SciPy Reference Guide

Release 1.7.0

Written by the SciPy community

June 21, 2021

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Download documentation: https://docs.scipy.org/doc/

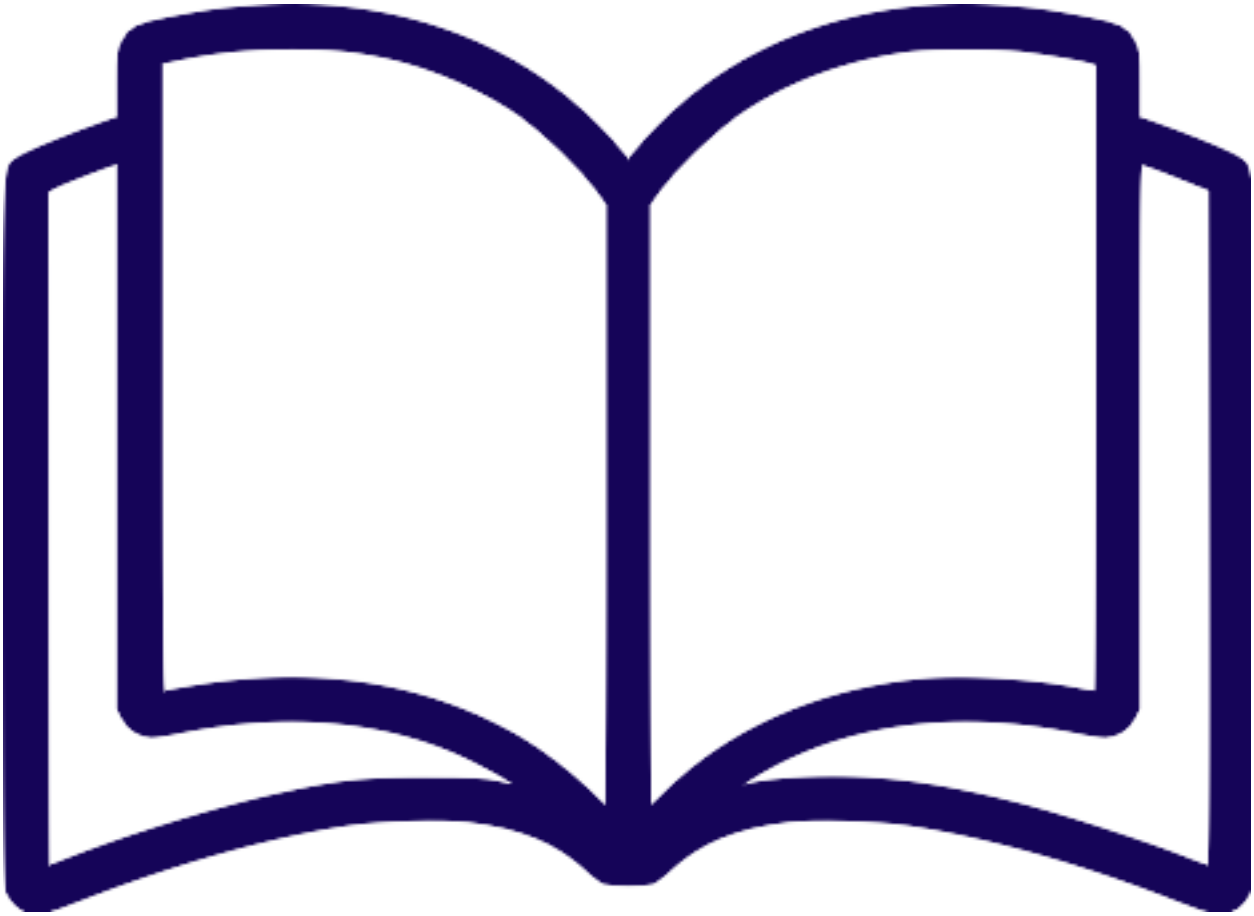
Useful links: Install | Source Repository | Issues & Ideas | Q&A Support | Mailing List

SciPy (pronounced "Sigh Pie") is an open-source software for mathematics, science, and engineering.

Getting started

New to *SciPy*? Check out the getting started guides. They contain an introduction to *SciPy'* main concepts and links to additional tutorials.

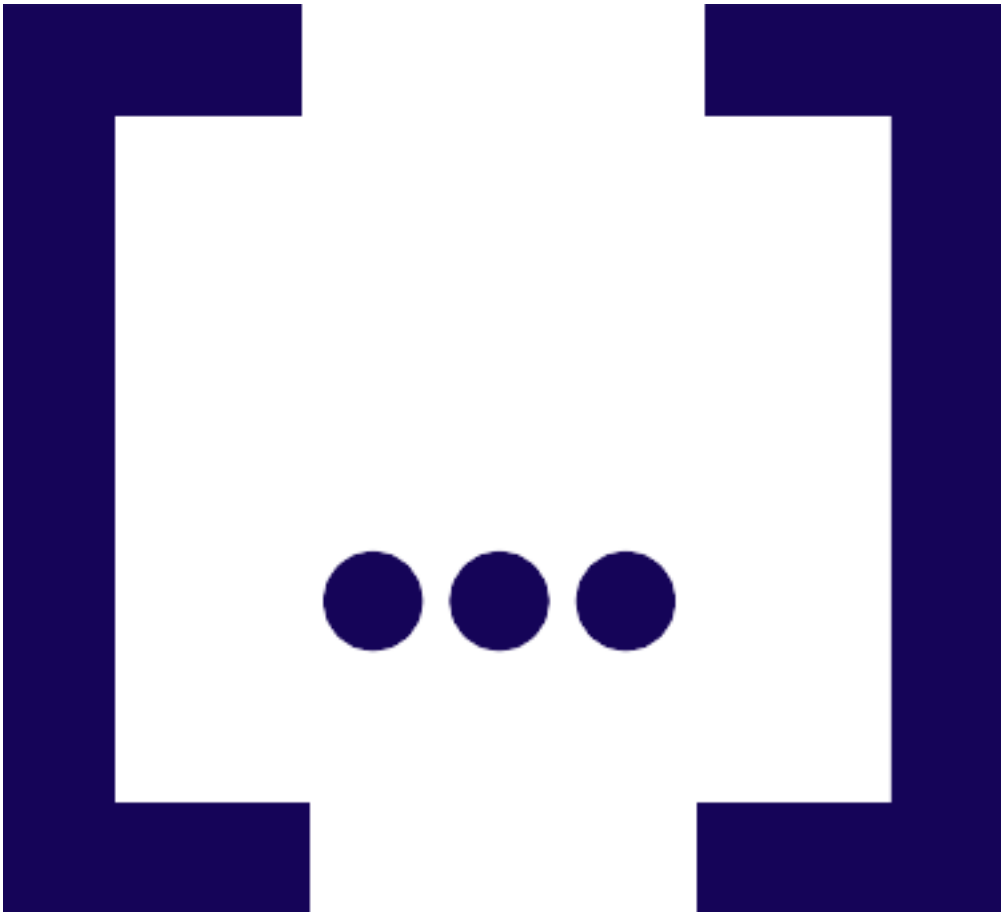
To the getting started guides



User guide

The user guide provides in-depth information on the key concepts of SciPy with useful background information and explanation.

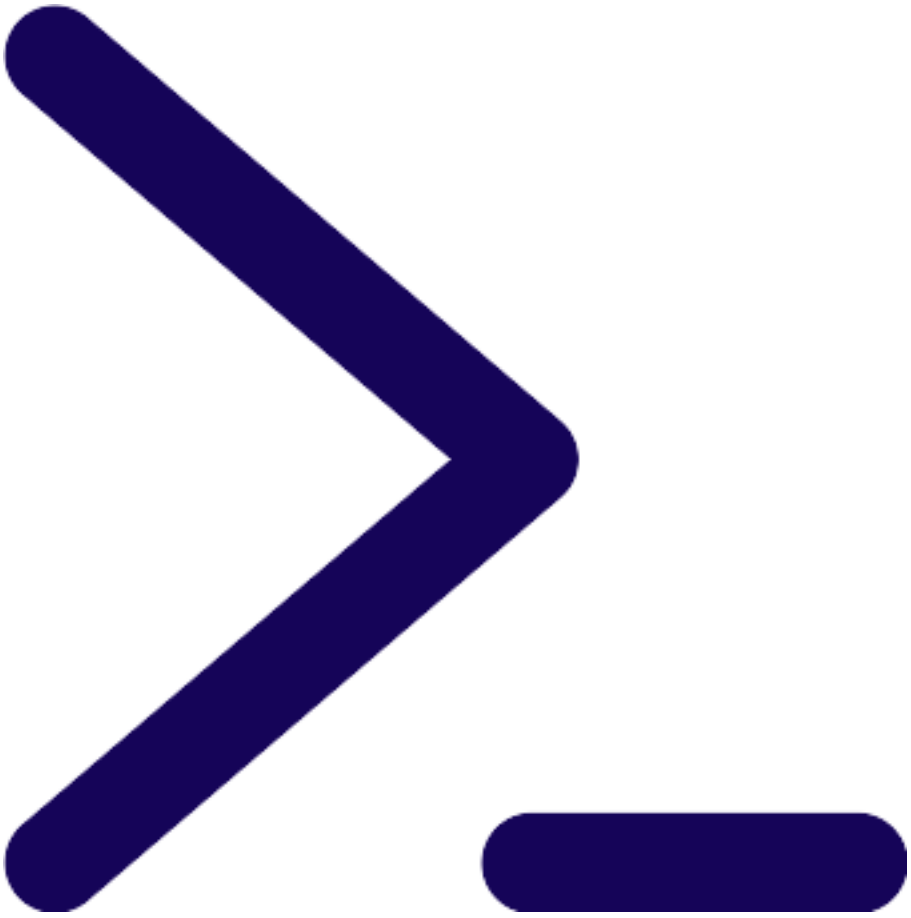
To the user guide



API reference

The reference guide contains a detailed description of the SciPy API. The reference describes how the methods work and which parameters can be used. It assumes that you have an understanding of the key concepts.

To the reference guide



Developer guide

Saw a typo in the documentation? Want to improve existing functionalities? The contributing guidelines will guide you through the process of improving pandas.

To the development guide

CHAPTER

ONE

GETTING STARTED

1.1 Installation

Working with conda?

SciPy is part of the Anaconda distribution and can be installed with Anaconda or Miniconda:

```
conda install scipy
```

Prefer pip?

SciPy can be installed via pip from PyPI.

```
pip install scipy
```

In-depth instructions?

Installing a specific version? Installing from source? Check the advanced installation page.

Learn more

1.1.1 Installing and upgrading

Information on how to install SciPy and/or the SciPy Stack (a larger set of packages for scientific computing with Python) can be found at https://scipy.org/install.html .

It is recommended that users use a scientific Python distribution or binaries for their platform. If building from source is required, documentation about that can be found at building/index.

If you already have SciPy installed and want to upgrade to a newer version, use the same install mechanism as you have used to install SciPy before. Before upgrading to a newer version, it is recommended to check that your own code does not use any deprecated SciPy functionality. To do so, run your code with `python -Wd`.

1.2 Tutorials

For a quick overview of SciPy functionality, see the *user guide*.

You can also refer to the *reference guide* for an exhaustive list of all what is possible with SciPy.

CHAPTER

TWO

SCIPY USER GUIDE

2.1 Introduction

Contents

- *Introduction*
  - *SciPy Organization*
  - *Finding Documentation*

SciPy is a collection of mathematical algorithms and convenience functions built on the NumPy extension of Python. It adds significant power to the interactive Python session by providing the user with high-level commands and classes for manipulating and visualizing data. With SciPy, an interactive Python session becomes a data-processing and system-prototyping environment rivaling systems, such as MATLAB, IDL, Octave, R-Lab, and SciLab.

The additional benefit of basing SciPy on Python is that this also makes a powerful programming language available for use in developing sophisticated programs and specialized applications. Scientific applications using SciPy benefit from the development of additional modules in numerous niches of the software landscape by developers across the world. Everything from parallel programming to web and data-base subroutines and classes have been made available to the Python programmer. All of this power is available in addition to the mathematical libraries in SciPy.

This tutorial will acquaint the first-time user of SciPy with some of its most important features. It assumes that the user has already installed the SciPy package. Some general Python facility is also assumed, such as could be acquired by working through the Python distribution's Tutorial. For further introductory help the user is directed to the NumPy documentation.

For brevity and convenience, we will often assume that the main packages (numpy, scipy, and matplotlib) have been imported as:

```
>>> import numpy as np
>>> import matplotlib as mpl
>>> import matplotlib.pyplot as plt
```

These are the import conventions that our community has adopted after discussion on public mailing lists. You will see these conventions used throughout NumPy and SciPy source code and documentation. While we obviously don't require you to follow these conventions in your own code, it is highly recommended.

2.1.1 SciPy Organization

SciPy is organized into subpackages covering different scientific computing domains. These are summarized in the following table:

Subpackage	Description
cluster	Clustering algorithms
constants	Physical and mathematical constants
fftpack	Fast Fourier Transform routines
integrate	Integration and ordinary differential equation solvers
interpolate	Interpolation and smoothing splines
io	Input and Output
linalg	Linear algebra
ndimage	N-dimensional image processing
odr	Orthogonal distance regression
optimize	Optimization and root-finding routines
signal	Signal processing
sparse	Sparse matrices and associated routines
spatial	Spatial data structures and algorithms
special	Special functions
stats	Statistical distributions and functions

SciPy sub-packages need to be imported separately, for example:

```
>>> from scipy import linalg, optimize
```

Because of their ubiquitousness, some of the functions in these subpackages are also made available in the *scipy* namespace to ease their use in interactive sessions and programs. In addition, many basic array functions from `numpy` are also available at the top-level of the *scipy* package. Before looking at the sub-packages individually, we will first look at some of these common functions.

2.1.2 Finding Documentation

SciPy and NumPy have documentation versions in both HTML and PDF format available at https://docs.scipy.org/, that cover nearly all available functionality. However, this documentation is still work-in-progress and some parts may be incomplete or sparse. As we are a volunteer organization and depend on the community for growth, your participation - everything from providing feedback to improving the documentation and code - is welcome and actively encouraged.

Python's documentation strings are used in SciPy for on-line documentation. There are two methods for reading them and getting help. One is Python's command `help` in the `pydoc` module. Entering this command with no arguments (i.e. `>>> help`) launches an interactive help session that allows searching through the keywords and modules available to all of Python. Secondly, running the command *help(obj)* with an object as the argument displays that object's calling signature, and documentation string.

The pydoc method of `help` is sophisticated but uses a pager to display the text. Sometimes this can interfere with the terminal within which you are running the interactive session. A numpy/scipy-specific help system is also available under the command `numpy.info`. The signature and documentation string for the object passed to the `help` command are printed to standard output (or to a writeable object passed as the third argument). The second keyword argument of `numpy.info` defines the maximum width of the line for printing. If a module is passed as the argument to `help` then a list of the functions and classes defined in that module is printed. For example:

```
>>> np.info(optimize.fmin)
 fmin(func, x0, args=(), xtol=0.0001, ftol=0.0001, maxiter=None, maxfun=None,
```

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```
      full_output=0, disp=1, retall=0, callback=None)

Minimize a function using the downhill simplex algorithm.

Parameters
----------
func : callable func(x,*args)
    The objective function to be minimized.
x0 : ndarray
    Initial guess.
args : tuple
    Extra arguments passed to func, i.e. ``f(x,*args)``.
callback : callable
    Called after each iteration, as callback(xk), where xk is the
    current parameter vector.

Returns
-------
xopt : ndarray
    Parameter that minimizes function.
fopt : float
    Value of function at minimum: ``fopt = func(xopt)``.
iter : int
    Number of iterations performed.
funcalls : int
    Number of function calls made.
warnflag : int
    1 : Maximum number of function evaluations made.
    2 : Maximum number of iterations reached.
allvecs : list
    Solution at each iteration.

Other parameters
----------------
xtol : float
    Relative error in xopt acceptable for convergence.
ftol : number
    Relative error in func(xopt) acceptable for convergence.
maxiter : int
    Maximum number of iterations to perform.
maxfun : number
    Maximum number of function evaluations to make.
full_output : bool
    Set to True if fopt and warnflag outputs are desired.
disp : bool
    Set to True to print convergence messages.
retall : bool
    Set to True to return list of solutions at each iteration.

Notes
-----
Uses a Nelder-Mead simplex algorithm to find the minimum of function of
```

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```
one or more variables.
```

Another useful command is `dir`, which can be used to look at the namespace of a module or package.

2.2 Special functions (`scipy.special`)

The main feature of the *scipy.special* package is the definition of numerous special functions of mathematical physics. Available functions include airy, elliptic, bessel, gamma, beta, hypergeometric, parabolic cylinder, mathieu, spheroidal wave, struve, and kelvin. There are also some low-level stats functions that are not intended for general use as an easier interface to these functions is provided by the `stats` module. Most of these functions can take array arguments and return array results following the same broadcasting rules as other math functions in Numerical Python. Many of these functions also accept complex numbers as input. For a complete list of the available functions with a one-line description type `>>> help(special)`. Each function also has its own documentation accessible using help. If you don't see a function you need, consider writing it and contributing it to the library. You can write the function in either C, Fortran, or Python. Look in the source code of the library for examples of each of these kinds of functions.

2.2.1 Bessel functions of real order(`jv`, `jn_zeros`)

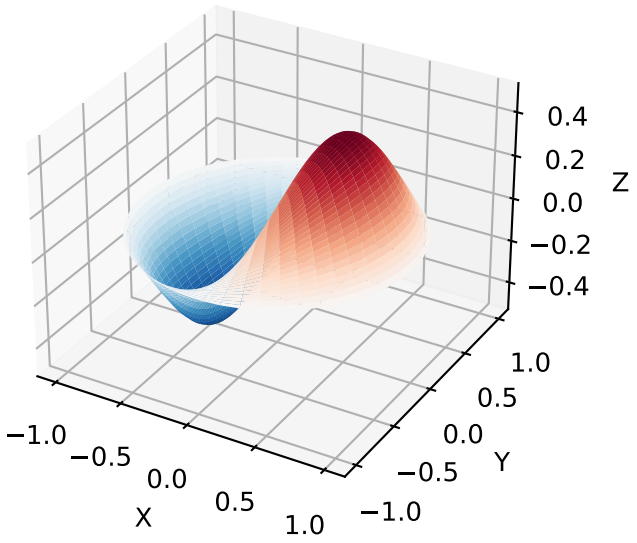
Bessel functions are a family of solutions to Bessel's differential equation with real or complex order alpha:

$$x^2 \frac{d^2y}{dx^2} + x\frac{dy}{dx} + (x^2 - \alpha^2)y = 0$$

Among other uses, these functions arise in wave propagation problems, such as the vibrational modes of a thin drum head. Here is an example of a circular drum head anchored at the edge:

```
>>> from scipy import special
>>> def drumhead_height(n, k, distance, angle, t):
...     kth_zero = special.jn_zeros(n, k)[-1]
...     return np.cos(t) * np.cos(n*angle) * special.jn(n, distance*kth_zero)
>>> theta = np.r_[0:2*np.pi:50j]
>>> radius = np.r_[0:1:50j]
>>> x = np.array([r * np.cos(theta) for r in radius])
>>> y = np.array([r * np.sin(theta) for r in radius])
>>> z = np.array([drumhead_height(1, 1, r, theta, 0.5) for r in radius])
```

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax = fig.add_axes(rect=(0, 0.05, 0.95, 0.95), projection='3d')
>>> ax.plot_surface(x, y, z, rstride=1, cstride=1, cmap='RdBu_r', vmin=-0.5,␣
↪vmax=0.5)
>>> ax.set_xlabel('X')
>>> ax.set_ylabel('Y')
>>> ax.set_xticks(np.arange(-1, 1.1, 0.5))
>>> ax.set_yticks(np.arange(-1, 1.1, 0.5))
>>> ax.set_zlabel('Z')
>>> plt.show()
```



2.2.2 Cython Bindings for Special Functions (`scipy.special.cython_special`)

SciPy also offers Cython bindings for scalar, typed versions of many of the functions in special. The following Cython code gives a simple example of how to use these functions:

```
cimport scipy.special.cython_special as csc

cdef:
    double x = 1
    double complex z = 1 + 1j
    double si, ci, rgam
    double complex cgam

rgam = csc.gamma(x)
print(rgam)
cgam = csc.gamma(z)
print(cgam)
csc.sici(x, &si, &ci)
print(si, ci)
```

(See the Cython documentation for help with compiling Cython.) In the example the function `csc.gamma` works essentially like its ufunc counterpart *gamma*, though it takes C types as arguments instead of NumPy arrays. Note, in particular, that the function is overloaded to support real and complex arguments; the correct variant is selected at compile time. The function `csc.sici` works slightly differently from *sici*; for the ufunc we could write `ai, bi = sici(x)`, whereas in the Cython version multiple return values are passed as pointers. It might help to think of this as analogous to calling a ufunc with an output array: `sici(x, out=(si, ci))`.

There are two potential advantages to using the Cython bindings:

- they avoid Python function overhead
- they do not require the Python Global Interpreter Lock (GIL)

The following sections discuss how to use these advantages to potentially speed up your code, though, of course, one should always profile the code first to make sure putting in the extra effort will be worth it.

Avoiding Python Function Overhead

For the ufuncs in special, Python function overhead is avoided by vectorizing, that is, by passing an array to the function. Typically, this approach works quite well, but sometimes it is more convenient to call a special function on scalar inputs inside a loop, for example, when implementing your own ufunc. In this case, the Python function overhead can become significant. Consider the following example:

```
import scipy.special as sc
cimport scipy.special.cython_special as csc

def python_tight_loop():
    cdef:
        int n
        double x = 1

    for n in range(100):
        sc.jv(n, x)

def cython_tight_loop():
    cdef:
        int n
        double x = 1

    for n in range(100):
        csc.jv(n, x)
```

On one computer `python_tight_loop` took about 131 microseconds to run and `cython_tight_loop` took about 18.2 microseconds to run. Obviously this example is contrived: one could just call `special.jv(np.arange(100), 1)` and get results just as fast as in `cython_tight_loop`. The point is that if Python function overhead becomes significant in your code, then the Cython bindings might be useful.

Releasing the GIL

One often needs to evaluate a special function at many points, and typically the evaluations are trivially parallelizable. Since the Cython bindings do not require the GIL, it is easy to run them in parallel using Cython's `prange` function. For example, suppose that we wanted to compute the fundamental solution to the Helmholtz equation:

$$\Delta_x G(x, y) + k^2 G(x, y) = \delta(x - y),$$

where k is the wavenumber and δ is the Dirac delta function. It is known that in two dimensions the unique (radiating) solution is

$$G(x, y) = \frac{i}{4} H_0^{(1)}(k|x - y|),$$

where $H_0^{(1)}$ is the Hankel function of the first kind, i.e., the function *hankel1*. The following example shows how we could compute this function in parallel:

```
from libc.math cimport fabs
cimport cython
from cython.parallel cimport prange

import numpy as np
import scipy.special as sc
```

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```
cimport scipy.special.cython_special as csc

def serial_G(k, x, y):
    return 0.25j*sc.hankel1(0, k*np.abs(x - y))

@cython.boundscheck(False)
@cython.wraparound(False)
cdef void _parallel_G(double k, double[:,:] x, double[:,:] y,
                      double complex[:,:] out) nogil:
    cdef int i, j

    for i in prange(x.shape[0]):
        for j in range(y.shape[0]):
            out[i,j] = 0.25j*csc.hankel1(0, k*fabs(x[i,j] - y[i,j]))

def parallel_G(k, x, y):
    out = np.empty_like(x, dtype='complex128')
    _parallel_G(k, x, y, out)
    return out
```

(For help with compiling parallel code in Cython see here.) If the above Cython code is in a file `test.pyx`, then we can write an informal benchmark which compares the parallel and serial versions of the function:

```
import timeit

import numpy as np

from test import serial_G, parallel_G

def main():
    k = 1
    x, y = np.linspace(-100, 100, 1000), np.linspace(-100, 100, 1000)
    x, y = np.meshgrid(x, y)

    def serial():
        serial_G(k, x, y)

    def parallel():
        parallel_G(k, x, y)

    time_serial = timeit.timeit(serial, number=3)
    time_parallel = timeit.timeit(parallel, number=3)
    print("Serial method took {:.3} seconds".format(time_serial))
    print("Parallel method took {:.3} seconds".format(time_parallel))

if __name__ == "__main__":
    main()
```

On one quad-core computer the serial method took 1.29 seconds and the parallel method took 0.29 seconds.

2.2.3 Functions not in `scipy.special`

Some functions are not included in special because they are straightforward to implement with existing functions in NumPy and SciPy. To prevent reinventing the wheel, this section provides implementations of several such functions, which hopefully illustrate how to handle similar functions. In all examples NumPy is imported as `np` and special is imported as `sc`.

The binary entropy function:

```
def binary_entropy(x):
    return -(sc.xlogy(x, x) + sc.xlog1py(1 - x, -x))/np.log(2)
```

A rectangular step function on [0, 1]:

```
def step(x):
    return 0.5*(np.sign(x) + np.sign(1 - x))
```

Translating and scaling can be used to get an arbitrary step function.

The ramp function:

```
def ramp(x):
    return np.maximum(0, x)
```

2.3 Integration (`scipy.integrate`)

The *`scipy.integrate`* sub-package provides several integration techniques including an ordinary differential equation integrator. An overview of the module is provided by the help command:

```
>>> help(integrate)
 Methods for Integrating Functions given function object.

   quad          -- General purpose integration.
   dblquad       -- General purpose double integration.
   tplquad       -- General purpose triple integration.
   fixed_quad    -- Integrate func(x) using Gaussian quadrature of order n.
   quadrature    -- Integrate with given tolerance using Gaussian quadrature.
   romberg       -- Integrate func using Romberg integration.

 Methods for Integrating Functions given fixed samples.

   trapezoid            -- Use trapezoidal rule to compute integral.
   cumulative_trapezoid -- Use trapezoidal rule to cumulatively compute␣
↪integral.
   simpson              -- Use Simpson's rule to compute integral from␣
↪samples.
   romb                 -- Use Romberg Integration to compute integral from
                        -- (2**k + 1) evenly-spaced samples.

   See the special module's orthogonal polynomials (special) for Gaussian
      quadrature roots and weights for other weighting factors and regions.

 Interface to numerical integrators of ODE systems.
```

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```
   odeint        -- General integration of ordinary differential equations.
   ode           -- Integrate ODE using VODE and ZVODE routines.
```

2.3.1 General integration (quad)

The function *quad* is provided to integrate a function of one variable between two points. The points can be $\pm\infty$ ($\pm$ `inf`) to indicate infinite limits. For example, suppose you wish to integrate a bessel function `jv(2.5, x)` along the interval $[0, 4.5]$.

$$I = \int_0^{4.5} J_{2.5}(x)\, dx.$$

This could be computed using *quad*:

```
>>> import scipy.integrate as integrate
>>> import scipy.special as special
>>> result = integrate.quad(lambda x: special.jv(2.5,x), 0, 4.5)
>>> result
(1.1178179380783249, 7.8663172481899801e-09)
```

```
>>> from numpy import sqrt, sin, cos, pi
>>> I = sqrt(2/pi)*(18.0/27*sqrt(2)*cos(4.5) - 4.0/27*sqrt(2)*sin(4.5) +
...                 sqrt(2*pi) * special.fresnel(3/sqrt(pi))[0])
>>> I
1.117817938088701
```

```
>>> print(abs(result[0]-I))
1.03761443881e-11
```

The first argument to quad is a "callable" Python object (i.e., a function, method, or class instance). Notice the use of a lambda- function in this case as the argument. The next two arguments are the limits of integration. The return value is a tuple, with the first element holding the estimated value of the integral and the second element holding an upper bound on the error. Notice, that in this case, the true value of this integral is

$$I = \sqrt{\frac{2}{\pi}}\left(\frac{18}{27}\sqrt{2}\cos(4.5) - \frac{4}{27}\sqrt{2}\sin(4.5) + \sqrt{2\pi}\,\mathrm{Si}\left(\frac{3}{\sqrt{\pi}}\right)\right),$$

where

$$\mathrm{Si}(x) = \int_0^x \sin\left(\frac{\pi}{2}t^2\right) dt.$$

is the Fresnel sine integral. Note that the numerically-computed integral is within 1.04×10^{-11} of the exact result — well below the reported error bound.

If the function to integrate takes additional parameters, they can be provided in the *args* argument. Suppose that the following integral shall be calculated:

$$I(a, b) = \int_0^1 ax^2 + b\, dx.$$

This integral can be evaluated by using the following code:

```
>>> from scipy.integrate import quad
>>> def integrand(x, a, b):
...     return a*x**2 + b
...
>>> a = 2
>>> b = 1
>>> I = quad(integrand, 0, 1, args=(a,b))
>>> I
(1.6666666666666667, 1.8503717077085944e-14)
```

Infinite inputs are also allowed in *quad* by using $\pm$ `inf` as one of the arguments. For example, suppose that a numerical value for the exponential integral:

$$E_n(x) = \int_1^\infty \frac{e^{-xt}}{t^n}\, dt.$$

is desired (and the fact that this integral can be computed as `special.expn(n,x)` is forgotten). The functionality of the function *special.expn* can be replicated by defining a new function `vec_expint` based on the routine *quad*:

```
>>> from scipy.integrate import quad
>>> def integrand(t, n, x):
...     return np.exp(-x*t) / t**n
...
```

```
>>> def expint(n, x):
...     return quad(integrand, 1, np.inf, args=(n, x))[0]
...
```

```
>>> vec_expint = np.vectorize(expint)
```

```
>>> vec_expint(3, np.arange(1.0, 4.0, 0.5))
array([ 0.1097,  0.0567,  0.0301,  0.0163,  0.0089,  0.0049])
>>> import scipy.special as special
>>> special.expn(3, np.arange(1.0,4.0,0.5))
array([ 0.1097,  0.0567,  0.0301,  0.0163,  0.0089,  0.0049])
```

The function which is integrated can even use the quad argument (though the error bound may underestimate the error due to possible numerical error in the integrand from the use of *quad*). The integral in this case is

$$I_n = \int_0^\infty \int_1^\infty \frac{e^{-xt}}{t^n}\, dt\, dx = \frac{1}{n}.$$

```
>>> result = quad(lambda x: expint(3, x), 0, np.inf)
>>> print(result)
(0.3333333324560266, 2.8548934485373678e-09)
```

```
>>> I3 = 1.0/3.0
>>> print(I3)
0.333333333333
```

```
>>> print(I3 - result[0])
8.77306560731e-11
```

This last example shows that multiple integration can be handled using repeated calls to *quad*.

2.3.2 General multiple integration (dblquad, tplquad, nquad)

The mechanics for double and triple integration have been wrapped up into the functions *dblquad* and *tplquad*. These functions take the function to integrate and four, or six arguments, respectively. The limits of all inner integrals need to be defined as functions.

An example of using double integration to compute several values of I_n is shown below:

```
>>> from scipy.integrate import quad, dblquad
>>> def I(n):
...     return dblquad(lambda t, x: np.exp(-x*t)/t**n, 0, np.inf, lambda x: 1,
↪ lambda x: np.inf)
...
```

```
>>> print(I(4))
(0.2500000000043577, 1.29830334693681e-08)
>>> print(I(3))
(0.33333333325010883, 1.3888461883425516e-08)
>>> print(I(2))
(0.4999999999985751, 1.3894083651858995e-08)
```

As example for non-constant limits consider the integral

$$I = \int_{y=0}^{1/2} \int_{x=0}^{1-2y} xy \, dx \, dy = \frac{1}{96}.$$

This integral can be evaluated using the expression below (Note the use of the non-constant lambda functions for the upper limit of the inner integral):

```
>>> from scipy.integrate import dblquad
>>> area = dblquad(lambda x, y: x*y, 0, 0.5, lambda x: 0, lambda x: 1-2*x)
>>> area
(0.010416666666666668, 1.1564823173178715e-16)
```

For n-fold integration, scipy provides the function *nquad*. The integration bounds are an iterable object: either a list of constant bounds, or a list of functions for the non-constant integration bounds. The order of integration (and therefore the bounds) is from the innermost integral to the outermost one.

The integral from above

$$I_n = \int_0^\infty \int_1^\infty \frac{e^{-xt}}{t^n} \, dt \, dx = \frac{1}{n}$$

can be calculated as

```
>>> from scipy import integrate
>>> N = 5
>>> def f(t, x):
...     return np.exp(-x*t) / t**N
...
>>> integrate.nquad(f, [[1, np.inf],[0, np.inf]])
(0.20000000000002294, 1.2239614263187945e-08)
```

Note that the order of arguments for f must match the order of the integration bounds; i.e., the inner integral with respect to t is on the interval $[1, \infty]$ and the outer integral with respect to x is on the interval $[0, \infty]$.

Non-constant integration bounds can be treated in a similar manner; the example from above

$$I = \int_{y=0}^{1/2} \int_{x=0}^{1-2y} xy \, dx \, dy = \frac{1}{96}.$$

can be evaluated by means of

```
>>> from scipy import integrate
>>> def f(x, y):
...     return x*y
...
>>> def bounds_y():
...     return [0, 0.5]
...
>>> def bounds_x(y):
...     return [0, 1-2*y]
...
>>> integrate.nquad(f, [bounds_x, bounds_y])
(0.010416666666666668, 4.101620128472366e-16)
```

which is the same result as before.

2.3.3 Gaussian quadrature

A few functions are also provided in order to perform simple Gaussian quadrature over a fixed interval. The first is *fixed_quad*, which performs fixed-order Gaussian quadrature. The second function is *quadrature*, which performs Gaussian quadrature of multiple orders until the difference in the integral estimate is beneath some tolerance supplied by the user. These functions both use the module `scipy.special.orthogonal`, which can calculate the roots and quadrature weights of a large variety of orthogonal polynomials (the polynomials themselves are available as special functions returning instances of the polynomial class — e.g., *special.legendre*).

2.3.4 Romberg Integration

Romberg's method [WPR] is another method for numerically evaluating an integral. See the help function for *romberg* for further details.

2.3.5 Integrating using Samples

If the samples are equally-spaced and the number of samples available is $2^k + 1$ for some integer k, then Romberg *romb* integration can be used to obtain high-precision estimates of the integral using the available samples. Romberg integration uses the trapezoid rule at step-sizes related by a power of two and then performs Richardson extrapolation on these estimates to approximate the integral with a higher degree of accuracy.

In case of arbitrary spaced samples, the two functions *trapezoid* and *simpson* are available. They are using Newton-Coates formulas of order 1 and 2 respectively to perform integration. The trapezoidal rule approximates the function as a straight line between adjacent points, while Simpson's rule approximates the function between three adjacent points as a parabola.

For an odd number of samples that are equally spaced Simpson's rule is exact if the function is a polynomial of order 3 or less. If the samples are not equally spaced, then the result is exact only if the function is a polynomial of order 2 or less.

```
>>> import numpy as np
>>> def f1(x):
...     return x**2
...
>>> def f2(x):
...     return x**3
...
>>> x = np.array([1,3,4])
>>> y1 = f1(x)
>>> from scipy import integrate
>>> I1 = integrate.simpson(y1, x)
>>> print(I1)
21.0
```

This corresponds exactly to

$$\int_1^4 x^2 \, dx = 21,$$

whereas integrating the second function

```
>>> y2 = f2(x)
>>> I2 = integrate.simpson(y2, x)
>>> print(I2)
61.5
```

does not correspond to

$$\int_1^4 x^3 \, dx = 63.75$$

because the order of the polynomial in f2 is larger than two.

2.3.6 Faster integration using low-level callback functions

A user desiring reduced integration times may pass a C function pointer through *scipy.LowLevelCallable* to *quad*, *dblquad*, *tplquad* or *nquad* and it will be integrated and return a result in Python. The performance increase here arises from two factors. The primary improvement is faster function evaluation, which is provided by compilation of the function itself. Additionally we have a speedup provided by the removal of function calls between C and Python in *quad*. This method may provide a speed improvements of ~2x for trivial functions such as sine but can produce a much more noticeable improvements (10x+) for more complex functions. This feature then, is geared towards a user with numerically intensive integrations willing to write a little C to reduce computation time significantly.

The approach can be used, for example, via `ctypes` in a few simple steps:

1.) Write an integrand function in C with the function signature `double f(int n, double *x, void *user_data)`, where `x` is an array containing the point the function f is evaluated at, and `user_data` to arbitrary additional data you want to provide.

```
/* testlib.c */
double f(int n, double *x, void *user_data) {
    double c = *(double *)user_data;
    return c + x[0] - x[1] * x[2]; /* corresponds to c + x - y * z */
}
```

2.) Now compile this file to a shared/dynamic library (a quick search will help with this as it is OS-dependent). The user must link any math libraries, etc., used. On linux this looks like:

```
$ gcc -shared -fPIC -o testlib.so testlib.c
```

The output library will be referred to as `testlib.so`, but it may have a different file extension. A library has now been created that can be loaded into Python with `ctypes`.

3.) Load shared library into Python using `ctypes` and set `restypes` and `argtypes` - this allows SciPy to interpret the function correctly:

```
import os, ctypes
from scipy import integrate, LowLevelCallable

lib = ctypes.CDLL(os.path.abspath('testlib.so'))
lib.f.restype = ctypes.c_double
lib.f.argtypes = (ctypes.c_int, ctypes.POINTER(ctypes.c_double), ctypes.c_
↪void_p)

c = ctypes.c_double(1.0)
user_data = ctypes.cast(ctypes.pointer(c), ctypes.c_void_p)

func = LowLevelCallable(lib.f, user_data)
```

The last `void *user_data` in the function is optional and can be omitted (both in the C function and ctypes argtypes) if not needed. Note that the coordinates are passed in as an array of doubles rather than a separate argument.

4.) Now integrate the library function as normally, here using *nquad*:

```
>>> integrate.nquad(func, [[0, 10], [-10, 0], [-1, 1]])
(1200.0, 1.1102230246251565e-11)
```

The Python tuple is returned as expected in a reduced amount of time. All optional parameters can be used with this method including specifying singularities, infinite bounds, etc.

2.3.7 Ordinary differential equations (`solve_ivp`)

Integrating a set of ordinary differential equations (ODEs) given initial conditions is another useful example. The function *solve_ivp* is available in SciPy for integrating a first-order vector differential equation:

$$\frac{d\mathbf{y}}{dt} = \mathbf{f}\left(\mathbf{y}, t\right),$$

given initial conditions $\mathbf{y}\left(0\right) = y_0$, where $\mathbf{y}$ is a length N vector and $\mathbf{f}$ is a mapping from $\mathcal{R}^N$ to $\mathcal{R}^N$. A higher-order ordinary differential equation can always be reduced to a differential equation of this type by introducing intermediate derivatives into the $\mathbf{y}$ vector.

For example, suppose it is desired to find the solution to the following second-order differential equation:

$$\frac{d^2w}{dz^2} - zw(z) = 0$$

with initial conditions $w\left(0\right) = \frac{1}{\sqrt[3]{3^2}\Gamma\left(\frac{2}{3}\right)}$ and $\left.\frac{dw}{dz}\right|_{z=0} = -\frac{1}{\sqrt[3]{3}\Gamma\left(\frac{1}{3}\right)}$. It is known that the solution to this differential equation with these boundary conditions is the Airy function

$$w = \mathrm{Ai}\left(z\right),$$

which gives a means to check the integrator using *special.airy*.

First, convert this ODE into standard form by setting $\mathbf{y} = \left[\frac{dw}{dz}, w\right]$ and $t = z$. Thus, the differential equation becomes

$$\frac{d\mathbf{y}}{dt} = \begin{bmatrix} ty_1 \\ y_0 \end{bmatrix} = \begin{bmatrix} 0 & t \\ 1 & 0 \end{bmatrix} \begin{bmatrix} y_0 \\ y_1 \end{bmatrix} = \begin{bmatrix} 0 & t \\ 1 & 0 \end{bmatrix} \mathbf{y}.$$

In other words,

$$\mathbf{f}(\mathbf{y}, t) = \mathbf{A}(t)\,\mathbf{y}.$$

As an interesting reminder, if $\mathbf{A}(t)$ commutes with $\int_0^t \mathbf{A}(\tau)\,d\tau$ under matrix multiplication, then this linear differential equation has an exact solution using the matrix exponential:

$$\mathbf{y}(t) = \exp\left(\int_0^t \mathbf{A}(\tau)\,d\tau\right)\mathbf{y}(0),$$

However, in this case, $\mathbf{A}(t)$ and its integral do not commute.

This differential equation can be solved using the function *solve_ivp*. It requires the derivative, *fprime*, the time span *[t_start, t_end]* and the initial conditions vector, *y0*, as input arguments and returns an object whose *y* field is an array with consecutive solution values as columns. The initial conditions are therefore given in the first output column.

```
>>> from scipy.integrate import solve_ivp
>>> from scipy.special import gamma, airy
>>> y1_0 = +1 / 3**(2/3) / gamma(2/3)
>>> y0_0 = -1 / 3**(1/3) / gamma(1/3)
>>> y0 = [y0_0, y1_0]
>>> def func(t, y):
...     return [t*y[1],y[0]]
...
>>> t_span = [0, 4]
>>> sol1 = solve_ivp(func, t_span, y0)
>>> print("sol1.t: {}".format(sol1.t))
sol1.t:    [0.         0.10097672 1.04643602 1.91060117 2.49872472 3.08684827
 3.62692846 4.        ]
```

As it can be seen *solve_ivp* determines its time steps automatically if not specified otherwise. To compare the solution of *solve_ivp* with the *airy* function the time vector created by *solve_ivp* is passed to the *airy* function.

```
>>> print("sol1.y[1]: {}".format(sol1.y[1]))
sol1.y[1]: [0.35502805 0.328952   0.12801343 0.04008508 0.01601291 0.00623879
 0.00356316 0.00405982]
>>> print("airy(sol.t)[0]:  {}".format(airy(sol1.t)[0]))
airy(sol.t)[0]: [0.35502805 0.328952   0.12804768 0.03995804 0.01575943 0.
↪00562799
 0.00201689 0.00095156]
```

The solution of *solve_ivp* with its standard parameters shows a big deviation to the airy function. To minimize this deviation, relative and absolute tolerances can be used.

```
>>> rtol, atol = (1e-8, 1e-8)
>>> sol2 = solve_ivp(func, t_span, y0, rtol=rtol, atol=atol)
>>> print("sol2.y[1][::6]: {}".format(sol2.y[1][0::6]))
sol2.y[1][::6]: [0.35502805 0.19145234 0.06368989 0.0205917  0.00554734 0.
↪00106409]
```

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```
>>> print("airy(sol2.t)[0][::6]: {}".format(airy(sol2.t)[0][::6]))
airy(sol2.t)[0][::6]: [0.35502805 0.19145234 0.06368989 0.0205917  0.00554733␣
↪0.00106406]
```

To specify user defined time points for the solution of *solve_ivp*, *solve_ivp* offers two possibilities that can also be used complementarily. By passing the *t_eval* option to the function call *solve_ivp* returns the solutions of these time points of *t_eval* in its output.

```
>>> import numpy as np
>>> t = np.linspace(0, 4, 100)
>>> sol3 = solve_ivp(func, t_span, y0, t_eval=t)
```

If the jacobian matrix of function is known, it can be passed to the *solve_ivp* to achieve better results. Please be aware however that the default integration method *RK45* does not support jacobian matrices and thereby another integration method has to be chosen. One of the integration methods that support a jacobian matrix is the for example the *Radau* method of following example.

```
>>> def gradient(t, y):
...     return [[0,t], [1,0]]
>>> sol4 = solve_ivp(func, t_span, y0, method='Radau', jac=gradient)
```

Solving a system with a banded Jacobian matrix

odeint can be told that the Jacobian is *banded*. For a large system of differential equations that are known to be stiff, this can improve performance significantly.

As an example, we'll solve the 1-D Gray-Scott partial differential equations using the method of lines [MOL]. The Gray-Scott equations for the functions $u(x,t)$ and $v(x,t)$ on the interval $x \in [0, L]$ are

$$\begin{aligned}\frac{\partial u}{\partial t} &= D_u \frac{\partial^2 u}{\partial x^2} - uv^2 + f(1-u)\\ \frac{\partial v}{\partial t} &= D_v \frac{\partial^2 v}{\partial x^2} + uv^2 - (f+k)v\end{aligned}$$

where D_u and D_v are the diffusion coefficients of the components u and v, respectively, and f and k are constants. (For more information about the system, see http://groups.csail.mit.edu/mac/projects/amorphous/GrayScott/)

We'll assume Neumann (i.e., "no flux") boundary conditions:

$$\frac{\partial u}{\partial x}(0,t) = 0, \quad \frac{\partial v}{\partial x}(0,t) = 0, \quad \frac{\partial u}{\partial x}(L,t) = 0, \quad \frac{\partial v}{\partial x}(L,t) = 0$$

To apply the method of lines, we discretize the x variable by defining the uniformly spaced grid of N points $\{x_0, x_1, \ldots, x_{N-1}\}$, with $x_0 = 0$ and $x_{N-1} = L$. We define $u_j(t) \equiv u(x_k, t)$ and $v_j(t) \equiv v(x_k, t)$, and replace the x derivatives with finite differences. That is,

$$\frac{\partial^2 u}{\partial x^2}(x_j, t) \to \frac{u_{j-1}(t) - 2u_j(t) + u_{j+1}(t)}{(\Delta x)^2}$$

We then have a system of $2N$ ordinary differential equations:

$$\begin{aligned}\frac{du_j}{dt} &= \frac{D_u}{(\Delta x)^2}(u_{j-1} - 2u_j + u_{j+1}) - u_j v_j^2 + f(1-u_j)\\ \frac{dv_j}{dt} &= \frac{D_v}{(\Delta x)^2}(v_{j-1} - 2v_j + v_{j+1}) + u_j v_j^2 - (f+k)v_j\end{aligned} \tag{2.1}$$

For convenience, the (t) arguments have been dropped.

To enforce the boundary conditions, we introduce "ghost" points x_{-1} and x_N, and define $u_{-1}(t) \equiv u_1(t)$, $u_N(t) \equiv u_{N-2}(t)$; $v_{-1}(t)$ and $v_N(t)$ are defined analogously.

Then

$$\begin{aligned} \frac{du_0}{dt} &= \frac{D_u}{(\Delta x)^2}(2u_1 - 2u_0) - u_0 v_0^2 + f(1 - u_0) \\ \frac{dv_0}{dt} &= \frac{D_v}{(\Delta x)^2}(2v_1 - 2v_0) + u_0 v_0^2 - (f + k)v_0 \end{aligned} \tag{2.2}$$

and

$$\begin{aligned} \frac{du_{N-1}}{dt} &= \frac{D_u}{(\Delta x)^2}(2u_{N-2} - 2u_{N-1}) - u_{N-1} v_{N-1}^2 + f(1 - u_{N-1}) \\ \frac{dv_{N-1}}{dt} &= \frac{D_v}{(\Delta x)^2}(2v_{N-2} - 2v_{N-1}) + u_{N-1} v_{N-1}^2 - (f + k)v_{N-1} \end{aligned} \tag{2.3}$$

Our complete system of $2N$ ordinary differential equations is (2.1) for $k = 1, 2, \ldots, N-2$, along with (2.2) and (2.3).

We can now starting implementing this system in code. We must combine $\{u_k\}$ and $\{v_k\}$ into a single vector of length $2N$. The two obvious choices are $\{u_0, u_1, \ldots, u_{N-1}, v_0, v_1, \ldots, v_{N-1}\}$ and $\{u_0, v_0, u_1, v_1, \ldots, u_{N-1}, v_{N-1}\}$. Mathematically, it does not matter, but the choice affects how efficiently `odeint` can solve the system. The reason is in how the order affects the pattern of the nonzero elements of the Jacobian matrix.

When the variables are ordered as $\{u_0, u_1, \ldots, u_{N-1}, v_0, v_1, \ldots, v_{N-1}\}$, the pattern of nonzero elements of the Jacobian matrix is

```
* * 0 0 0 0 0 * 0 0 0 0 0 0
* * * 0 0 0 0 0 * 0 0 0 0 0
0 * * * 0 0 0 0 0 * 0 0 0 0
0 0 * * * 0 0 0 0 0 * 0 0 0
0 0 0 * * * 0 0 0 0 0 * 0 0
0 0 0 0 * * * 0 0 0 0 0 * 0
0 0 0 0 0 * * * 0 0 0 0 0 *
* 0 0 0 0 0 0 * * 0 0 0 0 0
0 * 0 0 0 0 0 * * * 0 0 0 0
0 0 * 0 0 0 0 0 * * * 0 0 0
0 0 0 * 0 0 0 0 0 * * * 0 0
0 0 0 0 * 0 0 0 0 0 * * * 0
0 0 0 0 0 * 0 0 0 0 0 * * *
0 0 0 0 0 0 * 0 0 0 0 ) * *
```

The Jacobian pattern with variables interleaved as $\{u_0, v_0, u_1, v_1, \ldots, u_{N-1}, v_{N-1}\}$ is

```
* * * 0 0 0 0 0 0 0 0 0 0 0
* * 0 * 0 0 0 0 0 0 0 0 0 0
* 0 * * * 0 0 0 0 0 0 0 0 0
0 * * * 0 * 0 0 0 0 0 0 0 0
0 0 * 0 * * * 0 0 0 0 0 0 0
0 0 0 * * * 0 * 0 0 0 0 0 0
0 0 0 0 * 0 * * * 0 0 0 0 0
0 0 0 0 0 * * * 0 * 0 0 0 0
0 0 0 0 0 0 * 0 * * * 0 0 0
0 0 0 0 0 0 0 * * * 0 * 0 0
0 0 0 0 0 0 0 0 * 0 * * * 0
0 0 0 0 0 0 0 0 0 * * * 0 *
0 0 0 0 0 0 0 0 0 0 * 0 * *
0 0 0 0 0 0 0 0 0 0 0 * * *
```

In both cases, there are just five nontrivial diagonals, but when the variables are interleaved, the bandwidth is much smaller. That is, the main diagonal and the two diagonals immediately above and the two immediately below the main diagonal are the nonzero diagonals. This is important, because the inputs `mu` and `ml` of `odeint` are the upper and lower bandwidths of the Jacobian matrix. When the variables are interleaved, `mu` and `ml` are 2. When the variables are stacked with $\{v_k\}$ following $\{u_k\}$, the upper and lower bandwidths are N.

With that decision made, we can write the function that implements the system of differential equations.

First, we define the functions for the source and reaction terms of the system:

```
def G(u, v, f, k):
    return f * (1 - u) - u*v**2

def H(u, v, f, k):
    return -(f + k) * v + u*v**2
```

Next, we define the function that computes the right-hand side of the system of differential equations:

```
def grayscott1d(y, t, f, k, Du, Dv, dx):
    """
    Differential equations for the 1-D Gray-Scott equations.

    The ODEs are derived using the method of lines.
    """
    # The vectors u and v are interleaved in y.  We define
    # views of u and v by slicing y.
    u = y[::2]
    v = y[1::2]

    # dydt is the return value of this function.
    dydt = np.empty_like(y)

    # Just like u and v are views of the interleaved vectors
    # in y, dudt and dvdt are views of the interleaved output
    # vectors in dydt.
    dudt = dydt[::2]
    dvdt = dydt[1::2]

    # Compute du/dt and dv/dt.  The end points and the interior points
    # are handled separately.
    dudt[0]    = G(u[0],    v[0],    f, k) + Du * (-2.0*u[0] + 2.0*u[1]) /␣
↪dx**2
    dudt[1:-1] = G(u[1:-1], v[1:-1], f, k) + Du * np.diff(u,2) / dx**2
    dudt[-1]   = G(u[-1],   v[-1],   f, k) + Du * (- 2.0*u[-1] + 2.0*u[-2]) /␣
↪dx**2
    dvdt[0]    = H(u[0],    v[0],    f, k) + Dv * (-2.0*v[0] + 2.0*v[1]) /␣
↪dx**2
    dvdt[1:-1] = H(u[1:-1], v[1:-1], f, k) + Dv * np.diff(v,2) / dx**2
    dvdt[-1]   = H(u[-1],   v[-1],   f, k) + Dv * (-2.0*v[-1] + 2.0*v[-2]) /␣
↪dx**2

    return dydt
```

We won't implement a function to compute the Jacobian, but we will tell *odeint* that the Jacobian matrix is banded. This allows the underlying solver (LSODA) to avoid computing values that it knows are zero. For a large system, this improves the performance significantly, as demonstrated in the following ipython session.

First, we define the required inputs:

```
In [30]: rng = np.random.default_rng()

In [31]: y0 = rng.standard_normal(5000)

In [32]: t = np.linspace(0, 50, 11)
```

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```
In [33]: f = 0.024

In [34]: k = 0.055

In [35]: Du = 0.01

In [36]: Dv = 0.005

In [37]: dx = 0.025
```

Time the computation without taking advantage of the banded structure of the Jacobian matrix:

```
In [38]: %timeit sola = odeint(grayscott1d, y0, t, args=(f, k, Du, Dv, dx))
1 loop, best of 3: 25.2 s per loop
```

Now set `ml=2` and `mu=2`, so *`odeint`* knows that the Jacobian matrix is banded:

```
In [39]: %timeit solb = odeint(grayscott1d, y0, t, args=(f, k, Du, Dv, dx),␣
↪ml=2, mu=2)
10 loops, best of 3: 191 ms per loop
```

That is quite a bit faster!

Let's ensure that they have computed the same result:

```
In [41]: np.allclose(sola, solb)
Out[41]: True
```

References

2.4 Optimization (`scipy.optimize`)

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- *Optimization (`scipy.optimize`)*
  - *Unconstrained minimization of multivariate scalar functions (`minimize`)*
    - *Nelder-Mead Simplex algorithm (`method='Nelder-Mead'`)*
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The *`scipy.optimize`* package provides several commonly used optimization algorithms. A detailed listing is available: *`scipy.optimize`* (can also be found by `help(scipy.optimize)`).

2.4.1 Unconstrained minimization of multivariate scalar functions (`minimize`)

The *minimize* function provides a common interface to unconstrained and constrained minimization algorithms for multivariate scalar functions in *scipy.optimize*. To demonstrate the minimization function, consider the problem of minimizing the Rosenbrock function of N variables:

$$f(\mathbf{x}) = \sum_{i=1}^{N-1} 100\left(x_{i+1} - x_i^2\right)^2 + (1 - x_i)^2 .$$

The minimum value of this function is 0 which is achieved when $x_i = 1$.

Note that the Rosenbrock function and its derivatives are included in *scipy.optimize*. The implementations shown in the following sections provide examples of how to define an objective function as well as its jacobian and hessian functions.

Nelder-Mead Simplex algorithm (`method='Nelder-Mead'`)

In the example below, the *minimize* routine is used with the *Nelder-Mead* simplex algorithm (selected through the `method` parameter):

```
>>> import numpy as np
>>> from scipy.optimize import minimize
```

```
>>> def rosen(x):
...     """The Rosenbrock function"""
...     return sum(100.0*(x[1:]-x[:-1]**2.0)**2.0 + (1-x[:-1])**2.0)
```

```
>>> x0 = np.array([1.3, 0.7, 0.8, 1.9, 1.2])
>>> res = minimize(rosen, x0, method='nelder-mead',
...                options={'xatol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000066
         Iterations: 339
         Function evaluations: 571
```

```
>>> print(res.x)
[1. 1. 1. 1. 1.]
```

The simplex algorithm is probably the simplest way to minimize a fairly well-behaved function. It requires only function evaluations and is a good choice for simple minimization problems. However, because it does not use any gradient evaluations, it may take longer to find the minimum.

Another optimization algorithm that needs only function calls to find the minimum is *Powell*'s method available by setting `method='powell'` in *minimize*.

Broyden-Fletcher-Goldfarb-Shanno algorithm (`method='BFGS'`)

In order to converge more quickly to the solution, this routine uses the gradient of the objective function. If the gradient is not given by the user, then it is estimated using first-differences. The Broyden-Fletcher-Goldfarb-Shanno (BFGS) method typically requires fewer function calls than the simplex algorithm even when the gradient must be estimated.

To demonstrate this algorithm, the Rosenbrock function is again used. The gradient of the Rosenbrock function is the vector:

$$\begin{aligned}\frac{\partial f}{\partial x_j} &= \sum_{i=1}^{N} 200\left(x_i - x_{i-1}^2\right)\left(\delta_{i,j} - 2x_{i-1}\delta_{i-1,j}\right) - 2\left(1 - x_{i-1}\right)\delta_{i-1,j}. \\ &= 200\left(x_j - x_{j-1}^2\right) - 400x_j\left(x_{j+1} - x_j^2\right) - 2\left(1 - x_j\right).\end{aligned}$$

This expression is valid for the interior derivatives. Special cases are

$$\begin{aligned}\frac{\partial f}{\partial x_0} &= -400x_0\left(x_1 - x_0^2\right) - 2\left(1 - x_0\right), \\ \frac{\partial f}{\partial x_{N-1}} &= 200\left(x_{N-1} - x_{N-2}^2\right).\end{aligned}$$

A Python function which computes this gradient is constructed by the code-segment:

```
>>> def rosen_der(x):
...     xm = x[1:-1]
...     xm_m1 = x[:-2]
...     xm_p1 = x[2:]
...     der = np.zeros_like(x)
...     der[1:-1] = 200*(xm-xm_m1**2) - 400*(xm_p1 - xm**2)*xm - 2*(1-xm)
...     der[0] = -400*x[0]*(x[1]-x[0]**2) - 2*(1-x[0])
...     der[-1] = 200*(x[-1]-x[-2]**2)
...     return der
```

This gradient information is specified in the *minimize* function through the `jac` parameter as illustrated below.

```
>>> res = minimize(rosen, x0, method='BFGS', jac=rosen_der,
...                options={'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 51                    # may vary
         Function evaluations: 63
         Gradient evaluations: 63
>>> res.x
array([1., 1., 1., 1., 1.])
```

Newton-Conjugate-Gradient algorithm (`method='Newton-CG'`)

Newton-Conjugate Gradient algorithm is a modified Newton's method and uses a conjugate gradient algorithm to (approximately) invert the local Hessian [NW]. Newton's method is based on fitting the function locally to a quadratic form:

$$f\left(\mathbf{x}\right) \approx f\left(\mathbf{x}_0\right) + \nabla f\left(\mathbf{x}_0\right) \cdot \left(\mathbf{x} - \mathbf{x}_0\right) + \frac{1}{2}\left(\mathbf{x} - \mathbf{x}_0\right)^T \mathbf{H}\left(\mathbf{x}_0\right)\left(\mathbf{x} - \mathbf{x}_0\right).$$

where $\mathbf{H}\left(\mathbf{x}_0\right)$ is a matrix of second-derivatives (the Hessian). If the Hessian is positive definite then the local minimum of this function can be found by setting the gradient of the quadratic form to zero, resulting in

$$\mathbf{x}_{\text{opt}} = \mathbf{x}_0 - \mathbf{H}^{-1}\nabla f.$$

The inverse of the Hessian is evaluated using the conjugate-gradient method. An example of employing this method to minimizing the Rosenbrock function is given below. To take full advantage of the Newton-CG method, a function which computes the Hessian must be provided. The Hessian matrix itself does not need to be constructed, only a vector which is the product of the Hessian with an arbitrary vector needs to be available to the minimization routine. As a result, the user can provide either a function to compute the Hessian matrix, or a function to compute the product of the Hessian with an arbitrary vector.

Full Hessian example:

The Hessian of the Rosenbrock function is

$$\begin{aligned} H_{ij} = \frac{\partial^2 f}{\partial x_i \partial x_j} &= 200\left(\delta_{i,j} - 2x_{i-1}\delta_{i-1,j}\right) - 400x_i\left(\delta_{i+1,j} - 2x_i\delta_{i,j}\right) - 400\delta_{i,j}\left(x_{i+1} - x_i^2\right) + 2\delta_{i,j}, \\ &= \left(202 + 1200x_i^2 - 400x_{i+1}\right)\delta_{i,j} - 400x_i\delta_{i+1,j} - 400x_{i-1}\delta_{i-1,j}, \end{aligned}$$

if $i, j \in [1, N-2]$ with $i, j \in [0, N-1]$ defining the $N \times N$ matrix. Other non-zero entries of the matrix are

$$\begin{aligned} \frac{\partial^2 f}{\partial x_0^2} &= 1200x_0^2 - 400x_1 + 2, \\ \frac{\partial^2 f}{\partial x_0 \partial x_1} = \frac{\partial^2 f}{\partial x_1 \partial x_0} &= -400x_0, \\ \frac{\partial^2 f}{\partial x_{N-1} \partial x_{N-2}} = \frac{\partial^2 f}{\partial x_{N-2} \partial x_{N-1}} &= -400x_{N-2}, \\ \frac{\partial^2 f}{\partial x_{N-1}^2} &= 200. \end{aligned}$$

For example, the Hessian when $N = 5$ is

$$\mathbf{H} = \begin{bmatrix} 1200x_0^2 - 400x_1 + 2 & -400x_0 & 0 & 0 & 0 \\ -400x_0 & 202 + 1200x_1^2 - 400x_2 & -400x_1 & 0 & 0 \\ 0 & -400x_1 & 202 + 1200x_2^2 - 400x_3 & -400x_2 & 0 \\ 0 & & -400x_2 & 202 + 1200x_3^2 - 400x_4 & -400x_3 \\ 0 & 0 & 0 & -400x_3 & 200 \end{bmatrix}.$$

The code which computes this Hessian along with the code to minimize the function using Newton-CG method is shown in the following example:

```
>>> def rosen_hess(x):
...     x = np.asarray(x)
...     H = np.diag(-400*x[:-1],1) - np.diag(400*x[:-1],-1)
...     diagonal = np.zeros_like(x)
...     diagonal[0] = 1200*x[0]**2-400*x[1]+2
...     diagonal[-1] = 200
...     diagonal[1:-1] = 202 + 1200*x[1:-1]**2 - 400*x[2:]
...     H = H + np.diag(diagonal)
...     return H
```

```
>>> res = minimize(rosen, x0, method='Newton-CG',
...                jac=rosen_der, hess=rosen_hess,
...                options={'xtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 19                         # may vary
         Function evaluations: 22
```

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```
         Gradient evaluations: 19
         Hessian evaluations: 19
>>> res.x
array([1.,  1.,  1.,  1.,  1.])
```

Hessian product example:

For larger minimization problems, storing the entire Hessian matrix can consume considerable time and memory. The Newton-CG algorithm only needs the product of the Hessian times an arbitrary vector. As a result, the user can supply code to compute this product rather than the full Hessian by giving a `hess` function which take the minimization vector as the first argument and the arbitrary vector as the second argument (along with extra arguments passed to the function to be minimized). If possible, using Newton-CG with the Hessian product option is probably the fastest way to minimize the function.

In this case, the product of the Rosenbrock Hessian with an arbitrary vector is not difficult to compute. If $\mathbf{p}$ is the arbitrary vector, then $\mathbf{H}(\mathbf{x})\mathbf{p}$ has elements:

$$\mathbf{H}(\mathbf{x})\mathbf{p} = \begin{bmatrix} \left(1200x_0^2 - 400x_1 + 2\right)p_0 - 400x_0p_1 \\ \vdots \\ -400x_{i-1}p_{i-1} + \left(202 + 1200x_i^2 - 400x_{i+1}\right)p_i - 400x_ip_{i+1} \\ \vdots \\ -400x_{N-2}p_{N-2} + 200p_{N-1} \end{bmatrix}.$$

Code which makes use of this Hessian product to minimize the Rosenbrock function using *minimize* follows:

```
>>> def rosen_hess_p(x, p):
...     x = np.asarray(x)
...     Hp = np.zeros_like(x)
...     Hp[0] = (1200*x[0]**2 - 400*x[1] + 2)*p[0] - 400*x[0]*p[1]
...     Hp[1:-1] = -400*x[:-2]*p[:-2]+(202+1200*x[1:-1]**2-400*x[2:])*p[1:-1]␣
↪\
...                 -400*x[1:-1]*p[2:]
...     Hp[-1] = -400*x[-2]*p[-2] + 200*p[-1]
...     return Hp
```

```
>>> res = minimize(rosen, x0, method='Newton-CG',
...                jac=rosen_der, hessp=rosen_hess_p,
...                options={'xtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 20                    # may vary
         Function evaluations: 23
         Gradient evaluations: 20
         Hessian evaluations: 44
>>> res.x
array([1., 1., 1., 1., 1.])
```

According to [NW] p. 170 the `Newton-CG` algorithm can be inefficient when the Hessian is ill-conditioned because of the poor quality search directions provided by the method in those situations. The method `trust-ncg`, according to the authors, deals more effectively with this problematic situation and will be described next.

Trust-Region Newton-Conjugate-Gradient Algorithm (`method='trust-ncg'`)

The `Newton-CG` method is a line search method: it finds a direction of search minimizing a quadratic approximation of the function and then uses a line search algorithm to find the (nearly) optimal step size in that direction. An alternative approach is to, first, fix the step size limit Δ and then find the optimal step $\mathbf{p}$ inside the given trust-radius by solving the following quadratic subproblem:

$$\min_{\mathbf{p}} f(\mathbf{x}_k) + \nabla f(\mathbf{x}_k) \cdot \mathbf{p} + \frac{1}{2}\mathbf{p}^T \mathbf{H}(\mathbf{x}_k)\,\mathbf{p}; \quad \text{subject to: } \|\mathbf{p}\| \leq \Delta.$$

The solution is then updated $\mathbf{x}_{k+1} = \mathbf{x}_k + \mathbf{p}$ and the trust-radius Δ is adjusted according to the degree of agreement of the quadratic model with the real function. This family of methods is known as trust-region methods. The `trust-ncg` algorithm is a trust-region method that uses a conjugate gradient algorithm to solve the trust-region subproblem [NW].

Full Hessian example:

```
>>> res = minimize(rosen, x0, method='trust-ncg',
...                jac=rosen_der, hess=rosen_hess,
...                options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 20                    # may vary
         Function evaluations: 21
         Gradient evaluations: 20
         Hessian evaluations: 19
>>> res.x
array([1., 1., 1., 1., 1.])
```

Hessian product example:

```
>>> res = minimize(rosen, x0, method='trust-ncg',
...                jac=rosen_der, hessp=rosen_hess_p,
...                options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 20                    # may vary
         Function evaluations: 21
         Gradient evaluations: 20
         Hessian evaluations: 0
>>> res.x
array([1., 1., 1., 1., 1.])
```

Trust-Region Truncated Generalized Lanczos / Conjugate Gradient Algorithm (`method='trust-krylov'`)

Similar to the `trust-ncg` method, the `trust-krylov` method is a method suitable for large-scale problems as it uses the hessian only as linear operator by means of matrix-vector products. It solves the quadratic subproblem more accurately than the `trust-ncg` method.

$$\min_{\mathbf{p}} f(\mathbf{x}_k) + \nabla f(\mathbf{x}_k) \cdot \mathbf{p} + \frac{1}{2}\mathbf{p}^T \mathbf{H}(\mathbf{x}_k)\,\mathbf{p}; \quad \text{subject to: } \|\mathbf{p}\| \leq \Delta.$$

This method wraps the [TRLIB] implementation of the [GLTR] method solving exactly a trust-region subproblem restricted to a truncated Krylov subspace. For indefinite problems it is usually better to use this method as it reduces the number of nonlinear iterations at the expense of few more matrix-vector products per subproblem solve in comparison to the `trust-ncg` method.

Full Hessian example:

```
>>> res = minimize(rosen, x0, method='trust-krylov',
...                jac=rosen_der, hess=rosen_hess,
...                options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 19                    # may vary
         Function evaluations: 20
         Gradient evaluations: 20
         Hessian evaluations: 18
>>> res.x
array([1., 1., 1., 1., 1.])
```

Hessian product example:

```
>>> res = minimize(rosen, x0, method='trust-krylov',
...                jac=rosen_der, hessp=rosen_hess_p,
...                options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 19                    # may vary
         Function evaluations: 20
         Gradient evaluations: 20
         Hessian evaluations: 0
>>> res.x
array([1., 1., 1., 1., 1.])
```

Trust-Region Nearly Exact Algorithm (`method='trust-exact'`)

All methods `Newton-CG`, `trust-ncg` and `trust-krylov` are suitable for dealing with large-scale problems (problems with thousands of variables). That is because the conjugate gradient algorithm approximately solve the trust-region subproblem (or invert the Hessian) by iterations without the explicit Hessian factorization. Since only the product of the Hessian with an arbitrary vector is needed, the algorithm is specially suited for dealing with sparse Hessians, allowing low storage requirements and significant time savings for those sparse problems.

For medium-size problems, for which the storage and factorization cost of the Hessian are not critical, it is possible to obtain a solution within fewer iteration by solving the trust-region subproblems almost exactly. To achieve that, a certain nonlinear equations is solved iteratively for each quadratic subproblem [CGT]. This solution requires usually 3 or 4 Cholesky factorizations of the Hessian matrix. As the result, the method converges in fewer number of iterations and takes fewer evaluations of the objective function than the other implemented trust-region methods. The Hessian product option is not supported by this algorithm. An example using the Rosenbrock function follows:

```
>>> res = minimize(rosen, x0, method='trust-exact',
...                jac=rosen_der, hess=rosen_hess,
...                options={'gtol': 1e-8, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
```

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```
         Iterations: 13                    # may vary
         Function evaluations: 14
         Gradient evaluations: 13
         Hessian evaluations: 14
>>> res.x
array([1., 1., 1., 1., 1.])
```

2.4.2 Constrained minimization of multivariate scalar functions (`minimize`)

The *minimize* function provides algorithms for constrained minimization, namely `'trust-constr'` , `'SLSQP'` and `'COBYLA'`. They require the constraints to be defined using slightly different structures. The method `'trust-constr'` requires the constraints to be defined as a sequence of objects *LinearConstraint* and *NonlinearConstraint*. Methods `'SLSQP'` and `'COBYLA'`, on the other hand, require constraints to be defined as a sequence of dictionaries, with keys `type`, `fun` and `jac`.

As an example let us consider the constrained minimization of the Rosenbrock function:

$$\begin{aligned} \min_{x_0, x_1} \quad & 100\left(x_1 - x_0^2\right)^2 + (1 - x_0)^2 \\ \text{subject to:} \quad & x_0 + 2x_1 \leq 1 \\ & x_0^2 + x_1 \leq 1 \\ & x_0^2 - x_1 \leq 1 \\ & 2x_0 + x_1 = 1 \\ & 0 \leq x_0 \leq 1 \\ & -0.5 \leq x_1 \leq 2.0. \end{aligned}$$

This optimization problem has the unique solution $[x_0, x_1] = [0.4149,\ 0.1701]$, for which only the first and fourth constraints are active.

Trust-Region Constrained Algorithm (`method='trust-constr'`)

The trust-region constrained method deals with constrained minimization problems of the form:

$$\begin{aligned} \min_{x} \quad & f(x) \\ \text{subject to:} \quad & c^l \leq c(x) \leq c^u, \\ & x^l \leq x \leq x^u. \end{aligned}$$

When $c_j^l = c_j^u$ the method reads the j-th constraint as an equality constraint and deals with it accordingly. Besides that, one-sided constraint can be specified by setting the upper or lower bound to `np.inf` with the appropriate sign.

The implementation is based on [EQSQP] for equality-constraint problems and on [TRIP] for problems with inequality constraints. Both are trust-region type algorithms suitable for large-scale problems.

Defining Bounds Constraints:

The bound constraints $0 \leq x_0 \leq 1$ and $-0.5 \leq x_1 \leq 2.0$ are defined using a *Bounds* object.

```
>>> from scipy.optimize import Bounds
>>> bounds = Bounds([0, -0.5], [1.0, 2.0])
```

Defining Linear Constraints:

The constraints $x_0 + 2x_1 \leq 1$ and $2x_0 + x_1 = 1$ can be written in the linear constraint standard format:

$$\begin{bmatrix} -\infty \\ 1 \end{bmatrix} \leq \begin{bmatrix} 1 & 2 \\ 2 & 1 \end{bmatrix} \begin{bmatrix} x_0 \\ x_1 \end{bmatrix} \leq \begin{bmatrix} 1 \\ 1 \end{bmatrix},$$

and defined using a *LinearConstraint* object.

```
>>> from scipy.optimize import LinearConstraint
>>> linear_constraint = LinearConstraint([[1, 2], [2, 1]], [-np.inf, 1], [1,␣
↪1])
```

Defining Nonlinear Constraints:

The nonlinear constraint:

$$c(x) = \begin{bmatrix} x_0^2 + x_1 \\ x_0^2 - x_1 \end{bmatrix} \leq \begin{bmatrix} 1 \\ 1 \end{bmatrix},$$

with Jacobian matrix:

$$J(x) = \begin{bmatrix} 2x_0 & 1 \\ 2x_0 & -1 \end{bmatrix},$$

and linear combination of the Hessians:

$$H(x, v) = \sum_{i=0}^{1} v_i \nabla^2 c_i(x) = v_0 \begin{bmatrix} 2 & 0 \\ 0 & 0 \end{bmatrix} + v_1 \begin{bmatrix} 2 & 0 \\ 0 & 0 \end{bmatrix},$$

is defined using a *NonlinearConstraint* object.

```
>>> def cons_f(x):
...     return [x[0]**2 + x[1], x[0]**2 - x[1]]
>>> def cons_J(x):
...     return [[2*x[0], 1], [2*x[0], -1]]
>>> def cons_H(x, v):
...     return v[0]*np.array([[2, 0], [0, 0]]) + v[1]*np.array([[2, 0], [0,␣
↪0]])
>>> from scipy.optimize import NonlinearConstraint
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac=cons_J,
↪ hess=cons_H)
```

Alternatively, it is also possible to define the Hessian $H(x, v)$ as a sparse matrix,

```
>>> from scipy.sparse import csc_matrix
>>> def cons_H_sparse(x, v):
...     return v[0]*csc_matrix([[2, 0], [0, 0]]) + v[1]*csc_matrix([[2, 0],␣
↪[0, 0]])
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1,
...                                            jac=cons_J, hess=cons_H_sparse)
```

or as a *LinearOperator* object.

```
>>> from scipy.sparse.linalg import LinearOperator
>>> def cons_H_linear_operator(x, v):
...     def matvec(p):
...         return np.array([p[0]*2*(v[0]+v[1]), 0])
...     return LinearOperator((2, 2), matvec=matvec)
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1,
...                                            jac=cons_J, hess=cons_H_linear_
↪operator)
```

When the evaluation of the Hessian $H(x, v)$ is difficult to implement or computationally infeasible, one may use *HessianUpdateStrategy*. Currently available strategies are *BFGS* and *SR1*.

```
>>> from scipy.optimize import BFGS
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac=cons_J,
↪ hess=BFGS())
```

Alternatively, the Hessian may be approximated using finite differences.

```
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac=cons_J,
↪ hess='2-point')
```

The Jacobian of the constraints can be approximated by finite differences as well. In this case, however, the Hessian cannot be computed with finite differences and needs to be provided by the user or defined using *HessianUpdateStrategy*.

```
>>> nonlinear_constraint = NonlinearConstraint(cons_f, -np.inf, 1, jac='2-
↪point', hess=BFGS())
```

Solving the Optimization Problem:

The optimization problem is solved using:

```
>>> x0 = np.array([0.5, 0])
>>> res = minimize(rosen, x0, method='trust-constr', jac=rosen_der,␣
↪hess=rosen_hess,
...                constraints=[linear_constraint, nonlinear_constraint],
...                options={'verbose': 1}, bounds=bounds)
# may vary
`gtol` termination condition is satisfied.
Number of iterations: 12, function evaluations: 8, CG iterations: 7,␣
↪optimality: 2.99e-09, constraint violation: 1.11e-16, execution time: 0.016␣
↪s.
>>> print(res.x)
[0.41494531 0.17010937]
```

When needed, the objective function Hessian can be defined using a *LinearOperator* object,

```
>>> def rosen_hess_linop(x):
...     def matvec(p):
...         return rosen_hess_p(x, p)
...     return LinearOperator((2, 2), matvec=matvec)
>>> res = minimize(rosen, x0, method='trust-constr', jac=rosen_der,␣
↪hess=rosen_hess_linop,
...                constraints=[linear_constraint, nonlinear_constraint],
...                options={'verbose': 1}, bounds=bounds)
```

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```
# may vary
`gtol` termination condition is satisfied.
Number of iterations: 12, function evaluations: 8, CG iterations: 7,␣
↪optimality: 2.99e-09, constraint violation: 1.11e-16, execution time: 0.018␣
↪s.
>>> print(res.x)
[0.41494531 0.17010937]
```

or a Hessian-vector product through the parameter `hessp`.

```
>>> res = minimize(rosen, x0, method='trust-constr', jac=rosen_der,␣
↪hessp=rosen_hess_p,
...                constraints=[linear_constraint, nonlinear_constraint],
...                options={'verbose': 1}, bounds=bounds)
# may vary
`gtol` termination condition is satisfied.
Number of iterations: 12, function evaluations: 8, CG iterations: 7,␣
↪optimality: 2.99e-09, constraint violation: 1.11e-16, execution time: 0.018␣
↪s.
>>> print(res.x)
[0.41494531 0.17010937]
```

Alternatively, the first and second derivatives of the objective function can be approximated. For instance, the Hessian can be approximated with *SR1* quasi-Newton approximation and the gradient with finite differences.

```
>>> from scipy.optimize import SR1
>>> res = minimize(rosen, x0, method='trust-constr',  jac="2-point",␣
↪hess=SR1(),
...                constraints=[linear_constraint, nonlinear_constraint],
...                options={'verbose': 1}, bounds=bounds)
# may vary
`gtol` termination condition is satisfied.
Number of iterations: 12, function evaluations: 24, CG iterations: 7,␣
↪optimality: 4.48e-09, constraint violation: 0.00e+00, execution time: 0.016␣
↪s.
>>> print(res.x)
[0.41494531 0.17010937]
```

Sequential Least SQuares Programming (SLSQP) Algorithm (`method='SLSQP'`)

The SLSQP method deals with constrained minimization problems of the form:

$$\begin{aligned} \min_{x} \quad & f(x) \\ \text{subject to:} \quad & c_j(x) = 0, \quad && j \in \mathcal{E} \\ & c_j(x) \geq 0, \quad && j \in \mathcal{I} \\ & \text{lb}_i \leq x_i \leq \text{ub}_i, \quad && i = 1, ..., N. \end{aligned}$$

Where $\mathcal{E}$ or $\mathcal{I}$ are sets of indices containing equality and inequality constraints.

Both linear and nonlinear constraints are defined as dictionaries with keys `type`, `fun` and `jac`.

```
>>> ineq_cons = {'type': 'ineq',
...              'fun' : lambda x: np.array([1 - x[0] - 2*x[1],
...                                          1 - x[0]**2 - x[1],
...                                          1 - x[0]**2 + x[1]]),
...              'jac' : lambda x: np.array([[-1.0, -2.0],
...                                          [-2*x[0], -1.0],
...                                          [-2*x[0], 1.0]])}
>>> eq_cons = {'type': 'eq',
...            'fun' : lambda x: np.array([2*x[0] + x[1] - 1]),
...            'jac' : lambda x: np.array([2.0, 1.0])}
```

And the optimization problem is solved with:

```
>>> x0 = np.array([0.5, 0])
>>> res = minimize(rosen, x0, method='SLSQP', jac=rosen_der,
...                constraints=[eq_cons, ineq_cons], options={'ftol': 1e-9,
↪'disp': True},
...                bounds=bounds)
# may vary
Optimization terminated successfully.    (Exit mode 0)
            Current function value: 0.342717574857755
            Iterations: 5
            Function evaluations: 6
            Gradient evaluations: 5
>>> print(res.x)
[0.41494475 0.1701105 ]
```

Most of the options available for the method `'trust-constr'` are not available for `'SLSQP'`.

2.4.3 Global optimization

Global optimization aims to find the global minimum of a function within given bounds, in the presence of potentially many local minima. Typically, global minimizers efficiently search the parameter space, while using a local minimizer (e.g., *minimize*) under the hood. SciPy contains a number of good global optimizers. Here, we'll use those on the same objective function, namely the (aptly named) `eggholder` function:

```
>>> def eggholder(x):
...     return (-(x[1] + 47) * np.sin(np.sqrt(abs(x[0]/2 + (x[1]  + 47))))
...             -x[0] * np.sin(np.sqrt(abs(x[0] - (x[1]  + 47)))))

>>> bounds = [(-512, 512), (-512, 512)]
```

This function looks like an egg carton:

```
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.mplot3d import Axes3D

>>> x = np.arange(-512, 513)
>>> y = np.arange(-512, 513)
>>> xgrid, ygrid = np.meshgrid(x, y)
>>> xy = np.stack([xgrid, ygrid])
```

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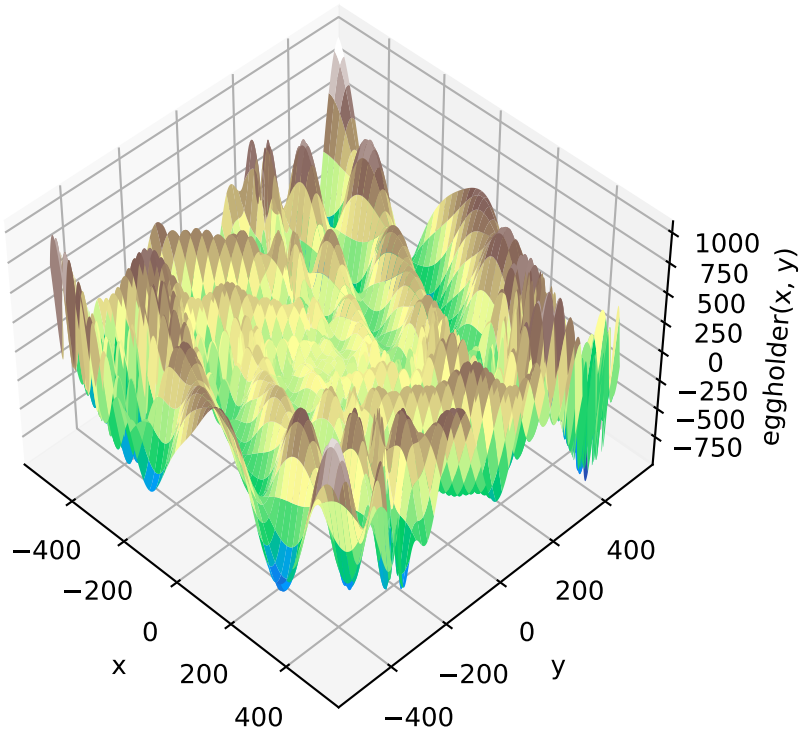
```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111, projection='3d')
>>> ax.view_init(45, -45)
>>> ax.plot_surface(xgrid, ygrid, eggholder(xy), cmap='terrain')
>>> ax.set_xlabel('x')
>>> ax.set_ylabel('y')
>>> ax.set_zlabel('eggholder(x, y)')
>>> plt.show()
```



We now use the global optimizers to obtain the minimum and the function value at the minimum. We'll store the results in a dictionary so we can compare different optimization results later.

```
>>> from scipy import optimize
>>> results = dict()
>>> results['shgo'] = optimize.shgo(eggholder, bounds)
>>> results['shgo']
     fun: -935.3379515604197  # may vary
    funl: array([-935.33795156])
 message: 'Optimization terminated successfully.'
    nfev: 42
     nit: 2
   nlfev: 37
   nlhev: 0
   nljev: 9
 success: True
       x: array([439.48096952, 453.97740589])
      xl: array([[439.48096952, 453.97740589]])
```

```
>>> results['DA'] = optimize.dual_annealing(eggholder, bounds)
>>> results['DA']
     fun: -956.9182316237413  # may vary
 message: ['Maximum number of iteration reached']
    nfev: 4091
    nhev: 0
     nit: 1000
    njev: 0
       x: array([482.35324114, 432.87892901])
```

All optimizers return an `OptimizeResult`, which in addition to the solution contains information on the number of function evaluations, whether the optimization was successful, and more. For brevity, we won't show the full output of the other optimizers:

```
>>> results['DE'] = optimize.differential_evolution(eggholder, bounds)
>>> results['BH'] = optimize.basinhopping(eggholder, bounds)
```

shgo has a second method, which returns all local minima rather than only what it thinks is the global minimum:

```
>>> results['shgo_sobol'] = optimize.shgo(eggholder, bounds, n=200, iters=5,
...                                       sampling_method='sobol')
```

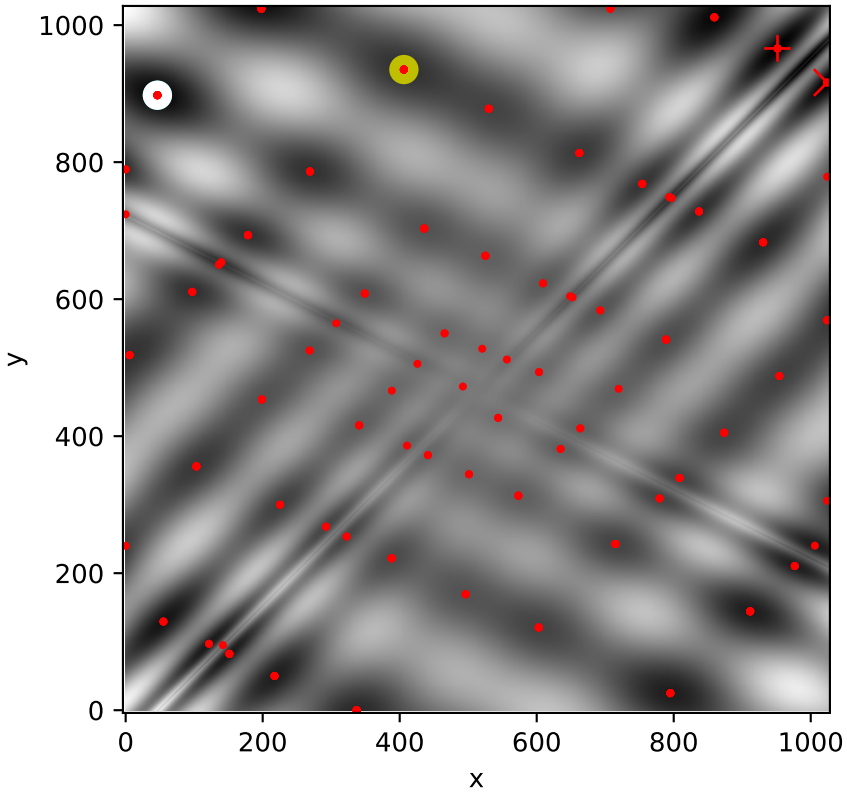
We'll now plot all found minima on a heatmap of the function:

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> im = ax.imshow(eggholder(xy), interpolation='bilinear', origin='lower',
...                cmap='gray')
>>> ax.set_xlabel('x')
>>> ax.set_ylabel('y')
>>>
>>> def plot_point(res, marker='o', color=None):
...     ax.plot(512+res.x[0], 512+res.x[1], marker=marker, color=color, ms=10)

>>> plot_point(results['BH'], color='y')  # basinhopping           - yellow
>>> plot_point(results['DE'], color='c')  # differential_evolution - cyan
>>> plot_point(results['DA'], color='w')  # dual_annealing.        - white

>>> # SHGO produces multiple minima, plot them all (with a smaller marker
↪size)
>>> plot_point(results['shgo'], color='r', marker='+')
>>> plot_point(results['shgo_sobol'], color='r', marker='x')
>>> for i in range(results['shgo_sobol'].xl.shape[0]):
...     ax.plot(512 + results['shgo_sobol'].xl[i, 0],
...             512 + results['shgo_sobol'].xl[i, 1],
...             'ro', ms=2)

>>> ax.set_xlim([-4, 514*2])
>>> ax.set_ylim([-4, 514*2])
>>> plt.show()
```



2.4.4 Least-squares minimization (`least_squares`)

SciPy is capable of solving robustified bound-constrained nonlinear least-squares problems:

$$\min_{\mathbf{x}} \frac{1}{2} \sum_{i=1}^{m} \rho\left(f_i(\mathbf{x})^2\right) \tag{2.4}$$

$$\text{subject to } \mathbf{lb} \leq \mathbf{x} \leq \mathbf{ub} \tag{2.5}$$

Here $f_i(\mathbf{x})$ are smooth functions from $\mathbb{R}^n$ to $\mathbb{R}$, we refer to them as residuals. The purpose of a scalar-valued function $\rho(\cdot)$ is to reduce the influence of outlier residuals and contribute to robustness of the solution, we refer to it as a loss function. A linear loss function gives a standard least-squares problem. Additionally, constraints in a form of lower and upper bounds on some of x_j are allowed.

All methods specific to least-squares minimization utilize a $m \times n$ matrix of partial derivatives called Jacobian and defined as $J_{ij} = \partial f_i / \partial x_j$. It is highly recommended to compute this matrix analytically and pass it to `least_squares`, otherwise, it will be estimated by finite differences, which takes a lot of additional time and can be very inaccurate in hard cases.

Function `least_squares` can be used for fitting a function $\varphi(t; \mathbf{x})$ to empirical data $\{(t_i, y_i), i = 0, \ldots, m-1\}$. To do this, one should simply precompute residuals as $f_i(\mathbf{x}) = w_i(\varphi(t_i; \mathbf{x}) - y_i)$, where w_i are weights assigned to each observation.

Example of solving a fitting problem

Here we consider an enzymatic reaction[1]. There are 11 residuals defined as

$$f_i(x) = \frac{x_0(u_i^2 + u_i x_1)}{u_i^2 + u_i x_2 + x_3} - y_i, \quad i = 0, \ldots, 10,$$

where y_i are measurement values and u_i are values of the independent variable. The unknown vector of parameters is $\mathbf{x} = (x_0, x_1, x_2, x_3)^T$. As was said previously, it is recommended to compute Jacobian matrix in a closed form:

$$J_{i0} = \frac{\partial f_i}{\partial x_0} = \frac{u_i^2 + u_i x_1}{u_i^2 + u_i x_2 + x_3} \tag{2.6}$$

$$J_{i1} = \frac{\partial f_i}{\partial x_1} = \frac{u_i x_0}{u_i^2 + u_i x_2 + x_3} \tag{2.7}$$

$$J_{i2} = \frac{\partial f_i}{\partial x_2} = -\frac{x_0(u_i^2 + u_i x_1)u_i}{(u_i^2 + u_i x_2 + x_3)^2} \tag{2.8}$$

$$J_{i3} = \frac{\partial f_i}{\partial x_3} = -\frac{x_0(u_i^2 + u_i x_1)}{(u_i^2 + u_i x_2 + x_3)^2} \tag{2.9}$$

We are going to use the "hard" starting point defined in[2]. To find a physically meaningful solution, avoid potential division by zero and assure convergence to the global minimum we impose constraints $0 \leq x_j \leq 100, j = 0, 1, 2, 3$.

The code below implements least-squares estimation of $\mathbf{x}$ and finally plots the original data and the fitted model function:

```
>>> from scipy.optimize import least_squares
```

```
>>> def model(x, u):
...     return x[0] * (u ** 2 + x[1] * u) / (u ** 2 + x[2] * u + x[3])
```

```
>>> def fun(x, u, y):
...     return model(x, u) - y
```

```
>>> def jac(x, u, y):
...     J = np.empty((u.size, x.size))
...     den = u ** 2 + x[2] * u + x[3]
...     num = u ** 2 + x[1] * u
...     J[:, 0] = num / den
...     J[:, 1] = x[0] * u / den
...     J[:, 2] = -x[0] * num * u / den ** 2
...     J[:, 3] = -x[0] * num / den ** 2
...     return J
```

```
>>> u = np.array([4.0, 2.0, 1.0, 5.0e-1, 2.5e-1, 1.67e-1, 1.25e-1, 1.0e-1,
...               8.33e-2, 7.14e-2, 6.25e-2])
>>> y = np.array([1.957e-1, 1.947e-1, 1.735e-1, 1.6e-1, 8.44e-2, 6.27e-2,
...               4.56e-2, 3.42e-2, 3.23e-2, 2.35e-2, 2.46e-2])
>>> x0 = np.array([2.5, 3.9, 4.15, 3.9])
>>> res = least_squares(fun, x0, jac=jac, bounds=(0, 100), args=(u, y),␣
↪verbose=1)
```

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[1] J. Kowalik and J. F. Morrison, "Analysis of kinetic data for allosteric enzyme reactions as a nonlinear regression problem", Math. Biosci., vol. 2, pp. 57-66, 1968.

[2] B. M. Averick et al., "The MINPACK-2 Test Problem Collection".

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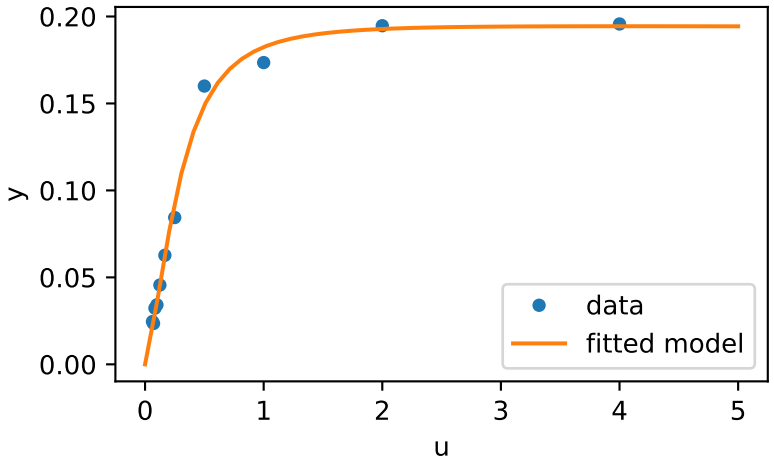
```
# may vary
`ftol` termination condition is satisfied.
Function evaluations 130, initial cost 4.4383e+00, final cost 1.5375e-04,␣
↪first-order optimality 4.92e-08.
>>> res.x
array([ 0.19280596,  0.19130423,  0.12306063,  0.13607247])
```

```
>>> import matplotlib.pyplot as plt
>>> u_test = np.linspace(0, 5)
>>> y_test = model(res.x, u_test)
>>> plt.plot(u, y, 'o', markersize=4, label='data')
>>> plt.plot(u_test, y_test, label='fitted model')
>>> plt.xlabel("u")
>>> plt.ylabel("y")
>>> plt.legend(loc='lower right')
>>> plt.show()
```



Further examples

Three interactive examples below illustrate usage of `least_squares` in greater detail.

1. Large-scale bundle adjustment in scipy demonstrates large-scale capabilities of `least_squares` and how to efficiently compute finite difference approximation of sparse Jacobian.
2. Robust nonlinear regression in scipy shows how to handle outliers with a robust loss function in a nonlinear regression.
3. Solving a discrete boundary-value problem in scipy examines how to solve a large system of equations and use bounds to achieve desired properties of the solution.

For the details about mathematical algorithms behind the implementation refer to documentation of `least_squares`.

2.4.5 Univariate function minimizers (`minimize_scalar`)

Often only the minimum of an univariate function (i.e., a function that takes a scalar as input) is needed. In these circumstances, other optimization techniques have been developed that can work faster. These are accessible from the *minimize_scalar* function, which proposes several algorithms.

Unconstrained minimization (`method='brent'`)

There are, actually, two methods that can be used to minimize an univariate function: *brent* and *golden*, but *golden* is included only for academic purposes and should rarely be used. These can be respectively selected through the *method* parameter in *minimize_scalar*. The *brent* method uses Brent's algorithm for locating a minimum. Optimally, a bracket (the *bracket* parameter) should be given which contains the minimum desired. A bracket is a triple (a, b, c) such that $f(a) > f(b) < f(c)$ and $a < b < c$. If this is not given, then alternatively two starting points can be chosen and a bracket will be found from these points using a simple marching algorithm. If these two starting points are not provided, *0* and *1* will be used (this may not be the right choice for your function and result in an unexpected minimum being returned).

Here is an example:

```
>>> from scipy.optimize import minimize_scalar
>>> f = lambda x: (x - 2) * (x + 1)**2
>>> res = minimize_scalar(f, method='brent')
>>> print(res.x)
1.0
```

Bounded minimization (`method='bounded'`)

Very often, there are constraints that can be placed on the solution space before minimization occurs. The *bounded* method in *minimize_scalar* is an example of a constrained minimization procedure that provides a rudimentary interval constraint for scalar functions. The interval constraint allows the minimization to occur only between two fixed endpoints, specified using the mandatory *bounds* parameter.

For example, to find the minimum of $J_1(x)$ near $x = 5$, *minimize_scalar* can be called using the interval $[4, 7]$ as a constraint. The result is $x_{\min} = 5.3314$:

```
>>> from scipy.special import j1
>>> res = minimize_scalar(j1, bounds=(4, 7), method='bounded')
>>> res.x
5.33144184241
```

2.4.6 Custom minimizers

Sometimes, it may be useful to use a custom method as a (multivariate or univariate) minimizer, for example, when using some library wrappers of *minimize* (e.g., *basinhopping*).

We can achieve that by, instead of passing a method name, passing a callable (either a function or an object implementing a *__call__* method) as the *method* parameter.

Let us consider an (admittedly rather virtual) need to use a trivial custom multivariate minimization method that will just search the neighborhood in each dimension independently with a fixed step size:

```
>>> from scipy.optimize import OptimizeResult
>>> def custmin(fun, x0, args=(), maxfev=None, stepsize=0.1,
...         maxiter=100, callback=None, **options):
...     bestx = x0
...     besty = fun(x0)
...     funcalls = 1
...     niter = 0
...     improved = True
...     stop = False
...
...     while improved and not stop and niter < maxiter:
...         improved = False
...         niter += 1
...         for dim in range(np.size(x0)):
...             for s in [bestx[dim] - stepsize, bestx[dim] + stepsize]:
...                 testx = np.copy(bestx)
...                 testx[dim] = s
...                 testy = fun(testx, *args)
...                 funcalls += 1
...                 if testy < besty:
...                     besty = testy
...                     bestx = testx
...                     improved = True
...             if callback is not None:
...                 callback(bestx)
...             if maxfev is not None and funcalls >= maxfev:
...                 stop = True
...                 break
...
...     return OptimizeResult(fun=besty, x=bestx, nit=niter,
...                           nfev=funcalls, success=(niter > 1))
>>> x0 = [1.35, 0.9, 0.8, 1.1, 1.2]
>>> res = minimize(rosen, x0, method=custmin, options=dict(stepsize=0.05))
>>> res.x
array([1., 1., 1., 1., 1.])
```

This will work just as well in case of univariate optimization:

```
>>> def custmin(fun, bracket, args=(), maxfev=None, stepsize=0.1,
...         maxiter=100, callback=None, **options):
...     bestx = (bracket[1] + bracket[0]) / 2.0
...     besty = fun(bestx)
...     funcalls = 1
...     niter = 0
...     improved = True
...     stop = False
...
...     while improved and not stop and niter < maxiter:
...         improved = False
...         niter += 1
...         for testx in [bestx - stepsize, bestx + stepsize]:
...             testy = fun(testx, *args)
...             funcalls += 1
```

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```
...                 if testy < besty:
...                     besty = testy
...                     bestx = testx
...                     improved = True
...             if callback is not None:
...                 callback(bestx)
...             if maxfev is not None and funcalls >= maxfev:
...                 stop = True
...                 break
...
...         return OptimizeResult(fun=besty, x=bestx, nit=niter,
...                               nfev=funcalls, success=(niter > 1))
>>> def f(x):
...     return (x - 2)**2 * (x + 2)**2
>>> res = minimize_scalar(f, bracket=(-3.5, 0), method=custmin,
...                       options=dict(stepsize = 0.05))
>>> res.x
-2.0
```

2.4.7 Root finding

Scalar functions

If one has a single-variable equation, there are multiple different root finding algorithms that can be tried. Most of these algorithms require the endpoints of an interval in which a root is expected (because the function changes signs). In general, `brentq` is the best choice, but the other methods may be useful in certain circumstances or for academic purposes. When a bracket is not available, but one or more derivatives are available, then `newton` (or `halley`, `secant`) may be applicable. This is especially the case if the function is defined on a subset of the complex plane, and the bracketing methods cannot be used.

Fixed-point solving

A problem closely related to finding the zeros of a function is the problem of finding a fixed point of a function. A fixed point of a function is the point at which evaluation of the function returns the point: $g(x) = x$. Clearly, the fixed point of g is the root of $f(x) = g(x) - x$. Equivalently, the root of f is the fixed point of $g(x) = f(x) + x$. The routine `fixed_point` provides a simple iterative method using Aitkens sequence acceleration to estimate the fixed point of g given a starting point.

Sets of equations

Finding a root of a set of non-linear equations can be achieved using the `root` function. Several methods are available, amongst which `hybr` (the default) and `lm`, which, respectively, use the hybrid method of Powell and the Levenberg-Marquardt method from MINPACK.

The following example considers the single-variable transcendental equation

$$x + 2\cos(x) = 0,$$

a root of which can be found as follows:

```
>>> import numpy as np
>>> from scipy.optimize import root
>>> def func(x):
...     return x + 2 * np.cos(x)
>>> sol = root(func, 0.3)
>>> sol.x
array([-1.02986653])
>>> sol.fun
array([ -6.66133815e-16])
```

Consider now a set of non-linear equations

$$\begin{aligned} x_0 \cos(x_1) &= 4, \\ x_0 x_1 - x_1 &= 5. \end{aligned}$$

We define the objective function so that it also returns the Jacobian and indicate this by setting the `jac` parameter to `True`. Also, the Levenberg-Marquardt solver is used here.

```
>>> def func2(x):
...     f = [x[0] * np.cos(x[1]) - 4,
...          x[1]*x[0] - x[1] - 5]
...     df = np.array([[np.cos(x[1]), -x[0] * np.sin(x[1])],
...                    [x[1], x[0] - 1]])
...     return f, df
>>> sol = root(func2, [1, 1], jac=True, method='lm')
>>> sol.x
array([ 6.50409711,  0.90841421])
```

Root finding for large problems

Methods `hybr` and `lm` in *root* cannot deal with a very large number of variables (*N*), as they need to calculate and invert a dense *N x N* Jacobian matrix on every Newton step. This becomes rather inefficient when *N* grows.

Consider, for instance, the following problem: we need to solve the following integrodifferential equation on the square $[0,1] \times [0,1]$:

$$(\partial_x^2 + \partial_y^2) P + 5 \left(\int_0^1 \int_0^1 \cosh(P)\, dx\, dy \right)^2 = 0$$

with the boundary condition $P(x,1) = 1$ on the upper edge and $P = 0$ elsewhere on the boundary of the square. This can be done by approximating the continuous function *P* by its values on a grid, $P_{n,m} \approx P(nh, mh)$, with a small grid spacing *h*. The derivatives and integrals can then be approximated; for instance $\partial_x^2 P(x,y) \approx (P(x+h,y) - 2P(x,y) + P(x-h,y))/h^2$. The problem is then equivalent to finding the root of some function `residual(P)`, where `P` is a vector of length $N_x N_y$.

Now, because $N_x N_y$ can be large, methods `hybr` or `lm` in *root* will take a long time to solve this problem. The solution can, however, be found using one of the large-scale solvers, for example `krylov`, `broyden2`, or `anderson`. These use what is known as the inexact Newton method, which instead of computing the Jacobian matrix exactly, forms an approximation for it.

The problem we have can now be solved as follows:

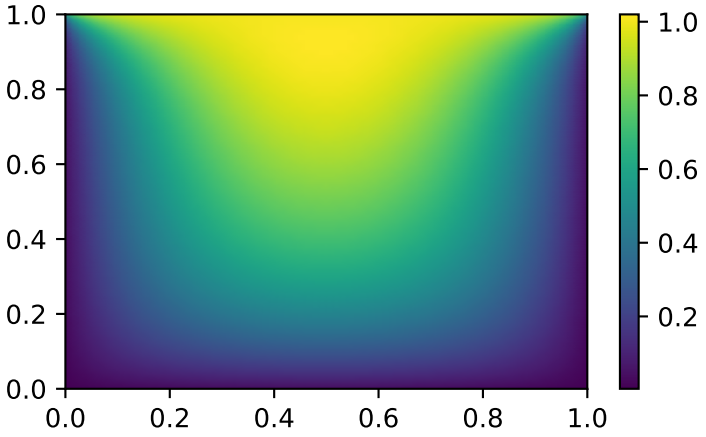
```
import numpy as np
from scipy.optimize import root
from numpy import cosh, zeros_like, mgrid, zeros

# parameters
nx, ny = 75, 75
hx, hy = 1./(nx-1), 1./(ny-1)

P_left, P_right = 0, 0
P_top, P_bottom = 1, 0

def residual(P):
   d2x = zeros_like(P)
   d2y = zeros_like(P)

   d2x[1:-1] = (P[2:]   - 2*P[1:-1] + P[:-2]) / hx/hx
   d2x[0]    = (P[1]    - 2*P[0]    + P_left)/hx/hx
   d2x[-1]   = (P_right - 2*P[-1]   + P[-2])/hx/hx

   d2y[:,1:-1] = (P[:,2:] - 2*P[:,1:-1] + P[:,:-2])/hy/hy
   d2y[:,0]    = (P[:,1]  - 2*P[:,0]    + P_bottom)/hy/hy
   d2y[:,-1]   = (P_top   - 2*P[:,-1]   + P[:,-2])/hy/hy

   return d2x + d2y + 5*cosh(P).mean()**2

# solve
guess = zeros((nx, ny), float)
sol = root(residual, guess, method='krylov', options={'disp': True})
#sol = root(residual, guess, method='broyden2', options={'disp': True, 'max_
↪rank': 50})
#sol = root(residual, guess, method='anderson', options={'disp': True, 'M':␣
↪10})
print('Residual: %g' % abs(residual(sol.x)).max())

# visualize
import matplotlib.pyplot as plt
x, y = mgrid[0:1:(nx*1j), 0:1:(ny*1j)]
plt.pcolormesh(x, y, sol.x, shading='gouraud')
plt.colorbar()
plt.show()
```

Still too slow? Preconditioning.

When looking for the zero of the functions $f_i(\mathbf{x}) = 0$, *i = 1, 2, ..., N*, the `krylov` solver spends most of the time inverting the Jacobian matrix,

$$J_{ij} = \frac{\partial f_i}{\partial x_j}.$$

If you have an approximation for the inverse matrix $M \approx J^{-1}$, you can use it for *preconditioning* the linear-inversion problem. The idea is that instead of solving $J\mathbf{s} = \mathbf{y}$ one solves $MJ\mathbf{s} = M\mathbf{y}$: since matrix MJ is "closer" to the identity matrix than J is, the equation should be easier for the Krylov method to deal with.



The matrix M can be passed to *root* with method `krylov` as an option `options['jac_options']['inner_M']`. It can be a (sparse) matrix or a *scipy.sparse.linalg.LinearOperator* instance.

For the problem in the previous section, we note that the function to solve consists of two parts: the first one is the application of the Laplace operator, $[\partial_x^2 + \partial_y^2]P$, and the second is the integral. We can actually easily compute the Jacobian corresponding to the Laplace operator part: we know that in 1-D

$$\partial_x^2 \approx \frac{1}{h_x^2} \begin{pmatrix} -2 & 1 & 0 & 0\cdots \\ 1 & -2 & 1 & 0\cdots \\ 0 & 1 & -2 & 1\cdots \\ \cdots & & & \end{pmatrix} = h_x^{-2} L$$

so that the whole 2-D operator is represented by

$$J_1 = \partial_x^2 + \partial_y^2 \simeq h_x^{-2} L \otimes I + h_y^{-2} I \otimes L$$

The matrix J_2 of the Jacobian corresponding to the integral is more difficult to calculate, and since *all* of it entries are nonzero, it will be difficult to invert. J_1 on the other hand is a relatively simple matrix, and can be inverted by *scipy.sparse.linalg.splu* (or the inverse can be approximated by *scipy.sparse.linalg.spilu*). So we are content to take $M \approx J_1^{-1}$ and hope for the best.

In the example below, we use the preconditioner $M = J_1^{-1}$.

```
import numpy as np
from scipy.optimize import root
from scipy.sparse import spdiags, kron
from scipy.sparse.linalg import spilu, LinearOperator
from numpy import cosh, zeros_like, mgrid, zeros, eye

# parameters
nx, ny = 75, 75
hx, hy = 1./(nx-1), 1./(ny-1)

P_left, P_right = 0, 0
P_top, P_bottom = 1, 0
```

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```
def get_preconditioner():
    """Compute the preconditioner M"""
    diags_x = zeros((3, nx))
    diags_x[0,:] = 1/hx/hx
    diags_x[1,:] = -2/hx/hx
    diags_x[2,:] = 1/hx/hx
    Lx = spdiags(diags_x, [-1,0,1], nx, nx)

    diags_y = zeros((3, ny))
    diags_y[0,:] = 1/hy/hy
    diags_y[1,:] = -2/hy/hy
    diags_y[2,:] = 1/hy/hy
    Ly = spdiags(diags_y, [-1,0,1], ny, ny)

    J1 = kron(Lx, eye(ny)) + kron(eye(nx), Ly)

    # Now we have the matrix `J_1`. We need to find its inverse `M` --
    # however, since an approximate inverse is enough, we can use
    # the *incomplete LU* decomposition

    J1_ilu = spilu(J1)

    # This returns an object with a method .solve() that evaluates
    # the corresponding matrix-vector product. We need to wrap it into
    # a LinearOperator before it can be passed to the Krylov methods:

    M = LinearOperator(shape=(nx*ny, nx*ny), matvec=J1_ilu.solve)
    return M

def solve(preconditioning=True):
    """Compute the solution"""
    count = [0]

    def residual(P):
        count[0] += 1

        d2x = zeros_like(P)
        d2y = zeros_like(P)

        d2x[1:-1] = (P[2:]   - 2*P[1:-1] + P[:-2])/hx/hx
        d2x[0]    = (P[1]    - 2*P[0]    + P_left)/hx/hx
        d2x[-1]   = (P_right - 2*P[-1]   + P[-2])/hx/hx

        d2y[:,1:-1] = (P[:,2:] - 2*P[:,1:-1] + P[:,:-2])/hy/hy
        d2y[:,0]    = (P[:,1]  - 2*P[:,0]    + P_bottom)/hy/hy
        d2y[:,-1]   = (P_top   - 2*P[:,-1]   + P[:,-2])/hy/hy

        return d2x + d2y + 5*cosh(P).mean()**2

    # preconditioner
    if preconditioning:
```

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```
        M = get_preconditioner()
    else:
        M = None

    # solve
    guess = zeros((nx, ny), float)

    sol = root(residual, guess, method='krylov',
               options={'disp': True,
                        'jac_options': {'inner_M': M}})
    print('Residual', abs(residual(sol.x)).max())
    print('Evaluations', count[0])

    return sol.x

def main():
    sol = solve(preconditioning=True)

    # visualize
    import matplotlib.pyplot as plt
    x, y = mgrid[0:1:(nx*1j), 0:1:(ny*1j)]
    plt.clf()
    plt.pcolor(x, y, sol)
    plt.clim(0, 1)
    plt.colorbar()
    plt.show()


if __name__ == "__main__":
    main()
```

Resulting run, first without preconditioning:

```
0:  |F(x)| = 803.614; step 1; tol 0.000257947
1:  |F(x)| = 345.912; step 1; tol 0.166755
2:  |F(x)| = 139.159; step 1; tol 0.145657
3:  |F(x)| = 27.3682; step 1; tol 0.0348109
4:  |F(x)| = 1.03303; step 1; tol 0.00128227
5:  |F(x)| = 0.0406634; step 1; tol 0.00139451
6:  |F(x)| = 0.00344341; step 1; tol 0.00645373
7:  |F(x)| = 0.000153671; step 1; tol 0.00179246
8:  |F(x)| = 6.7424e-06; step 1; tol 0.00173256
Residual 3.57078908664e-07
Evaluations 317
```

and then with preconditioning:

```
0:  |F(x)| = 136.993; step 1; tol 7.49599e-06
1:  |F(x)| = 4.80983; step 1; tol 0.00110945
2:  |F(x)| = 0.195942; step 1; tol 0.00149362
3:  |F(x)| = 0.000563597; step 1; tol 7.44604e-06
4:  |F(x)| = 1.00698e-09; step 1; tol 2.87308e-12
```

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```
Residual 9.29603061195e-11
Evaluations 77
```

Using a preconditioner reduced the number of evaluations of the `residual` function by a factor of *4*. For problems where the residual is expensive to compute, good preconditioning can be crucial — it can even decide whether the problem is solvable in practice or not.

Preconditioning is an art, science, and industry. Here, we were lucky in making a simple choice that worked reasonably well, but there is a lot more depth to this topic than is shown here.

2.4.8 Linear programming (`linprog`)

The function *`linprog`* can minimize a linear objective function subject to linear equality and inequality constraints. This kind of problem is well known as linear programming. Linear programming solves problems of the following form:

$$\begin{aligned} \min_x \ & c^T x \\ \text{such that } & A_{ub} x \leq b_{ub}, \\ & A_{eq} x = b_{eq}, \\ & l \leq x \leq u, \end{aligned}$$

where x is a vector of decision variables; c, b_{ub}, b_{eq}, l, and u are vectors; and A_{ub} and A_{eq} are matrices.

In this tutorial, we will try to solve a typical linear programming problem using *`linprog`*.

Linear programming example

Consider the following simple linear programming problem:

$$\begin{aligned} \max_{x_1, x_2, x_3, x_4} \ & 29x_1 + 45x_2 \\ \text{such that } & x_1 - x_2 - 3x_3 \leq 5 \\ & 2x_1 - 3x_2 - 7x_3 + 3x_4 \geq 10 \\ & 2x_1 + 8x_2 + x_3 = 60 \\ & 4x_1 + 4x_2 + x_4 = 60 \\ & 0 \leq x_0 \\ & 0 \leq x_1 \leq 5 \\ & x_2 \leq 0.5 \\ & -3 \leq x_3 \end{aligned}$$

We need some mathematical manipulations to convert the target problem to the form accepted by *`linprog`*.

First of all, let's consider the objective function. We want to maximize the objective function, but *`linprog`* can only accept a minimization problem. This is easily remedied by converting the maximize $29x_1 + 45x_2$ to minimizing $-29x_1 - 45x_2$. Also, x_3, x_4 are not shown in the objective function. That means the weights corresponding with x_3, x_4 are zero. So, the objective function can be converted to:

$$\min_{x_1, x_2, x_3, x_4} \ -29x_1 - 45x_2 + 0x_3 + 0x_4$$

If we define the vector of decision variables $x = [x_1, x_2, x_3, x_4]^T$, the objective weights vector c of *`linprog`* in this problem should be

$$c = [-29, -45, 0, 0]^T$$

Next, let's consider the two inequality constraints. The first one is a "less than" inequality, so it is already in the form accepted by *linprog*. The second one is a "greater than" inequality, so we need to multiply both sides by -1 to convert it to a "less than" inequality. Explicitly showing zero coefficients, we have:

$$x_1 - x_2 - 3x_3 + 0x_4 \leq 5$$
$$-2x_1 + 3x_2 + 7x_3 - 3x_4 \leq -10$$

These equations can be converted to matrix form:

$$A_{ub}x \leq b_{ub}$$

where

$$A_{ub} = \begin{bmatrix} 1 & -1 & -3 & 0 \\ -2 & 3 & 7 & -3 \end{bmatrix}$$

$$b_{ub} = \begin{bmatrix} 5 \\ -10 \end{bmatrix}$$

Next, let's consider the two equality constraints. Showing zero weights explicitly, these are:

$$2x_1 + 8x_2 + 1x_3 + 0x_4 = 60$$
$$4x_1 + 4x_2 + 0x_3 + 1x_4 = 60$$

These equations can be converted to matrix form:

$$A_{eq}x = b_{eq}$$

where

$$A_{eq} = \begin{bmatrix} 2 & 8 & 1 & 0 \\ 4 & 4 & 0 & 1 \end{bmatrix}$$

$$b_{eq} = \begin{bmatrix} 60 \\ 60 \end{bmatrix}$$

Lastly, let's consider the separate inequality constraints on individual decision variables, which are known as "box constraints" or "simple bounds". These constraints can be applied using the bounds argument of *linprog*. As noted in the *linprog* documentation, the default value of bounds is `(0, None)`, meaning that the lower bound on each decision variable is 0, and the upper bound on each decision variable is infinity: all the decision variables are non-negative. Our bounds are different, so we will need to specify the lower and upper bound on each decision variable as a tuple and group these tuples into a list.

Finally, we can solve the transformed problem using *linprog*.

```
>>> import numpy as np
>>> from scipy.optimize import linprog
>>> c = np.array([-29.0, -45.0, 0.0, 0.0])
>>> A_ub = np.array([[1.0, -1.0, -3.0, 0.0],
...                  [-2.0, 3.0, 7.0, -3.0]])
>>> b_ub = np.array([5.0, -10.0])
>>> A_eq = np.array([[2.0, 8.0, 1.0, 0.0],
...                  [4.0, 4.0, 0.0, 1.0]])
>>> b_eq = np.array([60.0, 60.0])
>>> x0_bounds = (0, None)
>>> x1_bounds = (0, 5.0)
>>> x2_bounds = (-np.inf, 0.5)  # +/- np.inf can be used instead of None
>>> x3_bounds = (-3.0, None)
>>> bounds = [x0_bounds, x1_bounds, x2_bounds, x3_bounds]
```

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```
>>> result = linprog(c, A_ub=A_ub, b_ub=b_ub, A_eq=A_eq, b_eq=b_eq,␣
↪bounds=bounds)
>>> print(result)
     con: array([15.5361242 , 16.61288005])  # may vary
     fun: -370.2321976308326  # may vary
 message: 'The algorithm terminated successfully and determined that the␣
↪problem is infeasible.'
     nit: 6  # may vary
   slack: array([ 0.79314989, -1.76308532])  # may vary
  status: 2
 success: False
       x: array([ 6.60059391,  3.97366609, -0.52664076,  1.09007993])  # may␣
↪vary
```

The result states that our problem is infeasible, meaning that there is no solution vector that satisfies all the constraints. That doesn't necessarily mean we did anything wrong; some problems truly are infeasible. Suppose, however, that we were to decide that our bound constraint on x_1 was too tight and that it could be loosened to $0 \leq x_1 \leq 6$. After adjusting our code `x1_bounds = (0, 6)` to reflect the change and executing it again:

```
>>> x1_bounds = (0, 6)
>>> bounds = [x0_bounds, x1_bounds, x2_bounds, x3_bounds]
>>> result = linprog(c, A_ub=A_ub, b_ub=b_ub, A_eq=A_eq, b_eq=b_eq,␣
↪bounds=bounds)
>>> print(result)
     con: array([9.78840831e-09, 1.04662945e-08])  # may vary
     fun: -505.97435889013434  # may vary
message: 'Optimization terminated successfully.'
     nit: 4  # may vary
   slack: array([ 6.52747190e-10, -2.26730279e-09])  # may vary
  status: 0
 success: True
       x: array([ 9.41025641,  5.17948718, -0.25641026,  1.64102564])  # may␣
↪vary
```

The result shows the optimization was successful. We can check the objective value (`result.fun`) is same as $c^T x$:

```
>>> x = np.array(result.x)
>>> print(c @ x)
-505.97435889013434  # may vary
```

We can also check that all constraints are satisfied within reasonable tolerances:

```
>>> print(b_ub - (A_ub @ x).flatten())  # this is equivalent to result.slack
[ 6.52747190e-10, -2.26730279e-09]  # may vary
>>> print(b_eq - (A_eq @ x).flatten())  # this is equivalent to result.con
[ 9.78840831e-09, 1.04662945e-08]]  # may vary
>>> print([0 <= result.x[0], 0 <= result.x[1] <= 6.0, result.x[2] <= 0.5, -3.
↪0 <= result.x[3]])
[True, True, True, True]
```

If we need greater accuracy, typically at the expense of speed, we can solve using the `revised simplex` method:

```
>>> result = linprog(c, A_ub=A_ub, b_ub=b_ub, A_eq=A_eq, b_eq=b_eq,␣
↪bounds=bounds, method='revised simplex')
>>> print(result)
    con: array([0.00000000e+00, 7.10542736e-15])  # may vary
    fun: -505.97435897435895    # may vary
message: 'Optimization terminated successfully.'
    nit: 5  # may vary
  slack: array([ 1.77635684e-15, -3.55271368e-15])  # may vary
 status: 0
success: True
      x: array([ 9.41025641,  5.17948718, -0.25641026,  1.64102564])  # may␣
↪vary
```

2.4.9 Assignment problems

Linear sum assignment problem example

Consider the problem of selecting students for a swimming medley relay team. We have a table showing times for each swimming style of five students:

Student	backstroke	breaststroke	butterfly	freestyle
A	43.5	47.1	48.4	38.2
B	45.5	42.1	49.6	36.8
C	43.4	39.1	42.1	43.2
D	46.5	44.1	44.5	41.2
E	46.3	47.8	50.4	37.2

We need to choose a student for each of the four swimming styles such that the total relay time is minimized. This is a typical linear sum assignment problem. We can use *linear_sum_assignment* to solve it.

The linear sum assignment problem is one of the most famous combinatorial optimization problems. Given a "cost matrix" C, the problem is to choose

- exactly one element from each row
- without choosing more than one element from any column
- such that the sum of the chosen elements is minimized

In other words, we need to assign each row to one column such that the sum of the corresponding entries is minimized.

Formally, let X be a boolean matrix where $X[i, j] = 1$ iff row i is assigned to column j. Then the optimal assignment has cost

$$\min \sum_i \sum_j C_{i,j} X_{i,j}$$

The first step is to define the cost matrix. In this example, we want to assign each swimming style to a student. *linear_sum_assignment* is able to assign each row of a cost matrix to a column. Therefore, to form the cost matrix, the table above needs to be transposed so that the rows correspond with swimming styles and the columns correspond with students:

```
>>> import numpy as np
>>> cost = np.array([[43.5, 45.5, 43.4, 46.5, 46.3],
```

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```
...                   [47.1, 42.1, 39.1, 44.1, 47.8],
...                   [48.4, 49.6, 42.1, 44.5, 50.4],
...                   [38.2, 36.8, 43.2, 41.2, 37.2]])
```

We can solve the assignment problem with *linear_sum_assignment*:

```
>>> from scipy.optimize import linear_sum_assignment
>>> row_ind, col_ind = linear_sum_assignment(cost)
```

The `row_ind` and `col_ind` are optimal assigned matrix indexes of the cost matrix:

```
>>> row_ind
array([0, 1, 2, 3])
>>> col_ind
array([0, 2, 3, 1])
```

The optimal assignment is:

```
>>> styles = np.array(["backstroke", "breaststroke", "butterfly", "freestyle
↪"])[row_ind]
>>> students = np.array(["A", "B", "C", "D", "E"])[col_ind]
>>> dict(zip(styles, students))
{'backstroke': 'A', 'breaststroke': 'C', 'butterfly': 'D', 'freestyle': 'B'}
```

The optimal total medley time is:

```
>>> cost[row_ind, col_ind].sum()
163.89999999999998
```

Note that this result is not the same as the sum of the minimum times for each swimming style:

```
>>> np.min(cost, axis=1).sum()
161.39999999999998
```

because student "C" is the best swimmer in both "breaststroke" and "butterfly" style. We cannot assign student "C" to both styles, so we assigned student C to the "breaststroke" style and D to the "butterfly" style to minimize the total time.

References

Some further reading and related software, such as Newton-Krylov [KK], PETSc [PP], and PyAMG [AMG]:

2.5 Interpolation (`scipy.interpolate`)

Contents

- *Interpolation (`scipy.interpolate`)*
  - *1-D interpolation (`interp1d`)*
  - *Multivariate data interpolation (`griddata`)*

- *Spline interpolation*
  - *Spline interpolation in 1-D: Procedural (interpolate.splXXX)*
  - *Spline interpolation in 1-d: Object-oriented (`UnivariateSpline`)*
  - *2-D spline representation: Procedural (`bisplrep`)*
  - *2-D spline representation: Object-oriented (`BivariateSpline`)*
- *Using radial basis functions for smoothing/interpolation*
  - *1-D Example*
  - *2-D Example*

There are several general interpolation facilities available in SciPy, for data in 1, 2, and higher dimensions:

- A class representing an interpolant (*`interp1d`*) in 1-D, offering several interpolation methods.
- Convenience function *`griddata`* offering a simple interface to interpolation in N dimensions (N = 1, 2, 3, 4, …). Object-oriented interface for the underlying routines is also available.
- Functions for 1- and 2-D (smoothed) cubic-spline interpolation, based on the FORTRAN library FITPACK. They are both procedural and object-oriented interfaces for the FITPACK library.
- Interpolation using radial basis functions.

2.5.1 1-D interpolation (`interp1d`)

The *`interp1d`* class in *`scipy.interpolate`* is a convenient method to create a function based on fixed data points, which can be evaluated anywhere within the domain defined by the given data using linear interpolation. An instance of this class is created by passing the 1-D vectors comprising the data. The instance of this class defines a __call__ method and can therefore by treated like a function which interpolates between known data values to obtain unknown values (it also has a docstring for help). Behavior at the boundary can be specified at instantiation time. The following example demonstrates its use, for linear and cubic spline interpolation:

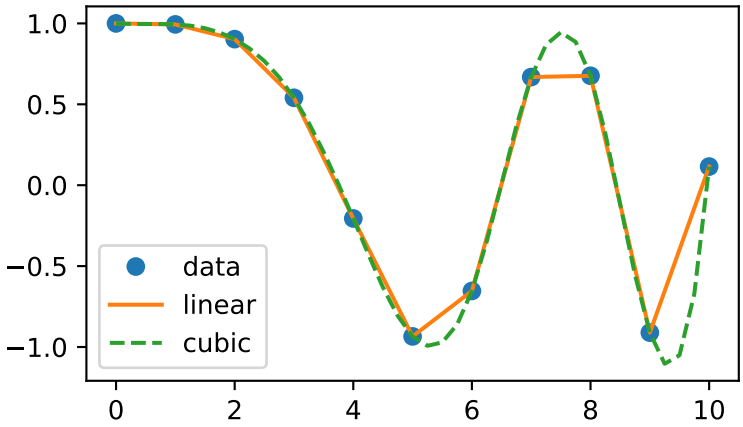
```
>>> from scipy.interpolate import interp1d
```

```
>>> x = np.linspace(0, 10, num=11, endpoint=True)
>>> y = np.cos(-x**2/9.0)
>>> f = interp1d(x, y)
>>> f2 = interp1d(x, y, kind='cubic')
```

```
>>> xnew = np.linspace(0, 10, num=41, endpoint=True)
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'o', xnew, f(xnew), '-', xnew, f2(xnew), '--')
>>> plt.legend(['data', 'linear', 'cubic'], loc='best')
>>> plt.show()
```

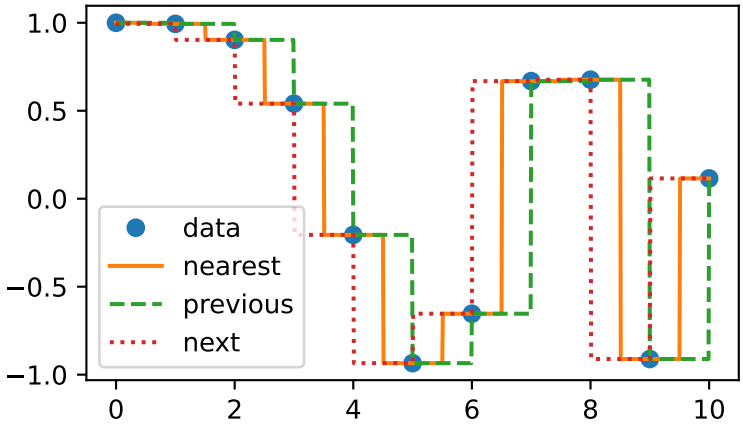
Another set of interpolations in *`interp1d`* is *nearest*, *previous*, and *next*, where they return the nearest, previous, or next point along the x-axis. Nearest and next can be thought of as a special case of a causal interpolating filter. The following example demonstrates their use, using the same data as in the previous example:

```
>>> from scipy.interpolate import interp1d
```




```
>>> x = np.linspace(0, 10, num=11, endpoint=True)
>>> y = np.cos(-x**2/9.0)
>>> f1 = interp1d(x, y, kind='nearest')
>>> f2 = interp1d(x, y, kind='previous')
>>> f3 = interp1d(x, y, kind='next')
```

```
>>> xnew = np.linspace(0, 10, num=1001, endpoint=True)
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'o')
>>> plt.plot(xnew, f1(xnew), '-', xnew, f2(xnew), '--', xnew, f3(xnew), ':')
>>> plt.legend(['data', 'nearest', 'previous', 'next'], loc='best')
>>> plt.show()
```



2.5.2 Multivariate data interpolation (griddata)

Suppose you have multidimensional data, for instance, for an underlying function *f(x, y)* you only know the values at points *(x[i], y[i])* that do not form a regular grid.

Suppose we want to interpolate the 2-D function

```
>>> def func(x, y):
...     return x*(1-x)*np.cos(4*np.pi*x) * np.sin(4*np.pi*y**2)**2
```

on a grid in [0, 1]x[0, 1]

```
>>> grid_x, grid_y = np.mgrid[0:1:100j, 0:1:200j]
```

but we only know its values at 1000 data points:

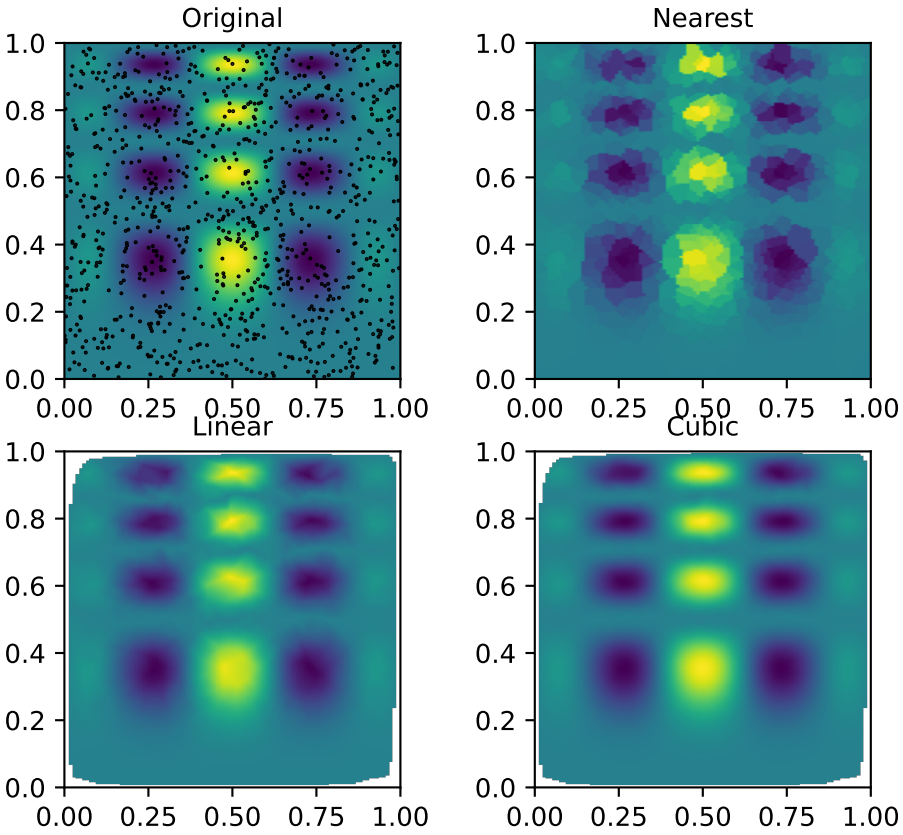
```
>>> rng = np.random.default_rng()
>>> points = rng.random((1000, 2))
>>> values = func(points[:,0], points[:,1])
```

This can be done with *griddata* – below, we try out all of the interpolation methods:

```
>>> from scipy.interpolate import griddata
>>> grid_z0 = griddata(points, values, (grid_x, grid_y), method='nearest')
>>> grid_z1 = griddata(points, values, (grid_x, grid_y), method='linear')
>>> grid_z2 = griddata(points, values, (grid_x, grid_y), method='cubic')
```

One can see that the exact result is reproduced by all of the methods to some degree, but for this smooth function the piecewise cubic interpolant gives the best results:

```
>>> import matplotlib.pyplot as plt
>>> plt.subplot(221)
>>> plt.imshow(func(grid_x, grid_y).T, extent=(0,1,0,1), origin='lower')
>>> plt.plot(points[:,0], points[:,1], 'k.', ms=1)
>>> plt.title('Original')
>>> plt.subplot(222)
>>> plt.imshow(grid_z0.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Nearest')
>>> plt.subplot(223)
>>> plt.imshow(grid_z1.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Linear')
>>> plt.subplot(224)
>>> plt.imshow(grid_z2.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Cubic')
>>> plt.gcf().set_size_inches(6, 6)
>>> plt.show()
```


Original
Nearest
Linear
Cubic
1.0
0.8
0.6
0.4
0.2
0.0
0.00
0.25
0.50
0.75
1.00

2.5.3 Spline interpolation

Spline interpolation in 1-D: Procedural (interpolate.splXXX)

Spline interpolation requires two essential steps: (1) a spline representation of the curve is computed, and (2) the spline is evaluated at the desired points. In order to find the spline representation, there are two different ways to represent a curve and obtain (smoothing) spline coefficients: directly and parametrically. The direct method finds the spline representation of a curve in a 2-D plane using the function *splrep*. The first two arguments are the only ones required, and these provide the x and y components of the curve. The normal output is a 3-tuple, (t, c, k) , containing the knot-points, t , the coefficients c and the order k of the spline. The default spline order is cubic, but this can be changed with the input keyword, *k*.

For curves in N-D space the function *splprep* allows defining the curve parametrically. For this function only 1 input argument is required. This input is a list of N-arrays representing the curve in N-D space. The length of each array is the number of curve points, and each array provides one component of the N-D data point. The parameter variable is given with the keyword argument, *u*,, which defaults to an equally-spaced monotonic sequence between 0 and 1 . The default output consists of two objects: a 3-tuple, (t, c, k) , containing the spline representation and the parameter variable u.

The keyword argument, s , is used to specify the amount of smoothing to perform during the spline fit. The default value of s is $s = m - \sqrt{2m}$ where m is the number of data-points being fit. Therefore, **if no smoothing is desired a value of** $\mathbf{s} = 0$ **should be passed to the routines.**

Once the spline representation of the data has been determined, functions are available for evaluating the spline (*splev*) and its derivatives (*splev*, *spalde*) at any point and the integral of the spline between any two points (*splint*). In addition, for cubic splines ($k = 3$) with 8 or more knots, the roots of the spline can be estimated (*sproot*). These functions are demonstrated in the example that follows.

```
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate
```

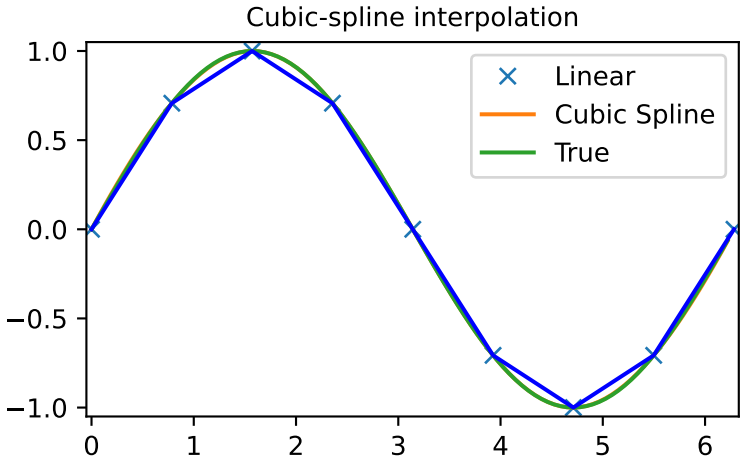
Cubic-spline

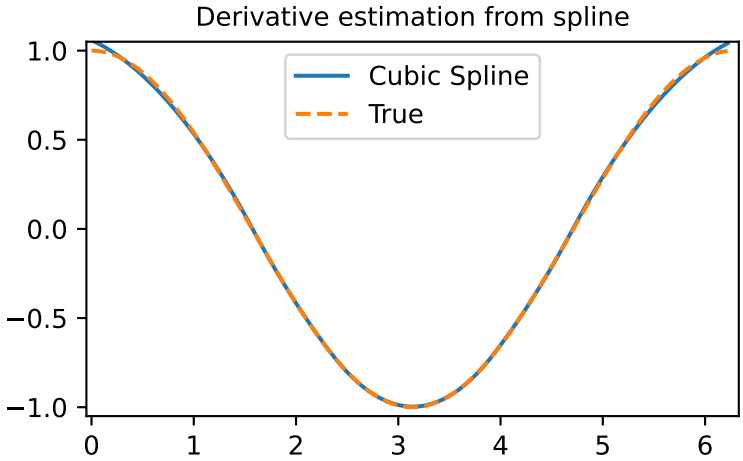
```
>>> x = np.arange(0, 2*np.pi+np.pi/4, 2*np.pi/8)
>>> y = np.sin(x)
>>> tck = interpolate.splrep(x, y, s=0)
>>> xnew = np.arange(0, 2*np.pi, np.pi/50)
>>> ynew = interpolate.splev(xnew, tck, der=0)
```

```
>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, np.sin(xnew), x, y, 'b')
>>> plt.legend(['Linear', 'Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Cubic-spline interpolation')
>>> plt.show()
```

Derivative of spline

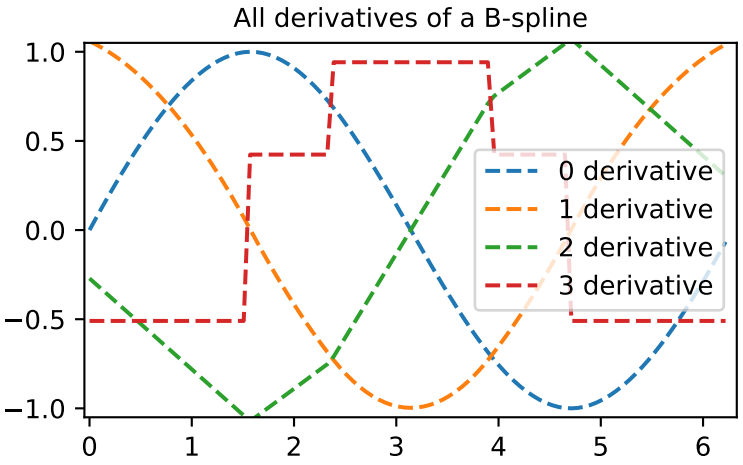
```
>>> yder = interpolate.splev(xnew, tck, der=1)
>>> plt.figure()
>>> plt.plot(xnew, yder, xnew, np.cos(xnew),'--')
>>> plt.legend(['Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Derivative estimation from spline')
>>> plt.show()
```


Cubic-spline interpolation
Linear
Cubic Spline
True
1.0
0.5
0.0
−0.5
−1.0
0
1
2
3
4
5
6


Derivative estimation from spline
Cubic Spline
True
1.0
0.5
0.0
−0.5
−1.0
0
1
2
3
4
5
6

All derivatives of spline

```
>>> yders = interpolate.spalde(xnew, tck)
>>> plt.figure()
>>> for i in range(len(yders[0])):
...     plt.plot(xnew, [d[i] for d in yders], '--', label=f"{i} derivative")
>>> plt.legend()
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('All derivatives of a B-spline')
>>> plt.show()
```



Integral of spline

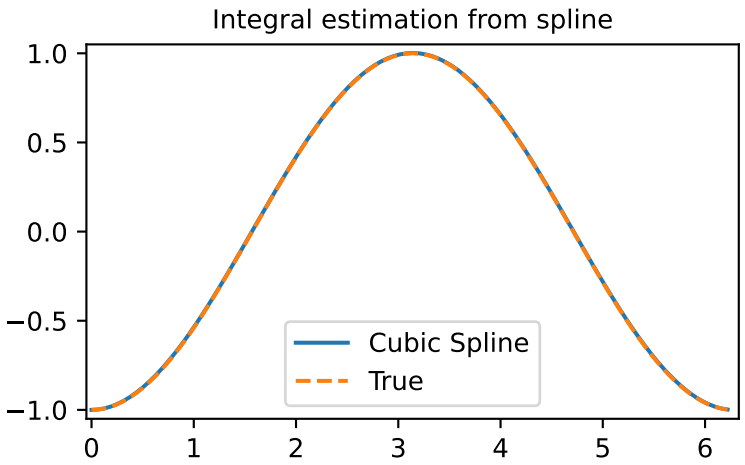
```
>>> def integ(x, tck, constant=-1):
...     x = np.atleast_1d(x)
...     out = np.zeros(x.shape, dtype=x.dtype)
...     for n in range(len(out)):
...         out[n] = interpolate.splint(0, x[n], tck)
...     out += constant
...     return out
```

```
>>> yint = integ(xnew, tck)
>>> plt.figure()
>>> plt.plot(xnew, yint, xnew, -np.cos(xnew), '--')
>>> plt.legend(['Cubic Spline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Integral estimation from spline')
>>> plt.show()
```

Roots of spline

```
>>> interpolate.sproot(tck)
array([3.1416])
```

Notice that *sproot* failed to find an obvious solution at the edge of the approximation interval, $x = 0$. If we define the

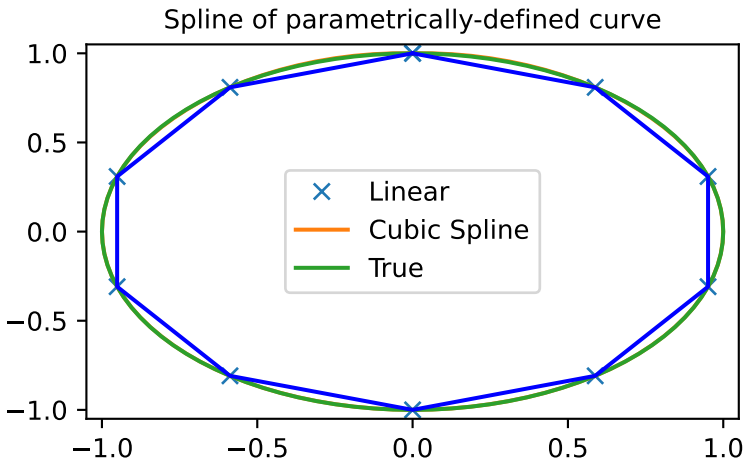


spline on a slightly larger interval, we recover both roots $x = 0$ and $x = 2\pi$:

```
>>> x = np.linspace(-np.pi/4, 2.*np.pi + np.pi/4, 21)
>>> y = np.sin(x)
>>> tck = interpolate.splrep(x, y, s=0)
>>> interpolate.sproot(tck)
array([0., 3.1416])
```

Parametric spline

```
>>> t = np.arange(0, 1.1, .1)
>>> x = np.sin(2*np.pi*t)
>>> y = np.cos(2*np.pi*t)
>>> tck, u = interpolate.splprep([x, y], s=0)
>>> unew = np.arange(0, 1.01, 0.01)
>>> out = interpolate.splev(unew, tck)
>>> plt.figure()
>>> plt.plot(x, y, 'x', out[0], out[1], np.sin(2*np.pi*unew), np.cos(2*np.
↪pi*unew), x, y, 'b')
>>> plt.legend(['Linear', 'Cubic Spline', 'True'])
>>> plt.axis([-1.05, 1.05, -1.05, 1.05])
>>> plt.title('Spline of parametrically-defined curve')
>>> plt.show()
```



Spline interpolation in 1-d: Object-oriented (`UnivariateSpline`)

The spline-fitting capabilities described above are also available via an objected-oriented interface. The 1-D splines are objects of the *`UnivariateSpline`* class, and are created with the x and y components of the curve provided as arguments to the constructor. The class defines *`__call__`*, allowing the object to be called with the x-axis values, at which the spline should be evaluated, returning the interpolated y-values. This is shown in the example below for the subclass *`InterpolatedUnivariateSpline`*. The *`integral`*, *`derivatives`*, and *`roots`* methods are also available on *`UnivariateSpline`* objects, allowing definite integrals, derivatives, and roots to be computed for the spline.

The UnivariateSpline class can also be used to smooth data by providing a non-zero value of the smoothing parameter *s*, with the same meaning as the *s* keyword of the *`splrep`* function described above. This results in a spline that has fewer knots than the number of data points, and hence is no longer strictly an interpolating spline, but rather a smoothing spline. If this is not desired, the *`InterpolatedUnivariateSpline`* class is available. It is a subclass of *`UnivariateSpline`* that always passes through all points (equivalent to forcing the smoothing parameter to 0). This class is demonstrated in the example below.

The *`LSQUnivariateSpline`* class is the other subclass of *`UnivariateSpline`*. It allows the user to specify the number and location of internal knots explicitly with the parameter *t*. This allows for the creation of customized splines with non-linear spacing, to interpolate in some domains and smooth in others, or change the character of the spline.

```
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate
```

InterpolatedUnivariateSpline

```
>>> x = np.arange(0, 2*np.pi+np.pi/4, 2*np.pi/8)
>>> y = np.sin(x)
>>> s = interpolate.InterpolatedUnivariateSpline(x, y)
>>> xnew = np.arange(0, 2*np.pi, np.pi/50)
>>> ynew = s(xnew)
```

```
>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, np.sin(xnew), x, y, 'b')
```

(continues on next page)

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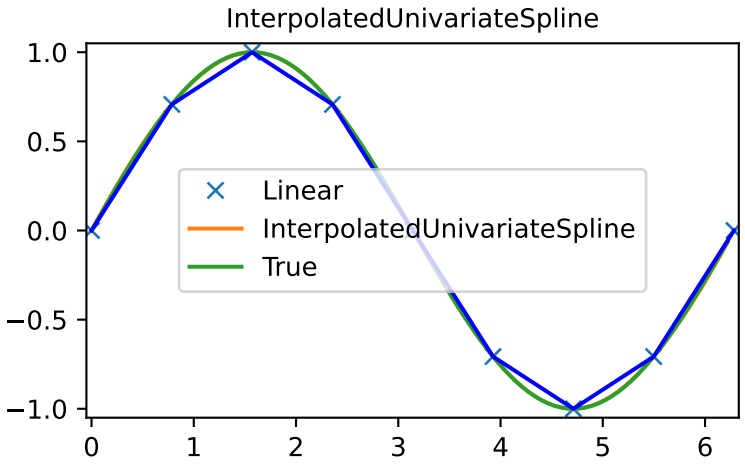
```
>>> plt.legend(['Linear', 'InterpolatedUnivariateSpline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('InterpolatedUnivariateSpline')
>>> plt.show()
```



LSQUnivarateSpline with non-uniform knots

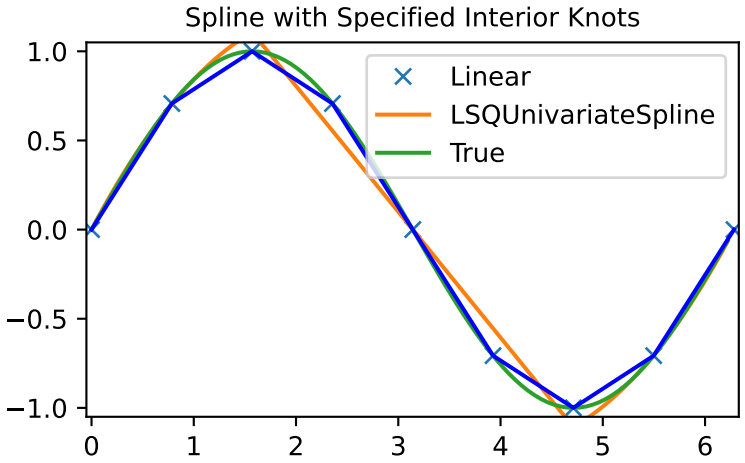
```
>>> t = [np.pi/2-.1, np.pi/2+.1, 3*np.pi/2-.1, 3*np.pi/2+.1]
>>> s = interpolate.LSQUnivariateSpline(x, y, t, k=2)
>>> ynew = s(xnew)
```

```
>>> plt.figure()
>>> plt.plot(x, y, 'x', xnew, ynew, xnew, np.sin(xnew), x, y, 'b')
>>> plt.legend(['Linear', 'LSQUnivariateSpline', 'True'])
>>> plt.axis([-0.05, 6.33, -1.05, 1.05])
>>> plt.title('Spline with Specified Interior Knots')
>>> plt.show()
```

2-D spline representation: Procedural (`bisplrep`)

For (smooth) spline-fitting to a 2-D surface, the function *bisplrep* is available. This function takes as required inputs the **1-D** arrays *x*, *y*, and *z*, which represent points on the surface $z = f(x, y)$. The default output is a list $[tx, ty, c, kx, ky]$ whose entries represent respectively, the components of the knot positions, the coefficients of the spline, and the order of the spline in each coordinate. It is convenient to hold this list in a single object, *tck,* so that it can be passed easily to the function *bisplev*. The keyword, *s* , can be used to change the amount of smoothing performed on the data while determining the appropriate spline. The default value is $s = m - \sqrt{2m}$, where m is the number of data points in the *x,* *y,* and *z* vectors. As a result, if no smoothing is desired, then $s = 0$ should be passed to *bisplrep*.

To evaluate the 2-D spline and its partial derivatives (up to the order of the spline), the function *bisplev* is required. This function takes as the first two arguments **two 1-D arrays** whose cross-product specifies the domain over which to evaluate the spline. The third argument is the *tck* list returned from *bisplrep*. If desired, the fourth and fifth arguments provide the orders of the partial derivative in the x and y direction, respectively.



It is important to note that 2-D interpolation should not be used to find the spline representation of images. The algorithm used is not amenable to large numbers of input points. The signal-processing toolbox contains more appropriate algorithms for finding the spline representation of an image. The 2-D interpolation commands are intended for use when interpolating a 2-D function as shown in the example that follows. This example uses the `mgrid` command in NumPy which is useful for defining a "mesh-grid" in many dimensions. (See also the `ogrid` command if the full-mesh is not needed). The number of output arguments and the number of dimensions of each argument is determined by the number of indexing objects passed in `mgrid`.

```
>>> import numpy as np
>>> from scipy import interpolate
>>> import matplotlib.pyplot as plt
```

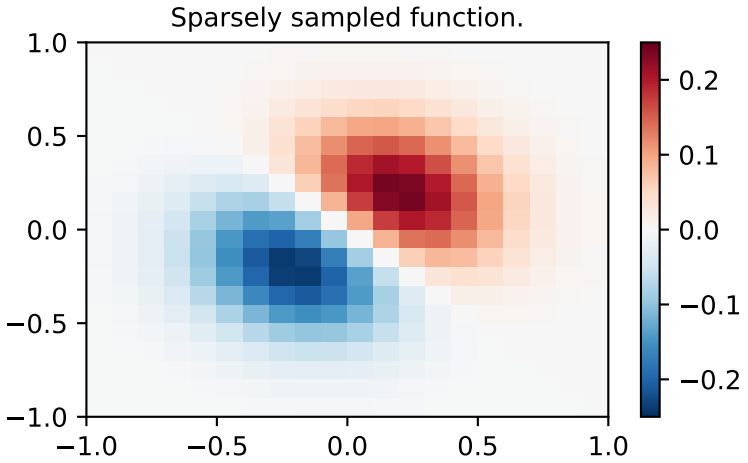
Define function over a sparse 20x20 grid

```
>>> x_edges, y_edges = np.mgrid[-1:1:21j, -1:1:21j]
>>> x = x_edges[:-1, :-1] + np.diff(x_edges[:2, 0])[0] / 2.
>>> y = y_edges[:-1, :-1] + np.diff(y_edges[0, :2])[0] / 2.
>>> z = (x+y) * np.exp(-6.0*(x*x+y*y))
```

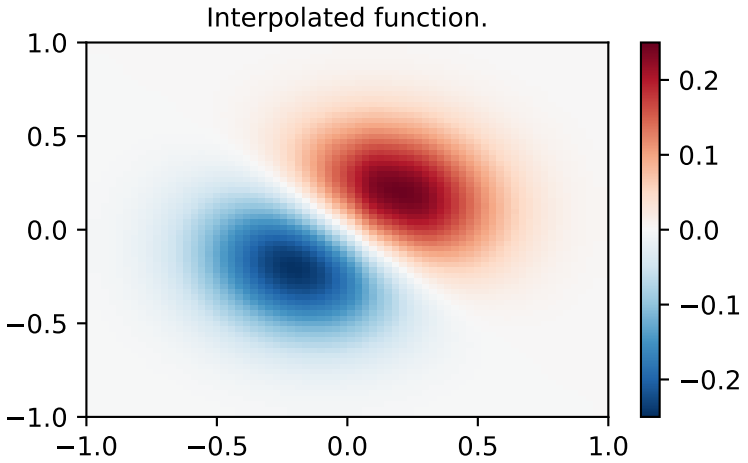
```
>>> plt.figure()
>>> lims = dict(cmap='RdBu_r', vmin=-0.25, vmax=0.25)
>>> plt.pcolormesh(x_edges, y_edges, z, shading='flat', **lims)
>>> plt.colorbar()
>>> plt.title("Sparsely sampled function.")
>>> plt.show()
```

Interpolate function over a new 70x70 grid

```
>>> xnew_edges, ynew_edges = np.mgrid[-1:1:71j, -1:1:71j]
>>> xnew = xnew_edges[:-1, :-1] + np.diff(xnew_edges[:2, 0])[0] / 2.
>>> ynew = ynew_edges[:-1, :-1] + np.diff(ynew_edges[0, :2])[0] / 2.
>>> tck = interpolate.bisplrep(x, y, z, s=0)
>>> znew = interpolate.bisplev(xnew[:,0], ynew[0,:], tck)
```




```
>>> plt.figure()
>>> plt.pcolormesh(xnew_edges, ynew_edges, znew, shading='flat', **lims)
>>> plt.colorbar()
>>> plt.title("Interpolated function.")
>>> plt.show()
```



2-D spline representation: Object-oriented (`BivariateSpline`)

The *`BivariateSpline`* class is the 2-D analog of the *`UnivariateSpline`* class. It and its subclasses implement the FITPACK functions described above in an object-oriented fashion, allowing objects to be instantiated that can be called to compute the spline value by passing in the two coordinates as the two arguments.

2.5.4 Using radial basis functions for smoothing/interpolation

Radial basis functions can be used for smoothing/interpolating scattered data in N dimensions, but should be used with caution for extrapolation outside of the observed data range.

1-D Example

This example compares the usage of the *`Rbf`* and *`UnivariateSpline`* classes from the scipy.interpolate module.

```
>>> import numpy as np
>>> from scipy.interpolate import Rbf, InterpolatedUnivariateSpline
>>> import matplotlib.pyplot as plt
```

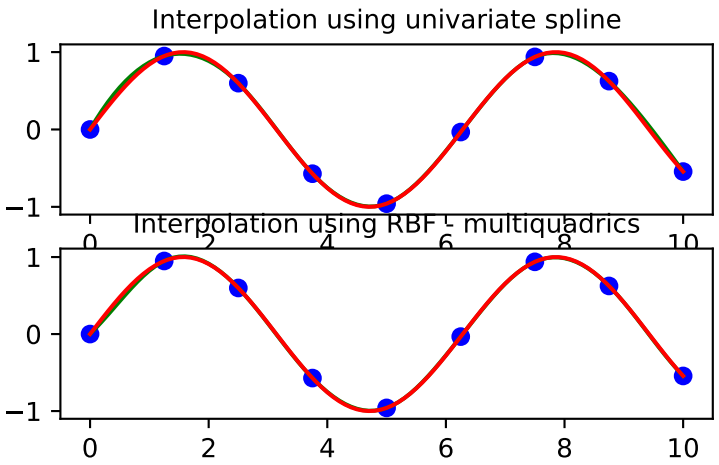
```
>>> # setup data
>>> x = np.linspace(0, 10, 9)
>>> y = np.sin(x)
>>> xi = np.linspace(0, 10, 101)
```

```
>>> # use fitpack2 method
>>> ius = InterpolatedUnivariateSpline(x, y)
>>> yi = ius(xi)
```

```
>>> plt.subplot(2, 1, 1)
>>> plt.plot(x, y, 'bo')
>>> plt.plot(xi, yi, 'g')
>>> plt.plot(xi, np.sin(xi), 'r')
>>> plt.title('Interpolation using univariate spline')
```

```
>>> # use RBF method
>>> rbf = Rbf(x, y)
>>> fi = rbf(xi)
```

```
>>> plt.subplot(2, 1, 2)
>>> plt.plot(x, y, 'bo')
>>> plt.plot(xi, fi, 'g')
>>> plt.plot(xi, np.sin(xi), 'r')
>>> plt.title('Interpolation using RBF - multiquadrics')
>>> plt.show()
```



2-D Example

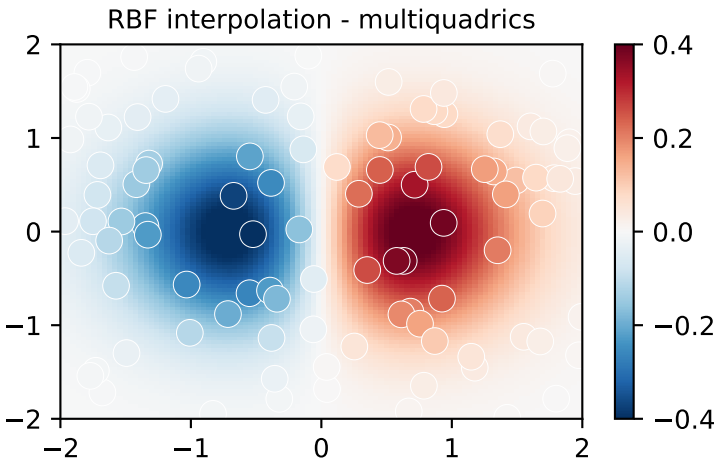
This example shows how to interpolate scattered 2-D data:

```
>>> import numpy as np
>>> from scipy.interpolate import Rbf
>>> import matplotlib.pyplot as plt
>>> from matplotlib import cm
```

```
>>> # 2-d tests - setup scattered data
>>> rng = np.random.default_rng()
>>> x = rng.random(100)*4.0-2.0
>>> y = rng.random(100)*4.0-2.0
>>> z = x*np.exp(-x**2-y**2)
>>> edges = np.linspace(-2.0, 2.0, 101)
>>> centers = edges[:-1] + np.diff(edges[:2])[0] / 2.
>>> XI, YI = np.meshgrid(centers, centers)
```

```
>>> # use RBF
>>> rbf = Rbf(x, y, z, epsilon=2)
>>> ZI = rbf(XI, YI)
```

```
>>> # plot the result
>>> plt.subplot(1, 1, 1)
>>> X_edges, Y_edges = np.meshgrid(edges, edges)
>>> lims = dict(cmap='RdBu_r', vmin=-0.4, vmax=0.4)
>>> plt.pcolormesh(X_edges, Y_edges, ZI, shading='flat', **lims)
>>> plt.scatter(x, y, 100, z, edgecolor='w', lw=0.1, **lims)
>>> plt.title('RBF interpolation - multiquadrics')
>>> plt.xlim(-2, 2)
>>> plt.ylim(-2, 2)
>>> plt.colorbar()
```



2.6 Fourier Transforms (`scipy.fft`)

Contents

- *Fourier Transforms (`scipy.fft`)*
  - *Fast Fourier transforms*
    - *1-D discrete Fourier transforms*
    - *2- and N-D discrete Fourier transforms*
  - *Discrete Cosine Transforms*
    - *Type I DCT*
    - *Type II DCT*
    - *Type III DCT*
    - *Type IV DCT*
    - *DCT and IDCT*
    - *Example*
  - *Discrete Sine Transforms*
    - *Type I DST*
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    - *Type IV DST*
    - *DST and IDST*
  - *Fast Hankel Transform*
  - *References*

Fourier analysis is a method for expressing a function as a sum of periodic components, and for recovering the signal from those components. When both the function and its Fourier transform are replaced with discretized counterparts, it is called the discrete Fourier transform (DFT). The DFT has become a mainstay of numerical computing in part because of a very fast algorithm for computing it, called the Fast Fourier Transform (FFT), which was known to Gauss (1805) and was brought to light in its current form by Cooley and Tukey [CT65]. Press et al. [NR07] provide an accessible introduction to Fourier analysis and its applications.

2.6.1 Fast Fourier transforms

1-D discrete Fourier transforms

The FFT *y[k]* of length N of the length-N sequence *x[n]* is defined as

$$y[k] = \sum_{n=0}^{N-1} e^{-2\pi j \frac{kn}{N}} x[n] \,,$$

and the inverse transform is defined as follows

$$x[n] = \frac{1}{N} \sum_{k=0}^{N-1} e^{2\pi j \frac{kn}{N}} y[k] \,.$$

These transforms can be calculated by means of `fft` and `ifft`, respectively, as shown in the following example.

```
>>> from scipy.fft import fft, ifft
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> y = fft(x)
>>> y
array([ 4.5       +0.j        ,  2.08155948-1.65109876j,
       -1.83155948+1.60822041j, -1.83155948-1.60822041j,
        2.08155948+1.65109876j])
>>> yinv = ifft(y)
>>> yinv
array([ 1.0+0.j,  2.0+0.j,  1.0+0.j, -1.0+0.j,  1.5+0.j])
```

From the definition of the FFT it can be seen that

$$y[0] = \sum_{n=0}^{N-1} x[n] \,.$$

In the example

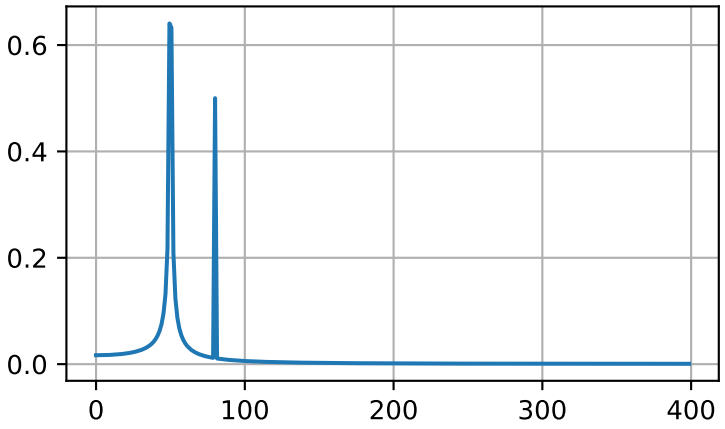
```
>>> np.sum(x)
4.5
```

which corresponds to $y[0]$. For N even, the elements $y[1]...y[N/2-1]$ contain the positive-frequency terms, and the elements $y[N/2]...y[N-1]$ contain the negative-frequency terms, in order of decreasingly negative frequency. For N odd, the elements $y[1]...y[(N-1)/2]$ contain the positive-frequency terms, and the elements $y[(N+1)/2]...y[N-1]$ contain the negative-frequency terms, in order of decreasingly negative frequency.

In case the sequence x is real-valued, the values of $y[n]$ for positive frequencies is the conjugate of the values $y[n]$ for negative frequencies (because the spectrum is symmetric). Typically, only the FFT corresponding to positive frequencies is plotted.

The example plots the FFT of the sum of two sines.

```
>>> from scipy.fft import fft, fftfreq
>>> # Number of sample points
>>> N = 600
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N, endpoint=False)
>>> y = np.sin(50.0 * 2.0*np.pi*x) + 0.5*np.sin(80.0 * 2.0*np.pi*x)
>>> yf = fft(y)
>>> xf = fftfreq(N, T)[:N//2]
>>> import matplotlib.pyplot as plt
>>> plt.plot(xf, 2.0/N * np.abs(yf[0:N//2]))
>>> plt.grid()
>>> plt.show()
```



The FFT input signal is inherently truncated. This truncation can be modeled as multiplication of an infinite signal with a rectangular window function. In the spectral domain this multiplication becomes convolution of the signal spectrum with the window function spectrum, being of form $\sin(x)/x$. This convolution is the cause of an effect called spectral leakage (see [WPW]). Windowing the signal with a dedicated window function helps mitigate spectral leakage. The example below uses a Blackman window from scipy.signal and shows the effect of windowing (the zero component of the FFT has been truncated for illustrative purposes).

```
>>> from scipy.fft import fft, fftfreq
>>> # Number of sample points
>>> N = 600
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N, endpoint=False)
>>> y = np.sin(50.0 * 2.0*np.pi*x) + 0.5*np.sin(80.0 * 2.0*np.pi*x)
>>> yf = fft(y)
>>> from scipy.signal import blackman
>>> w = blackman(N)
>>> ywf = fft(y*w)
>>> xf = fftfreq(N, T)[:N//2]
```

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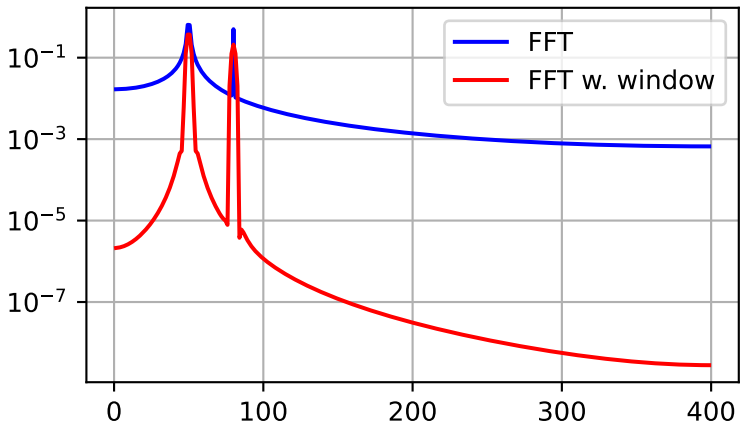
```
>>> import matplotlib.pyplot as plt
>>> plt.semilogy(xf[1:N//2], 2.0/N * np.abs(yf[1:N//2]), '-b')
>>> plt.semilogy(xf[1:N//2], 2.0/N * np.abs(ywf[1:N//2]), '-r')
>>> plt.legend(['FFT', 'FFT w. window'])
>>> plt.grid()
>>> plt.show()
```



In case the sequence x is complex-valued, the spectrum is no longer symmetric. To simplify working with the FFT functions, scipy provides the following two helper functions.

The function *fftfreq* returns the FFT sample frequency points.

```
>>> from scipy.fft import fftfreq
>>> freq = fftfreq(8, 0.125)
>>> freq
array([ 0., 1., 2., 3., -4., -3., -2., -1.])
```

In a similar spirit, the function *fftshift* allows swapping the lower and upper halves of a vector, so that it becomes suitable for display.

```
>>> from scipy.fft import fftshift
>>> x = np.arange(8)
>>> fftshift(x)
array([4, 5, 6, 7, 0, 1, 2, 3])
```

The example below plots the FFT of two complex exponentials; note the asymmetric spectrum.

```
>>> from scipy.fft import fft, fftfreq, fftshift
>>> # number of signal points
>>> N = 400
>>> # sample spacing
>>> T = 1.0 / 800.0
>>> x = np.linspace(0.0, N*T, N, endpoint=False)
>>> y = np.exp(50.0 * 1.j * 2.0*np.pi*x) + 0.5*np.exp(-80.0 * 1.j * 2.0*np.
↪pi*x)
```

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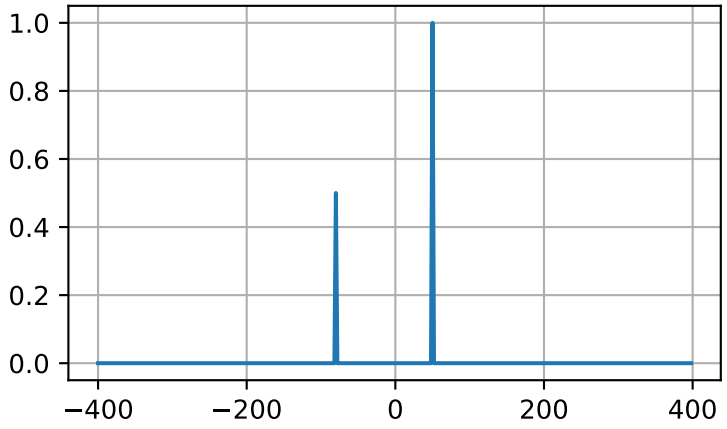
```
>>> yf = fft(y)
>>> xf = fftfreq(N, T)
>>> xf = fftshift(xf)
>>> yplot = fftshift(yf)
>>> import matplotlib.pyplot as plt
>>> plt.plot(xf, 1.0/N * np.abs(yplot))
>>> plt.grid()
>>> plt.show()
```



The function *rfft* calculates the FFT of a real sequence and outputs the complex FFT coefficients $y[n]$ for only half of the frequency range. The remaining negative frequency components are implied by the Hermitian symmetry of the FFT for a real input (`y[n] = conj(y[-n])`). In case of N being even: $[Re(y[0]) + 0j, y[1], ..., Re(y[N/2]) + 0j]$; in case of N being odd $[Re(y[0]) + 0j, y[1], ..., y[N/2]$. The terms shown explicitly as $Re(y[k]) + 0j$ are restricted to be purely real since, by the hermitian property, they are their own complex conjugate.

The corresponding function *irfft* calculates the IFFT of the FFT coefficients with this special ordering.

```
>>> from scipy.fft import fft, rfft, irfft
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5, 1.0])
>>> fft(x)
array([ 5.5 +0.j        ,  2.25-0.4330127j , -2.75-1.29903811j,
        1.5 +0.j        , -2.75+1.29903811j,  2.25+0.4330127j ])
>>> yr = rfft(x)
>>> yr
array([ 5.5 +0.j        ,  2.25-0.4330127j , -2.75-1.29903811j,
        1.5 +0.j        ])
>>> irfft(yr)
array([ 1. ,  2. ,  1. , -1. ,  1.5,  1. ])
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
>>> fft(x)
array([ 4.5       +0.j        ,  2.08155948-1.65109876j,
       -1.83155948+1.60822041j, -1.83155948-1.60822041j,
        2.08155948+1.65109876j])
```

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```
>>> yr = rfft(x)
>>> yr
array([ 4.5       +0.j        ,  2.08155948-1.65109876j,
       -1.83155948+1.60822041j])
```

Notice that the *rfft* of odd and even length signals are of the same shape. By default, *irfft* assumes the output signal should be of even length. And so, for odd signals, it will give the wrong result:

```
>>> irfft(yr)
array([ 1.70788987,  2.40843925, -0.37366961,  0.75734049])
```

To recover the original odd-length signal, we **must** pass the output shape by the *n* parameter.

```
>>> irfft(yr, n=len(x))
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

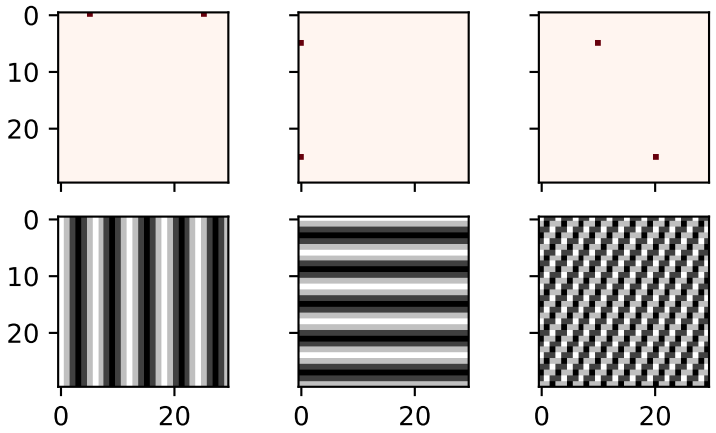
2- and N-D discrete Fourier transforms

The functions *fft2* and *ifft2* provide 2-D FFT and IFFT, respectively. Similarly, *fftn* and *ifftn* provide N-D FFT, and IFFT, respectively.

For real-input signals, similarly to *rfft*, we have the functions *rfft2* and *irfft2* for 2-D real transforms; *rfftn* and *irfftn* for N-D real transforms.

The example below demonstrates a 2-D IFFT and plots the resulting (2-D) time-domain signals.

```
>>> from scipy.fft import ifftn
>>> import matplotlib.pyplot as plt
>>> import matplotlib.cm as cm
>>> N = 30
>>> f, ((ax1, ax2, ax3), (ax4, ax5, ax6)) = plt.subplots(2, 3, sharex='col',␣
↪sharey='row')
>>> xf = np.zeros((N,N))
>>> xf[0, 5] = 1
>>> xf[0, N-5] = 1
>>> Z = ifftn(xf)
>>> ax1.imshow(xf, cmap=cm.Reds)
>>> ax4.imshow(np.real(Z), cmap=cm.gray)
>>> xf = np.zeros((N, N))
>>> xf[5, 0] = 1
>>> xf[N-5, 0] = 1
>>> Z = ifftn(xf)
>>> ax2.imshow(xf, cmap=cm.Reds)
>>> ax5.imshow(np.real(Z), cmap=cm.gray)
>>> xf = np.zeros((N, N))
>>> xf[5, 10] = 1
>>> xf[N-5, N-10] = 1
>>> Z = ifftn(xf)
>>> ax3.imshow(xf, cmap=cm.Reds)
>>> ax6.imshow(np.real(Z), cmap=cm.gray)
>>> plt.show()
```



2.6.2 Discrete Cosine Transforms

SciPy provides a DCT with the function `dct` and a corresponding IDCT with the function `idct`. There are 8 types of the DCT [WPC], [Mak]; however, only the first 4 types are implemented in scipy. "The" DCT generally refers to DCT type 2, and "the" Inverse DCT generally refers to DCT type 3. In addition, the DCT coefficients can be normalized differently (for most types, scipy provides `None` and `ortho`). Two parameters of the dct/idct function calls allow setting the DCT type and coefficient normalization.

For a single dimension array x, dct(x, norm='ortho') is equal to MATLAB dct(x).

Type I DCT

SciPy uses the following definition of the unnormalized DCT-I (`norm=None`):

$$y[k] = x_0 + (-1)^k x_{N-1} + 2\sum_{n=1}^{N-2} x[n] \cos\left(\frac{\pi nk}{N-1}\right), \qquad 0 \le k < N.$$

Note that the DCT-I is only supported for input size > 1.

Type II DCT

SciPy uses the following definition of the unnormalized DCT-II (`norm=None`):

$$y[k] = 2\sum_{n=0}^{N-1} x[n] \cos\left(\frac{\pi(2n+1)k}{2N}\right) \qquad 0 \le k < N.$$

In case of the normalized DCT (`norm='ortho'`), the DCT coefficients $y[k]$ are multiplied by a scaling factor f:

$$f = \begin{cases} \sqrt{1/(4N)}, & \text{if } k = 0 \\ \sqrt{1/(2N)}, & \text{otherwise} \end{cases}.$$

In this case, the DCT "base functions" $\phi_k[n] = 2f \cos\left(\frac{\pi(2n+1)k}{2N}\right)$ become orthonormal:

$$\sum_{n=0}^{N-1} \phi_k[n]\phi_l[n] = \delta_{lk}.$$

Type III DCT

SciPy uses the following definition of the unnormalized DCT-III (`norm=None`):

$$y[k] = x_0 + 2\sum_{n=1}^{N-1} x[n]\cos\left(\frac{\pi n(2k+1)}{2N}\right) \qquad 0 \le k < N,$$

or, for `norm='ortho'`:

$$y[k] = \frac{x_0}{\sqrt{N}} + \frac{2}{\sqrt{N}}\sum_{n=1}^{N-1} x[n]\cos\left(\frac{\pi n(2k+1)}{2N}\right) \qquad 0 \le k < N.$$

Type IV DCT

SciPy uses the following definition of the unnormalized DCT-IV (`norm=None`):

$$y[k] = 2\sum_{n=0}^{N-1} x[n]\cos\left(\frac{\pi(2n+1)(2k+1)}{4N}\right) \qquad 0 \le k < N,$$

or, for `norm='ortho'`:

$$y[k] = \sqrt{\frac{2}{N}}\sum_{n=0}^{N-1} x[n]\cos\left(\frac{\pi(2n+1)(2k+1)}{4N}\right) \qquad 0 \le k < N$$

DCT and IDCT

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor of *2N*. The orthonormalized DCT-III is exactly the inverse of the orthonormalized DCT- II. The function *idct* performs the mappings between the DCT and IDCT types, as well as the correct normalization.

The following example shows the relation between DCT and IDCT for different types and normalizations.

```
>>> from scipy.fft import dct, idct
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
```

The DCT-II and DCT-III are each other's inverses, so for an orthonormal transform we return back to the original signal.

```
>>> dct(dct(x, type=2, norm='ortho'), type=3, norm='ortho')
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

Doing the same under default normalization, however, we pick up an extra scaling factor of $2N = 10$ since the forward transform is unnormalized.

```
>>> dct(dct(x, type=2), type=3)
array([ 10.,  20.,  10., -10.,  15.])
```

For this reason, we should use the function *idct* using the same type for both, giving a correctly normalized result.

```
>>> # Normalized inverse: no scaling factor
>>> idct(dct(x, type=2), type=2)
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

Analogous results can be seen for the DCT-I, which is its own inverse up to a factor of $2(N-1)$.

```
>>> dct(dct(x, type=1, norm='ortho'), type=1, norm='ortho')
array([ 1. ,  2. ,  1. , -1. ,  1.5])
>>> # Unnormalized round-trip via DCT-I: scaling factor 2*(N-1) = 8
>>> dct(dct(x, type=1), type=1)
array([ 8. ,  16.,  8. , -8. ,  12.])
>>> # Normalized inverse: no scaling factor
>>> idct(dct(x, type=1), type=1)
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

And for the DCT-IV, which is also its own inverse up to a factor of $2N$.

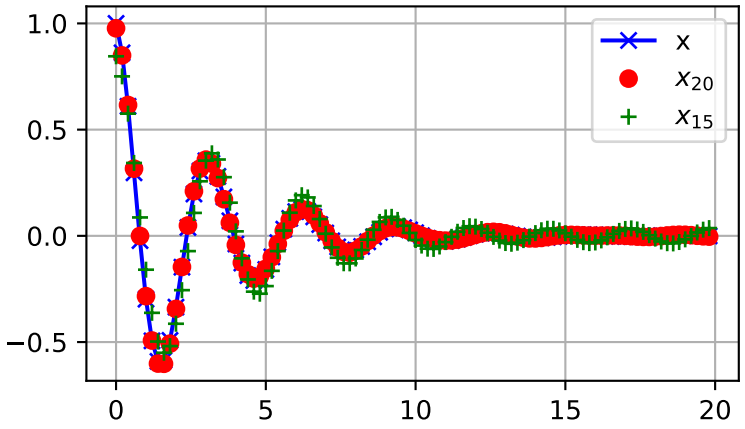
```
>>> dct(dct(x, type=4, norm='ortho'), type=4, norm='ortho')
array([ 1. ,  2. ,  1. , -1. ,  1.5])
>>> # Unnormalized round-trip via DCT-IV: scaling factor 2*N = 10
>>> dct(dct(x, type=4), type=4)
array([ 10.,  20.,  10., -10.,  15.])
>>> # Normalized inverse: no scaling factor
>>> idct(dct(x, type=4), type=4)
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

Example

The DCT exhibits the "energy compaction property", meaning that for many signals only the first few DCT coefficients have significant magnitude. Zeroing out the other coefficients leads to a small reconstruction error, a fact which is exploited in lossy signal compression (e.g. JPEG compression).

The example below shows a signal x and two reconstructions (x_{20} and x_{15}) from the signal's DCT coefficients. The signal x_{20} is reconstructed from the first 20 DCT coefficients, x_{15} is reconstructed from the first 15 DCT coefficients. It can be seen that the relative error of using 20 coefficients is still very small (~0.1%), but provides a five-fold compression rate.

```
>>> from scipy.fft import dct, idct
>>> import matplotlib.pyplot as plt
>>> N = 100
>>> t = np.linspace(0,20,N, endpoint=False)
>>> x = np.exp(-t/3)*np.cos(2*t)
>>> y = dct(x, norm='ortho')
>>> window = np.zeros(N)
>>> window[:20] = 1
>>> yr = idct(y*window, norm='ortho')
>>> sum(abs(x-yr)**2) / sum(abs(x)**2)
0.0009872817275276098
>>> plt.plot(t, x, '-bx')
>>> plt.plot(t, yr, 'ro')
>>> window = np.zeros(N)
>>> window[:15] = 1
>>> yr = idct(y*window, norm='ortho')
>>> sum(abs(x-yr)**2) / sum(abs(x)**2)
0.06196643004256714
>>> plt.plot(t, yr, 'g+')
>>> plt.legend(['x', '$x_{20}$', '$x_{15}$'])
>>> plt.grid()
>>> plt.show()
```



2.6.3 Discrete Sine Transforms

SciPy provides a DST [Mak] with the function `dst` and a corresponding IDST with the function `idst`.

There are, theoretically, 8 types of the DST for different combinations of even/odd boundary conditions and boundary offsets [WPS], only the first 4 types are implemented in scipy.

Type I DST

DST-I assumes the input is odd around n=-1 and n=N. SciPy uses the following definition of the unnormalized DST-I (`norm=None`):

$$y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin\left(\frac{\pi(n+1)(k+1)}{N+1}\right), \qquad 0 \le k < N.$$

Note also that the DST-I is only supported for input size > 1. The (unnormalized) DST-I is its own inverse, up to a factor of *2(N+1)*.

Type II DST

DST-II assumes the input is odd around n=-1/2 and even around n=N. SciPy uses the following definition of the unnormalized DST-II (`norm=None`):

$$y[k] = 2 \sum_{n=0}^{N-1} x[n] \sin\left(\frac{\pi(n+1/2)(k+1)}{N}\right), \qquad 0 \le k < N.$$

Type III DST

DST-III assumes the input is odd around n=-1 and even around n=N-1. SciPy uses the following definition of the unnormalized DST-III (`norm=None`):

$$y[k] = (-1)^k x[N-1] + 2\sum_{n=0}^{N-2} x[n] \sin\left(\frac{\pi(n+1)(k+1/2)}{N}\right), \qquad 0 \le k < N.$$

Type IV DST

SciPy uses the following definition of the unnormalized DST-IV (`norm=None`):

$$y[k] = 2\sum_{n=0}^{N-1} x[n] \sin\left(\frac{\pi(2n+1)(2k+1)}{4N}\right) \qquad 0 \le k < N,$$

or, for `norm='ortho'`:

$$y[k] = \sqrt{\frac{2}{N}}\sum_{n=0}^{N-1} x[n] \sin\left(\frac{\pi(2n+1)(2k+1)}{4N}\right) \qquad 0 \le k < N,$$

DST and IDST

The following example shows the relation between DST and IDST for different types and normalizations.

```
>>> from scipy.fft import dst, idst
>>> x = np.array([1.0, 2.0, 1.0, -1.0, 1.5])
```

The DST-II and DST-III are each other's inverses, so for an orthonormal transform we return back to the original signal.

```
>>> dst(dst(x, type=2, norm='ortho'), type=3, norm='ortho')
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

Doing the same under default normalization, however, we pick up an extra scaling factor of $2N = 10$ since the forward transform is unnormalized.

```
>>> dst(dst(x, type=2), type=3)
array([ 10.,  20.,  10., -10.,  15.])
```

For this reason, we should use the function *idst* using the same type for both, giving a correctly normalized result.

```
>>> idst(dst(x, type=2), type=2)
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

Analogous results can be seen for the DST-I, which is its own inverse up to a factor of $2(N-1)$.

```
>>> dst(dst(x, type=1, norm='ortho'), type=1, norm='ortho')
array([ 1. ,  2. ,  1. , -1. ,  1.5])
>>>  # scaling factor 2*(N+1) = 12
>>> dst(dst(x, type=1), type=1)
array([ 12.,  24.,  12., -12.,  18.])
>>>  # no scaling factor
>>> idst(dst(x, type=1), type=1)
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

And for the DST-IV, which is also its own inverse up to a factor of $2N$.

```
>>> dst(dst(x, type=4, norm='ortho'), type=4, norm='ortho')
array([ 1. ,  2. ,  1. , -1. ,  1.5])
>>>  # scaling factor 2*N = 10
>>> dst(dst(x, type=4), type=4)
array([ 10.,  20.,  10., -10.,  15.])
>>>  # no scaling factor
>>> idst(dst(x, type=4), type=4)
array([ 1. ,  2. ,  1. , -1. ,  1.5])
```

2.6.4 Fast Hankel Transform

SciPy provides the functions `fht` and `ifht` to perform the Fast Hankel Transform (FHT) and its inverse (IFHT) on logarithmically-spaced input arrays.

The FHT is the discretised version of the continuous Hankel transform defined by [Ham00]

$$A(k) = \int_0^\infty a(r)\, J_\mu(kr)\, k\, dr \;,$$

with J_μ the Bessel function of order μ. Under a change of variables $r \to \log r$, $k \to \log k$, this becomes

$$A(e^{\log k}) = \int_0^\infty a(e^{\log r})\, J_\mu(e^{\log k + \log r})\, e^{\log k + \log r}\, d\log r$$

which is a convolution in logarithmic space. The FHT algorithm uses the FFT to perform this convolution on discrete input data.

Care must be taken to minimise numerical ringing due to the circular nature of FFT convolution. To ensure that the low-ringing condition [Ham00] holds, the output array can be slightly shifted by an offset computed using the `fhtoffset` function.

2.6.5 References

2.7 Signal Processing (`scipy.signal`)

The signal processing toolbox currently contains some filtering functions, a limited set of filter design tools, and a few B-spline interpolation algorithms for 1- and 2-D data. While the B-spline algorithms could technically be placed under the interpolation category, they are included here because they only work with equally-spaced data and make heavy use of filter-theory and transfer-function formalism to provide a fast B-spline transform. To understand this section, you will need to understand that a signal in SciPy is an array of real or complex numbers.

2.7.1 B-splines

A B-spline is an approximation of a continuous function over a finite- domain in terms of B-spline coefficients and knot points. If the knot- points are equally spaced with spacing Δx, then the B-spline approximation to a 1-D function is the finite-basis expansion.

$$y\,(x) \approx \sum_j c_j \beta^o \left(\frac{x}{\Delta x} - j\right).$$

In two dimensions with knot-spacing Δx and Δy, the function representation is

$$z(x,y) \approx \sum_j \sum_k c_{jk} \beta^o \left(\frac{x}{\Delta x} - j \right) \beta^o \left(\frac{y}{\Delta y} - k \right).$$

In these expressions, $\beta^o(\cdot)$ is the space-limited B-spline basis function of order o. The requirement of equally-spaced knot-points and equally-spaced data points, allows the development of fast (inverse-filtering) algorithms for determining the coefficients, c_j, from sample-values, y_n. Unlike the general spline interpolation algorithms, these algorithms can quickly find the spline coefficients for large images.

The advantage of representing a set of samples via B-spline basis functions is that continuous-domain operators (derivatives, re- sampling, integral, etc.), which assume that the data samples are drawn from an underlying continuous function, can be computed with relative ease from the spline coefficients. For example, the second derivative of a spline is

$$y''(x) = \frac{1}{\Delta x^2} \sum_j c_j \beta^{o\prime\prime} \left(\frac{x}{\Delta x} - j \right).$$

Using the property of B-splines that

$$\frac{d^2 \beta^o(w)}{dw^2} = \beta^{o-2}(w+1) - 2\beta^{o-2}(w) + \beta^{o-2}(w-1),$$

it can be seen that

$$y''(x) = \frac{1}{\Delta x^2} \sum_j c_j \left[\beta^{o-2} \left(\frac{x}{\Delta x} - j + 1 \right) - 2\beta^{o-2} \left(\frac{x}{\Delta x} - j \right) + \beta^{o-2} \left(\frac{x}{\Delta x} - j - 1 \right) \right].$$

If $o = 3$, then at the sample points:

$$\begin{aligned} \Delta x^2 \, y'(x)|_{x=n\Delta x} &= \sum_j c_j \delta_{n-j+1} - 2c_j \delta_{n-j} + c_j \delta_{n-j-1}, \\ &= c_{n+1} - 2c_n + c_{n-1}. \end{aligned}$$

Thus, the second-derivative signal can be easily calculated from the spline fit. If desired, smoothing splines can be found to make the second derivative less sensitive to random errors.

The savvy reader will have already noticed that the data samples are related to the knot coefficients via a convolution operator, so that simple convolution with the sampled B-spline function recovers the original data from the spline coefficients. The output of convolutions can change depending on how the boundaries are handled (this becomes increasingly more important as the number of dimensions in the dataset increases). The algorithms relating to B-splines in the signal-processing subpackage assume mirror-symmetric boundary conditions. Thus, spline coefficients are computed based on that assumption, and data-samples can be recovered exactly from the spline coefficients by assuming them to be mirror-symmetric also.

Currently the package provides functions for determining second- and third- order cubic spline coefficients from equally-spaced samples in one and two dimensions (`qspline1d`, `qspline2d`, `cspline1d`, `cspline2d`). The package also supplies a function (`bspline`) for evaluating the B-spline basis function, $\beta^o(x)$ for arbitrary order and x. For large o, the B-spline basis function can be approximated well by a zero-mean Gaussian function with standard-deviation equal to $\sigma_o = (o+1)/12$:

$$\beta^o(x) \approx \frac{1}{\sqrt{2\pi\sigma_o^2}} \exp\left(-\frac{x^2}{2\sigma_o} \right).$$

A function to compute this Gaussian for arbitrary x and o is also available (`gauss_spline`). The following code and figure use spline-filtering to compute an edge-image (the second derivative of a smoothed spline) of a raccoon's face, which is an array returned by the command `scipy.misc.face`. The command `sepfir2d` was used to apply a separable 2-D FIR filter with mirror-symmetric boundary conditions to the spline coefficients. This function is ideally-suited for reconstructing samples from spline coefficients and is faster than `convolve2d`, which convolves arbitrary 2-D filters and allows for choosing mirror-symmetric boundary conditions.

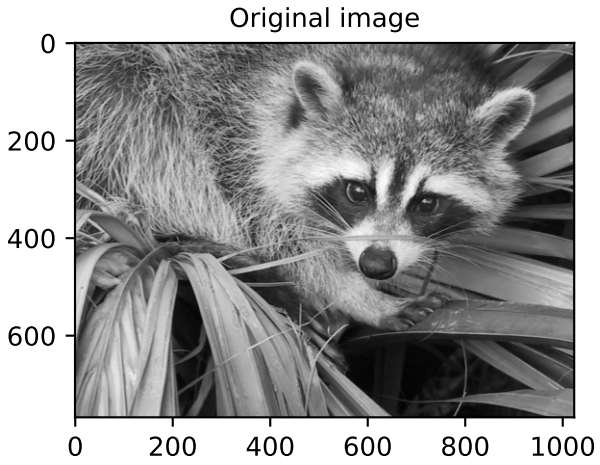
```
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt
```

```
>>> image = misc.face(gray=True).astype(np.float32)
>>> derfilt = np.array([1.0, -2, 1.0], dtype=np.float32)
>>> ck = signal.cspline2d(image, 8.0)
>>> deriv = (signal.sepfir2d(ck, derfilt, [1]) +
...          signal.sepfir2d(ck, [1], derfilt))
```

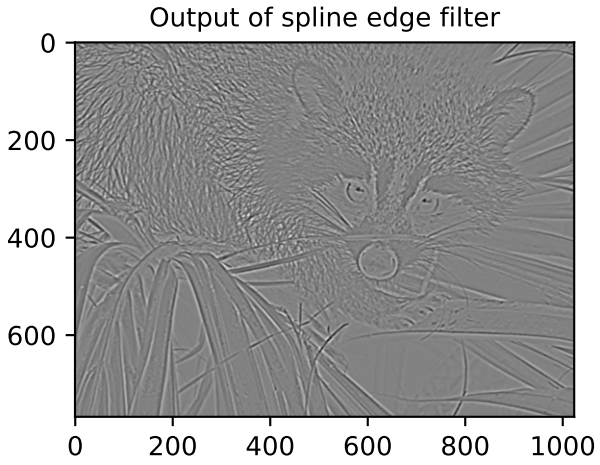
Alternatively, we could have done:

```
laplacian = np.array([[0,1,0], [1,-4,1], [0,1,0]], dtype=np.float32)
deriv2 = signal.convolve2d(ck,laplacian,mode='same',boundary='symm')
```

```
>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()
```




```
>>> plt.figure()
>>> plt.imshow(deriv)
>>> plt.gray()
>>> plt.title('Output of spline edge filter')
>>> plt.show()
```



2.7.2 Filtering

Filtering is a generic name for any system that modifies an input signal in some way. In SciPy, a signal can be thought of as a NumPy array. There are different kinds of filters for different kinds of operations. There are two broad kinds of filtering operations: linear and non-linear. Linear filters can always be reduced to multiplication of the flattened NumPy array by an appropriate matrix resulting in another flattened NumPy array. Of course, this is not usually the best way to compute the filter, as the matrices and vectors involved may be huge. For example, filtering a 512×512 image with this method would require multiplication of a $512^2 \times 512^2$ matrix with a 512^2 vector. Just trying to store the $512^2 \times 512^2$ matrix using a standard NumPy array would require $68,719,476,736$ elements. At 4 bytes per element this would require 256GB of memory. In most applications, most of the elements of this matrix are zero and a different method for computing the output of the filter is employed.

Convolution/Correlation

Many linear filters also have the property of shift-invariance. This means that the filtering operation is the same at different locations in the signal and it implies that the filtering matrix can be constructed from knowledge of one row (or column) of the matrix alone. In this case, the matrix multiplication can be accomplished using Fourier transforms.

Let $x[n]$ define a 1-D signal indexed by the integer n. Full convolution of two 1-D signals can be expressed as

$$y[n] = \sum_{k=-\infty}^{\infty} x[k]\, h[n-k].$$

This equation can only be implemented directly if we limit the sequences to finite-support sequences that can be stored in a computer, choose $n = 0$ to be the starting point of both sequences, let $K + 1$ be that value for which $x[n] = 0$ for all $n \geq K + 1$ and $M + 1$ be that value for which $h[n] = 0$ for all $n \geq M + 1$, then the discrete convolution expression is

$$y[n] = \sum_{k=\max(n-M,0)}^{\min(n,K)} x[k]\, h[n-k].$$

For convenience, assume $K \geq M$. Then, more explicitly, the output of this operation is

$$\begin{aligned}
y[0] &= x[0]\,h[0] \\
y[1] &= x[0]\,h[1] + x[1]\,h[0] \\
y[2] &= x[0]\,h[2] + x[1]\,h[1] + x[2]\,h[0] \\
&\vdots \\
y[M] &= x[0]\,h[M] + x[1]\,h[M-1] + \cdots + x[M]\,h[0] \\
y[M+1] &= x[1]\,h[M] + x[2]\,h[M-1] + \cdots + x[M+1]\,h[0] \\
&\vdots \\
y[K] &= x[K-M]\,h[M] + \cdots + x[K]\,h[0] \\
y[K+1] &= x[K+1-M]\,h[M] + \cdots + x[K]\,h[1] \\
&\vdots \\
y[K+M-1] &= x[K-1]\,h[M] + x[K]\,h[M-1] \\
y[K+M] &= x[K]\,h[M]\,.
\end{aligned}$$

Thus, the full discrete convolution of two finite sequences of lengths $K+1$ and $M+1$, respectively, results in a finite sequence of length $K+M+1 = (K+1)+(M+1)-1$.

1-D convolution is implemented in SciPy with the function `convolve`. This function takes as inputs the signals x, h, and two optional flags 'mode' and 'method', and returns the signal y.

The first optional flag, 'mode', allows for the specification of which part of the output signal to return. The default value of 'full' returns the entire signal. If the flag has a value of 'same', then only the middle K values are returned, starting at $y\left[\left\lfloor \frac{M-1}{2} \right\rfloor\right]$, so that the output has the same length as the first input. If the flag has a value of 'valid', then only the middle $K-M+1 = (K+1)-(M+1)+1$ output values are returned, where z depends on all of the values of the smallest input from $h[0]$ to $h[M]$. In other words, only the values $y[M]$ to $y[K]$ inclusive are returned.

The second optional flag, 'method', determines how the convolution is computed, either through the Fourier transform approach with `fftconvolve` or through the direct method. By default, it selects the expected faster method. The Fourier transform method has order $O(N \log N)$, while the direct method has order $O(N^2)$. Depending on the big O constant and the value of N, one of these two methods may be faster. The default value, 'auto', performs a rough calculation and chooses the expected faster method, while the values 'direct' and 'fft' force computation with the other two methods.

The code below shows a simple example for convolution of 2 sequences:

```
>>> x = np.array([1.0, 2.0, 3.0])
>>> h = np.array([0.0, 1.0, 0.0, 0.0, 0.0])
>>> signal.convolve(x, h)
array([ 0.,  1.,  2.,  3.,  0.,  0.,  0.])
>>> signal.convolve(x, h, 'same')
array([ 2.,  3.,  0.])
```

This same function `convolve` can actually take N-D arrays as inputs and will return the N-D convolution of the two arrays, as is shown in the code example below. The same input flags are available for that case as well.

```
>>> x = np.array([[1., 1., 0., 0.], [1., 1., 0., 0.], [0., 0., 0., 0.], [0.,␣
↪0., 0., 0.]])
>>> h = np.array([[1., 0., 0., 0.], [0., 0., 0., 0.], [0., 0., 1., 0.], [0.,␣
↪0., 0., 0.]])
>>> signal.convolve(x, h)
array([[ 1.,  1.,  0.,  0.,  0.,  0.,  0.],
```

(continues on next page)

(continued from previous page)

```
       [ 1.,  1.,  0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  1.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  1.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.,  0.,  0.]])
```

Correlation is very similar to convolution except that the minus sign becomes a plus sign. Thus,

$$w[n] = \sum_{k=-\infty}^{\infty} y[k]\, x[n+k],$$

is the (cross) correlation of the signals y and x. For finite-length signals with $y[n] = 0$ outside of the range $[0, K]$ and $x[n] = 0$ outside of the range $[0, M]$, the summation can simplify to

$$w[n] = \sum_{k=\max(0,-n)}^{\min(K,M-n)} y[k]\, x[n+k].$$

Assuming again that $K \geq M$, this is

$$\begin{aligned}
w[-K] &= y[K]\, x[0] \\
w[-K+1] &= y[K-1]\, x[0] + y[K]\, x[1] \\
&\vdots \quad \vdots \quad \vdots \\
w[M-K] &= y[K-M]\, x[0] + y[K-M+1]\, x[1] + \cdots + y[K]\, x[M] \\
w[M-K+1] &= y[K-M-1]\, x[0] + \cdots + y[K-1]\, x[M] \\
&\vdots \quad \vdots \quad \vdots \\
w[-1] &= y[1]\, x[0] + y[2]\, x[1] + \cdots + y[M+1]\, x[M] \\
w[0] &= y[0]\, x[0] + y[1]\, x[1] + \cdots + y[M]\, x[M] \\
w[1] &= y[0]\, x[1] + y[1]\, x[2] + \cdots + y[M-1]\, x[M] \\
w[2] &= y[0]\, x[2] + y[1]\, x[3] + \cdots + y[M-2]\, x[M] \\
&\vdots \quad \vdots \quad \vdots \\
w[M-1] &= y[0]\, x[M-1] + y[1]\, x[M] \\
w[M] &= y[0]\, x[M].
\end{aligned}$$

The SciPy function *correlate* implements this operation. Equivalent flags are available for this operation to return the full $K + M + 1$ length sequence ('full') or a sequence with the same size as the largest sequence starting at $w\left[-K + \left\lfloor \frac{M-1}{2} \right\rfloor\right]$ ('same') or a sequence where the values depend on all the values of the smallest sequence ('valid'). This final option returns the $K - M + 1$ values $w[M-K]$ to $w[0]$ inclusive.

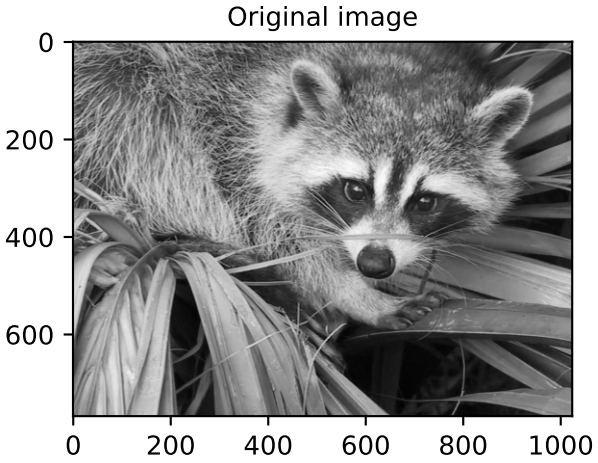
The function *correlate* can also take arbitrary N-D arrays as input and return the N-D convolution of the two arrays on output.

When $N = 2$, *correlate* and/or *convolve* can be used to construct arbitrary image filters to perform actions such as blurring, enhancing, and edge-detection for an image.

```
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt
```

```
>>> image = misc.face(gray=True)
>>> w = np.zeros((50, 50))
>>> w[0][0] = 1.0
>>> w[49][25] = 1.0
>>> image_new = signal.fftconvolve(image, w)
```

```
>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()
```




```
>>> plt.figure()
>>> plt.imshow(image_new)
>>> plt.gray()
>>> plt.title('Filtered image')
>>> plt.show()
```

Calculating the convolution in the time domain as above is mainly used for filtering when one of the signals is much smaller than the other ($K \gg M$), otherwise linear filtering is more efficiently calculated in the frequency domain provided by the function *fftconvolve*. By default, *convolve* estimates the fastest method using *choose_conv_method*.

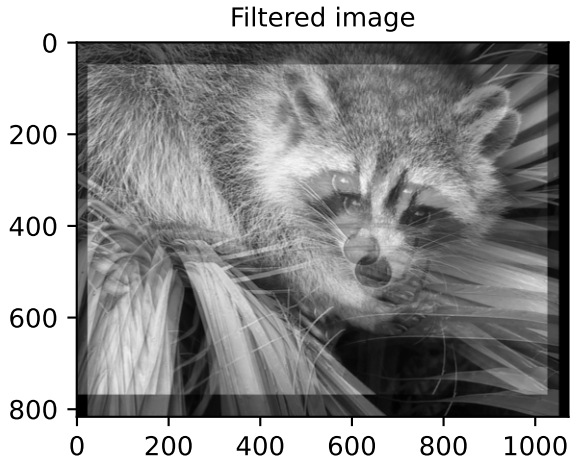
If the filter function $w[n, m]$ can be factored according to

$$h[n, m] = h_1[n]h_2[m],$$

convolution can be calculated by means of the function *sepfir2d*. As an example, we consider a Gaussian filter `gaussian`

$$h[n, m] \propto e^{-x^2-y^2} = e^{-x^2}e^{-y^2},$$

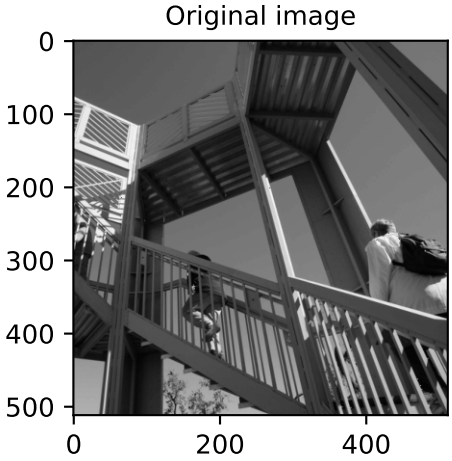
which is often used for blurring.



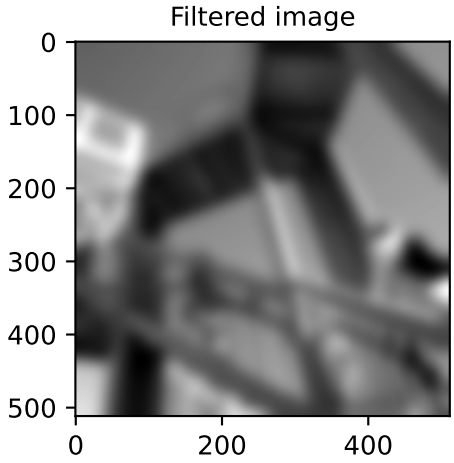

```
>>> import numpy as np
>>> from scipy import signal, misc
>>> import matplotlib.pyplot as plt
```

```
>>> image = misc.ascent()
>>> w = signal.windows.gaussian(51, 10.0)
>>> image_new = signal.sepfir2d(image, w, w)
```

```
>>> plt.figure()
>>> plt.imshow(image)
>>> plt.gray()
>>> plt.title('Original image')
>>> plt.show()
```



```
>>> plt.figure()
>>> plt.imshow(image_new)
>>> plt.gray()
>>> plt.title('Filtered image')
>>> plt.show()
```



Difference-equation filtering

A general class of linear 1-D filters (that includes convolution filters) are filters described by the difference equation

$$\sum_{k=0}^{N} a_k y\left[n-k\right] = \sum_{k=0}^{M} b_k x\left[n-k\right],$$

where $x\left[n\right]$ is the input sequence and $y\left[n\right]$ is the output sequence. If we assume initial rest so that $y\left[n\right] = 0$ for $n < 0$, then this kind of filter can be implemented using convolution. However, the convolution filter sequence $h\left[n\right]$ could be infinite if $a_k \neq 0$ for $k \geq 1$. In addition, this general class of linear filter allows initial conditions to be placed on $y\left[n\right]$ for $n < 0$ resulting in a filter that cannot be expressed using convolution.

The difference equation filter can be thought of as finding $y\left[n\right]$ recursively in terms of its previous values

$$a_0 y\left[n\right] = -a_1 y\left[n-1\right] - \cdots - a_N y\left[n-N\right] + \cdots + b_0 x\left[n\right] + \cdots + b_M x\left[n-M\right].$$

Often, $a_0 = 1$ is chosen for normalization. The implementation in SciPy of this general difference equation filter is a little more complicated than would be implied by the previous equation. It is implemented so that only one signal needs to be delayed. The actual implementation equations are (assuming $a_0 = 1$):

$$\begin{aligned}
y\left[n\right] &= b_0 x\left[n\right] + z_0\left[n-1\right] \\
z_0\left[n\right] &= b_1 x\left[n\right] + z_1\left[n-1\right] - a_1 y\left[n\right] \\
z_1\left[n\right] &= b_2 x\left[n\right] + z_2\left[n-1\right] - a_2 y\left[n\right] \\
&\vdots \quad \vdots \quad \vdots \\
z_{K-2}\left[n\right] &= b_{K-1} x\left[n\right] + z_{K-1}\left[n-1\right] - a_{K-1} y\left[n\right] \\
z_{K-1}\left[n\right] &= b_K x\left[n\right] - a_K y\left[n\right],
\end{aligned}$$

where $K = \max(N, M)$. Note that $b_K = 0$ if $K > M$ and $a_K = 0$ if $K > N$. In this way, the output at time n depends only on the input at time n and the value of z_0 at the previous time. This can always be calculated as long as the K values $z_0[n-1] \ldots z_{K-1}[n-1]$ are computed and stored at each time step.

The difference-equation filter is called using the command `lfilter` in SciPy. This command takes as inputs the vector b, the vector, a, a signal x and returns the vector y (the same length as x) computed using the equation given above. If x is N-D, then the filter is computed along the axis provided. If desired, initial conditions providing the values of $z_0[-1]$ to $z_{K-1}[-1]$ can be provided or else it will be assumed that they are all zero. If initial conditions are provided, then the final conditions on the intermediate variables are also returned. These could be used, for example, to restart the calculation in the same state.

Sometimes, it is more convenient to express the initial conditions in terms of the signals $x[n]$ and $y[n]$. In other words, perhaps you have the values of $x[-M]$ to $x[-1]$ and the values of $y[-N]$ to $y[-1]$ and would like to determine what values of $z_m[-1]$ should be delivered as initial conditions to the difference-equation filter. It is not difficult to show that, for $0 \leq m < K$,

$$z_m[n] = \sum_{p=0}^{K-m-1} \left(b_{m+p+1} x[n-p] - a_{m+p+1} y[n-p] \right).$$

Using this formula, we can find the initial-condition vector $z_0[-1]$ to $z_{K-1}[-1]$ given initial conditions on y (and x). The command `lfiltic` performs this function.

As an example, consider the following system:

$$y[n] = \frac{1}{2}x[n] + \frac{1}{4}x[n-1] + \frac{1}{3}y[n-1]$$

The code calculates the signal $y[n]$ for a given signal $x[n]$; first for initial conditions $y[-1] = 0$ (default case), then for $y[-1] = 2$ by means of `lfiltic`.

```
>>> import numpy as np
>>> from scipy import signal
```

```
>>> x = np.array([1., 0., 0., 0.])
>>> b = np.array([1.0/2, 1.0/4])
>>> a = np.array([1.0, -1.0/3])
>>> signal.lfilter(b, a, x)
array([0.5, 0.41666667, 0.13888889, 0.0462963])
>>> zi = signal.lfiltic(b, a, y=[2.])
>>> signal.lfilter(b, a, x, zi=zi)
(array([ 1.16666667,  0.63888889,  0.21296296,  0.07098765]), array([0.
↪02366]))
```

Note that the output signal $y[n]$ has the same length as the length as the input signal $x[n]$.

Analysis of Linear Systems

Linear system described a linear-difference equation can be fully described by the coefficient vectors a and b as was done above; an alternative representation is to provide a factor k, N_z zeros z_k and N_p poles p_k, respectively, to describe the system by means of its transfer function $H(z)$, according to

$$H(z) = k \frac{(z - z_1)(z - z_2)...(z - z_{N_z})}{(z - p_1)(z - p_2)...(z - p_{N_p})}.$$

This alternative representation can be obtained with the scipy function `tf2zpk`; the inverse is provided by `zpk2tf`.

For the above example we have

```
>>> b = np.array([1.0/2, 1.0/4])
>>> a = np.array([1.0, -1.0/3])
>>> signal.tf2zpk(b, a)
(array([-0.5]), array([ 0.33333333]), 0.5)
```

i.e., the system has a zero at $z = -1/2$ and a pole at $z = 1/3$.

The scipy function *freqz* allows calculation of the frequency response of a system described by the coefficients a_k and b_k. See the help of the *freqz* function for a comprehensive example.

Filter Design

Time-discrete filters can be classified into finite response (FIR) filters and infinite response (IIR) filters. FIR filters can provide a linear phase response, whereas IIR filters cannot. SciPy provides functions for designing both types of filters.

FIR Filter

The function *firwin* designs filters according to the window method. Depending on the provided arguments, the function returns different filter types (e.g., low-pass, band-pass…).

The example below designs a low-pass and a band-stop filter, respectively.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```

```
>>> b1 = signal.firwin(40, 0.5)
>>> b2 = signal.firwin(41, [0.3, 0.8])
>>> w1, h1 = signal.freqz(b1)
>>> w2, h2 = signal.freqz(b2)
```

```
>>> plt.title('Digital filter frequency response')
>>> plt.plot(w1, 20*np.log10(np.abs(h1)), 'b')
>>> plt.plot(w2, 20*np.log10(np.abs(h2)), 'r')
>>> plt.ylabel('Amplitude Response (dB)')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```

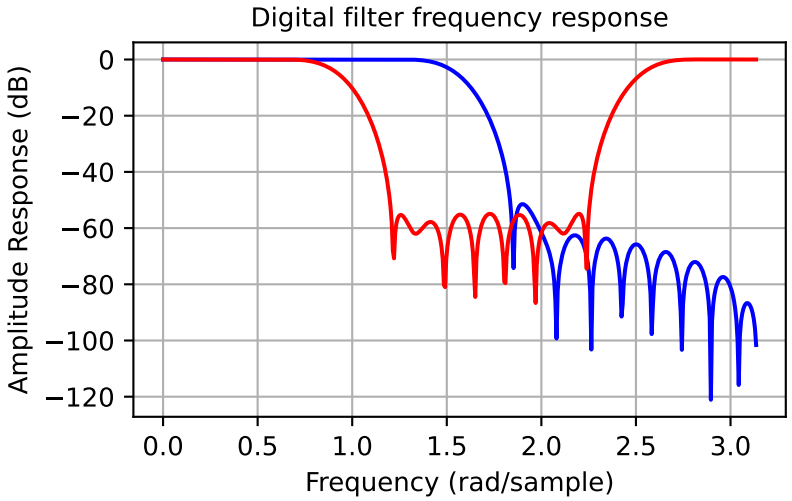
Note that *firwin* uses, per default, a normalized frequency defined such that the value 1 corresponds to the Nyquist frequency, whereas the function *freqz* is defined such that the value π corresponds to the Nyquist frequency.

The function *firwin2* allows design of almost arbitrary frequency responses by specifying an array of corner frequencies and corresponding gains, respectively.

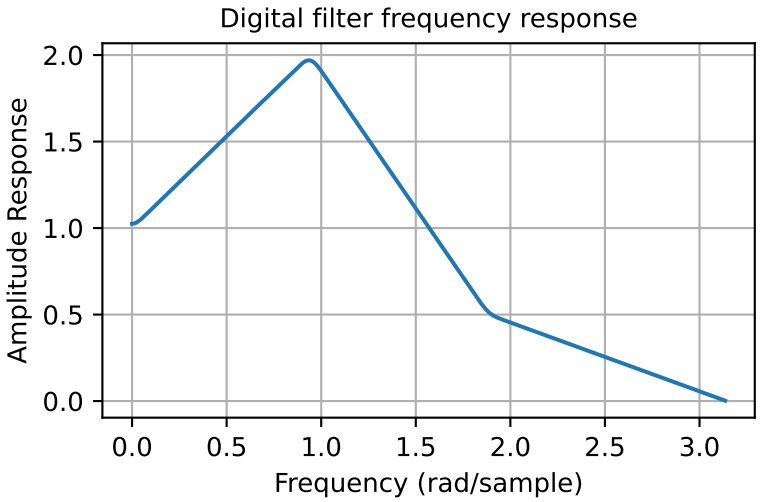
The example below designs a filter with such an arbitrary amplitude response.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```

```
>>> b = signal.firwin2(150, [0.0, 0.3, 0.6, 1.0], [1.0, 2.0, 0.5, 0.0])
>>> w, h = signal.freqz(b)
```




```
>>> plt.title('Digital filter frequency response')
>>> plt.plot(w, np.abs(h))
>>> plt.title('Digital filter frequency response')
>>> plt.ylabel('Amplitude Response')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```



Note the linear scaling of the y-axis and the different definition of the Nyquist frequency in *firwin2* and *freqz* (as explained above).

IIR Filter

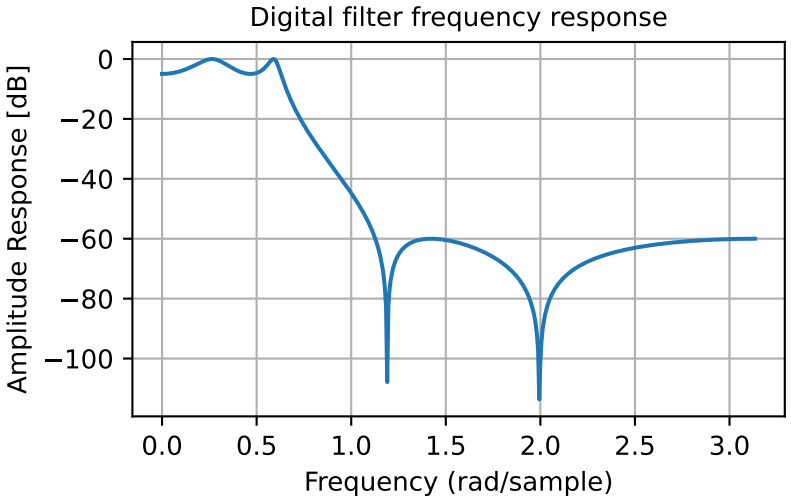
SciPy provides two functions to directly design IIR *iirdesign* and *iirfilter*, where the filter type (e.g., elliptic) is passed as an argument and several more filter design functions for specific filter types, e.g., *ellip*.

The example below designs an elliptic low-pass filter with defined pass-band and stop-band ripple, respectively. Note the much lower filter order (order 4) compared with the FIR filters from the examples above in order to reach the same stop-band attenuation of ≈ 60 dB.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.iirfilter(4, Wn=0.2, rp=5, rs=60, btype='lowpass', ftype=
↪'ellip')
>>> w, h = signal.freqz(b, a)
```

```
>>> plt.title('Digital filter frequency response')
>>> plt.plot(w, 20*np.log10(np.abs(h)))
>>> plt.title('Digital filter frequency response')
>>> plt.ylabel('Amplitude Response [dB]')
>>> plt.xlabel('Frequency (rad/sample)')
>>> plt.grid()
>>> plt.show()
```



Filter Coefficients

Filter coefficients can be stored in several different formats:

- 'ba' or 'tf' = transfer function coefficients
- 'zpk' = zeros, poles, and overall gain
- 'ss' = state-space system representation
- 'sos' = transfer function coefficients of second-order sections

Functions, such as *tf2zpk* and *zpk2ss*, can convert between them.

Transfer function representation

The `ba` or `tf` format is a 2-tuple `(b, a)` representing a transfer function, where *b* is a length `M+1` array of coefficients of the *M*-order numerator polynomial, and *a* is a length `N+1` array of coefficients of the *N*-order denominator, as positive, descending powers of the transfer function variable. So the tuple of $b = [b_0, b_1, ..., b_M]$ and $a = [a_0, a_1, ..., a_N]$ can represent an analog filter of the form:

$$H(s) = \frac{b_0 s^M + b_1 s^{(M-1)} + \cdots + b_M}{a_0 s^N + a_1 s^{(N-1)} + \cdots + a_N} = \frac{\sum_{i=0}^{M} b_i s^{(M-i)}}{\sum_{i=0}^{N} a_i s^{(N-i)}}$$

or a discrete-time filter of the form:

$$H(z) = \frac{b_0 z^M + b_1 z^{(M-1)} + \cdots + b_M}{a_0 z^N + a_1 z^{(N-1)} + \cdots + a_N} = \frac{\sum_{i=0}^{M} b_i z^{(M-i)}}{\sum_{i=0}^{N} a_i z^{(N-i)}}.$$

This "positive powers" form is found more commonly in controls engineering. If *M* and *N* are equal (which is true for all filters generated by the bilinear transform), then this happens to be equivalent to the "negative powers" discrete-time form preferred in DSP:

$$H(z) = \frac{b_0 + b_1 z^{-1} + \cdots + b_M z^{-M}}{a_0 + a_1 z^{-1} + \cdots + a_N z^{-N}} = \frac{\sum_{i=0}^{M} b_i z^{-i}}{\sum_{i=0}^{N} a_i z^{-i}}.$$

Although this is true for common filters, remember that this is not true in the general case. If *M* and *N* are not equal, the discrete-time transfer function coefficients must first be converted to the "positive powers" form before finding the poles and zeros.

This representation suffers from numerical error at higher orders, so other formats are preferred when possible.

Zeros and poles representation

The `zpk` format is a 3-tuple `(z, p, k)`, where *z* is an *M*-length array of the complex zeros of the transfer function $z = [z_0, z_1, ..., z_{M-1}]$, *p* is an *N*-length array of the complex poles of the transfer function $p = [p_0, p_1, ..., p_{N-1}]$, and *k* is a scalar gain. These represent the digital transfer function:

$$H(z) = k \cdot \frac{(z - z_0)(z - z_1) \cdots (z - z_{(M-1)})}{(z - p_0)(z - p_1) \cdots (z - p_{(N-1)})} = k \frac{\prod_{i=0}^{M-1} (z - z_i)}{\prod_{i=0}^{N-1} (z - p_i)}$$

or the analog transfer function:

$$H(s) = k \cdot \frac{(s - z_0)(s - z_1) \cdots (s - z_{(M-1)})}{(s - p_0)(s - p_1) \cdots (s - p_{(N-1)})} = k \frac{\prod_{i=0}^{M-1} (s - z_i)}{\prod_{i=0}^{N-1} (s - p_i)}.$$

Although the sets of roots are stored as ordered NumPy arrays, their ordering does not matter: `([-1, -2], [-3, -4], 1)` is the same filter as `([-2, -1], [-4, -3], 1)`.

State-space system representation

The `ss` format is a 4-tuple of arrays `(A, B, C, D)` representing the state-space of an *N*-order digital/discrete-time system of the form:

$$\mathbf{x}[k+1] = A\mathbf{x}[k] + B\mathbf{u}[k]$$
$$\mathbf{y}[k] = C\mathbf{x}[k] + D\mathbf{u}[k]$$

or a continuous/analog system of the form:

$$\dot{\mathbf{x}}(t) = A\mathbf{x}(t) + B\mathbf{u}(t)$$
$$\mathbf{y}(t) = C\mathbf{x}(t) + D\mathbf{u}(t),$$

with *P* inputs, *Q* outputs and *N* state variables, where:

- *x* is the state vector
- *y* is the output vector of length *Q*
- *u* is the input vector of length *P*
- *A* is the state matrix, with shape `(N, N)`
- *B* is the input matrix with shape `(N, P)`
- *C* is the output matrix with shape `(Q, N)`
- *D* is the feedthrough or feedforward matrix with shape `(Q, P)`. (In cases where the system does not have a direct feedthrough, all values in *D* are zero.)

State-space is the most general representation and the only one that allows for multiple-input, multiple-output (MIMO) systems. There are multiple state-space representations for a given transfer function. Specifically, the "controllable canonical form" and "observable canonical form" have the same coefficients as the `tf` representation, and, therefore, suffer from the same numerical errors.

Second-order sections representation

The `sos` format is a single 2-D array of shape `(n_sections, 6)`, representing a sequence of second-order transfer functions which, when cascaded in series, realize a higher-order filter with minimal numerical error. Each row corresponds to a second-order `tf` representation, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients:

$$[b_0, b_1, b_2, a_0, a_1, a_2]$$

The coefficients are typically normalized, such that a_0 is always 1. The section order is usually not important with floating-point computation; the filter output will be the same, regardless of the order.

Filter transformations

The IIR filter design functions first generate a prototype analog low-pass filter with a normalized cutoff frequency of 1 rad/sec. This is then transformed into other frequencies and band types using the following substitutions:

Type	Transformation
lp2lp	$s \to \frac{s}{\omega_0}$
lp2hp	$s \to \frac{\omega_0}{s}$
lp2bp	$s \to \frac{s^2+{\omega_0}^2}{s\cdot\mathrm{BW}}$
lp2bs	$s \to \frac{s\cdot\mathrm{BW}}{s^2+{\omega_0}^2}$

Here, ω_0 is the new cutoff or center frequency, and BW is the bandwidth. These preserve symmetry on a logarithmic frequency axis.

To convert the transformed analog filter into a digital filter, the *bilinear* transform is used, which makes the following substitution:

$$s \to \frac{2}{T}\frac{z-1}{z+1},$$

where T is the sampling time (the inverse of the sampling frequency).

Other filters

The signal processing package provides many more filters as well.

Median Filter

A median filter is commonly applied when noise is markedly non-Gaussian or when it is desired to preserve edges. The median filter works by sorting all of the array pixel values in a rectangular region surrounding the point of interest. The sample median of this list of neighborhood pixel values is used as the value for the output array. The sample median is the middle-array value in a sorted list of neighborhood values. If there are an even number of elements in the neighborhood, then the average of the middle two values is used as the median. A general purpose median filter that works on N-D arrays is `medfilt`. A specialized version that works only for 2-D arrays is available as `medfilt2d`.

Order Filter

A median filter is a specific example of a more general class of filters called order filters. To compute the output at a particular pixel, all order filters use the array values in a region surrounding that pixel. These array values are sorted and then one of them is selected as the output value. For the median filter, the sample median of the list of array values is used as the output. A general-order filter allows the user to select which of the sorted values will be used as the output. So, for example, one could choose to pick the maximum in the list or the minimum. The order filter takes an additional argument besides the input array and the region mask that specifies which of the elements in the sorted list of neighbor array values should be used as the output. The command to perform an order filter is `order_filter`.

Wiener filter

The Wiener filter is a simple deblurring filter for denoising images. This is not the Wiener filter commonly described in image-reconstruction problems but, instead, it is a simple, local-mean filter. Let x be the input signal, then the output is

$$y = \begin{cases} \frac{\sigma^2}{\sigma_x^2} m_x + \left(1 - \frac{\sigma^2}{\sigma_x^2}\right) x & \sigma_x^2 \geq \sigma^2, \\ m_x & \sigma_x^2 < \sigma^2, \end{cases}$$

where m_x is the local estimate of the mean and σ_x^2 is the local estimate of the variance. The window for these estimates is an optional input parameter (default is 3×3). The parameter σ^2 is a threshold noise parameter. If σ is not given, then it is estimated as the average of the local variances.

Hilbert filter

The Hilbert transform constructs the complex-valued analytic signal from a real signal. For example, if $x = \cos \omega n$, then $y = \text{hilbert}\,(x)$ would return (except near the edges) $y = \exp(j\omega n)$. In the frequency domain, the hilbert transform performs

$$Y = X \cdot H,$$

where H is 2 for positive frequencies, 0 for negative frequencies, and 1 for zero-frequencies.

Analog Filter Design

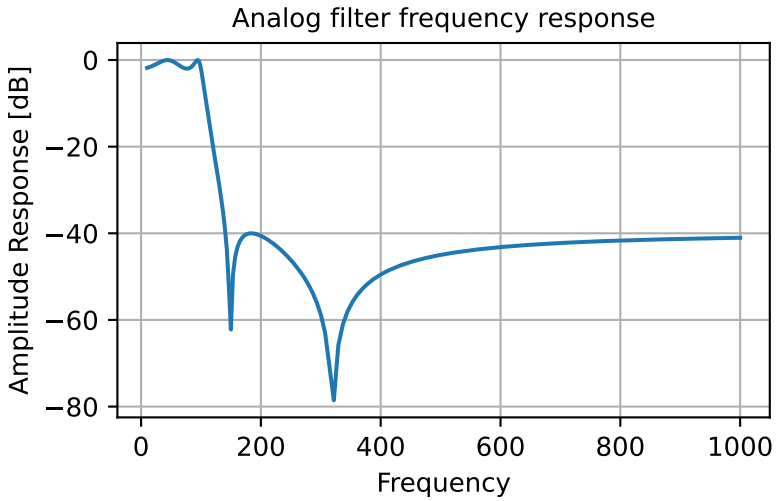
The functions `iirdesign`, `iirfilter`, and the filter design functions for specific filter types (e.g., `ellip`) all have a flag *analog*, which allows the design of analog filters as well.

The example below designs an analog (IIR) filter, obtains via `tf2zpk` the poles and zeros and plots them in the complex s-plane. The zeros at $\omega \approx 150$ and $\omega \approx 300$ can be clearly seen in the amplitude response.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.iirdesign(wp=100, ws=200, gpass=2.0, gstop=40., analog=True)
>>> w, h = signal.freqs(b, a)
```

```
>>> plt.title('Analog filter frequency response')
>>> plt.plot(w, 20*np.log10(np.abs(h)))
>>> plt.ylabel('Amplitude Response [dB]')
>>> plt.xlabel('Frequency')
>>> plt.grid()
>>> plt.show()
```




```
>>> z, p, k = signal.tf2zpk(b, a)
```

```
>>> plt.plot(np.real(z), np.imag(z), 'xb')
>>> plt.plot(np.real(p), np.imag(p), 'or')
>>> plt.legend(['Zeros', 'Poles'], loc=2)
```

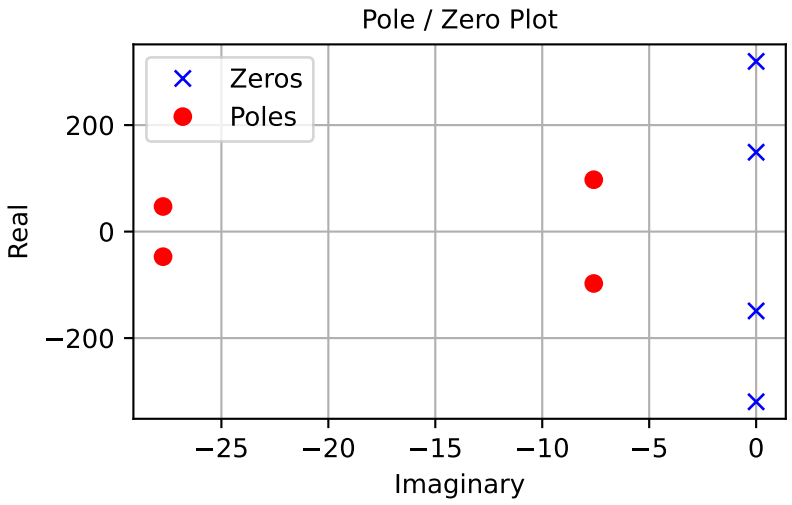
```
>>> plt.title('Pole / Zero Plot')
>>> plt.ylabel('Real')
>>> plt.xlabel('Imaginary')
>>> plt.grid()
>>> plt.show()
```

2.7.3 Spectral Analysis

Periodogram Measurements

The scipy function *periodogram* provides a method to estimate the spectral density using the periodogram method.

The example below calculates the periodogram of a sine signal in white Gaussian noise.




```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1270.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
```

```
>>> f, Pper_spec = signal.periodogram(x, fs, 'flattop', scaling='spectrum')
```

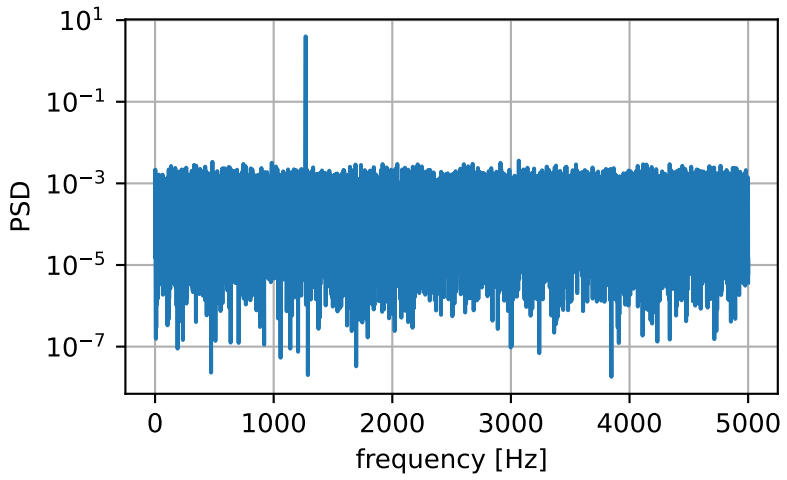
```
>>> plt.semilogy(f, Pper_spec)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD')
>>> plt.grid()
>>> plt.show()
```

Spectral Analysis using Welch's Method

An improved method, especially with respect to noise immunity, is Welch's method, which is implemented by the scipy function *welch*.

The example below estimates the spectrum using Welch's method and uses the same parameters as the example above. Note the much smoother noise floor of the spectrogram.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```




```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1270.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += np.random.normal(scale=np.sqrt(noise_power), size=time.shape)
```

```
>>> f, Pwelch_spec = signal.welch(x, fs, scaling='spectrum')
```

```
>>> plt.semilogy(f, Pwelch_spec)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD')
>>> plt.grid()
>>> plt.show()
```

Lomb-Scargle Periodograms (`lombscargle`)

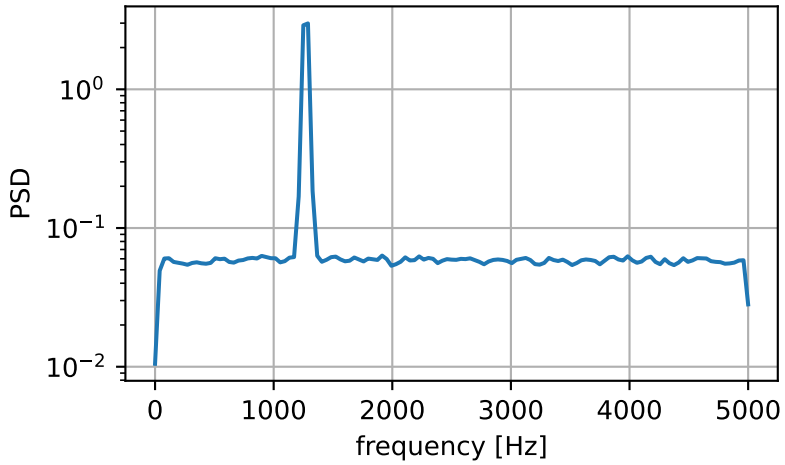
Least-squares spectral analysis (LSSA)[1][2] is a method of estimating a frequency spectrum, based on a least-squares fit of sinusoids to data samples, similar to Fourier analysis. Fourier analysis, the most used spectral method in science, generally boosts long-periodic noise in long-gapped records; LSSA mitigates such problems.

The Lomb-Scargle method performs spectral analysis on unevenly-sampled data and is known to be a powerful way to find, and test the significance of, weak periodic signals.

For a time series comprising N_t measurements $X_j \equiv X(t_j)$ sampled at times t_j, where $(j = 1, \ldots, N_t)$, assumed to have been scaled and shifted, such that its mean is zero and its variance is unity, the normalized Lomb-Scargle periodogram at

[1] N.R. Lomb "Least-squares frequency analysis of unequally spaced data", Astrophysics and Space Science, vol 39, pp. 447-462, 1976

[2] J.D. Scargle "Studies in astronomical time series analysis. II - Statistical aspects of spectral analysis of unevenly spaced data", The Astrophysical Journal, vol 263, pp. 835-853, 1982



frequency f is

$$P_n(f)\frac{1}{2}\left\{\frac{\left[\sum_j^{N_t} X_j \cos\omega(t_j-\tau)\right]^2}{\sum_j^{N_t}\cos^2\omega(t_j-\tau)}+\frac{\left[\sum_j^{N_t} X_j \sin\omega(t_j-\tau)\right]^2}{\sum_j^{N_t}\sin^2\omega(t_j-\tau)}\right\}.$$

Here, $\omega \equiv 2\pi f$ is the angular frequency. The frequency-dependent time offset τ is given by

$$\tan 2\omega\tau = \frac{\sum_j^{N_t}\sin 2\omega t_j}{\sum_j^{N_t}\cos 2\omega t_j}.$$

The `lombscargle` function calculates the periodogram using a slightly modified algorithm due to Townsend[3], which allows the periodogram to be calculated using only a single pass through the input arrays for each frequency.

The equation is refactored as:

$$P_n(f) = \frac{1}{2}\left[\frac{(c_\tau XC + s_\tau XS)^2}{c_\tau^2 CC + 2c_\tau s_\tau CS + s_\tau^2 SS} + \frac{(c_\tau XS - s_\tau XC)^2}{c_\tau^2 SS - 2c_\tau s_\tau CS + s_\tau^2 CC}\right]$$

and

$$\tan 2\omega\tau = \frac{2CS}{CC - SS}.$$

Here,

$$c_\tau = \cos\omega\tau, \qquad s_\tau = \sin\omega\tau,$$

[3] R.H.D. Townsend, "Fast calculation of the Lomb-Scargle periodogram using graphics processing units.", The Astrophysical Journal Supplement Series, vol 191, pp. 247-253, 2010

while the sums are

$$XC = \sum_j^{N_t} X_j \cos \omega t_j$$
$$XS = \sum_j^{N_t} X_j \sin \omega t_j$$
$$CC = \sum_j^{N_t} \cos^2 \omega t_j$$
$$SS = \sum_j^{N_t} \sin^2 \omega t_j$$
$$CS = \sum_j^{N_t} \cos \omega t_j \sin \omega t_j.$$

This requires $N_f(2N_t + 3)$ trigonometric function evaluations giving a factor of ~ 2 speed increase over the straightforward implementation.

2.7.4 Detrend

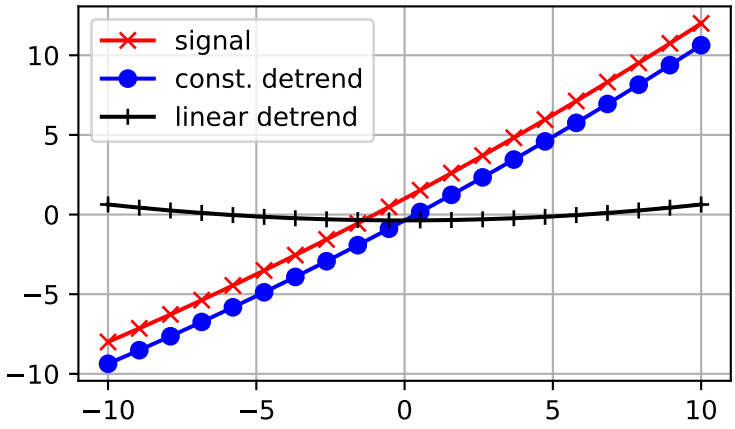
SciPy provides the function *detrend* to remove a constant or linear trend in a data series in order to see effect of higher order.

The example below removes the constant and linear trend of a second-order polynomial time series and plots the remaining signal components.

```
>>> import numpy as np
>>> import scipy.signal as signal
>>> import matplotlib.pyplot as plt
```

```
>>> t = np.linspace(-10, 10, 20)
>>> y = 1 + t + 0.01*t**2
>>> yconst = signal.detrend(y, type='constant')
>>> ylin = signal.detrend(y, type='linear')
```

```
>>> plt.plot(t, y, '-rx')
>>> plt.plot(t, yconst, '-bo')
>>> plt.plot(t, ylin, '-k+')
>>> plt.grid()
>>> plt.legend(['signal', 'const. detrend', 'linear detrend'])
>>> plt.show()
```



References

Some further reading and related software:

2.8 Linear Algebra (`scipy.linalg`)

When SciPy is built using the optimized ATLAS LAPACK and BLAS libraries, it has very fast linear algebra capabilities. If you dig deep enough, all of the raw LAPACK and BLAS libraries are available for your use for even more speed. In this section, some easier-to-use interfaces to these routines are described.

All of these linear algebra routines expect an object that can be converted into a 2-D array. The output of these routines is also a 2-D array.

2.8.1 scipy.linalg vs numpy.linalg

`scipy.linalg` contains all the functions in numpy.linalg. plus some other more advanced ones not contained in `numpy.linalg`.

Another advantage of using `scipy.linalg` over `numpy.linalg` is that it is always compiled with BLAS/LAPACK support, while for numpy this is optional. Therefore, the scipy version might be faster depending on how numpy was installed.

Therefore, unless you don't want to add `scipy` as a dependency to your `numpy` program, use `scipy.linalg` instead of `numpy.linalg`.

2.8.2 numpy.matrix vs 2-D numpy.ndarray

The classes that represent matrices, and basic operations, such as matrix multiplications and transpose are a part of `numpy`. For convenience, we summarize the differences between `numpy.matrix` and `numpy.ndarray` here.

`numpy.matrix` is matrix class that has a more convenient interface than `numpy.ndarray` for matrix operations. This class supports, for example, MATLAB-like creation syntax via the semicolon, has matrix multiplication as default for the `*` operator, and contains `I` and `T` members that serve as shortcuts for inverse and transpose:

```
>>> import numpy as np
>>> A = np.mat('[1 2;3 4]')
>>> A
matrix([[1, 2],
        [3, 4]])
>>> A.I
matrix([[-2. ,  1. ],
        [ 1.5, -0.5]])
>>> b = np.mat('[5 6]')
>>> b
matrix([[5, 6]])
>>> b.T
matrix([[5],
        [6]])
>>> A*b.T
matrix([[17],
        [39]])
```

Despite its convenience, the use of the `numpy.matrix` class is discouraged, since it adds nothing that cannot be accomplished with 2-D `numpy.ndarray` objects, and may lead to a confusion of which class is being used. For example, the above code can be rewritten as:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2],[3,4]])
>>> A
array([[1, 2],
       [3, 4]])
>>> linalg.inv(A)
array([[-2. ,  1. ],
       [ 1.5, -0.5]])
>>> b = np.array([[5,6]]) #2D array
>>> b
array([[5, 6]])
>>> b.T
array([[5],
       [6]])
>>> A*b #not matrix multiplication!
array([[ 5, 12],
       [15, 24]])
>>> A.dot(b.T) #matrix multiplication
array([[17],
       [39]])
>>> b = np.array([5,6]) #1D array
>>> b
```

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```
array([5, 6])
>>> b.T  #not matrix transpose!
array([5, 6])
>>> A.dot(b)  #does not matter for multiplication
array([17, 39])
```

`scipy.linalg` operations can be applied equally to `numpy.matrix` or to 2D `numpy.ndarray` objects.

2.8.3 Basic routines

Finding the inverse

The inverse of a matrix $\mathbf{A}$ is the matrix $\mathbf{B}$, such that $\mathbf{AB} = \mathbf{I}$, where $\mathbf{I}$ is the identity matrix consisting of ones down the main diagonal. Usually, $\mathbf{B}$ is denoted $\mathbf{B} = \mathbf{A}^{-1}$. In SciPy, the matrix inverse of the NumPy array, A, is obtained using *`linalg.inv`* `(A)`, or using `A.I` if `A` is a Matrix. For example, let

$$\mathbf{A} = \begin{bmatrix} 1 & 3 & 5 \\ 2 & 5 & 1 \\ 2 & 3 & 8 \end{bmatrix},$$

then

$$\mathbf{A^{-1}} = \frac{1}{25} \begin{bmatrix} -37 & 9 & 22 \\ 14 & 2 & -9 \\ 4 & -3 & 1 \end{bmatrix} = \begin{bmatrix} -1.48 & 0.36 & 0.88 \\ 0.56 & 0.08 & -0.36 \\ 0.16 & -0.12 & 0.04 \end{bmatrix}.$$

The following example demonstrates this computation in SciPy

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,3,5],[2,5,1],[2,3,8]])
>>> A
array([[1, 3, 5],
       [2, 5, 1],
       [2, 3, 8]])
>>> linalg.inv(A)
array([[-1.48,  0.36,  0.88],
       [ 0.56,  0.08, -0.36],
       [ 0.16, -0.12,  0.04]])
>>> A.dot(linalg.inv(A)) #double check
array([[  1.00000000e+00,  -1.11022302e-16,  -5.55111512e-17],
       [  3.05311332e-16,   1.00000000e+00,   1.87350135e-16],
       [  2.22044605e-16,  -1.11022302e-16,   1.00000000e+00]])
```

Solving a linear system

Solving linear systems of equations is straightforward using the scipy command `linalg.solve`. This command expects an input matrix and a right-hand side vector. The solution vector is then computed. An option for entering a symmetric matrix is offered, which can speed up the processing when applicable. As an example, suppose it is desired to solve the following simultaneous equations:

$$\begin{aligned} x + 3y + 5z &= 10 \\ 2x + 5y + z &= 8 \\ 2x + 3y + 8z &= 3 \end{aligned}$$

We could find the solution vector using a matrix inverse:

$$\begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} 1 & 3 & 5 \\ 2 & 5 & 1 \\ 2 & 3 & 8 \end{bmatrix}^{-1} \begin{bmatrix} 10 \\ 8 \\ 3 \end{bmatrix} = \frac{1}{25} \begin{bmatrix} -232 \\ 129 \\ 19 \end{bmatrix} = \begin{bmatrix} -9.28 \\ 5.16 \\ 0.76 \end{bmatrix}.$$

However, it is better to use the linalg.solve command, which can be faster and more numerically stable. In this case, it, however, gives the same answer as shown in the following example:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1, 2], [3, 4]])
>>> A
array([[1, 2],
       [3, 4]])
>>> b = np.array([[5], [6]])
>>> b
array([[5],
       [6]])
>>> linalg.inv(A).dot(b)  # slow
array([[-4. ],
       [ 4.5]])
>>> A.dot(linalg.inv(A).dot(b)) - b  # check
array([[  8.88178420e-16],
       [  2.66453526e-15]])
>>> np.linalg.solve(A, b)  # fast
array([[-4. ],
       [ 4.5]])
>>> A.dot(np.linalg.solve(A, b)) - b  # check
array([[ 0.],
       [ 0.]])
```

Finding the determinant

The determinant of a square matrix $\mathbf{A}$ is often denoted $|\mathbf{A}|$ and is a quantity often used in linear algebra. Suppose a_{ij} are the elements of the matrix $\mathbf{A}$ and let $M_{ij} = |\mathbf{A}_{ij}|$ be the determinant of the matrix left by removing the i^{th} row and j^{th} column from $\mathbf{A}$. Then, for any row i,

$$|\mathbf{A}| = \sum_j (-1)^{i+j} a_{ij} M_{ij}.$$

This is a recursive way to define the determinant, where the base case is defined by accepting that the determinant of a 1×1 matrix is the only matrix element. In SciPy the determinant can be calculated with `linalg.det`. For example,

the determinant of

$$\mathbf{A} = \begin{bmatrix} 1 & 3 & 5 \\ 2 & 5 & 1 \\ 2 & 3 & 8 \end{bmatrix}$$

is

$$\begin{aligned} |\mathbf{A}| &= 1\begin{vmatrix} 5 & 1 \\ 3 & 8 \end{vmatrix} - 3\begin{vmatrix} 2 & 1 \\ 2 & 8 \end{vmatrix} + 5\begin{vmatrix} 2 & 5 \\ 2 & 3 \end{vmatrix} \\ &= 1\,(5\cdot 8 - 3\cdot 1) - 3\,(2\cdot 8 - 2\cdot 1) + 5\,(2\cdot 3 - 2\cdot 5) = -25. \end{aligned}$$

. In SciPy, this is computed as shown in this example:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2],[3,4]])
>>> A
array([[1, 2],
       [3, 4]])
>>> linalg.det(A)
-2.0
```

Computing norms

Matrix and vector norms can also be computed with SciPy. A wide range of norm definitions are available using different parameters to the order argument of *linalg.norm*. This function takes a rank-1 (vectors) or a rank-2 (matrices) array and an optional order argument (default is 2). Based on these inputs, a vector or matrix norm of the requested order is computed.

For vector *x*, the order parameter can be any real number including `inf` or `-inf`. The computed norm is

$$\|\mathbf{x}\| = \begin{cases} \max|x_i| & \text{ord} = \text{inf} \\ \min|x_i| & \text{ord} = -\text{inf} \\ \left(\sum_i |x_i|^{\text{ord}}\right)^{1/\text{ord}} & |\text{ord}| < \infty. \end{cases}$$

For matrix $\mathbf{A}$, the only valid values for norm are $\pm 2, \pm 1, \pm$ inf, and 'fro' (or 'f') Thus,

$$\|\mathbf{A}\| = \begin{cases} \max_i \sum_j |a_{ij}| & \text{ord} = \text{inf} \\ \min_i \sum_j |a_{ij}| & \text{ord} = -\text{inf} \\ \max_j \sum_i |a_{ij}| & \text{ord} = 1 \\ \min_j \sum_i |a_{ij}| & \text{ord} = -1 \\ \max \sigma_i & \text{ord} = 2 \\ \min \sigma_i & \text{ord} = -2 \\ \sqrt{\text{trace}\,(\mathbf{A}^H\mathbf{A})} & \text{ord} = \text{'fro'} \end{cases}$$

where σ_i are the singular values of $\mathbf{A}$.

Examples:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A=np.array([[1,2],[3,4]])
>>> A
```

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```
array([[1, 2],
       [3, 4]])
>>> linalg.norm(A)
5.4772255750516612
>>> linalg.norm(A,'fro') # frobenius norm is the default
5.4772255750516612
>>> linalg.norm(A,1) # L1 norm (max column sum)
6
>>> linalg.norm(A,-1)
4
>>> linalg.norm(A,np.inf) # L inf norm (max row sum)
7
```

Solving linear least-squares problems and pseudo-inverses

Linear least-squares problems occur in many branches of applied mathematics. In this problem, a set of linear scaling coefficients is sought that allows a model to fit the data. In particular, it is assumed that data y_i is related to data $\mathbf{x}_i$ through a set of coefficients c_j and model functions $f_j\left(\mathbf{x}_i\right)$ via the model

$$y_i = \sum_j c_j f_j\left(\mathbf{x}_i\right) + \epsilon_i,$$

where ϵ_i represents uncertainty in the data. The strategy of least squares is to pick the coefficients c_j to minimize

$$J\left(\mathbf{c}\right) = \sum_i \left| y_i - \sum_j c_j f_j\left(x_i\right) \right|^2.$$

Theoretically, a global minimum will occur when

$$\frac{\partial J}{\partial c_n^*} = 0 = \sum_i \left(y_i - \sum_j c_j f_j\left(x_i\right) \right) \left(-f_n^*\left(x_i\right)\right)$$

or

$$\begin{aligned} \sum_j c_j \sum_i f_j\left(x_i\right) f_n^*\left(x_i\right) &= \sum_i y_i f_n^*\left(x_i\right) \\ \mathbf{A}^H\mathbf{A}\mathbf{c} &= \mathbf{A}^H\mathbf{y} \end{aligned}$$

, where

$$\left\{\mathbf{A}\right\}_{ij} = f_j\left(x_i\right).$$

When $\mathbf{A^H A}$ is invertible, then

$$\mathbf{c} = \left(\mathbf{A}^H\mathbf{A}\right)^{-1}\mathbf{A}^H\mathbf{y} = \mathbf{A}^\dagger\mathbf{y},$$

where $\mathbf{A}^\dagger$ is called the pseudo-inverse of $\mathbf{A}$. Notice that using this definition of $\mathbf{A}$ the model can be written

$$\mathbf{y} = \mathbf{A}\mathbf{c} + \boldsymbol{\epsilon}.$$

The command *linalg.lstsq* will solve the linear least-squares problem for $\mathbf{c}$ given $\mathbf{A}$ and $\mathbf{y}$. In addition, *linalg.pinv* or *linalg.pinv2* (uses a different method based on singular value decomposition) will find $\mathbf{A}^\dagger$ given $\mathbf{A}$.

The following example and figure demonstrate the use of *linalg.lstsq* and *linalg.pinv* for solving a data-fitting problem. The data shown below were generated using the model:

$$y_i = c_1 e^{-x_i} + c_2 x_i,$$

where $x_i = 0.1i$ for $i = 1 \ldots 10$, $c_1 = 5$, and $c_2 = 4$. Noise is added to y_i and the coefficients c_1 and c_2 are estimated using linear least squares.

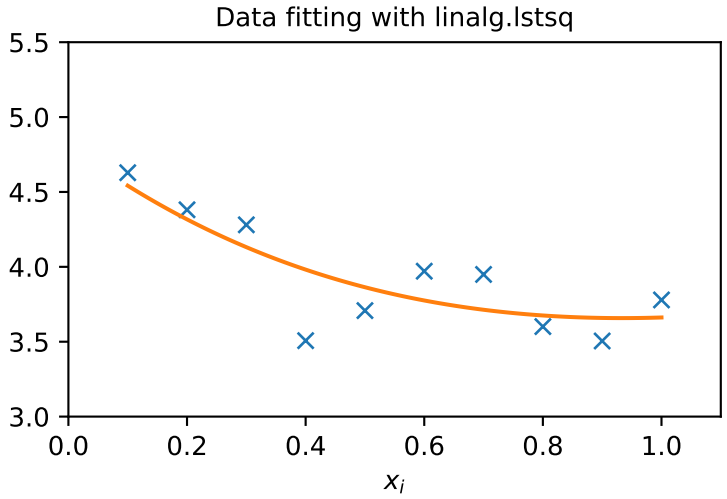
```
>>> import numpy as np
>>> from scipy import linalg
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

```
>>> c1, c2 = 5.0, 2.0
>>> i = np.r_[1:11]
>>> xi = 0.1*i
>>> yi = c1*np.exp(-xi) + c2*xi
>>> zi = yi + 0.05 * np.max(yi) * rng.standard_normal(len(yi))
```

```
>>> A = np.c_[np.exp(-xi)[:, np.newaxis], xi[:, np.newaxis]]
>>> c, resid, rank, sigma = linalg.lstsq(A, zi)
```

```
>>> xi2 = np.r_[0.1:1.0:100j]
>>> yi2 = c[0]*np.exp(-xi2) + c[1]*xi2
```

```
>>> plt.plot(xi,zi,'x',xi2,yi2)
>>> plt.axis([0,1.1,3.0,5.5])
>>> plt.xlabel('$x_i$')
>>> plt.title('Data fitting with linalg.lstsq')
>>> plt.show()
```



Generalized inverse

The generalized inverse is calculated using the command `linalg.pinv` or `linalg.pinv2`. These two commands differ in how they compute the generalized inverse. The first uses the linalg.lstsq algorithm, while the second uses singular value decomposition. Let $\mathbf{A}$ be an $M \times N$ matrix, then if $M > N$, the generalized inverse is

$$\mathbf{A}^{\dagger} = \left(\mathbf{A}^H \mathbf{A}\right)^{-1} \mathbf{A}^H,$$

while if $M < N$ matrix, the generalized inverse is

$$\mathbf{A}^{\#} = \mathbf{A}^H \left(\mathbf{A}\mathbf{A}^H\right)^{-1}.$$

In the case that $M = N$, then

$$\mathbf{A}^{\dagger} = \mathbf{A}^{\#} = \mathbf{A}^{-1},$$

as long as $\mathbf{A}$ is invertible.

2.8.4 Decompositions

In many applications, it is useful to decompose a matrix using other representations. There are several decompositions supported by SciPy.

Eigenvalues and eigenvectors

The eigenvalue-eigenvector problem is one of the most commonly employed linear algebra operations. In one popular form, the eigenvalue-eigenvector problem is to find for some square matrix $\mathbf{A}$ scalars λ and corresponding vectors $\mathbf{v}$, such that

$$\mathbf{A}\mathbf{v} = \lambda\mathbf{v}.$$

For an $N \times N$ matrix, there are N (not necessarily distinct) eigenvalues — roots of the (characteristic) polynomial

$$|\mathbf{A} - \lambda\mathbf{I}| = 0.$$

The eigenvectors, $\mathbf{v}$, are also sometimes called right eigenvectors to distinguish them from another set of left eigenvectors that satisfy

$$\mathbf{v}_L^H \mathbf{A} = \lambda \mathbf{v}_L^H$$

or

$$\mathbf{A}^H \mathbf{v}_L = \lambda^* \mathbf{v}_L.$$

With its default optional arguments, the command `linalg.eig` returns λ and $\mathbf{v}$. However, it can also return $\mathbf{v}_L$ and just λ by itself (`linalg.eigvals` returns just λ as well).

In addition, `linalg.eig` can also solve the more general eigenvalue problem

$$\begin{aligned} \mathbf{A}\mathbf{v} &= \lambda\mathbf{B}\mathbf{v} \\ \mathbf{A}^H\mathbf{v}_L &= \lambda^*\mathbf{B}^H\mathbf{v}_L \end{aligned}$$

for square matrices $\mathbf{A}$ and $\mathbf{B}$. The standard eigenvalue problem is an example of the general eigenvalue problem for $\mathbf{B} = \mathbf{I}$. When a generalized eigenvalue problem can be solved, it provides a decomposition of $\mathbf{A}$ as

$$\mathbf{A} = \mathbf{B}\mathbf{V}\mathbf{\Lambda}\mathbf{V}^{-1},$$

where $\mathbf{V}$ is the collection of eigenvectors into columns and $\mathbf{\Lambda}$ is a diagonal matrix of eigenvalues.

By definition, eigenvectors are only defined up to a constant scale factor. In SciPy, the scaling factor for the eigenvectors is chosen so that $\|\mathbf{v}\|^2 = \sum_i v_i^2 = 1$.

As an example, consider finding the eigenvalues and eigenvectors of the matrix

$$\mathbf{A} = \begin{bmatrix} 1 & 5 & 2 \\ 2 & 4 & 1 \\ 3 & 6 & 2 \end{bmatrix}.$$

The characteristic polynomial is

$$\begin{aligned} |\mathbf{A} - \lambda\mathbf{I}| &= (1-\lambda)\left[(4-\lambda)(2-\lambda) - 6\right] - \\ &\quad 5\left[2(2-\lambda) - 3\right] + 2\left[12 - 3(4-\lambda)\right] \\ &= -\lambda^3 + 7\lambda^2 + 8\lambda - 3. \end{aligned}$$

The roots of this polynomial are the eigenvalues of $\mathbf{A}$:

$$\begin{aligned} \lambda_1 &= 7.9579 \\ \lambda_2 &= -1.2577 \\ \lambda_3 &= 0.2997. \end{aligned}$$

The eigenvectors corresponding to each eigenvalue can be found using the original equation. The eigenvectors associated with these eigenvalues can then be found.

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1, 2], [3, 4]])
>>> la, v = linalg.eig(A)
>>> l1, l2 = la
>>> print(l1, l2)   # eigenvalues
(-0.3722813232690143+0j) (5.372281323269014+0j)
>>> print(v[:, 0])   # first eigenvector
[-0.82456484  0.56576746]
>>> print(v[:, 1])   # second eigenvector
[-0.41597356 -0.90937671]
>>> print(np.sum(abs(v**2), axis=0))  # eigenvectors are unitary
[1. 1.]
>>> v1 = np.array(v[:, 0]).T
>>> print(linalg.norm(A.dot(v1) - l1*v1))  # check the computation
3.23682852457e-16
```

Singular value decomposition

Singular value decomposition (SVD) can be thought of as an extension of the eigenvalue problem to matrices that are not square. Let $\mathbf{A}$ be an $M \times N$ matrix with M and N arbitrary. The matrices $\mathbf{A}^H\mathbf{A}$ and $\mathbf{A}\mathbf{A}^H$ are square hermitian matrices[1] of size $N \times N$ and $M \times M$, respectively. It is known that the eigenvalues of square hermitian matrices are real and non-negative. In addition, there are at most $\min(M, N)$ identical non-zero eigenvalues of $\mathbf{A}^H\mathbf{A}$ and $\mathbf{A}\mathbf{A}^H$. Define these positive eigenvalues as σ_i^2. The square-root of these are called singular values of $\mathbf{A}$. The eigenvectors of $\mathbf{A}^H\mathbf{A}$ are collected by columns into an $N \times N$ unitary[2] matrix $\mathbf{V}$, while the eigenvectors of $\mathbf{A}\mathbf{A}^H$ are collected by columns in

[1] A hermitian matrix $\mathbf{D}$ satisfies $\mathbf{D}^H = \mathbf{D}$.
[2] A unitary matrix $\mathbf{D}$ satisfies $\mathbf{D}^H\mathbf{D} = \mathbf{I} = \mathbf{D}\mathbf{D}^H$ so that $\mathbf{D}^{-1} = \mathbf{D}^H$.

the unitary matrix $\mathbf{U}$, the singular values are collected in an $M \times N$ zero matrix $\mathbf{\Sigma}$ with main diagonal entries set to the singular values. Then

$$\mathbf{A} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^H$$

is the singular value decomposition of $\mathbf{A}$. Every matrix has a singular value decomposition. Sometimes, the singular values are called the spectrum of $\mathbf{A}$. The command *linalg.svd* will return $\mathbf{U}$, $\mathbf{V}^H$, and σ_i as an array of the singular values. To obtain the matrix $\mathbf{\Sigma}$, use *linalg.diagsvd*. The following example illustrates the use of *linalg.svd*:

```
>>> import numpy as np
>>> from scipy import linalg
>>> A = np.array([[1,2,3],[4,5,6]])
>>> A
array([[1, 2, 3],
       [4, 5, 6]])
>>> M,N = A.shape
>>> U,s,Vh = linalg.svd(A)
>>> Sig = linalg.diagsvd(s,M,N)
>>> U, Vh = U, Vh
>>> U
array([[-0.3863177 , -0.92236578],
       [-0.92236578,  0.3863177 ]])
>>> Sig
array([[ 9.508032  ,  0.        ,  0.        ],
       [ 0.        ,  0.77286964,  0.        ]])
>>> Vh
array([[-0.42866713, -0.56630692, -0.7039467 ],
       [ 0.80596391,  0.11238241, -0.58119908],
       [ 0.40824829, -0.81649658,  0.40824829]])
>>> U.dot(Sig.dot(Vh)) #check computation
array([[ 1.,  2.,  3.],
       [ 4.,  5.,  6.]])
```

LU decomposition

The LU decomposition finds a representation for the $M \times N$ matrix $\mathbf{A}$ as

$$\mathbf{A} = \mathbf{P}\,\mathbf{L}\,\mathbf{U},$$

where $\mathbf{P}$ is an $M \times M$ permutation matrix (a permutation of the rows of the identity matrix), $\mathbf{L}$ is in $M \times K$ lower triangular or trapezoidal matrix ($K = \min(M, N)$) with unit-diagonal, and $\mathbf{U}$ is an upper triangular or trapezoidal matrix. The SciPy command for this decomposition is *linalg.lu*.

Such a decomposition is often useful for solving many simultaneous equations where the left-hand side does not change but the right-hand side does. For example, suppose we are going to solve

$$\mathbf{A}\mathbf{x}_i = \mathbf{b}_i$$

for many different $\mathbf{b}_i$. The LU decomposition allows this to be written as

$$\mathbf{P}\mathbf{L}\mathbf{U}\mathbf{x}_i = \mathbf{b}_i.$$

Because $\mathbf{L}$ is lower-triangular, the equation can be solved for $\mathbf{U}\mathbf{x}_i$ and, finally, $\mathbf{x}_i$ very rapidly using forward- and back-substitution. An initial time spent factoring $\mathbf{A}$ allows for very rapid solution of similar systems of equations in the future. If the intent for performing LU decomposition is for solving linear systems, then the command *linalg.lu_factor* should be used followed by repeated applications of the command *linalg.lu_solve* to solve the system for each new right-hand side.

Cholesky decomposition

Cholesky decomposition is a special case of LU decomposition applicable to Hermitian positive definite matrices. When $\mathbf{A} = \mathbf{A}^H$ and $\mathbf{x}^H\mathbf{A}\mathbf{x} \geq 0$ for all $\mathbf{x}$, then decompositions of $\mathbf{A}$ can be found so that

$$\begin{aligned}\mathbf{A} &= \mathbf{U}^H\mathbf{U} \\ \mathbf{A} &= \mathbf{L}\mathbf{L}^H\end{aligned}$$

, where $\mathbf{L}$ is lower triangular and $\mathbf{U}$ is upper triangular. Notice that $\mathbf{L} = \mathbf{U}^H$. The command *linalg.cholesky* computes the Cholesky factorization. For using the Cholesky factorization to solve systems of equations, there are also *linalg.cho_factor* and *linalg.cho_solve* routines that work similarly to their LU decomposition counterparts.

QR decomposition

The QR decomposition (sometimes called a polar decomposition) works for any $M \times N$ array and finds an $M \times M$ unitary matrix $\mathbf{Q}$ and an $M \times N$ upper-trapezoidal matrix $\mathbf{R}$, such that

$$\mathbf{A} = \mathbf{Q}\mathbf{R}.$$

Notice that if the SVD of $\mathbf{A}$ is known, then the QR decomposition can be found.

$$\mathbf{A} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^H = \mathbf{Q}\mathbf{R}$$

implies that $\mathbf{Q} = \mathbf{U}$ and $\mathbf{R} = \mathbf{\Sigma}\mathbf{V}^H$. Note, however, that in SciPy independent algorithms are used to find QR and SVD decompositions. The command for QR decomposition is *linalg.qr*.

Schur decomposition

For a square $N \times N$ matrix, $\mathbf{A}$, the Schur decomposition finds (not necessarily unique) matrices $\mathbf{T}$ and $\mathbf{Z}$, such that

$$\mathbf{A} = \mathbf{Z}\mathbf{T}\mathbf{Z}^H,$$

where $\mathbf{Z}$ is a unitary matrix and $\mathbf{T}$ is either upper triangular or quasi upper triangular, depending on whether or not a real Schur form or complex Schur form is requested. For a real Schur form both $\mathbf{T}$ and $\mathbf{Z}$ are real-valued when $\mathbf{A}$ is real-valued. When $\mathbf{A}$ is a real-valued matrix, the real Schur form is only quasi upper triangular because 2×2 blocks extrude from the main diagonal corresponding to any complex-valued eigenvalues. The command *linalg.schur* finds the Schur decomposition, while the command *linalg.rsf2csf* converts $\mathbf{T}$ and $\mathbf{Z}$ from a real Schur form to a complex Schur form. The Schur form is especially useful in calculating functions of matrices.

The following example illustrates the Schur decomposition:

```
>>> from scipy import linalg
>>> A = np.mat('[1 3 2; 1 4 5; 2 3 6]')
>>> T, Z = linalg.schur(A)
>>> T1, Z1 = linalg.schur(A, 'complex')
>>> T2, Z2 = linalg.rsf2csf(T, Z)
>>> T
array([[ 9.90012467,  1.78947961, -0.65498528],
       [ 0.        ,  0.54993766, -1.57754789],
       [ 0.        ,  0.51260928,  0.54993766]])
>>> T2
array([[ 9.90012467+0.00000000e+00j, -0.32436598+1.55463542e+00j,
```

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```
        -0.88619748+5.69027615e-01j],
       [ 0.        +0.00000000e+00j,  0.54993766+8.99258408e-01j,
         1.06493862+3.05311332e-16j],
       [ 0.        +0.00000000e+00j,  0.        +0.00000000e+00j,
         0.54993766-8.99258408e-01j]])
>>> abs(T1 - T2) # different
array([[  1.06604538e-14,   2.06969555e+00,   1.69375747e+00],  # may vary
       [  0.00000000e+00,   1.33688556e-15,   4.74146496e-01],
       [  0.00000000e+00,   0.00000000e+00,   1.13220977e-15]])
>>> abs(Z1 - Z2) # different
array([[ 0.06833781,  0.88091091,  0.79568503],    # may vary
       [ 0.11857169,  0.44491892,  0.99594171],
       [ 0.12624999,  0.60264117,  0.77257633]])
>>> T, Z, T1, Z1, T2, Z2 = map(np.mat,(T,Z,T1,Z1,T2,Z2))
>>> abs(A - Z*T*Z.H)  # same
matrix([[  5.55111512e-16,   1.77635684e-15,   2.22044605e-15],
        [  0.00000000e+00,   3.99680289e-15,   8.88178420e-16],
        [  1.11022302e-15,   4.44089210e-16,   3.55271368e-15]])
>>> abs(A - Z1*T1*Z1.H)  # same
matrix([[  4.26993904e-15,   6.21793362e-15,   8.00007092e-15],
        [  5.77945386e-15,   6.21798014e-15,   1.06653681e-14],
        [  7.16681444e-15,   8.90271058e-15,   1.77635764e-14]])
>>> abs(A - Z2*T2*Z2.H)  # same
matrix([[  6.02594127e-16,   1.77648931e-15,   2.22506907e-15],
        [  2.46275555e-16,   3.99684548e-15,   8.91642616e-16],
        [  8.88225111e-16,   8.88312432e-16,   4.44104848e-15]])
```

Interpolative decomposition

scipy.linalg.interpolative contains routines for computing the interpolative decomposition (ID) of a matrix. For a matrix $A \in \mathbb{C}^{m\times n}$ of rank $k \leq \min\{m, n\}$ this is a factorization

$$A\Pi = \begin{bmatrix} A\Pi_1 & A\Pi_2 \end{bmatrix} = A\Pi_1 \begin{bmatrix} I & T \end{bmatrix},$$

where $\Pi = [\Pi_1, \Pi_2]$ is a permutation matrix with $\Pi_1 \in \{0, 1\}^{n\times k}$, i.e., $A\Pi_2 = A\Pi_1 T$. This can equivalently be written as $A = BP$, where $B = A\Pi_1$ and $P = [I, T]\Pi^{\mathsf{T}}$ are the *skeleton* and *interpolation matrices*, respectively.

See also:

scipy.linalg.interpolative — for more information.

2.8.5 Matrix functions

Consider the function $f(x)$ with Taylor series expansion

$$f(x) = \sum_{k=0}^{\infty} \frac{f^{(k)}(0)}{k!} x^k.$$

A matrix function can be defined using this Taylor series for the square matrix $\mathbf{A}$ as

$$f(\mathbf{A}) = \sum_{k=0}^{\infty} \frac{f^{(k)}(0)}{k!} \mathbf{A}^k.$$

While this serves as a useful representation of a matrix function, it is rarely the best way to calculate a matrix function.

Exponential and logarithm functions

The matrix exponential is one of the more common matrix functions. The preferred method for implementing the matrix exponential is to use scaling and a Padé approximation for e^x. This algorithm is implemented as `linalg.expm`.

The inverse of the matrix exponential is the matrix logarithm defined as the inverse of the matrix exponential:

$$\mathbf{A} \equiv \exp(\log(\mathbf{A})).$$

The matrix logarithm can be obtained with `linalg.logm`.

Trigonometric functions

The trigonometric functions, $\sin$, $\cos$, and $\tan$, are implemented for matrices in `linalg.sinm`, `linalg.cosm`, and `linalg.tanm`, respectively. The matrix sine and cosine can be defined using Euler's identity as

$$\begin{aligned}\sin(\mathbf{A}) &= \frac{e^{j\mathbf{A}} - e^{-j\mathbf{A}}}{2j} \\ \cos(\mathbf{A}) &= \frac{e^{j\mathbf{A}} + e^{-j\mathbf{A}}}{2}.\end{aligned}$$

The tangent is

$$\tan(x) = \frac{\sin(x)}{\cos(x)} = [\cos(x)]^{-1}\sin(x)$$

and so the matrix tangent is defined as

$$[\cos(\mathbf{A})]^{-1}\sin(\mathbf{A}).$$

Hyperbolic trigonometric functions

The hyperbolic trigonometric functions, $\sinh$, $\cosh$, and $\tanh$, can also be defined for matrices using the familiar definitions:

$$\begin{aligned}\sinh(\mathbf{A}) &= \frac{e^{\mathbf{A}} - e^{-\mathbf{A}}}{2} \\ \cosh(\mathbf{A}) &= \frac{e^{\mathbf{A}} + e^{-\mathbf{A}}}{2} \\ \tanh(\mathbf{A}) &= [\cosh(\mathbf{A})]^{-1}\sinh(\mathbf{A}).\end{aligned}$$

These matrix functions can be found using `linalg.sinhm`, `linalg.coshm`, and `linalg.tanhm`.

Arbitrary function

Finally, any arbitrary function that takes one complex number and returns a complex number can be called as a matrix function using the command `linalg.funm`. This command takes the matrix and an arbitrary Python function. It then implements an algorithm from Golub and Van Loan's book "Matrix Computations" to compute the function applied to the matrix using a Schur decomposition. Note that *the function needs to accept complex numbers* as input in order to work with this algorithm. For example, the following code computes the zeroth-order Bessel function applied to a matrix.

```
>>> from scipy import special, linalg
>>> rng = np.random.default_rng()
>>> A = rng.random((3, 3))
>>> B = linalg.funm(A, lambda x: special.jv(0, x))
>>> A
array([[0.06369197, 0.90647174, 0.98024544],
       [0.68752227, 0.5604377 , 0.49142032],
       [0.86754578, 0.9746787 , 0.37932682]])
>>> B
array([[ 0.6929219 , -0.29728805, -0.15930896],
       [-0.16226043,  0.71967826, -0.22709386],
       [-0.19945564, -0.33379957,  0.70259022]])
>>> linalg.eigvals(A)
array([ 1.94835336+0.j, -0.72219681+0.j, -0.22270006+0.j])
>>> special.jv(0, linalg.eigvals(A))
array([0.25375345+0.j, 0.87379738+0.j, 0.98763955+0.j])
>>> linalg.eigvals(B)
array([0.25375345+0.j, 0.87379738+0.j, 0.98763955+0.j])
```

Note how, by virtue of how matrix analytic functions are defined, the Bessel function has acted on the matrix eigenvalues.

2.8.6 Special matrices

SciPy and NumPy provide several functions for creating special matrices that are frequently used in engineering and science.

Type	Function	Description
block diagonal	*scipy.linalg.block_diag*	Create a block diagonal matrix from the provided arrays.
circulant	*scipy.linalg.circulant*	Create a circulant matrix.
companion	*scipy.linalg.companion*	Create a companion matrix.
convolution	*scipy.linalg.convolution_matrix*	Create a convolution matrix.
Discrete Fourier	*scipy.linalg.dft*	Create a discrete Fourier transform matrix.
Fiedler	*scipy.linalg.fiedler*	Create a symmetric Fiedler matrix.
Fiedler Companion	*scipy.linalg.fiedler_companion*	Create a Fiedler companion matrix.
Hadamard	*scipy.linalg.hadamard*	Create an Hadamard matrix.
Hankel	*scipy.linalg.hankel*	Create a Hankel matrix.
Helmert	*scipy.linalg.helmert*	Create a Helmert matrix.
Hilbert	*scipy.linalg.hilbert*	Create a Hilbert matrix.
Inverse Hilbert	*scipy.linalg.invhilbert*	Create the inverse of a Hilbert matrix.
Leslie	*scipy.linalg.leslie*	Create a Leslie matrix.
Pascal	*scipy.linalg.pascal*	Create a Pascal matrix.
Inverse Pascal	*scipy.linalg.invpascal*	Create the inverse of a Pascal matrix.
Toeplitz	*scipy.linalg.toeplitz*	Create a Toeplitz matrix.
Van der Monde	numpy.vander	Create a Van der Monde matrix.

For examples of the use of these functions, see their respective docstrings.

2.9 Sparse eigenvalue problems with ARPACK

2.9.1 Introduction

ARPACK[1] is a Fortran package which provides routines for quickly finding a few eigenvalues/eigenvectors of large sparse matrices. In order to find these solutions, it requires only left-multiplication by the matrix in question. This operation is performed through a *reverse-communication* interface. The result of this structure is that ARPACK is able to find eigenvalues and eigenvectors of any linear function mapping a vector to a vector.

All of the functionality provided in ARPACK is contained within the two high-level interfaces `scipy.sparse.linalg.eigs` and `scipy.sparse.linalg.eigsh`. `eigs` provides interfaces for finding the eigenvalues/vectors of real or complex nonsymmetric square matrices, while `eigsh` provides interfaces for real-symmetric or complex-hermitian matrices.

2.9.2 Basic functionality

ARPACK can solve either standard eigenvalue problems of the form

$$A\mathbf{x} = \lambda\mathbf{x}$$

or general eigenvalue problems of the form

$$A\mathbf{x} = \lambda M\mathbf{x}.$$

The power of ARPACK is that it can compute only a specified subset of eigenvalue/eigenvector pairs. This is accomplished through the keyword `which`. The following values of `which` are available:

- `which = 'LM'` : Eigenvalues with largest magnitude (`eigs`, `eigsh`), that is, largest eigenvalues in the euclidean norm of complex numbers.
- `which = 'SM'` : Eigenvalues with smallest magnitude (`eigs`, `eigsh`), that is, smallest eigenvalues in the euclidean norm of complex numbers.
- `which = 'LR'` : Eigenvalues with largest real part (`eigs`).
- `which = 'SR'` : Eigenvalues with smallest real part (`eigs`).
- `which = 'LI'` : Eigenvalues with largest imaginary part (`eigs`).
- `which = 'SI'` : Eigenvalues with smallest imaginary part (`eigs`).
- `which = 'LA'` : Eigenvalues with largest algebraic value (`eigsh`), that is, largest eigenvalues inclusive of any negative sign.
- `which = 'SA'` : Eigenvalues with smallest algebraic value (`eigsh`), that is, smallest eigenvalues inclusive of any negative sign.
- `which = 'BE'` : Eigenvalues from both ends of the spectrum (`eigsh`).

Note that ARPACK is generally better at finding extremal eigenvalues, that is, eigenvalues with large magnitudes. In particular, using `which = 'SM'` may lead to slow execution time and/or anomalous results. A better approach is to use *shift-invert mode*.

[1] http://www.caam.rice.edu/software/ARPACK/

2.9.3 Shift-invert mode

Shift-invert mode relies on the following observation. For the generalized eigenvalue problem

$$A\mathbf{x} = \lambda M\mathbf{x},$$

it can be shown that

$$(A - \sigma M)^{-1}M\mathbf{x} = \nu\mathbf{x},$$

where

$$\nu = \frac{1}{\lambda - \sigma}.$$

2.9.4 Examples

Imagine you'd like to find the smallest and largest eigenvalues and the corresponding eigenvectors for a large matrix. ARPACK can handle many forms of input: dense matrices ,such as `numpy.ndarray` instances, sparse matrices, such as *`scipy.sparse.csr_matrix`*, or a general linear operator derived from *`scipy.sparse.linalg.LinearOperator`*. For this example, for simplicity, we'll construct a symmetric, positive-definite matrix.

```
>>> import numpy as np
>>> from scipy.linalg import eig, eigh
>>> from scipy.sparse.linalg import eigs, eigsh
>>> np.set_printoptions(suppress=True)
>>> rng = np.random.default_rng()
>>>
>>> X = rng.random((100, 100)) - 0.5
>>> X = np.dot(X, X.T)  # create a symmetric matrix
```

We now have a symmetric matrix `X`, with which to test the routines. First, compute a standard eigenvalue decomposition using `eigh`:

```
>>> evals_all, evecs_all = eigh(X)
```

As the dimension of `X` grows, this routine becomes very slow. Especially, if only a few eigenvectors and eigenvalues are needed, `ARPACK` can be a better option. First let's compute the largest eigenvalues (`which = 'LM'`) of `X` and compare them to the known results:

```
>>> evals_large, evecs_large = eigsh(X, 3, which='LM')
>>> print(evals_all[-3:])
[29.22435321 30.05590784 30.58591252]
>>> print(evals_large)
[29.22435321 30.05590784 30.58591252]
>>> print(np.dot(evecs_large.T, evecs_all[:,-3:]))
array([[-1.  0.  0.],       # may vary (signs)
       [ 0.  1.  0.],
       [-0.  0. -1.]])
```

The results are as expected. ARPACK recovers the desired eigenvalues and they match the previously known results. Furthermore, the eigenvectors are orthogonal, as we'd expect. Now, let's attempt to solve for the eigenvalues with smallest magnitude:

```
>>> evals_small, evecs_small = eigsh(X, 3, which='SM')
Traceback (most recent call last):       # may vary (convergence)
...
scipy.sparse.linalg.eigen.arpack.arpack.ArpackNoConvergence:
ARPACK error -1: No convergence (1001 iterations, 0/3 eigenvectors converged)
```

Oops. We see that, as mentioned above, ARPACK is not quite as adept at finding small eigenvalues. There are a few ways this problem can be addressed. We could increase the tolerance (`tol`) to lead to faster convergence:

```
>>> evals_small, evecs_small = eigsh(X, 3, which='SM', tol=1E-2)
>>> evals_all[:3]
array([0.00053181, 0.00298319, 0.01387821])
>>> evals_small
array([0.00053181, 0.00298319, 0.01387821])
>>> np.dot(evecs_small.T, evecs_all[:,:3])
array([[ 0.99999999  0.00000024 -0.00000049],    # may vary (signs)
       [-0.00000023  0.99999999  0.00000056],
       [ 0.00000031 -0.00000037  0.99999852]])
```

This works, but we lose the precision in the results. Another option is to increase the maximum number of iterations (`maxiter`) from 1000 to 5000:

```
>>> evals_small, evecs_small = eigsh(X, 3, which='SM', maxiter=5000)
>>> evals_all[:3]
array([0.00053181, 0.00298319, 0.01387821])
>>> evals_small
array([0.00053181, 0.00298319, 0.01387821])
>>> np.dot(evecs_small.T, evecs_all[:,:3])
array([[ 1.  0.  0.],           # may vary (signs)
       [-0.  1.  0.],
       [ 0.  0. -1.]])
```

We get the results we'd hoped for, but the computation time is much longer. Fortunately, ARPACK contains a mode that allows a quick determination of non-external eigenvalues: *shift-invert mode*. As mentioned above, this mode involves transforming the eigenvalue problem to an equivalent problem with different eigenvalues. In this case, we hope to find eigenvalues near zero, so we'll choose `sigma = 0`. The transformed eigenvalues will then satisfy $\nu = 1/(\lambda - \sigma) = 1/\lambda$, so our small eigenvalues λ become large eigenvalues ν.

```
>>> evals_small, evecs_small = eigsh(X, 3, sigma=0, which='LM')
>>> evals_all[:3]
array([0.00053181, 0.00298319, 0.01387821])
>>> evals_small
array([0.00053181, 0.00298319, 0.01387821])
>>> np.dot(evecs_small.T, evecs_all[:,:3])
array([[ 1.  0.  0.],    # may vary (signs)
       [ 0. -1. -0.],
       [-0. -0.  1.]])
```

We get the results we were hoping for, with much less computational time. Note that the transformation from $\nu \to \lambda$ takes place entirely in the background. The user need not worry about the details.

The shift-invert mode provides more than just a fast way to obtain a few small eigenvalues. Say, you desire to find internal eigenvalues and eigenvectors, e.g., those nearest to $\lambda = 1$. Simply set `sigma = 1` and ARPACK will take care of the rest:

```
>>> evals_mid, evecs_mid = eigsh(X, 3, sigma=1, which='LM')
>>> i_sort = np.argsort(abs(1. / (1 - evals_all)))[-3:]
>>> evals_all[i_sort]
array([0.94164107, 1.05464515, 0.99090277])
>>> evals_mid
array([0.94164107, 0.99090277, 1.05464515])
>>> print(np.dot(evecs_mid.T, evecs_all[:,i_sort]))
array([[-0.  1.  0.],     # may vary (signs)
       [-0. -0.  1.],
       [ 1.  0.  0.]]
```

The eigenvalues come out in a different order, but they're all there. Note that the shift-invert mode requires the internal solution of a matrix inverse. This is taken care of automatically by `eigsh` and *eigs*, but the operation can also be specified by the user. See the docstring of *scipy.sparse.linalg.eigsh* and *scipy.sparse.linalg.eigs* for details.

2.9.5 Use of LinearOperator

We consider now the case where you'd like to avoid creating a dense matrix and use *scipy.sparse.linalg.LinearOperator* instead. Our first linear operator applies element-wise multiplication between the input vector and a vector $\mathbf{d}$ provided by the user to the operator itself. This operator mimics a diagonal matrix with the elements of $\mathbf{d}$ along the main diagonal and it has the main benefit that the forward and adjoint operations are simple element-wise multiplications other than matrix-vector multiplications. For a diagonal matrix, we expect the eigenvalues to be equal to the elements along the main diagonal, in this case $\mathbf{d}$. The eigenvalues and eigenvectors obtained with `eigsh` are compared to those obtained by using `eigh` when applied to the dense matrix:

```
>>> from scipy.sparse.linalg import LinearOperator
>>> class Diagonal(LinearOperator):
...     def __init__(self, diag, dtype='float32'):
...         self.diag = diag
...         self.shape = (len(self.diag), len(self.diag))
...         self.dtype = np.dtype(dtype)
...     def _matvec(self, x):
...         return self.diag*x
...     def _rmatvec(self, x):
...         return self.diag*x
```

```
>>> N = 100
>>> rng = np.random.default_rng()
>>> d = rng.normal(0, 1, N).astype(np.float64)
>>> D = np.diag(d)
>>> Dop = Diagonal(d, dtype=np.float64)
```

```
>>> evals_all, evecs_all = eigh(D)
>>> evals_large, evecs_large = eigsh(Dop, 3, which='LA', maxiter=1e3)
>>> evals_all[-3:]
array([1.53092498, 1.77243671, 2.00582508])
>>> evals_large
array([1.53092498, 1.77243671, 2.00582508])
>>> print(np.dot(evecs_large.T, evecs_all[:,-3:]))
array([[-1.  0.  0.],     # may vary (signs)
```

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```
       [-0. -1.  0.],
       [ 0.  0. -1.]]
```

In this case, we have created a quick and easy `Diagonal` operator. The external library PyLops provides similar capabilities in the Diagonal operator, as well as several other operators.

Finally, we consider a linear operator that mimics the application of a first-derivative stencil. In this case, the operator is equivalent to a real nonsymmetric matrix. Once again, we compare the estimated eigenvalues and eigenvectors with those from a dense matrix that applies the same first derivative to an input signal:

```
>>> class FirstDerivative(LinearOperator):
...     def __init__(self, N, dtype='float32'):
...         self.N = N
...         self.shape = (self.N, self.N)
...         self.dtype = np.dtype(dtype)
...     def _matvec(self, x):
...         y = np.zeros(self.N, self.dtype)
...         y[1:-1] = (0.5*x[2:]-0.5*x[0:-2])
...         return y
...     def _rmatvec(self, x):
...         y = np.zeros(self.N, self.dtype)
...         y[0:-2] = y[0:-2] - (0.5*x[1:-1])
...         y[2:] = y[2:] + (0.5*x[1:-1])
...         return y
```

```
>>> N = 21
>>> D = np.diag(0.5*np.ones(N-1), k=1) - np.diag(0.5*np.ones(N-1), k=-1)
>>> D[0] = D[-1] = 0 # take away edge effects
>>> Dop = FirstDerivative(N, dtype=np.float64)
```

```
>>> evals_all, evecs_all = eig(D)
>>> evals_large, evecs_large = eigs(Dop, 4, which='LI')
>>> evals_all_imag = evals_all.imag
>>> isort_imag = np.argsort(np.abs(evals_all_imag))
>>> evals_all_imag = evals_all_imag[isort_imag]
>>> evals_large_imag = evals_large.imag
>>> isort_imag = np.argsort(np.abs(evals_large_imag))
>>> evals_large_imag = evals_large_imag[isort_imag]
>>> evals_all_imag[-4:]
array([-0.95105652, 0.95105652, -0.98768834, 0.98768834])
>>> evals_large_imag
array([0.95105652, -0.95105652, 0.98768834, -0.98768834])
```

Note that the eigenvalues of this operator are all imaginary. Moreover, the keyword `which='LI'` of *scipy.sparse.linalg.eigs* produces the eigenvalues with largest absolute imaginary part (both positive and negative). Again, a more advanced implementation of the first-derivative operator is available in the PyLops library under the name of FirstDerivative operator.

2.9.6 References

2.10 Compressed Sparse Graph Routines (`scipy.sparse.csgraph`)

2.10.1 Example: Word Ladders

A Word Ladder is a word game invented by Lewis Carroll, in which players find paths between words by switching one letter at a time. For example, one can link "ape" and "man" in the following way:

$$\text{ape} \to \text{apt} \to \text{ait} \to \text{bit} \to \text{big} \to \text{bag} \to \text{mag} \to \text{man}$$

Note that each step involves changing just one letter of the word. This is just one possible path from "ape" to "man", but is it the shortest possible path? If we desire to find the shortest word-ladder path between two given words, the sparse graph submodule can help.

First, we need a list of valid words. Many operating systems have such a list built in. For example, on linux, a word list can often be found at one of the following locations:

```
/usr/share/dict
/var/lib/dict
```

Another easy source for words are the Scrabble word lists available at various sites around the internet (search with your favorite search engine). We'll first create this list. The system word lists consist of a file with one word per line. The following should be modified to use the particular word list you have available:

```
>>> word_list = open('/usr/share/dict/words').readlines()
>>> word_list = map(str.strip, word_list)
```

We want to look at words of length 3, so let's select just those words of the correct length. We'll also eliminate words which start with upper-case (proper nouns) or contain non-alphanumeric characters, like apostrophes and hyphens. Finally, we'll make sure everything is lower-case for comparison later:

```
>>> word_list = [word for word in word_list if len(word) == 3]
>>> word_list = [word for word in word_list if word[0].islower()]
>>> word_list = [word for word in word_list if word.isalpha()]
>>> word_list = list(map(str.lower, word_list))
>>> len(word_list)
586    # may vary
```

Now we have a list of 586 valid three-letter words (the exact number may change depending on the particular list used). Each of these words will become a node in our graph, and we will create edges connecting the nodes associated with each pair of words which differs by only one letter.

There are efficient ways to do this, and inefficient ways to do this. To do this as efficiently as possible, we're going to use some sophisticated numpy array manipulation:

```
>>> import numpy as np
>>> word_list = np.asarray(word_list)
>>> word_list.dtype   # these are unicode characters in Python 3
dtype('<U3')
>>> word_list.sort()  # sort for quick searching later
```

We have an array where each entry is three unicode characters long. We'd like to find all pairs where exactly one character is different. We'll start by converting each word to a 3-D vector:

```
>>> word_bytes = np.ndarray((word_list.size, word_list.itemsize),
...                         dtype='uint8',
...                         buffer=word_list.data)
>>> # each unicode character is four bytes long. We only need first byte
>>> # we know that there are three characters in each word
>>> word_bytes = word_bytes[:, ::word_list.itemsize//3]
>>> word_bytes.shape
(586, 3)    # may vary
```

Now, we'll use the Hamming distance between each point to determine which pairs of words are connected. The Hamming distance measures the fraction of entries between two vectors which differ: any two words with a Hamming distance equal to $1/N$, where N is the number of letters, are connected in the word ladder:

```
>>> from scipy.spatial.distance import pdist, squareform
>>> from scipy.sparse import csr_matrix
>>> hamming_dist = pdist(word_bytes, metric='hamming')
>>> # there are three characters in each word
>>> graph = csr_matrix(squareform(hamming_dist < 1.5 / 3))
```

When comparing the distances, we don't use an equality because this can be unstable for floating point values. The inequality produces the desired result, as long as no two entries of the word list are identical. Now, that our graph is set up, we'll use a shortest path search to find the path between any two words in the graph:

```
>>> i1 = word_list.searchsorted('ape')
>>> i2 = word_list.searchsorted('man')
>>> word_list[i1]
'ape'
>>> word_list[i2]
'man'
```

We need to check that these match, because if the words are not in the list, that will not be the case. Now, all we need is to find the shortest path between these two indices in the graph. We'll use Dijkstra's algorithm, because it allows us to find the path for just one node:

```
>>> from scipy.sparse.csgraph import dijkstra
>>> distances, predecessors = dijkstra(graph, indices=i1,
...                                    return_predecessors=True)
>>> print(distances[i2])
5.0    # may vary
```

So we see that the shortest path between "ape" and "man" contains only five steps. We can use the predecessors returned by the algorithm to reconstruct this path:

```
>>> path = []
>>> i = i2
>>> while i != i1:
...     path.append(word_list[i])
...     i = predecessors[i]
>>> path.append(word_list[i1])
>>> print(path[::-1])
['ape', 'apt', 'opt', 'oat', 'mat', 'man']    # may vary
```

This is three fewer links than our initial example: the path from "ape" to "man" is only five steps.

Using other tools in the module, we can answer other questions. For example, are there three-letter words which are not linked in a word ladder? This is a question of connected components in the graph:

```
>>> from scipy.sparse.csgraph import connected_components
>>> N_components, component_list = connected_components(graph)
>>> print(N_components)
15    # may vary
```

In this particular sample of three-letter words, there are 15 connected components: that is, 15 distinct sets of words with no paths between the sets. How many words are there in each of these sets? We can learn this from the list of components:

```
>>> [np.sum(component_list == i) for i in range(N_components)]
[571, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1]    # may vary
```

There is one large connected set and 14 smaller ones. Let's look at the words in the smaller ones:

```
>>> [list(word_list[np.nonzero(component_list == i)]) for i in range(1, N_
↪components)]
[['aha'],    # may vary
 ['chi'],
 ['ebb'],
 ['ems', 'emu'],
 ['gnu'],
 ['ism'],
 ['khz'],
 ['nth'],
 ['ova'],
 ['qua'],
 ['ugh'],
 ['ups'],
 ['urn'],
 ['use']]
```

These are all the three-letter words which do not connect to others via a word ladder.

We might also be curious about which words are maximally separated. Which two words take the most links to connect? We can determine this by computing the matrix of all shortest paths. Note that, by convention, the distance between two non-connected points is reported to be infinity, so we'll need to remove these before finding the maximum:

```
>>> distances, predecessors = dijkstra(graph, return_predecessors=True)
>>> max_distance = np.max(distances[~np.isinf(distances)])
>>> print(max_distance)
13.0    # may vary
```

So, there is at least one pair of words which takes 13 steps to get from one to the other! Let's determine which these are:

```
>>> i1, i2 = np.nonzero(distances == max_distance)
>>> list(zip(word_list[i1], word_list[i2]))
[('imp', 'ohm'),    # may vary
 ('imp', 'ohs'),
 ('ohm', 'imp'),
 ('ohm', 'ump'),
 ('ohs', 'imp'),
 ('ohs', 'ump'),
```

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```
 ('ump', 'ohm'),
 ('ump', 'ohs')]
```

We see that there are two pairs of words which are maximally separated from each other: 'imp' and 'ump' on the one hand, and 'ohm' and 'ohs' on the other. We can find the connecting list in the same way as above:

```
>>> path = []
>>> i = i2[0]
>>> while i != i1[0]:
...     path.append(word_list[i])
...     i = predecessors[i1[0], i]
>>> path.append(word_list[i1[0]])
>>> print(path[::-1])
['imp', 'amp', 'asp', 'ass', 'ads', 'add', 'aid', 'mid', 'mod', 'moo', 'too',
 ↪'tho', 'oho', 'ohm']    # may vary
```

This gives us the path we desired to see.

Word ladders are just one potential application of scipy's fast graph algorithms for sparse matrices. Graph theory makes appearances in many areas of mathematics, data analysis, and machine learning. The sparse graph tools are flexible enough to handle many of these situations.

2.11 Spatial data structures and algorithms (`scipy.spatial`)

scipy.spatial can compute triangulations, Voronoi diagrams, and convex hulls of a set of points, by leveraging the Qhull library.

Moreover, it contains *KDTree* implementations for nearest-neighbor point queries, and utilities for distance computations in various metrics.

2.11.1 Delaunay triangulations

The Delaunay triangulation is a subdivision of a set of points into a non-overlapping set of triangles, such that no point is inside the circumcircle of any triangle. In practice, such triangulations tend to avoid triangles with small angles.

Delaunay triangulation can be computed using *scipy.spatial* as follows:

```
>>> from scipy.spatial import Delaunay
>>> points = np.array([[0, 0], [0, 1.1], [1, 0], [1, 1]])
>>> tri = Delaunay(points)
```

We can visualize it:

```
>>> import matplotlib.pyplot as plt
>>> plt.triplot(points[:,0], points[:,1], tri.simplices)
>>> plt.plot(points[:,0], points[:,1], 'o')
```

And add some further decorations:

```
>>> for j, p in enumerate(points):
...     plt.text(p[0]-0.03, p[1]+0.03, j, ha='right') # label the points
```

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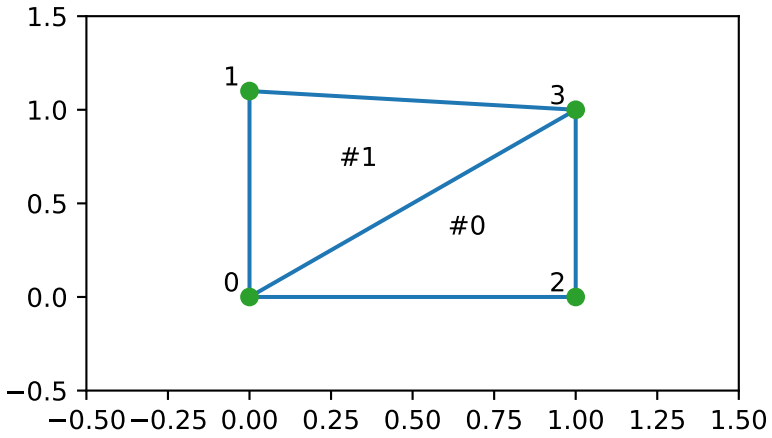
```
>>> for j, s in enumerate(tri.simplices):
...     p = points[s].mean(axis=0)
...     plt.text(p[0], p[1], '#%d' % j, ha='center') # label triangles
>>> plt.xlim(-0.5, 1.5); plt.ylim(-0.5, 1.5)
>>> plt.show()
```



The structure of the triangulation is encoded in the following way: the `simplices` attribute contains the indices of the points in the `points` array that make up the triangle. For instance:

```
>>> i = 1
>>> tri.simplices[i,:]
array([3, 1, 0], dtype=int32)
>>> points[tri.simplices[i,:]]
array([[ 1. ,  1. ],
       [ 0. ,  1.1],
       [ 0. ,  0. ]])
```

Moreover, neighboring triangles can also be found:

```
>>> tri.neighbors[i]
array([-1,  0, -1], dtype=int32)
```

What this tells us is that this triangle has triangle #0 as a neighbor, but no other neighbors. Moreover, it tells us that neighbor 0 is opposite the vertex 1 of the triangle:

```
>>> points[tri.simplices[i, 1]]
array([ 0. ,  1.1])
```

Indeed, from the figure, we see that this is the case.

Qhull can also perform tessellations to simplices for higher-dimensional point sets (for instance, subdivision into tetrahedra in 3-D).

Coplanar points

It is important to note that not *all* points necessarily appear as vertices of the triangulation, due to numerical precision issues in forming the triangulation. Consider the above with a duplicated point:

```
>>> points = np.array([[0, 0], [0, 1], [1, 0], [1, 1], [1, 1]])
>>> tri = Delaunay(points)
>>> np.unique(tri.simplices.ravel())
array([0, 1, 2, 3], dtype=int32)
```

Observe that point #4, which is a duplicate, does not occur as a vertex of the triangulation. That this happened is recorded:

```
>>> tri.coplanar
array([[4, 0, 3]], dtype=int32)
```

This means that point 4 resides near triangle 0 and vertex 3, but is not included in the triangulation.

Note that such degeneracies can occur not only because of duplicated points, but also for more complicated geometrical reasons, even in point sets that at first sight seem well-behaved.

However, Qhull has the "QJ" option, which instructs it to perturb the input data randomly until degeneracies are resolved:

```
>>> tri = Delaunay(points, qhull_options="QJ Pp")
>>> points[tri.simplices]
array([[[1, 0],
        [1, 1],
        [0, 0]],
       [[1, 1],
        [1, 1],
        [1, 0]],
       [[1, 1],
        [0, 1],
        [0, 0]],
       [[0, 1],
        [1, 1],
        [1, 1]]])
```

Two new triangles appeared. However, we see that they are degenerate and have zero area.

2.11.2 Convex hulls

A convex hull is the smallest convex object containing all points in a given point set.

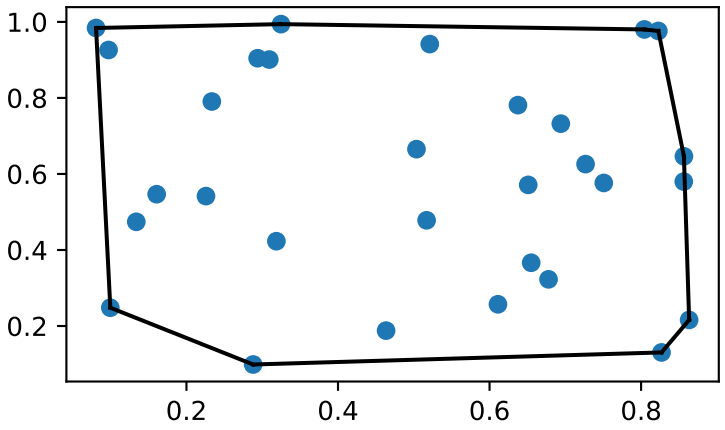
These can be computed via the Qhull wrappers in *scipy.spatial* as follows:

```
>>> from scipy.spatial import ConvexHull
>>> rng = np.random.default_rng()
>>> points = rng.random((30, 2))   # 30 random points in 2-D
>>> hull = ConvexHull(points)
```

The convex hull is represented as a set of N 1-D simplices, which in 2-D means line segments. The storage scheme is exactly the same as for the simplices in the Delaunay triangulation discussed above.

We can illustrate the above result:

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> for simplex in hull.simplices:
...     plt.plot(points[simplex,0], points[simplex,1], 'k-')
>>> plt.show()
```



The same can be achieved with *scipy.spatial.convex_hull_plot_2d*.

2.11.3 Voronoi diagrams

A Voronoi diagram is a subdivision of the space into the nearest neighborhoods of a given set of points.

There are two ways to approach this object using *scipy.spatial*. First, one can use the *KDTree* to answer the question "which of the points is closest to this one", and define the regions that way:

```
>>> from scipy.spatial import KDTree
>>> points = np.array([[0, 0], [0, 1], [0, 2], [1, 0], [1, 1], [1, 2],
...                    [2, 0], [2, 1], [2, 2]])
>>> tree = KDTree(points)
>>> tree.query([0.1, 0.1])
(0.14142135623730953, 0)
```

So the point `(0.1, 0.1)` belongs to region `0`. In color:

```
>>> x = np.linspace(-0.5, 2.5, 31)
>>> y = np.linspace(-0.5, 2.5, 33)
>>> xx, yy = np.meshgrid(x, y)
>>> xy = np.c_[xx.ravel(), yy.ravel()]
>>> import matplotlib.pyplot as plt
>>> dx_half, dy_half = np.diff(x[:2])[0] / 2., np.diff(y[:2])[0] / 2.
>>> x_edges = np.concatenate((x - dx_half, [x[-1] + dx_half]))
>>> y_edges = np.concatenate((y - dy_half, [y[-1] + dy_half]))
>>> plt.pcolormesh(x_edges, y_edges, tree.query(xy)[1].reshape(33, 31),␣
↪shading='flat')
```

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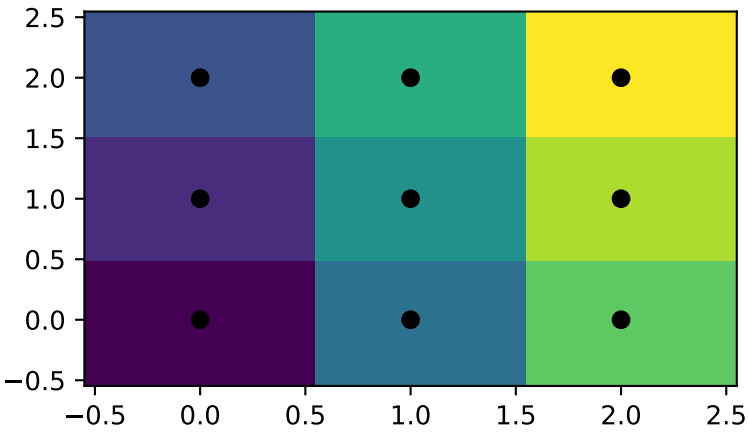
```
>>> plt.plot(points[:,0], points[:,1], 'ko')
>>> plt.show()
```



This does not, however, give the Voronoi diagram as a geometrical object.

The representation in terms of lines and points can be again obtained via the Qhull wrappers in *scipy.spatial*:

```
>>> from scipy.spatial import Voronoi
>>> vor = Voronoi(points)
>>> vor.vertices
array([[0.5, 0.5],
       [0.5, 1.5],
       [1.5, 0.5],
       [1.5, 1.5]])
```

The Voronoi vertices denote the set of points forming the polygonal edges of the Voronoi regions. In this case, there are 9 different regions:

```
>>> vor.regions
[[], [-1, 0], [-1, 1], [1, -1, 0], [3, -1, 2], [-1, 3], [-1, 2], [0, 1, 3, 2],
 ↪ [2, -1, 0], [3, -1, 1]]
```

Negative value `-1` again indicates a point at infinity. Indeed, only one of the regions, `[0, 1, 3, 2]`, is bounded. Note here that due to similar numerical precision issues as in Delaunay triangulation above, there may be fewer Voronoi regions than input points.

The ridges (lines in 2-D) separating the regions are described as a similar collection of simplices as the convex hull pieces:

```
>>> vor.ridge_vertices
[[-1, 0], [-1, 0], [-1, 1], [-1, 1], [0, 1], [-1, 3], [-1, 2], [2, 3], [-1,␣
 ↪3], [-1, 2], [1, 3], [0, 2]]
```

These numbers present the indices of the Voronoi vertices making up the line segments. `-1` is again a point at infinity — only 4 of the 12 lines are a bounded line segment, while others extend to infinity.

The Voronoi ridges are perpendicular to the lines drawn between the input points. To which two points each ridge corresponds is also recorded:

```
>>> vor.ridge_points
array([[0, 3],
       [0, 1],
       [2, 5],
       [2, 1],
       [1, 4],
       [7, 8],
       [7, 6],
       [7, 4],
       [8, 5],
       [6, 3],
       [4, 5],
       [4, 3]], dtype=int32)
```

This information, taken together, is enough to construct the full diagram.

We can plot it as follows. First, the points and the Voronoi vertices:

```
>>> plt.plot(points[:, 0], points[:, 1], 'o')
>>> plt.plot(vor.vertices[:, 0], vor.vertices[:, 1], '*')
>>> plt.xlim(-1, 3); plt.ylim(-1, 3)
```

Plotting the finite line segments goes as for the convex hull, but now we have to guard for the infinite edges:

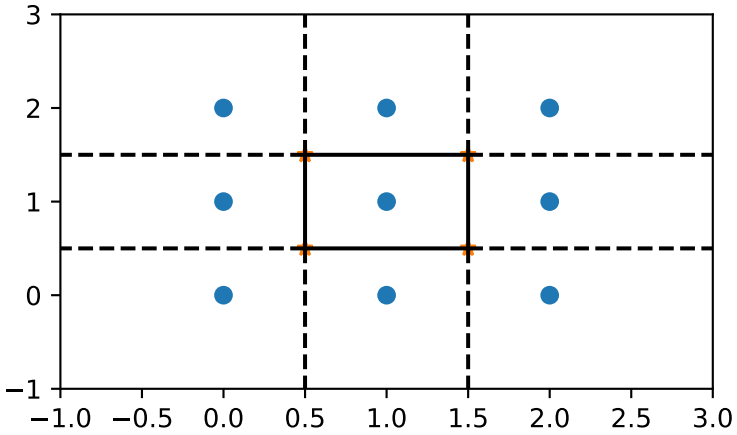
```
>>> for simplex in vor.ridge_vertices:
...     simplex = np.asarray(simplex)
...     if np.all(simplex >= 0):
...         plt.plot(vor.vertices[simplex, 0], vor.vertices[simplex, 1], 'k-')
```

The ridges extending to infinity require a bit more care:

```
>>> center = points.mean(axis=0)
>>> for pointidx, simplex in zip(vor.ridge_points, vor.ridge_vertices):
...     simplex = np.asarray(simplex)
...     if np.any(simplex < 0):
...         i = simplex[simplex >= 0][0] # finite end Voronoi vertex
...         t = points[pointidx[1]] - points[pointidx[0]]  # tangent
...         t = t / np.linalg.norm(t)
...         n = np.array([-t[1], t[0]]) # normal
...         midpoint = points[pointidx].mean(axis=0)
...         far_point = vor.vertices[i] + np.sign(np.dot(midpoint - center,␣
↪n)) * n * 100
...         plt.plot([vor.vertices[i,0], far_point[0]],
...                  [vor.vertices[i,1], far_point[1]], 'k--')
>>> plt.show()
```

This plot can also be created using *scipy.spatial.voronoi_plot_2d*.

Voronoi diagrams can be used to create interesting generative art. Try playing with the settings of this `mandala` function to create your own!




```
>>> import numpy as np
>>> from scipy import spatial
>>> import matplotlib.pyplot as plt
```

```
>>> def mandala(n_iter, n_points, radius):
...     """Creates a mandala figure using Voronoi tesselations.
...
...     Parameters
...     ----------
...     n_iter : int
...         Number of iterations, i.e. how many times the equidistant points␣
↪will
...         be generated.
...     n_points : int
...         Number of points to draw per iteration.
...     radius : scalar
...         The radial expansion factor.
...
...     Returns
...     -------
...     fig : matplotlib.Figure instance
...
...     Notes
...     -----
...     This code is adapted from the work of Audrey Roy Greenfeld [1]_ and␣
↪Carlos
...     Focil-Espinosa [2]_, who created beautiful mandalas with Python code.␣
↪ That
...     code in turn was based on Antonio Sánchez Chinchón's R code [3]_.
...
...     References
...     ----------
...     .. [1] https://www.codemakesmehappy.com/2019/09/voronoi-mandalas.html
```

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```
...
...     .. [2] https://github.com/CarlosFocil/mandalapy
...
...     .. [3] https://github.com/aschinchon/mandalas
...
...     """
...     fig = plt.figure(figsize=(10, 10))
...     ax = fig.add_subplot(111)
...     ax.set_axis_off()
...     ax.set_aspect('equal', adjustable='box')
...
...     angles = np.linspace(0, 2*np.pi * (1 - 1/n_points), num=n_points) +␣
↪np.pi/2
...     # Starting from a single center point, add points iteratively
...     xy = np.array([[0, 0]])
...     for k in range(n_iter):
...         t1 = np.array([])
...         t2 = np.array([])
...         # Add `n_points` new points around each existing point in this␣
↪iteration
...         for i in range(xy.shape[0]):
...             t1 = np.append(t1, xy[i, 0] + radius**k * np.cos(angles))
...             t2 = np.append(t2, xy[i, 1] + radius**k * np.sin(angles))
...
...         xy = np.column_stack((t1, t2))
...
...     # Create the Mandala figure via a Voronoi plot
...     spatial.voronoi_plot_2d(spatial.Voronoi(xy), ax=ax)
...
...     return fig
```

```
>>> # Modify the following parameters in order to get different figures
>>> n_iter = 3
>>> n_points = 6
>>> radius = 4
```

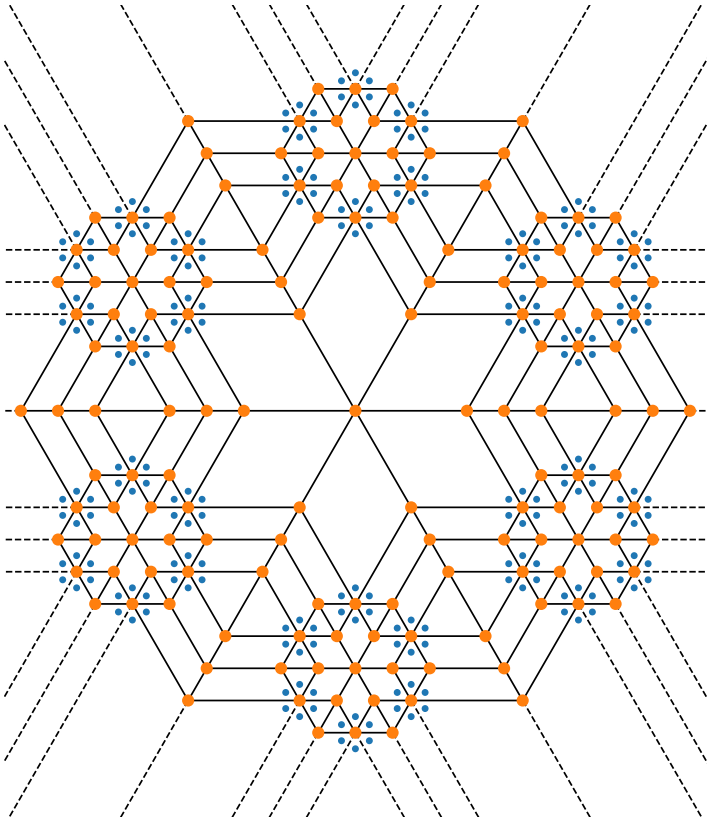
```
>>> fig = mandala(n_iter, n_points, radius)
>>> plt.show()
```

2.12 Statistics (`scipy.stats`)

2.12.1 Introduction

In this tutorial, we discuss many, but certainly not all, features of `scipy.stats`. The intention here is to provide a user with a working knowledge of this package. We refer to the *reference manual* for further details.

Note: This documentation is work in progress.



Discrete Statistical Distributions

Discrete random variables take on only a countable number of values. The commonly used distributions are included in SciPy and described in this document. Each discrete distribution can take one extra integer parameter: L. The relationship between the general distribution p and the standard distribution p_0 is

$$p(x) = p_0(x - L)$$

which allows for shifting of the input. When a distribution generator is initialized, the discrete distribution can either specify the beginning and ending (integer) values a and b which must be such that

$$p_0(x) = 0 \quad x < a \text{ or } x > b$$

in which case, it is assumed that the pdf function is specified on the integers $a + mk \leq b$ where k is a non-negative integer ($0, 1, 2, \ldots$) and m is a positive integer multiplier. Alternatively, the two lists x_k and $p(x_k)$ can be provided directly in which case a dictionary is set up internally to evaluate probabilities and generate random variates.

Probability Mass Function (PMF)

The probability mass function of a random variable X is defined as the probability that the random variable takes on a particular value.

$$p(x_k) = P[X = x_k]$$

This is also sometimes called the probability density function, although technically

$$f(x) = \sum_k p(x_k)\,\delta(x - x_k)$$

is the probability density function for a discrete distribution[1] .

Cumulative Distribution Function (CDF)

The cumulative distribution function is

$$F(x) = P[X \leq x] = \sum_{x_k \leq x} p(x_k)$$

and is also useful to be able to compute. Note that

$$F(x_k) - F(x_{k-1}) = p(x_k)$$

Survival Function

The survival function is just

$$S(x) = 1 - F(x) = P[X > k]$$

the probability that the random variable is strictly larger than k .

Percent Point Function (Inverse CDF)

The percent point function is the inverse of the cumulative distribution function and is

$$G(q) = F^{-1}(q)$$

for discrete distributions, this must be modified for cases where there is no x_k such that $F(x_k) = q$. In these cases we choose $G(q)$ to be the smallest value $x_k = G(q)$ for which $F(x_k) \geq q$. If $q = 0$ then we define $G(0) = a - 1$. This definition allows random variates to be defined in the same way as with continuous rv's using the inverse cdf on a uniform distribution to generate random variates.

[1] XXX: Unknown layout Plain Layout: Note that we will be using p to represent the probability mass function and a parameter (a XXX: probability). The usage should be obvious from context.

Inverse survival function

The inverse survival function is the inverse of the survival function

$$Z(\alpha) = S^{-1}(\alpha) = G(1-\alpha)$$

and is thus the smallest non-negative integer k for which $F(k) \geq 1-\alpha$ or the smallest non-negative integer k for which $S(k) \leq \alpha$.

Hazard functions

If desired, the hazard function and the cumulative hazard function could be defined as

$$h(x_k) = \frac{p(x_k)}{1 - F(x_k)}$$

and

$$H(x) = \sum_{x_k \leq x} h(x_k) = \sum_{x_k \leq x} \frac{F(x_k) - F(x_{k-1})}{1 - F(x_k)}.$$

Moments

Non-central moments are defined using the PDF

$$\mu'_m = E[X^m] = \sum_k x_k^m p(x_k).$$

Central moments are computed similarly $\mu = \mu'_1$

$$\begin{aligned}\mu_m = E[(X-\mu)^m] &= \sum_k (x_k - \mu)^m p(x_k) \\ &= \sum_{k=0}^{m} (-1)^{m-k} \left(\begin{array}{c} m \\ k \end{array} \right) \mu^{m-k} \mu'_k\end{aligned}$$

The mean is the first moment

$$\mu = \mu'_1 = E[X] = \sum_k x_k p(x_k)$$

the variance is the second central moment

$$\mu_2 = E\left[(X-\mu)^2\right] = \sum_{x_k} x_k^2 p(x_k) - \mu^2.$$

Skewness is defined as

$$\gamma_1 = \frac{\mu_3}{\mu_2^{3/2}}$$

while (Fisher) kurtosis is

$$\gamma_2 = \frac{\mu_4}{\mu_2^2} - 3,$$

so that a normal distribution has a kurtosis of zero.

Moment generating function

The moment generating function is defined as

$$M_X(t) = E\left[e^{Xt}\right] = \sum_{x_k} e^{x_k t} p(x_k)$$

Moments are found as the derivatives of the moment generating function evaluated at 0.

Fitting data

To fit data to a distribution, maximizing the likelihood function is common. Alternatively, some distributions have well-known minimum variance unbiased estimators. These will be chosen by default, but the likelihood function will always be available for minimizing.

If $f_i(k;\boldsymbol{\theta})$ is the PDF of a random-variable where $\boldsymbol{\theta}$ is a vector of parameters (*e.g.* L and S), then for a collection of N independent samples from this distribution, the joint distribution the random vector $\mathbf{k}$ is

$$f(\mathbf{k};\boldsymbol{\theta}) = \prod_{i=1}^{N} f_i(k_i;\boldsymbol{\theta}).$$

The maximum likelihood estimate of the parameters $\boldsymbol{\theta}$ are the parameters which maximize this function with $\mathbf{x}$ fixed and given by the data:

$$\begin{aligned}\hat{\boldsymbol{\theta}} &= \arg\max_{\boldsymbol{\theta}} f(\mathbf{k};\boldsymbol{\theta}) \\ &= \arg\min_{\boldsymbol{\theta}} l_{\mathbf{k}}(\boldsymbol{\theta}).\end{aligned}$$

Where

$$\begin{aligned}l_{\mathbf{k}}(\boldsymbol{\theta}) &= -\sum_{i=1}^{N} \log f(k_i;\boldsymbol{\theta}) \\ &= -N\overline{\log f(k_i;\boldsymbol{\theta})}\end{aligned}$$

Standard notation for mean

We will use

$$\overline{y(\mathbf{x})} = \frac{1}{N}\sum_{i=1}^{N} y(x_i)$$

where N should be clear from context.

Combinations

Note that

$$k! = k\cdot(k-1)\cdot(k-2)\cdot\cdots\cdot 1 = \Gamma(k+1)$$

and has special cases of

$$\begin{aligned}0! &\equiv 1 \\ k! &\equiv 0 \quad k<0\end{aligned}$$

and

$$\left(\begin{array}{c} n \\ k \end{array}\right) = \frac{n!}{(n-k)!k!}.$$

If $n<0$ or $k<0$ or $k>n$ we define $\left(\begin{array}{c} n \\ k \end{array}\right) = 0$

Discrete Distributions in `scipy.stats`

Bernoulli Distribution

A Bernoulli random variable of parameter p takes one of only two values $X = 0$ or $X = 1$. The probability of success ($X = 1$) is p , and the probability of failure ($X = 0$) is $1 - p$. It can be thought of as a binomial random variable with $n = 1$. The PMF is $p(k) = 0$ for $k \neq 0, 1$ and

$$\begin{aligned}
p(k; p) &= \begin{cases} 1-p & k = 0 \\ p & k = 1 \end{cases} \\
F(x; p) &= \begin{cases} 0 & x < 0 \\ 1-p & 0 \leq x < 1 \\ 1 & 1 \leq x \end{cases} \\
G(q; p) &= \begin{cases} 0 & 0 \leq q < 1-p \\ 1 & 1-p \leq q \leq 1 \end{cases} \\
\mu &= p \\
\mu_2 &= p(1-p) \\
\gamma_3 &= \frac{1-2p}{\sqrt{p(1-p)}} \\
\gamma_4 &= \frac{1-6p(1-p)}{p(1-p)}
\end{aligned}$$

$$M(t) = 1 - p\left(1 - e^t\right)$$

$$\mu'_m = p$$

$$h[X] = p \log p + (1-p) \log(1-p)$$

Implementation: *scipy.stats.bernoulli*

Beta-Binomial Distribution

The beta-binomial distribution is a binomial distribution with a probability of success *p* that follows a beta distribution. The probability mass function for *betabinom*, defined for $0 \leq k \leq n$, is:

$$f(k; n, a, b) = \binom{n}{k} \frac{B(k+a, n-k+b)}{B(a, b)}$$

for `k` in `{0, 1, ..., n}`, where $B(a, b)$ is the Beta function.

In the limiting case of $a = b = 1$, the beta-binomial distribution reduces to a discrete uniform distribution:

$$f(k; n, 1, 1) = \frac{1}{n+1}$$

In the limiting case of $n = 1$, the beta-binomial distribution reduces to a Bernoulli distribution with the shape parameter $p = a/(a+b)$:

$$f(k; 1, a, b) = \begin{cases} a/(a+b) & \text{if } k = 0 \\ b/(a+b) & \text{if } k = 1 \end{cases}$$

Implementation: *scipy.stats.betabinom*

Binomial Distribution

A binomial random variable with parameters (n, p) can be described as the sum of n independent Bernoulli random variables of parameter p;

$$Y = \sum_{i=1}^{n} X_i.$$

Therefore, this random variable counts the number of successes in n independent trials of a random experiment where the probability of success is p.

$$\begin{aligned} p(k; n, p) &= \binom{n}{k} p^k (1-p)^{n-k} \quad k \in \{0, 1, \ldots n\}, \\ F(x; n, p) &= \sum_{k \le x} \binom{n}{k} p^k (1-p)^{n-k} = I_{1-p}(n - \lfloor x \rfloor, \lfloor x \rfloor + 1) \quad x \ge 0 \end{aligned}$$

where the incomplete beta integral is

$$I_x(a, b) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \int_0^x t^{a-1} (1-t)^{b-1} \, dt.$$

Now

$$\begin{aligned} \mu &= np \\ \mu_2 &= np(1-p) \\ \gamma_1 &= \frac{1-2p}{\sqrt{np(1-p)}} \\ \gamma_2 &= \frac{1-6p(1-p)}{np(1-p)}. \end{aligned}$$

$$M(t) = \left[1 - p\left(1 - e^t\right)\right]^n$$

Implementation: `scipy.stats.binom`

Boltzmann (truncated Planck) Distribution

$$\begin{aligned} p(k; N, \lambda) &= \frac{1 - e^{-\lambda}}{1 - e^{-\lambda N}} \exp(-\lambda k) \quad k \in \{0, 1, \ldots, N-1\} \\ F(x; N, \lambda) &= \begin{cases} 0 & x < 0 \\ \frac{1 - \exp[-\lambda(\lfloor x \rfloor + 1)]}{1 - \exp(-\lambda N)} & 0 \le x \le N-1 \\ 1 & x \ge N-1 \end{cases} \\ G(q, \lambda) &= \left\lceil -\frac{1}{\lambda} \log\left[1 - q\left(1 - e^{-\lambda N}\right)\right] - 1 \right\rceil \end{aligned}$$

Define $z = e^{-\lambda}$

$$\begin{aligned}
\mu &= \frac{z}{1-z} - \frac{Nz^N}{1-z^N} \\
\mu_2 &= \frac{z}{(1-z)^2} - \frac{N^2 z^N}{(1-z^N)^2} \\
\gamma_1 &= \frac{z(1+z)\left(\frac{1-z^N}{1-z}\right)^3 - N^3 z^N \left(1+z^N\right)}{\left[z\left(\frac{1-z^N}{1-z}\right)^2 - N^2 z^N\right]^{3/2}} \\
\gamma_2 &= \frac{z\left(1+4z+z^2\right)\left(\frac{1-z^N}{1-z}\right)^4 - N^4 z^N \left(1+4z^N+z^{2N}\right)}{\left[z\left(\frac{1-z^N}{1-z}\right)^2 - N^2 z^N\right]^2}
\end{aligned}$$

$$M(t) = \frac{1-e^{N(t-\lambda)}}{1-e^{t-\lambda}} \frac{1-e^{-\lambda}}{1-e^{-\lambda N}}$$

Implementation: `scipy.stats.boltzmann`

Planck (discrete exponential) Distribution

Named Planck because of its relationship to the black-body problem he solved.

$$\begin{aligned}
p(k;\lambda) &= \left(1-e^{-\lambda}\right) e^{-\lambda k} \quad k\lambda \geq 0 \\
F(x;\lambda) &= 1 - e^{-\lambda(\lfloor x \rfloor + 1)} \quad x\lambda \geq 0 \\
G(q;\lambda) &= \left\lceil -\frac{1}{\lambda}\log[1-q] - 1 \right\rceil .
\end{aligned}$$

$$\begin{aligned}
\mu &= \frac{1}{e^{\lambda}-1} \\
\mu_2 &= \frac{e^{-\lambda}}{(1-e^{-\lambda})^2} \\
\gamma_1 &= 2\cosh\left(\frac{\lambda}{2}\right) \\
\gamma_2 &= 4 + 2\cosh(\lambda)
\end{aligned}$$

$$M(t) = \frac{1-e^{-\lambda}}{1-e^{t-\lambda}}$$

$$h[X] = \frac{\lambda e^{-\lambda}}{1-e^{-\lambda}} - \log\left(1-e^{-\lambda}\right)$$

Implementation: `scipy.stats.planck`

Poisson Distribution

The Poisson random variable counts the number of successes in n independent Bernoulli trials in the limit as $n \to \infty$ and $p \to 0$ where the probability of success in each trial is p and $np = \lambda \geq 0$ is a constant. It can be used to approximate the Binomial random variable or in its own right to count the number of events that occur in the interval $[0, t]$ for a process satisfying certain "sparsity" constraints. The functions are:

$$\begin{aligned}
p(k;\lambda) &= e^{-\lambda}\frac{\lambda^k}{k!} \quad k \geq 0, \\
F(x;\lambda) &= \sum_{n=0}^{\lfloor x \rfloor} e^{-\lambda}\frac{\lambda^n}{n!} = \frac{1}{\Gamma(\lfloor x \rfloor + 1)}\int_{\lambda}^{\infty} t^{\lfloor x \rfloor} e^{-t} dt, \\
\mu &= \lambda \\
\mu_2 &= \lambda \\
\gamma_1 &= \frac{1}{\sqrt{\lambda}} \\
\gamma_2 &= \frac{1}{\lambda}.
\end{aligned}$$

$$M(t) = \exp\left[\lambda\left(e^t - 1\right)\right].$$

Implementation: *scipy.stats.poisson*

Geometric Distribution

The geometric random variable with parameter $p \in (0, 1)$ can be defined as the number of trials required to obtain a success where the probability of success on each trial is p . Thus,

$$\begin{aligned}
p(k;p) &= (1-p)^{k-1}p \quad k \geq 1 \\
F(x;p) &= 1 - (1-p)^{\lfloor x \rfloor} \quad x \geq 1 \\
G(q;p) &= \left\lceil \frac{\log(1-q)}{\log(1-p)} \right\rceil \\
\mu &= \frac{1}{p} \\
\mu_2 &= \frac{1-p}{p^2} \\
\gamma_1 &= \frac{2-p}{\sqrt{1-p}} \\
\gamma_2 &= \frac{p^2 - 6p + 6}{1-p}.
\end{aligned}$$

$$M(t) = \frac{p}{e^{-t} - (1-p)}$$

Implementation: *scipy.stats.geom*

Negative Binomial Distribution

The negative binomial random variable with parameters n and $p \in (0,1)$ can be defined as the number of *extra* independent trials (beyond n) required to accumulate a total of n successes where the probability of a success on each trial is p. Equivalently, this random variable is the number of failures encountered while accumulating n successes during independent trials of an experiment that succeeds with probability p. Thus,

$$\begin{aligned}
p(k;n,p) &= \left(\begin{array}{c} k+n-1 \\ n-1 \end{array}\right) p^n (1-p)^k \quad k \geq 0 \\
F(x;n,p) &= \sum_{i=0}^{\lfloor x \rfloor} \left(\begin{array}{c} i+n-1 \\ i \end{array}\right) p^n (1-p)^i \quad x \geq 0 \\
&= I_p(n, \lfloor x \rfloor + 1) \quad x \geq 0 \\
\mu &= n\frac{1-p}{p} \\
\mu_2 &= n\frac{1-p}{p^2} \\
\gamma_1 &= \frac{2-p}{\sqrt{n(1-p)}} \\
\gamma_2 &= \frac{p^2+6(1-p)}{n(1-p)}.
\end{aligned}$$

Recall that $I_p(a,b)$ is the incomplete beta integral.

Implementation: `scipy.stats.nbinom`

Hypergeometric Distribution

The hypergeometric random variable with parameters (M,n,N) counts the number of "good "objects in a sample of size N chosen without replacement from a population of M objects where n is the number of "good "objects in the total population.

$$\begin{aligned}
p(k;N,n,M) &= \frac{\left(\begin{array}{c} n \\ k \end{array}\right)\left(\begin{array}{c} M-n \\ N-k \end{array}\right)}{\left(\begin{array}{c} M \\ N \end{array}\right)} \quad N-(M-n) \leq k \leq \min(n,N) \\
F(x;N,n,M) &= \sum_{k=0}^{\lfloor x \rfloor} \frac{\left(\begin{array}{c} m \\ k \end{array}\right)\left(\begin{array}{c} N-m \\ n-k \end{array}\right)}{\left(\begin{array}{c} N \\ n \end{array}\right)}, \\
\mu &= \frac{nN}{M} \\
\mu_2 &= \frac{nN(M-n)(M-N)}{M^2(M-1)} \\
\gamma_1 &= \frac{(M-2n)(M-2N)}{M-2}\sqrt{\frac{M-1}{nN(M-m)(M-n)}} \\
\gamma_2 &= \frac{g(N,n,M)}{nN(M-n)(M-3)(M-2)(N-M)}
\end{aligned}$$

where (defining $m = M - n$)

$$\begin{aligned} g(N,n,M) &= m^3 - m^5 + 3m^2n - 6m^3n + m^4n + 3mn^2 \\ &\quad -12m^2n^2 + 8m^3n^2 + n^3 - 6mn^3 + 8m^2n^3 \\ &\quad +mn^4 - n^5 - 6m^3N + 6m^4N + 18m^2nN \\ &\quad -6m^3nN + 18mn^2N - 24m^2n^2N - 6n^3N \\ &\quad -6mn^3N + 6n^4N + 6m^2N^2 - 6m^3N^2 - 24mnN^2 \\ &\quad +12m^2nN^2 + 6n^2N^2 + 12mn^2N^2 - 6n^3N^2. \end{aligned}$$

Implementation: *scipy.stats.hypergeom*

Fisher's Noncentral Hypergeometric Distribution

A random variable has Fisher's Noncentral Hypergeometric distribution with parameters

$M \in \mathbb{N}, n \in [0, M], N \in [0, M], \omega > 0,$

if its probability mass function is given by

$$p(x; M, n, N, \omega) = \frac{\binom{n}{x}\binom{M-n}{N-x}\omega^x}{P_0},$$

for $x \in [x_l, x_u]$, where $x_l = \max(0, N - (M - n))$, $x_u = \min(N, n)$,

$$P_k = \sum_{y=x_l}^{x_u} \binom{n}{y}\binom{M-n}{N-y}\omega^y y^k,$$

and the binomial coefficients are

$$\binom{n}{k} \equiv \frac{n!}{k!(n-k)!}.$$

Other functions of this distribution are

$$\begin{aligned} \mu &= \frac{P_0}{P_1}, \\ \mu_2 &= \frac{P_2}{P_0} - \left(\frac{P_1}{P_0}\right)^2, \end{aligned}$$

References

- Agner Fog, "Biased Urn Theory", https://cran.r-project.org/web/packages/BiasedUrn/vignettes/UrnTheory.pdf
- "Fisher's noncentral hypergeometric distribution", Wikipedia, https://en.wikipedia.org/wiki/Fisher's_noncentral_hypergeometric_dist

Implementation: *scipy.stats.nchypergeom_fisher*

Wallenius' Noncentral Hypergeometric Distribution

A random variable has Wallenius' Noncentral Hypergeometric distribution with parameters

$M \in \mathbb{N}, n \in [0, M], N \in [0, M], \omega > 0,$

if its probability mass function is given by

$$p(x; N, n, M) = \binom{n}{x}\binom{M-n}{N-x}\int_0^1 \left(1-t^{\omega/D}\right)^x \left(1-t^{1/D}\right)^{N-x} dt$$

for $x \in [x_l, x_u]$, where $x_l = \max(0, N-(M-n))$, $x_u = \min(N, n)$,

$$D = \omega(n-x) + ((M-n)-(N-x)),$$

and the binomial coefficients are

$$\binom{n}{k} \equiv \frac{n!}{k!(n-k)!}.$$

References

- Agner Fog, "Biased Urn Theory", https://cran.r-project.org/web/packages/BiasedUrn/vignettes/UrnTheory.pdf
- "Wallenius' noncentral hypergeometric distribution", Wikipedia, https://en.wikipedia.org/wiki/Wallenius'_noncentral_hypergeometri

Implementation: *scipy.stats.nchypergeom_wallenius*

Negative Hypergeometric Distribution

Consider a box containing M balls: n red and $M-n$ blue. We randomly sample balls from the box, one at a time and *without* replacement, until we have picked r blue balls. *nhypergeom* is the distribution of the number of red balls k we have picked.

$$\begin{aligned}
p(k; M, n, r) &= \frac{\binom{k+r-1}{k}\binom{M-r-k}{n-k}}{\binom{M}{n}} \quad 0 \le k \le M-n, \\
F(x; M, n, r) &= \sum_{k=0}^{\lfloor x \rfloor} p\left(k; M, n, r\right), \\
\mu &= \frac{rn}{M-n+1}, \\
\mu_2 &= \frac{rn(M+1)}{(M-n+1)(M-n+2)}\left(1-\frac{r}{M-n+1}\right)
\end{aligned}$$

for $k \in 0, 1, 2, ..., n$, where the binomial coefficients are defined as,

$$\binom{n}{k} \equiv \frac{n!}{k!(n-k)!}$$

The cumulative distribution, survivor function, hazard function, cumulative hazard function, inverse distribution function, moment generating function, and characteristic function on the support of k are mathematically intractable.

Implementation: *scipy.stats.nhypergeom*

Zipf (Zeta) Distribution

A random variable has the zeta distribution (also called the zipf distribution) with parameter $\alpha > 1$ if it's probability mass function is given by

$$p(k;\alpha) = \frac{1}{\zeta(\alpha)\,k^{\alpha}} \quad k \geq 1$$

where

$$\zeta(\alpha) = \sum_{n=1}^{\infty} \frac{1}{n^{\alpha}}$$

is the Riemann zeta function. Other functions of this distribution are

$$\begin{aligned} F(x;\alpha) &= \frac{1}{\zeta(\alpha)} \sum_{k=1}^{\lfloor x \rfloor} \frac{1}{k^{\alpha}} \\ \mu &= \frac{\zeta_1}{\zeta_0} \quad \alpha > 2 \\ \mu_2 &= \frac{\zeta_2\zeta_0 - \zeta_1^2}{\zeta_0^2} \quad \alpha > 3 \\ \gamma_1 &= \frac{\zeta_3\zeta_0^2 - 3\zeta_0\zeta_1\zeta_2 + 2\zeta_1^3}{\left[\zeta_2\zeta_0 - \zeta_1^2\right]^{3/2}} \quad \alpha > 4 \\ \gamma_2 &= \frac{\zeta_4\zeta_0^3 - 4\zeta_3\zeta_1\zeta_0^2 + 12\zeta_2\zeta_1^2\zeta_0 - 6\zeta_1^4 - 3\zeta_2^2\zeta_0^2}{\left(\zeta_2\zeta_0 - \zeta_1^2\right)^2}. \end{aligned}$$

$$M(t) = \frac{\mathrm{Li}_{\alpha}(e^t)}{\zeta(\alpha)}$$

where $\zeta_i = \zeta(\alpha - i)$ and $\mathrm{Li}_n(z)$ is the n^{th} polylogarithm function of z defined as

$$\mathrm{Li}_n(z) \equiv \sum_{k=1}^{\infty} \frac{z^k}{k^n}$$

$$\mu'_n = M^{(n)}(t)\Big|_{t=0} = \frac{\mathrm{Li}_{\alpha-n}(e^t)}{\zeta(a)}\Big|_{t=0} = \frac{\zeta(\alpha-n)}{\zeta(\alpha)}$$

Implementation: `scipy.stats.zipf`

Zipfian Distribution

A random variable has the Zipfian distribution with parameters $s \geq 0$ and $N \in \{1, 2, 3, \dots\}$ if its probability mass function is given by

$$p(k;s,N) = \frac{1}{H_{N,s}k^s} \quad k \in \{1, 2, \dots, n-1, n\}$$

where

$$H_{N,s} = \sum_{n=1}^{N} \frac{1}{n^s}$$

is the N^{th} generalized harmonic number of order s. Other functions of this distribution are

$$\begin{aligned} F\left(x;s,N\right) &= \frac{H_{k,s}}{H_{N,s}}, \\ \mu &= \frac{H_{N,s-1}}{H_{N,s}}, \\ \mu_2 &= \frac{H_{N,s-2}}{H_{N,s}} - \frac{H_{N,s-1}^2}{H_{N,s}^2}, \\ \gamma_1 &= \frac{\frac{H_{N,s-3}}{H_{N,s}} - 3\frac{H_{N,s-1}H_{N,s-2}}{H_{N,s}^2} + 2\frac{H_{N,s-1}^3}{H_{N,s}^3}}{\left(\frac{H_{N,s-2}H_{N,s}-H_{N,s-1}^2}{H_{N,s}^2}\right)^{\frac{3}{2}}}, \text{and} \\ \gamma_2 &= \frac{H_{N,s}^3 H_{N,s-4} - 4H_{N,s}^2 H_{N,s-1}H_{N,s-3} + 6H_{N,s}H_{N,s-1}^2 H_{N,s-2} - 3H_{N,s-1}^4}{\left(H_{N,s-2}H_{N,s} - H_{N,s-1}^2\right)^2}. \end{aligned}$$

References

- "Zipf's Law", Wikipedia, https://en.wikipedia.org/wiki/Zipf%27s_law
- Larry Leemis, "Zipf Distribution", Univariate Distribution Relationships. http://www.math.wm.edu/~leemis/chart/UDR/PDFs/Zipf.pdf

Implementation: `scipy.stats.zipfian`

Logarithmic (Log-Series, Series) Distribution

The logarithmic distribution with parameter p has a probability mass function with terms proportional to the Taylor series expansion of $\log\left(1-p\right)$

$$\begin{aligned} p\left(k;p\right) &= -\frac{p^k}{k\log\left(1-p\right)} \quad k \geq 1 \\ F\left(x;p\right) &= -\frac{1}{\log\left(1-p\right)}\sum_{k=1}^{\lfloor x \rfloor}\frac{p^k}{k} = 1 + \frac{p^{1+\lfloor x \rfloor}\Phi\left(p,1,1+\lfloor x \rfloor\right)}{\log\left(1-p\right)} \end{aligned}$$

where

$$\Phi\left(z,s,a\right) = \sum_{k=0}^{\infty}\frac{z^k}{\left(a+k\right)^s}$$

is the Lerch Transcendent. Also define $r = \log\left(1-p\right)$

$$\begin{aligned} \mu &= -\frac{p}{\left(1-p\right)r} \\ \mu_2 &= -\frac{p\left[p+r\right]}{\left(1-p\right)^2 r^2} \\ \gamma_1 &= -\frac{2p^2+3pr+\left(1+p\right)r^2}{r\left(p+r\right)\sqrt{-p\left(p+r\right)}}r \\ \gamma_2 &= -\frac{6p^3+12p^2r+p\left(4p+7\right)r^2+\left(p^2+4p+1\right)r^3}{p\left(p+r\right)^2}. \end{aligned}$$

$$\begin{aligned} M\left(t\right) &= -\frac{1}{\log\left(1-p\right)}\sum_{k=1}^{\infty}\frac{e^{tk}p^{k}}{k} \\ &= \frac{\log\left(1-pe^{t}\right)}{\log\left(1-p\right)} \end{aligned}$$

Thus,

$$\mu_{n}' = M^{(n)}\left(t\right)\Big|_{t=0} = \frac{\mathrm{Li}_{1-n}\left(pe^{t}\right)}{\log\left(1-p\right)}\Big|_{t=0} = -\frac{\mathrm{Li}_{1-n}\left(p\right)}{\log\left(1-p\right)}.$$

Implementation: `scipy.stats.logser`

Discrete Uniform (randint) Distribution

The discrete uniform distribution with parameters (a, b) constructs a random variable that has an equal probability of being any one of the integers in the half-open range $[a, b)$. If a is not given it is assumed to be zero and the only parameter is b. Therefore,

$$\begin{aligned} p\left(k,a,b\right) &= \frac{1}{b-a} \quad a \le k < b \\ F\left(x;a,b\right) &= \frac{\lfloor x\rfloor - a}{b-a} \quad a \le x \le b \\ G\left(q;a,b\right) &= \lceil q\left(b-a\right)+a\rceil \\ \mu &= \frac{b+a-1}{2} \\ \mu_{2} &= \frac{\left(b-a-1\right)\left(b-a+1\right)}{12} \\ \gamma_{1} &= 0 \\ \gamma_{2} &= -\frac{6}{5}\frac{\left(b-a\right)^{2}+1}{\left(b-a-1\right)\left(b-a+1\right)}. \end{aligned}$$

$$\begin{aligned} M\left(t\right) &= \frac{1}{b-a}\sum_{k=a}^{b-1}e^{tk} \\ &= \frac{e^{bt}-e^{at}}{\left(b-a\right)\left(e^{t}-1\right)} \end{aligned}$$

Implementation: `scipy.stats.randint`

Discrete Laplacian Distribution

Defined over all integers for $a > 0$

$$\begin{aligned} p\left(k\right) &= \tanh\left(\frac{a}{2}\right)e^{-a|k|}, \\ F\left(x\right) &= \begin{cases} \frac{e^{a(\lfloor x\rfloor+1)}}{e^{a}+1} & \lfloor x\rfloor < 0, \\ 1-\frac{e^{-a\lfloor x\rfloor}}{e^{a}+1} & \lfloor x\rfloor \ge 0. \end{cases} \\ G\left(q\right) &= \begin{cases} \left\lceil \frac{1}{a}\log\left[q\left(e^{a}+1\right)\right]-1\right\rceil & q < \frac{1}{1+e^{-a}}, \\ \left\lceil -\frac{1}{a}\log\left[\left(1-q\right)\left(1+e^{a}\right)\right]\right\rceil & q \ge \frac{1}{1+e^{-a}}. \end{cases} \end{aligned}$$

$$\begin{aligned} M(t) &= \tanh\left(\frac{a}{2}\right) \sum_{k=-\infty}^{\infty} e^{tk} e^{-a|k|} \\ &= C\left(1 + \sum_{k=1}^{\infty} e^{-(t+a)k} + \sum_{1}^{\infty} e^{(t-a)k}\right) \\ &= \tanh\left(\frac{a}{2}\right)\left(1 + \frac{e^{-(t+a)}}{1 - e^{-(t+a)}} + \frac{e^{t-a}}{1 - e^{t-a}}\right) \\ &= \frac{\tanh\left(\frac{a}{2}\right) \sinh a}{\cosh a - \cosh t}. \end{aligned}$$

Thus,

$$\mu_n' = M^{(n)}(0) = [1 + (-1)^n] \operatorname{Li}_{-n}\left(e^{-a}\right)$$

where $\operatorname{Li}_{-n}(z)$ is the polylogarithm function of order $-n$ evaluated at z.

$$h[X] = -\log\left(\tanh\left(\frac{a}{2}\right)\right) + \frac{a}{\sinh a}$$

Implementation: *scipy.stats.dlaplace*

Yule-Simon Distribution

A Yule-Simon random variable with parameter $\alpha > 0$ can be represented as a mixture of exponential random variates. To see this write W as an exponential random variate with rate ρ and a Geometric random variate K with probability $1 - exp(-W)$ then K marginally has a Yule-Simon distribution. The latent variable representation described above is used for random variate generation.

$$\begin{aligned} p(k;\alpha) &= \alpha \frac{\Gamma(k)\,\Gamma(\alpha+1)}{\Gamma(k+\alpha+1)} \\ F(k;\alpha) &= 1 - \frac{k\Gamma(k)\,\Gamma(\alpha+1)}{\Gamma(k+\alpha+1)} \end{aligned}$$

for $k = 1, 2, ...$

Now

$$\begin{aligned} \mu &= \frac{\alpha}{\alpha - 1} \\ \mu_2 &= \frac{\alpha^2}{(\alpha-1)^2(\alpha-2)} \\ \gamma_1 &= \frac{\sqrt{(\alpha-2)}\,(\alpha+1)^2}{\alpha(\alpha-3)} \\ \gamma_2 &= \frac{(\alpha+3) + \left(\alpha^3 - 49\alpha - 22\right)}{\alpha(\alpha-4)(\alpha-3)} \end{aligned}$$

for $\alpha > 1$ otherwise the mean is infinite and the variance does not exist. For the variance, $\alpha > 2$ otherwise the variance does not exist. Similarly, for the skewness and kurtosis to be finite, $\alpha > 3$ and $\alpha > 4$ respectively.

Implementation: *scipy.stats.yulesimon*

Continuous Statistical Distributions

Overview

All distributions will have location (L) and Scale (S) parameters along with any shape parameters needed, the names for the shape parameters will vary. Standard form for the distributions will be given where $L = 0.0$ and $S = 1.0$. The nonstandard forms can be obtained for the various functions using (note U is a standard uniform random variate).

Function Name	Standard Function	Transformation
Cumulative Distribution Function (CDF)	$F(x)$	$F(x;L,S) = F\left(\frac{(x-L)}{S}\right)$
Probability Density Function (PDF)	$f(x) = F'(x)$	$f(x;L,S) = \frac{1}{S}f\left(\frac{(x-L)}{S}\right)$
Percent Point Function (PPF)	$G(q) = F^{-1}(q)$	$G(q;L,S) = L + SG(q)$
Probability Sparsity Function (PSF)	$g(q) = G'(q)$	$g(q;L,S) = Sg(q)$
Hazard Function (HF)	$h_a(x) = \frac{f(x)}{1-F(x)}$	$h_a(x;L,S) = \frac{1}{S}h_a\left(\frac{(x-L)}{S}\right)$
Cumulative Hazard Function (CHF)	$H_a(x) = \log\frac{1}{1-F(x)}$	$H_a(x;L,S) = H_a\left(\frac{(x-L)}{S}\right)$
Survival Function (SF)	$S(x) = 1 - F(x)$	$S(x;L,S) = S\left(\frac{(x-L)}{S}\right)$
Inverse Survival Function (ISF)	$Z(\alpha) = S^{-1}(\alpha) = G(1-\alpha)$	$Z(\alpha;L,S) = L + SZ(\alpha)$
Moment Generating Function (MGF)	$M_Y(t) = E\left[e^{Yt}\right]$	$M_X(t) = e^{Lt}M_Y(St)$
Random Variates	$Y = G(U)$	$X = L + SY$
(Differential) Entropy	$h[Y] = -\int f(y)\log f(y)\,dy$	$h[X] = h[Y] + \log S$
(Non-central) Moments	$\mu'_n = E[Y^n]$	$E[X^n] = L^n\sum_{k=0}^{N}\binom{n}{k}\left(\frac{S}{L}\right)^k\mu'_k$
Central Moments	$\mu_n = E[(Y-\mu)^n]$	$E[(X-\mu_X)^n] = S^n\mu_n$
mean (mode, median), var	$\mu,\ \mu_2$	$L + S\mu,\ S^2\mu_2$
skewness	$\gamma_1 = \frac{\mu_3}{(\mu_2)^{3/2}}$	γ_1
kurtosis	$\gamma_2 = \frac{\mu_4}{(\mu_2)^2} - 3$	γ_2

Moments

Non-central moments are defined using the PDF

$$\mu'_n = \int_{-\infty}^{\infty} x^n f(x)\,dx.$$

Note, that these can always be computed using the PPF. Substitute $x = G(q)$ in the above equation and get

$$\mu'_n = \int_0^1 G^n(q)\,dq$$

which may be easier to compute numerically. Note that $q = F(x)$ so that $dq = f(x)\,dx$. Central moments are computed similarly $\mu = \mu'_1$

$$\begin{aligned}\mu_n &= \int_{-\infty}^{\infty}(x-\mu)^n f(x)\,dx \\ &= \int_0^1 (G(q)-\mu)^n\,dq \\ &= \sum_{k=0}^{n}\binom{n}{k}(-\mu)^k\mu'_{n-k}\end{aligned}$$

In particular

$$\begin{aligned}\mu_3 &= \mu_3' - 3\mu\mu_2' + 2\mu^3 \\ &= \mu_3' - 3\mu\mu_2 - \mu^3 \\ \mu_4 &= \mu_4' - 4\mu\mu_3' + 6\mu^2\mu_2' - 3\mu^4 \\ &= \mu_4' - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4\end{aligned}$$

Skewness is defined as

$$\gamma_1 = \sqrt{\beta_1} = \frac{\mu_3}{\mu_2^{3/2}}$$

while (Fisher) kurtosis is

$$\gamma_2 = \frac{\mu_4}{\mu_2^2} - 3,$$

so that a normal distribution has a kurtosis of zero.

Median and mode

The median, m_n is defined as the point at which half of the density is on one side and half on the other. In other words, $F(m_n) = \frac{1}{2}$ so that

$$m_n = G\left(\frac{1}{2}\right).$$

In addition, the mode, m_d , is defined as the value for which the probability density function reaches it's peak

$$m_d = \arg\max_x f(x).$$

Fitting data

To fit data to a distribution, maximizing the likelihood function is common. Alternatively, some distributions have well-known minimum variance unbiased estimators. These will be chosen by default, but the likelihood function will always be available for minimizing.

If $f(x;\boldsymbol{\theta})$ is the PDF of a random-variable where $\boldsymbol{\theta}$ is a vector of parameters (*e.g.* L and S), then for a collection of N independent samples from this distribution, the joint distribution the random vector $\mathbf{x}$ is

$$f(\mathbf{x};\boldsymbol{\theta}) = \prod_{i=1}^{N} f(x_i;\boldsymbol{\theta}).$$

The maximum likelihood estimate of the parameters $\boldsymbol{\theta}$ are the parameters which maximize this function with $\mathbf{x}$ fixed and given by the data:

$$\begin{aligned}\boldsymbol{\theta}_{es} &= \arg\max_{\boldsymbol{\theta}} f(\mathbf{x};\boldsymbol{\theta}) \\ &= \arg\min_{\boldsymbol{\theta}} l_{\mathbf{x}}(\boldsymbol{\theta}).\end{aligned}$$

Where

$$\begin{aligned}l_{\mathbf{x}}(\boldsymbol{\theta}) &= -\sum_{i=1}^{N} \log f(x_i;\boldsymbol{\theta}) \\ &= -N\overline{\log f(x_i;\boldsymbol{\theta})}\end{aligned}$$

Note that if $\boldsymbol{\theta}$ includes only shape parameters, the location and scale-parameters can be fit by replacing x_i with $(x_i - L)/S$ in the log-likelihood function adding $N \log S$ and minimizing, thus

$$\begin{aligned} l_{\mathbf{x}}(L, S; \boldsymbol{\theta}) &= N \log S - \sum_{i=1}^{N} \log f\left(\frac{x_i - L}{S}; \boldsymbol{\theta}\right) \\ &= N \log S + l_{\frac{\mathbf{x}-S}{L}}(\boldsymbol{\theta}) \end{aligned}$$

If desired, sample estimates for L and S (not necessarily maximum likelihood estimates) can be obtained from samples estimates of the mean and variance using

$$\begin{aligned} \hat{S} &= \sqrt{\frac{\hat{\mu}_2}{\mu_2}} \\ \hat{L} &= \hat{\mu} - \hat{S}\mu \end{aligned}$$

where μ and μ_2 are assumed known as the mean and variance of the **untransformed** distribution (when $L = 0$ and $S = 1$) and

$$\begin{aligned} \hat{\mu} &= \frac{1}{N}\sum_{i=1}^{N} x_i = \bar{\mathbf{x}} \\ \hat{\mu}_2 &= \frac{1}{N-1}\sum_{i=1}^{N}(x_i - \hat{\mu})^2 = \frac{N}{N-1}\overline{(\mathbf{x} - \bar{\mathbf{x}})^2} \end{aligned}$$

Standard notation for mean

We will use

$$\overline{y(\mathbf{x})} = \frac{1}{N}\sum_{i=1}^{N} y(x_i)$$

where N should be clear from context as the number of samples x_i

References

- Documentation for ranlib, rv2, cdflib
- Eric Weisstein's world of mathematics http://mathworld.wolfram.com/, http://mathworld.wolfram.com/topics/StatisticalDistributions.html
- Documentation to Regress+ by Michael McLaughlin item Engineering and Statistics Handbook (NIST), https://www.itl.nist.gov/div898/handbook/
- Documentation for DATAPLOT from NIST, https://www.itl.nist.gov/div898/software/dataplot/distribu.htm
- Norman Johnson, Samuel Kotz, and N. Balakrishnan Continuous Univariate Distributions, second edition, Volumes I and II, Wiley & Sons, 1994.

In the tutorials several special functions appear repeatedly and are listed here.

Symbol	Description	Definition
$\gamma(s,x)$	lower incomplete Gamma function	$\int_0^x t^{s-1}e^{-t}dt$
$\Gamma(s,x)$	upper incomplete Gamma function	$\int_x^\infty t^{s-1}e^{-t}dt$
$B(x;a,b)$	incomplete Beta function	$\int_0^x t^{a-1}(1-t)^{b-1}dt$
$I(x;a,b)$	regularized incomplete Beta function	$\frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)}\int_0^x t^{a-1}(1-t)^{b-1}dt$
$\phi(x)$	PDF for normal distribution	$\frac{1}{\sqrt{2\pi}}e^{-x^2/2}$
$\Phi(x)$	CDF for normal distribution	$\int_{-\infty}^x \phi(t)\,dt = \frac{1}{2}+\frac{1}{2}\text{erf}\left(\frac{x}{\sqrt{2}}\right)$
$\psi(z)$	digamma function	$\frac{d}{dz}\log(\Gamma(z))$
$\psi_n(z)$	polygamma function	$\frac{d^{n+1}}{dz^{n+1}}\log(\Gamma(z))$
$I_\nu(y)$	modified Bessel function of the first kind	
Ei(z)	exponential integral	$-\int_{-x}^\infty \frac{e^{-t}}{t}dt$
$\zeta(n)$	Riemann zeta function	$\sum_{k=1}^\infty \frac{1}{k^n}$
$\zeta(n,z)$	Hurwitz zeta function	$\sum_{k=0}^\infty \frac{1}{(k+z)^n}$
${}_pF_q(a_1,\ldots,a_p;b_1,\ldots,b_q;z)$	Hypergeometric function	$\sum_{n=0}^\infty \frac{(a_1)_n\cdots(a_p)_n}{(b_1)_n\cdots(b_q)_n}\frac{z^n}{n!}$

Continuous Distributions in `scipy.stats`

Alpha Distribution

One shape parameter $\alpha > 0$ (parameter β in DATAPLOT is a scale-parameter). The support for the standard form is $x > 0$.

$$\begin{aligned} f(x;\alpha) &= \frac{1}{x^2\Phi(\alpha)\sqrt{2\pi}}\exp\left(-\frac{1}{2}\left(\alpha-\frac{1}{x}\right)^2\right) \\ F(x;\alpha) &= \frac{\Phi\left(\alpha-\frac{1}{x}\right)}{\Phi(\alpha)} \\ G(q;\alpha) &= \left[\alpha-\Phi^{-1}(q\Phi(\alpha))\right]^{-1} \end{aligned}$$

$$M(t) = \frac{1}{\Phi(a)\sqrt{2\pi}}\int_0^\infty \frac{e^{xt}}{x^2}\exp\left(-\frac{1}{2}\left(\alpha-\frac{1}{x}\right)^2\right)dx$$

No moments?

$$l_{\mathbf{x}}(\alpha) = N\log\left[\Phi(\alpha)\sqrt{2\pi}\right] + 2N\overline{\log\mathbf{x}} + \frac{N}{2}\alpha^2 - \alpha\overline{\mathbf{x}^{-1}} + \frac{1}{2}\overline{\mathbf{x}^{-2}}$$

Implementation: *scipy.stats.alpha*

Anglit Distribution

Defined over $x \in \left[-\frac{\pi}{4},\frac{\pi}{4}\right]$.

$$\begin{aligned} f(x) &= \sin\left(2x+\frac{\pi}{2}\right) = \cos(2x) \\ F(x) &= \sin^2\left(x+\frac{\pi}{4}\right) \\ G(q) &= \arcsin(\sqrt{q}) - \frac{\pi}{4} \end{aligned}$$

$$\begin{aligned}\mu &= 0\\ \mu_2 &= \frac{\pi^2}{16}-\frac{1}{2}\\ \gamma_1 &= 0\\ \gamma_2 &= -2\frac{\pi^4-96}{\left(\pi^2-8\right)^2}\end{aligned}$$

$$\begin{aligned}h\left[X\right] &= 1-\log 2\\ &\approx 0.30685281944005469058\end{aligned}$$

$$\begin{aligned}M\left(t\right) &= \int_{-\frac{\pi}{4}}^{\frac{\pi}{4}}\cos\left(2x\right)e^{xt}dx\\ &= \frac{4\cosh\left(\frac{\pi t}{4}\right)}{t^2+4}\end{aligned}$$

$$l_{\mathbf{x}}\left(\cdot\right) = -N\overline{\log\left[\cos\left(2\mathbf{x}\right)\right]}$$

Implementation: *scipy.stats.anglit*

Arcsine Distribution

Defined over $x\in[0,1]$. To get the definition presented in Johnson, Kotz, and Balakrishnan, substitute $x=\frac{u+1}{2}$. i.e. $L=-1$ and $S=2$.

$$\begin{aligned}f\left(x\right) &= \frac{1}{\pi\sqrt{x\left(1-x\right)}}\\ F\left(x\right) &= \frac{2}{\pi}\arcsin\left(\sqrt{x}\right)\\ G\left(q\right) &= \sin^2\left(\frac{\pi}{2}q\right)\end{aligned}$$

$$M\left(t\right) = 1+\sum_{k=1}^{\infty}\left(\prod_{r=0}^{k-1}\frac{2r+1}{2r+2}\right)\frac{t^k}{k!}$$

$$\begin{aligned}\mu_n' &= \frac{1}{\pi}\int_0^1 x^{n-1/2}\left(1-x\right)^{-1/2}dx\\ &= \frac{1}{\pi}B\left(\frac{1}{2},n+\frac{1}{2}\right) = \frac{\left(2n-1\right)!!}{2^n n!}\end{aligned}$$

$$\begin{aligned}\mu &= \frac{1}{2}\\ \mu_2 &= \frac{1}{8}\\ \gamma_1 &= 0\\ \gamma_2 &= -\frac{3}{2}\end{aligned}$$

$$h\left[X\right] = \log(\frac{\pi}{4}) \approx -0.24156447527049044468$$

$$l_{\mathbf{x}}\left(\cdot\right) = N\log\pi+\frac{N}{2}\overline{\log\mathbf{x}}+\frac{N}{2}\overline{\log\left(1-\mathbf{x}\right)}$$

References

- Norman Johnson, Samuel Kotz, and N. Balakrishnan, Continuous Univariate Distributions, second edition, Volumes I and II, Wiley & Sons, 1994.
- "Arcsine Distribution", Wikipedia, https://en.wikipedia.org/wiki/Arcsine_distribution

Implementation: `scipy.stats.arcsine`

Beta Distribution

There are two shape parameters $a, b > 0$ and the support is $x \in [0, 1]$.

$$\begin{aligned}
f(x; a, b) &= \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} x^{a-1}(1-x)^{b-1} \\
F(x; a, b) &= \int_0^x f(y; a, b)\, dy = I(x; a, b) \\
G(q; a, b) &= I^{-1}(q; a, b) \\
M(t) &= \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)}\, {}_1F_1(a; a+b; t) \\
\mu &= \frac{a}{a+b} \\
\mu_2 &= \frac{ab(a+b+1)}{(a+b)^2} \\
\gamma_1 &= 2\frac{b-a}{a+b+2}\sqrt{\frac{a+b+1}{ab}} \\
\gamma_2 &= \frac{6\left(a^3 + a^2(1-2b) + b^2(b+1) - 2ab(b+2)\right)}{ab(a+b+2)(a+b+3)} \\
m_d &= \frac{(a-1)}{(a+b-2)}\; a+b \neq 2
\end{aligned}$$

where $I(x; a, b)$ is the regularized incomplete Beta function. $f(x; a, 1)$ is also called the Power-function distribution.

$$l_{\mathbf{x}}(a, b) = -N\log\Gamma(a+b) + N\log\Gamma(a) + N\log\Gamma(b) - N(a-1)\overline{\log \mathbf{x}} - N(b-1)\overline{\log(1-\mathbf{x})}$$

Implementation: `scipy.stats.beta`

Beta Prime Distribution

There are two shape parameters $a, b > 0$ and the support is $x \in [0, \infty)$. Note the CDF evaluation uses Eq. 3.194.1 on pg. 313 of Gradshteyn & Ryzhik (sixth edition).

$$\begin{aligned}
f(x; \alpha, \beta) &= \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} x^{\alpha-1}(1+x)^{-\alpha-\beta} \\
F(x; \alpha, \beta) &= \frac{\Gamma(\alpha+\beta)}{\alpha\Gamma(\alpha)\Gamma(\beta)} x^{\alpha}\, {}_2F_1(\alpha+\beta, \alpha; 1+\alpha; -x) \\
G(q; \alpha, \beta) &= F^{-1}(x; \alpha, \beta)
\end{aligned}$$

$$\mu'_n = \begin{cases} \frac{\Gamma(n+\alpha)\Gamma(\beta-n)}{\Gamma(\alpha)\Gamma(\beta)} = \frac{(\alpha)_n}{(\beta-n)_n} & \beta > n \\ \infty & \text{otherwise} \end{cases}$$

Therefore,

$$\begin{aligned}
\mu &= \frac{\alpha}{\beta-1} \quad \text{for } \beta > 1 \\
\mu_2 &= \frac{\alpha\left(\alpha+1\right)}{\left(\beta-2\right)\left(\beta-1\right)} - \frac{\alpha^2}{\left(\beta-1\right)^2} \quad \text{for } \beta > 2 \\
\gamma_1 &= \frac{\frac{\alpha(\alpha+1)(\alpha+2)}{(\beta-3)(\beta-2)(\beta-1)} - 3\mu\mu_2 - \mu^3}{\mu_2^{3/2}} \quad \text{for } \beta > 3 \\
\gamma_2 &= \frac{\mu_4}{\mu_2^2} - 3 \\
\mu_4 &= \frac{\alpha\left(\alpha+1\right)\left(\alpha+2\right)\left(\alpha+3\right)}{\left(\beta-4\right)\left(\beta-3\right)\left(\beta-2\right)\left(\beta-1\right)} - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4 \quad \text{for } \beta > 4
\end{aligned}$$

Implementation: `scipy.stats.betaprime`

Bradford Distribution

There is one shape parameter, $c > 0$, and the support is $x \in [0, 1]$.

$$\begin{aligned}
\text{Let } k &= \log\left(1+c\right) \\
\text{Then} & \\
f\left(x;c\right) &= \frac{c}{k\left(1+cx\right)} \\
F\left(x;c\right) &= \frac{\log\left(1+cx\right)}{k} \\
G\left(q\ c\right) &= \frac{\left(1+c\right)^q - 1}{c} \\
M\left(t\right) &= \frac{1}{k}e^{-t/c}\left[\mathrm{Ei}\left(t+\frac{t}{c}\right) - \mathrm{Ei}\left(\frac{t}{c}\right)\right] \\
\mu &= \frac{c-k}{ck} \\
\mu_2 &= \frac{\left(c+2\right)k - 2c}{2ck^2} \\
\gamma_1 &= \frac{\sqrt{2}\left(12c^2 - 9kc\left(c+2\right) + 2k^2\left(c\left(c+3\right)+3\right)\right)}{\sqrt{c\left(c\left(k-2\right)+2k\right)}\left(3c\left(k-2\right)+6k\right)} \\
\gamma_2 &= \frac{c^3\left(k-3\right)\left(k\left(3k-16\right)+24\right) + 12kc^2\left(k-4\right)\left(k-3\right) + 6ck^2\left(3k-14\right) + 12k^3}{3c\left(c\left(k-2\right)+2k\right)^2} \\
m_d &= 0 \\
m_n &= \sqrt{1+c} - 1 \\
h\left[X\right] &= \frac{1}{2}\log\left(1+c\right) - \log\left(\frac{c}{\log\left(1+c\right)}\right)
\end{aligned}$$

where $\mathrm{Ei}\left(z\right)$ is the exponential integral function.

Implementation: `scipy.stats.bradford`

Burr Distribution

There are two shape parameters $c, d > 0$ and the support is $x \in [0, \infty)$.

$$
\begin{aligned}
\text{Let } k &= \Gamma(d)\,\Gamma\left(1-\frac{2}{c}\right)\Gamma\left(\frac{2}{c}+d\right) - \Gamma^2\left(1-\frac{1}{c}\right)\Gamma^2\left(\frac{1}{c}+d\right) \\
f(x;c,d) &= \frac{cd}{x^{c+1}\left(1+x^{-c}\right)^{d+1}} \\
F(x;c,d) &= \left(1+x^{-c}\right)^{-d} \\
G(q;c,d) &= \left(q^{-1/d}-1\right)^{-1/c} \\
\mu &= \frac{\Gamma\left(1-\frac{1}{c}\right)\Gamma\left(\frac{1}{c}+d\right)}{\Gamma(d)} \\
\mu_2 &= \frac{k}{\Gamma^2(d)} \\
\gamma_1 &= \frac{1}{\sqrt{k^3}}\left[2\Gamma^3\left(1-\frac{1}{c}\right)\Gamma^3\left(\frac{1}{c}+d\right) + \Gamma^2(d)\,\Gamma\left(1-\frac{3}{c}\right)\Gamma\left(\frac{3}{c}+d\right)\right. \\
&\quad \left. -3\Gamma(d)\,\Gamma\left(1-\frac{2}{c}\right)\Gamma\left(1-\frac{1}{c}\right)\Gamma\left(\frac{1}{c}+d\right)\Gamma\left(\frac{2}{c}+d\right)\right] \\
\gamma_2 &= -3 + \frac{1}{k^2}\left[6\Gamma(d)\,\Gamma\left(1-\frac{2}{c}\right)\Gamma^2\left(1-\frac{1}{c}\right)\Gamma^2\left(\frac{1}{c}+d\right)\Gamma\left(\frac{2}{c}+d\right)\right. \\
&\quad -3\Gamma^4\left(1-\frac{1}{c}\right)\Gamma^4\left(\frac{1}{c}+d\right) + \Gamma^3(d)\,\Gamma\left(1-\frac{4}{c}\right)\Gamma\left(\frac{4}{c}+d\right) \\
&\quad \left. -4\Gamma^2(d)\,\Gamma\left(1-\frac{3}{c}\right)\Gamma\left(1-\frac{1}{c}\right)\Gamma\left(\frac{1}{c}+d\right)\Gamma\left(\frac{3}{c}+d\right)\right] \\
m_d &= \left(\frac{cd-1}{c+1}\right)^{1/c} \text{ if } \quad cd > 1, \text{ otherwise } \quad 0 \\
m_n &= \left(2^{1/d}-1\right)^{-1/c}
\end{aligned}
$$

Implementation: `scipy.stats.burr`

Burr12 Distribution

There are two shape parameters $c, d > 0$ and the support is $x \in [0, \infty)$. The Burr12 distribution is also known as the Singh-Maddala distribution.

$$\begin{aligned}
f(x; c, d) &= cd\frac{x^{c-1}}{(1+x^c)^{d+1}} \\
F(x; c, d) &= 1 - (1+x^c)^{-d} \\
G(q; c, d) &= \left((1-q)^{-1/d} - 1\right)^{-1/c} \\
S(x; c, d) &= (1+x^c)^{-d} \\
\mu &= d\,B\left(d - \frac{1}{c}, 1 + \frac{1}{c}\right) \\
\mu_n &= d\,B\left(d - \frac{n}{c}, 1 + \frac{n}{c}\right) \\
m_d &= \left(\frac{c-1}{cd+1}\right)^{1/c} \text{ if } \quad c > 1, \text{ otherwise } \quad 0 \\
m_n &= \left(2^{1/d} - 1\right)^{-1/c}
\end{aligned}$$

where $B(a, b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)}$ is the Beta function.

Implementation: `scipy.stats.burr12`

Cauchy Distribution

The support is $x \in \mathbb{R}$.

$$\begin{aligned}
f(x) &= \frac{1}{\pi\,(1+x^2)} \\
F(x) &= \frac{1}{2} + \frac{1}{\pi}\tan^{-1} x \\
G(q) &= \tan\left(\pi q - \frac{\pi}{2}\right) \\
m_d &= 0 \\
m_n &= 0
\end{aligned}$$

No finite moments. This is the t distribution with one degree of freedom.

$$\begin{aligned}
h[X] &= \log(4\pi) \\
&\approx 2.5310242469692907930.
\end{aligned}$$

Implementation: `scipy.stats.cauchy`

Skewed Cauchy Distribution

This distribution is a generalization of the Cauchy distribution. It has a single shape parameter $-1 < a < 1$ that skews the distribution. The special case $a = 0$ yields the Cauchy distribution.

Functions

$$
\begin{aligned}
f(x, a) &= \frac{1}{\pi\left(\frac{x^2}{(ax+1)^2}+1\right)}, \quad x \geq 0; \\
&= \frac{1}{\pi\left(\frac{x^2}{(-ax+1)^2}+1\right)}, \quad x < 0. \\
F(x, a) &= \frac{1-a}{2} + \frac{1+a}{\pi}\arctan\left(\frac{x}{1+a}\right), \quad x \geq 0; \\
&= \frac{1-a}{2} + \frac{1-a}{\pi}\arctan\left(\frac{x}{1-a}\right), \quad x < 0.
\end{aligned}
$$

The mean, variance, skewness, and kurtosis are all undefined.

References

- "Skewed generalized *t* distribution", Wikipedia https://en.wikipedia.org/wiki/Skewed_generalized_t_distribution#Skewed_Cauchy_distribution

Implementation: `scipy.stats.skewcauchy`

Chi Distribution

Generated by taking the (positive) square-root of chi-squared variates. The one shape parameter is ν, a positive integer, the degrees of freedom. The support is $x \geq 0$.

$$
\begin{aligned}
f(x;\nu) &= \frac{x^{\nu-1}e^{-x^2/2}}{2^{\nu/2-1}\Gamma\left(\frac{\nu}{2}\right)} \\
F(x;\nu) &= \frac{\gamma\left(\frac{\nu}{2},\frac{x^2}{2}\right)}{\Gamma(\frac{\nu}{2})} \\
G(q;\nu) &= \sqrt{2\gamma^{-1}\left(\frac{\nu}{2},q\Gamma(\frac{\nu}{2})\right)} \\
M(t) &= \Gamma\left(\frac{v}{2}\right)\,{}_1F_1\left(\frac{v}{2};\frac{1}{2};\frac{t^2}{2}\right)+\frac{t}{\sqrt{2}}\Gamma\left(\frac{1+\nu}{2}\right)\,{}_1F_1\left(\frac{1+\nu}{2};\frac{3}{2};\frac{t^2}{2}\right) \\
\mu &= \frac{\sqrt{2}\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \\
\mu_2 &= \nu-\mu^2 \\
\gamma_1 &= \frac{2\mu^3+\mu\left(1-2\nu\right)}{\mu_2^{3/2}} \\
\gamma_2 &= \frac{2\nu\left(1-\nu\right)-6\mu^4+4\mu^2\left(2\nu-1\right)}{\mu_2^2} \\
m_d &= \sqrt{\nu-1}\quad \nu\geq 1 \\
m_n &= \sqrt{2\gamma^{-1}\left(\frac{\nu}{2},\frac{1}{2}\Gamma(\frac{\nu}{2})\right)}
\end{aligned}
$$

Implementation: *scipy.stats.chi*

Chi-squared Distribution

This is the gamma distribution with $L = 0.0$ and $S = 2.0$ and $\alpha = \nu/2$ where ν is called the degrees of freedom. If $Z_1 \ldots Z_\nu$ are all standard normal distributions, then $W = \sum_k Z_k^2$ has (standard) chi-square distribution with ν degrees of freedom.

The standard form (most often used in standard form only) has support $x \geq 0$.

$$
\begin{aligned}
f(x;\alpha) &= \frac{1}{2\Gamma\left(\frac{\nu}{2}\right)}\left(\frac{x}{2}\right)^{\nu/2-1}e^{-x/2} \\
F(x;\alpha) &= \frac{\gamma\left(\frac{\nu}{2},\frac{x}{2}\right)}{\Gamma(\frac{\nu}{2})} \\
G(q;\alpha) &= 2\gamma^{-1}\left(\frac{\nu}{2},q\Gamma(\frac{\nu}{2})\right)
\end{aligned}
$$

where γ is the lower incomplete gamma function, $\gamma(s,x) = \int_0^x t^{s-1}e^{-t}dt$.

$$
M(t) = \frac{\Gamma\left(\frac{\nu}{2}\right)}{\left(\frac{1}{2}-t\right)^{\nu/2}}
$$

$$\begin{aligned}
\mu &= \nu \\
\mu_2 &= 2\nu \\
\gamma_1 &= \frac{2\sqrt{2}}{\sqrt{\nu}} \\
\gamma_2 &= \frac{12}{\nu} \\
m_d &= \frac{\nu}{2} - 1
\end{aligned}$$

Implementation: *scipy.stats.chi2*

Cosine Distribution

Approximation to the normal distribution. The support is $[-\pi, \pi]$.

$$\begin{aligned}
f(x) &= \frac{1}{2\pi}(1 + \cos x) \\
F(x) &= \frac{1}{2\pi}(\pi + x + \sin x) \\
G(q) &= F^{-1}(q) \\
M(t) &= \frac{\sinh(\pi t)}{\pi t(1 + t^2)} \\
\mu = m_d = m_n &= 0 \\
\mu_2 &= \frac{\pi^2}{3} - 2 \\
\gamma_1 &= 0 \\
\gamma_2 &= \frac{-6\left(\pi^4 - 90\right)}{5\left(\pi^2 - 6\right)^2}
\end{aligned}$$

$$\begin{aligned}
h[X] &= \log(4\pi) - 1 \\
&\approx 1.5310242469692907930.
\end{aligned}$$

Implementation: *scipy.stats.cosine*

Double Gamma Distribution

The double gamma is the signed version of the Gamma distribution. For $\alpha > 0$:

$$\begin{aligned}
f(x;\alpha) &= \frac{1}{2\Gamma(\alpha)}|x|^{\alpha-1}e^{-|x|} \\
F(x;\alpha) &= \begin{cases} \frac{1}{2} - \frac{\gamma(\alpha,|x|)}{2\Gamma(\alpha)} & x \le 0 \\ \frac{1}{2} + \frac{\gamma(\alpha,|x|)}{2\Gamma(\alpha)} & x > 0 \end{cases} \\
G(q;\alpha) &= \begin{cases} -\gamma^{-1}(\alpha, |2q-1|\,\Gamma(\alpha)) & q \le \frac{1}{2} \\ \gamma^{-1}(\alpha, |2q-1|\,\Gamma(\alpha)) & q > \frac{1}{2} \end{cases}
\end{aligned}$$

$$M(t) = \frac{1}{2(1-t)^a} + \frac{1}{2(1+t)^a}$$

$$\begin{aligned}
\mu = m_n &= 0 \\
\mu_2 &= \alpha(\alpha+1) \\
\gamma_1 &= 0 \\
\gamma_2 &= \frac{(\alpha+2)(\alpha+3)}{\alpha(\alpha+1)} - 3 \\
m_d &= \text{NA}
\end{aligned}$$

Implementation: *scipy.stats.dgamma*

Double Weibull Distribution

This is a signed form of the Weibull distribution. There is one shape parameter $c > 0$. Support is $x \in \mathbb{R}$.

$$\begin{aligned}
f(x;c) &= \frac{c}{2}|x|^{c-1}\exp\left(-|x|^c\right) \\
F(x;c) &= \begin{cases} \frac{1}{2}\exp\left(-|x|^c\right) & x \le 0 \\ 1 - \frac{1}{2}\exp\left(-|x|^c\right) & x > 0 \end{cases} \\
G(q;c) &= \begin{cases} -\log^{1/c}\left(\frac{1}{2q}\right) & q \le \frac{1}{2} \\ \log^{1/c}\left(\frac{1}{2q-1}\right) & q > \frac{1}{2} \end{cases}
\end{aligned}$$

$$\mu'_n = \mu_n = \begin{cases} \Gamma\left(1+\frac{n}{c}\right) & n \text{ even} \\ 0 & n \text{ odd} \end{cases}$$

$$\begin{aligned}
m_n = \mu &= 0 \\
\mu_2 &= \Gamma\left(\frac{c+2}{c}\right) \\
\gamma_1 &= 0 \\
\gamma_2 &= \frac{\Gamma\left(1+\frac{4}{c}\right)}{\Gamma^2\left(1+\frac{2}{c}\right)} \\
m_d &= \text{NA bimodal}
\end{aligned}$$

Implementation: *scipy.stats.dweibull*

Erlang Distribution

This is just the Gamma distribution with shape parameter $\alpha = n$ an integer.

Implementation: *scipy.stats.erlang*

Exponential Distribution

This is a special case of the Gamma (and Erlang) distributions with shape parameter $(\alpha = 1)$ and the same location and scale parameters. The standard form is therefore ($x \ge 0$)

$$\begin{aligned}
f(x) &= e^{-x} \\
F(x) &= \gamma(1,x) = 1 - e^{-x} \\
G(q) &= -\log(1-q)
\end{aligned}$$

$$\mu'_n = n!$$

$$M(t) = \frac{1}{1-t}$$

$$\begin{aligned}
\mu &= 1 \\
\mu_2 &= 1 \\
\gamma_1 &= 2 \\
\gamma_2 &= 6 \\
m_d &= 0
\end{aligned}$$

$$h[X] = 1.$$

Implementation: `scipy.stats.expon`

Exponentiated Weibull Distribution

Two positive shape parameters $a, c > 0$, and the support is $x \in [0, \infty)$.

$$\begin{aligned}
f(x; a, c) &= ac\left[1 - \exp\left(-x^c\right)\right]^{a-1} \exp\left(-x^c\right) x^{c-1} \\
F(x; a, c) &= \left[1 - \exp\left(-x^c\right)\right]^a \\
G(q; a, c) &= \left[-\log\left(1 - q^{1/a}\right)\right]^{1/c}
\end{aligned}$$

Implementation: `scipy.stats.exponweib`

Exponential Power Distribution

One positive shape parameter b. The support is $x \geq 0$.

$$\begin{aligned}
f(x; b) &= ebx^{b-1} \exp\left(x^b - e^{x^b}\right) \\
F(x; b) &= 1 - \exp\left(1 - e^{x^b}\right) \\
G(q; b) &= \log\left(1 - \log\left(1 - q\right)\right)^{1/b}
\end{aligned}$$

Implementation: `scipy.stats.exponpow`

Fatigue Life (Birnbaum-Saunders) Distribution

This distribution's pdf is the average of the inverse-Gaussian $(\mu = 1)$ and reciprocal inverse-Gaussian pdf $(\mu = 1)$. We follow the notation of JKB here with $\beta = S$. There is one shape parameter $c > 0$, and the support is $x \geq 0$.

$$\begin{aligned}
f(x; c) &= \frac{x+1}{2c\sqrt{2\pi x^3}} \exp\left(-\frac{(x-1)^2}{2xc^2}\right) \\
F(x; c) &= \Phi\left(\frac{1}{c}\left(\sqrt{x} - \frac{1}{\sqrt{x}}\right)\right) \\
G(q; c) &= \frac{1}{4}\left[c\Phi^{-1}(q) + \sqrt{c^2\left(\Phi^{-1}(q)\right)^2 + 4}\right]^2
\end{aligned}$$

$$M(t) = c\sqrt{2\pi} \exp\left(\frac{1}{c^2}\left(1 - \sqrt{1 - 2c^2 t}\right)\right)\left(1 + \frac{1}{\sqrt{1 - 2c^2 t}}\right)$$

$$\begin{aligned}
\mu &= \frac{c^2}{2} + 1 \\
\mu_2 &= c^2\left(\frac{5}{4}c^2 + 1\right) \\
\gamma_1 &= \frac{4c\sqrt{11c^2+6}}{\left(5c^2+4\right)^{3/2}} \\
\gamma_2 &= \frac{6c^2\left(93c^2+41\right)}{\left(5c^2+4\right)^2}
\end{aligned}$$

Implementation: *scipy.stats.fatiguelife*

Fisk (Log Logistic) Distribution

Special case of the Burr distribution with $d = 1$. There is are one shape parameter $c > 0$ and the support is $x \in [0, \infty)$.

$$\begin{aligned}
\text{Let } k &= \Gamma\left(1-\frac{2}{c}\right)\Gamma\left(\frac{2}{c}+1\right) - \Gamma^2\left(1-\frac{1}{c}\right)\Gamma^2\left(\frac{1}{c}+1\right) \\
f\left(x;c,d\right) &= \frac{cx^{c-1}}{\left(1+x^c\right)^2} \\
F\left(x;c,d\right) &= \left(1+x^{-c}\right)^{-1} \\
G\left(q;c,d\right) &= \left(q^{-1}-1\right)^{-1/c} \\
\mu &= \Gamma\left(1-\frac{1}{c}\right)\Gamma\left(\frac{1}{c}+1\right) \\
\mu_2 &= k \\
\gamma_1 &= \frac{1}{\sqrt{k^3}}\left[2\Gamma^3\left(1-\frac{1}{c}\right)\Gamma^3\left(\frac{1}{c}+1\right) + \Gamma\left(1-\frac{3}{c}\right)\Gamma\left(\frac{3}{c}+1\right)\right. \\
&\quad \left. -3\Gamma\left(1-\frac{2}{c}\right)\Gamma\left(1-\frac{1}{c}\right)\Gamma\left(\frac{1}{c}+1\right)\Gamma\left(\frac{2}{c}+1\right)\right] \\
\gamma_2 &= -3 + \frac{1}{k^2}\left[6\Gamma\left(1-\frac{2}{c}\right)\Gamma^2\left(1-\frac{1}{c}\right)\Gamma^2\left(\frac{1}{c}+1\right)\Gamma\left(\frac{2}{c}+1\right)\right. \\
&\quad -3\Gamma^4\left(1-\frac{1}{c}\right)\Gamma^4\left(\frac{1}{c}+1\right) + \Gamma\left(1-\frac{4}{c}\right)\Gamma\left(\frac{4}{c}+1\right) \\
&\quad \left. -4\Gamma\left(1-\frac{3}{c}\right)\Gamma\left(1-\frac{1}{c}\right)\Gamma\left(\frac{1}{c}+1\right)\Gamma\left(\frac{3}{c}+1\right)\right] \\
m_d &= \left(\frac{c-1}{c+1}\right)^{1/c} \text{ if } c > 1, \text{otherwise } 0 \\
m_n &= 1 \\
h\left[X\right] &= 2 - \log c
\end{aligned}$$

Implementation: *scipy.stats.fisk*

Folded Cauchy Distribution

This formula can be expressed in terms of the standard formulas for the Cauchy distribution (call the cdf $C(x)$ and the pdf $d(x)$). If Y is cauchy then $|Y|$ is folded cauchy. There is one shape parameter c and the support is $x \geq 0$.

$$\begin{aligned} f(x;c) &= \frac{1}{\pi\left(1+(x-c)^2\right)} + \frac{1}{\pi\left(1+(x+c)^2\right)} \\ F(x;c) &= \frac{1}{\pi}\tan^{-1}(x-c) + \frac{1}{\pi}\tan^{-1}(x+c) \\ G(q;c) &= F^{-1}(q;c) \end{aligned}$$

No moments

Implementation: `scipy.stats.foldcauchy`

Folded Normal Distribution

If Z is Normal with mean L and $\sigma = S$, then $|Z|$ is a folded normal with shape parameter $c = |L|/S$, location parameter 0 and scale parameter S . This is a special case of the non-central chi distribution with one- degree of freedom and non-centrality parameter c^2. Note that $c \geq 0$. The standard form of the folded normal is

$$\begin{aligned} f(x;c) &= \sqrt{\frac{2}{\pi}}\cosh(cx)\exp\left(-\frac{x^2+c^2}{2}\right) \\ F(x;c) &= \Phi(x-c) - \Phi(-x-c) = \Phi(x-c) + \Phi(x+c) - 1 \\ G(q;c) &= F^{-1}(q;c) \\ M(t) &= \exp\left(\frac{t}{2}(t-2c)\right)\left(1+e^{2ct}\right) \\ k &= \operatorname{erf}\left(\frac{c}{\sqrt{2}}\right) \\ p &= \exp\left(-\frac{c^2}{2}\right) \\ \mu &= \sqrt{\frac{2}{\pi}}p + ck \\ \mu_2 &= c^2 + 1 - \mu^2 \\ \gamma_1 &= \frac{\sqrt{\frac{2}{\pi}}p^3\left(4-\frac{\pi}{p^2}\left(2c^2+1\right)\right) + 2ck\left(6p^2 + 3cpk\sqrt{2\pi} + \pi c\left(k^2-1\right)\right)}{\pi\mu_2^{3/2}} \\ \gamma_2 &= \frac{c^4 + 6c^2 + 3 + 6\left(c^2+1\right)\mu^2 - 3\mu^4 - 4p\mu\left(\sqrt{\frac{2}{\pi}}\left(c^2+2\right) + \frac{ck}{p}\left(c^2+3\right)\right)}{\mu_2^2} \end{aligned}$$

Implementation: `scipy.stats.foldnorm`

Fratio (or F) Distribution

The distribution of $(X_1/X_2)\,(\nu_2/\nu_1)$ if X_1 is chi-squared with v_1 degrees of freedom and X_2 is chi-squared with v_2 degrees of freedom. The support is $x \geq 0$.

$$\begin{aligned}
f\left(x;\nu_1,\nu_2\right) &= \frac{\nu_2^{\nu_2/2}\nu_1^{\nu_1/2}x^{\nu_1/2-1}}{\left(\nu_2+\nu_1 x\right)^{(\nu_1+\nu_2)/2}B\left(\frac{\nu_1}{2},\frac{\nu_2}{2}\right)} \\
F\left(x;v_1,v_2\right) &= I\left(\frac{\nu_1 x}{\nu_2+\nu_1 x};\frac{\nu_1}{2},\frac{\nu_2}{2}\right) \\
G\left(q;\nu_1,\nu_2\right) &= \left(\frac{\nu_2}{I^{-1}\left(q;\nu_1/2,\nu_2/2\right)}-\frac{\nu_1}{\nu_2}\right)^{-1} \\
\mu &= \frac{\nu_2}{\nu_2-2} \quad \text{for } \nu_2>2 \\
\mu_2 &= \frac{2\nu_2^2\left(\nu_1+\nu_2-2\right)}{\nu_1\left(\nu_2-2\right)^2\left(\nu_2-4\right)} \quad \text{for } v_2>4 \\
\gamma_1 &= \frac{2\left(2\nu_1+\nu_2-2\right)}{\nu_2-6}\sqrt{\frac{2\left(\nu_2-4\right)}{\nu_1\left(\nu_1+\nu_2-2\right)}} \quad \text{for } \nu_2>6 \\
\gamma_2 &= \frac{3\left(8+\left(\nu_2-6\right)\gamma_1^2\right)}{2\nu-16} \quad \text{for } \nu_2>8
\end{aligned}$$

where $I\left(x;a,b\right)=I_x\left(a,b\right)$ is the regularized incomplete Beta function.

Implementation: `scipy.stats.f`

Gamma Distribution

The standard form for the gamma distribution is $(\alpha>0)$ valid for $x \geq 0$.

$$\begin{aligned}
f\left(x;\alpha\right) &= \frac{1}{\Gamma\left(\alpha\right)}x^{\alpha-1}e^{-x} \\
F\left(x;\alpha\right) &= \frac{\gamma\left(\alpha,x\right)}{\Gamma(\alpha)} \\
G\left(q;\alpha\right) &= \gamma^{-1}\left(\alpha,q\Gamma(\alpha)\right)
\end{aligned}$$

where γ is the lower incomplete gamma function, $\gamma\left(s,x\right)=\int_0^x t^{s-1}e^{-t}dt$.

$$M\left(t\right)=\frac{1}{\left(1-t\right)^{\alpha}}$$

$$\begin{aligned}
\mu &= \alpha \\
\mu_2 &= \alpha \\
\gamma_1 &= \frac{2}{\sqrt{\alpha}} \\
\gamma_2 &= \frac{6}{\alpha} \\
m_d &= \alpha-1
\end{aligned}$$

$$h\left[X\right]=\Psi\left(a\right)\left[1-a\right]+a+\log\Gamma\left(a\right)$$

where

$$\Psi\left(a\right)=\frac{\Gamma'\left(a\right)}{\Gamma\left(a\right)}.$$

Implementation: `scipy.stats.gamma`

Generalized Logistic Distribution

Has been used in the analysis of extreme values. There is one shape parameter $c > 0$. The support is $x \geq 0$.

$$\begin{aligned} f(x;c) &= \frac{c\exp(-x)}{[1+\exp(-x)]^{c+1}} \\ F(x;c) &= \frac{1}{[1+\exp(-x)]^{c}} \\ G(q;c) &= -\log\left(q^{-1/c}-1\right) \end{aligned}$$

$$M(t) = \frac{c}{1-t}\,{}_2F_1(1+c,\,1-t\,;\,2-t\,;-1)$$

$$\begin{aligned} \mu &= \gamma+\psi_0(c) \\ \mu_2 &= \frac{\pi^2}{6}+\psi_1(c) \\ \gamma_1 &= \frac{\psi_2(c)+2\zeta(3)}{\mu_2^{3/2}} \\ \gamma_2 &= \frac{\left(\frac{\pi^4}{15}+\psi_3(c)\right)}{\mu_2^2} \\ m_d &= \log c \\ m_n &= -\log\left(2^{1/c}-1\right) \end{aligned}$$

Note that the polygamma function is

$$\begin{aligned} \psi_n(z) &= \frac{d^{n+1}}{dz^{n+1}}\log\Gamma(z) \\ &= (-1)^{n+1}\,n!\sum_{k=0}^{\infty}\frac{1}{(z+k)^{n+1}} \\ &= (-1)^{n+1}\,n!\zeta(n+1,z) \end{aligned}$$

where $\zeta(k,x)$ is a generalization of the Riemann zeta function called the Hurwitz zeta function. Note that $\zeta(n) \equiv \zeta(n,1)$.

Implementation: *scipy.stats.genlogistic*

Generalized Pareto Distribution

There is one shape parameter $c \neq 0$. The support is $x \geq 0$ if $c > 0$, and $0 \leq x < \frac{1}{|c|}$ if c is negative.

$$\begin{aligned} f(x;c) &= (1+cx)^{-1-\frac{1}{c}} \\ F(x;c) &= 1-\frac{1}{(1+cx)^{1/c}} \\ G(q;c) &= \frac{1}{c}\left[\left(\frac{1}{1-q}\right)^{c}-1\right] \end{aligned}$$

$$M(t) = \begin{cases} \left(-\frac{t}{c}\right)^{\frac{1}{c}}e^{-\frac{t}{c}}\left[\Gamma\left(1-\frac{1}{c}\right)+\left(\gamma\left(-\frac{1}{c},-\frac{t}{c}\right)/\Gamma\left(\frac{1}{-c}\right)\right)-\pi\csc\left(\frac{\pi}{c}\right)/\Gamma\left(\frac{1}{c}\right)\right] & c>0 \\ \left(\frac{|c|}{t}\right)^{1/|c|}\Gamma\left(\frac{1}{|c|},\frac{t}{|c|}\right)\frac{1}{\Gamma\left(\frac{1}{|c|}\right)} & c<0 \end{cases}$$

$$\mu'_n = \frac{(-1)^n}{c^n} \sum_{k=0}^{n} \binom{n}{k} \frac{(-1)^k}{1-ck} \quad \text{if } cn < 1$$

$$\begin{aligned}
\mu'_1 &= \frac{1}{1-c} \quad c < 1 \\
\mu'_2 &= \frac{2}{(1-2c)(1-c)} \quad c < \frac{1}{2} \\
\mu'_3 &= \frac{6}{(1-c)(1-2c)(1-3c)} \quad c < \frac{1}{3} \\
\mu'_4 &= \frac{24}{(1-c)(1-2c)(1-3c)(1-4c)} \quad c < \frac{1}{4}
\end{aligned}$$

Thus,

$$\begin{aligned}
\mu &= \mu'_1 \\
\mu_2 &= \mu'_2 - \mu^2 \\
\gamma_1 &= \frac{\mu'_3 - 3\mu\mu_2 - \mu^3}{\mu_2^{3/2}} \\
\gamma_2 &= \frac{\mu'_4 - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4}{\mu_2^2} - 3
\end{aligned}$$

$$h[X] = 1 + c \quad c > 0$$

Implementation: *scipy.stats.genpareto*

Generalized Exponential Distribution

Three positive shape parameters $a, b, c > 0$ with support $x \geq 0$.

$$\begin{aligned}
f(x; a, b, c) &= \left(a + b\left(1 - e^{-cx}\right)\right) \exp\left(ax - bx + \frac{b}{c}\left(1 - e^{-cx}\right)\right) \\
F(x; a, b, c) &= 1 - \exp\left(ax - bx + \frac{b}{c}\left(1 - e^{-cx}\right)\right) \\
G(q; a, b, c) &= F^{-1}
\end{aligned}$$

Implementation: *scipy.stats.genexpon*

Generalized Extreme Value Distribution

Extreme value distributions with one shape parameter c.

If $c > 0$, the support is $-\infty < x \leq 1/c$. If $c < 0$, the support is $\frac{1}{c} \leq x < \infty$.

$$\begin{aligned}
f(x; c) &= \exp\left(-(1-cx)^{1/c}\right)(1-cx)^{1/c-1} \\
F(x; c) &= \exp\left(-(1-cx)^{1/c}\right) \\
G(q; c) &= \frac{1}{c}\left(1 - (-\log q)^c\right)
\end{aligned}$$

$$\mu'_n = \frac{1}{c^n} \sum_{k=0}^{n} \binom{n}{k} (-1)^k \Gamma(ck+1) \quad \text{if } cn > -1$$

So,

$$\begin{aligned}
\mu_1' &= \frac{1}{c}\left(1-\Gamma\left(1+c\right)\right) \quad c>-1\\
\mu_2' &= \frac{1}{c^2}\left(1-2\Gamma\left(1+c\right)+\Gamma\left(1+2c\right)\right) \quad c>-\frac{1}{2}\\
\mu_3' &= \frac{1}{c^3}\left(1-3\Gamma\left(1+c\right)+3\Gamma\left(1+2c\right)-\Gamma\left(1+3c\right)\right) \quad c>-\frac{1}{3}\\
\mu_4' &= \frac{1}{c^4}\left(1-4\Gamma\left(1+c\right)+6\Gamma\left(1+2c\right)-4\Gamma\left(1+3c\right)+\Gamma\left(1+4c\right)\right) \quad c>-\frac{1}{4}
\end{aligned}$$

For $c=0$ the distribution is the same as the (left-skewed) Gumbel distribution, and the support is $\mathbb{R}$.

$$\begin{aligned}
f\left(x;0\right) &= \exp\left(-e^{-x}\right)e^{-x}\\
F\left(x;0\right) &= \exp\left(-e^{-x}\right)\\
G\left(q;0\right) &= -\log\left(-\log q\right)
\end{aligned}$$

$$\begin{aligned}
\mu &= \gamma=-\psi_0\left(1\right)\\
\mu_2 &= \frac{\pi^2}{6}\\
\gamma_1 &= \frac{12\sqrt{6}}{\pi^3}\zeta\left(3\right)\\
\gamma_2 &= \frac{12}{5}
\end{aligned}$$

Implementation: *scipy.stats.genextreme*

Generalized Gamma Distribution

A general probability form that reduces to many common distributions. There are two shape parameters $a>0$ and $c\neq 0$. The support is $x\geq 0$.

$$\begin{aligned}
f\left(x;a,c\right) &= \frac{\left|c\right|x^{ca-1}}{\Gamma\left(a\right)}\exp\left(-x^c\right)\\
F\left(x;a,c\right) &= \begin{cases}\frac{\gamma(a,x^c)}{\Gamma(a)} & c>0\\ 1-\frac{\gamma(a,x^c)}{\Gamma(a)} & c<0\end{cases}\\
G\left(q;a,c\right) &= \begin{cases}\gamma^{-1}\left(a,\Gamma\left(a\right)q\right)^{1/c} & c>0\\ \gamma^{-1}\left(a,\Gamma\left(a\right)\left(1-q\right)\right)^{1/c} & c<0\end{cases}
\end{aligned}$$

where γ is the lower incomplete gamma function, $\gamma(s,x) = \int_0^x t^{s-1}e^{-t}dt$.

$$\begin{aligned}
\mu'_n &= \frac{\Gamma\left(a+\frac{n}{c}\right)}{\Gamma(a)} \\
\mu &= \frac{\Gamma\left(a+\frac{1}{c}\right)}{\Gamma(a)} \\
\mu_2 &= \frac{\Gamma\left(a+\frac{2}{c}\right)}{\Gamma(a)} - \mu^2 \\
\gamma_1 &= \frac{\Gamma\left(a+\frac{3}{c}\right)/\Gamma(a) - 3\mu\mu_2 - \mu^3}{\mu_2^{3/2}} \\
\gamma_2 &= \frac{\Gamma\left(a+\frac{4}{c}\right)/\Gamma(a) - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4}{\mu_2^2} - 3 \\
m_d &= \left(\frac{ac-1}{c}\right)^{1/c}
\end{aligned}$$

Special cases are Weibull $(a=1)$, half-normal $(a=1/2, c=2)$ and ordinary gamma distributions $c=1$. If $c=-1$ then it is the inverted gamma distribution.

$$h[X] = a - a\Psi(a) + \frac{1}{c}\Psi(a) + \log\Gamma(a) - \log|c|.$$

Implementation: `scipy.stats.gengamma`

Generalized Half-Logistic Distribution

One shape parameter $c > 0$ and support $x \in [0, 1/c]$.

$$\begin{aligned}
f(x;c) &= \frac{2(1-cx)^{\frac{1}{c}-1}}{\left(1+(1-cx)^{1/c}\right)^2} \\
F(x;c) &= \frac{1-(1-cx)^{1/c}}{1+(1-cx)^{1/c}} \\
G(q;c) &= \frac{1}{c}\left[1-\left(\frac{1-q}{1+q}\right)^c\right]
\end{aligned}$$

$$h[X] = 2 - (2c+1)\log 2.$$

Implementation: `scipy.stats.genhalflogistic`

Generalized Hyperbolic Distribution

The Generalized Hyperbolic Distribution is defined as the normal variance-mean mixture with Generalized Inverse Gaussian distribution as the mixing distribution. The "hyperbolic" characterization refers to the fact that the shape of the log-probability distribution can be described as a hyperbola. Hyperbolic distributions are sometime referred to as semi-fat tailed because their probability density decrease slower than "sub-hyperbolic" distributions (e.g. normal distribution, whose log-probability decreases quadratically), but faster than other "extreme value" distributions (e.g. *pareto* distribution, whose log-probability decreases logarithmically).

Functions

Different parameterizations exist in the literature; SciPy implements the "4th parametrization" in Prause (1999).

$$f(x, p, a, b) \quad = \quad \frac{(a^2 - b^2)^{p/2}}{\sqrt{2\pi} a^{p-0.5} K_p\Big(\sqrt{a^2 - b^2}\Big)} e^{bx} \times \frac{K_{p-1/2}(a\sqrt{1 + x^2})}{(\sqrt{1 + x^2})^{1/2-p}}$$

for:

- $x, p \in (-\infty; \infty)$
- $|b| < a$ if $p \geq 0$
- $|b| \leq a$ if $p < 0$
- $K_p(.)$ denotes the modified Bessel function of the second kind and order p (`scipy.special.kn`)

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, $f(x, p, a, b, \text{loc}, \text{scale})$ is identically equivalent to $\frac{1}{\text{scale}} f(y, p, a, b)$ with $y = \frac{1}{\text{scale}}(x - \text{loc})$.

This parameterization derives from the original $(\lambda, \alpha, \beta, \delta, \mu)$ parameterization in Barndorff (1978) by setting:

- $\lambda = p$
- $\alpha = \frac{a}{\delta} = \frac{\hat{\alpha}}{\delta}$
- $\beta = \frac{b}{\delta} = \frac{\hat{\beta}}{\delta}$
- $\delta = \text{scale}$
- $\mu = \text{location}$

Random variates for the `scipy.stats.genhyperbolic` can be efficiently sampled from the above-mentioned normal variance-mean mixture where `scipy.stats.geninvgauss` is parametrized as $GIG\Big(p = p, b = \sqrt{\hat{\alpha}^2 - \hat{\beta}^2}, \text{loc} = \text{location}, \text{scale} = \frac{1}{\sqrt{\hat{\alpha}^2 - \hat{\beta}^2}}\Big)$ so that: $GH(p, \hat{\alpha}, \hat{\beta}) = \hat{\beta} \cdot GIG + \sqrt{GIG} \cdot N(0, 1)$

The "generalized" characterization suggests the fact that this distribution is a superclass of several other probability distribution, for instance:

- $f(p = -\nu/2, a = 0, b = 0, \text{loc} = 0, \text{scale} = \sqrt{\nu})$ has a Student's t-distribution (`scipy.stats.t`) with ν degrees of freedom.
- $f(p = 1, a = \hat{\alpha}, b = \hat{\beta}, \text{loc} = \mu, \text{scale} = \delta)$ has a Hyperbolic Distribution.
- $f(p = -1/2, a = \hat{\alpha}, b = \hat{\beta}, \text{loc} = \mu, \text{scale} = \delta)$ has a Normal Inverse Gaussian Distribution (`scipy.stats.norminvgauss`).
- $f(p = 1, a = \delta, b = 0, loc = \mu, \text{scale} = \delta)$ has a Laplace Distribution (`scipy.stats.laplace`) for $\delta \to 0$

Examples

It is useful to understand how the parameters affect the shape of the distribution. While it is fairly straightforward to interpret the meaning of b as the skewness, understanding the difference between a and p is not as obvious, as both affect the kurtosis of the distribution. a can be interpreted as the speed of the decay of the probability density (where $a > 1$ the asymptotic decay is faster than log_e and vice versa) or - equivalently - as the slope of the log-probability hyperbola asymptote (where $a > 1$ decay is faster than $|1|$ and vice versa). p can be seen as the width of the shoulders of the probability density distribution (where $p < 1$ results in narrow shoulders and vice versa) or - equivalently - as the shape of the log-probability hyperbola, which is convex for $p < 1$ and concave otherwise.

```
import numpy as np
from matplotlib import pyplot as plt
from scipy import stats

p, a, b, loc, scale = 1, 1, 0, 0, 1
x = np.linspace(-10, 10, 100)

# plot GH for different values of p
plt.figure(0)
plt.title("Generalized Hyperbolic | -10 < p < 10")
plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        label = 'GH(p=1, a=1, b=0, loc=0, scale=1)')
plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        color = 'red', alpha = 0.5, label='GH(p>1, a=1, b=0, loc=0, scale=1)')
[plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        color = 'red', alpha = 0.1) for p in np.linspace(1, 10, 10)]
plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        color = 'blue', alpha = 0.5, label='GH(p<1, a=1, b=0, loc=0, scale=1)
↪')
[plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        color = 'blue', alpha = 0.1) for p in np.linspace(-10, 1, 10)]
plt.plot(x, stats.norm.pdf(x, loc, scale), label = 'N(loc=0, scale=1)')
plt.plot(x, stats.laplace.pdf(x, loc, scale), label = 'Laplace(loc=0, scale=1)
↪')
plt.plot(x, stats.pareto.pdf(x+1, 1, loc, scale), label = 'Pareto(a=1, loc=0,␣
↪scale=1)')
plt.ylim(1e-15, 1e2)
plt.yscale('log')
plt.legend(bbox_to_anchor=(1.1, 1))
plt.subplots_adjust(right=0.5)

# plot GH for different values of a
plt.figure(1)
plt.title("Generalized Hyperbolic | 0 < a < 10")
plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        label = 'GH(p=1, a=1, b=0, loc=0, scale=1)')
plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        color = 'blue', alpha = 0.5, label='GH(p=1, a>1, b=0, loc=0, scale=1)
↪')
[plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        color = 'blue', alpha = 0.1) for a in np.linspace(1, 10, 10)]
plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        color = 'red', alpha = 0.5, label='GH(p=1, 0<a<1, b=0, loc=0, scale=1)
↪')
[plt.plot(x, stats.genhyperbolic.pdf(x, p, a, b, loc, scale),
        color = 'red', alpha = 0.1) for a in np.linspace(0, 1, 10)]
plt.plot(x, stats.norm.pdf(x, loc, scale),  label = 'N(loc=0, scale=1)')
plt.plot(x, stats.laplace.pdf(x, loc, scale), label = 'Laplace(loc=0, scale=1)
↪')
plt.plot(x, stats.pareto.pdf(x+1, 1, loc, scale), label = 'Pareto(a=1, loc=0,␣
↪scale=1)')
plt.ylim(1e-15, 1e2)
plt.yscale('log')
```

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```
plt.legend(bbox_to_anchor=(1.1, 1))
plt.subplots_adjust(right=0.5)

plt.show()
```

References

- Normal Variance-Mean Mixture https://en.wikipedia.org/wiki/Normal_variance-mean_mixture
- Generalized Hyperbolic Distribution https://en.wikipedia.org/wiki/Generalised_hyperbolic_distribution
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- Scott, David J, Würtz, Diethelm, Dong, Christine and Tran, Thanh Tam, (2009), Moments of the generalized hyperbolic distribution, MPRA Paper, University Library of Munich, Germany, https://EconPapers.repec.org/RePEc:pra:mprapa:19081.

Implementation: *scipy.stats.genhyperbolic*

Generalized Inverse Gaussian Distribution

The probability density function is given by:

$$f(x; p, b) = x^{p-1} \exp(-b(x + 1/x)/2)/(2K_p(b)),$$

where $x > 0$ is a real number and the parameters p, b satisfy $b > 0$. K_v is the modified Bessel function of second kind of order v (*scipy.special.kv*).

If *X* is *geninvgauss(p, b)*, then the distribution of *1/X* is *geninvgauss(-p, b)*. The inverse Gaussian distribution (*scipy.stats.invgauss*) is a special case with p=-1/2.

Implementation: *scipy.stats.geninvgauss*

Generalized Normal Distribution

This distribution is also known as the exponential power distribution. It has a single shape parameter $\beta > 0$. It reduces to a number of common distributions.

Functions

$$f(x; \beta) = \frac{\beta}{2\Gamma(1/\beta)} e^{-|x|^\beta}$$

$$F(x; \beta) = \frac{1}{2} + \operatorname{sgn}(x) \frac{\gamma\left(1/\beta, x^\beta\right)}{2\Gamma(1/\beta)}$$

γ is the lower incomplete gamma function. $\gamma(s, x) = \int_0^x t^{s-1} e^{-t} dt$.

$$h[X; \beta] = \frac{1}{\beta} - \log\left(\frac{\beta}{2\Gamma(1/\beta)}\right)$$

Moments

$$\begin{aligned}
\mu &= 0 \\
m_n &= 0 \\
m_d &= 0 \\
\mu_2 &= \frac{\Gamma(3/\beta)}{\gamma(1/\beta)} \\
\gamma_1 &= 0 \\
\gamma_2 &= \frac{\Gamma(5/\beta)\Gamma(1/\beta)}{\Gamma(3/\beta)^2} - 3
\end{aligned}$$

Special Cases

- Laplace distribution ($\beta = 1$)
- Normal distribution with $\mu_2 = 1/2$ ($\beta = 2$)
- Uniform distribution over the interval $[-1, 1]$ ($\beta \to \infty$)

Sources

- https://en.wikipedia.org/wiki/Generalized_normal_distribution#Version_1
- https://en.wikipedia.org/wiki/Incomplete_gamma_function#Lower_incomplete_Gamma_function

Implementation: *scipy.stats.gennorm*

Gilbrat Distribution

Special case of the log-normal with $\sigma = 1$ and $S = 1.0$, typically also $L = 0.0$.)

$$\begin{aligned}
f(x; \sigma) &= \frac{1}{x\sqrt{2\pi}} \exp\left(-\frac{1}{2}(\log x)^2\right) \\
F(x; \sigma) &= \Phi(\log x) = \frac{1}{2}\left(1 + \operatorname{erf}\left(\frac{\log x}{\sqrt{2}}\right)\right) \\
G(q; \sigma) &= \exp\left(\Phi^{-1}(q)\right)
\end{aligned}$$

$$\begin{aligned}
\mu &= \sqrt{e} \\
\mu_2 &= e[e - 1] \\
\gamma_1 &= \sqrt{e - 1}(2 + e) \\
\gamma_2 &= e^4 + 2e^3 + 3e^2 - 6
\end{aligned}$$

$$\begin{aligned} h\left[X\right] &= \log\left(\sqrt{2\pi e}\right) \\ &\approx 1.4189385332046727418 \end{aligned}$$

Implementation: *scipy.stats.gilbrat*

Gompertz (Truncated Gumbel) Distribution

For $x \geq 0$ and $c > 0$. In JKB the two shape parameters b, a are reduced to the single shape-parameter $c = b/a$. As a is just a scale parameter when $a \neq 0$. If $a = 0$, the distribution reduces to the exponential distribution scaled by $1/b$. Thus, the standard form is given as

$$\begin{aligned} f\left(x; c\right) &= ce^{x}\exp\left(-c\left(e^{x}-1\right)\right) \\ F\left(x; c\right) &= 1-\exp\left(-c\left(e^{x}-1\right)\right) \\ G\left(q; c\right) &= \log\left(1-\frac{1}{c}\log\left(1-q\right)\right) \end{aligned}$$

$$h\left[X\right] = 1-\log\left(c\right)-e^{c}\mathrm{Ei}\left(1, c\right),$$

where

$$\mathrm{Ei}\left(n, x\right) = \int_{1}^{\infty} t^{-n}\exp\left(-xt\right)dt$$

Implementation: *scipy.stats.gompertz*

Gumbel (LogWeibull, Fisher-Tippetts, Type I Extreme Value) Distribution

One of a class of extreme value distributions (right-skewed).

$$\begin{aligned} f\left(x\right) &= \exp\left(-\left(x+e^{-x}\right)\right) \\ F\left(x\right) &= \exp\left(-e^{-x}\right) \\ G\left(q\right) &= -\log\left(-\log\left(q\right)\right) \end{aligned}$$

$$M\left(t\right) = \Gamma\left(1-t\right)$$

$$\begin{aligned} \mu &= \gamma = -\psi_{0}\left(1\right) \\ \mu_{2} &= \frac{\pi^{2}}{6} \\ \gamma_{1} &= \frac{12\sqrt{6}}{\pi^{3}}\zeta\left(3\right) \\ \gamma_{2} &= \frac{12}{5} \\ m_{d} &= 0 \\ m_{n} &= -\log\left(\log 2\right) \end{aligned}$$

$$h\left[X\right] \approx 1.0608407169541684911$$

Implementation: *scipy.stats.gumbel_r*

Gumbel Left-skewed (for minimum order statistic) Distribution

$$\begin{aligned} f(x) &= \exp(x - e^x) \\ F(x) &= 1 - \exp(-e^x) \\ G(q) &= \log(-\log(1-q)) \end{aligned}$$

$$M(t) = \Gamma(1+t)$$

Note, that μ is negative the mean for the right-skewed distribution. Similar for median and mode. All other moments are the same.

$$h[X] \approx 1.0608407169541684911.$$

Implementation: *scipy.stats.gumbel_l*

HalfCauchy Distribution

If Z is Hyperbolic Secant distributed then e^Z is Half-Cauchy distributed. Also, if W is (standard) Cauchy distributed, then $|W|$ is Half-Cauchy distributed. Special case of the Folded Cauchy distribution with $c = 0$. The support is $x \geq 0$. The standard form is

$$\begin{aligned} f(x) &= \frac{2}{\pi(1+x^2)} \\ F(x) &= \frac{2}{\pi}\arctan(x) \\ G(q) &= \tan\left(\frac{\pi}{2}q\right) \end{aligned}$$

$$M(t) = \cos t + \frac{2}{\pi}\left[\mathrm{Si}(t)\cos t - \mathrm{Ci}(-t)\sin t\right]$$

where $\mathrm{Si}(t) = \int_0^t \frac{\sin x}{x}dx$, $\mathrm{Ci}(t) = -\int_t^\infty \frac{\cos x}{x}dx$.

$$\begin{aligned} m_d &= 0 \\ m_n &= \tan\left(\frac{\pi}{4}\right) \end{aligned}$$

No moments, as the integrals diverge.

$$\begin{aligned} h[X] &= \log(2\pi) \\ &\approx 1.8378770664093454836. \end{aligned}$$

Implementation: *scipy.stats.halfcauchy*

HalfNormal Distribution

This is a special case of the chi distribution with $L = a$ and $S = b$ and $\nu = 1$. This is also a special case of the folded normal with shape parameter $c = 0$ and $S = S$. If Z is (standard) normally distributed then, $|Z|$ is half-normal. The standard form is

$$\begin{aligned} f(x) &= \sqrt{\frac{2}{\pi}}e^{-x^2/2} \\ F(x) &= 2\Phi(x) - 1 \\ G(q) &= \Phi^{-1}\left(\frac{1+q}{2}\right) \end{aligned}$$

$$M\left(t\right)=\sqrt{2\pi}e^{t^{2}/2}\Phi\left(t\right)$$

$$\begin{aligned}\mu &= \sqrt{\frac{2}{\pi}}\\ \mu_{2} &= 1-\frac{2}{\pi}\\ \gamma_{1} &= \frac{\sqrt{2}\left(4-\pi\right)}{\left(\pi-2\right)^{3/2}}\\ \gamma_{2} &= \frac{8\left(\pi-3\right)}{\left(\pi-2\right)^{2}}\\ m_{d} &= 0\\ m_{n} &= \Phi^{-1}\left(\frac{3}{4}\right)\end{aligned}$$

$$\begin{aligned}h\left[X\right] &= \log\left(\sqrt{\frac{\pi e}{2}}\right)\\ &\approx 0.72579135264472743239.\end{aligned}$$

Implementation: *scipy.stats.halfnorm*

Half-Logistic Distribution

In the limit as $c\to\infty$ for the generalized half-logistic we have the half-logistic defined over $x\geq 0$. Also, the distribution of $|X|$ where X has logistic distribution.

$$\begin{aligned}f\left(x\right) &= \frac{2e^{-x}}{\left(1+e^{-x}\right)^{2}}=\frac{1}{2}\mathrm{sech}^{2}\left(\frac{x}{2}\right)\\ F\left(x\right) &= \frac{1-e^{-x}}{1+e^{-x}}=\tanh\left(\frac{x}{2}\right)\\ G\left(q\right) &= \log\left(\frac{1+q}{1-q}\right)=2\mathrm{arctanh}\left(q\right)\end{aligned}$$

$$M\left(t\right)=1-t\psi_{0}\left(\frac{1}{2}-\frac{t}{2}\right)+t\psi_{0}\left(1-\frac{t}{2}\right)$$

where ψ_{m} is the polygamma function $\psi_{m}(z)=\frac{d^{m+1}}{dz^{m+1}}\log(\Gamma(z))$.

$$\mu_{n}^{\prime}=2\left(1-2^{1-n}\right)n!\zeta\left(n\right)\quad n\neq 1$$

$$\begin{aligned}\mu_{1}^{\prime} &= 2\log\left(2\right)\\ \mu_{2}^{\prime} &= 2\zeta\left(2\right)=\frac{\pi^{2}}{3}\\ \mu_{3}^{\prime} &= 9\zeta\left(3\right)\\ \mu_{4}^{\prime} &= 42\zeta\left(4\right)=\frac{7\pi^{4}}{15}\end{aligned}$$

$$\begin{aligned}h\left[X\right] &= 2-\log\left(2\right)\\ &\approx 1.3068528194400546906.\end{aligned}$$

Implementation: *scipy.stats.halflogistic*

Hyperbolic Secant Distribution

Related to the logistic distribution and used in lifetime analysis. Standard form is (defined over all x)

$$\begin{aligned} f(x) &= \frac{1}{\pi}\operatorname{sech}(x) \\ F(x) &= \frac{2}{\pi}\arctan\left(e^{x}\right) \\ G(q) &= \log\left(\tan\left(\frac{\pi}{2}q\right)\right) \end{aligned}$$

$$M(t) = \sec\left(\frac{\pi}{2}t\right)$$

$$\begin{aligned} \mu_n' &= \frac{1+(-1)^n}{2\pi 2^{2n}} n! \left[\zeta\left(n+1,\frac{1}{4}\right) - \zeta\left(n+1,\frac{3}{4}\right)\right] \\ &= \begin{cases} 0 & n \text{ odd} \\ C_{n/2}\frac{\pi^n}{2^n} & n \text{ even} \end{cases} \end{aligned}$$

where C_m is an integer given by

$$\begin{aligned} C_m &= \frac{(2m)!\left[\zeta\left(2m+1,\frac{1}{4}\right) - \zeta\left(2m+1,\frac{3}{4}\right)\right]}{\pi^{2m+1}2^{2m}} \\ &= 4(-1)^{m-1}\frac{16^m}{2m+1}B_{2m+1}\left(\frac{1}{4}\right) \end{aligned}$$

where $B_{2m+1}\left(\frac{1}{4}\right)$ is the Bernoulli polynomial of order $2m+1$ evaluated at $1/4$. Thus

$$\mu_n' = \begin{cases} 0 & n \text{ odd} \\ 4(-1)^{n/2-1}\frac{(2\pi)^n}{n+1}B_{n+1}\left(\frac{1}{4}\right) & n \text{ even} \end{cases}$$

$$\begin{aligned} m_d = m_n = \mu &= 0 \\ \mu_2 &= \frac{\pi^2}{4} \\ \gamma_1 &= 0 \\ \gamma_2 &= 2 \end{aligned}$$

$$h[X] = \log(2\pi).$$

Implementation: *scipy.stats.hypsecant*

Gauss Hypergeometric Distribution

The four shape parameters are $\alpha > 0$, $\beta > 0$, $-\infty < \gamma < \infty$, and $z > -1$. The support is $x \in [0,1]$.

$$\text{Let } C = \frac{1}{B(\alpha,\beta)\ {}_2F_1(\gamma,\alpha;\alpha+\beta;-z)}$$

$$\begin{aligned} f(x;\alpha,\beta,\gamma,z) &= Cx^{\alpha-1}\frac{(1-x)^{\beta-1}}{(1+zx)^{\gamma}} \\ \mu_n' &= \frac{B(n+\alpha,\beta)}{B(\alpha,\beta)}\frac{{}_2F_1(\gamma,\alpha+n;\alpha+\beta+n;-z)}{{}_2F_1(\gamma,\alpha;\alpha+\beta;-z)} \end{aligned}$$

Implementation: *scipy.stats.gausshyper*

Inverted Gamma Distribution

Special case of the generalized Gamma distribution with $c = -1$ and $a > 0$ and support $x \geq 0$.

$$\begin{aligned} f(x;a) &= \frac{x^{-a-1}}{\Gamma(a)} \exp\left(-\frac{1}{x}\right) \\ F(x;a) &= \frac{\Gamma\left(a, \frac{1}{x}\right)}{\Gamma(a)} \\ G(q;a) &= \left\{\Gamma^{-1}(a, \Gamma(a)\, q)\right\}^{-1} \end{aligned}$$

$$\mu_n' = \frac{\Gamma(a-n)}{\Gamma(a)} \quad a > n$$

$$\begin{aligned} \mu &= \frac{1}{a-1} \quad a > 1 \\ \mu_2 &= \frac{1}{(a-2)(a-1)} - \mu^2 \quad a > 2 \\ \gamma_1 &= \frac{\frac{1}{(a-3)(a-2)(a-1)} - 3\mu\mu_2 - \mu^3}{\mu_2^{3/2}} \\ \gamma_2 &= \frac{\frac{1}{(a-4)(a-3)(a-2)(a-1)} - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4}{\mu_2^2} - 3 \end{aligned}$$

$$m_d = \frac{1}{a+1}$$

$$h[X] = a - (a+1)\,\psi(a) + \log\Gamma(a)\,.$$

where Ψ is the digamma function $\psi(z) = \frac{d}{dz}\log(\Gamma(z))$.

Implementation: `scipy.stats.invgamma`

Inverse Normal (Inverse Gaussian) Distribution

The standard form involves the shape parameter μ (in most definitions, $L = 0.0$ is used). (In terms of the regress documentation $\mu = A/B$) and $B = S$ and L is not a parameter in that distribution. A standard form is $x > 0$

$$\begin{aligned} f(x;\mu) &= \frac{1}{\sqrt{2\pi x^3}} \exp\left(-\frac{(x-\mu)^2}{2x\mu^2}\right). \\ F(x;\mu) &= \Phi\left(\frac{1}{\sqrt{x}}\frac{x-\mu}{\mu}\right) + \exp\left(\frac{2}{\mu}\right)\Phi\left(-\frac{1}{\sqrt{x}}\frac{x+\mu}{\mu}\right) \\ G(q;\mu) &= F^{-1}(q;\mu) \end{aligned}$$

$$\begin{aligned} \mu &= \mu \\ \mu_2 &= \mu^3 \\ \gamma_1 &= 3\sqrt{\mu} \\ \gamma_2 &= 15\mu \\ m_d &= \frac{\mu}{2}\left(\sqrt{9\mu^2+4} - 3\mu\right) \end{aligned}$$

This is related to the canonical form or JKB "two-parameter" inverse Gaussian when written in it's full form with scale parameter S and location parameter L by taking $L = 0$ and $S \equiv \lambda$, then μS is equal to μ_2 where μ_2 is the parameter

used by JKB. We prefer this form because of it's consistent use of the scale parameter. Notice that in JKB the skew $\left(\sqrt{\beta_1}\right)$ and the kurtosis ($\beta_2 - 3$) are both functions only of $\mu_2/\lambda = \mu S/S = \mu$ as shown here, while the variance and mean of the standard form here are transformed appropriately.

Implementation: `scipy.stats.invgauss`

Inverted Weibull Distribution

There is one shape parameter $c > 0$ and the support is $x \geq 0$. Then

$$\begin{aligned} f(x;c) &= cx^{-c-1}\exp\left(-x^{-c}\right) \\ F(x;c) &= \exp\left(-x^{-c}\right) \\ G(q;c) &= (-\log q)^{-1/c} \end{aligned}$$

$$h[X] = 1 + \gamma + \frac{\gamma}{c} - \log(c)$$

where γ is Euler's constant.

Implementation: `scipy.stats.invweibull`

Johnson SB Distribution

There are two shape parameters $a \in \mathbb{R}$ and $b > 0$, and the support is $x \in [0, 1]$.

$$\begin{aligned} f(x;a,b) &= \frac{b}{x(1-x)}\phi\left(a + b\log\frac{x}{1-x}\right) \\ F(x;a,b) &= \Phi\left(a + b\log\frac{x}{1-x}\right) \\ G(q;a,b) &= \frac{1}{1+\exp\left(-\frac{1}{b}\left(\Phi^{-1}(q) - a\right)\right)} \end{aligned}$$

Implementation: `scipy.stats.johnsonsb`

Johnson SU Distribution

There are two shape parameters $a \in \mathbb{R}$ and $b > 0$, and the support is $x \in \mathbb{R}$.

$$\begin{aligned} f(x;a,b) &= \frac{b}{\sqrt{x^2+1}}\phi\left(a + b\log\left(x + \sqrt{x^2+1}\right)\right) \\ F(x;a,b) &= \Phi\left(a + b\log\left(x + \sqrt{x^2+1}\right)\right) \\ G(q;a,b) &= \sinh\left(\frac{\Phi^{-1}(q) - a}{b}\right) \end{aligned}$$

Implementation: `scipy.stats.johnsonsu`

KSone Distribution

This is the distribution of maximum positive differences between an empirical distribution function, computed from n samples or observations, and a comparison (or target) cumulative distribution function.

Writing $D_n^+ = \sup_t \left(F_{empirical,n}(t) - F_{target}(t)\right)$, `ksone` is the distribution of the D_n^+ values. (The distribution of $D_n^- = \sup_t \left(F_{target}(t) - F_{empirical,n}(t)\right)$ differences follows the same distribution, so `ksone` can be used for one-sided tests on either side.)

There is one shape parameter n, a positive integer, and the support is $x \in [0, 1]$.

$$\begin{aligned} F\left(n, x\right) &= 1 - \sum_{j=0}^{\lfloor n(1-x)\rfloor} \binom{n}{j} x \left(x + \frac{j}{n}\right)^{j-1} \left(1 - x - \frac{j}{n}\right)^{n-j} \\ &= 1 - \text{scipy.special.smirnov}(n, x) \\ \lim_{n\to\infty} F\left(n, \frac{x}{\sqrt{n}}\right) &= e^{-2x^2} \end{aligned}$$

References

- "Kolmogorov-Smirnov test", Wikipedia https://en.wikipedia.org/wiki/Kolmogorov-Smirnov_test
- Birnbaum, Z. W.; Tingey, Fred H. "One-Sided Confidence Contours for Probability Distribution Functions." *Ann. Math. Statist.* 22 (1951), no. 4, 592–596.

Implementation: *scipy.stats.ksone*

KStwo Distribution

This is the distribution of the maximum absolute differences between an empirical distribution function, computed from n samples or observations, and a comparison (or target) cumulative distribution function, which is assumed to be continuous. (The "two" in the name is because this is the two-sided difference. `ksone` is the distribution of the positive differences, D_n^+, hence it concerns one-sided differences. `kstwobign` is the limiting distribution of the *normalized* maximum absolute differences $\sqrt{n}D_n$.)

Writing $D_n = \sup_t |F_{empirical,n}(t) - F_{target}(t)|$, `kstwo` is the distribution of the D_n values.

`kstwo` can also be used with the differences between two empirical distribution functions, for sets of observations with m and n samples respectively. Writing $D_{m,n} = \sup_t |F_{1,m}(t) - F_{2,n}(t)|$, where $F_{1,m}$ and $F_{2,n}$ are the two empirical distribution functions, then $Pr(D_{m,n} \le x) \approx Pr(D_N \le x)$ under appropriate conditions, where $N = \sqrt{\left(\frac{mn}{m+n}\right)}$.

There is one shape parameter n, a positive integer, and the support is $x \in [0, 1]$.

The implementation follows Simard & L'Ecuyer, which combines exact algorithms of Durbin and Pomeranz with asymptotic estimates of Li-Chien, Pelz and Good to compute the CDF with 5-15 accurate digits.

Examples

```
>>> from scipy.stats import kstwo
```

Show the probability of a gap at least as big as 0, 0.5 and 1.0 for a sample of size 5

```
>>> kstwo.sf([0, 0.5, 1.0], 5)
array([1.   , 0.112, 0.   ])
```

Compare a sample of size 5 drawn from a source N(0.5, 1) distribution against a target N(0, 1) CDF.

```
>>> from scipy.stats import norm
>>> n = 5
>>> gendist = norm(0.5, 1)        # Normal distribution, mean 0.5, stddev 1
>>> x = np.sort(gendist.rvs(size=n, random_state=np.random.default_rng()))
>>> x
array([-1.59113056, -0.66335147,  0.54791569,  0.78009321,  1.27641365])
>>> target = norm(0, 1)
>>> cdfs = target.cdf(x)
>>> cdfs
array([0.0557901 , 0.25355274, 0.7081251 , 0.78233199, 0.89909533])
# Construct the Empirical CDF and the K-S statistics (Dn+, Dn-, Dn)
>>> ecdfs = np.arange(n+1, dtype=float)/n
>>> cols = np.column_stack([x, ecdfs[1:], cdfs, cdfs - ecdfs[:n], ecdfs[1:] -␣
↪cdfs])
>>> np.set_printoptions(precision=3)
>>> cols
array([[-1.591,  0.2  ,  0.056,  0.056,  0.144],
       [-0.663,  0.4  ,  0.254,  0.054,  0.146],
       [ 0.548,  0.6  ,  0.708,  0.308, -0.108],
       [ 0.78 ,  0.8  ,  0.782,  0.182,  0.018],
       [ 1.276,  1.   ,  0.899,  0.099,  0.101]])
>>> gaps = cols[:, -2:]
>>> Dnpm = np.max(gaps, axis=0)
>>> Dn = np.max(Dnpm)
>>> iminus, iplus = np.argmax(gaps, axis=0)
>>> print('Dn- = %f (at x=%.2f)' % (Dnpm[0], x[iminus]))
Dn- = 0.308125 (at x=0.55)
>>> print('Dn+ = %f (at x=%.2f)' % (Dnpm[1], x[iplus]))
Dn+ = 0.146447 (at x=-0.66)
>>> print('Dn  = %f' % (Dn))
Dn  = 0.308125
```

```
>>> probs = kstwo.sf(Dn, n)
>>> print(chr(10).join(['For a sample of size %d drawn from a N(0, 1)␣
↪distribution:' % n,
...      ' Kolmogorov-Smirnov 2-sided n=%d: Prob(Dn >= %f) = %.4f' % (n, Dn,␣
↪probs)]))
For a sample of size 5 drawn from a N(0, 1) distribution:
 Kolmogorov-Smirnov 2-sided n=5: Prob(Dn >= 0.308125) = 0.6319
```

Plot the Empirical CDF against the target N(0, 1) CDF

```
>>> import matplotlib.pyplot as plt
>>> plt.step(np.concatenate([[-3], x]), ecdfs, where='post', label='Empirical␣
↪CDF')
>>> x3 = np.linspace(-3, 3, 100)
>>> plt.plot(x3, target.cdf(x3), label='CDF for N(0, 1)')
>>> plt.ylim([0, 1]); plt.grid(True); plt.legend();
>>> plt.vlines([x[iminus]], ecdfs[iminus], cdfs[iminus], color='r', linestyle=
↪'solid', lw=4)
>>> plt.vlines([x[iplus]], cdfs[iplus], ecdfs[iplus+1], color='m', linestyle=
↪'solid', lw=4)
>>> plt.annotate('Dn-', xy=(x[iminus], (ecdfs[iminus]+ cdfs[iminus])/2),
...              xytext=(x[iminus]+1, (ecdfs[iminus]+ cdfs[iminus])/2 - 0.02),
...              arrowprops=dict(facecolor='white', edgecolor='r', shrink=0.
↪05), size=15, color='r');
>>> plt.annotate('Dn+', xy=(x[iplus], (ecdfs[iplus+1]+ cdfs[iplus])/2),
...             xytext=(x[iplus]-2, (ecdfs[iplus+1]+ cdfs[iplus])/2 - 0.02),
...             arrowprops=dict(facecolor='white', edgecolor='m', shrink=0.
↪05), size=15, color='m');
>>> plt.show()
```

References

- "Kolmogorov-Smirnov test", Wikipedia https://en.wikipedia.org/wiki/Kolmogorov-Smirnov_test
- Durbin J. "The Probability that the Sample Distribution Function Lies Between Two Parallel Straight Lines." *Ann. Math. Statist.*, 39 (1968) 39, 398-411.
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- Simard, R., L'Ecuyer, P. "Computing the Two-Sided Kolmogorov-Smirnov Distribution", *Journal of Statistical Software*, Vol 39, (2011) 11.

Implementation: *scipy.stats.kstwo*

KStwobign Distribution

This is the limiting distribution of the normalized maximum absolute differences between an empirical distribution function, computed from n samples or observations, and a comparison (or target) cumulative distribution function. (`ksone` is the distribution of the unnormalized positive differences, D_n^+.)

Writing $D_n = \sup_t |F_{empirical,n}(t) - F_{target}(t)|$, the normalization factor is $\sqrt{n}$, and `kstwobign` is the limiting distribution of the $\sqrt{n}D_n$ values as $n \to \infty$.

Note that $D_n = \max(D_n^+, D_n^-)$, but D_n^+ and D_n^- are not independent.

`kstwobign` can also be used with the differences between two empirical distribution functions, for sets of observations with m and n samples respectively, where m and n are "big". Writing $D_{m,n} = \sup_t |F_{1,m}(t) - F_{2,n}(t)|$, where

$F_{1,m}$ and $F_{2,n}$ are the two empirical distribution functions, then `kstwobign` is also the limiting distribution of the $\sqrt{\left(\frac{mn}{m+n}\right) D_{m,n}}$ values, as $m, n \to \infty$ and $m/n \to a \neq 0, \infty$.

There are no shape parameters, and the support is $x \in [0, \infty)$.

$$\begin{aligned} F(x) &= 1 - 2\sum_{k=1}^{\infty}(-1)^{k-1} e^{-2k^2x^2} \\ &= \frac{\sqrt{2\pi}}{x}\sum_{k=1}^{\infty} e^{-(2k-1)^2\pi^2/(8x^2)} \\ &= 1 - \text{scipy.special.kolmogorov}(n, x) \\ f(x) &= 8x\sum_{k=1}^{\infty}(-1)^{k-1} k^2 e^{-2k^2x^2} \end{aligned}$$

References

- "Kolmogorov-Smirnov test", Wikipedia https://en.wikipedia.org/wiki/Kolmogorov-Smirnov_test
- Kolmogoroff, A. "Confidence Limits for an Unknown Distribution Function."" *Ann. Math. Statist.* 12 (1941), no. 4, 461–463.
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Implementation: *`scipy.stats.kstwobign`*

Laplace (Double Exponential, Bilateral Exponential) Distribution

$$\begin{aligned} f(x) &= \frac{1}{2}e^{-|x|} \\ F(x) &= \begin{cases} \frac{1}{2}e^{x} & x \leq 0 \\ 1 - \frac{1}{2}e^{-x} & x > 0 \end{cases} \\ G(q) &= \begin{cases} \log(2q) & q \leq \frac{1}{2} \\ -\log(2-2q) & q > \frac{1}{2} \end{cases} \end{aligned}$$

$$\begin{aligned} m_d = m_n = \mu &= 0 \\ \mu_2 &= 2 \\ \gamma_1 &= 0 \\ \gamma_2 &= 3 \end{aligned}$$

The ML estimator of the location parameter is

$$\hat{L} = \text{median}(X_i)$$

where X_i is a sequence of N mutually independent Laplace RV's and the median is some number between the $\frac{1}{2}N\text{th}$ and the $(N/2+1)\text{th}$ order statistic (*e.g.* take the average of these two) when N is even. Also,

$$\hat{S} = \frac{1}{N}\sum_{j=1}^{N}\left|X_j - \hat{L}\right|.$$

Replace $\hat{L}$ with L if it is known. If L is known then this estimator is distributed as $(2N)^{-1} S \cdot \chi^2_{2N}$.

$$\begin{aligned} h[X] &= \log(2e) \\ &\approx 1.6931471805599453094. \end{aligned}$$

Implementation: `scipy.stats.laplace`

Asymmetric Laplace Distribution

This distribution is a generalization of the Laplace distribution. It has a single shape parameter $\kappa > 0$ that species the distribution's asymmetry. The special case $\kappa = 1$ yields the Laplace distribution.

Functions

$$\begin{aligned} F(x,\kappa) &= 1 - \frac{\kappa^{-1}}{\kappa+\kappa^{-1}} \exp(-x\kappa), \quad x \geq 0; \\ &= \frac{\kappa}{\kappa+\kappa^{-1}} \exp(x/\kappa), \quad x < 0. \\ f(x,\kappa) &= \frac{1}{\kappa+\kappa^{-1}} \exp(-x\kappa), \quad x \geq 0; \\ &= \frac{1}{\kappa+\kappa^{-1}} \exp(x/\kappa), \quad x < 0. \end{aligned}$$

$$\begin{aligned} \mu &= \kappa^{-1} - \kappa \\ \mu_2 &= \kappa^{-2} + \kappa^2 \\ \gamma_1 &= \frac{2(1-\kappa^6)}{(1+\kappa^4)^{3/2}} \\ \gamma_2 &= \frac{6(1+\kappa^8)}{(1+\kappa^4)^2} \end{aligned}$$

References

- "Asymmetric Laplace distribution", Wikipedia https://en.wikipedia.org/wiki/Asymmetric_Laplace_distribution
- Kozubowski TJ and Podgórski K, "A Multivariate and Asymmetric Generalization of Laplace Distribution," *Computational Statistics* 15, 531–540 (2000). DOI:10.1007/PL00022717

Implementation: `scipy.stats.laplace_asymmetric`

Left-skewed Lévy Distribution

Special case of Lévy-stable distribution with $\alpha = \frac{1}{2}$ and $\beta = -1$. The support is $x \leq 0$. In standard form

$$\begin{aligned} f(x) &= \frac{1}{|x|\sqrt{2\pi|x|}} \exp\left(-\frac{1}{2|x|}\right) \\ F(x) &= 2\Phi\left(\frac{1}{\sqrt{|x|}}\right) - 1 \\ G(q) &= -\left[\Phi^{-1}\left(\frac{q+1}{2}\right)\right]^{-2}. \end{aligned}$$

No moments.

Implementation: *scipy.stats.levy_l*

Lévy Distribution

A special case of Lévy-stable distributions with $\alpha = \frac{1}{2}$ and $\beta = 1$ and support $x \geq 0$. In standard form it is defined for $x > 0$ as

$$\begin{aligned} f(x) &= \frac{1}{x\sqrt{2\pi x}} \exp\left(-\frac{1}{2x}\right) \\ F(x) &= 2\left[1 - \Phi\left(\frac{1}{\sqrt{x}}\right)\right] \\ G(q) &= \left[\Phi^{-1}\left(1 - \frac{q}{2}\right)\right]^{-2}. \end{aligned}$$

It has no finite moments.

Implementation: *scipy.stats.levy*

Logistic (Sech-squared) Distribution

A special case of the Generalized Logistic distribution with $c = 1$. Defined for $x \geq 0$

$$\begin{aligned} f(x) &= \frac{\exp(-x)}{(1 + \exp(-x))^2} \\ F(x) &= \frac{1}{1 + \exp(-x)} \\ G(q) &= -\log(1/q - 1) \end{aligned}$$

$$\begin{aligned} \mu &= \gamma + \psi_0(1) = 0 \\ \mu_2 &= \frac{\pi^2}{6} + \psi_1(1) = \frac{\pi^2}{3} \\ \gamma_1 &= \frac{\psi_2(1) + 2\zeta(3)}{\mu_2^{3/2}} = 0 \\ \gamma_2 &= \frac{\left(\frac{\pi^4}{15} + \psi_3(1)\right)}{\mu_2^2} = \frac{6}{5} \\ m_d &= \log 1 = 0 \\ m_n &= -\log(2 - 1) = 0 \end{aligned}$$

where ψ_m is the polygamma function $\psi_m(z) = \frac{d^{m+1}}{dz^{m+1}} \log(\Gamma(z))$.

$$h[X] = 1.$$

Implementation: *scipy.stats.logistic*

Log Double Exponential (Log-Laplace) Distribution

One shape parameter $c > 0$. The support is $x \geq 0$.

$$\begin{aligned} f(x;c) &= \begin{cases} \frac{c}{2}x^{c-1} & 0 < x < 1 \\ \frac{c}{2}x^{-c-1} & x \geq 1 \end{cases} \\ F(x;c) &= \begin{cases} \frac{1}{2}x^{c} & 0 < x < 1 \\ 1 - \frac{1}{2}x^{-c} & x \geq 1 \end{cases} \\ G(q;c) &= \begin{cases} (2q)^{1/c} & 0 \leq q < \frac{1}{2} \\ (2-2q)^{-1/c} & \frac{1}{2} \leq q \leq 1 \end{cases} \end{aligned}$$

$$h[X] = \log\left(\frac{2e}{c}\right)$$

Implementation: `scipy.stats.loglaplace`

Log Gamma Distribution

A single shape parameter $c > 0$. The support is $x \in \mathbb{R}$.

$$\begin{aligned} f(x;c) &= \frac{\exp(cx - e^x)}{\Gamma(c)} \\ F(x;c) &= \frac{\gamma(c, e^x)}{\Gamma(c)} \\ G(q;c) &= \log\left(\gamma^{-1}(c, q\Gamma(c))\right) \end{aligned}$$

where γ is the lower incomplete gamma function, $\gamma(s,x) = \int_0^x t^{s-1}e^{-t}dt$.

$$\mu'_n = \int_0^\infty [\log y]^n y^{c-1} \exp(-y)\, dy.$$

$$\begin{aligned} \mu &= \mu'_1 \\ \mu_2 &= \mu'_2 - \mu^2 \\ \gamma_1 &= \frac{\mu'_3 - 3\mu\mu_2 - \mu^3}{\mu_2^{3/2}} \\ \gamma_2 &= \frac{\mu'_4 - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4}{\mu_2^2} - 3 \end{aligned}$$

Implementation: `scipy.stats.loggamma`

Log Normal (Cobb-Douglass) Distribution

Has one shape parameter σ >0. (Notice that the "Regress" $A = \log S$ where S is the scale parameter and A is the mean of the underlying normal distribution). The support is $x \geq 0$.

$$\begin{aligned} f(x;\sigma) &= \frac{1}{\sigma x\sqrt{2\pi}} \exp\left(-\frac{1}{2}\left(\frac{\log x}{\sigma}\right)^2\right) \\ F(x;\sigma) &= \Phi\left(\frac{\log x}{\sigma}\right) \\ G(q;\sigma) &= \exp\left(\sigma\Phi^{-1}(q)\right) \end{aligned}$$

$$\begin{aligned}
\mu &= \exp\left(\sigma^2/2\right) \\
\mu_2 &= \exp\left(\sigma^2\right)\left[\exp\left(\sigma^2\right)-1\right] \\
\gamma_1 &= \sqrt{p-1}\,(2+p) \\
\gamma_2 &= p^4+2p^3+3p^2-6 \qquad p=e^{\sigma^2}
\end{aligned}$$

Notice that using JKB notation we have $\theta = L, \zeta = \log S$ and we have given the so-called antilognormal form of the distribution. This is more consistent with the location, scale parameter description of general probability distributions.

$$h\left[X\right] = \frac{1}{2}\left[1+\log\left(2\pi\right)+2\log\left(\sigma\right)\right].$$

Also, note that if X is a log-normally distributed random-variable with $L = 0$ and S and shape parameter σ. Then, $\log X$ is normally distributed with variance σ^2 and mean $\log S$.

Implementation: *scipy.stats.lognorm*

Log-Uniform Distribution

This random variable is log-uniform. That is, if `loguniform(10**-1, 10**1)` is specified, `0.1`, `1`, `10` are all equally likely.

There are two shape parameters $a, b > 0$ and the support is $x \in [a, b]$.

$$\begin{aligned}
f\left(x;a,b\right) &= \frac{1}{x\log\left(b/a\right)} \\
F\left(x;a,b\right) &= \frac{\log\left(x/a\right)}{\log\left(b/a\right)} \\
G\left(q;a,b\right) &= a\exp\left(q\log\left(b/a\right)\right) = a\left(\frac{b}{a}\right)^q
\end{aligned}$$

$$\begin{aligned}
d &= \log\left(a/b\right) \\
\mu &= \frac{a-b}{d} \\
\mu_2 &= \mu\frac{a+b}{2}-\mu^2 = \frac{\left(a-b\right)\left[a\left(d-2\right)+b\left(d+2\right)\right]}{2d^2} \\
\gamma_1 &= \frac{\sqrt{2}\left[12d\left(a-b\right)^2+d^2\left(a^2\left(2d-9\right)+2abd+b^2\left(2d+9\right)\right)\right]}{3d\sqrt{a-b}\left[a\left(d-2\right)+b\left(d+2\right)\right]^{3/2}} \\
\gamma_2 &= \frac{-36\left(a-b\right)^3+36d\left(a-b\right)^2\left(a+b\right)-16d^2\left(a^3-b^3\right)+3d^3\left(a^2+b^2\right)\left(a+b\right)}{3\left(a-b\right)\left[a\left(d-2\right)+b\left(d+2\right)\right]^2}-3 \\
m_d &= a \\
m_n &= \sqrt{ab}
\end{aligned}$$

$$h\left[X\right] = \frac{1}{2}\log\left(ab\right)+\log\left[\log\left(\frac{b}{a}\right)\right].$$

Implementation: *scipy.stats.loguniform*.

Maxwell Distribution

This is a special case of the Chi distribution with $L = 0$ and $S = \frac{1}{\sqrt{a}}$ and $\nu = 3$. The support is $x \geq 0$.

$$\begin{aligned} f(x) &= \sqrt{\frac{2}{\pi}} x^2 e^{-x^2/2} \\ F(x) &= \frac{\gamma\left(\frac{3}{2}, \frac{x^2}{2}\right)}{\Gamma(\frac{3}{2})} \\ G(q) &= \sqrt{2\gamma^{-1}\left(\frac{3}{2}, q\Gamma(\frac{3}{2})\right)} \end{aligned}$$

$$\begin{aligned} \mu &= 2\sqrt{\frac{2}{\pi}} \\ \mu_2 &= 3 - \frac{8}{\pi} \\ \gamma_1 &= \sqrt{2}\frac{32 - 10\pi}{(3\pi - 8)^{3/2}} \\ \gamma_2 &= \frac{-12\pi^2 + 160\pi - 384}{(3\pi - 8)^2} \\ m_d &= \sqrt{2} \\ m_n &= \sqrt{2\gamma^{-1}\left(\frac{3}{2}, \frac{1}{2}\Gamma(\frac{3}{2})\right)} \end{aligned}$$

$$h[X] = \log\left(\sqrt{\frac{2\pi}{e}}\right) + \gamma.$$

Implementation: `scipy.stats.maxwell`

Mielke's Beta-Kappa Distribution

A generalized F distribution. Two shape parameters κ and θ, with support $x \geq 0$. The β in the DATAPLOT reference is a scale parameter.

$$\begin{aligned} f(x; \kappa, \theta) &= \frac{\kappa x^{\kappa - 1}}{(1 + x^\theta)^{1 + \frac{\kappa}{\theta}}} \\ F(x; \kappa, \theta) &= \frac{x^\kappa}{(1 + x^\theta)^{\kappa/\theta}} \\ G(q; \kappa, \theta) &= \left(\frac{q^{\theta/\kappa}}{1 - q^{\theta/\kappa}}\right)^{1/\theta} \end{aligned}$$

Implementation: `scipy.stats.mielke`

Nakagami Distribution

Generalization of the chi distribution. Shape parameter is $\nu > 0$. The support is $x \geq 0$.

$$\begin{aligned} f(x;\nu) &= \frac{2\nu^{\nu}}{\Gamma(\nu)} x^{2\nu-1} \exp\left(-\nu x^2\right) \\ F(x;\nu) &= \frac{\gamma\left(\nu, \nu x^2\right)}{\Gamma(\nu)} \\ G(q;\nu) &= \sqrt{\frac{1}{\nu}\gamma^{-1}\left(\nu, q\Gamma(\nu)\right)} \end{aligned}$$

where γ is the lower incomplete gamma function, $\gamma(\nu, x) = \int_0^x t^{\nu-1} e^{-t} dt$.

$$\begin{aligned} \mu &= \frac{\Gamma\left(\nu+\frac{1}{2}\right)}{\sqrt{\nu}\Gamma(\nu)} \\ \mu_2 &= \left[1-\mu^2\right] \\ \gamma_1 &= \frac{\mu\left(1-4v\mu_2\right)}{2\nu\mu_2^{3/2}} \\ \gamma_2 &= \frac{-6\mu^4\nu + (8\nu-2)\mu^2 - 2\nu + 1}{\nu\mu_2^2} \end{aligned}$$

Implementation: *scipy.stats.nakagami*

MLE of the Nakagami Distribution in SciPy (`nakagami.fit`)

The probability density function of the `nakagami` distribution in SciPy is

$$f(x;\nu,\mu,\sigma) = 2\frac{\nu^{\nu}}{\sigma\Gamma(\nu)}\left(\frac{x-\mu}{\sigma}\right)^{2\nu-1}\exp\left(-\nu\left(\frac{x-\mu}{\sigma}\right)^2\right), \tag{1}$$

for x such that $\frac{x-\mu}{\sigma} \geq 0$, where $\nu \geq \frac{1}{2}$ is the shape parameter, μ is the location, and σ is the scale.

The log-likelihood function is therefore

$$l(\nu,\mu,\sigma) = \sum_{i=1}^{N}\log\left(2\frac{\nu^{\nu}}{\sigma\Gamma(\nu)}\left(\frac{x_i-\mu}{\sigma}\right)^{2\nu-1}\exp\left(-\nu\left(\frac{x_i-\mu}{\sigma}\right)^2\right)\right), \tag{2}$$

which can be expanded as

$$l(\nu,\mu,\sigma) = N\log(2) + N\nu\log(\nu) - N\log\left(\Gamma(\nu)\right) - 2N\nu\log(\sigma) + (2\nu-1)\sum_{i=1}^{N}\log(x_i-\mu) - \nu\sigma^{-2}\sum_{i=1}^{N}(x_i-\mu)^2, \tag{3}$$

Leaving supports constraints out, the first-order condition for optimality on the likelihood derivatives gives estimates of parameters:

$$\frac{\partial l}{\partial\nu}(\nu,\mu,\sigma) = N\left(1+\log(\nu)-\psi^{(0)}(\nu)\right) + 2\sum_{i=1}^{N}\log\left(\frac{x_i-\mu}{\sigma}\right) - \sum_{i=1}^{N}\left(\frac{x_i-\mu}{\sigma}\right)^2 = 0, \tag{4}$$

$$\frac{\partial l}{\partial\mu}(\nu,\mu,\sigma) = (1-2\nu)\sum_{i=1}^{N}\frac{1}{x_i-\mu} + \frac{2\nu}{\sigma^2}\sum_{i=1}^{N}x_i - \mu = 0, \text{ and} \tag{5}$$

$$\frac{\partial l}{\partial\sigma}(\nu,\mu,\sigma) = -2N\nu\frac{1}{\sigma} + 2\nu\sigma^{-3}\sum_{i=1}^{N}(x_i-\mu)^2 = 0, \tag{6}$$

where $\psi^{(0)}$ is the polygamma function of order 0; i.e. $\psi^{(0)}(\nu) = \frac{d}{d\nu}\log\Gamma(\nu)$.

However, the support of the distribution is the values of x for which $\frac{x-\mu}{\sigma} \geq 0$, and this provides an additional constraint that

$$\mu \leq \min_i x_i. \tag{7}$$

For $\nu = \frac{1}{2}$, the partial derivative of the log-likelihood with respect to μ reduces to:

$$\frac{\partial l}{\partial \mu}(\nu, \mu, \sigma) = \sigma^2 \sum_{i=1}^{N}(x_i - \mu), \tag{2.10}$$

which is positive when the support constraint is satisfied. Because the partial derivative with respect to μ is positive, increasing μ increases the log-likelihood, and therefore the constraint is active at the maximum likelihood estimate for μ

$$\mu = \min_i x_i, \quad \nu = \frac{1}{2}. \tag{8}$$

For ν sufficiently greater than $\frac{1}{2}$, the likelihood equation $\frac{\partial l}{\partial \mu}(\nu, \mu, \sigma) = 0$ has a solution, and this solution provides the maximum likelihood estimate for μ. In either case, however, the condition $\mu = \min_i x_i$ provides a reasonable initial guess for numerical optimization.

Furthermore, the likelihood equation for σ can be solved explicitly, and it provides the maximum likelihood estimate

$$\sigma = \sqrt{\frac{\sum_{i=1}^{N}(x_i - \mu)^2}{N}}. \tag{9}$$

Hence, the `_fitstart` method for `nakagami` uses

$$\mu_0 = \min_i x_i \text{ and} \tag{2.11}$$

$$\sigma_0 = \sqrt{\frac{\sum_{i=1}^{N}(x_i - \mu_0)^2}{N}} \tag{2.12}$$

as initial guesses for numerical optimization accordingly.

Noncentral chi-squared Distribution

The distribution of $\sum_{i=1}^{\nu}(Z_i + \delta_i)^2$ where Z_i are independent standard normal variables and δ_i are constants. $\lambda = \sum_{i=1}^{\nu}\delta_i^2 > 0$. (In communications it is called the Marcum-Q function). It can be thought of as a Generalized Rayleigh-Rice distribution.

The two shape parameters are ν, a positive integer, and λ, a positive real number. The support is $x \geq 0$.

$$\begin{aligned}
f(x;\nu,\lambda) &= e^{-(\lambda+x)/2}\frac{1}{2}\left(\frac{x}{\lambda}\right)^{(\nu-2)/4} I_{(\nu-2)/2}\left(\sqrt{\lambda x}\right) \\
F(x;\nu,\lambda) &= \sum_{j=0}^{\infty}\left\{\frac{(\lambda/2)^j}{j!}e^{-\lambda/2}\right\}\Pr\left[\chi^2_{\nu+2j} \leq x\right] \\
G(q;\nu,\lambda) &= F^{-1}(q;\nu,\lambda) \\
\mu &= \nu + \lambda \\
\mu_2 &= 2(\nu + 2\lambda) \\
\gamma_1 &= \frac{\sqrt{8}(\nu + 3\lambda)}{(\nu + 2\lambda)^{3/2}} \\
\gamma_2 &= \frac{12(\nu + 4\lambda)}{(\nu + 2\lambda)^2}
\end{aligned}$$

where $I_\nu(y)$ is a modified Bessel function of the first kind.

References

- "Noncentral chi-squared distribution", Wikipedia https://en.wikipedia.org/wiki/Noncentral_chi-squared_distribution

Implementation: *scipy.stats.ncx2*

Noncentral F Distribution

The distribution of $(X_1/X_2)(\nu_2/\nu_1)$ if X_1 is non-central chi-squared with ν_1 degrees of freedom and parameter λ, and X_2 is chi-squared with ν_2 degrees of freedom.

There are 3 shape parameters: the degrees of freedom $\nu_1 > 0$ and $\nu_2 > 0$; and $\lambda \geq 0$.

$$\begin{aligned} f(x;\lambda,\nu_1,\nu_2) &= \exp\left[\frac{\lambda}{2}+\frac{(\lambda\nu_1 x)}{2(\nu_1 x+\nu_2)}\right]\nu_1^{\nu_1/2}\nu_2^{\nu_2/2}x^{\nu_1/2-1} \\ &\quad\times(\nu_2+\nu_1 x)^{-(\nu_1+\nu_2)/2}\,\frac{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(1+\frac{\nu_2}{2}\right)L_{\nu_2/2}^{\nu_1/2-1}\left(-\frac{\lambda\nu_1 x}{2(\nu_1 x+\nu_2)}\right)}{B\left(\frac{\nu_1}{2},\frac{\nu_2}{2}\right)\Gamma\left(\frac{\nu_1+\nu_2}{2}\right)} \end{aligned}$$

where $L_{\nu_2/2}^{\nu_1/2-1}(x)$ is an associated Laguerre polynomial.

If $\lambda = 0$, the distribution becomes equivalent to the Fisher distribution with ν_1 and ν_2 degrees of freedom.

Implementation: *scipy.stats.ncf*

Noncentral t Distribution

The distribution of the ratio

$$\frac{U+\lambda}{\chi_\nu/\sqrt{\nu}}$$

where U and χ_ν are independent and distributed as a standard normal and chi with ν degrees of freedom. Note $\lambda > 0$ and $\nu > 0$.

$$\begin{aligned}
f(x;\lambda,\nu) &= \frac{\nu^{\nu/2}\Gamma(\nu+1)}{2^\nu e^{\lambda^2/2}(\nu+x^2)^{\nu/2}\Gamma(\nu/2)} \\
&\quad \times \left\{ \frac{\sqrt{2}\lambda x\, {}_1F_1\left(\frac{\nu}{2}+1;\frac{3}{2};\frac{\lambda^2x^2}{2(\nu+x^2)}\right)}{(\nu+x^2)\Gamma\left(\frac{\nu+1}{2}\right)} \right. \\
&\quad \left. - \frac{{}_1F_1\left(\frac{\nu+1}{2};\frac{1}{2};\frac{\lambda^2x^2}{2(\nu+x^2)}\right)}{\sqrt{\nu+x^2}\Gamma\left(\frac{\nu}{2}+1\right)} \right\} \\
&= \frac{\Gamma(\nu+1)}{2^{(\nu-1)/2}\sqrt{\pi\nu}\Gamma(\nu/2)} \exp\left[-\frac{\nu\lambda^2}{\nu+x^2}\right] \\
&\quad \times \left(\frac{\nu}{\nu+x^2}\right)^{(\nu-1)/2} Hh_\nu\left(-\frac{\lambda x}{\sqrt{\nu+x^2}}\right) \\
F(x;\lambda,\nu) &= \begin{cases} \tilde{F}_{\nu,\mu}(x) & x \geq 0 \\ 1-\tilde{F}_{\nu,-\mu}(x) & x < 0 \end{cases}
\end{aligned}$$

where

$$\begin{aligned}
\tilde{F}_{\nu,\mu}(x) &= \Phi(-\mu) + \frac{1}{2}\sum_{j=0}^{\infty}\left[p_j I_y\left(j+\frac{1}{2},\frac{\nu}{2}\right) + q_j I_y\left(j+1,\frac{\nu}{2}\right)\right] \\
y &= \frac{x^2}{x^2+\nu} \\
p_j &= \frac{e^{\left(-\frac{\mu^2}{2}\right)}}{j!}\left(\frac{\mu^2}{2}\right)^j \\
q_j &= \frac{\mu e^{\left(-\frac{\mu^2}{2}\right)}}{\sqrt{2}\Gamma(j+3/2)}\left(\frac{\mu^2}{2}\right)^j
\end{aligned}$$

where $I_y(a,b)$ is the regularized incomplete beta function and Airy's Hh function is $Hh_\nu(x) = \frac{1}{\Gamma(\nu+1)}\int_0^\infty t^\nu e^{\frac{-(t+x)^2}{2}}dt$.

Implementation: `scipy.stats.nct`

Normal Distribution

$$\begin{aligned}
f(x) &= \frac{e^{-x^2/2}}{\sqrt{2\pi}} \\
F(x) &= \Phi(x) = \frac{1}{2} + \frac{1}{2}\text{erf}\left(\frac{x}{\sqrt{2}}\right) \\
G(q) &= \Phi^{-1}(q)
\end{aligned}$$

$$\begin{aligned}
m_d = m_n = \mu &= 0 \\
\mu_2 &= 1 \\
\gamma_1 &= 0 \\
\gamma_2 &= 0
\end{aligned}$$

$$\begin{aligned} h\left[X\right] &= \log\left(\sqrt{2\pi e}\right) \\ &\approx 1.4189385332046727418 \end{aligned}$$

Implementation: `scipy.stats.norm`

Normal Inverse Gaussian Distribution

The probability density function is given by:

$$f(x;a,b) = \frac{a\exp\left(\sqrt{a^2-b^2}+bx\right)}{\pi\sqrt{1+x^2}}\,K_1\left(a*sqrt1+x^2\right),$$

where x is a real number, the parameter a is the tail heaviness and b is the asymmetry parameter satisfying $a > 0$ and $|b| \leq a$. K_1 is the modified Bessel function of second kind (`scipy.special.k1`).

A normal inverse Gaussian random variable with parameters a and b can be expressed as $X = bV + \sqrt{(V)}X$ where X is *norm(0,1)* and V is *invgauss(mu=1/sqrt(a**2 - b**2))*. Hence, the normal inverse Gaussian distribution is a special case of normal variance-mean mixtures.

Implementation: `scipy.stats.norminvgauss`

Pareto Distribution

One shape parameter $b > 0$ and support $x \geq 1$. The standard form is

$$\begin{aligned} f\left(x;b\right) &= \frac{b}{x^{b+1}} \\ F\left(x;b\right) &= 1-\frac{1}{x^b} \\ G\left(q;b\right) &= \left(1-q\right)^{-1/b} \end{aligned}$$

$$\begin{aligned} \mu &= \frac{b}{b-1} \quad b>1 \\ \mu_2 &= \frac{b}{\left(b-2\right)\left(b-1\right)^2} \quad b>2 \\ \gamma_1 &= \frac{2\left(b+1\right)\sqrt{b-2}}{\left(b-3\right)\sqrt{b}} \quad b>3 \\ \gamma_2 &= \frac{6\left(b^3+b^2-6b-2\right)}{b\left(b^2-7b+12\right)} \quad b>4 \end{aligned}$$

$$h\left(X\right) = \frac{1}{c}+1-\log\left(c\right)$$

Implementation: `scipy.stats.pareto`

Pareto Second Kind (Lomax) Distribution

This is Pareto of the first kind with $L = -1.0$. There is one shape parameter $c > 0$ and support $x \geq 0$.

$$\begin{aligned} f(x;c) &= \frac{c}{(1+x)^{c+1}} \\ F(x;c) &= 1 - \frac{1}{(1+x)^{c}} \\ G(q;c) &= (1-q)^{-1/c} - 1 \end{aligned}$$

$$h[X] = \frac{1}{c} + 1 - \log(c).$$

Implementation: `scipy.stats.lomax`

Power Log Normal Distribution

A generalization of the log-normal distribution with shape parameters $\sigma > 0$, $c > 0$ and support $x \geq 0$.

$$\begin{aligned} f(x;\sigma,c) &= \frac{c}{x\sigma}\phi\left(\frac{\log x}{\sigma}\right)\left(\Phi\left(-\frac{\log x}{\sigma}\right)\right)^{c-1} \\ F(x;\sigma,c) &= 1 - \left(\Phi\left(-\frac{\log x}{\sigma}\right)\right)^{c} \\ G(q;\sigma,c) &= \exp\left(-\sigma\Phi^{-1}\left(\left(1-q\right)^{1/c}\right)\right) \end{aligned}$$

$$\mu_n' = \int_0^1 \exp\left(-n\sigma\Phi^{-1}\left(y^{1/c}\right)\right) dy$$

$$\begin{aligned} \mu &= \mu_1' \\ \mu_2 &= \mu_2' - \mu^2 \\ \gamma_1 &= \frac{\mu_3' - 3\mu\mu_2 - \mu^3}{\mu_2^{3/2}} \\ \gamma_2 &= \frac{\mu_4' - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4}{\mu_2^2} - 3 \end{aligned}$$

This distribution reduces to the log-normal distribution when $c = 1$.

Implementation: `scipy.stats.powerlognorm`

Power Normal Distribution

A generalization of the normal distribution, with one shape parameter $c > 0$ and support $x \geq 0$.

$$\begin{aligned} f(x;c) &= c\phi(x)\left(\Phi(-x)\right)^{c-1} \\ F(x;c) &= 1 - \left(\Phi(-x)\right)^{c} \\ G(q;c) &= -\Phi^{-1}\left(\left(1-q\right)^{1/c}\right) \end{aligned}$$

$$\mu_n' = (-1)^n \int_0^1 \left[\Phi^{-1}\left(y^{1/c}\right)\right]^n dy$$

$$\begin{aligned}
\mu &= \mu_1' \\
\mu_2 &= \mu_2' - \mu^2 \\
\gamma_1 &= \frac{\mu_3' - 3\mu\mu_2 - \mu^3}{\mu_2^{3/2}} \\
\gamma_2 &= \frac{\mu_4' - 4\mu\mu_3 - 6\mu^2\mu_2 - \mu^4}{\mu_2^2} - 3
\end{aligned}$$

For $c = 1$ this reduces to the normal distribution.

Implementation: *scipy.stats.powernorm*

Power-function Distribution

A special case of the beta distribution with $b = 1$. There is one shape parameter $a > 0$ and support $x \in [0, 1]$.

$$\begin{aligned}
f(x; a) &= ax^{a-1} \\
F(x; a) &= x^a \\
G(q; a) &= q^{1/a} \\
\mu &= \frac{a}{a+1} \\
\mu_2 &= \frac{a(a+2)}{(a+1)^2} \\
\gamma_1 &= 2(1-a)\sqrt{\frac{a+2}{a(a+3)}} \\
\gamma_2 &= \frac{6\left(a^3 - a^2 - 6a + 2\right)}{a(a+3)(a+4)} \\
m_d &= 1
\end{aligned}$$

$$h[X] = 1 - \frac{1}{a} - \log(a)$$

Implementation: *scipy.stats.powerlaw*

R-distribution Distribution

A general-purpose distribution with a variety of shapes controlled by one shape parameter $c > 0$. The support of the standard distribution is $x \in [-1, 1]$.

$$\begin{aligned}
f(x; c) &= \frac{\left(1 - x^2\right)^{c/2-1}}{B\left(\frac{1}{2}, \frac{c}{2}\right)} \\
F(x; c) &= \frac{1}{2} + \frac{x}{B\left(\frac{1}{2}, \frac{c}{2}\right)} {}_2F_1\left(\frac{1}{2}, 1 - \frac{c}{2}; \frac{3}{2}; x^2\right)
\end{aligned}$$

$$\mu_n' = \frac{\left(1 + (-1)^n\right)}{2} B\left(\frac{n+1}{2}, \frac{c}{2}\right)$$

The R-distribution with parameter n is the distribution of the correlation coefficient of a random sample of size n drawn from a bivariate normal distribution with $\rho = 0$. The mean of the standard distribution is always zero and as the sample size grows, the distribution's mass concentrates more closely about this mean.

Implementation: *scipy.stats.rdist*

Rayleigh Distribution

This is a special case of the Chi distribution with $L = 0.0$ and $\nu = 2$ (no location parameter is generally used), the mode of the distribution is S.

$$\begin{aligned} f(r) &= re^{-r^2/2} \\ F(r) &= 1 - e^{-r^2/2} \\ G(q) &= \sqrt{-2\log(1-q)} \end{aligned}$$

$$\begin{aligned} \mu &= \sqrt{\frac{\pi}{2}} \\ \mu_2 &= \frac{4-\pi}{2} \\ \gamma_1 &= \frac{2(\pi-3)\sqrt{\pi}}{(4-\pi)^{3/2}} \\ \gamma_2 &= \frac{24\pi - 6\pi^2 - 16}{(4-\pi)^2} \\ m_d &= 1 \\ m_n &= \sqrt{2\log(2)} \end{aligned}$$

$$h[X] = \frac{\gamma}{2} + \log\left(\frac{e}{\sqrt{2}}\right).$$

$$\mu'_n = \sqrt{2^n}\Gamma\left(\frac{n}{2}+1\right)$$

Implementation: `scipy.stats.rayleigh`

Rice Distribution

There is one shape parameter $b \geq 0$ (the "distance from the origin") and the support is $x \geq 0$.

$$\begin{aligned} f(x;b) &= x\exp\left(-\frac{x^2+b^2}{2}\right) I_0(xb) \\ F(x;b) &= \int_0^x \alpha\exp\left(-\frac{\alpha^2+b^2}{2}\right) I_0(\alpha b)\, d\alpha \end{aligned}$$

were $I_0(y)$ is the modified Bessel function of the first kind of order 0.

$$\mu'_n = \sqrt{2^n}\Gamma\left(1+\frac{n}{2}\right) {}_1F_1\left(-\frac{n}{2};1;-\frac{b^2}{2}\right)$$

Implementation: `scipy.stats.rice`

Reciprocal Inverse Gaussian Distribution

The pdf is found from the inverse gaussian (IG), $f_{RIG}(x;\mu) = \frac{1}{x^2} f_{IG}\left(\frac{1}{x};\mu\right)$ defined for $x \geq 0$ as

$$\begin{aligned} f_{IG}(x;\mu) &= \frac{1}{\sqrt{2\pi x^3}}\exp\left(-\frac{(x-\mu)^2}{2x\mu^2}\right). \\ F_{IG}(x;\mu) &= \Phi\left(\frac{1}{\sqrt{x}}\frac{x-\mu}{\mu}\right) + \exp\left(\frac{2}{\mu}\right)\Phi\left(-\frac{1}{\sqrt{x}}\frac{x+\mu}{\mu}\right) \end{aligned}$$

$$
\begin{aligned}
f_{RIG}\left(x;\mu\right) &= \frac{1}{\sqrt{2\pi x}}\exp\left(-\frac{\left(1-\mu x\right)^{2}}{2x\mu^{2}}\right)\\
F_{RIG}\left(x;\mu\right) &= 1-F_{IG}\left(\frac{1}{x},\mu\right)\\
&= 1-\Phi\left(\frac{1}{\sqrt{x}}\frac{1-\mu x}{\mu}\right)-\exp\left(\frac{2}{\mu}\right)\Phi\left(-\frac{1}{\sqrt{x}}\frac{1+\mu x}{\mu}\right)
\end{aligned}
$$

Implementation: `scipy.stats.recipinvgauss`

Semicircular Distribution

Defined on $x \in [-1, 1]$

$$
\begin{aligned}
f\left(x\right) &= \frac{2}{\pi}\sqrt{1-x^{2}}\\
F\left(x\right) &= \frac{1}{2}+\frac{1}{\pi}\left[x\sqrt{1-x^{2}}+\arcsin x\right]\\
G\left(q\right) &= F^{-1}\left(q\right)
\end{aligned}
$$

$$
\begin{aligned}
m_{d}=m_{n}=\mu &= 0\\
\mu_{2} &= \frac{1}{4}\\
\gamma_{1} &= 0\\
\gamma_{2} &= -1
\end{aligned}
$$

$$h\left[X\right] = 0.64472988584940017414.$$

Implementation: `scipy.stats.semicircular`

Studentized Range Distribution

This distribution has two shape parameters, $k > 1$ and $\nu > 0$, and the support is $x \geq 0$.

$$f(x;k,\nu) = \frac{k(k-1)\nu^{\nu/2}}{\Gamma(\nu/2)2^{\nu/2-1}}\int_{0}^{\infty}\int_{-\infty}^{\infty}s^{\nu}e^{-\nu s^{2}/2}\phi(z)\phi(sx+z)[\Phi(sx+z)-\Phi(z)]^{k-2}\,dz\,ds$$

$$F(q;k,\nu) = \frac{k\nu^{\nu/2}}{\Gamma(\nu/2)2^{\nu/2-1}}\int_{0}^{\infty}\int_{-\infty}^{\infty}s^{\nu-1}e^{-\nu s^{2}/2}\phi(z)[\Phi(sq+z)-\Phi(z)]^{k-1}\,dz\,ds$$

Note: $\phi(z)$ and $\Phi(z)$ represent the normal PDF and normal CDF, respectively.

When ν exceeds 100,000, the asymptopic approximation of $F(x;k,\nu=\infty)$ is used:

$$F(x;k,\nu=\infty) = k\int_{-\infty}^{\infty}\phi(z)[\Phi(x+z)-\Phi(z)]^{k-1}\,dz$$

Implementation: `scipy.stats.studentized_range`

Student t Distribution

There is one shape parameter $\nu > 0$ and the support is $x \in \mathbb{R}$.

$$
\begin{aligned}
f\left(x;\nu\right) &= \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\sqrt{\pi\nu}\Gamma\left(\frac{\nu}{2}\right)\left[1+\frac{x^2}{\nu}\right]^{\frac{\nu+1}{2}}} \\
F\left(x;\nu\right) &= \begin{cases} \frac{1}{2}I\left(\frac{\nu}{\nu+x^2};\frac{\nu}{2},\frac{1}{2}\right) & x \leq 0 \\ 1-\frac{1}{2}I\left(\frac{\nu}{\nu+x^2};\frac{\nu}{2},\frac{1}{2}\right) & x \geq 0 \end{cases} \\
G\left(q;\nu\right) &= \begin{cases} -\sqrt{\frac{\nu}{I^{-1}\left(2q;\frac{\nu}{2},\frac{1}{2}\right)}-\nu} & q \leq \frac{1}{2} \\ \sqrt{\frac{\nu}{I^{-1}\left(2-2q;\frac{\nu}{2},\frac{1}{2}\right)}-\nu} & q \geq \frac{1}{2} \end{cases}
\end{aligned}
$$

$$
\begin{aligned}
m_n = m_d = \mu &= 0 \\
\mu_2 &= \frac{\nu}{\nu-2} \quad \nu > 2 \\
\gamma_1 &= 0 \quad \nu > 3 \\
\gamma_2 &= \frac{6}{\nu-4} \quad \nu > 4
\end{aligned}
$$

where $I\left(x;a,b\right)$ is the incomplete beta integral and $I^{-1}\left(I\left(x;a,b\right);a,b\right) = x$. As $\nu \to \infty$, this distribution approaches the standard normal distribution.

$$
h\left[X\right] = \frac{\nu+1}{2}\left[\psi\left(\frac{1+\nu}{2}\right)-\psi\left(\frac{\nu}{2}\right)\right]+\ln\left[\sqrt{\nu}B\left(\frac{\nu}{2},\frac{1}{2}\right)\right]
$$

where $\psi(x)$ is the digamma function and $B(x,y)$ is the beta function.

References

- "Student's t-distribution", Wikipedia, https://en.wikipedia.org/wiki/Student%27s_t-distribution

Implementation: `scipy.stats.t`

Trapezoidal Distribution

Two shape parameters $c \in [0,1], d \in [0,1]$ giving the distances to the first and second modes as a percentage of the total extent of the non-zero portion. The location parameter is the start of the non- zero portion, and the scale-parameter is the width of the non-zero portion. In standard form we have $x \in [0,1]$.

$$
\begin{aligned}
u(c,d) &= \frac{2}{d-c+1} \\
f\left(x;c,d\right) &= \begin{cases} \frac{ux}{c} & x < c \\ u & c \leq x \leq d \\ u\frac{1-x}{1-d} & x > d \end{cases} \\
F\left(x;c,d\right) &= \begin{cases} \frac{ux^2}{2c} & x < c \\ \frac{uc}{2}+u(x-c) & c \leq x \leq d \\ 1-\frac{u(1-x)^2}{2(1-d)} & x > d \end{cases} \\
G\left(q;c,d\right) &= \begin{cases} \sqrt{qc(d-c+1)} & q < c \\ \frac{q}{u}+\frac{c}{2} & q \leq d \\ 1-\sqrt{\frac{2(1-q)(1-d)}{u}} & q > d \end{cases}
\end{aligned}
$$

Implementation: `scipy.stats.trapezoid`

Triangular Distribution

One shape parameter $c \in [0, 1]$ giving the distance to the peak as a percentage of the total extent of the non-zero portion. The location parameter is the start of the non- zero portion, and the scale-parameter is the width of the non-zero portion. In standard form we have $x \in [0, 1]$.

$$\begin{aligned} f(x; c) &= \begin{cases} 2\frac{x}{c} & x < c \\ 2\frac{1-x}{1-c} & x \geq c \end{cases} \\ F(x; c) &= \begin{cases} \frac{x^2}{c} & x < c \\ \frac{x^2-2x+c}{c-1} & x \geq c \end{cases} \\ G(q; c) &= \begin{cases} \sqrt{cq} & q < c \\ 1 - \sqrt{(1-c)(1-q)} & q \geq c \end{cases} \end{aligned}$$

$$\begin{aligned} \mu &= \frac{c}{3} + \frac{1}{3} \\ \mu_2 &= \frac{1 - c + c^2}{18} \\ \gamma_1 &= \frac{\sqrt{2}(2c-1)(c+1)(c-2)}{5(1-c+c^2)^{3/2}} \\ \gamma_2 &= -\frac{3}{5} \end{aligned}$$

$$\begin{aligned} h(X) &= \log\left(\frac{1}{2}\sqrt{e}\right) \\ &\approx -0.19314718055994530942. \end{aligned}$$

Implementation: `scipy.stats.triang`

Truncated Exponential Distribution

This is an exponential distribution defined only over a certain region $0 \leq x \leq B$. In standard form this is

$$\begin{aligned} f(x; B) &= \frac{e^{-x}}{1 - e^{-B}} \\ F(x; B) &= \frac{1 - e^{-x}}{1 - e^{-B}} \\ G(q; B) &= -\log\left(1 - q + qe^{-B}\right) \end{aligned}$$

$$\mu'_n = \Gamma(1 + n) - \Gamma(1 + n, B)$$

$$h[X] = \log\left(e^B - 1\right) + \frac{1 + e^B(B - 1)}{1 - e^B}.$$

Implementation: `scipy.stats.truncexpon`

Truncated Normal Distribution

A normal distribution restricted to lie within a certain range given by two parameters A and B . Notice that this A and B correspond to the bounds on x in standard form. For $x \in [A, B]$ we get

$$\begin{aligned} f(x; A, B) &= \frac{\phi(x)}{\Phi(B) - \Phi(A)} \\ F(x; A, B) &= \frac{\Phi(x) - \Phi(A)}{\Phi(B) - \Phi(A)} \\ G(q; A, B) &= \Phi^{-1}(q\Phi(B) + \Phi(A)(1-q)) \end{aligned}$$

where

$$\begin{aligned} \phi(x) &= \frac{1}{\sqrt{2\pi}} e^{-x^2/2} \\ \Phi(x) &= \int_{-\infty}^{x} \phi(u)\, du. \end{aligned}$$

$$\begin{aligned} \mu &= \frac{\phi(A) - \phi(B)}{\Phi(B) - \Phi(A)} \\ \mu_2 &= 1 + \frac{A\phi(A) - B\phi(B)}{\Phi(B) - \Phi(A)} - \left(\frac{\phi(A) - \phi(B)}{\Phi(B) - \Phi(A)}\right)^2 \end{aligned}$$

Implementation: `scipy.stats.truncnorm`

Tukey-Lambda Distribution

There is one shape parameter λ. The support is $x \in \mathbb{R}$.

$$\begin{aligned} f(x; \lambda) &= F'(x; \lambda) = \frac{1}{G'(F(x; \lambda); \lambda)} = \frac{1}{F^{\lambda-1}(x; \lambda) + [1 - F(x; \lambda)]^{\lambda-1}} \\ F(x; \lambda) &= G^{-1}(x; \lambda) \\ G(p; \lambda) &= \frac{p^\lambda - (1-p)^\lambda}{\lambda} \end{aligned}$$

$$\begin{aligned} \mu &= 0 \\ \mu_2 &= \int_0^1 G^2(p; \lambda)\, dp \\ &= \frac{2\Gamma\left(\lambda + \frac{3}{2}\right) - \lambda 4^{-\lambda}\sqrt{\pi}\Gamma(\lambda)(1 - 2\lambda)}{\lambda^2(1 + 2\lambda)\Gamma\left(\lambda + \frac{3}{2}\right)} \\ \gamma_1 &= 0 \\ \gamma_2 &= \frac{\mu_4}{\mu_2^2} - 3 \\ \mu_4 &= \frac{3\Gamma(\lambda)\Gamma\left(\lambda + \frac{1}{2}\right) 2^{-2\lambda}}{\lambda^3\Gamma\left(2\lambda + \frac{3}{2}\right)} + \frac{2}{\lambda^4(1 + 4\lambda)} \\ &\quad - \frac{2\sqrt{3}\Gamma(\lambda) 2^{-6\lambda} 3^{3\lambda}\Gamma\left(\lambda + \frac{1}{3}\right)\Gamma\left(\lambda + \frac{2}{3}\right)}{\lambda^3\Gamma\left(2\lambda + \frac{3}{2}\right)\Gamma\left(\lambda + \frac{1}{2}\right)}. \end{aligned}$$

Notice that the $\lim_{\lambda\to 0} G(p;\lambda) = \log(p/(1-p))$

$$\begin{aligned} h[X] &= \int_0^1 \log[G'(p)]\,dp \\ &= \int_0^1 \log\left[p^{\lambda-1} + (1-p)^{\lambda-1}\right] dp. \end{aligned}$$

Implementation: *scipy.stats.tukeylambda*

Uniform Distribution

Standard form $x \in [0,1]$. In general form, the lower limit is L, the upper limit is $S+L$.

$$\begin{aligned} f(x) &= 1 \\ F(x) &= x \\ G(q) &= q \end{aligned}$$

$$\begin{aligned} \mu &= \frac{1}{2} \\ \mu_2 &= \frac{1}{12} \\ \gamma_1 &= 0 \\ \gamma_2 &= -\frac{6}{5} \end{aligned}$$

$$h[X] = 0$$

Implementation: *scipy.stats.uniform*

Von Mises Distribution

There is one shape parameter $\kappa > 0$, with support $x \in [-\pi,\pi]$. For values of $\kappa < 100$ the PDF and CDF formulas below are used. Otherwise, a normal approximation with variance $1/\kappa$ is used. [Note that the PDF and CDF functions below are periodic with period 2π. If an input outside $x \in [-\pi,\pi]$ is given, it is converted to the equivalent angle in this range.]

$$\begin{aligned} f(x;\kappa) &= \frac{e^{\kappa\cos x}}{2\pi I_0(\kappa)} \\ F(x;\kappa) &= \frac{1}{2} + \frac{x}{2\pi} + \sum_{k=1}^{\infty} \frac{I_k(\kappa)\sin(kx)}{I_0(\kappa)\,\pi k} \\ G(q;\kappa) &= F^{-1}(x;\kappa) \end{aligned}$$

where $I_k(\kappa)$ is a modified Bessel function of the first kind.

$$\begin{aligned} \mu &= 0 \\ \mu_2 &= \int_{-\pi}^{\pi} x^2 f(x;\kappa)\,dx \\ \gamma_1 &= 0 \\ \gamma_2 &= \frac{\int_{-\pi}^{\pi} x^4 f(x;\kappa)\,dx}{\mu_2^2} - 3 \end{aligned}$$

This can be used for defining circular variance.

Implementation: *scipy.stats.vonmises*

Wald Distribution

Special case of the Inverse Normal with shape parameter set to 1.0. It has support $x \geq 0$.

$$\begin{aligned} f(x) &= \frac{1}{\sqrt{2\pi x^3}} \exp\left(-\frac{(x-1)^2}{2x}\right). \\ F(x) &= \Phi\left(\frac{x-1}{\sqrt{x}}\right) + \exp(2)\,\Phi\left(-\frac{x+1}{\sqrt{x}}\right) \\ G(q;\mu) &= F^{-1}(q;\mu) \end{aligned}$$

$$\begin{aligned} \mu &= 1 \\ \mu_2 &= 1 \\ \gamma_1 &= 3 \\ \gamma_2 &= 15 \\ m_d &= \frac{1}{2}\left(\sqrt{13}-3\right) \end{aligned}$$

Implementation: *scipy.stats.wald*

Weibull Maximum Extreme Value Distribution

Defined for $x < 0$ and $c > 0$.

$$\begin{aligned} f(x;c) &= c(-x)^{c-1} \exp(-(-x)^c) \\ F(x;c) &= \exp(-(-x)^c) \\ G(q;c) &= -(-\log q)^{1/c} \end{aligned}$$

The mean is the negative of the right-skewed Frechet distribution given above, and the other statistical parameters can be computed from

$$\mu_n' = (-1)^n \Gamma\left(1+\frac{n}{c}\right).$$

$$\begin{aligned} \mu &= -\Gamma\left(1+\frac{1}{c}\right) \\ \mu_2 &= \Gamma\left(1+\frac{2}{c}\right) - \Gamma^2\left(1+\frac{1}{c}\right) \\ \gamma_1 &= -\frac{\Gamma\left(1+\frac{3}{c}\right) - 3\Gamma\left(1+\frac{2}{c}\right)\Gamma\left(1+\frac{1}{c}\right) + 2\Gamma^3\left(1+\frac{1}{c}\right)}{\mu_2^{3/2}} \\ \gamma_2 &= \frac{\Gamma\left(1+\frac{4}{c}\right) - 4\Gamma\left(1+\frac{1}{c}\right)\Gamma\left(1+\frac{3}{c}\right) + 6\Gamma^2\left(1+\frac{1}{c}\right)\Gamma\left(1+\frac{2}{c}\right) - 3\Gamma^4\left(1+\frac{1}{c}\right)}{\mu_2^2} - 3 \\ m_d &= \begin{cases} -\left(\frac{c-1}{c}\right)^{\frac{1}{c}} & \text{if } c > 1 \\ 0 & \text{if } c <= 1 \end{cases} \\ m_n &= -\ln(2)^{\frac{1}{c}} \end{aligned}$$

$$h[X] = -\frac{\gamma}{c} - \log(c) + \gamma + 1$$

where γ is Euler's constant and equal to

$$\gamma \approx 0.57721566490153286061.$$

Implementation: *scipy.stats.weibull_max*

Weibull Minimum Extreme Value Distribution

A type of extreme-value distribution with a lower bound. Defined for $x > 0$ and $c > 0$

$$\begin{aligned} f(x;c) &= cx^{c-1}\exp\left(-x^c\right) \\ F(x;c) &= 1-\exp\left(-x^c\right) \\ G(q;c) &= \left[-\log\left(1-q\right)\right]^{1/c} \end{aligned}$$

$$\mu_n' = \Gamma\left(1+\frac{n}{c}\right)$$

$$\begin{aligned} \mu &= \Gamma\left(1+\frac{1}{c}\right) \\ \mu_2 &= \Gamma\left(1+\frac{2}{c}\right)-\Gamma^2\left(1+\frac{1}{c}\right) \\ \gamma_1 &= \frac{\Gamma\left(1+\frac{3}{c}\right)-3\Gamma\left(1+\frac{2}{c}\right)\Gamma\left(1+\frac{1}{c}\right)+2\Gamma^3\left(1+\frac{1}{c}\right)}{\mu_2^{3/2}} \\ \gamma_2 &= \frac{\Gamma\left(1+\frac{4}{c}\right)-4\Gamma\left(1+\frac{1}{c}\right)\Gamma\left(1+\frac{3}{c}\right)+6\Gamma^2\left(1+\frac{1}{c}\right)\Gamma\left(1+\frac{2}{c}\right)-3\Gamma^4\left(1+\frac{1}{c}\right)}{\mu_2^2}-3 \\ m_d &= \begin{cases} \left(\frac{c-1}{c}\right)^{\frac{1}{c}} & \text{if } c>1 \\ 0 & \text{if } c<=1 \end{cases} \\ m_n &= \ln\left(2\right)^{\frac{1}{c}} \end{aligned}$$

$$h\left[X\right] = -\frac{\gamma}{c}-\log\left(c\right)+\gamma+1$$

where γ is Euler's constant and equal to

$$\gamma \approx 0.57721566490153286061.$$

Implementation: *scipy.stats.weibull_min*

Wrapped Cauchy Distribution

There is one shape parameter $c \in (0,1)$ with support $x \in [0, 2\pi]$.

$$\begin{aligned} f(x;c) &= \frac{1-c^2}{2\pi\left(1+c^2-2c\cos x\right)} \\ g_c(x) &= \frac{1}{\pi}\arctan\left(\frac{1+c}{1-c}\tan\left(\frac{x}{2}\right)\right) \\ r_c(q) &= 2\arctan\left(\frac{1-c}{1+c}\tan\left(\pi q\right)\right) \\ F(x;c) &= \begin{cases} g_c(x) & 0 \le x < \pi \\ 1-g_c\left(2\pi-x\right) & \pi \le x \le 2\pi \end{cases} \\ G(q;c) &= \begin{cases} r_c(q) & 0 \le q < \frac{1}{2} \\ 2\pi-r_c\left(1-q\right) & \frac{1}{2} \le q \le 1 \end{cases} \end{aligned}$$

$$h\left[X\right] = \log\left(2\pi\left(1-c^2\right)\right).$$

Implementation: *scipy.stats.wrapcauchy*

2.12.2 Random variables

There are two general distribution classes that have been implemented for encapsulating *continuous random variables* and *discrete random variables*. Over 80 continuous random variables (RVs) and 10 discrete random variables have been implemented using these classes. Besides this, new routines and distributions can be easily added by the end user. (If you create one, please contribute it.)

All of the statistics functions are located in the sub-package `scipy.stats` and a fairly complete listing of these functions can be obtained using `info(stats)`. The list of the random variables available can also be obtained from the docstring for the stats sub-package.

In the discussion below, we mostly focus on continuous RVs. Nearly everything also applies to discrete variables, but we point out some differences here: *Specific points for discrete distributions*.

In the code samples below, we assume that the `scipy.stats` package is imported as

```
>>> from scipy import stats
```

and in some cases we assume that individual objects are imported as

```
>>> from scipy.stats import norm
```

Getting help

First of all, all distributions are accompanied with help functions. To obtain just some basic information, we print the relevant docstring: `print(stats.norm.__doc__)`.

To find the support, i.e., upper and lower bounds of the distribution, call:

```
>>> print('bounds of distribution lower: %s, upper: %s' % norm.support())
bounds of distribution lower: -inf, upper: inf
```

We can list all methods and properties of the distribution with `dir(norm)`. As it turns out, some of the methods are private, although they are not named as such (their names do not start with a leading underscore), for example `veccdf`, are only available for internal calculation (those methods will give warnings when one tries to use them, and will be removed at some point).

To obtain the *real* main methods, we list the methods of the frozen distribution. (We explain the meaning of a *frozen* distribution below).

```
>>> rv = norm()
>>> dir(rv)  # reformatted
['__class__', '__delattr__', '__dict__', '__dir__', '__doc__', '__eq__',
 '__format__', '__ge__', '__getattribute__', '__gt__', '__hash__',
 '__init__', '__le__', '__lt__', '__module__', '__ne__', '__new__',
 '__reduce__', '__reduce_ex__', '__repr__', '__setattr__', '__sizeof__',
 '__str__', '__subclasshook__', '__weakref__', 'a', 'args', 'b', 'cdf',
 'dist', 'entropy', 'expect', 'interval', 'isf', 'kwds', 'logcdf',
 'logpdf', 'logpmf', 'logsf', 'mean', 'median', 'moment', 'pdf', 'pmf',
 'ppf', 'random_state', 'rvs', 'sf', 'stats', 'std', 'var']
```

Finally, we can obtain the list of available distribution through introspection:

```
>>> dist_continu = [d for d in dir(stats) if
...                 isinstance(getattr(stats, d), stats.rv_continuous)]
```

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(continued from previous page)

```
>>> dist_discrete = [d for d in dir(stats) if
...                  isinstance(getattr(stats, d), stats.rv_discrete)]
>>> print('number of continuous distributions: %d' % len(dist_continu))
number of continuous distributions: 104
>>> print('number of discrete distributions:   %d' % len(dist_discrete))
number of discrete distributions:   19
```

Common methods

The main public methods for continuous RVs are:

- rvs: Random Variates
- pdf: Probability Density Function
- cdf: Cumulative Distribution Function
- sf: Survival Function (1-CDF)
- ppf: Percent Point Function (Inverse of CDF)
- isf: Inverse Survival Function (Inverse of SF)
- stats: Return mean, variance, (Fisher's) skew, or (Fisher's) kurtosis
- moment: non-central moments of the distribution

Let's take a normal RV as an example.

```
>>> norm.cdf(0)
0.5
```

To compute the `cdf` at a number of points, we can pass a list or a numpy array.

```
>>> norm.cdf([-1., 0, 1])
array([ 0.15865525,  0.5,  0.84134475])
>>> import numpy as np
>>> norm.cdf(np.array([-1., 0, 1]))
array([ 0.15865525,  0.5,  0.84134475])
```

Thus, the basic methods, such as *pdf*, *cdf*, and so on, are vectorized.

Other generally useful methods are supported too:

```
>>> norm.mean(), norm.std(), norm.var()
(0.0, 1.0, 1.0)
>>> norm.stats(moments="mv")
(array(0.0), array(1.0))
```

To find the median of a distribution, we can use the percent point function `ppf`, which is the inverse of the `cdf`:

```
>>> norm.ppf(0.5)
0.0
```

To generate a sequence of random variates, use the `size` keyword argument:

```
>>> norm.rvs(size=3)
array([-0.35687759,  1.34347647, -0.11710531])  # random
```

Don't think that `norm.rvs(5)` generates 5 variates:

```
>>> norm.rvs(5)
5.471435163732493  # random
```

Here, `5` with no keyword is being interpreted as the first possible keyword argument, `loc`, which is the first of a pair of keyword arguments taken by all continuous distributions. This brings us to the topic of the next subsection.

Random number generation

Drawing random numbers relies on generators from `numpy.random` package. In the examples above, the specific stream of random numbers is not reproducible across runs. To achieve reproducibility, you can explicitly *seed* a random number generator. In NumPy, a generator is an instance of `numpy.random.Generator`. Here is the canonical way to create a generator:

```
>>> from numpy.random import default_rng
>>> rng = default_rng()
```

And fixing the seed can be done like this:

```
>>> # do NOT copy this value
>>> rng = default_rng(301439351238479871608357552876690613766)
```

Warning: Do not use this number or common values such as 0. Using just a small set of seeds to instantiate larger state spaces means that there are some initial states that are impossible to reach. This creates some biases if everyone uses such values. A good way to get a seed is to use a `numpy.random.SeedSequence`:

```
>>> from numpy.random import SeedSequence
>>> print(SeedSequence().entropy)
301439351238479871608357552876690613766  # random
```

The *random_state* parameter in distributions accepts an instance of `numpy.random.Generator` class, or an integer, which is then used to seed an internal `Generator` object:

```
>>> norm.rvs(size=5, random_state=rng)
array([ 0.47143516, -1.19097569,  1.43270697, -0.3126519 , -0.72058873])  #␣
↪random
```

For further info, see NumPy's documentation.

Shifting and scaling

All continuous distributions take `loc` and `scale` as keyword parameters to adjust the location and scale of the distribution, e.g., for the standard normal distribution, the location is the mean and the scale is the standard deviation.

```
>>> norm.stats(loc=3, scale=4, moments="mv")
(array(3.0), array(16.0))
```

In many cases, the standardized distribution for a random variable `X` is obtained through the transformation `(X - loc) / scale`. The default values are `loc = 0` and `scale = 1`.

Smart use of `loc` and `scale` can help modify the standard distributions in many ways. To illustrate the scaling further, the `cdf` of an exponentially distributed RV with mean $1/\lambda$ is given by

$$F(x) = 1 - \exp(-\lambda x)$$

By applying the scaling rule above, it can be seen that by taking `scale = 1./lambda` we get the proper scale.

```
>>> from scipy.stats import expon
>>> expon.mean(scale=3.)
3.0
```

Note: Distributions that take shape parameters may require more than simple application of `loc` and/or `scale` to achieve the desired form. For example, the distribution of 2-D vector lengths given a constant vector of length R perturbed by independent N(0, σ^2) deviations in each component is rice(R/σ, scale= σ). The first argument is a shape parameter that needs to be scaled along with x.

The uniform distribution is also interesting:

```
>>> from scipy.stats import uniform
>>> uniform.cdf([0, 1, 2, 3, 4, 5], loc=1, scale=4)
array([ 0.  ,  0.  ,  0.25,  0.5 ,  0.75,  1.  ])
```

Finally, recall from the previous paragraph that we are left with the problem of the meaning of `norm.rvs(5)`. As it turns out, calling a distribution like this, the first argument, i.e., the 5, gets passed to set the `loc` parameter. Let's see:

```
>>> np.mean(norm.rvs(5, size=500))
5.0098355106969992  # random
```

Thus, to explain the output of the example of the last section: `norm.rvs(5)` generates a single normally distributed random variate with mean `loc=5`, because of the default `size=1`.

We recommend that you set `loc` and `scale` parameters explicitly, by passing the values as keywords rather than as arguments. Repetition can be minimized when calling more than one method of a given RV by using the technique of *Freezing a Distribution*, as explained below.

Shape parameters

While a general continuous random variable can be shifted and scaled with the `loc` and `scale` parameters, some distributions require additional shape parameters. For instance, the gamma distribution with density

$$\gamma(x, a) = \frac{\lambda(\lambda x)^{a-1}}{\Gamma(a)} e^{-\lambda x},$$

requires the shape parameter a. Observe that setting λ can be obtained by setting the `scale` keyword to $1/\lambda$.

Let's check the number and name of the shape parameters of the gamma distribution. (We know from the above that this should be 1.)

```
>>> from scipy.stats import gamma
>>> gamma.numargs
1
>>> gamma.shapes
'a'
```

Now, we set the value of the shape variable to 1 to obtain the exponential distribution, so that we compare easily whether we get the results we expect.

```
>>> gamma(1, scale=2.).stats(moments="mv")
(array(2.0), array(4.0))
```

Notice that we can also specify shape parameters as keywords:

```
>>> gamma(a=1, scale=2.).stats(moments="mv")
(array(2.0), array(4.0))
```

Freezing a distribution

Passing the `loc` and `scale` keywords time and again can become quite bothersome. The concept of *freezing* a RV is used to solve such problems.

```
>>> rv = gamma(1, scale=2.)
```

By using `rv` we no longer have to include the scale or the shape parameters anymore. Thus, distributions can be used in one of two ways, either by passing all distribution parameters to each method call (such as we did earlier) or by freezing the parameters for the instance of the distribution. Let us check this:

```
>>> rv.mean(), rv.std()
(2.0, 2.0)
```

This is, indeed, what we should get.

Broadcasting

The basic methods `pdf`, and so on, satisfy the usual numpy broadcasting rules. For example, we can calculate the critical values for the upper tail of the t distribution for different probabilities and degrees of freedom.

```
>>> stats.t.isf([0.1, 0.05, 0.01], [[10], [11]])
array([[ 1.37218364,  1.81246112,  2.76376946],
       [ 1.36343032,  1.79588482,  2.71807918]])
```

Here, the first row contains the critical values for 10 degrees of freedom and the second row for 11 degrees of freedom (d.o.f.). Thus, the broadcasting rules give the same result of calling `isf` twice:

```
>>> stats.t.isf([0.1, 0.05, 0.01], 10)
array([ 1.37218364,  1.81246112,  2.76376946])
>>> stats.t.isf([0.1, 0.05, 0.01], 11)
array([ 1.36343032,  1.79588482,  2.71807918])
```

If the array with probabilities, i.e., `[0.1, 0.05, 0.01]` and the array of degrees of freedom i.e., `[10, 11, 12]`, have the same array shape, then element-wise matching is used. As an example, we can obtain the 10% tail for 10 d.o.f., the 5% tail for 11 d.o.f. and the 1% tail for 12 d.o.f. by calling

```
>>> stats.t.isf([0.1, 0.05, 0.01], [10, 11, 12])
array([ 1.37218364,  1.79588482,  2.68099799])
```

Specific points for discrete distributions

Discrete distributions have mostly the same basic methods as the continuous distributions. However `pdf` is replaced by the probability mass function `pmf`, no estimation methods, such as fit, are available, and `scale` is not a valid keyword parameter. The location parameter, keyword `loc`, can still be used to shift the distribution.

The computation of the cdf requires some extra attention. In the case of continuous distribution, the cumulative distribution function is, in most standard cases, strictly monotonic increasing in the bounds (a,b) and has, therefore, a unique inverse. The cdf of a discrete distribution, however, is a step function, hence the inverse cdf, i.e., the percent point function, requires a different definition:

```
ppf(q) = min{x : cdf(x) >= q, x integer}
```

For further info, see the docs here.

We can look at the hypergeometric distribution as an example

```
>>> from scipy.stats import hypergeom
>>> [M, n, N] = [20, 7, 12]
```

If we use the cdf at some integer points and then evaluate the ppf at those cdf values, we get the initial integers back, for example

```
>>> x = np.arange(4) * 2
>>> x
array([0, 2, 4, 6])
>>> prb = hypergeom.cdf(x, M, n, N)
>>> prb
array([  1.03199174e-04,   5.21155831e-02,   6.08359133e-01,
         9.89783282e-01])
```

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```
>>> hypergeom.ppf(prb, M, n, N)
array([ 0.,  2.,  4.,  6.])
```

If we use values that are not at the kinks of the cdf step function, we get the next higher integer back:

```
>>> hypergeom.ppf(prb + 1e-8, M, n, N)
array([ 1.,  3.,  5.,  7.])
>>> hypergeom.ppf(prb - 1e-8, M, n, N)
array([ 0.,  2.,  4.,  6.])
```

Fitting distributions

The main additional methods of the not frozen distribution are related to the estimation of distribution parameters:

- ***fit: maximum likelihood estimation of distribution parameters, including location***

  and scale

- fit_loc_scale: estimation of location and scale when shape parameters are given
- nnlf: negative log likelihood function
- expect: calculate the expectation of a function against the pdf or pmf

Performance issues and cautionary remarks

The performance of the individual methods, in terms of speed, varies widely by distribution and method. The results of a method are obtained in one of two ways: either by explicit calculation, or by a generic algorithm that is independent of the specific distribution.

Explicit calculation, on the one hand, requires that the method is directly specified for the given distribution, either through analytic formulas or through special functions in `scipy.special` or `numpy.random` for `rvs`. These are usually relatively fast calculations.

The generic methods, on the other hand, are used if the distribution does not specify any explicit calculation. To define a distribution, only one of pdf or cdf is necessary; all other methods can be derived using numeric integration and root finding. However, these indirect methods can be *very* slow. As an example, `rgh = stats.gausshyper.rvs(0.5, 2, 2, 2, size=100)` creates random variables in a very indirect way and takes about 19 seconds for 100 random variables on my computer, while one million random variables from the standard normal or from the t distribution take just above one second.

Remaining issues

The distributions in `scipy.stats` have recently been corrected and improved and gained a considerable test suite; however, a few issues remain:

- The distributions have been tested over some range of parameters; however, in some corner ranges, a few incorrect results may remain.
- The maximum likelihood estimation in *fit* does not work with default starting parameters for all distributions and the user needs to supply good starting parameters. Also, for some distribution using a maximum likelihood estimator might inherently not be the best choice.

2.12.3 Building specific distributions

The next examples shows how to build your own distributions. Further examples show the usage of the distributions and some statistical tests.

Making a continuous distribution, i.e., subclassing `rv_continuous`

Making continuous distributions is fairly simple.

```
>>> from scipy import stats
>>> class deterministic_gen(stats.rv_continuous):
...     def _cdf(self, x):
...         return np.where(x < 0, 0., 1.)
...     def _stats(self):
...         return 0., 0., 0., 0.
```

```
>>> deterministic = deterministic_gen(name="deterministic")
>>> deterministic.cdf(np.arange(-3, 3, 0.5))
array([ 0.,  0.,  0.,  0.,  0.,  0.,  1.,  1.,  1.,  1.,  1.,  1.])
```

Interestingly, the `pdf` is now computed automatically:

```
>>> deterministic.pdf(np.arange(-3, 3, 0.5))
array([  0.00000000e+00,   0.00000000e+00,   0.00000000e+00,
         0.00000000e+00,   0.00000000e+00,   0.00000000e+00,
         5.83333333e+04,   4.16333634e-12,   4.16333634e-12,
         4.16333634e-12,   4.16333634e-12,   4.16333634e-12])
```

Be aware of the performance issues mentioned in *Performance issues and cautionary remarks*. The computation of unspecified common methods can become very slow, since only general methods are called, which, by their very nature, cannot use any specific information about the distribution. Thus, as a cautionary example:

```
>>> from scipy.integrate import quad
>>> quad(deterministic.pdf, -1e-1, 1e-1)
(4.163336342344337e-13, 0.0)
```

But this is not correct: the integral over this pdf should be 1. Let's make the integration interval smaller:

```
>>> quad(deterministic.pdf, -1e-3, 1e-3)  # warning removed
(1.000076872229173, 0.0010625571718182458)
```

This looks better. However, the problem originated from the fact that the pdf is not specified in the class definition of the deterministic distribution.

Subclassing `rv_discrete`

In the following, we use *stats.rv_discrete* to generate a discrete distribution that has the probabilities of the truncated normal for the intervals centered around the integers.

General info

From the docstring of rv_discrete, `help(stats.rv_discrete)`,

> "You can construct an arbitrary discrete rv where P{X=xk} = pk by passing to the rv_discrete initialization method (through the values= keyword) a tuple of sequences (xk, pk) which describes only those values of X (xk) that occur with nonzero probability (pk)."

Next to this, there are some further requirements for this approach to work:

- The keyword *name* is required.
- The support points of the distribution xk have to be integers.
- The number of significant digits (decimals) needs to be specified.

In fact, if the last two requirements are not satisfied, an exception may be raised or the resulting numbers may be incorrect.

An example

Let's do the work. First:

```
>>> npoints = 20   # number of integer support points of the distribution␣
 ↪minus 1
>>> npointsh = npoints // 2
>>> npointsf = float(npoints)
>>> nbound = 4   # bounds for the truncated normal
>>> normbound = (1+1/npointsf) * nbound   # actual bounds of truncated normal
>>> grid = np.arange(-npointsh, npointsh+2, 1)   # integer grid
>>> gridlimitsnorm = (grid-0.5) / npointsh * nbound   # bin limits for the␣
 ↪truncnorm
>>> gridlimits = grid - 0.5   # used later in the analysis
>>> grid = grid[:-1]
>>> probs = np.diff(stats.truncnorm.cdf(gridlimitsnorm, -normbound,␣
 ↪normbound))
>>> gridint = grid
```

And, finally, we can subclass `rv_discrete`:

```
>>> normdiscrete = stats.rv_discrete(values=(gridint,
...              np.round(probs, decimals=7)), name='normdiscrete')
```

Now that we have defined the distribution, we have access to all common methods of discrete distributions.

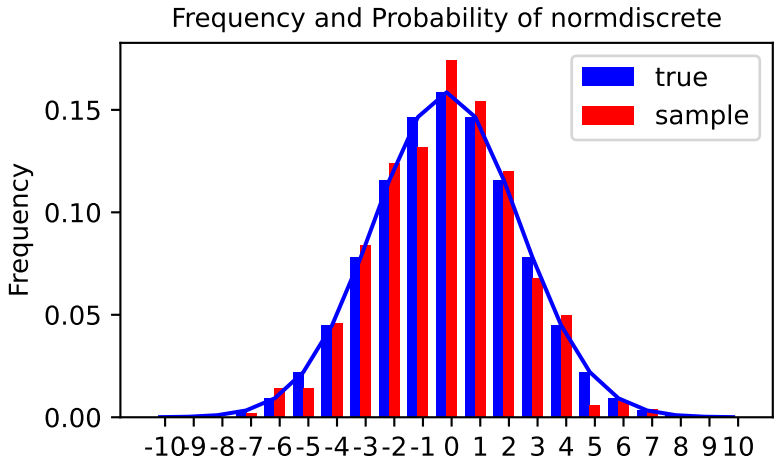
```
>>> print('mean = %6.4f, variance = %6.4f, skew = %6.4f, kurtosis = %6.4f' %
...       normdiscrete.stats(moments='mvsk'))
mean = -0.0000, variance = 6.3302, skew = 0.0000, kurtosis = -0.0076
```

```
>>> nd_std = np.sqrt(normdiscrete.stats(moments='v'))
```

Testing the implementation

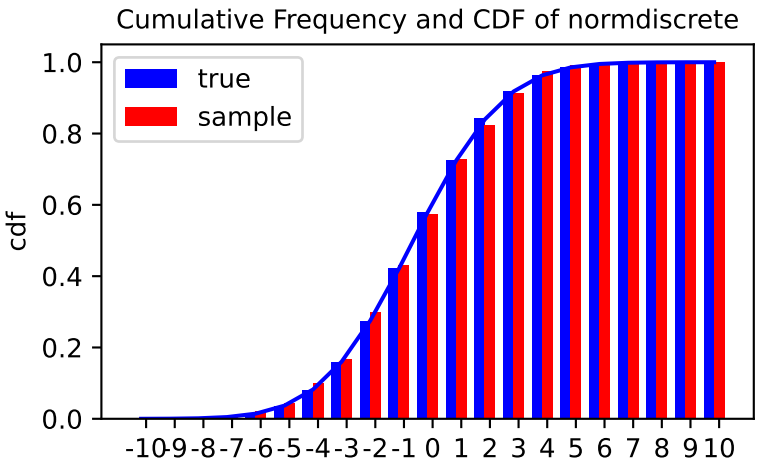
Let's generate a random sample and compare observed frequencies with the probabilities.

```
>>> n_sample = 500
>>> rvs = normdiscrete.rvs(size=n_sample)
>>> f, l = np.histogram(rvs, bins=gridlimits)
>>> sfreq = np.vstack([gridint, f, probs*n_sample]).T
>>> print(sfreq)
[[-1.00000000e+01  0.00000000e+00  2.95019349e-02]  # random
 [-9.00000000e+00  0.00000000e+00  1.32294142e-01]
 [-8.00000000e+00  0.00000000e+00  5.06497902e-01]
 [-7.00000000e+00  2.00000000e+00  1.65568919e+00]
 [-6.00000000e+00  1.00000000e+00  4.62125309e+00]
 [-5.00000000e+00  9.00000000e+00  1.10137298e+01]
 [-4.00000000e+00  2.60000000e+01  2.24137683e+01]
 [-3.00000000e+00  3.70000000e+01  3.89503370e+01]
 [-2.00000000e+00  5.10000000e+01  5.78004747e+01]
 [-1.00000000e+00  7.10000000e+01  7.32455414e+01]
 [ 0.00000000e+00  7.40000000e+01  7.92618251e+01]
 [ 1.00000000e+00  8.90000000e+01  7.32455414e+01]
 [ 2.00000000e+00  5.50000000e+01  5.78004747e+01]
 [ 3.00000000e+00  5.00000000e+01  3.89503370e+01]
 [ 4.00000000e+00  1.70000000e+01  2.24137683e+01]
 [ 5.00000000e+00  1.10000000e+01  1.10137298e+01]
 [ 6.00000000e+00  4.00000000e+00  4.62125309e+00]
 [ 7.00000000e+00  3.00000000e+00  1.65568919e+00]
 [ 8.00000000e+00  0.00000000e+00  5.06497902e-01]
 [ 9.00000000e+00  0.00000000e+00  1.32294142e-01]
 [ 1.00000000e+01  0.00000000e+00  2.95019349e-02]]
```



Next, we can test whether our sample was generated by our norm-discrete distribution. This also verifies whether the random numbers were generated correctly.

The chisquare test requires that there are a minimum number of observations in each bin. We combine the tail bins into larger bins so that they contain enough observations.




```
>>> f2 = np.hstack([f[:5].sum(), f[5:-5], f[-5:].sum()])
>>> p2 = np.hstack([probs[:5].sum(), probs[5:-5], probs[-5:].sum()])
>>> ch2, pval = stats.chisquare(f2, p2*n_sample)
```

```
>>> print('chisquare for normdiscrete: chi2 = %6.3f pvalue = %6.4f' % (ch2,␣
↪pval))
chisquare for normdiscrete: chi2 = 12.466 pvalue = 0.4090  # random
```

The pvalue in this case is high, so we can be quite confident that our random sample was actually generated by the distribution.

2.12.4 Analysing one sample

First, we create some random variables. We set a seed so that in each run we get identical results to look at. As an example we take a sample from the Student t distribution:

```
>>> x = stats.t.rvs(10, size=1000)
```

Here, we set the required shape parameter of the t distribution, which in statistics corresponds to the degrees of freedom, to 10. Using size=1000 means that our sample consists of 1000 independently drawn (pseudo) random numbers. Since we did not specify the keyword arguments *loc* and *scale*, those are set to their default values zero and one.

Descriptive statistics

x is a numpy array, and we have direct access to all array methods, e.g.,

```
>>> print(x.min())    # equivalent to np.min(x)
-3.78975572422  # random
>>> print(x.max())    # equivalent to np.max(x)
5.26327732981  # random
>>> print(x.mean())   # equivalent to np.mean(x)
```

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```
0.0140610663985  # random
>>> print(x.var())    # equivalent to np.var(x))
1.28899386208  # random
```

How do the sample properties compare to their theoretical counterparts?

```
>>> m, v, s, k = stats.t.stats(10, moments='mvsk')
>>> n, (smin, smax), sm, sv, ss, sk = stats.describe(x)
```

```
>>> sstr = '%-14s mean = %6.4f, variance = %6.4f, skew = %6.4f, kurtosis =
↪%6.4f'
>>> print(sstr % ('distribution:', m, v, s ,k))
distribution:  mean = 0.0000, variance = 1.2500, skew = 0.0000, kurtosis = 1.
↪0000  # random
>>> print(sstr % ('sample:', sm, sv, ss, sk))
sample:        mean = 0.0141, variance = 1.2903, skew = 0.2165, kurtosis = 1.
↪0556  # random
```

Note: *stats.describe* uses the unbiased estimator for the variance, while np.var is the biased estimator.

For our sample the sample statistics differ a by a small amount from their theoretical counterparts.

T-test and KS-test

We can use the t-test to test whether the mean of our sample differs in a statistically significant way from the theoretical expectation.

```
>>> print('t-statistic = %6.3f pvalue = %6.4f' %  stats.ttest_1samp(x, m))
t-statistic =  0.391 pvalue = 0.6955  # random
```

The pvalue is 0.7, this means that with an alpha error of, for example, 10%, we cannot reject the hypothesis that the sample mean is equal to zero, the expectation of the standard t-distribution.

As an exercise, we can calculate our ttest also directly without using the provided function, which should give us the same answer, and so it does:

```
>>> tt = (sm-m)/np.sqrt(sv/float(n))  # t-statistic for mean
>>> pval = stats.t.sf(np.abs(tt), n-1)*2  # two-sided pvalue = Prob(abs(t)>tt)
>>> print('t-statistic = %6.3f pvalue = %6.4f' % (tt, pval))
t-statistic =  0.391 pvalue = 0.6955  # random
```

The Kolmogorov-Smirnov test can be used to test the hypothesis that the sample comes from the standard t-distribution

```
>>> print('KS-statistic D = %6.3f pvalue = %6.4f' % stats.kstest(x, 't', (10,
↪)))
KS-statistic D =  0.016 pvalue = 0.9571  # random
```

Again, the p-value is high enough that we cannot reject the hypothesis that the random sample really is distributed according to the t-distribution. In real applications, we don't know what the underlying distribution is. If we perform the Kolmogorov-Smirnov test of our sample against the standard normal distribution, then we also cannot reject the hypothesis that our sample was generated by the normal distribution given that, in this example, the p-value is almost 40%.

```
>>> print('KS-statistic D = %6.3f pvalue = %6.4f' % stats.kstest(x, 'norm'))
KS-statistic D =  0.028 pvalue = 0.3918  # random
```

However, the standard normal distribution has a variance of 1, while our sample has a variance of 1.29. If we standardize our sample and test it against the normal distribution, then the p-value is again large enough that we cannot reject the hypothesis that the sample came form the normal distribution.

```
>>> d, pval = stats.kstest((x-x.mean())/x.std(), 'norm')
>>> print('KS-statistic D = %6.3f pvalue = %6.4f' % (d, pval))
KS-statistic D =  0.032 pvalue = 0.2397  # random
```

Note: The Kolmogorov-Smirnov test assumes that we test against a distribution with given parameters, since, in the last case, we estimated mean and variance, this assumption is violated and the distribution of the test statistic, on which the p-value is based, is not correct.

Tails of the distribution

Finally, we can check the upper tail of the distribution. We can use the percent point function ppf, which is the inverse of the cdf function, to obtain the critical values, or, more directly, we can use the inverse of the survival function

```
>>> crit01, crit05, crit10 = stats.t.ppf([1-0.01, 1-0.05, 1-0.10], 10)
>>> print('critical values from ppf at 1%%, 5%% and 10%% %8.4f %8.4f %8.4f'
 ↪% (crit01, crit05, crit10))
critical values from ppf at 1%, 5% and 10%   2.7638   1.8125   1.3722
>>> print('critical values from isf at 1%%, 5%% and 10%% %8.4f %8.4f %8.4f'
 ↪% tuple(stats.t.isf([0.01,0.05,0.10],10)))
critical values from isf at 1%, 5% and 10%   2.7638   1.8125   1.3722
```

```
>>> freq01 = np.sum(x>crit01) / float(n) * 100
>>> freq05 = np.sum(x>crit05) / float(n) * 100
>>> freq10 = np.sum(x>crit10) / float(n) * 100
>>> print('sample %%-frequency at 1%%, 5%% and 10%% tail %8.4f %8.4f %8.4f'
 ↪% (freq01, freq05, freq10))
sample %-frequency at 1%, 5% and 10% tail   1.4000   5.8000  10.5000  # random
```

In all three cases, our sample has more weight in the top tail than the underlying distribution. We can briefly check a larger sample to see if we get a closer match. In this case, the empirical frequency is quite close to the theoretical probability, but if we repeat this several times, the fluctuations are still pretty large.

```
>>> freq05l = np.sum(stats.t.rvs(10, size=10000) > crit05) / 10000.0 * 100
>>> print('larger sample %%-frequency at 5%% tail %8.4f' % freq05l)
larger sample %-frequency at 5% tail   4.8000  # random
```

We can also compare it with the tail of the normal distribution, which has less weight in the tails:

```
>>> print('tail prob. of normal at 1%%, 5%% and 10%% %8.4f %8.4f %8.4f' %
...       tuple(stats.norm.sf([crit01, crit05, crit10])*100))
tail prob. of normal at 1%, 5% and 10%   0.2857   3.4957   8.5003
```

The chisquare test can be used to test whether for a finite number of bins, the observed frequencies differ significantly from the probabilities of the hypothesized distribution.

```
>>> quantiles = [0.0, 0.01, 0.05, 0.1, 1-0.10, 1-0.05, 1-0.01, 1.0]
>>> crit = stats.t.ppf(quantiles, 10)
>>> crit
array([       -inf, -2.76376946, -1.81246112, -1.37218364,  1.37218364,
        1.81246112,  2.76376946,         inf])
>>> n_sample = x.size
>>> freqcount = np.histogram(x, bins=crit)[0]
>>> tprob = np.diff(quantiles)
>>> nprob = np.diff(stats.norm.cdf(crit))
>>> tch, tpval = stats.chisquare(freqcount, tprob*n_sample)
>>> nch, npval = stats.chisquare(freqcount, nprob*n_sample)
>>> print('chisquare for t:      chi2 = %6.2f pvalue = %6.4f' % (tch, tpval))
chisquare for t:      chi2 =  2.30 pvalue = 0.8901  # random
>>> print('chisquare for normal: chi2 = %6.2f pvalue = %6.4f' % (nch, npval))
chisquare for normal: chi2 = 64.60 pvalue = 0.0000  # random
```

We see that the standard normal distribution is clearly rejected, while the standard t-distribution cannot be rejected. Since the variance of our sample differs from both standard distributions, we can again redo the test taking the estimate for scale and location into account.

The fit method of the distributions can be used to estimate the parameters of the distribution, and the test is repeated using probabilities of the estimated distribution.

```
>>> tdof, tloc, tscale = stats.t.fit(x)
>>> nloc, nscale = stats.norm.fit(x)
>>> tprob = np.diff(stats.t.cdf(crit, tdof, loc=tloc, scale=tscale))
>>> nprob = np.diff(stats.norm.cdf(crit, loc=nloc, scale=nscale))
>>> tch, tpval = stats.chisquare(freqcount, tprob*n_sample)
>>> nch, npval = stats.chisquare(freqcount, nprob*n_sample)
>>> print('chisquare for t:      chi2 = %6.2f pvalue = %6.4f' % (tch, tpval))
chisquare for t:      chi2 =  1.58 pvalue = 0.9542  # random
>>> print('chisquare for normal: chi2 = %6.2f pvalue = %6.4f' % (nch, npval))
chisquare for normal: chi2 = 11.08 pvalue = 0.0858  # random
```

Taking account of the estimated parameters, we can still reject the hypothesis that our sample came from a normal distribution (at the 5% level), but again, with a p-value of 0.95, we cannot reject the t-distribution.

Special tests for normal distributions

Since the normal distribution is the most common distribution in statistics, there are several additional functions available to test whether a sample could have been drawn from a normal distribution.

First, we can test if skew and kurtosis of our sample differ significantly from those of a normal distribution:

```
>>> print('normal skewtest teststat = %6.3f pvalue = %6.4f' % stats.
↪skewtest(x))
normal skewtest teststat =  2.785 pvalue = 0.0054  # random
>>> print('normal kurtosistest teststat = %6.3f pvalue = %6.4f' % stats.
↪kurtosistest(x))
normal kurtosistest teststat =  4.757 pvalue = 0.0000  # random
```

These two tests are combined in the normality test

```
>>> print('normaltest teststat = %6.3f pvalue = %6.4f' % stats.normaltest(x))
normaltest teststat = 30.379 pvalue = 0.0000  # random
```

In all three tests, the p-values are very low and we can reject the hypothesis that the our sample has skew and kurtosis of the normal distribution.

Since skew and kurtosis of our sample are based on central moments, we get exactly the same results if we test the standardized sample:

```
>>> print('normaltest teststat = %6.3f pvalue = %6.4f' %
...       stats.normaltest((x-x.mean())/x.std()))
normaltest teststat = 30.379 pvalue = 0.0000  # random
```

Because normality is rejected so strongly, we can check whether the normaltest gives reasonable results for other cases:

```
>>> print('normaltest teststat = %6.3f pvalue = %6.4f' %
...       stats.normaltest(stats.t.rvs(10, size=100)))
normaltest teststat =  4.698 pvalue = 0.0955  # random
>>> print('normaltest teststat = %6.3f pvalue = %6.4f' %
...              stats.normaltest(stats.norm.rvs(size=1000)))
normaltest teststat =  0.613 pvalue = 0.7361  # random
```

When testing for normality of a small sample of t-distributed observations and a large sample of normal-distributed observations, then in neither case can we reject the null hypothesis that the sample comes from a normal distribution. In the first case, this is because the test is not powerful enough to distinguish a t and a normally distributed random variable in a small sample.

2.12.5 Comparing two samples

In the following, we are given two samples, which can come either from the same or from different distribution, and we want to test whether these samples have the same statistical properties.

Comparing means

Test with sample with identical means:

```
>>> rvs1 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> rvs2 = stats.norm.rvs(loc=5, scale=10, size=500)
>>> stats.ttest_ind(rvs1, rvs2)
Ttest_indResult(statistic=-0.5489036175088705, pvalue=0.5831943748663959)  #␣
↪random
```

Test with sample with different means:

```
>>> rvs3 = stats.norm.rvs(loc=8, scale=10, size=500)
>>> stats.ttest_ind(rvs1, rvs3)
Ttest_indResult(statistic=-4.533414290175026, pvalue=6.507128186389019e-06)
↪# random
```

Kolmogorov-Smirnov test for two samples ks_2samp

For the example, where both samples are drawn from the same distribution, we cannot reject the null hypothesis, since the pvalue is high

```
>>> stats.ks_2samp(rvs1, rvs2)
KstestResult(statistic=0.026, pvalue=0.9959527565364388)  # random
```

In the second example, with different location, i.e., means, we can reject the null hypothesis, since the pvalue is below 1%

```
>>> stats.ks_2samp(rvs1, rvs3)
KstestResult(statistic=0.114, pvalue=0.00299005061044668)  # random
```

2.12.6 Kernel density estimation

A common task in statistics is to estimate the probability density function (PDF) of a random variable from a set of data samples. This task is called density estimation. The most well-known tool to do this is the histogram. A histogram is a useful tool for visualization (mainly because everyone understands it), but doesn't use the available data very efficiently. Kernel density estimation (KDE) is a more efficient tool for the same task. The *gaussian_kde* estimator can be used to estimate the PDF of univariate as well as multivariate data. It works best if the data is unimodal.

Univariate estimation

We start with a minimal amount of data in order to see how *gaussian_kde* works and what the different options for bandwidth selection do. The data sampled from the PDF are shown as blue dashes at the bottom of the figure (this is called a rug plot):

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

```
>>> x1 = np.array([-7, -5, 1, 4, 5], dtype=np.float64)
>>> kde1 = stats.gaussian_kde(x1)
>>> kde2 = stats.gaussian_kde(x1, bw_method='silverman')
```

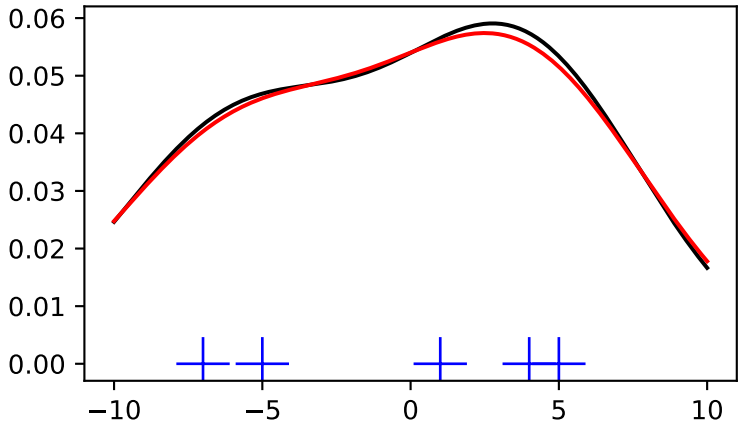
```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
```

```
>>> ax.plot(x1, np.zeros(x1.shape), 'b+', ms=20)  # rug plot
>>> x_eval = np.linspace(-10, 10, num=200)
>>> ax.plot(x_eval, kde1(x_eval), 'k-', label="Scott's Rule")
>>> ax.plot(x_eval, kde2(x_eval), 'r-', label="Silverman's Rule")
```

```
>>> plt.show()
```

We see that there is very little difference between Scott's Rule and Silverman's Rule, and that the bandwidth selection with a limited amount of data is probably a bit too wide. We can define our own bandwidth function to get a less smoothed-out result.

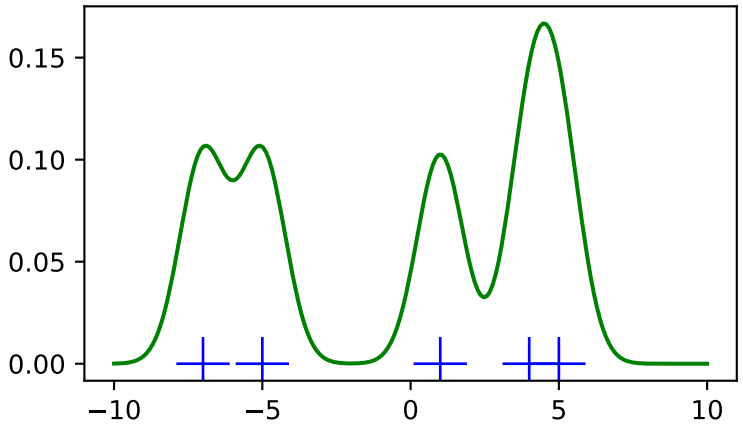
```
>>> def my_kde_bandwidth(obj, fac=1./5):
...     """We use Scott's Rule, multiplied by a constant factor."""
...     return np.power(obj.n, -1./(obj.d+4)) * fac
```




```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
```

```
>>> ax.plot(x1, np.zeros(x1.shape), 'b+', ms=20)  # rug plot
>>> kde3 = stats.gaussian_kde(x1, bw_method=my_kde_bandwidth)
>>> ax.plot(x_eval, kde3(x_eval), 'g-', label="With smaller BW")
```

```
>>> plt.show()
```



We see that if we set bandwidth to be very narrow, the obtained estimate for the probability density function (PDF) is simply the sum of Gaussians around each data point.

We now take a more realistic example and look at the difference between the two available bandwidth selection rules. Those rules are known to work well for (close to) normal distributions, but even for unimodal distributions that are quite

strongly non-normal they work reasonably well. As a non-normal distribution we take a Student's T distribution with 5 degrees of freedom.

```
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats


rng = np.random.default_rng()
x1 = rng.normal(size=200)  # random data, normal distribution
xs = np.linspace(x1.min()-1, x1.max()+1, 200)

kde1 = stats.gaussian_kde(x1)
kde2 = stats.gaussian_kde(x1, bw_method='silverman')

fig = plt.figure(figsize=(8, 6))

ax1 = fig.add_subplot(211)
ax1.plot(x1, np.zeros(x1.shape), 'b+', ms=12)  # rug plot
ax1.plot(xs, kde1(xs), 'k-', label="Scott's Rule")
ax1.plot(xs, kde2(xs), 'b-', label="Silverman's Rule")
ax1.plot(xs, stats.norm.pdf(xs), 'r--', label="True PDF")

ax1.set_xlabel('x')
ax1.set_ylabel('Density')
ax1.set_title("Normal (top) and Student's T$_{df=5}$ (bottom) distributions")
ax1.legend(loc=1)

x2 = stats.t.rvs(5, size=200, random_state=rng)  # random data, T distribution
xs = np.linspace(x2.min() - 1, x2.max() + 1, 200)

kde3 = stats.gaussian_kde(x2)
kde4 = stats.gaussian_kde(x2, bw_method='silverman')

ax2 = fig.add_subplot(212)
ax2.plot(x2, np.zeros(x2.shape), 'b+', ms=12)  # rug plot
ax2.plot(xs, kde3(xs), 'k-', label="Scott's Rule")
ax2.plot(xs, kde4(xs), 'b-', label="Silverman's Rule")
ax2.plot(xs, stats.t.pdf(xs, 5), 'r--', label="True PDF")

ax2.set_xlabel('x')
ax2.set_ylabel('Density')

plt.show()
```

We now take a look at a bimodal distribution with one wider and one narrower Gaussian feature. We expect that this will be a more difficult density to approximate, due to the different bandwidths required to accurately resolve each feature.

```
>>> from functools import partial
```

```
>>> loc1, scale1, size1 = (-2, 1, 175)
>>> loc2, scale2, size2 = (2, 0.2, 50)
>>> x2 = np.concatenate([np.random.normal(loc=loc1, scale=scale1, size=size1),
```

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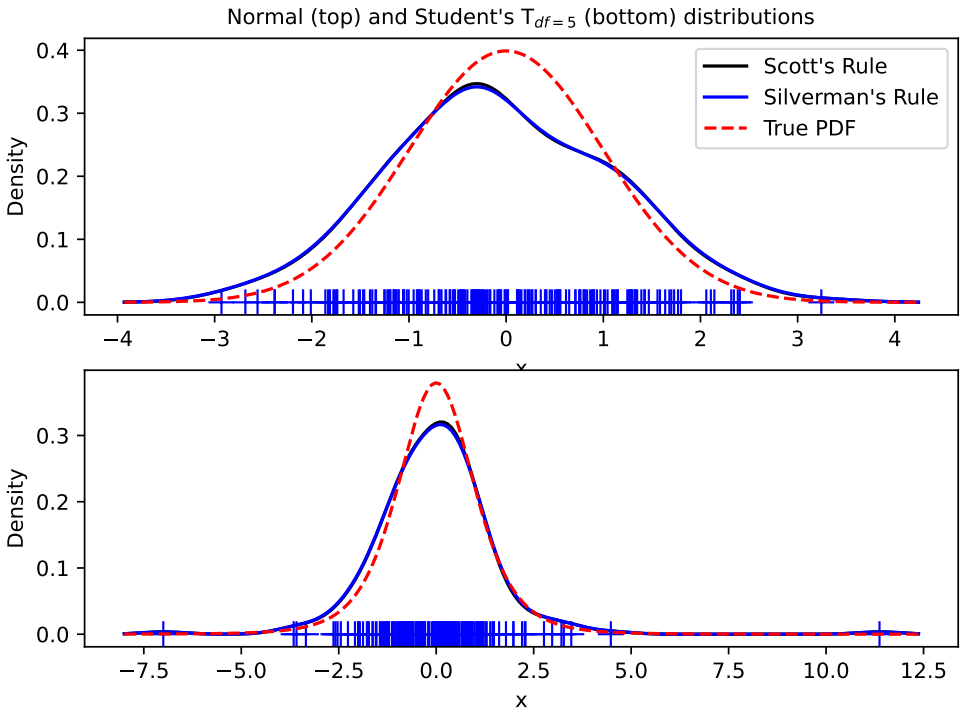
Normal (top) and Student's T$_{df=5}$ (bottom) distributions
Scott's Rule
Silverman's Rule
True PDF
Density
0.4
0.3
0.2
0.1
0.0
−4
−3
−2
−1
0
1
2
3
4
Density
0.3
0.2
0.1
0.0
−7.5
−5.0
−2.5
0.0
2.5
5.0
7.5
10.0
12.5
x

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```
...                       np.random.normal(loc=loc2, scale=scale2,␣
↪size=size2)])
```

```
>>> x_eval = np.linspace(x2.min() - 1, x2.max() + 1, 500)
```

```
>>> kde = stats.gaussian_kde(x2)
>>> kde2 = stats.gaussian_kde(x2, bw_method='silverman')
>>> kde3 = stats.gaussian_kde(x2, bw_method=partial(my_kde_bandwidth, fac=0.
↪2))
>>> kde4 = stats.gaussian_kde(x2, bw_method=partial(my_kde_bandwidth, fac=0.
↪5))
```

```
>>> pdf = stats.norm.pdf
>>> bimodal_pdf = pdf(x_eval, loc=loc1, scale=scale1) * float(size1) / x2.
↪size + \
...               pdf(x_eval, loc=loc2, scale=scale2) * float(size2) / x2.size
```

```
>>> fig = plt.figure(figsize=(8, 6))
>>> ax = fig.add_subplot(111)
```

```
>>> ax.plot(x2, np.zeros(x2.shape), 'b+', ms=12)
>>> ax.plot(x_eval, kde(x_eval), 'k-', label="Scott's Rule")
>>> ax.plot(x_eval, kde2(x_eval), 'b-', label="Silverman's Rule")
>>> ax.plot(x_eval, kde3(x_eval), 'g-', label="Scott * 0.2")
>>> ax.plot(x_eval, kde4(x_eval), 'c-', label="Scott * 0.5")
>>> ax.plot(x_eval, bimodal_pdf, 'r--', label="Actual PDF")
```

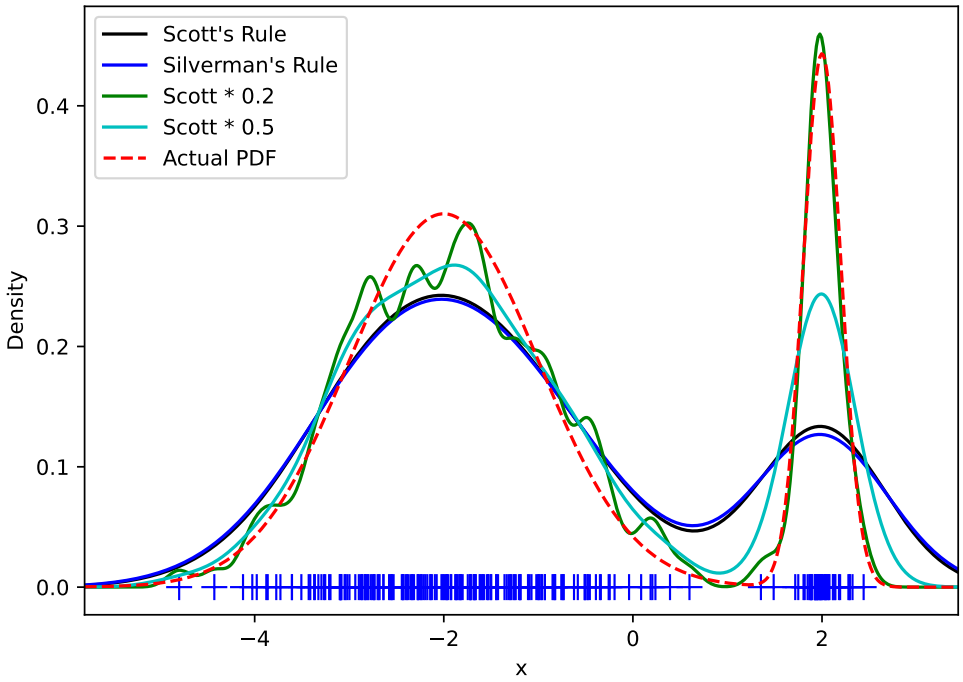
```
>>> ax.set_xlim([x_eval.min(), x_eval.max()])
>>> ax.legend(loc=2)
>>> ax.set_xlabel('x')
>>> ax.set_ylabel('Density')
>>> plt.show()
```

As expected, the KDE is not as close to the true PDF as we would like due to the different characteristic size of the two features of the bimodal distribution. By halving the default bandwidth (`Scott * 0.5`), we can do somewhat better, while using a factor 5 smaller bandwidth than the default doesn't smooth enough. What we really need, though, in this case, is a non-uniform (adaptive) bandwidth.

Multivariate estimation

With *gaussian_kde* we can perform multivariate, as well as univariate estimation. We demonstrate the bivariate case. First, we generate some random data with a model in which the two variates are correlated.

```
>>> def measure(n):
...     """Measurement model, return two coupled measurements."""
...     m1 = np.random.normal(size=n)
...     m2 = np.random.normal(scale=0.5, size=n)
...     return m1+m2, m1-m2
```


Scott's Rule
Silverman's Rule
Scott * 0.2
Scott * 0.5
Actual PDF
Density
0.0
0.1
0.2
0.3
0.4
−4
−2
0
2
x

```
>>> m1, m2 = measure(2000)
>>> xmin = m1.min()
>>> xmax = m1.max()
>>> ymin = m2.min()
>>> ymax = m2.max()
```

Then we apply the KDE to the data:

```
>>> X, Y = np.mgrid[xmin:xmax:100j, ymin:ymax:100j]
>>> positions = np.vstack([X.ravel(), Y.ravel()])
>>> values = np.vstack([m1, m2])
>>> kernel = stats.gaussian_kde(values)
>>> Z = np.reshape(kernel.evaluate(positions).T, X.shape)
```

Finally, we plot the estimated bivariate distribution as a colormap and plot the individual data points on top.

```
>>> fig = plt.figure(figsize=(8, 6))
>>> ax = fig.add_subplot(111)
```

```
>>> ax.imshow(np.rot90(Z), cmap=plt.cm.gist_earth_r,
...           extent=[xmin, xmax, ymin, ymax])
>>> ax.plot(m1, m2, 'k.', markersize=2)
```

```
>>> ax.set_xlim([xmin, xmax])
>>> ax.set_ylim([ymin, ymax])
```

```
>>> plt.show()
```

Multiscale Graph Correlation (MGC)

With *multiscale_graphcorr*, we can test for independence on high dimensional and nonlinear data. Before we start, let's import some useful packages:

```
>>> import numpy as np
>>> import matplotlib.pyplot as plt; plt.style.use('classic')
>>> from scipy.stats import multiscale_graphcorr
```

Let's use a custom plotting function to plot the data relationship:

```
>>> def mgc_plot(x, y, sim_name, mgc_dict=None, only_viz=False,
...              only_mgc=False):
...     """Plot sim and MGC-plot"""
...     if not only_mgc:
...         # simulation
...         plt.figure(figsize=(8, 8))
...         ax = plt.gca()
...         ax.set_title(sim_name + " Simulation", fontsize=20)
...         ax.scatter(x, y)
...         ax.set_xlabel('X', fontsize=15)
...         ax.set_ylabel('Y', fontsize=15)
...         ax.axis('equal')
```

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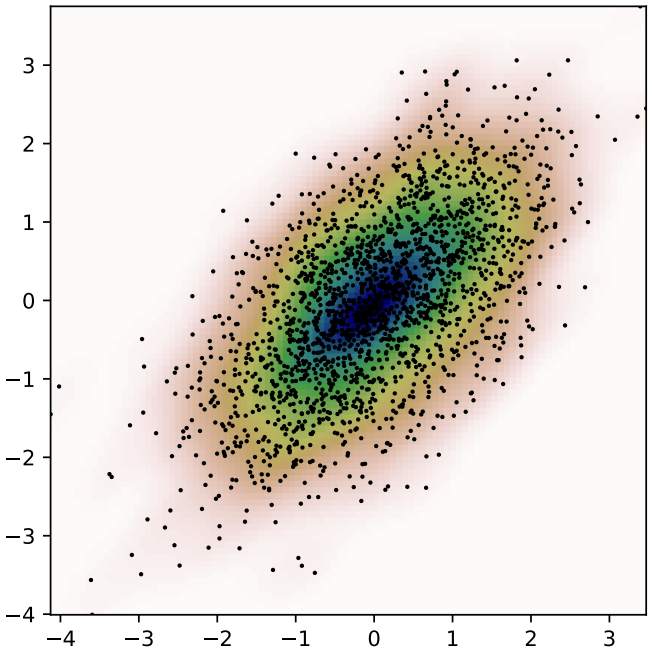
3
2
1
0
−1
−2
−3
−4
−4
−3
−2
−1
0
1
2
3

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```
...         ax.tick_params(axis="x", labelsize=15)
...         ax.tick_params(axis="y", labelsize=15)
...         plt.show()
...     if not only_viz:
...         # local correlation map
...         plt.figure(figsize=(8,8))
...         ax = plt.gca()
...         mgc_map = mgc_dict["mgc_map"]
...         # draw heatmap
...         ax.set_title("Local Correlation Map", fontsize=20)
...         im = ax.imshow(mgc_map, cmap='YlGnBu')
...         # colorbar
...         cbar = ax.figure.colorbar(im, ax=ax)
...         cbar.ax.set_ylabel("", rotation=-90, va="bottom")
...         ax.invert_yaxis()
...         # Turn spines off and create white grid.
...         for edge, spine in ax.spines.items():
...             spine.set_visible(False)
...         # optimal scale
...         opt_scale = mgc_dict["opt_scale"]
...         ax.scatter(opt_scale[0], opt_scale[1],
...                    marker='X', s=200, color='red')
...         # other formatting
...         ax.tick_params(bottom="off", left="off")
...         ax.set_xlabel('#Neighbors for X', fontsize=15)
...         ax.set_ylabel('#Neighbors for Y', fontsize=15)
...         ax.tick_params(axis="x", labelsize=15)
...         ax.tick_params(axis="y", labelsize=15)
...         ax.set_xlim(0, 100)
...         ax.set_ylim(0, 100)
...         plt.show()
```

Let's look at some linear data first:

```
>>> rng = np.random.default_rng()
>>> x = np.linspace(-1, 1, num=100)
>>> y = x + 0.3 * rng.random(x.size)
```

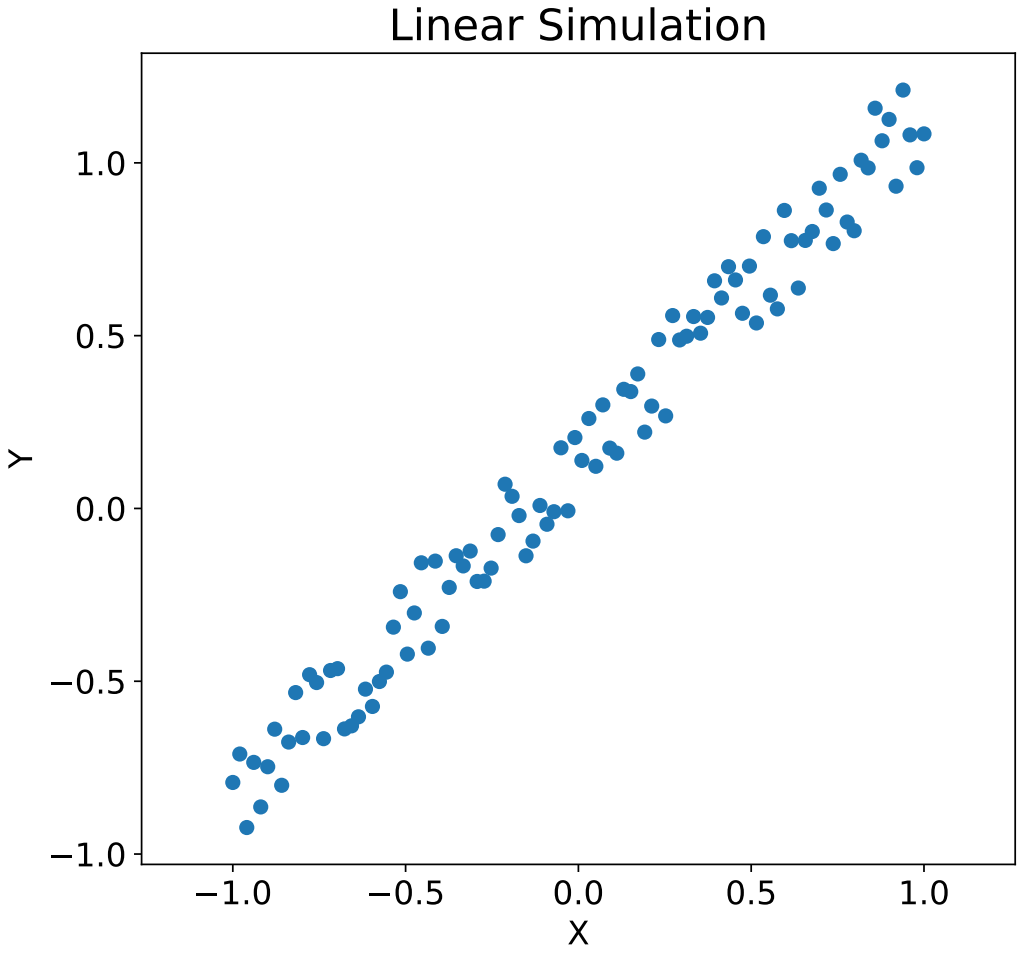
The simulation relationship can be plotted below:

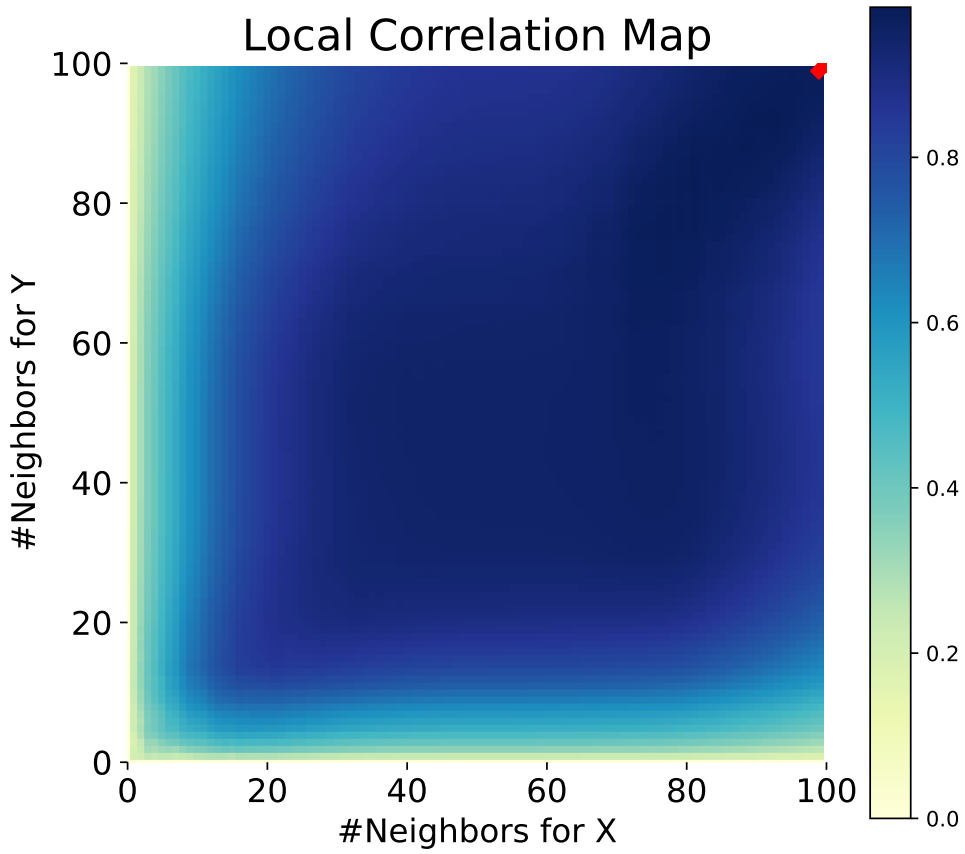
```
>>> mgc_plot(x, y, "Linear", only_viz=True)
```

Now, we can see the test statistic, p-value, and MGC map visualized below. The optimal scale is shown on the map as a red "x":

```
>>> stat, pvalue, mgc_dict = multiscale_graphcorr(x, y)
>>> print("MGC test statistic: ", round(stat, 1))
MGC test statistic:  1.0
>>> print("P-value: ", round(pvalue, 1))
P-value:  0.0
>>> mgc_plot(x, y, "Linear", mgc_dict, only_mgc=True)
```

It is clear from here, that MGC is able to determine a relationship between the input data matrices because the p-value is


Linear Simulation
1.0
0.5
0.0
−0.5
−1.0
Y
−1.0
−0.5
0.0
0.5
1.0
X


Local Correlation Map
100
80
60
40
20
0
#Neighbors for Y
0
20
40
60
80
100
#Neighbors for X
0.8
0.6
0.4
0.2
0.0

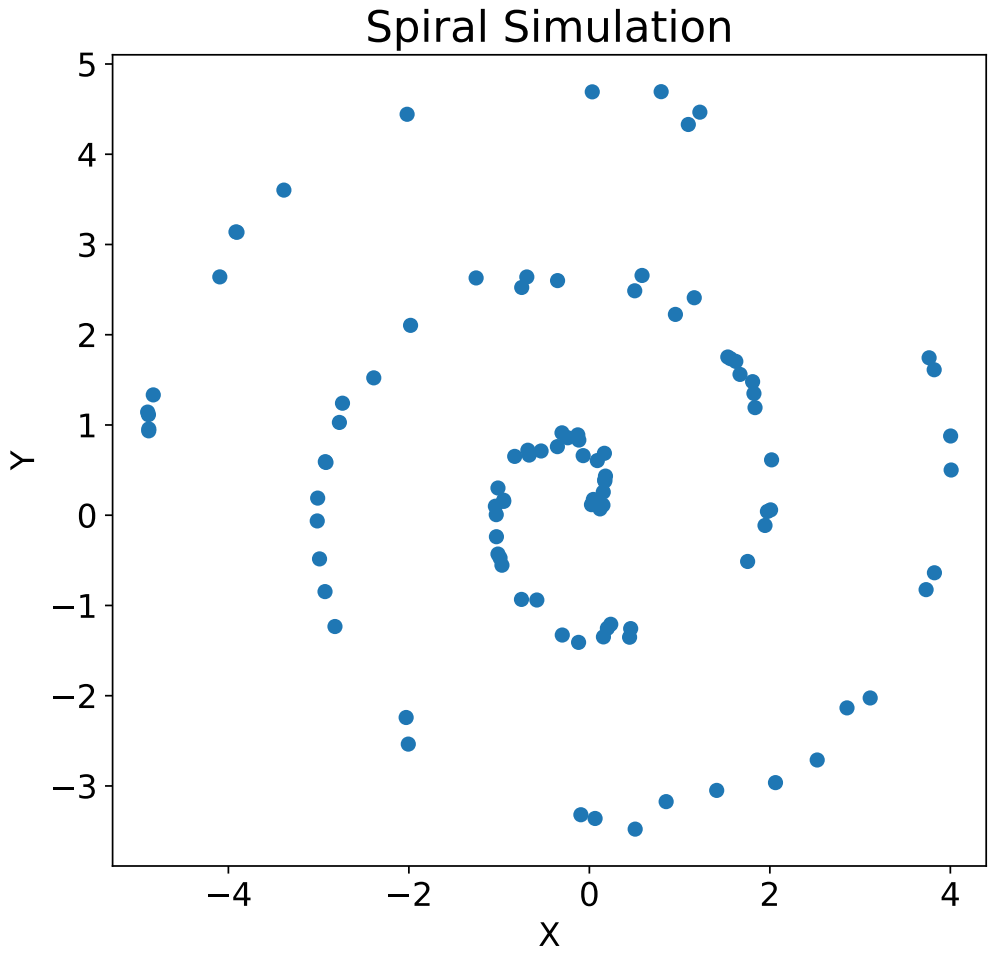
very low and the MGC test statistic is relatively high. The MGC-map indicates a **strongly linear relationship**. Intuitively, this is because having more neighbors will help in identifying a linear relationship between x and y. The optimal scale in this case is **equivalent to the global scale**, marked by a red spot on the map.

The same can be done for nonlinear data sets. The following x and y arrays are derived from a nonlinear simulation:

```
>>> unif = np.array(rng.uniform(0, 5, size=100))
>>> x = unif * np.cos(np.pi * unif)
>>> y = unif * np.sin(np.pi * unif) + 0.4 * rng.random(x.size)
```

The simulation relationship can be plotted below:

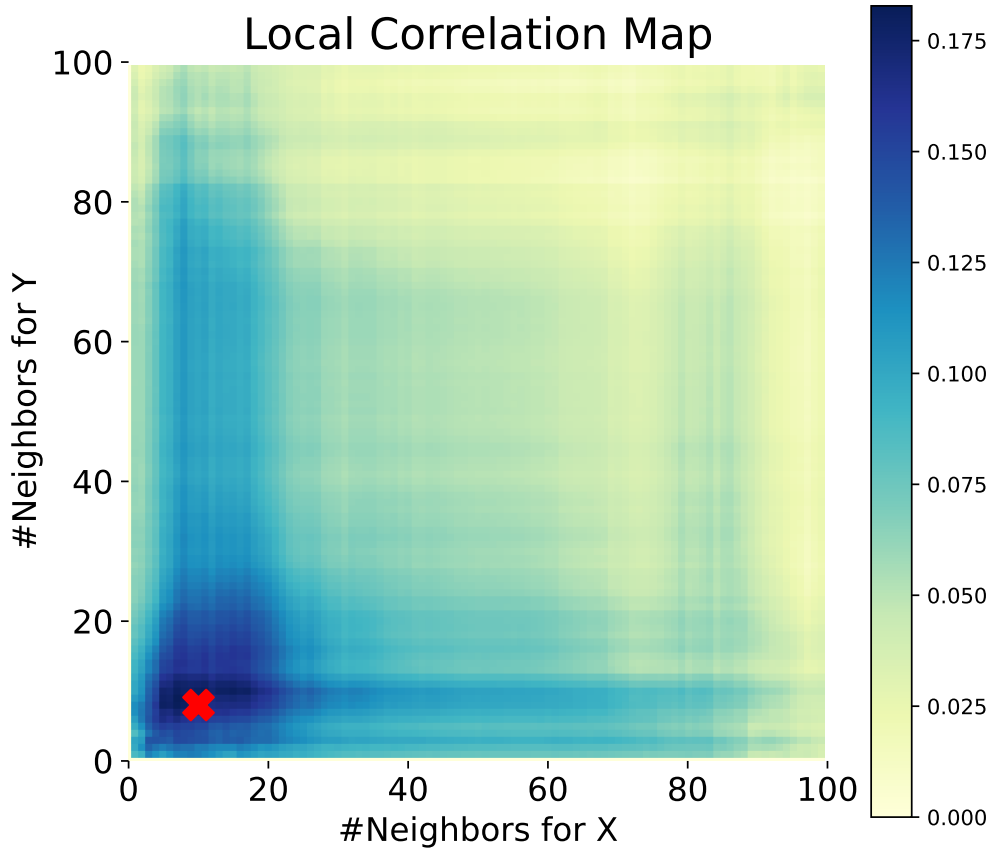
```
>>> mgc_plot(x, y, "Spiral", only_viz=True)
```



Now, we can see the test statistic, p-value, and MGC map visualized below. The optimal scale is shown on the map as a

red “x”:

```
>>> stat, pvalue, mgc_dict = multiscale_graphcorr(x, y)
>>> print("MGC test statistic: ", round(stat, 1))
MGC test statistic:  0.2  # random
>>> print("P-value: ", round(pvalue, 1))
P-value:  0.0
>>> mgc_plot(x, y, "Spiral", mgc_dict, only_mgc=True)
```

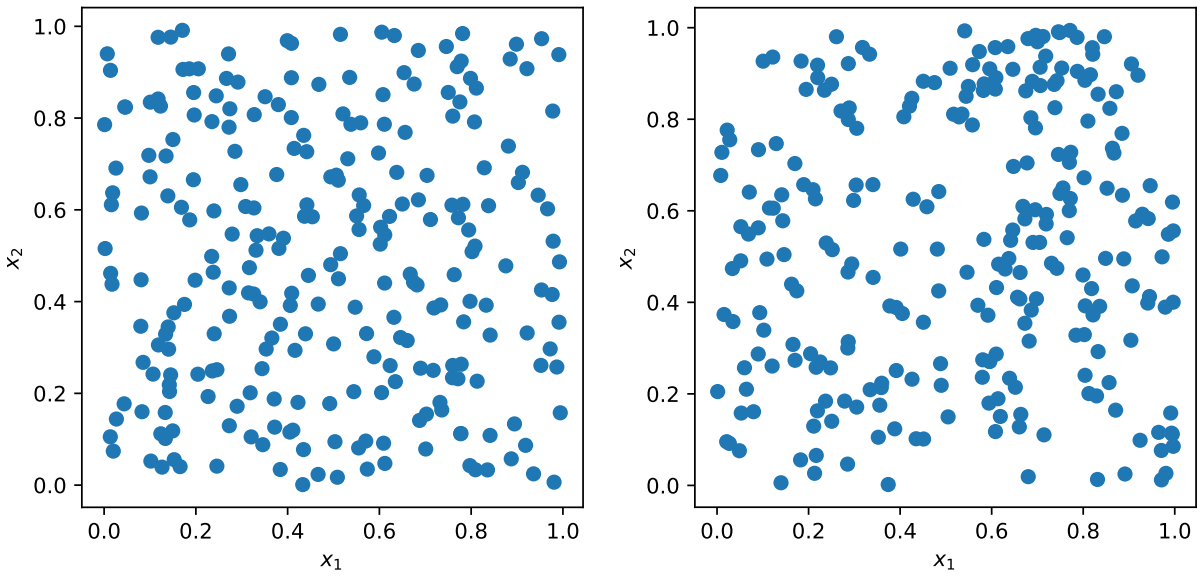


It is clear from here, that MGC is able to determine a relationship again because the p-value is very low and the MGC test statistic is relatively high. The MGC-map indicates a **strongly nonlinear relationship**. The optimal scale in this case is **equivalent to the local scale**, marked by a red spot on the map.

2.12.7 Quasi-Monte Carlo

Before talking about Quasi-Monte Carlo (QMC), a quick introduction about Monte Carlo (MC). MC methods, or MC experiments, are a broad class of computational algorithms that rely on repeated random sampling to obtain numerical results. The underlying concept is to use randomness to solve problems that might be deterministic in principle. They are often used in physical and mathematical problems and are most useful when it is difficult or impossible to use other approaches. MC methods are mainly used in three problem classes: optimization, numerical integration, and generating draws from a probability distribution.

Generating random numbers with specific properties is a more complex problem than it sounds. Simple MC methods are designed to sample points to be independent and identically distributed (IID). But generating multiple sets of random points can produce radically different results.



In both cases in the plot above, points are generated randomly without any knowledge about previously drawn points. It is clear that some regions of the space are left unexplored - which can cause problems in simulations as a particular set of points might trigger a totally different behaviour.

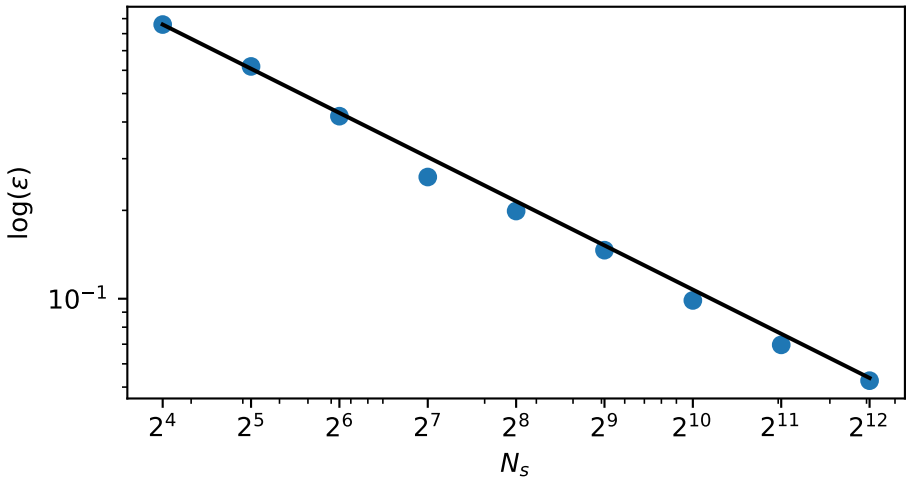
A great benefit of MC is that it has known convergence properties. Let's look at the mean of the squared sum in 5 dimensions:

$$f(\mathbf{x}) = \left(\sum_{j=1}^{5} x_j \right)^2 ,$$

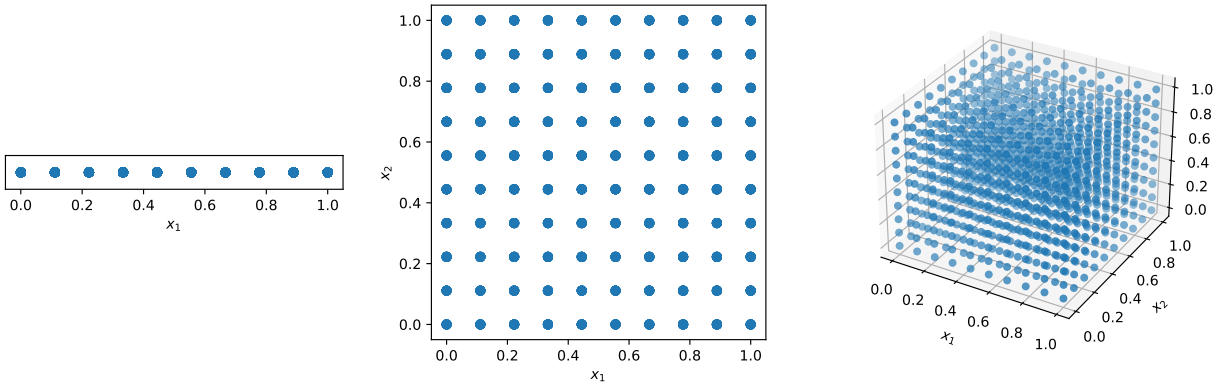
with $x_j \sim \mathcal{U}(0, 1)$. It has a known mean value, $\mu = 5/3 + 5(5-1)/4$. Using MC sampling, we can compute that mean numerically, and the approximation error follows a theoretical rate of $O(n^{-1/2})$.

Although the convergence is ensured, practitioners tend to want to have an exploration process which is more deterministic. With normal MC, a seed can be used to have a repeatable process. But fixing the seed would break the convergence property: a given seed could work for a given class of problem and break for another one.

What is commonly done to walk through the space in a deterministic manner, is to use a regular grid spanning all parameter dimensions, also called a saturated design. Let's consider the unit-hypercube, with all bounds ranging from 0 to 1. Now, having a distance of 0.1 between points, the number of points required to fill the unit interval would be 10. In a 2-dimensional hypercube the same spacing would require 100, and in 3 dimensions 1,000 points. As the number of dimensions grows, the number of experiments which is required to fill the space rises exponentially as the dimensionality of the space increases. This exponential growth is called "the curse of dimensionality".




```
>>> import numpy as np
>>> disc = 10
>>> x1 = np.linspace(0, 1, disc)
>>> x2 = np.linspace(0, 1, disc)
>>> x3 = np.linspace(0, 1, disc)
>>> x1, x2, x3 = np.meshgrid(x1, x2, x3)
```

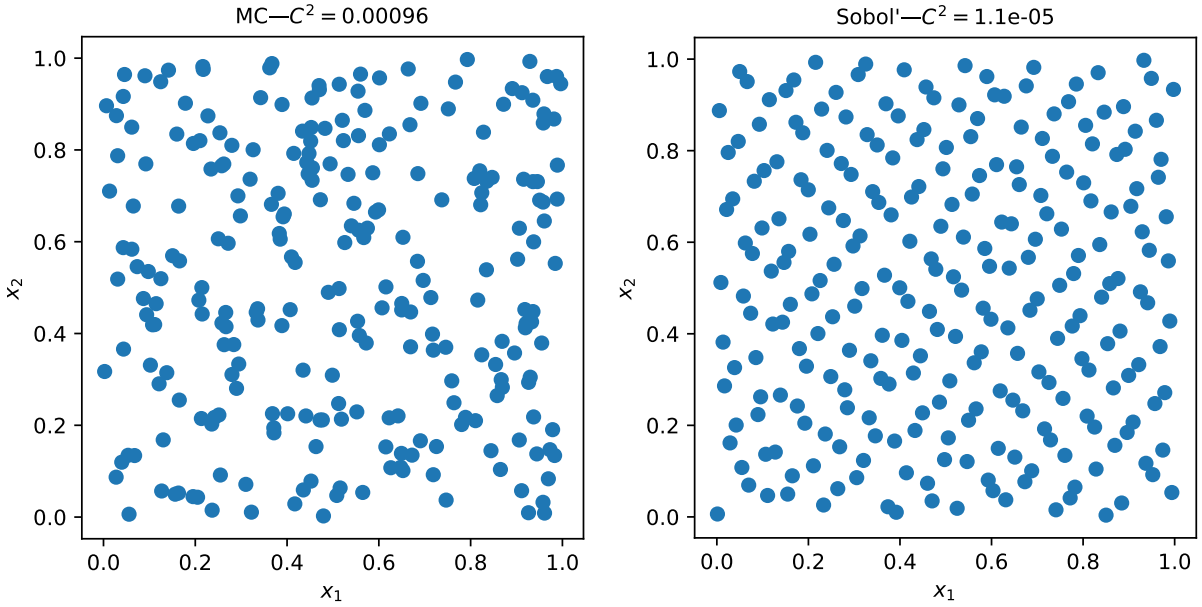


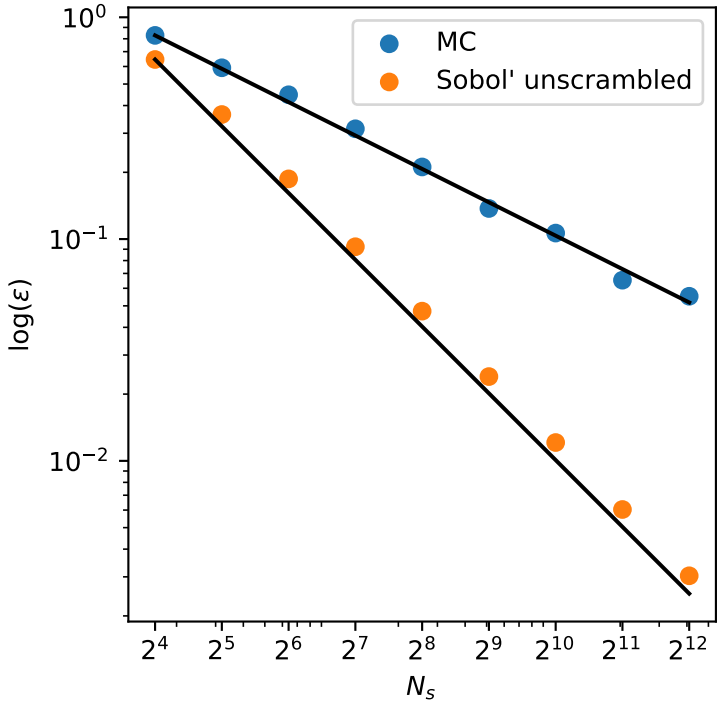
To mitigate this issue, QMC methods have been designed. They are deterministic, have a good coverage of the space and some of them can be continued and retain good properties. The main difference with MC methods is that the points are not IID but they know about previous points. Hence, some methods are also referred to as sequences.

This figure presents 2 sets of 256 points. The design of the left is a plain MC whereas the design of the right is a QMC design using the *Sobol'* method. We clearly see that the QMC version is more uniform. The points sample better near the boundaries and there are less clusters or gaps.

One way to assess the uniformity is to use a measure called the discrepancy. Here the discrepancy of *Sobol'* points is better than crude MC.

Coming back to the computation of the mean, QMC methods also have better rates of convergence for the error. They can achieve $O(n^{-1})$ for this function, and even better rates on very smooth functions. This figure shows that the *Sobol'* method has a rate of $O(n^{-1})$:


MC—$C^2 = 0.00096$
Sobol'—$C^2 = 1.1e-05$
x_1
x_2
0.0
0.2
0.4
0.6
0.8
1.0

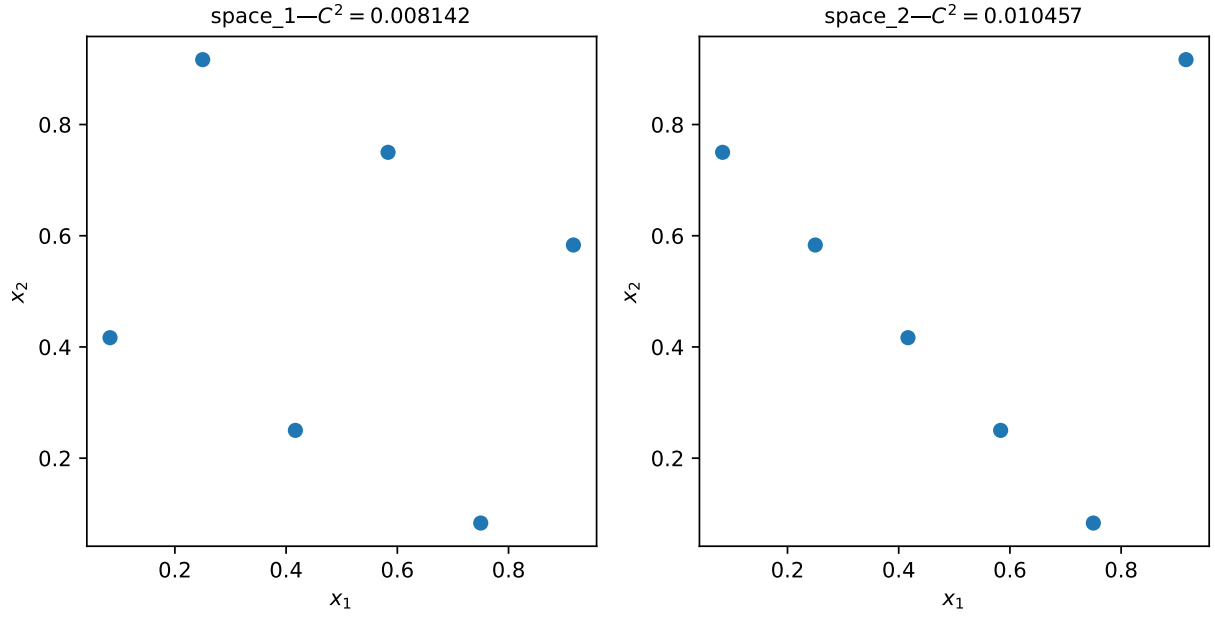

MC
Sobol' unscrambled
10^0
10^{-1}
10^{-2}
log(ε)
2^4 2^5 2^6 2^7 2^8 2^9 2^{10} 2^{11} 2^{12}
N_s

We refer to the documentation of *scipy.stats.qmc* for more mathematical details.

Calculate the discrepancy

Let's consider two sets of points. From the figure below, it is clear that the design on the left covers more of the space than the design on the right. This can be quantified using a *discrepancy* measure. The lower the discrepancy, the more uniform a sample is.

```
>>> import numpy as np
>>> from scipy.stats import qmc
>>> space_1 = np.array([[1, 3], [2, 6], [3, 2], [4, 5], [5, 1], [6, 4]])
>>> space_2 = np.array([[1, 5], [2, 4], [3, 3], [4, 2], [5, 1], [6, 6]])
>>> l_bounds = [0.5, 0.5]
>>> u_bounds = [6.5, 6.5]
>>> space_1 = qmc.scale(space_1, l_bounds, u_bounds, reverse=True)
>>> space_2 = qmc.scale(space_2, l_bounds, u_bounds, reverse=True)
>>> qmc.discrepancy(space_1)
0.008142039609053464
>>> qmc.discrepancy(space_2)
0.010456854423869011
```



Using a QMC engine

Several QMC samplers/engines are implemented. Here we look at two of the most used QMC methods: *Sobol* and *Halton* sequences.

```
"""Sobol' and Halton sequences."""
from scipy.stats import qmc
import numpy as np

import matplotlib.pyplot as plt
```

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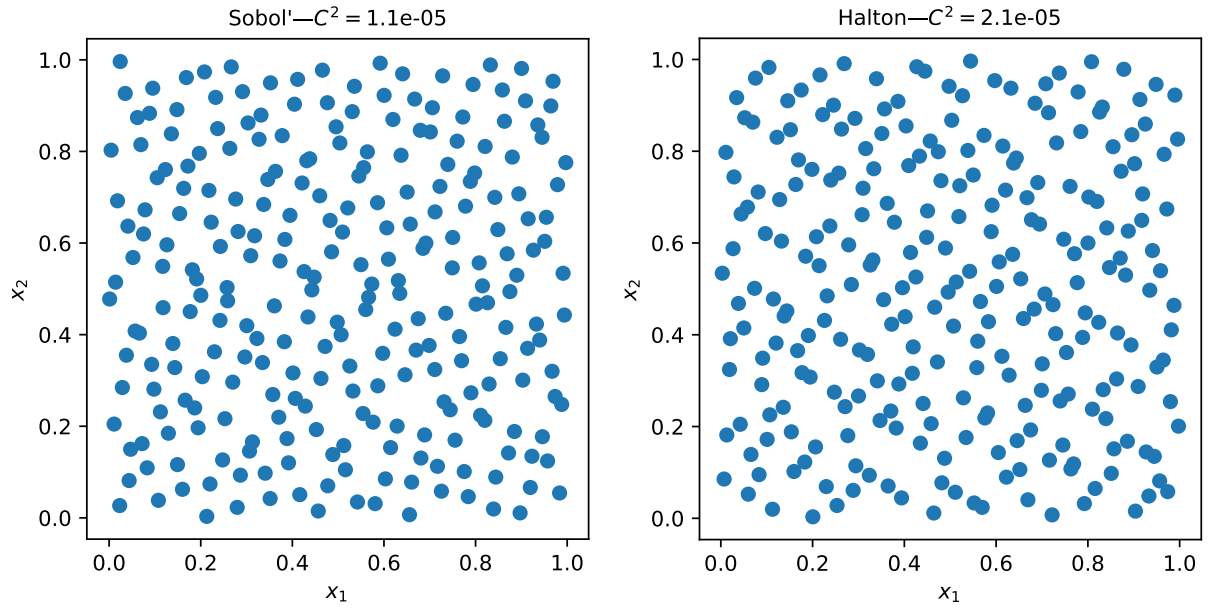
```
rng = np.random.default_rng()

n_sample = 256
dim = 2

sample = {}

# Sobol'
engine = qmc.Sobol(d=dim, seed=rng)
sample["Sobol'"] = engine.random(n_sample)

# Halton
engine = qmc.Halton(d=dim, seed=rng)
sample["Halton"] = engine.random(n_sample)

fig, axs = plt.subplots(1, 2, figsize=(8, 4))

for i, kind in enumerate(sample):
    axs[i].scatter(sample[kind][:, 0], sample[kind][:, 1])

    axs[i].set_aspect('equal')
    axs[i].set_xlabel(r'$x_1$')
    axs[i].set_ylabel(r'$x_2$')
    axs[i].set_title(f'{kind}—$C^2 = ${qmc.discrepancy(sample[kind]):.2}')

plt.tight_layout()
plt.show()
```



Warning: QMC methods require particular care and the user must read the documentation to avoid common pitfalls. *Sobol'* for instance requires a number of points following a power of 2. Also, thinning, burning or other point selection can break the properties of the sequence and result in a set of points which would not be better than MC.

QMC engines are state-aware. Meaning that you can continue the sequence, skip some points, or reset it. Let's take 5 points from *Halton*. And then ask for a second set of 5 points:

```
>>> from scipy.stats import qmc
>>> engine = qmc.Halton(d=2)
>>> engine.random(5)
array([[0.22166437, 0.07980522],  # random
       [0.72166437, 0.93165708],
       [0.47166437, 0.41313856],
       [0.97166437, 0.19091633],
       [0.01853937, 0.74647189]])
>>> engine.random(5)
array([[0.51853937, 0.52424967],  # random
       [0.26853937, 0.30202745],
       [0.76853937, 0.857583  ],
       [0.14353937, 0.63536078],
       [0.64353937, 0.01807683]])
```

Now we reset the sequence. Asking for 5 points leads to the same first 5 points:

```
>>> engine.reset()
>>> engine.random(5)
array([[0.22166437, 0.07980522],  # random
       [0.72166437, 0.93165708],
       [0.47166437, 0.41313856],
       [0.97166437, 0.19091633],
       [0.01853937, 0.74647189]])
```

And here we advance the sequence to get the same second set of 5 points:

```
>>> engine.reset()
>>> engine.fast_forward(5)
>>> engine.random(5)
array([[0.51853937, 0.52424967],  # random
       [0.26853937, 0.30202745],
       [0.76853937, 0.857583  ],
       [0.14353937, 0.63536078],
       [0.64353937, 0.01807683]])
```

Note: By default, both *Sobol* and *Halton* are scrambled. The convergence properties are better, and it prevents the appearance of fringes or noticeable patterns of points in high dimensions. There should be no practical reason not to use the scrambled version.

Making a QMC engine, i.e., subclassing `QMCEngine`

To make your own *QMCEngine*, a few methods have to be defined. Following is an example wrapping `numpy.random.Generator`.

```
>>> import numpy as np
>>> from scipy.stats import qmc
>>> class RandomEngine(qmc.QMCEngine):
...     def __init__(self, d, seed=None):
...         super().__init__(d=d, seed=seed)
...         self.rng = np.random.default_rng(self.rng_seed)
...
...
...     def random(self, n=1):
...         self.num_generated += n
...         return self.rng.random((n, self.d))
...
...
...     def reset(self):
...         self.rng = np.random.default_rng(self.rng_seed)
...         self.num_generated = 0
...         return self
...
...
...     def fast_forward(self, n):
...         self.random(n)
...         return self
```

Then we use it as any other QMC engine:

```
>>> engine = RandomEngine(2)
>>> engine.random(5)
array([[0.22733602, 0.31675834],  # random
       [0.79736546, 0.67625467],
       [0.39110955, 0.33281393],
       [0.59830875, 0.18673419],
       [0.67275604, 0.94180287]])
>>> engine.reset()
>>> engine.random(5)
array([[0.22733602, 0.31675834],  # random
       [0.79736546, 0.67625467],
       [0.39110955, 0.33281393],
       [0.59830875, 0.18673419],
       [0.67275604, 0.94180287]])
```

Guidelines on using QMC

- QMC has rules! Be sure to read the documentation or you might have no benefit over MC.
- Use `Sobol` if you need **exactly** 2^m points.
- `Halton` allows to sample, or skip, an arbitrary number of points. This is at the cost of a slower rate of convergence than *Sobol'*.
- Never remove the first points of the sequence. It will destroy the properties.
- Scrambling is always better.
- If you use LHS based methods, you cannot add points without losing the LHS properties. (There are some methods to do so, but this is not implemented.)

2.13 Multidimensional image processing (`scipy.ndimage`)

2.13.1 Introduction

Image processing and analysis are generally seen as operations on 2-D arrays of values. There are, however, a number of fields where images of higher dimensionality must be analyzed. Good examples of these are medical imaging and biological imaging. `numpy` is suited very well for this type of applications due to its inherent multidimensional nature. The `scipy.ndimage` packages provides a number of general image processing and analysis functions that are designed to operate with arrays of arbitrary dimensionality. The packages currently includes: functions for linear and non-linear filtering, binary morphology, B-spline interpolation, and object measurements.

2.13.2 Properties shared by all functions

All functions share some common properties. Notably, all functions allow the specification of an output array with the *output* argument. With this argument, you can specify an array that will be changed in-place with the result with the operation. In this case, the result is not returned. Usually, using the *output* argument is more efficient, since an existing array is used to store the result.

The type of arrays returned is dependent on the type of operation, but it is, in most cases, equal to the type of the input. If, however, the *output* argument is used, the type of the result is equal to the type of the specified output argument. If no output argument is given, it is still possible to specify what the result of the output should be. This is done by simply assigning the desired `numpy` type object to the output argument. For example:

```
>>> from scipy.ndimage import correlate
>>> correlate(np.arange(10), [1, 2.5])
array([ 0,  2,  6,  9, 13, 16, 20, 23, 27, 30])
>>> correlate(np.arange(10), [1, 2.5], output=np.float64)
array([  0. ,   2.5,   6. ,   9.5,  13. ,  16.5,  20. ,  23.5,  27. ,  30.5])
```

2.13.3 Filter functions

The functions described in this section all perform some type of spatial filtering of the input array: the elements in the output are some function of the values in the neighborhood of the corresponding input element. We refer to this neighborhood of elements as the filter kernel, which is often rectangular in shape but may also have an arbitrary footprint. Many of the functions described below allow you to define the footprint of the kernel by passing a mask through the *footprint* parameter. For example, a cross-shaped kernel can be defined as follows:

```
>>> footprint = np.array([[0, 1, 0], [1, 1, 1], [0, 1, 0]])
>>> footprint
array([[0, 1, 0],
       [1, 1, 1],
       [0, 1, 0]])
```

Usually, the origin of the kernel is at the center calculated by dividing the dimensions of the kernel shape by two. For instance, the origin of a 1-D kernel of length three is at the second element. Take, for example, the correlation of a 1-D array with a filter of length 3 consisting of ones:

```
>>> from scipy.ndimage import correlate1d
>>> a = [0, 0, 0, 1, 0, 0, 0]
>>> correlate1d(a, [1, 1, 1])
array([0, 0, 1, 1, 1, 0, 0])
```

Sometimes, it is convenient to choose a different origin for the kernel. For this reason, most functions support the *origin* parameter, which gives the origin of the filter relative to its center. For example:

```
>>> a = [0, 0, 0, 1, 0, 0, 0]
>>> correlate1d(a, [1, 1, 1], origin = -1)
array([0, 1, 1, 1, 0, 0, 0])
```

The effect is a shift of the result towards the left. This feature will not be needed very often, but it may be useful, especially for filters that have an even size. A good example is the calculation of backward and forward differences:

```
>>> a = [0, 0, 1, 1, 1, 0, 0]
>>> correlate1d(a, [-1, 1])               # backward difference
array([ 0,  0,  1,  0,  0, -1,  0])
>>> correlate1d(a, [-1, 1], origin = -1)  # forward difference
array([ 0,  1,  0,  0, -1,  0,  0])
```

We could also have calculated the forward difference as follows:

```
>>> correlate1d(a, [0, -1, 1])
array([ 0,  1,  0,  0, -1,  0,  0])
```

However, using the origin parameter instead of a larger kernel is more efficient. For multidimensional kernels, *origin* can be a number, in which case the origin is assumed to be equal along all axes, or a sequence giving the origin along each axis.

Since the output elements are a function of elements in the neighborhood of the input elements, the borders of the array need to be dealt with appropriately by providing the values outside the borders. This is done by assuming that the arrays are extended beyond their boundaries according to certain boundary conditions. In the functions described below, the boundary conditions can be selected using the *mode* parameter, which must be a string with the name of the boundary condition. The following boundary conditions are currently supported:

mode	description	example
“nearest”	use the value at the boundary	[1 2 3]->[1 1 2 3 3]
“wrap”	periodically replicate the array	[1 2 3]->[3 1 2 3 1]
“reflect”	reflect the array at the boundary	[1 2 3]->[1 1 2 3 3]
“mirror”	mirror the array at the boundary	[1 2 3]->[2 1 2 3 2]
“constant”	use a constant value, default is 0.0	[1 2 3]->[0 1 2 3 0]

The following synonyms are also supported for consistency with the interpolation routines:

mode	description
“grid-constant”	equivalent to “constant”*
“grid-mirror”	equivalent to “reflect”
“grid-wrap”	equivalent to “wrap”

* “grid-constant” and “constant” are equivalent for filtering operations, but have different behavior in interpolation functions. For API consistency, the filtering functions accept either name.

The “constant” mode is special since it needs an additional parameter to specify the constant value that should be used.

Note that modes mirror and reflect differ only in whether the sample at the boundary is repeated upon reflection. For mode mirror, the point of symmetry is exactly at the final sample, so that value is not repeated. This mode is also known as whole-sample symmetric since the point of symmetry falls on the final sample. Similarly, reflect is often refered to as half-sample symmetric as the point of symmetry is half a sample beyond the array boundary.

Note: The easiest way to implement such boundary conditions would be to copy the data to a larger array and extend the data at the borders according to the boundary conditions. For large arrays and large filter kernels, this would be very memory consuming, and the functions described below, therefore, use a different approach that does not require allocating large temporary buffers.

Correlation and convolution

- The `correlate1d` function calculates a 1-D correlation along the given axis. The lines of the array along the given axis are correlated with the given *weights*. The *weights* parameter must be a 1-D sequence of numbers.
- The function `correlate` implements multidimensional correlation of the input array with a given kernel.
- The `convolve1d` function calculates a 1-D convolution along the given axis. The lines of the array along the given axis are convoluted with the given *weights*. The *weights* parameter must be a 1-D sequence of numbers.
- The function `convolve` implements multidimensional convolution of the input array with a given kernel.

Note: A convolution is essentially a correlation after mirroring the kernel. As a result, the *origin* parameter behaves differently than in the case of a correlation: the results is shifted in the opposite direction.

Smoothing filters

- The *gaussian_filter1d* function implements a 1-D Gaussian filter. The standard deviation of the Gaussian filter is passed through the parameter *sigma*. Setting *order* = 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second, or third derivatives of a Gaussian. Higher-order derivatives are not implemented.
- The *gaussian_filter* function implements a multidimensional Gaussian filter. The standard deviations of the Gaussian filter along each axis are passed through the parameter *sigma* as a sequence or numbers. If *sigma* is not a sequence but a single number, the standard deviation of the filter is equal along all directions. The order of the filter can be specified separately for each axis. An order of 0 corresponds to convolution with a Gaussian kernel. An order of 1, 2, or 3 corresponds to convolution with the first, second, or third derivatives of a Gaussian. Higher-order derivatives are not implemented. The *order* parameter must be a number, to specify the same order for all axes, or a sequence of numbers to specify a different order for each axis.

Note: The multidimensional filter is implemented as a sequence of 1-D Gaussian filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a lower precision, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a more precise output type.

- The *uniform_filter1d* function calculates a 1-D uniform filter of the given *size* along the given axis.
- The *uniform_filter* implements a multidimensional uniform filter. The sizes of the uniform filter are given for each axis as a sequence of integers by the *size* parameter. If *size* is not a sequence, but a single number, the sizes along all axes are assumed to be equal.

Note: The multidimensional filter is implemented as a sequence of 1-D uniform filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a lower precision, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a more precise output type.

Filters based on order statistics

- The *minimum_filter1d* function calculates a 1-D minimum filter of the given *size* along the given axis.
- The *maximum_filter1d* function calculates a 1-D maximum filter of the given *size* along the given axis.
- The *minimum_filter* function calculates a multidimensional minimum filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number, in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.
- The *maximum_filter* function calculates a multidimensional maximum filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number, in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.
- The *rank_filter* function calculates a multidimensional rank filter. The *rank* may be less then zero, i.e., *rank* = -1 indicates the largest element. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number, in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

- The *percentile_filter* function calculates a multidimensional percentile filter. The *percentile* may be less then zero, i.e., *percentile* = -20 equals *percentile* = 80. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number, in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.
- The *median_filter* function calculates a multidimensional median filter. Either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number, in which case the size of the filter is assumed to be equal along each axis. The *footprint* if provided, must be an array that defines the shape of the kernel by its non-zero elements.

Derivatives

Derivative filters can be constructed in several ways. The function *gaussian_filter1d*, described in *Smoothing filters*, can be used to calculate derivatives along a given axis using the *order* parameter. Other derivative filters are the Prewitt and Sobel filters:

- The *prewitt* function calculates a derivative along the given axis.
- The *sobel* function calculates a derivative along the given axis.

The Laplace filter is calculated by the sum of the second derivatives along all axes. Thus, different Laplace filters can be constructed using different second-derivative functions. Therefore, we provide a general function that takes a function argument to calculate the second derivative along a given direction.

- The function *generic_laplace* calculates a Laplace filter using the function passed through `derivative2` to calculate second derivatives. The function `derivative2` should have the following signature

```
derivative2(input, axis, output, mode, cval, *extra_arguments, **extra_
↪keywords)
```

It should calculate the second derivative along the dimension *axis*. If *output* is not `None`, it should use that for the output and return `None`, otherwise it should return the result. *mode*, *cval* have the usual meaning.

The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and a dictionary of named arguments that are passed to `derivative2` at each call.

For example

```
>>> def d2(input, axis, output, mode, cval):
...     return correlate1d(input, [1, -2, 1], axis, output, mode, cval, 0)
...
>>> a = np.zeros((5, 5))
>>> a[2, 2] = 1
>>> from scipy.ndimage import generic_laplace
>>> generic_laplace(a, d2)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1., -4.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
```

To demonstrate the use of the *extra_arguments* argument, we could do

```
>>> def d2(input, axis, output, mode, cval, weights):
...     return correlate1d(input, weights, axis, output, mode, cval, 0,)
```

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```
...
>>> a = np.zeros((5, 5))
>>> a[2, 2] = 1
>>> generic_laplace(a, d2, extra_arguments = ([1, -2, 1],))
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1., -4.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
```

or

```
>>> generic_laplace(a, d2, extra_keywords = {'weights': [1, -2, 1]})
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1., -4.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
```

The following two functions are implemented using *generic_laplace* by providing appropriate functions for the second-derivative function:

- The function *laplace* calculates the Laplace using discrete differentiation for the second derivative (i.e., convolution with `[1, -2, 1]`).
- The function *gaussian_laplace* calculates the Laplace filter using *gaussian_filter* to calculate the second derivatives. The standard deviations of the Gaussian filter along each axis are passed through the parameter *sigma* as a sequence or numbers. If *sigma* is not a sequence but a single number, the standard deviation of the filter is equal along all directions.

The gradient magnitude is defined as the square root of the sum of the squares of the gradients in all directions. Similar to the generic Laplace function, there is a *generic_gradient_magnitude* function that calculates the gradient magnitude of an array.

- The function *generic_gradient_magnitude* calculates a gradient magnitude using the function passed through `derivative` to calculate first derivatives. The function `derivative` should have the following signature

```
derivative(input, axis, output, mode, cval, *extra_arguments, **extra_
↪keywords)
```

  It should calculate the derivative along the dimension *axis*. If *output* is not `None`, it should use that for the output and return `None`, otherwise it should return the result. *mode*, *cval* have the usual meaning.

  The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and a dictionary of named arguments that are passed to *derivative* at each call.

  For example, the *sobel* function fits the required signature

```
>>> a = np.zeros((5, 5))
>>> a[2, 2] = 1
>>> from scipy.ndimage import sobel, generic_gradient_magnitude
>>> generic_gradient_magnitude(a, sobel)
array([[ 0.        ,  0.        ,  0.        ,  0.        ,  0.        ],
       [ 0.        ,  1.41421356,  2.        ,  1.41421356,  0.        ],
```

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```
       [ 0.        ,  2.        ,  0.        ,  2.        ,  0.        ],
       [ 0.        ,  1.41421356,  2.        ,  1.41421356,  0.        ],
       [ 0.        ,  0.        ,  0.        ,  0.        ,  0.        ]])
```

See the documentation of *generic_laplace* for examples of using the *extra_arguments* and *extra_keywords* arguments.

The *sobel* and *prewitt* functions fit the required signature and can, therefore, be used directly with *generic_gradient_magnitude*.

- The function *gaussian_gradient_magnitude* calculates the gradient magnitude using *gaussian_filter* to calculate the first derivatives. The standard deviations of the Gaussian filter along each axis are passed through the parameter *sigma* as a sequence or numbers. If *sigma* is not a sequence but a single number, the standard deviation of the filter is equal along all directions.

Generic filter functions

To implement filter functions, generic functions can be used that accept a callable object that implements the filtering operation. The iteration over the input and output arrays is handled by these generic functions, along with such details as the implementation of the boundary conditions. Only a callable object implementing a callback function that does the actual filtering work must be provided. The callback function can also be written in C and passed using a `PyCapsule` (see *Extending scipy.ndimage in C* for more information).

- The *generic_filter1d* function implements a generic 1-D filter function, where the actual filtering operation must be supplied as a python function (or other callable object). The *generic_filter1d* function iterates over the lines of an array and calls `function` at each line. The arguments that are passed to `function` are 1-D arrays of the `numpy.float64` type. The first contains the values of the current line. It is extended at the beginning and the end, according to the *filter_size* and *origin* arguments. The second array should be modified in-place to provide the output values of the line. For example, consider a correlation along one dimension:

```
>>> a = np.arange(12).reshape(3,4)
>>> correlate1d(a, [1, 2, 3])
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

The same operation can be implemented using *generic_filter1d*, as follows:

```
>>> def fnc(iline, oline):
...     oline[...] = iline[:-2] + 2 * iline[1:-1] + 3 * iline[2:]
...
>>> from scipy.ndimage import generic_filter1d
>>> generic_filter1d(a, fnc, 3)
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

Here, the origin of the kernel was (by default) assumed to be in the middle of the filter of length 3. Therefore, each input line had been extended by one value at the beginning and at the end, before the function was called.

Optionally, extra arguments can be defined and passed to the filter function. The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and/or a dictionary of named arguments that are passed to derivative at each call. For example, we can pass the parameters of our filter as an argument

```
>>> def fnc(iline, oline, a, b):
...     oline[...] = iline[:-2] + a * iline[1:-1] + b * iline[2:]
...
>>> generic_filter1d(a, fnc, 3, extra_arguments = (2, 3))
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

or

```
>>> generic_filter1d(a, fnc, 3, extra_keywords = {'a':2, 'b':3})
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

- The *generic_filter* function implements a generic filter function, where the actual filtering operation must be supplied as a python function (or other callable object). The *generic_filter* function iterates over the array and calls `function` at each element. The argument of `function` is a 1-D array of the `numpy.float64` type that contains the values around the current element that are within the footprint of the filter. The function should return a single value that can be converted to a double precision number. For example, consider a correlation:

```
>>> a = np.arange(12).reshape(3,4)
>>> correlate(a, [[1, 0], [0, 3]])
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

The same operation can be implemented using *generic_filter*, as follows:

```
>>> def fnc(buffer):
...     return (buffer * np.array([1, 3])).sum()
...
>>> from scipy.ndimage import generic_filter
>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]])
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

Here, a kernel footprint was specified that contains only two elements. Therefore, the filter function receives a buffer of length equal to two, which was multiplied with the proper weights and the result summed.

When calling *generic_filter*, either the sizes of a rectangular kernel or the footprint of the kernel must be provided. The *size* parameter, if provided, must be a sequence of sizes or a single number, in which case the size of the filter is assumed to be equal along each axis. The *footprint*, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

Optionally, extra arguments can be defined and passed to the filter function. The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and/or a dictionary of named arguments that are passed to derivative at each call. For example, we can pass the parameters of our filter as an argument

```
>>> def fnc(buffer, weights):
...     weights = np.asarray(weights)
...     return (buffer * weights).sum()
...
```

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```
>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]], extra_arguments␣
↪= ([1, 3],))
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

or

```
>>> generic_filter(a, fnc, footprint = [[1, 0], [0, 1]], extra_keywords= {
↪'weights': [1, 3]})
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

These functions iterate over the lines or elements starting at the last axis, i.e., the last index changes the fastest. This order of iteration is guaranteed for the case that it is important to adapt the filter depending on spatial location. Here is an example of using a class that implements the filter and keeps track of the current coordinates while iterating. It performs the same filter operation as described above for *generic_filter*, but additionally prints the current coordinates:

```
>>> a = np.arange(12).reshape(3,4)
>>>
>>> class fnc_class:
...     def __init__(self, shape):
...         # store the shape:
...         self.shape = shape
...         # initialize the coordinates:
...         self.coordinates = [0] * len(shape)
...
...     def filter(self, buffer):
...         result = (buffer * np.array([1, 3])).sum()
...         print(self.coordinates)
...         # calculate the next coordinates:
...         axes = list(range(len(self.shape)))
...         axes.reverse()
...         for jj in axes:
...             if self.coordinates[jj] < self.shape[jj] - 1:
...                 self.coordinates[jj] += 1
...                 break
...             else:
...                 self.coordinates[jj] = 0
...         return result
...
>>> fnc = fnc_class(shape = (3,4))
>>> generic_filter(a, fnc.filter, footprint = [[1, 0], [0, 1]])
[0, 0]
[0, 1]
[0, 2]
[0, 3]
[1, 0]
[1, 1]
[1, 2]
[1, 3]
```

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```
[2, 0]
[2, 1]
[2, 2]
[2, 3]
array([[ 0,  3,  7, 11],
       [12, 15, 19, 23],
       [28, 31, 35, 39]])
```

For the *generic_filter1d* function, the same approach works, except that this function does not iterate over the axis that is being filtered. The example for *generic_filter1d* then becomes this:

```
>>> a = np.arange(12).reshape(3,4)
>>>
>>> class fnc1d_class:
...     def __init__(self, shape, axis = -1):
...         # store the filter axis:
...         self.axis = axis
...         # store the shape:
...         self.shape = shape
...         # initialize the coordinates:
...         self.coordinates = [0] * len(shape)
...
...     def filter(self, iline, oline):
...         oline[...] = iline[:-2] + 2 * iline[1:-1] + 3 * iline[2:]
...         print(self.coordinates)
...         # calculate the next coordinates:
...         axes = list(range(len(self.shape)))
...         # skip the filter axis:
...         del axes[self.axis]
...         axes.reverse()
...         for jj in axes:
...             if self.coordinates[jj] < self.shape[jj] - 1:
...                 self.coordinates[jj] += 1
...                 break
...             else:
...                 self.coordinates[jj] = 0
...
>>> fnc = fnc1d_class(shape = (3,4))
>>> generic_filter1d(a, fnc.filter, 3)
[0, 0]
[1, 0]
[2, 0]
array([[ 3,  8, 14, 17],
       [27, 32, 38, 41],
       [51, 56, 62, 65]])
```

Fourier domain filters

The functions described in this section perform filtering operations in the Fourier domain. Thus, the input array of such a function should be compatible with an inverse Fourier transform function, such as the functions from the `numpy.fft` module. We, therefore, have to deal with arrays that may be the result of a real or a complex Fourier transform. In the case of a real Fourier transform, only half of the of the symmetric complex transform is stored. Additionally, it needs to be known what the length of the axis was that was transformed by the real fft. The functions described here provide a parameter *n* that, in the case of a real transform, must be equal to the length of the real transform axis before transformation. If this parameter is less than zero, it is assumed that the input array was the result of a complex Fourier transform. The parameter *axis* can be used to indicate along which axis the real transform was executed.

- The *fourier_shift* function multiplies the input array with the multidimensional Fourier transform of a shift operation for the given shift. The *shift* parameter is a sequence of shifts for each dimension or a single value for all dimensions.
- The *fourier_gaussian* function multiplies the input array with the multidimensional Fourier transform of a Gaussian filter with given standard deviations *sigma*. The *sigma* parameter is a sequence of values for each dimension or a single value for all dimensions.
- The *fourier_uniform* function multiplies the input array with the multidimensional Fourier transform of a uniform filter with given sizes *size*. The *size* parameter is a sequence of values for each dimension or a single value for all dimensions.
- The *fourier_ellipsoid* function multiplies the input array with the multidimensional Fourier transform of an elliptically-shaped filter with given sizes *size*. The *size* parameter is a sequence of values for each dimension or a single value for all dimensions. This function is only implemented for dimensions 1, 2, and 3.

2.13.4 Interpolation functions

This section describes various interpolation functions that are based on B-spline theory. A good introduction to B-splines can be found in[1] with detailed algorithms for image interpolation given in[5].

Spline pre-filters

Interpolation using splines of an order larger than 1 requires a pre-filtering step. The interpolation functions described in section *Interpolation functions* apply pre-filtering by calling *spline_filter*, but they can be instructed not to do this by setting the *prefilter* keyword equal to False. This is useful if more than one interpolation operation is done on the same array. In this case, it is more efficient to do the pre-filtering only once and use a pre-filtered array as the input of the interpolation functions. The following two functions implement the pre-filtering:

- The *spline_filter1d* function calculates a 1-D spline filter along the given axis. An output array can optionally be provided. The order of the spline must be larger than 1 and less than 6.
- The *spline_filter* function calculates a multidimensional spline filter.

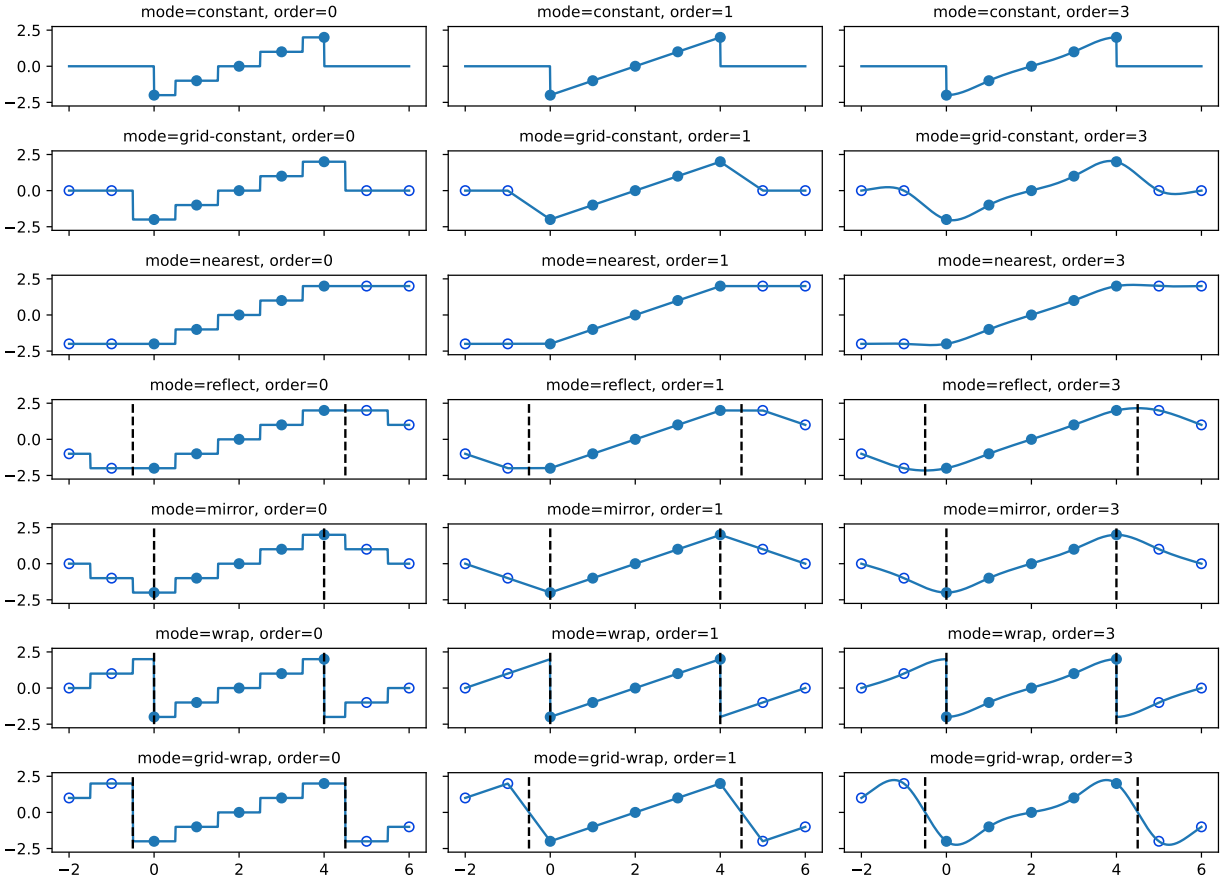
> **Note:** The multidimensional filter is implemented as a sequence of 1-D spline filters. The intermediate arrays are stored in the same data type as the output. Therefore, if an output with a limited precision is requested, the results may be imprecise because intermediate results may be stored with insufficient precision. This can be prevented by specifying a output type of high precision.

[1] M. Unser, "Splines: A Perfect Fit for Signal and Image Processing," IEEE Signal Processing Magazine, vol. 16, no. 6, pp. 22-38, November 1999.

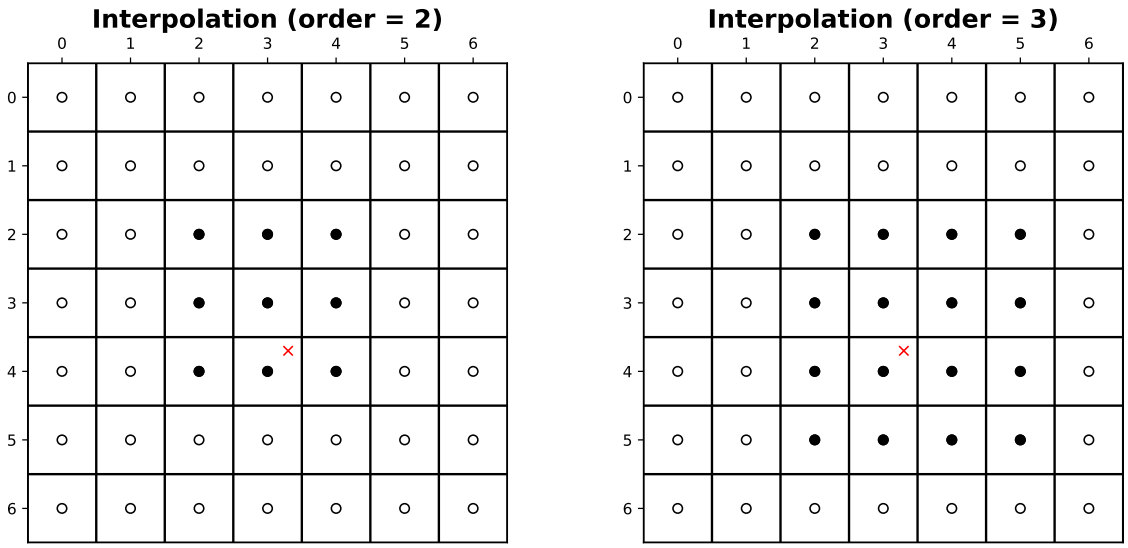
[5] T. Briand and P. Monasse, "Theory and Practice of Image B-Spline Interpolation", Image Processing On Line, 8, pp. 99–141, 2018. https://doi.org/10.5201/ipol.2018.221

Interpolation boundary handling

The interpolation functions all employ spline interpolation to effect some type of geometric transformation of the input array. This requires a mapping of the output coordinates to the input coordinates, and therefore, the possibility arises that input values outside the boundaries may be needed. This problem is solved in the same way as described in *Filter functions* for the multidimensional filter functions. Therefore, these functions all support a *mode* parameter that determines how the boundaries are handled, and a *cval* parameter that gives a constant value in case that the 'constant' mode is used. The behavior of all modes, including at non-integer locations is illustrated below. Note the boundaries are not handled the same for all modes; *reflect* (aka *grid-mirror*) and *grid-wrap* involve symmetry or repetition about a point that is half way between image samples (dashed vertical lines) while modes *mirror* and *wrap* treat the image as if it's extent ends exactly at the first and last sample point rather than 0.5 samples past it.



The coordinates of image samples fall on integer sampling locations in the range from 0 to `shape[i] - 1` along each axis, `i`. The figure below illustrates the interpolation of a point at location `(3.7, 3.3)` within an image of shape `(7, 7)`. For an interpolation of order `n`, `n + 1` samples are involved along each axis. The filled circles illustrate the sampling locations involved in the interpolation of the value at the location of the red x.



Interpolation functions

- The *geometric_transform* function applies an arbitrary geometric transform to the input. The given *mapping* function is called at each point in the output to find the corresponding coordinates in the input. *mapping* must be a callable object that accepts a tuple of length equal to the output array rank and returns the corresponding input coordinates as a tuple of length equal to the input array rank. The output shape and output type can optionally be provided. If not given, they are equal to the input shape and type.

  For example:

```
>>> a = np.arange(12).reshape(4,3).astype(np.float64)
>>> def shift_func(output_coordinates):
...     return (output_coordinates[0] - 0.5, output_coordinates[1] - 0.5)
...
>>> from scipy.ndimage import geometric_transform
>>> geometric_transform(a, shift_func)
array([[ 0.    ,  0.    ,  0.    ],
       [ 0.    ,  1.3625,  2.7375],
       [ 0.    ,  4.8125,  6.1875],
       [ 0.    ,  8.2625,  9.6375]])
```

  Optionally, extra arguments can be defined and passed to the filter function. The *extra_arguments* and *extra_keywords* arguments can be used to pass a tuple of extra arguments and/or a dictionary of named arguments that are passed to derivative at each call. For example, we can pass the shifts in our example as arguments

```
>>> def shift_func(output_coordinates, s0, s1):
...     return (output_coordinates[0] - s0, output_coordinates[1] - s1)
...
>>> geometric_transform(a, shift_func, extra_arguments = (0.5, 0.5))
array([[ 0.    ,  0.    ,  0.    ],
       [ 0.    ,  1.3625,  2.7375],
       [ 0.    ,  4.8125,  6.1875],
       [ 0.    ,  8.2625,  9.6375]])
```

  or

```
>>> geometric_transform(a, shift_func, extra_keywords = {'s0': 0.5, 's1':␣
↪0.5})
array([[ 0.    ,  0.    ,  0.    ],
       [ 0.    ,  1.3625,  2.7375],
       [ 0.    ,  4.8125,  6.1875],
       [ 0.    ,  8.2625,  9.6375]])
```

Note: The mapping function can also be written in C and passed using a *scipy.LowLevelCallable*. See *Extending scipy.ndimage in C* for more information.

- The function *map_coordinates* applies an arbitrary coordinate transformation using the given array of coordinates. The shape of the output is derived from that of the coordinate array by dropping the first axis. The parameter *coordinates* is used to find for each point in the output the corresponding coordinates in the input. The values of *coordinates* along the first axis are the coordinates in the input array at which the output value is found. (See also the numarray *coordinates* function.) Since the coordinates may be non- integer coordinates, the value of the input at these coordinates is determined by spline interpolation of the requested order.

  Here is an example that interpolates a 2D array at `(0.5, 0.5)` and `(1, 2)`:

```
>>> a = np.arange(12).reshape(4,3).astype(np.float64)
>>> a
array([[  0.,   1.,   2.],
       [  3.,   4.,   5.],
       [  6.,   7.,   8.],
       [  9.,  10.,  11.]])
>>> from scipy.ndimage import map_coordinates
>>> map_coordinates(a, [[0.5, 2], [0.5, 1]])
array([ 1.3625,  7.])
```

- The *affine_transform* function applies an affine transformation to the input array. The given transformation *matrix* and *offset* are used to find for each point in the output the corresponding coordinates in the input. The value of the input at the calculated coordinates is determined by spline interpolation of the requested order. The transformation *matrix* must be 2-D or can also be given as a 1-D sequence or array. In the latter case, it is assumed that the matrix is diagonal. A more efficient interpolation algorithm is then applied that exploits the separability of the problem. The output shape and output type can optionally be provided. If not given, they are equal to the input shape and type.
- The *shift* function returns a shifted version of the input, using spline interpolation of the requested *order*.
- The *zoom* function returns a rescaled version of the input, using spline interpolation of the requested *order*.
- The *rotate* function returns the input array rotated in the plane defined by the two axes given by the parameter *axes*, using spline interpolation of the requested *order*. The angle must be given in degrees. If *reshape* is true, then the size of the output array is adapted to contain the rotated input.

2.13.5 Morphology

Binary morphology

- The *generate_binary_structure* functions generates a binary structuring element for use in binary morphology operations. The *rank* of the structure must be provided. The size of the structure that is returned is equal to three in each direction. The value of each element is equal to one if the square of the Euclidean distance from the element to the center is less than or equal to *connectivity*. For instance, 2-D 4-connected and 8-connected structures are generated as follows:

```
>>> from scipy.ndimage import generate_binary_structure
>>> generate_binary_structure(2, 1)
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> generate_binary_structure(2, 2)
array([[ True,  True,  True],
       [ True,  True,  True],
       [ True,  True,  True]], dtype=bool)
```

Most binary morphology functions can be expressed in terms of the basic operations erosion and dilation.

- The *binary_erosion* function implements binary erosion of arrays of arbitrary rank with the given structuring element. The origin parameter controls the placement of the structuring element, as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using *generate_binary_structure*. The *border_value* parameter gives the value of the array outside boundaries. The erosion is repeated *iterations* times. If *iterations* is less than one, the erosion is repeated until the result does not change anymore. If a *mask* array is given, only those elements with a true value at the corresponding mask element are modified at each iteration.
- The *binary_dilation* function implements binary dilation of arrays of arbitrary rank with the given structuring element. The origin parameter controls the placement of the structuring element, as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using *generate_binary_structure*. The *border_value* parameter gives the value of the array outside boundaries. The dilation is repeated *iterations* times. If *iterations* is less than one, the dilation is repeated until the result does not change anymore. If a *mask* array is given, only those elements with a true value at the corresponding mask element are modified at each iteration.

Here is an example of using *binary_dilation* to find all elements that touch the border, by repeatedly dilating an empty array from the border using the data array as the mask:

```
>>> struct = np.array([[0, 1, 0], [1, 1, 1], [0, 1, 0]])
>>> a = np.array([[1,0,0,0,0], [1,1,0,1,0], [0,0,1,1,0], [0,0,0,0,0]])
>>> a
array([[1, 0, 0, 0, 0],
       [1, 1, 0, 1, 0],
       [0, 0, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> from scipy.ndimage import binary_dilation
>>> binary_dilation(np.zeros(a.shape), struct, -1, a, border_value=1)
array([[ True, False, False, False, False],
       [ True,  True, False, False, False],
       [False, False, False, False, False],
       [False, False, False, False, False]], dtype=bool)
```

The *binary_erosion* and *binary_dilation* functions both have an *iterations* parameter, which allows the erosion or dilation to be repeated a number of times. Repeating an erosion or a dilation with a given structure *n* times is equivalent to an erosion or a dilation with a structure that is *n-1* times dilated with itself. A function is provided that allows the calculation of a structure that is dilated a number of times with itself:

- The *iterate_structure* function returns a structure by dilation of the input structure *iteration* - 1 times with itself.

  For instance:

```
>>> struct = generate_binary_structure(2, 1)
>>> struct
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> from scipy.ndimage import iterate_structure
>>> iterate_structure(struct, 2)
array([[False, False,  True, False, False],
       [False,  True,  True,  True, False],
       [ True,  True,  True,  True,  True],
       [False,  True,  True,  True, False],
       [False, False,  True, False, False]], dtype=bool)

If the origin of the original structure is equal to 0, then it is
also equal to 0 for the iterated structure. If not, the origin
must also be adapted if the equivalent of the *iterations*
erosions or dilations must be achieved with the iterated
structure. The adapted origin is simply obtained by multiplying
with the number of iterations. For convenience, the
:func:`iterate_structure` also returns the adapted origin if the
*origin* parameter is not ``None``:

.. code:: python

   >>> iterate_structure(struct, 2, -1)
   (array([[False, False,  True, False, False],
           [False,  True,  True,  True, False],
           [ True,  True,  True,  True,  True],
           [False,  True,  True,  True, False],
           [False, False,  True, False, False]], dtype=bool), [-2, -2])
```

Other morphology operations can be defined in terms of erosion and dilation. The following functions provide a few of these operations for convenience:

- The *binary_opening* function implements binary opening of arrays of arbitrary rank with the given structuring element. Binary opening is equivalent to a binary erosion followed by a binary dilation with the same structuring element. The origin parameter controls the placement of the structuring element, as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using *generate_binary_structure*. The *iterations* parameter gives the number of erosions that is performed followed by the same number of dilations.
- The *binary_closing* function implements binary closing of arrays of arbitrary rank with the given structuring element. Binary closing is equivalent to a binary dilation followed by a binary erosion with the same structuring element. The origin parameter controls the placement of the structuring element, as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using *generate_binary_structure*. The *iterations* parameter gives the number of dilations that is performed followed

by the same number of erosions.

- The *binary_fill_holes* function is used to close holes in objects in a binary image, where the structure defines the connectivity of the holes. The origin parameter controls the placement of the structuring element, as described in *Filter functions*. If no structuring element is provided, an element with connectivity equal to one is generated using *generate_binary_structure*.
- The *binary_hit_or_miss* function implements a binary hit-or-miss transform of arrays of arbitrary rank with the given structuring elements. The hit-or-miss transform is calculated by erosion of the input with the first structure, erosion of the logical *not* of the input with the second structure, followed by the logical *and* of these two erosions. The origin parameters control the placement of the structuring elements, as described in *Filter functions*. If *origin2* equals `None`, it is set equal to the *origin1* parameter. If the first structuring element is not provided, a structuring element with connectivity equal to one is generated using *generate_binary_structure*. If *structure2* is not provided, it is set equal to the logical *not* of *structure1*.

Grey-scale morphology

Grey-scale morphology operations are the equivalents of binary morphology operations that operate on arrays with arbitrary values. Below, we describe the grey-scale equivalents of erosion, dilation, opening and closing. These operations are implemented in a similar fashion as the filters described in *Filter functions*, and we refer to this section for the description of filter kernels and footprints, and the handling of array borders. The grey-scale morphology operations optionally take a *structure* parameter that gives the values of the structuring element. If this parameter is not given, the structuring element is assumed to be flat with a value equal to zero. The shape of the structure can optionally be defined by the *footprint* parameter. If this parameter is not given, the structure is assumed to be rectangular, with sizes equal to the dimensions of the *structure* array, or by the *size* parameter if *structure* is not given. The *size* parameter is only used if both *structure* and *footprint* are not given, in which case the structuring element is assumed to be rectangular and flat with the dimensions given by *size*. The *size* parameter, if provided, must be a sequence of sizes or a single number in which case the size of the filter is assumed to be equal along each axis. The *footprint* parameter, if provided, must be an array that defines the shape of the kernel by its non-zero elements.

Similarly to binary erosion and dilation, there are operations for grey-scale erosion and dilation:

- The *grey_erosion* function calculates a multidimensional grey-scale erosion.
- The *grey_dilation* function calculates a multidimensional grey-scale dilation.

Grey-scale opening and closing operations can be defined similarly to their binary counterparts:

- The *grey_opening* function implements grey-scale opening of arrays of arbitrary rank. Grey-scale opening is equivalent to a grey-scale erosion followed by a grey-scale dilation.
- The *grey_closing* function implements grey-scale closing of arrays of arbitrary rank. Grey-scale opening is equivalent to a grey-scale dilation followed by a grey-scale erosion.
- The *morphological_gradient* function implements a grey-scale morphological gradient of arrays of arbitrary rank. The grey-scale morphological gradient is equal to the difference of a grey-scale dilation and a grey-scale erosion.
- The *morphological_laplace* function implements a grey-scale morphological laplace of arrays of arbitrary rank. The grey-scale morphological laplace is equal to the sum of a grey-scale dilation and a grey-scale erosion minus twice the input.
- The *white_tophat* function implements a white top-hat filter of arrays of arbitrary rank. The white top-hat is equal to the difference of the input and a grey-scale opening.
- The *black_tophat* function implements a black top-hat filter of arrays of arbitrary rank. The black top-hat is equal to the difference of a grey-scale closing and the input.

2.13.6 Distance transforms

Distance transforms are used to calculate the minimum distance from each element of an object to the background. The following functions implement distance transforms for three different distance metrics: Euclidean, city block, and chessboard distances.

- The function *distance_transform_cdt* uses a chamfer type algorithm to calculate the distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest distance to the background (all non-object elements). The structure determines the type of chamfering that is done. If the structure is equal to 'cityblock', a structure is generated using *generate_binary_structure* with a squared distance equal to 1. If the structure is equal to 'chessboard', a structure is generated using *generate_binary_structure* with a squared distance equal to the rank of the array. These choices correspond to the common interpretations of the city block and the chessboard distance metrics in two dimensions.

  In addition to the distance transform, the feature transform can be calculated. In this case, the index of the closest background element is returned along the first axis of the result. The *return_distances*, and *return_indices* flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

  The *distances* and *indices* arguments can be used to give optional output arrays that must be of the correct size and type (both `numpy.int32`). The basics of the algorithm used to implement this function are described in[2].

- The function *distance_transform_edt* calculates the exact Euclidean distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest Euclidean distance to the background (all non-object elements).

  In addition to the distance transform, the feature transform can be calculated. In this case, the index of the closest background element is returned along the first axis of the result. The *return_distances* and *return_indices* flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

  Optionally, the sampling along each axis can be given by the *sampling* parameter, which should be a sequence of length equal to the input rank, or a single number in which the sampling is assumed to be equal along all axes.

  The *distances* and *indices* arguments can be used to give optional output arrays that must be of the correct size and type (`numpy.float64` and `numpy.int32`).The algorithm used to implement this function is described in[3].

- The function *distance_transform_bf* uses a brute-force algorithm to calculate the distance transform of the input, by replacing each object element (defined by values larger than zero) with the shortest distance to the background (all non-object elements). The metric must be one of "euclidean", "cityblock", or "chessboard".

  In addition to the distance transform, the feature transform can be calculated. In this case, the index of the closest background element is returned along the first axis of the result. The *return_distances* and *return_indices* flags can be used to indicate if the distance transform, the feature transform, or both must be returned.

  Optionally, the sampling along each axis can be given by the *sampling* parameter, which should be a sequence of length equal to the input rank, or a single number in which the sampling is assumed to be equal along all axes. This parameter is only used in the case of the Euclidean distance transform.

  The *distances* and *indices* arguments can be used to give optional output arrays that must be of the correct size and type (`numpy.float64` and `numpy.int32`).

Note: This function uses a slow brute-force algorithm, the function *distance_transform_cdt* can be used to more efficiently calculate city block and chessboard distance transforms. The function *distance_transform_edt* can be used to more efficiently calculate the exact Euclidean distance transform.

---

[2] G. Borgefors, "Distance transformations in arbitrary dimensions.", Computer Vision, Graphics, and Image Processing, 27:321-345, 1984.

[3] C. R. Maurer, Jr., R. Qi, and V. Raghavan, "A linear time algorithm for computing exact euclidean distance transforms of binary images in arbitrary dimensions." IEEE Trans. PAMI 25, 265-270, 2003.

2.13.7 Segmentation and labeling

Segmentation is the process of separating objects of interest from the background. The most simple approach is, probably, intensity thresholding, which is easily done with `numpy` functions:

```
>>> a = np.array([[1,2,2,1,1,0],
...               [0,2,3,1,2,0],
...               [1,1,1,3,3,2],
...               [1,1,1,1,2,1]])
>>> np.where(a > 1, 1, 0)
array([[0, 1, 1, 0, 0, 0],
       [0, 1, 1, 0, 1, 0],
       [0, 0, 0, 1, 1, 1],
       [0, 0, 0, 0, 1, 0]])
```

The result is a binary image, in which the individual objects still need to be identified and labeled. The function *label* generates an array where each object is assigned a unique number:

- The *label* function generates an array where the objects in the input are labeled with an integer index. It returns a tuple consisting of the array of object labels and the number of objects found, unless the *output* parameter is given, in which case only the number of objects is returned. The connectivity of the objects is defined by a structuring element. For instance, in 2D using a 4-connected structuring element gives:

```
>>> a = np.array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,
↪0]])
>>> s = [[0, 1, 0], [1,1,1], [0,1,0]]
>>> from scipy.ndimage import label
>>> label(a, s)
(array([[0, 1, 1, 0, 0, 0],
        [0, 1, 1, 0, 2, 0],
        [0, 0, 0, 2, 2, 2],
        [0, 0, 0, 0, 2, 0]]), 2)
```

  These two objects are not connected because there is no way in which we can place the structuring element, such that it overlaps with both objects. However, an 8-connected structuring element results in only a single object:

```
>>> a = np.array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,
↪0]])
>>> s = [[1,1,1], [1,1,1], [1,1,1]]
>>> label(a, s)[0]
array([[0, 1, 1, 0, 0, 0],
       [0, 1, 1, 0, 1, 0],
       [0, 0, 0, 1, 1, 1],
       [0, 0, 0, 0, 1, 0]])
```

  If no structuring element is provided, one is generated by calling *generate_binary_structure* (see *Binary morphology*) using a connectivity of one (which in 2D is the 4-connected structure of the first example). The input can be of any type, any value not equal to zero is taken to be part of an object. This is useful if you need to 're-label' an array of object indices, for instance, after removing unwanted objects. Just apply the label function again to the index array. For instance:

```
>>> l, n = label([1, 0, 1, 0, 1])
>>> l
array([1, 0, 2, 0, 3])
```

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```
>>> l = np.where(l != 2, l, 0)
>>> l
array([1, 0, 0, 0, 3])
>>> label(l)[0]
array([1, 0, 0, 0, 2])
```

Note: The structuring element used by *label* is assumed to be symmetric.

There is a large number of other approaches for segmentation, for instance, from an estimation of the borders of the objects that can be obtained by derivative filters. One such approach is watershed segmentation. The function *watershed_ift* generates an array where each object is assigned a unique label, from an array that localizes the object borders, generated, for instance, by a gradient magnitude filter. It uses an array containing initial markers for the objects:

- The *watershed_ift* function applies a watershed from markers algorithm, using Image Foresting Transform, as described in[4].
- The inputs of this function are the array to which the transform is applied, and an array of markers that designate the objects by a unique label, where any non-zero value is a marker. For instance:

```
>>> input = np.array([[0, 0, 0, 0, 0, 0, 0],
...                   [0, 1, 1, 1, 1, 1, 0],
...                   [0, 1, 0, 0, 0, 1, 0],
...                   [0, 1, 0, 0, 0, 1, 0],
...                   [0, 1, 0, 0, 0, 1, 0],
...                   [0, 1, 1, 1, 1, 1, 0],
...                   [0, 0, 0, 0, 0, 0, 0]], np.uint8)
>>> markers = np.array([[1, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 2, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0]], np.int8)
>>> from scipy.ndimage import watershed_ift
>>> watershed_ift(input, markers)
array([[1, 1, 1, 1, 1, 1, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 2, 2, 2, 2, 2, 1],
       [1, 2, 2, 2, 2, 2, 1],
       [1, 2, 2, 2, 2, 2, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 1, 1, 1, 1, 1, 1]], dtype=int8)
```

Here, two markers were used to designate an object (*marker* = 2) and the background (*marker* = 1). The order in which these are processed is arbitrary: moving the marker for the background to the lower-right corner of the array yields a different result:

```
>>> markers = np.array([[0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
```

(continues on next page)

[4] A. X. Falcão, J. Stolfi, and R. A. Lotufo. "The image foresting transform: Theory, algorithms, and applications." IEEE Trans. PAMI 26, 19-29. 2004.

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```
...                       [0, 0, 0, 0, 0, 0, 0],
...                       [0, 0, 0, 2, 0, 0, 0],
...                       [0, 0, 0, 0, 0, 0, 0],
...                       [0, 0, 0, 0, 0, 0, 0],
...                       [0, 0, 0, 0, 0, 0, 1]], np.int8)
>>> watershed_ift(input, markers)
array([[1, 1, 1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1, 1, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 1, 2, 2, 2, 1, 1],
       [1, 1, 1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1, 1, 1]], dtype=int8)
```

The result is that the object (*marker* = 2) is smaller because the second marker was processed earlier. This may not be the desired effect if the first marker was supposed to designate a background object. Therefore, *watershed_ift* treats markers with a negative value explicitly as background markers and processes them after the normal markers. For instance, replacing the first marker by a negative marker gives a result similar to the first example:

```
>>> markers = np.array([[0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 2, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, 0],
...                     [0, 0, 0, 0, 0, 0, -1]], np.int8)
>>> watershed_ift(input, markers)
array([[-1, -1, -1, -1, -1, -1, -1],
       [-1, -1,  2,  2,  2, -1, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1, -1,  2,  2,  2, -1, -1],
       [-1, -1, -1, -1, -1, -1, -1]], dtype=int8)
```

The connectivity of the objects is defined by a structuring element. If no structuring element is provided, one is generated by calling *generate_binary_structure* (see *Binary morphology*) using a connectivity of one (which in 2D is a 4-connected structure.) For example, using an 8-connected structure with the last example yields a different object:

```
>>> watershed_ift(input, markers,
...                structure = [[1,1,1], [1,1,1], [1,1,1]])
array([[-1, -1, -1, -1, -1, -1, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1,  2,  2,  2,  2,  2, -1],
       [-1, -1, -1, -1, -1, -1, -1]], dtype=int8)
```

Note: The implementation of *watershed_ift* limits the data types of the input to `numpy.uint8` and

numpy.uint16.

2.13.8 Object measurements

Given an array of labeled objects, the properties of the individual objects can be measured. The *find_objects* function can be used to generate a list of slices that for each object, give the smallest sub-array that fully contains the object:

- The *find_objects* function finds all objects in a labeled array and returns a list of slices that correspond to the smallest regions in the array that contains the object.

  For instance:

```
>>> a = np.array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,
↪0]])
>>> l, n = label(a)
>>> from scipy.ndimage import find_objects
>>> f = find_objects(l)
>>> a[f[0]]
array([[1, 1],
       [1, 1]])
>>> a[f[1]]
array([[0, 1, 0],
       [1, 1, 1],
       [0, 1, 0]])
```

  The function *find_objects* returns slices for all objects, unless the *max_label* parameter is larger then zero, in which case only the first *max_label* objects are returned. If an index is missing in the *label* array, `None` is return instead of a slice. For example:

```
>>> from scipy.ndimage import find_objects
>>> find_objects([1, 0, 3, 4], max_label = 3)
[(slice(0, 1, None),), None, (slice(2, 3, None),)]
```

The list of slices generated by *find_objects* is useful to find the position and dimensions of the objects in the array, but can also be used to perform measurements on the individual objects. Say, we want to find the sum of the intensities of an object in image:

```
>>> image = np.arange(4 * 6).reshape(4, 6)
>>> mask = np.array([[0,1,1,0,0,0],[0,1,1,0,1,0],[0,0,0,1,1,1],[0,0,0,0,1,0]])
>>> labels = label(mask)[0]
>>> slices = find_objects(labels)
```

Then we can calculate the sum of the elements in the second object:

```
>>> np.where(labels[slices[1]] == 2, image[slices[1]], 0).sum()
80
```

That is, however, not particularly efficient and may also be more complicated for other types of measurements. Therefore, a few measurements functions are defined that accept the array of object labels and the index of the object to be measured. For instance, calculating the sum of the intensities can be done by:

```
>>> from scipy.ndimage import sum as ndi_sum
>>> ndi_sum(image, labels, 2)
80
```

For large arrays and small objects, it is more efficient to call the measurement functions after slicing the array:

```
>>> ndi_sum(image[slices[1]], labels[slices[1]], 2)
80
```

Alternatively, we can do the measurements for a number of labels with a single function call, returning a list of results. For instance, to measure the sum of the values of the background and the second object in our example, we give a list of labels:

```
>>> ndi_sum(image, labels, [0, 2])
array([178.0, 80.0])
```

The measurement functions described below all support the *index* parameter to indicate which object(s) should be measured. The default value of *index* is `None`. This indicates that all elements where the label is larger than zero should be treated as a single object and measured. Thus, in this case the *labels* array is treated as a mask defined by the elements that are larger than zero. If *index* is a number or a sequence of numbers it gives the labels of the objects that are measured. If *index* is a sequence, a list of the results is returned. Functions that return more than one result return their result as a tuple if *index* is a single number, or as a tuple of lists if *index* is a sequence.

- The `sum` function calculates the sum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *mean* function calculates the mean of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *variance* function calculates the variance of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *standard_deviation* function calculates the standard deviation of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *minimum* function calculates the minimum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *maximum* function calculates the maximum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *minimum_position* function calculates the position of the minimum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *maximum_position* function calculates the position of the maximum of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *extrema* function calculates the minimum, the maximum, and their positions, of the elements of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation. The

result is a tuple giving the minimum, the maximum, the position of the minimum, and the position of the maximum. The result is the same as a tuple formed by the results of the functions *minimum*, *maximum*, *minimum_position*, and *maximum_position* that are described above.

- The *center_of_mass* function calculates the center of mass of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation.
- The *histogram* function calculates a histogram of the object with label(s) given by *index*, using the *labels* array for the object labels. If *index* is `None`, all elements with a non-zero label value are treated as a single object. If *label* is `None`, all elements of *input* are used in the calculation. Histograms are defined by their minimum (*min*), maximum (*max*), and the number of bins (*bins*). They are returned as 1-D arrays of type `numpy.int32`.

2.13.9 Extending `scipy.ndimage` in C

A few functions in *scipy.ndimage* take a callback argument. This can be either a python function or a *scipy.LowLevelCallable* containing a pointer to a C function. Using a C function will generally be more efficient, since it avoids the overhead of calling a python function on many elements of an array. To use a C function, you must write a C extension that contains the callback function and a Python function that returns a *scipy.LowLevelCallable* containing a pointer to the callback.

An example of a function that supports callbacks is *geometric_transform*, which accepts a callback function that defines a mapping from all output coordinates to corresponding coordinates in the input array. Consider the following python example, which uses *geometric_transform* to implement a shift function.

```
from scipy import ndimage

def transform(output_coordinates, shift):
    input_coordinates = output_coordinates[0] - shift, output_coordinates[1] -
↪ shift
    return input_coordinates

im = np.arange(12).reshape(4, 3).astype(np.float64)
shift = 0.5
print(ndimage.geometric_transform(im, transform, extra_arguments=(shift,)))
```

We can also implement the callback function with the following C code:

```
/* example.c */

#include <Python.h>
#include <numpy/npy_common.h>

static int
_transform(npy_intp *output_coordinates, double *input_coordinates,
           int output_rank, int input_rank, void *user_data)
{
    npy_intp i;
    double shift = *(double *)user_data;

    for (i = 0; i < input_rank; i++) {
        input_coordinates[i] = output_coordinates[i] - shift;
    }
    return 1;
```

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```
}

static char *transform_signature = "int (npy_intp *, double *, int, int, void␣
↪*)";

static PyObject *
py_get_transform(PyObject *obj, PyObject *args)
{
    if (!PyArg_ParseTuple(args, "")) return NULL;
    return PyCapsule_New(_transform, transform_signature, NULL);
}

static PyMethodDef ExampleMethods[] = {
    {"get_transform", (PyCFunction)py_get_transform, METH_VARARGS, ""},
    {NULL, NULL, 0, NULL}
};

/* Initialize the module */
static struct PyModuleDef example = {
    PyModuleDef_HEAD_INIT,
    "example",
    NULL,
    -1,
    ExampleMethods,
    NULL,
    NULL,
    NULL,
    NULL
};

PyMODINIT_FUNC
PyInit_example(void)
{
    return PyModule_Create(&example);
}
```

More information on writing Python extension modules can be found here. If the C code is in the file `example.c`, then it can be compiled with the following `setup.py`,

```
from distutils.core import setup, Extension
import numpy

shift = Extension('example',
                  ['example.c'],
                  include_dirs=[numpy.get_include()]
)

setup(name='example',
      ext_modules=[shift]
)
```

and now running the script

```
import ctypes
import numpy as np
from scipy import ndimage, LowLevelCallable

from example import get_transform

shift = 0.5

user_data = ctypes.c_double(shift)
ptr = ctypes.cast(ctypes.pointer(user_data), ctypes.c_void_p)
callback = LowLevelCallable(get_transform(), ptr)
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))
```

produces the same result as the original python script.

In the C version, `_transform` is the callback function and the parameters `output_coordinates` and `input_coordinates` play the same role as they do in the python version, while `output_rank` and `input_rank` provide the equivalents of `len(output_coordinates)` and `len(input_coordinates)`. The variable `shift` is passed through `user_data` instead of `extra_arguments`. Finally, the C callback function returns an integer status, which is one upon success and zero otherwise.

The function `py_transform` wraps the callback function in a `PyCapsule`. The main steps are:

- Initialize a `PyCapsule`. The first argument is a pointer to the callback function.
- The second argument is the function signature, which must match exactly the one expected by *`ndimage`*.
- Above, we used *`scipy.LowLevelCallable`* to specify `user_data` that we generated with `ctypes`.

  A different approach would be to supply the data in the capsule context, that can be set by *PyCapsule_SetContext* and omit specifying `user_data` in *`scipy.LowLevelCallable`*. However, in this approach we would need to deal with allocation/freeing of the data — freeing the data after the capsule has been destroyed can be done by specifying a non-NULL callback function in the third argument of *PyCapsule_New*.

C callback functions for *`ndimage`* all follow this scheme. The next section lists the *`ndimage`* functions that accept a C callback function and gives the prototype of the function.

See also:

The functions that support low-level callback arguments are:

`generic_filter`, *`generic_filter1d`*, *`geometric_transform`*

Below, we show alternative ways to write the code, using Numba, Cython, ctypes, or cffi instead of writing wrapper code in C.

Numba

Numba provides a way to write low-level functions easily in Python. We can write the above using Numba as:

```
# example.py
import numpy as np
import ctypes
from scipy import ndimage, LowLevelCallable
from numba import cfunc, types, carray
```

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```
@cfunc(types.intc(types.CPointer(types.intp),
                  types.CPointer(types.double),
                  types.intc,
                  types.intc,
                  types.voidptr))
def transform(output_coordinates_ptr, input_coordinates_ptr,
              output_rank, input_rank, user_data):
    input_coordinates = carray(input_coordinates_ptr, (input_rank,))
    output_coordinates = carray(output_coordinates_ptr, (output_rank,))
    shift = carray(user_data, (1,), types.double)[0]

    for i in range(input_rank):
        input_coordinates[i] = output_coordinates[i] - shift

    return 1

shift = 0.5

# Then call the function
user_data = ctypes.c_double(shift)
ptr = ctypes.cast(ctypes.pointer(user_data), ctypes.c_void_p)
callback = LowLevelCallable(transform.ctypes, ptr)

im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))
```

Cython

Functionally the same code as above can be written in Cython with somewhat less boilerplate as follows:

```
# example.pyx

from numpy cimport npy_intp as intp

cdef api int transform(intp *output_coordinates, double *input_coordinates,
                       int output_rank, int input_rank, void *user_data):
    cdef intp i
    cdef double shift = (<double *>user_data)[0]

    for i in range(input_rank):
        input_coordinates[i] = output_coordinates[i] - shift
    return 1
```

```
# script.py

import ctypes
import numpy as np
from scipy import ndimage, LowLevelCallable

import example
```

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```
shift = 0.5

user_data = ctypes.c_double(shift)
ptr = ctypes.cast(ctypes.pointer(user_data), ctypes.c_void_p)
callback = LowLevelCallable.from_cython(example, "transform", ptr)
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))
```

cffi

With cffi, you can interface with a C function residing in a shared library (DLL). First, we need to write the shared library, which we do in C — this example is for Linux/OSX:

```
/*
  example.c
  Needs to be compiled with "gcc -std=c99 -shared -fPIC -o example.so example.
↪c"
  or similar
 */

#include <stdint.h>

int
_transform(intptr_t *output_coordinates, double *input_coordinates,
           int output_rank, int input_rank, void *user_data)
{
    int i;
    double shift = *(double *)user_data;

    for (i = 0; i < input_rank; i++) {
        input_coordinates[i] = output_coordinates[i] - shift;
    }
    return 1;
}
```

The Python code calling the library is:

```
import os
import numpy as np
from scipy import ndimage, LowLevelCallable
import cffi

# Construct the FFI object, and copypaste the function declaration
ffi = cffi.FFI()
ffi.cdef("""
int _transform(intptr_t *output_coordinates, double *input_coordinates,
               int output_rank, int input_rank, void *user_data);
""")

# Open library
lib = ffi.dlopen(os.path.abspath("example.so"))
```

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```
# Do the function call
user_data = ffi.new('double *', 0.5)
callback = LowLevelCallable(lib._transform, user_data)
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))
```

You can find more information in the cffi documentation.

ctypes

With *ctypes*, the C code and the compilation of the so/DLL is as for cffi above. The Python code is different:

```
# script.py

import os
import ctypes
import numpy as np
from scipy import ndimage, LowLevelCallable

lib = ctypes.CDLL(os.path.abspath('example.so'))

shift = 0.5

user_data = ctypes.c_double(shift)
ptr = ctypes.cast(ctypes.pointer(user_data), ctypes.c_void_p)

# Ctypes has no built-in intptr type, so override the signature
# instead of trying to get it via ctypes
callback = LowLevelCallable(lib._transform, ptr,
    "int _transform(intptr_t *, double *, int, int, void *)")

# Perform the call
im = np.arange(12).reshape(4, 3).astype(np.float64)
print(ndimage.geometric_transform(im, callback))
```

You can find more information in the ctypes documentation.

2.13.10 References

2.14 File IO (`scipy.io`)

See also:

NumPy IO routines

2.14.1 MATLAB files

loadmat(file_name[, mdict, appendmat])	Load MATLAB file.
savemat(file_name, mdict[, appendmat, …])	Save a dictionary of names and arrays into a MATLAB-style .mat file.
whosmat(file_name[, appendmat])	List variables inside a MATLAB file.

The basic functions

We'll start by importing *scipy.io* and calling it `sio` for convenience:

```
>>> import scipy.io as sio
```

If you are using IPython, try tab-completing on `sio`. Among the many options, you will find:

```
sio.loadmat
sio.savemat
sio.whosmat
```

These are the high-level functions you will most likely use when working with MATLAB files. You'll also find:

```
sio.matlab
```

This is the package from which `loadmat`, `savemat`, and `whosmat` are imported. Within `sio.matlab`, you will find the `mio` module This module contains the machinery that `loadmat` and `savemat` use. From time to time you may find yourself re-using this machinery.

How do I start?

You may have a `.mat` file that you want to read into SciPy. Or, you want to pass some variables from SciPy / NumPy into MATLAB.

To save us using a MATLAB license, let's start in Octave. Octave has MATLAB-compatible save and load functions. Start Octave (`octave` at the command line for me):

```
octave:1> a = 1:12
a =

   1   2   3   4   5   6   7   8   9  10  11  12

octave:2> a = reshape(a, [1 3 4])
a =

ans(:,:,1) =

   1   2   3

ans(:,:,2) =

   4   5   6

ans(:,:,3) =
```

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```
   7   8   9

ans(:,:,4) =

   10   11   12

octave:3> save -6 octave_a.mat a % MATLAB 6 compatible
octave:4> ls octave_a.mat
octave_a.mat
```

Now, to Python:

```
>>> mat_contents = sio.loadmat('octave_a.mat')
>>> mat_contents
{'a': array([[[  1.,   4.,   7.,  10.],
        [  2.,   5.,   8.,  11.],
        [  3.,   6.,   9.,  12.]]]),
 '__version__': '1.0',
 '__header__': 'MATLAB 5.0 MAT-file, written by
 Octave 3.6.3, 2013-02-17 21:02:11 UTC',
 '__globals__': []}
>>> oct_a = mat_contents['a']
>>> oct_a
array([[[  1.,   4.,   7.,  10.],
        [  2.,   5.,   8.,  11.],
        [  3.,   6.,   9.,  12.]]])
>>> oct_a.shape
(1, 3, 4)
```

Now let's try the other way round:

```
>>> import numpy as np
>>> vect = np.arange(10)
>>> vect.shape
(10,)
>>> sio.savemat('np_vector.mat', {'vect':vect})
```

Then back to Octave:

```
octave:8> load np_vector.mat
octave:9> vect
vect =

  0  1  2  3  4  5  6  7  8  9

octave:10> size(vect)
ans =

    1   10
```

If you want to inspect the contents of a MATLAB file without reading the data into memory, use the `whosmat` command:

```
>>> sio.whosmat('octave_a.mat')
[('a', (1, 3, 4), 'double')]
```

`whosmat` returns a list of tuples, one for each array (or other object) in the file. Each tuple contains the name, shape and data type of the array.

MATLAB structs

MATLAB structs are a little bit like Python dicts, except the field names must be strings. Any MATLAB object can be a value of a field. As for all objects in MATLAB, structs are, in fact, arrays of structs, where a single struct is an array of shape (1, 1).

```
octave:11> my_struct = struct('field1', 1, 'field2', 2)
my_struct =
{
  field1 =  1
  field2 =  2
}

octave:12> save -6 octave_struct.mat my_struct
```

We can load this in Python:

```
>>> mat_contents = sio.loadmat('octave_struct.mat')
>>> mat_contents
{'my_struct': array([[([[1.0]], [[2.0]])]],
      dtype=[('field1', 'O'), ('field2', 'O')]), '__version__': '1.0', '__
 ↪header__': 'MATLAB 5.0 MAT-file, written by Octave 3.6.3, 2013-02-17␣
 ↪21:23:14 UTC', '__globals__': []}
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct.shape
(1, 1)
>>> val = oct_struct[0,0]
>>> val
([[1.0]], [[2.0]])
>>> val['field1']
array([[ 1.]])
>>> val['field2']
array([[ 2.]])
>>> val.dtype
dtype([('field1', 'O'), ('field2', 'O')])
```

In the SciPy versions from 0.12.0, MATLAB structs come back as NumPy structured arrays, with fields named for the struct fields. You can see the field names in the `dtype` output above. Note also:

```
>>> val = oct_struct[0,0]
```

and:

```
octave:13> size(my_struct)
ans =

   1   1
```

So, in MATLAB, the struct array must be at least 2-D, and we replicate that when we read into SciPy. If you want all length 1 dimensions squeezed out, try this:

```
>>> mat_contents = sio.loadmat('octave_struct.mat', squeeze_me=True)
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct.shape
()
```

Sometimes, it's more convenient to load the MATLAB structs as Python objects rather than NumPy structured arrays - it can make the access syntax in Python a bit more similar to that in MATLAB. In order to do this, use the `struct_as_record=False` parameter setting to `loadmat`.

```
>>> mat_contents = sio.loadmat('octave_struct.mat', struct_as_record=False)
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct[0,0].field1
array([[ 1.]])
```

`struct_as_record=False` works nicely with `squeeze_me`:

```
>>> mat_contents = sio.loadmat('octave_struct.mat', struct_as_record=False,␣
↪squeeze_me=True)
>>> oct_struct = mat_contents['my_struct']
>>> oct_struct.shape # but no - it's a scalar
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
AttributeError: 'mat_struct' object has no attribute 'shape'
>>> type(oct_struct)
<class 'scipy.io.matlab.mio5_params.mat_struct'>
>>> oct_struct.field1
1.0
```

Saving struct arrays can be done in various ways. One simple method is to use dicts:

```
>>> a_dict = {'field1': 0.5, 'field2': 'a string'}
>>> sio.savemat('saved_struct.mat', {'a_dict': a_dict})
```

loaded as:

```
octave:21> load saved_struct
octave:22> a_dict
a_dict =

  scalar structure containing the fields:

    field2 = a string
    field1 =  0.50000
```

You can also save structs back again to MATLAB (or Octave in our case) like this:

```
>>> dt = [('f1', 'f8'), ('f2', 'S10')]
>>> arr = np.zeros((2,), dtype=dt)
>>> arr
array([(0.0, ''), (0.0, '')],
      dtype=[('f1', '<f8'), ('f2', 'S10')])
```

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```
>>> arr[0]['f1'] = 0.5
>>> arr[0]['f2'] = 'python'
>>> arr[1]['f1'] = 99
>>> arr[1]['f2'] = 'not perl'
>>> sio.savemat('np_struct_arr.mat', {'arr': arr})
```

MATLAB cell arrays

Cell arrays in MATLAB are rather like Python lists, in the sense that the elements in the arrays can contain any type of MATLAB object. In fact, they are most similar to NumPy object arrays, and that is how we load them into NumPy.

```
octave:14> my_cells = {1, [2, 3]}
my_cells =
{
  [1,1] =  1
  [1,2] =

     2   3

}

octave:15> save -6 octave_cells.mat my_cells
```

Back to Python:

```
>>> mat_contents = sio.loadmat('octave_cells.mat')
>>> oct_cells = mat_contents['my_cells']
>>> print(oct_cells.dtype)
object
>>> val = oct_cells[0,0]
>>> val
array([[ 1.]])
>>> print(val.dtype)
float64
```

Saving to a MATLAB cell array just involves making a NumPy object array:

```
>>> obj_arr = np.zeros((2,), dtype=np.object)
>>> obj_arr[0] = 1
>>> obj_arr[1] = 'a string'
>>> obj_arr
array([1, 'a string'], dtype=object)
>>> sio.savemat('np_cells.mat', {'obj_arr':obj_arr})
```

```
octave:16> load np_cells.mat
octave:17> obj_arr
obj_arr =
{
  [1,1] = 1
  [2,1] = a string
}
```

2.14.2 IDL files

readsav(file_name[, idict, python_dict, …])	Read an IDL .sav file.

2.14.3 Matrix Market files

mminfo(source)	Return size and storage parameters from Matrix Market file-like 'source'.
mmread(source)	Reads the contents of a Matrix Market file-like 'source' into a matrix.
mmwrite(target, a[, comment, field, …])	Writes the sparse or dense array *a* to Matrix Market file-like *target*.

2.14.4 Wav sound files (`scipy.io.wavfile`)

read(filename[, mmap])	Open a WAV file.
write(filename, rate, data)	Write a NumPy array as a WAV file.

2.14.5 Arff files (`scipy.io.arff`)

loadarff(f)	Read an arff file.

2.14.6 Netcdf

netcdf_file(filename[, mode, mmap, version, …])	A file object for NetCDF data.

Allows reading of NetCDF files (version of pupynere package)

CHAPTER

THREE

SCIPY API

3.1 Importing from SciPy

In Python the distinction between what is the public API of a library and what are private implementation details is not always clear. Unlike in other languages like Java, it is possible in Python to access "private" function or objects. Occasionally this may be convenient, but be aware that if you do so your code may break without warning in future releases. Some widely understood rules for what is and isn't public in Python are:

- Methods / functions / classes and module attributes whose names begin with a leading underscore are private.
- If a class name begins with a leading underscore, none of its members are public, whether or not they begin with a leading underscore.
- If a module name in a package begins with a leading underscore none of its members are public, whether or not they begin with a leading underscore.
- If a module or package defines `__all__`, that authoritatively defines the public interface.
- If a module or package doesn't define `__all__`, then all names that don't start with a leading underscore are public.

Note: Reading the above guidelines one could draw the conclusion that every private module or object starts with an underscore. This is not the case; the presence of underscores do mark something as private, but the absence of underscores do not mark something as public.

In SciPy there are modules whose names don't start with an underscore, but that should be considered private. To clarify which modules these are, we define below what the public API is for SciPy, and give some recommendations for how to import modules/functions/objects from SciPy.

3.2 Guidelines for importing functions from SciPy

The scipy namespace itself only contains functions imported from numpy. These functions still exist for backwards compatibility, but should be imported from numpy directly.

Everything in the namespaces of scipy submodules is public. In general, it is recommended to import functions from submodule namespaces. For example, the function `curve_fit` (defined in scipy/optimize/minpack.py) should be imported like this:

```
from scipy import optimize
result = optimize.curve_fit(...)
```

This form of importing submodules is preferred for all submodules except `scipy.io` (because `io` is also the name of a module in the Python stdlib):

```
from scipy import interpolate
from scipy import integrate
import scipy.io as spio
```

In some cases, the public API is one level deeper. For example, the `scipy.sparse.linalg` module is public, and the functions it contains are not available in the `scipy.sparse` namespace. Sometimes it may result in more easily understandable code if functions are imported from one level deeper. For example, in the following it is immediately clear that `lomax` is a distribution if the second form is chosen:

```
# first form
from scipy import stats
stats.lomax(...)

# second form
from scipy.stats import distributions
distributions.lomax(...)
```

In that case, the second form can be chosen **if** it is documented in the next section that the submodule in question is public.

3.3 API definition

Every submodule listed below is public. That means that these submodules are unlikely to be renamed or changed in an incompatible way, and if that is necessary, a deprecation warning will be raised for one SciPy release before the change is made.

- *scipy.cluster*
  - *scipy.cluster.vq*
  - *scipy.cluster.hierarchy*
- *scipy.constants*
- *scipy.fft*
- *scipy.fftpack*
- *scipy.integrate*
- *scipy.interpolate*
- *scipy.io*
  - *scipy.io.arff*
  - scipy.io.harwell_boeing
  - scipy.io.idl
  - scipy.io.matlab
  - scipy.io.netcdf
  - *scipy.io.wavfile*
- *scipy.linalg*
  - *scipy.linalg.blas*

  - *scipy.linalg.cython_blas*
  - *scipy.linalg.lapack*
  - *scipy.linalg.cython_lapack*
  - *scipy.linalg.interpolative*
- *scipy.misc*
- *scipy.ndimage*
- *scipy.odr*
- *scipy.optimize*
- *scipy.signal*
  - scipy.signal.windows
- *scipy.sparse*
  - *scipy.sparse.linalg*
  - *scipy.sparse.csgraph*
- *scipy.spatial*
  - *scipy.spatial.distance*
  - scipy.spatial.transform
- *scipy.special*
- *scipy.stats*
  - scipy.stats.distributions
  - *scipy.stats.mstats*
  - *scipy.stats.qmc*

3.3.1 Clustering package (`scipy.cluster`)

scipy.cluster.vq

Clustering algorithms are useful in information theory, target detection, communications, compression, and other areas. The *vq* module only supports vector quantization and the k-means algorithms.

scipy.cluster.hierarchy

The *hierarchy* module provides functions for hierarchical and agglomerative clustering. Its features include generating hierarchical clusters from distance matrices, calculating statistics on clusters, cutting linkages to generate flat clusters, and visualizing clusters with dendrograms.

3.3.2 K-means clustering and vector quantization (`scipy.cluster.vq`)

Provides routines for k-means clustering, generating code books from k-means models and quantizing vectors by comparing them with centroids in a code book.

whiten(obs[, check_finite])	Normalize a group of observations on a per feature basis.
vq(obs, code_book[, check_finite])	Assign codes from a code book to observations.
kmeans(obs, k_or_guess[, iter, thresh, …])	Performs k-means on a set of observation vectors forming k clusters.
kmeans2(data, k[, iter, thresh, minit, …])	Classify a set of observations into k clusters using the k-means algorithm.

scipy.cluster.vq.whiten

scipy.cluster.vq.**whiten**(*obs*, *check_finite=True*)

Normalize a group of observations on a per feature basis.

Before running k-means, it is beneficial to rescale each feature dimension of the observation set by its standard deviation (i.e. "whiten" it - as in "white noise" where each frequency has equal power). Each feature is divided by its standard deviation across all observations to give it unit variance.

Parameters

obs [ndarray] Each row of the array is an observation. The columns are the features seen during each observation.

```
>>> #          f0    f1    f2
>>> obs = [[  1.,   1.,   1.],  #o0
...        [  2.,   2.,   2.],  #o1
...        [  3.,   3.,   3.],  #o2
...        [  4.,   4.,   4.]]  #o3
```

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns

result [ndarray] Contains the values in *obs* scaled by the standard deviation of each column.

Examples

```
>>> from scipy.cluster.vq import whiten
>>> features  = np.array([[1.9, 2.3, 1.7],
...                       [1.5, 2.5, 2.2],
...                       [0.8, 0.6, 1.7,]])
>>> whiten(features)
array([[ 4.17944278,  2.69811351,  7.21248917],
       [ 3.29956009,  2.93273208,  9.33380951],
       [ 1.75976538,  0.7038557 ,  7.21248917]])
```

scipy.cluster.vq.vq

scipy.cluster.vq.**vq**(*obs*, *code_book*, *check_finite=True*)

Assign codes from a code book to observations.

Assigns a code from a code book to each observation. Each observation vector in the 'M' by 'N' *obs* array is compared with the centroids in the code book and assigned the code of the closest centroid.

The features in *obs* should have unit variance, which can be achieved by passing them through the whiten function. The code book can be created with the k-means algorithm or a different encoding algorithm.

Parameters

obs [ndarray] Each row of the 'M' x 'N' array is an observation. The columns are the "features" seen during each observation. The features must be whitened first using the whiten function or something equivalent.

code_book [ndarray] The code book is usually generated using the k-means algorithm. Each row of the array holds a different code, and the columns are the features of the code.

```
>>> #              f0    f1    f2   f3
>>> code_book = [
...             [  1.,   2.,   3.,   4.],  #c0
...             [  1.,   2.,   3.,   4.],  #c1
...             [  1.,   2.,   3.,   4.]]  #c2
```

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

Returns

code [ndarray] A length M array holding the code book index for each observation.

dist [ndarray] The distortion (distance) between the observation and its nearest code.

Examples

```
>>> from numpy import array
>>> from scipy.cluster.vq import vq
>>> code_book = array([[1.,1.,1.],
...                    [2.,2.,2.]])
>>> features  = array([[  1.9,2.3,1.7],
...                    [  1.5,2.5,2.2],
...                    [  0.8,0.6,1.7]])
>>> vq(features,code_book)
(array([1, 1, 0],'i'), array([ 0.43588989,  0.73484692,  0.83066239]))
```

scipy.cluster.vq.kmeans

scipy.cluster.vq.**kmeans**(*obs*, *k_or_guess*, *iter=20*, *thresh=1e-05*, *check_finite=True*, ***, *seed=None*)

Performs k-means on a set of observation vectors forming k clusters.

The k-means algorithm adjusts the classification of the observations into clusters and updates the cluster centroids until the position of the centroids is stable over successive iterations. In this implementation of the algorithm, the stability of the centroids is determined by comparing the absolute value of the change in the average Euclidean distance between the observations and their corresponding centroids against a threshold. This yields a code book mapping centroids to codes and vice versa.

Parameters

obs [ndarray] Each row of the M by N array is an observation vector. The columns are the features seen during each observation. The features must be whitened first with the *whiten* function.

k_or_guess [int or ndarray] The number of centroids to generate. A code is assigned to each centroid, which is also the row index of the centroid in the code_book matrix generated.
The initial k centroids are chosen by randomly selecting observations from the observation matrix. Alternatively, passing a k by N array specifies the initial k centroids.

iter [int, optional] The number of times to run k-means, returning the codebook with the lowest distortion. This argument is ignored if initial centroids are specified with an array for the `k_or_guess` parameter. This parameter does not represent the number of iterations of the k-means algorithm.

thresh [float, optional] Terminates the k-means algorithm if the change in distortion since the last k-means iteration is less than or equal to threshold.

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

seed [{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
Seed for initializing the pseudo-random number generator. If *seed* is None (or `numpy.random`), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used. The default is None.

Returns

codebook [ndarray] A k by N array of k centroids. The ith centroid codebook[i] is represented with the code i. The centroids and codes generated represent the lowest distortion seen, not necessarily the globally minimal distortion. Note that the number of centroids is not necessarily the same as the `k_or_guess` parameter, because centroids assigned to no observations are removed during iterations.

distortion [float] The mean (non-squared) Euclidean distance between the observations passed and the centroids generated. Note the difference to the standard definition of distortion in the context of the k-means algorithm, which is the sum of the squared distances.

See also:

kmeans2

a different implementation of k-means clustering with more methods for generating initial centroids but without using a distortion change threshold as a stopping criterion.

whiten

must be called prior to passing an observation matrix to kmeans.

Notes

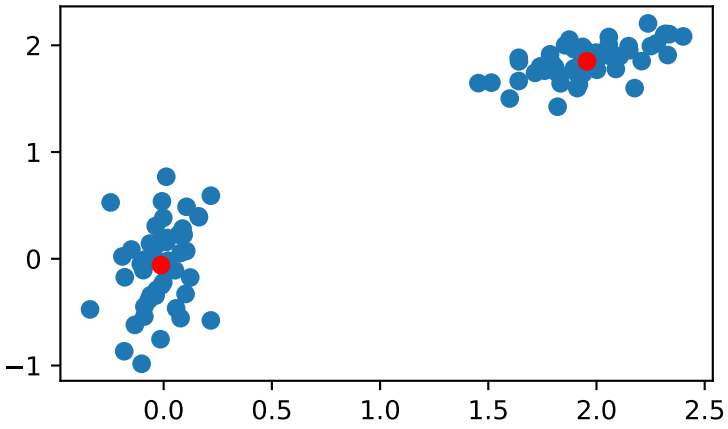
For more functionalities or optimal performance, you can use sklearn.cluster.KMeans. This is a benchmark result of several implementations.

Examples

```
>>> from numpy import array
>>> from scipy.cluster.vq import vq, kmeans, whiten
>>> import matplotlib.pyplot as plt
>>> features  = array([[ 1.9,2.3],
...                    [ 1.5,2.5],
...                    [ 0.8,0.6],
...                    [ 0.4,1.8],
...                    [ 0.1,0.1],
...                    [ 0.2,1.8],
...                    [ 2.0,0.5],
...                    [ 0.3,1.5],
...                    [ 1.0,1.0]])
>>> whitened = whiten(features)
>>> book = np.array((whitened[0],whitened[2]))
>>> kmeans(whitened,book)
(array([[ 2.3110306 ,  2.86287398],    # random
       [ 0.93218041,  1.24398691]]), 0.85684700941625547)
```

```
>>> codes = 3
>>> kmeans(whitened,codes)
(array([[ 2.3110306 ,  2.86287398],    # random
       [ 1.32544402,  0.65607529],
       [ 0.40782893,  2.02786907]]), 0.5196582527686241)
```

```
>>> # Create 50 datapoints in two clusters a and b
>>> pts = 50
>>> rng = np.random.default_rng()
>>> a = rng.multivariate_normal([0, 0], [[4, 1], [1, 4]], size=pts)
>>> b = rng.multivariate_normal([30, 10],
...                             [[10, 2], [2, 1]],
...                             size=pts)
>>> features = np.concatenate((a, b))
>>> # Whiten data
>>> whitened = whiten(features)
>>> # Find 2 clusters in the data
>>> codebook, distortion = kmeans(whitened, 2)
>>> # Plot whitened data and cluster centers in red
>>> plt.scatter(whitened[:, 0], whitened[:, 1])
>>> plt.scatter(codebook[:, 0], codebook[:, 1], c='r')
>>> plt.show()
```



scipy.cluster.vq.kmeans2

scipy.cluster.vq.**kmeans2**(*data*, *k*, *iter=10*, *thresh=1e-05*, *minit='random'*, *missing='warn'*, *check_finite=True*, ***, *seed=None*)

Classify a set of observations into k clusters using the k-means algorithm.

The algorithm attempts to minimize the Euclidean distance between observations and centroids. Several initialization methods are included.

Parameters

data [ndarray] A 'M' by 'N' array of 'M' observations in 'N' dimensions or a length 'M' array of 'M' 1-D observations.

k [int or ndarray] The number of clusters to form as well as the number of centroids to generate. If *minit* initialization string is 'matrix', or if a ndarray is given instead, it is interpreted as initial cluster to use instead.

iter [int, optional] Number of iterations of the k-means algorithm to run. Note that this differs in meaning from the iters parameter to the kmeans function.

thresh [float, optional] (not used yet)

minit [str, optional] Method for initialization. Available methods are 'random', 'points', '++' and 'matrix':
'random': generate k centroids from a Gaussian with mean and variance estimated from the data.
'points': choose k observations (rows) at random from data for the initial centroids.
'++': choose k observations accordingly to the kmeans++ method (careful seeding)
'matrix': interpret the k parameter as a k by M (or length k array for 1-D data) array of initial centroids.

missing [str, optional] Method to deal with empty clusters. Available methods are 'warn' and 'raise':
'warn': give a warning and continue.
'raise': raise an ClusterError and terminate the algorithm.

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default: True

seed [{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional

Seed for initializing the pseudo-random number generator. If *seed* is None (or `numpy.random`), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used. The default is None.

Returns

centroid [ndarray] A 'k' by 'N' array of centroids found at the last iteration of k-means.
label [ndarray] label[i] is the code or index of the centroid the ith observation is closest to.

See also:

kmeans

References

[1]

Examples

```
>>> from scipy.cluster.vq import kmeans2
>>> import matplotlib.pyplot as plt
```

Create z, an array with shape (100, 2) containing a mixture of samples from three multivariate normal distributions.

```
>>> rng = np.random.default_rng()
>>> a = rng.multivariate_normal([0, 6], [[2, 1], [1, 1.5]], size=45)
>>> b = rng.multivariate_normal([2, 0], [[1, -1], [-1, 3]], size=30)
>>> c = rng.multivariate_normal([6, 4], [[5, 0], [0, 1.2]], size=25)
>>> z = np.concatenate((a, b, c))
>>> rng.shuffle(z)
```

Compute three clusters.

```
>>> centroid, label = kmeans2(z, 3, minit='points')
>>> centroid
array([[ 2.22274463, -0.61666946],  # may vary
       [ 0.54069047,  5.86541444],
       [ 6.73846769,  4.01991898]])
```

How many points are in each cluster?

```
>>> counts = np.bincount(label)
>>> counts
array([29, 51, 20])  # may vary
```

Plot the clusters.

```
>>> w0 = z[label == 0]
>>> w1 = z[label == 1]
>>> w2 = z[label == 2]
>>> plt.plot(w0[:, 0], w0[:, 1], 'o', alpha=0.5, label='cluster 0')
>>> plt.plot(w1[:, 0], w1[:, 1], 'd', alpha=0.5, label='cluster 1')
>>> plt.plot(w2[:, 0], w2[:, 1], 's', alpha=0.5, label='cluster 2')
```

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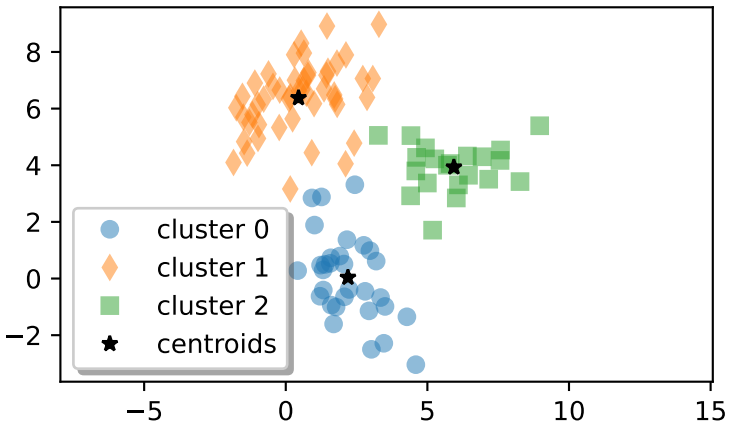
```
>>> plt.plot(centroid[:, 0], centroid[:, 1], 'k*', label='centroids')
>>> plt.axis('equal')
>>> plt.legend(shadow=True)
>>> plt.show()
```



Background information

The k-means algorithm takes as input the number of clusters to generate, k, and a set of observation vectors to cluster. It returns a set of centroids, one for each of the k clusters. An observation vector is classified with the cluster number or centroid index of the centroid closest to it.

A vector v belongs to cluster i if it is closer to centroid i than any other centroid. If v belongs to i, we say centroid i is the dominating centroid of v. The k-means algorithm tries to minimize distortion, which is defined as the sum of the squared distances between each observation vector and its dominating centroid. The minimization is achieved by iteratively reclassifying the observations into clusters and recalculating the centroids until a configuration is reached in which the centroids are stable. One can also define a maximum number of iterations.

Since vector quantization is a natural application for k-means, information theory terminology is often used. The centroid index or cluster index is also referred to as a "code" and the table mapping codes to centroids and, vice versa, is often referred to as a "code book". The result of k-means, a set of centroids, can be used to quantize vectors. Quantization aims to find an encoding of vectors that reduces the expected distortion.

All routines expect obs to be an M by N array, where the rows are the observation vectors. The codebook is a k by N array, where the ith row is the centroid of code word i. The observation vectors and centroids have the same feature dimension.

As an example, suppose we wish to compress a 24-bit color image (each pixel is represented by one byte for red, one for blue, and one for green) before sending it over the web. By using a smaller 8-bit encoding, we can reduce the amount of data by two thirds. Ideally, the colors for each of the 256 possible 8-bit encoding values should be chosen to minimize distortion of the color. Running k-means with k=256 generates a code book of 256 codes, which fills up all possible 8-bit sequences. Instead of sending a 3-byte value for each pixel, the 8-bit centroid index (or code word) of the dominating centroid is transmitted. The code book is also sent over the wire so each 8-bit code can be translated back to a 24-bit pixel value representation. If the image of interest was of an ocean, we would expect many 24-bit blues to be represented by 8-bit codes. If it was an image of a human face, more flesh-tone colors would be represented in the code book.

3.3.3 Hierarchical clustering (`scipy.cluster.hierarchy`)

These functions cut hierarchical clusterings into flat clusterings or find the roots of the forest formed by a cut by providing the flat cluster ids of each observation.

fcluster(Z, t[, criterion, depth, R, monocrit])	Form flat clusters from the hierarchical clustering defined by the given linkage matrix.
fclusterdata(X, t[, criterion, metric, …])	Cluster observation data using a given metric.
leaders(Z, T)	Return the root nodes in a hierarchical clustering.

scipy.cluster.hierarchy.fcluster

scipy.cluster.hierarchy.**fcluster**(*Z*, *t*, *criterion='inconsistent'*, *depth=2*, *R=None*, *monocrit=None*)

Form flat clusters from the hierarchical clustering defined by the given linkage matrix.

Parameters

Z [ndarray] The hierarchical clustering encoded with the matrix returned by the *linkage* function.

t [scalar]
For criteria 'inconsistent', 'distance' or 'monocrit',
this is the threshold to apply when forming flat clusters.
For 'maxclust' or 'maxclust_monocrit' criteria,
this would be max number of clusters requested.

criterion [str, optional] The criterion to use in forming flat clusters. This can be any of the following values:

inconsistent :
If a cluster node and all its descendants have an inconsistent value less than or equal to *t*, then all its leaf descendants belong to the same flat cluster. When no non-singleton cluster meets this criterion, every node is assigned to its own cluster. (Default)

distance :
Forms flat clusters so that the original observations in each flat cluster have no greater a cophenetic distance than *t*.

maxclust :
Finds a minimum threshold `r` so that the cophenetic distance between any two original observations in the same flat cluster is no more than `r` and no more than *t* flat clusters are formed.

monocrit :
Forms a flat cluster from a cluster node c with index i when `monocrit[j] <= t`.
For example, to threshold on the maximum mean distance as computed in the inconsistency matrix R with a threshold of 0.8 do:

```
MR = maxRstat(Z, R, 3)
fcluster(Z, t=0.8, criterion='monocrit',␣
↪monocrit=MR)
```

maxclust_monocrit :
Forms a flat cluster from a non-singleton cluster node `c` when `monocrit[i] <= r` for all cluster indices `i` below and including `c`. `r` is minimized such that no more than `t` flat clusters are formed. monocrit must

be monotonic. For example, to minimize the threshold t on maximum inconsistency values so that no more than 3 flat clusters are formed, do:

```
MI = maxinconsts(Z, R)
fcluster(Z, t=3, criterion='maxclust_monocrit',␣
↪monocrit=MI)
```

depth [int, optional] The maximum depth to perform the inconsistency calculation. It has no meaning for the other criteria. Default is 2.

R [ndarray, optional] The inconsistency matrix to use for the 'inconsistent' criterion. This matrix is computed if not provided.

monocrit [ndarray, optional] An array of length n-1. *monocrit[i]* is the statistics upon which non-singleton i is thresholded. The monocrit vector must be monotonic, i.e., given a node c with index i, for all node indices j corresponding to nodes below c, `monocrit[i] >= monocrit[j]`.

Returns

fcluster [ndarray] An array of length `n`. `T[i]` is the flat cluster number to which original observation `i` belongs.

See also:

`linkage`

for information about hierarchical clustering methods work.

Examples

```
>>> from scipy.cluster.hierarchy import ward, fcluster
>>> from scipy.spatial.distance import pdist
```

All cluster linkage methods - e.g., *`scipy.cluster.hierarchy.ward`* generate a linkage matrix `Z` as their output:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...       [0, 4], [0, 3], [1, 4],
...       [4, 0], [3, 0], [4, 1],
...       [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = ward(pdist(X))
```

```
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.29099445,  3.        ],
       [ 5.        , 13.        ,  1.29099445,  3.        ],
       [ 8.        , 14.        ,  1.29099445,  3.        ],
       [11.        , 15.        ,  1.29099445,  3.        ],
       [16.        , 17.        ,  5.77350269,  6.        ],
       [18.        , 19.        ,  5.77350269,  6.        ],
       [20.        , 21.        ,  8.16496581, 12.        ]])
```

This matrix represents a dendrogram, where the first and second elements are the two clusters merged at each step, the third element is the distance between these clusters, and the fourth element is the size of the new cluster - the number of original data points included.

scipy.cluster.hierarchy.fcluster can be used to flatten the dendrogram, obtaining as a result an assignation of the original data points to single clusters.

This assignation mostly depends on a distance threshold `t` - the maximum inter-cluster distance allowed:

```
>>> fcluster(Z, t=0.9, criterion='distance')
array([ 1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12], dtype=int32)
```

```
>>> fcluster(Z, t=1.1, criterion='distance')
array([1, 1, 2, 3, 3, 4, 5, 5, 6, 7, 7, 8], dtype=int32)
```

```
>>> fcluster(Z, t=3, criterion='distance')
array([1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4], dtype=int32)
```

```
>>> fcluster(Z, t=9, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

In the first case, the threshold `t` is too small to allow any two samples in the data to form a cluster, so 12 different clusters are returned.

In the second case, the threshold is large enough to allow the first 4 points to be merged with their nearest neighbors. So, here, only 8 clusters are returned.

The third case, with a much higher threshold, allows for up to 8 data points to be connected - so 4 clusters are returned here.

Lastly, the threshold of the fourth case is large enough to allow for all data points to be merged together - so a single cluster is returned.

scipy.cluster.hierarchy.fclusterdata

scipy.cluster.hierarchy.**fclusterdata**(*X*, *t*, *criterion='inconsistent'*, *metric='euclidean'*, *depth=2*, *method='single'*, *R=None*)

Cluster observation data using a given metric.

Clusters the original observations in the n-by-m data matrix X (n observations in m dimensions), using the euclidean distance metric to calculate distances between original observations, performs hierarchical clustering using the single linkage algorithm, and forms flat clusters using the inconsistency method with *t* as the cut-off threshold.

A 1-D array `T` of length `n` is returned. `T[i]` is the index of the flat cluster to which the original observation `i` belongs.

Parameters

X [(N, M) ndarray] N by M data matrix with N observations in M dimensions.

t [scalar]
For criteria 'inconsistent', 'distance' or 'monocrit',
this is the threshold to apply when forming flat clusters.
For 'maxclust' or 'maxclust_monocrit' criteria,
this would be max number of clusters requested.

criterion [str, optional] Specifies the criterion for forming flat clusters. Valid values are 'inconsistent' (default), 'distance', or 'maxclust' cluster formation algorithms. See *fcluster* for descriptions.

metric [str or function, optional] The distance metric for calculating pairwise distances. See `distance.pdist` for descriptions and linkage to verify compatibility with the linkage method.

depth [int, optional] The maximum depth for the inconsistency calculation. See *inconsistent* for more information.

method [str, optional] The linkage method to use (single, complete, average, weighted, median centroid, ward). See *linkage* for more information. Default is "single".

R [ndarray, optional] The inconsistency matrix. It will be computed if necessary if it is not passed.

Returns

fclusterdata

[ndarray] A vector of length n. T[i] is the flat cluster number to which original observation i belongs.

See also:

scipy.spatial.distance.pdist

pairwise distance metrics

Notes

This function is similar to the MATLAB function `clusterdata`.

Examples

```
>>> from scipy.cluster.hierarchy import fclusterdata
```

This is a convenience method that abstracts all the steps to perform in a typical SciPy's hierarchical clustering workflow.

- Transform the input data into a condensed matrix with *scipy.spatial.distance.pdist*.
- Apply a clustering method.
- Obtain flat clusters at a user defined distance threshold `t` using *scipy.cluster.hierarchy.fcluster*.

```
>>> X = [[0, 0], [0, 1], [1, 0],
...       [0, 4], [0, 3], [1, 4],
...       [4, 0], [3, 0], [4, 1],
...       [4, 4], [3, 4], [4, 3]]
```

```
>>> fclusterdata(X, t=1)
array([3, 3, 3, 4, 4, 4, 2, 2, 2, 1, 1, 1], dtype=int32)
```

The output here (for the dataset `X`, distance threshold `t`, and the default settings) is four clusters with three data points each.

scipy.cluster.hierarchy.leaders

scipy.cluster.hierarchy.**leaders**(*Z*, *T*)

Return the root nodes in a hierarchical clustering.

Returns the root nodes in a hierarchical clustering corresponding to a cut defined by a flat cluster assignment vector `T`. See the `fcluster` function for more information on the format of `T`.

For each flat cluster j of the k flat clusters represented in the n-sized flat cluster assignment vector `T`, this function finds the lowest cluster node i in the linkage tree Z, such that:

- leaf descendants belong only to flat cluster j (i.e., `T[p]==j` for all p in $S(i)$, where $S(i)$ is the set of leaf ids of descendant leaf nodes with cluster node i)
- there does not exist a leaf that is not a descendant with i that also belongs to cluster j (i.e., `T[q]!=j` for all q not in $S(i)$). If this condition is violated, `T` is not a valid cluster assignment vector, and an exception will be thrown.

Parameters

Z [ndarray] The hierarchical clustering encoded as a matrix. See *linkage* for more information.

T [ndarray] The flat cluster assignment vector.

Returns

L [ndarray] The leader linkage node id's stored as a k-element 1-D array, where `k` is the number of flat clusters found in `T`.
`L[j]=i` is the linkage cluster node id that is the leader of flat cluster with id M[j]. If `i < n`, `i` corresponds to an original observation, otherwise it corresponds to a non-singleton cluster.

M [ndarray] The leader linkage node id's stored as a k-element 1-D array, where `k` is the number of flat clusters found in `T`. This allows the set of flat cluster ids to be any arbitrary set of `k` integers.
For example: if `L[3]=2` and `M[3]=8`, the flat cluster with id 8's leader is linkage node 2.

See also:

fcluster

for the creation of flat cluster assignments.

Examples

```
>>> from scipy.cluster.hierarchy import ward, fcluster, leaders
>>> from scipy.spatial.distance import pdist
```

Given a linkage matrix `Z` - obtained after apply a clustering method to a dataset `X` - and a flat cluster assignment array `T`:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = ward(pdist(X))
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.29099445,  3.        ],
       [ 5.        , 13.        ,  1.29099445,  3.        ],
       [ 8.        , 14.        ,  1.29099445,  3.        ],
       [11.        , 15.        ,  1.29099445,  3.        ],
       [16.        , 17.        ,  5.77350269,  6.        ],
       [18.        , 19.        ,  5.77350269,  6.        ],
       [20.        , 21.        ,  8.16496581, 12.        ]])
```

```
>>> T = fcluster(Z, 3, criterion='distance')
>>> T
array([1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4], dtype=int32)
```

scipy.cluster.hierarchy.leaders returns the indices of the nodes in the dendrogram that are the leaders of each flat cluster:

```
>>> L, M = leaders(Z, T)
>>> L
array([16, 17, 18, 19], dtype=int32)
```

(remember that indices 0-11 point to the 12 data points in `X`, whereas indices 12-22 point to the 11 rows of `Z`)

scipy.cluster.hierarchy.leaders also returns the indices of the flat clusters in `T`:

```
>>> M
array([1, 2, 3, 4], dtype=int32)
```

These are routines for agglomerative clustering.

linkage(y[, method, metric, optimal_ordering])	Perform hierarchical/agglomerative clustering.
single(y)	Perform single/min/nearest linkage on the condensed distance matrix `y`.
complete(y)	Perform complete/max/farthest point linkage on a condensed distance matrix.
average(y)	Perform average/UPGMA linkage on a condensed distance matrix.
weighted(y)	Perform weighted/WPGMA linkage on the condensed distance matrix.
centroid(y)	Perform centroid/UPGMC linkage.
median(y)	Perform median/WPGMC linkage.
ward(y)	Perform Ward's linkage on a condensed distance matrix.

scipy.cluster.hierarchy.linkage

scipy.cluster.hierarchy.**linkage**(*y*, *method='single'*, *metric='euclidean'*, *optimal_ordering=False*)

Perform hierarchical/agglomerative clustering.

The input y may be either a 1-D condensed distance matrix or a 2-D array of observation vectors.

If y is a 1-D condensed distance matrix, then y must be a $\binom{n}{2}$ sized vector, where n is the number of original observations paired in the distance matrix. The behavior of this function is very similar to the MATLAB linkage function.

A $(n-1)$ by 4 matrix `Z` is returned. At the i-th iteration, clusters with indices `Z[i, 0]` and `Z[i, 1]` are combined to form cluster $n+i$. A cluster with an index less than n corresponds to one of the n original observations. The distance between clusters `Z[i, 0]` and `Z[i, 1]` is given by `Z[i, 2]`. The fourth value `Z[i, 3]` represents the number of original observations in the newly formed cluster.

The following linkage methods are used to compute the distance $d(s,t)$ between two clusters s and t. The algorithm begins with a forest of clusters that have yet to be used in the hierarchy being formed. When two clusters s and t from this forest are combined into a single cluster u, s and t are removed from the forest, and u is added to the forest. When only one cluster remains in the forest, the algorithm stops, and this cluster becomes the root.

A distance matrix is maintained at each iteration. The `d[i,j]` entry corresponds to the distance between cluster i and j in the original forest.

At each iteration, the algorithm must update the distance matrix to reflect the distance of the newly formed cluster u with the remaining clusters in the forest.

Suppose there are $|u|$ original observations $u[0], \ldots, u[|u|-1]$ in cluster u and $|v|$ original objects $v[0], \ldots, v[|v|-1]$ in cluster v. Recall, s and t are combined to form cluster u. Let v be any remaining cluster in the forest that is not u.

The following are methods for calculating the distance between the newly formed cluster u and each v.

- method='single' assigns

$$d(u,v) = \min(dist(u[i], v[j]))$$

  for all points i in cluster u and j in cluster v. This is also known as the Nearest Point Algorithm.

- method='complete' assigns

$$d(u,v) = \max(dist(u[i], v[j]))$$

  for all points i in cluster u and j in cluster v. This is also known by the Farthest Point Algorithm or Voor Hees Algorithm.

- method='average' assigns

$$d(u,v) = \sum_{ij} \frac{d(u[i], v[j])}{(|u| * |v|)}$$

  for all points i and j where $|u|$ and $|v|$ are the cardinalities of clusters u and v, respectively. This is also called the UPGMA algorithm.

- method='weighted' assigns

$$d(u,v) = (dist(s,v) + dist(t,v))/2$$

  where cluster u was formed with cluster s and t and v is a remaining cluster in the forest (also called WPGMA).

- method='centroid' assigns

$$dist(s,t) = ||c_s - c_t||_2$$

where c_s and c_t are the centroids of clusters s and t, respectively. When two clusters s and t are combined into a new cluster u, the new centroid is computed over all the original objects in clusters s and t. The distance then becomes the Euclidean distance between the centroid of u and the centroid of a remaining cluster v in the forest. This is also known as the UPGMC algorithm.

- method='median' assigns $d(s,t)$ like the `centroid` method. When two clusters s and t are combined into a new cluster u, the average of centroids s and t give the new centroid u. This is also known as the WPGMC algorithm.

- method='ward' uses the Ward variance minimization algorithm. The new entry $d(u,v)$ is computed as follows,

$$d(u,v) = \sqrt{\frac{|v|+|s|}{T}d(v,s)^2 + \frac{|v|+|t|}{T}d(v,t)^2 - \frac{|v|}{T}d(s,t)^2}$$

where u is the newly joined cluster consisting of clusters s and t, v is an unused cluster in the forest, $T = |v| + |s| + |t|$, and $|*|$ is the cardinality of its argument. This is also known as the incremental algorithm.

Warning: When the minimum distance pair in the forest is chosen, there may be two or more pairs with the same minimum distance. This implementation may choose a different minimum than the MATLAB version.

Parameters

y [ndarray] A condensed distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of m observation vectors in n dimensions may be passed as an m by n array. All elements of the condensed distance matrix must be finite, i.e., no NaNs or infs.

method [str, optional] The linkage algorithm to use. See the `Linkage Methods` section below for full descriptions.

metric [str or function, optional] The distance metric to use in the case that y is a collection of observation vectors; ignored otherwise. See the `pdist` function for a list of valid distance metrics. A custom distance function can also be used.

optimal_ordering
[bool, optional] If True, the linkage matrix will be reordered so that the distance between successive leaves is minimal. This results in a more intuitive tree structure when the data are visualized. defaults to False, because this algorithm can be slow, particularly on large datasets [2]. See also the *`optimal_leaf_ordering`* function.
New in version 1.0.0.

Returns

Z [ndarray] The hierarchical clustering encoded as a linkage matrix.

See also:

`scipy.spatial.distance.pdist`

pairwise distance metrics

Notes

1. For method 'single', an optimized algorithm based on minimum spanning tree is implemented. It has time complexity $O(n^2)$. For methods 'complete', 'average', 'weighted' and 'ward', an algorithm called nearest-neighbors chain is implemented. It also has time complexity $O(n^2)$. For other methods, a naive algorithm is implemented with $O(n^3)$ time complexity. All algorithms use $O(n^2)$ memory. Refer to [1] for details about the algorithms.
2. Methods 'centroid', 'median', and 'ward' are correctly defined only if Euclidean pairwise metric is used. If y is passed as precomputed pairwise distances, then it is the user's responsibility to assure that these distances are in fact Euclidean, otherwise the produced result will be incorrect.

References

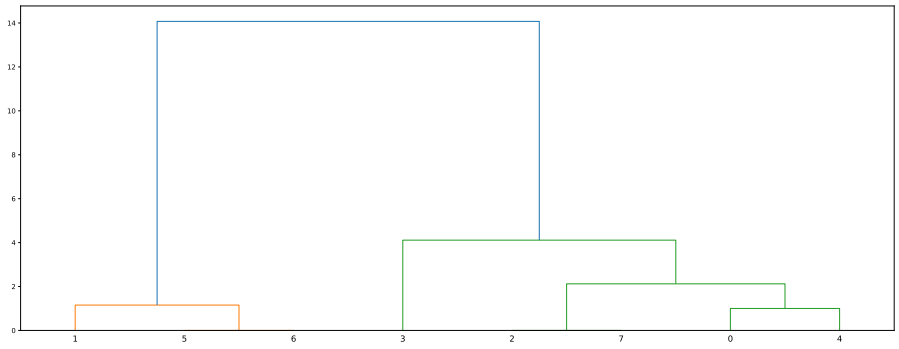
[1], [2]

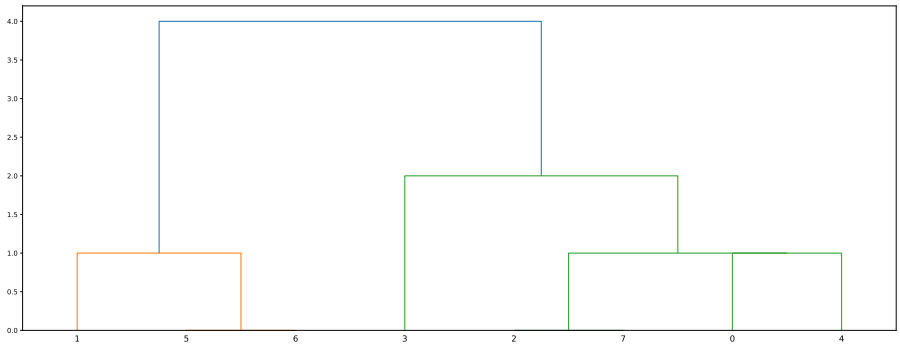
Examples

```
>>> from scipy.cluster.hierarchy import dendrogram, linkage
>>> from matplotlib import pyplot as plt
>>> X = [[i] for i in [2, 8, 0, 4, 1, 9, 9, 0]]
```

```
>>> Z = linkage(X, 'ward')
>>> fig = plt.figure(figsize=(25, 10))
>>> dn = dendrogram(Z)
```

```
>>> Z = linkage(X, 'single')
>>> fig = plt.figure(figsize=(25, 10))
>>> dn = dendrogram(Z)
>>> plt.show()
```





scipy.cluster.hierarchy.single

scipy.cluster.hierarchy.**single**(*y*)

Perform single/min/nearest linkage on the condensed distance matrix `y`.

Parameters

y [ndarray] The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

Returns

Z [ndarray] The linkage matrix.

See also:

`linkage`

for advanced creation of hierarchical clusterings.

`scipy.spatial.distance.pdist`

pairwise distance metrics

Examples

```
>>> from scipy.cluster.hierarchy import single, fcluster
>>> from scipy.spatial.distance import pdist
```

First, we need a toy dataset to play with:

```
x x     x x
x         x


x         x
x x     x x
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

Then, we get a condensed distance matrix from this dataset:

```
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```
>>> Z = single(y)
>>> Z
array([[ 0.,  1.,  1.,  2.],
       [ 2., 12.,  1.,  3.],
       [ 3.,  4.,  1.,  2.],
       [ 5., 14.,  1.,  3.],
       [ 6.,  7.,  1.,  2.],
       [ 8., 16.,  1.,  3.],
       [ 9., 10.,  1.,  2.],
       [11., 18.,  1.,  3.],
       [13., 15.,  2.,  6.],
       [17., 20.,  2.,  9.],
       [19., 21.,  2., 12.]])
```

The linkage matrix `Z` represents a dendrogram - see *scipy.cluster.hierarchy.linkage* for a detailed explanation of its contents.

We can use *scipy.cluster.hierarchy.fcluster* to see to which cluster each initial point would belong given a distance threshold:

```
>>> fcluster(Z, 0.9, criterion='distance')
array([ 7,  8,  9, 10, 11, 12,  4,  5,  6,  1,  2,  3], dtype=int32)
>>> fcluster(Z, 1, criterion='distance')
array([3, 3, 3, 4, 4, 4, 2, 2, 2, 1, 1, 1], dtype=int32)
>>> fcluster(Z, 2, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also, *scipy.cluster.hierarchy.dendrogram* can be used to generate a plot of the dendrogram.

scipy.cluster.hierarchy.complete

scipy.cluster.hierarchy.**complete**(*y*)

Perform complete/max/farthest point linkage on a condensed distance matrix.

Parameters

y [ndarray] The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

Returns

Z [ndarray] A linkage matrix containing the hierarchical clustering. See the *linkage* function documentation for more information on its structure.

See also:

linkage

for advanced creation of hierarchical clusterings.

scipy.spatial.distance.pdist

pairwise distance metrics

Examples

```
>>> from scipy.cluster.hierarchy import complete, fcluster
>>> from scipy.spatial.distance import pdist
```

First, we need a toy dataset to play with:

```
x x    x x
x        x

x        x
x x    x x
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

Then, we get a condensed distance matrix from this dataset:

```
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```
>>> Z = complete(y)
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.41421356,  3.        ],
       [ 5.        , 13.        ,  1.41421356,  3.        ],
       [ 8.        , 14.        ,  1.41421356,  3.        ],
       [11.        , 15.        ,  1.41421356,  3.        ],
       [16.        , 17.        ,  4.12310563,  6.        ],
       [18.        , 19.        ,  4.12310563,  6.        ],
       [20.        , 21.        ,  5.65685425, 12.        ]])
```

The linkage matrix `Z` represents a dendrogram - see *scipy.cluster.hierarchy.linkage* for a detailed explanation of its contents.

We can use *scipy.cluster.hierarchy.fcluster* to see to which cluster each initial point would belong given a distance threshold:

```
>>> fcluster(Z, 0.9, criterion='distance')
array([ 1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12], dtype=int32)
>>> fcluster(Z, 1.5, criterion='distance')
```

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```
array([1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4], dtype=int32)
>>> fcluster(Z, 4.5, criterion='distance')
array([1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2], dtype=int32)
>>> fcluster(Z, 6, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also, *scipy.cluster.hierarchy.dendrogram* can be used to generate a plot of the dendrogram.

scipy.cluster.hierarchy.average

scipy.cluster.hierarchy.**average**(*y*)

Perform average/UPGMA linkage on a condensed distance matrix.

Parameters

y [ndarray] The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

Returns

Z [ndarray] A linkage matrix containing the hierarchical clustering. See *linkage* for more information on its structure.

See also:

linkage

for advanced creation of hierarchical clusterings.

scipy.spatial.distance.pdist

pairwise distance metrics

Examples

```
>>> from scipy.cluster.hierarchy import average, fcluster
>>> from scipy.spatial.distance import pdist
```

First, we need a toy dataset to play with:

```
x x     x x
x         x

x         x
x x     x x
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...       [0, 4], [0, 3], [1, 4],
...       [4, 0], [3, 0], [4, 1],
...       [4, 4], [3, 4], [4, 3]]
```

Then, we get a condensed distance matrix from this dataset:

```
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```
>>> Z = average(y)
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.20710678,  3.        ],
       [ 5.        , 13.        ,  1.20710678,  3.        ],
       [ 8.        , 14.        ,  1.20710678,  3.        ],
       [11.        , 15.        ,  1.20710678,  3.        ],
       [16.        , 17.        ,  3.39675184,  6.        ],
       [18.        , 19.        ,  3.39675184,  6.        ],
       [20.        , 21.        ,  4.09206523, 12.        ]])
```

The linkage matrix `Z` represents a dendrogram - see *scipy.cluster.hierarchy.linkage* for a detailed explanation of its contents.

We can use *scipy.cluster.hierarchy.fcluster* to see to which cluster each initial point would belong given a distance threshold:

```
>>> fcluster(Z, 0.9, criterion='distance')
array([ 1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12], dtype=int32)
>>> fcluster(Z, 1.5, criterion='distance')
array([1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4], dtype=int32)
>>> fcluster(Z, 4, criterion='distance')
array([1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2], dtype=int32)
>>> fcluster(Z, 6, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also, *scipy.cluster.hierarchy.dendrogram* can be used to generate a plot of the dendrogram.

scipy.cluster.hierarchy.weighted

scipy.cluster.hierarchy.**weighted**(*y*)

Perform weighted/WPGMA linkage on the condensed distance matrix.

See *linkage* for more information on the return structure and algorithm.

Parameters

y [ndarray] The upper triangular of the distance matrix. The result of `pdist` is returned in this form.

Returns

Z [ndarray] A linkage matrix containing the hierarchical clustering. See *linkage* for more information on its structure.

See also:

linkage

for advanced creation of hierarchical clusterings.

scipy.spatial.distance.pdist

pairwise distance metrics

Examples

```
>>> from scipy.cluster.hierarchy import weighted, fcluster
>>> from scipy.spatial.distance import pdist
```

First, we need a toy dataset to play with:

```
x x    x x
x        x

x        x
x x    x x
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

Then, we get a condensed distance matrix from this dataset:

```
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```
>>> Z = weighted(y)
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 9.        , 11.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.20710678,  3.        ],
       [ 8.        , 13.        ,  1.20710678,  3.        ],
       [ 5.        , 14.        ,  1.20710678,  3.        ],
       [10.        , 15.        ,  1.20710678,  3.        ],
       [18.        , 19.        ,  3.05595762,  6.        ],
       [16.        , 17.        ,  3.32379407,  6.        ],
       [20.        , 21.        ,  4.06357713, 12.        ]])
```

The linkage matrix `Z` represents a dendrogram - see *scipy.cluster.hierarchy.linkage* for a detailed explanation of its contents.

We can use *scipy.cluster.hierarchy.fcluster* to see to which cluster each initial point would belong given a distance threshold:

```
>>> fcluster(Z, 0.9, criterion='distance')
array([ 7,  8,  9,  1,  2,  3, 10, 11, 12,  4,  6,  5], dtype=int32)
>>> fcluster(Z, 1.5, criterion='distance')
array([3, 3, 3, 1, 1, 1, 4, 4, 4, 2, 2, 2], dtype=int32)
>>> fcluster(Z, 4, criterion='distance')
array([2, 2, 2, 1, 1, 1, 2, 2, 2, 1, 1, 1], dtype=int32)
>>> fcluster(Z, 6, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also, *scipy.cluster.hierarchy.dendrogram* can be used to generate a plot of the dendrogram.

scipy.cluster.hierarchy.centroid

scipy.cluster.hierarchy.**centroid**(*y*)

Perform centroid/UPGMC linkage.

See *linkage* for more information on the input matrix, return structure, and algorithm.

The following are common calling conventions:

1. `Z = centroid(y)`

   Performs centroid/UPGMC linkage on the condensed distance matrix `y`.

2. `Z = centroid(X)`

   Performs centroid/UPGMC linkage on the observation matrix `X` using Euclidean distance as the distance metric.

Parameters

y [ndarray] A condensed distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of m observation vectors in n dimensions may be passed as an m by n array.

Returns

Z [ndarray] A linkage matrix containing the hierarchical clustering. See the *linkage* function documentation for more information on its structure.

See also:

linkage

for advanced creation of hierarchical clusterings.

scipy.spatial.distance.pdist

pairwise distance metrics

Examples

```
>>> from scipy.cluster.hierarchy import centroid, fcluster
>>> from scipy.spatial.distance import pdist
```

First, we need a toy dataset to play with:

```
x x    x x
x        x


x        x
x x    x x
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

Then, we get a condensed distance matrix from this dataset:

```
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```
>>> Z = centroid(y)
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.11803399,  3.        ],
       [ 5.        , 13.        ,  1.11803399,  3.        ],
       [ 8.        , 15.        ,  1.11803399,  3.        ],
       [11.        , 14.        ,  1.11803399,  3.        ],
       [18.        , 19.        ,  3.33333333,  6.        ],
       [16.        , 17.        ,  3.33333333,  6.        ],
       [20.        , 21.        ,  3.33333333, 12.        ]])
```

The linkage matrix `Z` represents a dendrogram - see *scipy.cluster.hierarchy.linkage* for a detailed explanation of its contents.

We can use *scipy.cluster.hierarchy.fcluster* to see to which cluster each initial point would belong given a distance threshold:

```
>>> fcluster(Z, 0.9, criterion='distance')
array([ 7,  8,  9, 10, 11, 12,  1,  2,  3,  4,  5,  6], dtype=int32)
>>> fcluster(Z, 1.1, criterion='distance')
array([5, 5, 6, 7, 7, 8, 1, 1, 2, 3, 3, 4], dtype=int32)
>>> fcluster(Z, 2, criterion='distance')
array([3, 3, 3, 4, 4, 4, 1, 1, 1, 2, 2, 2], dtype=int32)
>>> fcluster(Z, 4, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also, *scipy.cluster.hierarchy.dendrogram* can be used to generate a plot of the dendrogram.

scipy.cluster.hierarchy.median

scipy.cluster.hierarchy.**median**(*y*)

Perform median/WPGMC linkage.

See *linkage* for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = median(y)`
   Performs median/WPGMC linkage on the condensed distance matrix `y`. See `linkage` for more information on the return structure and algorithm.
2. `Z = median(X)`
   Performs median/WPGMC linkage on the observation matrix `X` using Euclidean distance as the distance metric. See *linkage* for more information on the return structure and algorithm.

Parameters

y [ndarray] A condensed distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns.

Alternatively, a collection of m observation vectors in n dimensions may be passed as an m by n array.

Returns

Z [ndarray] The hierarchical clustering encoded as a linkage matrix.

See also:

`linkage`

for advanced creation of hierarchical clusterings.

`scipy.spatial.distance.pdist`

pairwise distance metrics

Examples

```
>>> from scipy.cluster.hierarchy import median, fcluster
>>> from scipy.spatial.distance import pdist
```

First, we need a toy dataset to play with:

```
x x    x x
x        x

x        x
x x    x x
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

Then, we get a condensed distance matrix from this dataset:

```
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```
>>> Z = median(y)
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.11803399,  3.        ],
       [ 5.        , 13.        ,  1.11803399,  3.        ],
       [ 8.        , 15.        ,  1.11803399,  3.        ],
       [11.        , 14.        ,  1.11803399,  3.        ],
       [18.        , 19.        ,  3.        ,  6.        ],
       [16.        , 17.        ,  3.5       ,  6.        ],
       [20.        , 21.        ,  3.25      , 12.        ]])
```

The linkage matrix `Z` represents a dendrogram - see *scipy.cluster.hierarchy.linkage* for a detailed explanation of its contents.

We can use *scipy.cluster.hierarchy.fcluster* to see to which cluster each initial point would belong given a distance threshold:

```
>>> fcluster(Z, 0.9, criterion='distance')
array([ 7,  8,  9, 10, 11, 12,  1,  2,  3,  4,  5,  6], dtype=int32)
>>> fcluster(Z, 1.1, criterion='distance')
array([5, 5, 6, 7, 7, 8, 1, 1, 2, 3, 3, 4], dtype=int32)
>>> fcluster(Z, 2, criterion='distance')
array([3, 3, 3, 4, 4, 4, 1, 1, 1, 2, 2, 2], dtype=int32)
>>> fcluster(Z, 4, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also, *scipy.cluster.hierarchy.dendrogram* can be used to generate a plot of the dendrogram.

scipy.cluster.hierarchy.ward

scipy.cluster.hierarchy.**ward**(*y*)

Perform Ward's linkage on a condensed distance matrix.

See *linkage* for more information on the return structure and algorithm.

The following are common calling conventions:

1. `Z = ward(y)` Performs Ward's linkage on the condensed distance matrix `y`.
2. `Z = ward(X)` Performs Ward's linkage on the observation matrix `X` using Euclidean distance as the distance metric.

Parameters

y [ndarray] A condensed distance matrix. A condensed distance matrix is a flat array containing the upper triangular of the distance matrix. This is the form that `pdist` returns. Alternatively, a collection of m observation vectors in n dimensions may be passed as an m by n array.

Returns

Z [ndarray] The hierarchical clustering encoded as a linkage matrix. See *linkage* for more information on the return structure and algorithm.

See also:

linkage

for advanced creation of hierarchical clusterings.

scipy.spatial.distance.pdist

pairwise distance metrics

Examples

```
>>> from scipy.cluster.hierarchy import ward, fcluster
>>> from scipy.spatial.distance import pdist
```

First, we need a toy dataset to play with:

```
x x    x x
x        x

x        x
x x    x x
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

Then, we get a condensed distance matrix from this dataset:

```
>>> y = pdist(X)
```

Finally, we can perform the clustering:

```
>>> Z = ward(y)
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.29099445,  3.        ],
       [ 5.        , 13.        ,  1.29099445,  3.        ],
       [ 8.        , 14.        ,  1.29099445,  3.        ],
       [11.        , 15.        ,  1.29099445,  3.        ],
       [16.        , 17.        ,  5.77350269,  6.        ],
       [18.        , 19.        ,  5.77350269,  6.        ],
       [20.        , 21.        ,  8.16496581, 12.        ]])
```

The linkage matrix `Z` represents a dendrogram - see *scipy.cluster.hierarchy.linkage* for a detailed explanation of its contents.

We can use *scipy.cluster.hierarchy.fcluster* to see to which cluster each initial point would belong given a distance threshold:

```
>>> fcluster(Z, 0.9, criterion='distance')
array([ 1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12], dtype=int32)
>>> fcluster(Z, 1.1, criterion='distance')
array([1, 1, 2, 3, 3, 4, 5, 5, 6, 7, 7, 8], dtype=int32)
>>> fcluster(Z, 3, criterion='distance')
array([1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4], dtype=int32)
>>> fcluster(Z, 9, criterion='distance')
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], dtype=int32)
```

Also, *scipy.cluster.hierarchy.dendrogram* can be used to generate a plot of the dendrogram.

These routines compute statistics on hierarchies.

cophenet(Z[, Y])	Calculate the cophenetic distances between each observation in the hierarchical clustering defined by the linkage Z.
from_mlab_linkage(Z)	Convert a linkage matrix generated by MATLAB(TM) to a new linkage matrix compatible with this module.
inconsistent(Z[, d])	Calculate inconsistency statistics on a linkage matrix.
maxinconsts(Z, R)	Return the maximum inconsistency coefficient for each non-singleton cluster and its children.
maxdists(Z)	Return the maximum distance between any non-singleton cluster.
maxRstat(Z, R, i)	Return the maximum statistic for each non-singleton cluster and its children.
to_mlab_linkage(Z)	Convert a linkage matrix to a MATLAB(TM) compatible one.

scipy.cluster.hierarchy.cophenet

scipy.cluster.hierarchy.**cophenet**(*Z*, *Y=None*)

Calculate the cophenetic distances between each observation in the hierarchical clustering defined by the linkage Z.

Suppose p and q are original observations in disjoint clusters s and t, respectively and s and t are joined by a direct parent cluster u. The cophenetic distance between observations i and j is simply the distance between clusters s and t.

Parameters

Z [ndarray] The hierarchical clustering encoded as an array (see *linkage* function).

Y [ndarray (optional)] Calculates the cophenetic correlation coefficient c of a hierarchical clustering defined by the linkage matrix Z of a set of n observations in m dimensions. Y is the condensed distance matrix from which Z was generated.

Returns

c [ndarray] The cophentic correlation distance (if Y is passed).

d [ndarray] The cophenetic distance matrix in condensed form. The ij th entry is the cophenetic distance between original observations i and j.

See also:

linkage

for a description of what a linkage matrix is.

scipy.spatial.distance.squareform

transforming condensed matrices into square ones.

Examples

```
>>> from scipy.cluster.hierarchy import single, cophenet
>>> from scipy.spatial.distance import pdist, squareform
```

Given a dataset `X` and a linkage matrix `Z`, the cophenetic distance between two points of `X` is the distance between the largest two distinct clusters that each of the points:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

`X` corresponds to this dataset

```
x x     x x
x         x

x         x
x x     x x
```

```
>>> Z = single(pdist(X))
>>> Z
array([[ 0.,  1.,  1.,  2.],
       [ 2., 12.,  1.,  3.],
       [ 3.,  4.,  1.,  2.],
       [ 5., 14.,  1.,  3.],
       [ 6.,  7.,  1.,  2.],
       [ 8., 16.,  1.,  3.],
       [ 9., 10.,  1.,  2.],
       [11., 18.,  1.,  3.],
       [13., 15.,  2.,  6.],
       [17., 20.,  2.,  9.],
       [19., 21.,  2., 12.]])
>>> cophenet(Z)
array([1., 1., 2., 2., 2., 2., 2., 2., 2., 2., 2., 1., 2., 2., 2., 2., 2.,
       2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 1., 1., 2., 2.,
       2., 2., 2., 2., 1., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2., 2.,
       1., 1., 2., 2., 2., 1., 2., 2., 2., 2., 2., 2., 1., 1., 1.])
```

The output of the *scipy.cluster.hierarchy.cophenet* method is represented in condensed form. We can use *scipy.spatial.distance.squareform* to see the output as a regular matrix (where each element `ij` denotes the cophenetic distance between each `i`, `j` pair of points in `X`):

```
>>> squareform(cophenet(Z))
array([[0., 1., 1., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
       [1., 0., 1., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
       [1., 1., 0., 2., 2., 2., 2., 2., 2., 2., 2., 2.],
       [2., 2., 2., 0., 1., 1., 2., 2., 2., 2., 2., 2.],
       [2., 2., 2., 1., 0., 1., 2., 2., 2., 2., 2., 2.],
       [2., 2., 2., 1., 1., 0., 2., 2., 2., 2., 2., 2.],
       [2., 2., 2., 2., 2., 2., 0., 1., 1., 2., 2., 2.],
       [2., 2., 2., 2., 2., 2., 1., 0., 1., 2., 2., 2.],
```

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```
       [2., 2., 2., 2., 2., 2., 1., 1., 0., 2., 2., 2.],
       [2., 2., 2., 2., 2., 2., 2., 2., 2., 0., 1., 1.],
       [2., 2., 2., 2., 2., 2., 2., 2., 2., 1., 0., 1.],
       [2., 2., 2., 2., 2., 2., 2., 2., 2., 1., 1., 0.]])
```

In this example, the cophenetic distance between points on `X` that are very close (i.e., in the same corner) is 1. For other pairs of points is 2, because the points will be located in clusters at different corners - thus, the distance between these clusters will be larger.

scipy.cluster.hierarchy.from_mlab_linkage

`scipy.cluster.hierarchy.`**`from_mlab_linkage`**`(Z)`

Convert a linkage matrix generated by MATLAB(TM) to a new linkage matrix compatible with this module.

The conversion does two things:

- the indices are converted from `1..N` to `0..(N-1)` form, and
- a fourth column `Z[:,3]` is added where `Z[i,3]` represents the number of original observations (leaves) in the non-singleton cluster `i`.

This function is useful when loading in linkages from legacy data files generated by MATLAB.

Parameters

Z [ndarray] A linkage matrix generated by MATLAB(TM).

Returns

ZS [ndarray] A linkage matrix compatible with `scipy.cluster.hierarchy`.

See also:

`linkage`

for a description of what a linkage matrix is.

`to_mlab_linkage`

transform from SciPy to MATLAB format.

Examples

```
>>> import numpy as np
>>> from scipy.cluster.hierarchy import ward, from_mlab_linkage
```

Given a linkage matrix in MATLAB format `mZ`, we can use *`scipy.cluster.hierarchy.from_mlab_linkage`* to import it into SciPy format:

```
>>> mZ = np.array([[1, 2, 1], [4, 5, 1], [7, 8, 1],
...                [10, 11, 1], [3, 13, 1.29099445],
...                [6, 14, 1.29099445],
...                [9, 15, 1.29099445],
...                [12, 16, 1.29099445],
...                [17, 18, 5.77350269],
...                [19, 20, 5.77350269],
...                [21, 22,  8.16496581]])
```

```
>>> Z = from_mlab_linkage(mZ)
>>> Z
array([[  0.        ,   1.        ,   1.        ,   2.        ],
       [  3.        ,   4.        ,   1.        ,   2.        ],
       [  6.        ,   7.        ,   1.        ,   2.        ],
       [  9.        ,  10.        ,   1.        ,   2.        ],
       [  2.        ,  12.        ,   1.29099445,   3.        ],
       [  5.        ,  13.        ,   1.29099445,   3.        ],
       [  8.        ,  14.        ,   1.29099445,   3.        ],
       [ 11.        ,  15.        ,   1.29099445,   3.        ],
       [ 16.        ,  17.        ,   5.77350269,   6.        ],
       [ 18.        ,  19.        ,   5.77350269,   6.        ],
       [ 20.        ,  21.        ,   8.16496581,  12.        ]])
```

As expected, the linkage matrix `Z` returned includes an additional column counting the number of original samples in each cluster. Also, all cluster indices are reduced by 1 (MATLAB format uses 1-indexing, whereas SciPy uses 0-indexing).

scipy.cluster.hierarchy.inconsistent

`scipy.cluster.hierarchy.`**`inconsistent`**(*Z*, *d=2*)

Calculate inconsistency statistics on a linkage matrix.

Parameters

Z [ndarray] The $(n-1)$ by 4 matrix encoding the linkage (hierarchical clustering). See *`linkage`* documentation for more information on its form.

d [int, optional] The number of links up to d levels below each non-singleton cluster.

Returns

R [ndarray] A $(n-1)$ by 4 matrix where the `i`'th row contains the link statistics for the non-singleton cluster `i`. The link statistics are computed over the link heights for links d levels below the cluster `i`. `R[i,0]` and `R[i,1]` are the mean and standard deviation of the link heights, respectively; `R[i,2]` is the number of links included in the calculation; and `R[i,3]` is the inconsistency coefficient,

$$\frac{\mathtt{Z}[\mathtt{i},2] - \mathtt{R}[\mathtt{i},0]}{R[i,1]}$$

Notes

This function behaves similarly to the MATLAB(TM) `inconsistent` function.

Examples

```
>>> from scipy.cluster.hierarchy import inconsistent, linkage
>>> from matplotlib import pyplot as plt
>>> X = [[i] for i in [2, 8, 0, 4, 1, 9, 9, 0]]
>>> Z = linkage(X, 'ward')
>>> print(Z)
[[ 5.          6.          0.          2.        ]
 [ 2.          7.          0.          2.        ]
 [ 0.          4.          1.          2.        ]
 [ 1.          8.          1.15470054  3.        ]
 [ 9.         10.          2.12132034  4.        ]
 [ 3.         12.          4.11096096  5.        ]
 [11.         13.         14.07183949  8.        ]]
>>> inconsistent(Z)
array([[ 0.        ,  0.        ,  1.        ,  0.        ],
       [ 0.        ,  0.        ,  1.        ,  0.        ],
       [ 1.        ,  0.        ,  1.        ,  0.        ],
       [ 0.57735027,  0.81649658,  2.        ,  0.70710678],
       [ 1.04044011,  1.06123822,  3.        ,  1.01850858],
       [ 3.11614065,  1.40688837,  2.        ,  0.70710678],
       [ 6.44583366,  6.76770586,  3.        ,  1.12682288]])
```

scipy.cluster.hierarchy.maxinconsts

scipy.cluster.hierarchy.**maxinconsts**(*Z*, *R*)

Return the maximum inconsistency coefficient for each non-singleton cluster and its children.

Parameters

Z [ndarray] The hierarchical clustering encoded as a matrix. See *linkage* for more information.

R [ndarray] The inconsistency matrix.

Returns

MI [ndarray] A monotonic (n-1)-sized numpy array of doubles.

See also:

linkage

for a description of what a linkage matrix is.

inconsistent

for the creation of a inconsistency matrix.

Examples

```
>>> from scipy.cluster.hierarchy import median, inconsistent, maxinconsts
>>> from scipy.spatial.distance import pdist
```

Given a data set `X`, we can apply a clustering method to obtain a linkage matrix `Z`. *scipy.cluster.hierarchy.inconsistent* can be also used to obtain the inconsistency matrix `R` associated to this clustering process:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = median(pdist(X))
>>> R = inconsistent(Z)
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.11803399,  3.        ],
       [ 5.        , 13.        ,  1.11803399,  3.        ],
       [ 8.        , 15.        ,  1.11803399,  3.        ],
       [11.        , 14.        ,  1.11803399,  3.        ],
       [18.        , 19.        ,  3.        ,  6.        ],
       [16.        , 17.        ,  3.5       ,  6.        ],
       [20.        , 21.        ,  3.25      , 12.        ]])
>>> R
array([[1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.05901699, 0.08346263, 2.        , 0.70710678],
       [1.05901699, 0.08346263, 2.        , 0.70710678],
       [1.05901699, 0.08346263, 2.        , 0.70710678],
       [1.05901699, 0.08346263, 2.        , 0.70710678],
       [1.74535599, 1.08655358, 3.        , 1.15470054],
       [1.91202266, 1.37522872, 3.        , 1.15470054],
       [3.25      , 0.25      , 3.        , 0.        ]])
```

Here, *scipy.cluster.hierarchy.maxinconsts* can be used to compute the maximum value of the inconsistency statistic (the last column of `R`) for each non-singleton cluster and its children:

```
>>> maxinconsts(Z, R)
array([0.        , 0.        , 0.        , 0.        , 0.70710678,
       0.70710678, 0.70710678, 0.70710678, 1.15470054, 1.15470054,
       1.15470054])
```

scipy.cluster.hierarchy.maxdists

scipy.cluster.hierarchy.**maxdists**(*Z*)

Return the maximum distance between any non-singleton cluster.

Parameters

Z [ndarray] The hierarchical clustering encoded as a matrix. See `linkage` for more information.

Returns

maxdists [ndarray] A `(n-1)` sized numpy array of doubles; `MD[i]` represents the maximum distance between any cluster (including singletons) below and including the node with index i. More specifically, `MD[i] = Z[Q(i)-n, 2].max()` where `Q(i)` is the set of all node indices below and including node i.

See also:

linkage

for a description of what a linkage matrix is.

is_monotonic

for testing for monotonicity of a linkage matrix.

Examples

```
>>> from scipy.cluster.hierarchy import median, maxdists
>>> from scipy.spatial.distance import pdist
```

Given a linkage matrix `Z`, *scipy.cluster.hierarchy.maxdists* computes for each new cluster generated (i.e., for each row of the linkage matrix) what is the maximum distance between any two child clusters.

Due to the nature of hierarchical clustering, in many cases this is going to be just the distance between the two child clusters that were merged to form the current one - that is, Z[:,2].

However, for non-monotonic cluster assignments such as *scipy.cluster.hierarchy.median* clustering this is not always the case: There may be cluster formations were the distance between the two clusters merged is smaller than the distance between their children.

We can see this in an example:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = median(pdist(X))
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.11803399,  3.        ],
       [ 5.        , 13.        ,  1.11803399,  3.        ],
```

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```
       [ 8.        , 15.        ,  1.11803399,  3.        ],
       [11.        , 14.        ,  1.11803399,  3.        ],
       [18.        , 19.        ,  3.        ,  6.        ],
       [16.        , 17.        ,  3.5       ,  6.        ],
       [20.        , 21.        ,  3.25      , 12.        ]])
>>> maxdists(Z)
array([1.        , 1.        , 1.        , 1.        , 1.11803399,
       1.11803399, 1.11803399, 1.11803399, 3.        , 3.5       ,
       3.5       ])
```

Note that while the distance between the two clusters merged when creating the last cluster is 3.25, there are two children (clusters 16 and 17) whose distance is larger (3.5). Thus, *scipy.cluster.hierarchy.maxdists* returns 3.5 in this case.

scipy.cluster.hierarchy.maxRstat

scipy.cluster.hierarchy.**maxRstat**(*Z*, *R*, *i*)

Return the maximum statistic for each non-singleton cluster and its children.

Parameters

Z	[array_like] The hierarchical clustering encoded as a matrix. See *linkage* for more information.
R	[array_like] The inconsistency matrix.
i	[int] The column of *R* to use as the statistic.

Returns

MR	[ndarray] Calculates the maximum statistic for the i'th column of the inconsistency matrix *R* for each non-singleton cluster node. `MR[j]` is the maximum over `R[Q(j)-n, i]`, where `Q(j)` the set of all node ids corresponding to nodes below and including `j`.

See also:

linkage

for a description of what a linkage matrix is.

inconsistent

for the creation of a inconsistency matrix.

Examples

```
>>> from scipy.cluster.hierarchy import median, inconsistent, maxRstat
>>> from scipy.spatial.distance import pdist
```

Given a data set `X`, we can apply a clustering method to obtain a linkage matrix `Z`. *scipy.cluster.hierarchy.inconsistent* can be also used to obtain the inconsistency matrix `R` associated to this clustering process:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = median(pdist(X))
>>> R = inconsistent(Z)
>>> R
array([[1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.05901699, 0.08346263, 2.        , 0.70710678],
       [1.05901699, 0.08346263, 2.        , 0.70710678],
       [1.05901699, 0.08346263, 2.        , 0.70710678],
       [1.05901699, 0.08346263, 2.        , 0.70710678],
       [1.74535599, 1.08655358, 3.        , 1.15470054],
       [1.91202266, 1.37522872, 3.        , 1.15470054],
       [3.25      , 0.25      , 3.        , 0.        ]])
```

scipy.cluster.hierarchy.maxRstat can be used to compute the maximum value of each column of `R`, for each non-singleton cluster and its children:

```
>>> maxRstat(Z, R, 0)
array([1.        , 1.        , 1.        , 1.        , 1.05901699,
       1.05901699, 1.05901699, 1.05901699, 1.74535599, 1.91202266,
       3.25      ])
>>> maxRstat(Z, R, 1)
array([0.        , 0.        , 0.        , 0.        , 0.08346263,
       0.08346263, 0.08346263, 0.08346263, 1.08655358, 1.37522872,
       1.37522872])
>>> maxRstat(Z, R, 3)
array([0.        , 0.        , 0.        , 0.        , 0.70710678,
       0.70710678, 0.70710678, 0.70710678, 1.15470054, 1.15470054,
       1.15470054])
```

scipy.cluster.hierarchy.to_mlab_linkage

scipy.cluster.hierarchy.**to_mlab_linkage**(*Z*)

Convert a linkage matrix to a MATLAB(TM) compatible one.

Converts a linkage matrix `Z` generated by the linkage function of this module to a MATLAB(TM) compatible one. The return linkage matrix has the last column removed and the cluster indices are converted to `1..N` indexing.

Parameters

Z [ndarray] A linkage matrix generated by `scipy.cluster.hierarchy`.

Returns

to_mlab_linkage

[ndarray] A linkage matrix compatible with MATLAB(TM)'s hierarchical clustering functions.
The return linkage matrix has the last column removed and the cluster indices are converted to `1..N` indexing.

See also:

linkage

for a description of what a linkage matrix is.

from_mlab_linkage

transform from Matlab to SciPy format.

Examples

```
>>> from scipy.cluster.hierarchy import ward, to_mlab_linkage
>>> from scipy.spatial.distance import pdist
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = ward(pdist(X))
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.29099445,  3.        ],
       [ 5.        , 13.        ,  1.29099445,  3.        ],
       [ 8.        , 14.        ,  1.29099445,  3.        ],
       [11.        , 15.        ,  1.29099445,  3.        ],
       [16.        , 17.        ,  5.77350269,  6.        ],
       [18.        , 19.        ,  5.77350269,  6.        ],
       [20.        , 21.        ,  8.16496581, 12.        ]])
```

After a linkage matrix `Z` has been created, we can use *scipy.cluster.hierarchy.to_mlab_linkage* to convert it into MATLAB format:

```
>>> mZ = to_mlab_linkage(Z)
>>> mZ
array([[  1.        ,   2.        ,   1.        ],
       [  4.        ,   5.        ,   1.        ],
       [  7.        ,   8.        ,   1.        ],
       [ 10.        ,  11.        ,   1.        ],
       [  3.        ,  13.        ,   1.29099445],
       [  6.        ,  14.        ,   1.29099445],
       [  9.        ,  15.        ,   1.29099445],
       [ 12.        ,  16.        ,   1.29099445],
       [ 17.        ,  18.        ,   5.77350269],
       [ 19.        ,  20.        ,   5.77350269],
       [ 21.        ,  22.        ,   8.16496581]])
```

The new linkage matrix `mZ` uses 1-indexing for all the clusters (instead of 0-indexing). Also, the last column of the original linkage matrix has been dropped.

Routines for visualizing flat clusters.

dendrogram(Z[, p, truncate_mode, …])	Plot the hierarchical clustering as a dendrogram.

scipy.cluster.hierarchy.dendrogram

scipy.cluster.hierarchy.**dendrogram**(*Z*, *p=30*, *truncate_mode=None*, *color_threshold=None*, *get_leaves=True*, *orientation='top'*, *labels=None*, *count_sort=False*, *distance_sort=False*, *show_leaf_counts=True*, *no_plot=False*, *no_labels=False*, *leaf_font_size=None*, *leaf_rotation=None*, *leaf_label_func=None*, *show_contracted=False*, *link_color_func=None*, *ax=None*, *above_threshold_color='C0'*)

Plot the hierarchical clustering as a dendrogram.

The dendrogram illustrates how each cluster is composed by drawing a U-shaped link between a non-singleton cluster and its children. The top of the U-link indicates a cluster merge. The two legs of the U-link indicate which clusters were merged. The length of the two legs of the U-link represents the distance between the child clusters. It is also the cophenetic distance between original observations in the two children clusters.

Parameters

Z [ndarray] The linkage matrix encoding the hierarchical clustering to render as a dendrogram. See the `linkage` function for more information on the format of `Z`.

p [int, optional] The `p` parameter for `truncate_mode`.

truncate_mode

[str, optional] The dendrogram can be hard to read when the original observation matrix from which the linkage is derived is large. Truncation is used to condense the dendrogram. There are several modes:

- **None** No truncation is performed (default). Note: `'none'` is an alias for `None` that's kept for backward compatibility.
- **'lastp'** The last `p` non-singleton clusters formed in the linkage are the only non-leaf nodes in the linkage; they correspond to rows `Z[n-p-2:end]` in `Z`. All other non-singleton clusters are contracted into leaf nodes.
- **'level'** No more than `p` levels of the dendrogram tree are displayed. A "level" includes all nodes with `p` merges from the final merge.
  Note: `'mtica'` is an alias for `'level'` that's kept for backward compatibility.

color_threshold

[double, optional] For brevity, let t be the `color_threshold`. Colors all the descendent links below a cluster node k the same color if k is the first node below the cut threshold t. All links connecting nodes with distances greater than or equal to the threshold are colored with de default matplotlib color `'C0'`. If t is less than or equal to zero, all nodes are colored `'C0'`. If `color_threshold` is None or 'default', corresponding with MATLAB(TM) behavior, the threshold is set to `0.7*max(Z[:,2])`.

get_leaves [bool, optional] Includes a list `R['leaves']=H` in the result dictionary. For each i, `H[i] == j`, cluster node `j` appears in position `i` in the left-to-right traversal of the leaves, where $j < 2n-1$ and $i < n$.

orientation

[str, optional] The direction to plot the dendrogram, which can be any of the following strings:

- **'top'** Plots the root at the top, and plot descendent links going downwards. (default).
- **'bottom'** Plots the root at the bottom, and plot descendent links going upwards.
- **'left'** Plots the root at the left, and plot descendent links going right.
- **'right'** Plots the root at the right, and plot descendent links going left.

labels [ndarray, optional] By default, `labels` is None so the index of the original observation is used to label the leaf nodes. Otherwise, this is an n-sized sequence, with `n == Z.shape[0] + 1`. The `labels[i]` value is the text to put under the i th leaf node only if it corresponds to an original observation and not a non-singleton cluster.

count_sort

[str or bool, optional] For each node n, the order (visually, from left-to-right) n's two descendent links are plotted is determined by this parameter, which can be any of the following values:

False Nothing is done.

'ascending' or True
The child with the minimum number of original objects in its cluster is plotted first.

'descending'
The child with the maximum number of original objects in its cluster is plotted first.

Note, `distance_sort` and `count_sort` cannot both be True.

distance_sort

[str or bool, optional] For each node n, the order (visually, from left-to-right) n's two descendent links are plotted is determined by this parameter, which can be any of the following values:

False Nothing is done.

'ascending' or True
The child with the minimum distance between its direct descendents is plotted first.

'descending'
The child with the maximum distance between its direct descendents is plotted first.

Note `distance_sort` and `count_sort` cannot both be True.

show_leaf_counts

[bool, optional] When True, leaf nodes representing $k > 1$ original observation are labeled with the number of observations they contain in parentheses.

no_plot [bool, optional] When True, the final rendering is not performed. This is useful if only the data structures computed for the rendering are needed or if matplotlib is not available.

no_labels [bool, optional] When True, no labels appear next to the leaf nodes in the rendering of the dendrogram.

leaf_rotation

[double, optional] Specifies the angle (in degrees) to rotate the leaf labels. When unspecified, the rotation is based on the number of nodes in the dendrogram (default is 0).

leaf_font_size

[int, optional] Specifies the font size (in points) of the leaf labels. When unspecified, the size based on the number of nodes in the dendrogram.

leaf_label_func

[lambda or function, optional] When `leaf_label_func` is a callable function, for each leaf with cluster index $k < 2n - 1$. The function is expected to return a string with the label for the leaf.

Indices $k < n$ correspond to original observations while indices $k \geq n$ correspond to non-singleton clusters.

For example, to label singletons with their node id and non-singletons with their id, count, and inconsistency coefficient, simply do:

```
# First define the leaf label function.
def llf(id):
    if id < n:
        return str(id)
    else:
        return '[%d %d %1.2f]' % (id, count, R[n-id,3])
```

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```
# The text for the leaf nodes is going to be big so force
# a rotation of 90 degrees.
dendrogram(Z, leaf_label_func=llf, leaf_rotation=90)

# leaf_label_func can also be used together with
↪``truncate_mode`` parameter,
# in which case you will get your leaves labeled after
↪truncation:
dendrogram(Z, leaf_label_func=llf, leaf_rotation=90,
           truncate_mode='level', p=2)
```

show_contracted
: [bool, optional] When True the heights of non-singleton nodes contracted into a leaf node are plotted as crosses along the link connecting that leaf node. This really is only useful when truncation is used (see `truncate_mode` parameter).

link_color_func
: [callable, optional] If given, *link_color_function* is called with each non-singleton id corresponding to each U-shaped link it will paint. The function is expected to return the color to paint the link, encoded as a matplotlib color string code. For example:

```
dendrogram(Z, link_color_func=lambda k: colors[k])
```

colors the direct links below each untruncated non-singleton node `k` using `colors[k]`.

ax
: [matplotlib Axes instance, optional] If None and *no_plot* is not True, the dendrogram will be plotted on the current axes. Otherwise if *no_plot* is not True the dendrogram will be plotted on the given `Axes` instance. This can be useful if the dendrogram is part of a more complex figure.

above_threshold_color
: [str, optional] This matplotlib color string sets the color of the links above the color_threshold. The default is `'C0'`.

Returns

R
: [dict] A dictionary of data structures computed to render the dendrogram. Its has the following keys:

  `'color_list'`
  : A list of color names. The k'th element represents the color of the k'th link.

  `'icoord'` and `'dcoord'`
  : Each of them is a list of lists. Let `icoord = [I1, I2, ..., Ip]` where `Ik = [xk1, xk2, xk3, xk4]` and `dcoord = [D1, D2, ..., Dp]` where `Dk = [yk1, yk2, yk3, yk4]`, then the k'th link painted is `(xk1, yk1) - (xk2, yk2) - (xk3, yk3) - (xk4, yk4)`.

  `'ivl'`
  : A list of labels corresponding to the leaf nodes.

  `'leaves'`
  : For each i, `H[i] == j`, cluster node `j` appears in position `i` in the left-to-right traversal of the leaves, where $j < 2n-1$ and $i < n$. If `j` is less than `n`, the `i`-th leaf node corresponds to an original observation. Otherwise, it corresponds to a non-singleton cluster.

  `'leaves_color_list'`
  : A list of color names. The k'th element represents the color of the k'th leaf.

See also:

`linkage`, **`set_link_color_palette`**

Notes

It is expected that the distances in `Z[:,2]` be monotonic, otherwise crossings appear in the dendrogram.

Examples

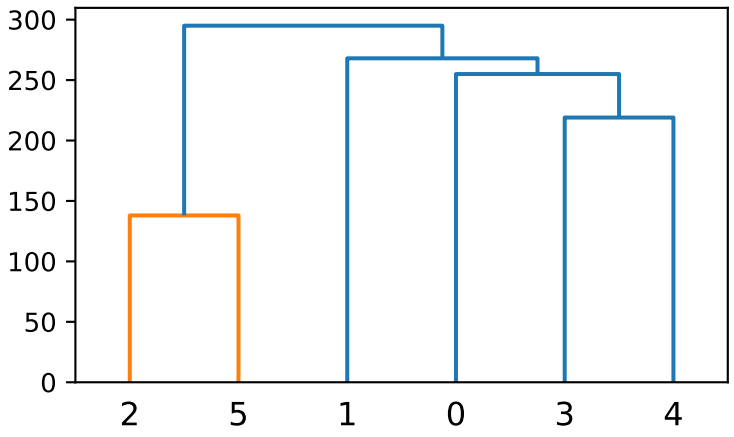
```
>>> from scipy.cluster import hierarchy
>>> import matplotlib.pyplot as plt
```

A very basic example:

```
>>> ytdist = np.array([662., 877., 255., 412., 996., 295., 468., 268.,
...                    400., 754., 564., 138., 219., 869., 669.])
>>> Z = hierarchy.linkage(ytdist, 'single')
>>> plt.figure()
>>> dn = hierarchy.dendrogram(Z)
```

Now, plot in given axes, improve the color scheme and use both vertical and horizontal orientations:

```
>>> hierarchy.set_link_color_palette(['m', 'c', 'y', 'k'])
>>> fig, axes = plt.subplots(1, 2, figsize=(8, 3))
>>> dn1 = hierarchy.dendrogram(Z, ax=axes[0], above_threshold_color='y',
...                            orientation='top')
>>> dn2 = hierarchy.dendrogram(Z, ax=axes[1],
...                            above_threshold_color='#bcbddc',
...                            orientation='right')
>>> hierarchy.set_link_color_palette(None)  # reset to default after use
>>> plt.show()
```



These are data structures and routines for representing hierarchies as tree objects.

ClusterNode(id[, left, right, dist, count])	A tree node class for representing a cluster.

continues on next page

Table 6 – continued from previous page

leaves_list(Z)	Return a list of leaf node ids.
to_tree(Z[, rd])	Convert a linkage matrix into an easy-to-use tree object.
cut_tree(Z[, n_clusters, height])	Given a linkage matrix Z, return the cut tree.
optimal_leaf_ordering(Z, y[, metric])	Given a linkage matrix Z and distance, reorder the cut tree.

scipy.cluster.hierarchy.ClusterNode

class scipy.cluster.hierarchy.**ClusterNode**(*id*, *left=None*, *right=None*, *dist=0*, *count=1*)

A tree node class for representing a cluster.

Leaf nodes correspond to original observations, while non-leaf nodes correspond to non-singleton clusters.

The *to_tree* function converts a matrix returned by the linkage function into an easy-to-use tree representation.

All parameter names are also attributes.

Parameters

id	[int] The node id.
left	[ClusterNode instance, optional] The left child tree node.
right	[ClusterNode instance, optional] The right child tree node.
dist	[float, optional] Distance for this cluster in the linkage matrix.
count	[int, optional] The number of samples in this cluster.

See also:

to_tree

for converting a linkage matrix Z into a tree object.

Methods

get_count()	The number of leaf nodes (original observations) belonging to the cluster node nd.
get_id()	The identifier of the target node.
get_left()	Return a reference to the left child tree object.
get_right()	Return a reference to the right child tree object.
is_leaf()	Return True if the target node is a leaf.
pre_order([func])	Perform pre-order traversal without recursive function calls.

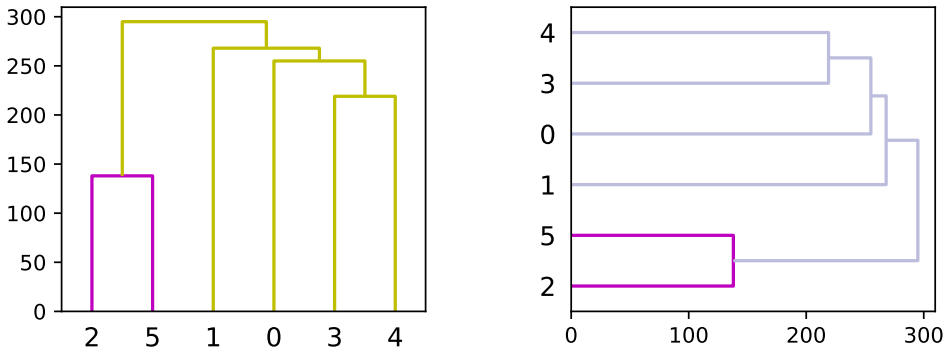
scipy.cluster.hierarchy.ClusterNode.get_count

ClusterNode.**get_count**()

The number of leaf nodes (original observations) belonging to the cluster node nd. If the target node is a leaf, 1 is returned.

Returns

get_count [int] The number of leaf nodes below the target node.



scipy.cluster.hierarchy.ClusterNode.get_id

`ClusterNode.`**`get_id`**`()`

The identifier of the target node.

For `0 <= i < n`, *i* corresponds to original observation i. For `n <= i < 2n-1`, *i* corresponds to non-singleton cluster formed at iteration `i-n`.

Returns

id [int] The identifier of the target node.

scipy.cluster.hierarchy.ClusterNode.get_left

`ClusterNode.`**`get_left`**`()`

Return a reference to the left child tree object.

Returns

left [ClusterNode] The left child of the target node. If the node is a leaf, None is returned.

scipy.cluster.hierarchy.ClusterNode.get_right

`ClusterNode.`**`get_right`**`()`

Return a reference to the right child tree object.

Returns

right [ClusterNode] The left child of the target node. If the node is a leaf, None is returned.

scipy.cluster.hierarchy.ClusterNode.is_leaf

`ClusterNode.`**`is_leaf`**`()`

Return True if the target node is a leaf.

Returns

leafness [bool] True if the target node is a leaf node.

scipy.cluster.hierarchy.ClusterNode.pre_order

ClusterNode.**pre_order**(*func=<function ClusterNode.<lambda>>*)

Perform pre-order traversal without recursive function calls.

When a leaf node is first encountered, `func` is called with the leaf node as its argument, and its result is appended to the list.

For example, the statement:

```
ids = root.pre_order(lambda x: x.id)
```

returns a list of the node ids corresponding to the leaf nodes of the tree as they appear from left to right.

Parameters

func [function] Applied to each leaf ClusterNode object in the pre-order traversal. Given the `i`-th leaf node in the pre-order traversal `n[i]`, the result of `func(n[i])` is stored in `L[i]`. If not provided, the index of the original observation to which the node corresponds is used.

Returns

L [list] The pre-order traversal.

scipy.cluster.hierarchy.leaves_list

scipy.cluster.hierarchy.**leaves_list**(*Z*)

Return a list of leaf node ids.

The return corresponds to the observation vector index as it appears in the tree from left to right. Z is a linkage matrix.

Parameters

Z [ndarray] The hierarchical clustering encoded as a matrix. *Z* is a linkage matrix. See *linkage* for more information.

Returns

leaves_list [ndarray] The list of leaf node ids.

See also:

dendrogram

for information about dendrogram structure.

Examples

```
>>> from scipy.cluster.hierarchy import ward, dendrogram, leaves_list
>>> from scipy.spatial.distance import pdist
>>> from matplotlib import pyplot as plt
```

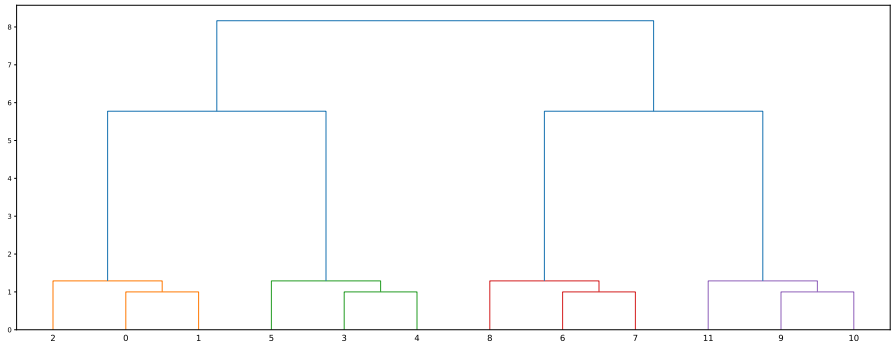
```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = ward(pdist(X))
```

The linkage matrix `Z` represents a dendrogram, that is, a tree that encodes the structure of the clustering performed. *scipy.cluster.hierarchy.leaves_list* shows the mapping between indices in the `X` dataset and leaves in the dendrogram:

```
>>> leaves_list(Z)
array([ 2,  0,  1,  5,  3,  4,  8,  6,  7, 11,  9, 10], dtype=int32)
```

```
>>> fig = plt.figure(figsize=(25, 10))
>>> dn = dendrogram(Z)
>>> plt.show()
```



scipy.cluster.hierarchy.to_tree

`scipy.cluster.hierarchy.`**`to_tree`**(*Z*, *rd=False*)

Convert a linkage matrix into an easy-to-use tree object.

The reference to the root *ClusterNode* object is returned (by default).

Each *ClusterNode* object has a `left`, `right`, `dist`, `id`, and `count` attribute. The left and right attributes point to ClusterNode objects that were combined to generate the cluster. If both are None then the *ClusterNode* object is a leaf node, its count must be 1, and its distance is meaningless but set to 0.

Note: This function is provided for the convenience of the library user. ClusterNodes are not used as input to any of the functions in this library.

Parameters

Z [ndarray] The linkage matrix in proper form (see the *linkage* function documentation).

rd [bool, optional] When False (default), a reference to the root *ClusterNode* object is returned. Otherwise, a tuple `(r, d)` is returned. `r` is a reference to the root node while `d` is a list of *ClusterNode* objects - one per original entry in the linkage matrix plus entries for all clustering steps. If a cluster id is less than the number of samples `n` in the data that the linkage matrix describes, then it corresponds to a singleton cluster (leaf node). See *linkage* for more information on the assignment of cluster ids to clusters.

Returns

tree [ClusterNode or tuple (ClusterNode, list of ClusterNode)] If `rd` is False, a *ClusterNode*. If `rd` is True, a list of length `2*n - 1`, with `n` the number of samples. See the description of *rd* above for more details.

See also:

linkage, **is_valid_linkage**, **ClusterNode**

Examples

```
>>> from scipy.cluster import hierarchy
>>> rng = np.random.default_rng()
>>> x = rng.random((5, 2))
>>> Z = hierarchy.linkage(x)
>>> hierarchy.to_tree(Z)
<scipy.cluster.hierarchy.ClusterNode object at ...
>>> rootnode, nodelist = hierarchy.to_tree(Z, rd=True)
>>> rootnode
<scipy.cluster.hierarchy.ClusterNode object at ...
>>> len(nodelist)
9
```

scipy.cluster.hierarchy.cut_tree

scipy.cluster.hierarchy.**cut_tree**(*Z*, *n_clusters=None*, *height=None*)

Given a linkage matrix Z, return the cut tree.

Parameters

Z [scipy.cluster.linkage array] The linkage matrix.
n_clusters [array_like, optional] Number of clusters in the tree at the cut point.
height [array_like, optional] The height at which to cut the tree. Only possible for ultrametric trees.

Returns

cutree [array] An array indicating group membership at each agglomeration step. I.e., for a full cut tree, in the first column each data point is in its own cluster. At the next step, two nodes are merged. Finally, all singleton and non-singleton clusters are in one group. If *n_clusters* or *height* are given, the columns correspond to the columns of *n_clusters* or *height*.

Examples

```
>>> from scipy import cluster
>>> import numpy as np
>>> from numpy.random import default_rng
>>> rng = default_rng()
>>> X = rng.random((50, 4))
>>> Z = cluster.hierarchy.ward(X)
>>> cutree = cluster.hierarchy.cut_tree(Z, n_clusters=[5, 10])
>>> cutree[:10]
array([[0, 0],
       [1, 1],
```

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```
        [2, 2],
        [3, 3],
        [3, 4],
        [2, 2],
        [0, 0],
        [1, 5],
        [3, 6],
        [4, 7]])  # random
```

scipy.cluster.hierarchy.optimal_leaf_ordering

scipy.cluster.hierarchy.**optimal_leaf_ordering**(*Z*, *y*, *metric='euclidean'*)

Given a linkage matrix Z and distance, reorder the cut tree.

Parameters

Z [ndarray] The hierarchical clustering encoded as a linkage matrix. See *linkage* for more information on the return structure and algorithm.

y [ndarray] The condensed distance matrix from which Z was generated. Alternatively, a collection of m observation vectors in n dimensions may be passed as an m by n array.

metric [str or function, optional] The distance metric to use in the case that y is a collection of observation vectors; ignored otherwise. See the pdist function for a list of valid distance metrics. A custom distance function can also be used.

Returns

Z_ordered [ndarray] A copy of the linkage matrix Z, reordered to minimize the distance between adjacent leaves.

Examples

```
>>> from scipy.cluster import hierarchy
>>> rng = np.random.default_rng()
>>> X = rng.standard_normal((10, 10))
>>> Z = hierarchy.ward(X)
>>> hierarchy.leaves_list(Z)
array([0, 3, 1, 9, 2, 5, 7, 4, 6, 8], dtype=int32)
>>> hierarchy.leaves_list(hierarchy.optimal_leaf_ordering(Z, X))
array([3, 0, 2, 5, 7, 4, 8, 6, 9, 1], dtype=int32)
```

These are predicates for checking the validity of linkage and inconsistency matrices as well as for checking isomorphism of two flat cluster assignments.

is_valid_im(R[, warning, throw, name])	Return True if the inconsistency matrix passed is valid.
is_valid_linkage(Z[, warning, throw, name])	Check the validity of a linkage matrix.
is_isomorphic(T1, T2)	Determine if two different cluster assignments are equivalent.
is_monotonic(Z)	Return True if the linkage passed is monotonic.
correspond(Z, Y)	Check for correspondence between linkage and condensed distance matrices.

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Table 8 – continued from previous page

num_obs_linkage(Z)	Return the number of original observations of the linkage matrix passed.

scipy.cluster.hierarchy.is_valid_im

scipy.cluster.hierarchy.**is_valid_im**(*R*, *warning=False*, *throw=False*, *name=None*)

Return True if the inconsistency matrix passed is valid.

It must be a n by 4 array of doubles. The standard deviations `R[:,1]` must be nonnegative. The link counts `R[:,2]` must be positive and no greater than $n-1$.

Parameters

R	[ndarray] The inconsistency matrix to check for validity.
warning	[bool, optional] When True, issues a Python warning if the linkage matrix passed is invalid.
throw	[bool, optional] When True, throws a Python exception if the linkage matrix passed is invalid.
name	[str, optional] This string refers to the variable name of the invalid linkage matrix.

Returns

b	[bool] True if the inconsistency matrix is valid.

See also:

linkage

for a description of what a linkage matrix is.

inconsistent

for the creation of a inconsistency matrix.

Examples

```
>>> from scipy.cluster.hierarchy import ward, inconsistent, is_valid_im
>>> from scipy.spatial.distance import pdist
```

Given a data set `X`, we can apply a clustering method to obtain a linkage matrix `Z`. *scipy.cluster.hierarchy.inconsistent* can be also used to obtain the inconsistency matrix `R` associated to this clustering process:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = ward(pdist(X))
>>> R = inconsistent(Z)
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.29099445,  3.        ],
```

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```
       [ 5.        , 13.        ,  1.29099445,  3.        ],
       [ 8.        , 14.        ,  1.29099445,  3.        ],
       [11.        , 15.        ,  1.29099445,  3.        ],
       [16.        , 17.        ,  5.77350269,  6.        ],
       [18.        , 19.        ,  5.77350269,  6.        ],
       [20.        , 21.        ,  8.16496581, 12.        ]])
>>> R
array([[1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.        , 0.        , 1.        , 0.        ],
       [1.14549722, 0.20576415, 2.        , 0.70710678],
       [1.14549722, 0.20576415, 2.        , 0.70710678],
       [1.14549722, 0.20576415, 2.        , 0.70710678],
       [1.14549722, 0.20576415, 2.        , 0.70710678],
       [2.78516386, 2.58797734, 3.        , 1.15470054],
       [2.78516386, 2.58797734, 3.        , 1.15470054],
       [6.57065706, 1.38071187, 3.        , 1.15470054]])
```

Now we can use *scipy.cluster.hierarchy.is_valid_im* to verify that `R` is correct:

```
>>> is_valid_im(R)
True
```

However, if `R` is wrongly constructed (e.g., one of the standard deviations is set to a negative value), then the check will fail:

```
>>> R[-1,1] = R[-1,1] * -1
>>> is_valid_im(R)
False
```

scipy.cluster.hierarchy.is_valid_linkage

`scipy.cluster.hierarchy.`**`is_valid_linkage`**(*Z*, *warning=False*, *throw=False*, *name=None*)

Check the validity of a linkage matrix.

A linkage matrix is valid if it is a 2-D array (type double) with n rows and 4 columns. The first two columns must contain indices between 0 and $2n - 1$. For a given row `i`, the following two expressions have to hold:

$$0 \leq \texttt{Z[i,0]} \leq i + n - 1 0 \leq Z[i, 1] \leq i + n - 1$$

I.e., a cluster cannot join another cluster unless the cluster being joined has been generated.

Parameters

Z	[array_like] Linkage matrix.
warning	[bool, optional] When True, issues a Python warning if the linkage matrix passed is invalid.
throw	[bool, optional] When True, throws a Python exception if the linkage matrix passed is invalid.
name	[str, optional] This string refers to the variable name of the invalid linkage matrix.

Returns

b	[bool] True if the inconsistency matrix is valid.

See also:

linkage

for a description of what a linkage matrix is.

Examples

```
>>> from scipy.cluster.hierarchy import ward, is_valid_linkage
>>> from scipy.spatial.distance import pdist
```

All linkage matrices generated by the clustering methods in this module will be valid (i.e., they will have the appropriate dimensions and the two required expressions will hold for all the rows).

We can check this using *scipy.cluster.hierarchy.is_valid_linkage*:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = ward(pdist(X))
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.29099445,  3.        ],
       [ 5.        , 13.        ,  1.29099445,  3.        ],
       [ 8.        , 14.        ,  1.29099445,  3.        ],
       [11.        , 15.        ,  1.29099445,  3.        ],
       [16.        , 17.        ,  5.77350269,  6.        ],
       [18.        , 19.        ,  5.77350269,  6.        ],
       [20.        , 21.        ,  8.16496581, 12.        ]])
>>> is_valid_linkage(Z)
True
```

However, if we create a linkage matrix in a wrong way - or if we modify a valid one in a way that any of the required expressions don't hold anymore, then the check will fail:

```
>>> Z[3][1] = 20    # the cluster number 20 is not defined at this point
>>> is_valid_linkage(Z)
False
```

scipy.cluster.hierarchy.is_isomorphic

scipy.cluster.hierarchy.**is_isomorphic**(*T1*, *T2*)

Determine if two different cluster assignments are equivalent.

Parameters

T1	[array_like] An assignment of singleton cluster ids to flat cluster ids.
T2	[array_like] An assignment of singleton cluster ids to flat cluster ids.

Returns

b	[bool] Whether the flat cluster assignments *T1* and *T2* are equivalent.

See also:

`linkage`

for a description of what a linkage matrix is.

`fcluster`

for the creation of flat cluster assignments.

Examples

```
>>> from scipy.cluster.hierarchy import fcluster, is_isomorphic
>>> from scipy.cluster.hierarchy import single, complete
>>> from scipy.spatial.distance import pdist
```

Two flat cluster assignments can be isomorphic if they represent the same cluster assignment, with different labels.

For example, we can use the *scipy.cluster.hierarchy.single*: method and flatten the output to four clusters:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = single(pdist(X))
>>> T = fcluster(Z, 1, criterion='distance')
>>> T
array([3, 3, 3, 4, 4, 4, 2, 2, 2, 1, 1, 1], dtype=int32)
```

We can then do the same using the *scipy.cluster.hierarchy.complete*: method:

```
>>> Z = complete(pdist(X))
>>> T_ = fcluster(Z, 1.5, criterion='distance')
>>> T_
array([1, 1, 1, 2, 2, 2, 3, 3, 3, 4, 4, 4], dtype=int32)
```

As we can see, in both cases we obtain four clusters and all the data points are distributed in the same way - the only thing that changes are the flat cluster labels (3 => 1, 4 =>2, 2 =>3 and 4 =>1), so both cluster assignments are isomorphic:

```
>>> is_isomorphic(T, T_)
True
```

scipy.cluster.hierarchy.is_monotonic

scipy.cluster.hierarchy.**is_monotonic**(*Z*)

Return True if the linkage passed is monotonic.

The linkage is monotonic if for every cluster s and t joined, the distance between them is no less than the distance between any previously joined clusters.

Parameters

Z [ndarray] The linkage matrix to check for monotonicity.

Returns

b [bool] A boolean indicating whether the linkage is monotonic.

See also:

linkage

for a description of what a linkage matrix is.

Examples

```
>>> from scipy.cluster.hierarchy import median, ward, is_monotonic
>>> from scipy.spatial.distance import pdist
```

By definition, some hierarchical clustering algorithms - such as *scipy.cluster.hierarchy.ward* - produce monotonic assignments of samples to clusters; however, this is not always true for other hierarchical methods - e.g. *scipy.cluster.hierarchy.median*.

Given a linkage matrix `Z` (as the result of a hierarchical clustering method) we can test programmatically whether it has the monotonicity property or not, using *scipy.cluster.hierarchy.is_monotonic*:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...      [0, 4], [0, 3], [1, 4],
...      [4, 0], [3, 0], [4, 1],
...      [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = ward(pdist(X))
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.29099445,  3.        ],
       [ 5.        , 13.        ,  1.29099445,  3.        ],
       [ 8.        , 14.        ,  1.29099445,  3.        ],
       [11.        , 15.        ,  1.29099445,  3.        ],
       [16.        , 17.        ,  5.77350269,  6.        ],
       [18.        , 19.        ,  5.77350269,  6.        ],
       [20.        , 21.        ,  8.16496581, 12.        ]])
>>> is_monotonic(Z)
True
```

```
>>> Z = median(pdist(X))
>>> Z
array([[ 0.        ,  1.        ,  1.        ,  2.        ],
       [ 3.        ,  4.        ,  1.        ,  2.        ],
       [ 9.        , 10.        ,  1.        ,  2.        ],
       [ 6.        ,  7.        ,  1.        ,  2.        ],
       [ 2.        , 12.        ,  1.11803399,  3.        ],
       [ 5.        , 13.        ,  1.11803399,  3.        ],
       [ 8.        , 15.        ,  1.11803399,  3.        ],
       [11.        , 14.        ,  1.11803399,  3.        ],
       [18.        , 19.        ,  3.        ,  6.        ],
       [16.        , 17.        ,  3.5       ,  6.        ],
       [20.        , 21.        ,  3.25      , 12.        ]])
>>> is_monotonic(Z)
False
```

Note that this method is equivalent to just verifying that the distances in the third column of the linkage matrix appear in a monotonically increasing order.

scipy.cluster.hierarchy.correspond

scipy.cluster.hierarchy.**correspond**(*Z*, *Y*)

Check for correspondence between linkage and condensed distance matrices.

They must have the same number of original observations for the check to succeed.

This function is useful as a sanity check in algorithms that make extensive use of linkage and distance matrices that must correspond to the same set of original observations.

Parameters

Z	[array_like] The linkage matrix to check for correspondence.
Y	[array_like] The condensed distance matrix to check for correspondence.

Returns

b	[bool] A boolean indicating whether the linkage matrix and distance matrix could possibly correspond to one another.

See also:

linkage

for a description of what a linkage matrix is.

Examples

```
>>> from scipy.cluster.hierarchy import ward, correspond
>>> from scipy.spatial.distance import pdist
```

This method can be used to check if a given linkage matrix `Z` has been obtained from the application of a cluster method over a dataset `X`:

```
>>> X = [[0, 0], [0, 1], [1, 0],
...       [0, 4], [0, 3], [1, 4],
...       [4, 0], [3, 0], [4, 1],
...       [4, 4], [3, 4], [4, 3]]
>>> X_condensed = pdist(X)
>>> Z = ward(X_condensed)
```

Here, we can compare `Z` and `X` (in condensed form):

```
>>> correspond(Z, X_condensed)
True
```

scipy.cluster.hierarchy.num_obs_linkage

scipy.cluster.hierarchy.**num_obs_linkage**(*Z*)

Return the number of original observations of the linkage matrix passed.

Parameters

Z [ndarray] The linkage matrix on which to perform the operation.

Returns

n [int] The number of original observations in the linkage.

Examples

```
>>> from scipy.cluster.hierarchy import ward, num_obs_linkage
>>> from scipy.spatial.distance import pdist
```

```
>>> X = [[0, 0], [0, 1], [1, 0],
...       [0, 4], [0, 3], [1, 4],
...       [4, 0], [3, 0], [4, 1],
...       [4, 4], [3, 4], [4, 3]]
```

```
>>> Z = ward(pdist(X))
```

`Z` is a linkage matrix obtained after using the Ward clustering method with `X`, a dataset with 12 data points.

```
>>> num_obs_linkage(Z)
12
```

Utility routines for plotting:

set_link_color_palette(palette)	Set list of matplotlib color codes for use by dendrogram.

scipy.cluster.hierarchy.set_link_color_palette

scipy.cluster.hierarchy.**set_link_color_palette**(*palette*)

Set list of matplotlib color codes for use by dendrogram.

Note that this palette is global (i.e., setting it once changes the colors for all subsequent calls to *dendrogram*) and that it affects only the the colors below `color_threshold`.

Note that *dendrogram* also accepts a custom coloring function through its `link_color_func` keyword, which is more flexible and non-global.

Parameters

palette : [list of str or None] A list of matplotlib color codes. The order of the color codes is the order in which the colors are cycled through when color thresholding in the dendrogram.
If `None`, resets the palette to its default (which are matplotlib default colors C1 to C9).

Returns

None

See also:

dendrogram

Notes

Ability to reset the palette with `None` added in SciPy 0.17.0.

Examples

```
>>> from scipy.cluster import hierarchy
>>> ytdist = np.array([662., 877., 255., 412., 996., 295., 468., 268.,
...                    400., 754., 564., 138., 219., 869., 669.])
>>> Z = hierarchy.linkage(ytdist, 'single')
>>> dn = hierarchy.dendrogram(Z, no_plot=True)
>>> dn['color_list']
['C1', 'C0', 'C0', 'C0', 'C0']
>>> hierarchy.set_link_color_palette(['c', 'm', 'y', 'k'])
>>> dn = hierarchy.dendrogram(Z, no_plot=True, above_threshold_color='b')
>>> dn['color_list']
['c', 'b', 'b', 'b', 'b']
>>> dn = hierarchy.dendrogram(Z, no_plot=True, color_threshold=267,
...                           above_threshold_color='k')
>>> dn['color_list']
['c', 'm', 'm', 'k', 'k']
```

Now, reset the color palette to its default:

```
>>> hierarchy.set_link_color_palette(None)
```

Utility classes:

DisjointSet([elements])	Disjoint set data structure for incremental connectivity queries.

scipy.cluster.hierarchy.DisjointSet

class scipy.cluster.hierarchy.**DisjointSet**(*elements=None*)

Disjoint set data structure for incremental connectivity queries.

New in version 1.6.0.

Notes

This class implements the disjoint set [1], also known as the *union-find* or *merge-find* data structure. The *find* operation (implemented in *__getitem__*) implements the *path halving* variant. The *merge* method implements the *merge by size* variant.

References

[1]

Examples

```
>>> from scipy.cluster.hierarchy import DisjointSet
```

Initialize a disjoint set:

```
>>> disjoint_set = DisjointSet([1, 2, 3, 'a', 'b'])
```

Merge some subsets:

```
>>> disjoint_set.merge(1, 2)
True
>>> disjoint_set.merge(3, 'a')
True
>>> disjoint_set.merge('a', 'b')
True
>>> disjoint_set.merge('b', 'b')
False
```

Find root elements:

```
>>> disjoint_set[2]
1
>>> disjoint_set['b']
3
```

Test connectivity:

```
>>> disjoint_set.connected(1, 2)
True
>>> disjoint_set.connected(1, 'b')
False
```

List elements in disjoint set:

```
>>> list(disjoint_set)
[1, 2, 3, 'a', 'b']
```

Get the subset containing 'a':

```
>>> disjoint_set.subset('a')
{'a', 3, 'b'}
```

Get all subsets in the disjoint set:

```
>>> disjoint_set.subsets()
[{1, 2}, {'a', 3, 'b'}]
```

Attributes

n_subsets [int] The number of subsets.

Methods

add(x)	Add element *x* to disjoint set
merge(x, y)	Merge the subsets of *x* and *y*.
connected(x, y)	Test whether *x* and *y* are in the same subset.
subset(x)	Get the subset containing *x*.
subsets()	Get all the subsets in the disjoint set.
__getitem__(x)	Find the root element of *x*.

scipy.cluster.hierarchy.DisjointSet.add

DisjointSet.**add**(*x*)

Add element *x* to disjoint set

scipy.cluster.hierarchy.DisjointSet.merge

DisjointSet.**merge**(*x*, *y*)

Merge the subsets of *x* and *y*.

The smaller subset (the child) is merged into the larger subset (the parent). If the subsets are of equal size, the root element which was first inserted into the disjoint set is selected as the parent.

Parameters

x, y [hashable object] Elements to merge.

Returns

merged [bool] True if *x* and *y* were in disjoint sets, False otherwise.

scipy.cluster.hierarchy.DisjointSet.connected

DisjointSet.**connected**(*x*, *y*)
Test whether *x* and *y* are in the same subset.

Parameters

x, y [hashable object] Elements to test.

Returns

result [bool] True if *x* and *y* are in the same set, False otherwise.

scipy.cluster.hierarchy.DisjointSet.subset

DisjointSet.**subset**(*x*)
Get the subset containing *x*.

Parameters

x [hashable object] Input element.

Returns

result [set] Subset containing *x*.

scipy.cluster.hierarchy.DisjointSet.subsets

DisjointSet.**subsets**()
Get all the subsets in the disjoint set.

Returns

result [list] Subsets in the disjoint set.

scipy.cluster.hierarchy.DisjointSet.__getitem__

DisjointSet.**__getitem__**(*x*)
Find the root element of *x*.

Parameters

x [hashable object] Input element.

Returns

root [hashable object] Root element of *x*.

3.3.4 Constants (`scipy.constants`)

Physical and mathematical constants and units.

Mathematical constants

pi	Pi
golden	Golden ratio
golden_ratio	Golden ratio

Physical constants

c	speed of light in vacuum
speed_of_light	speed of light in vacuum
mu_0	the magnetic constant μ_0
epsilon_0	the electric constant (vacuum permittivity), ϵ_0
h	the Planck constant h
Planck	the Planck constant h
hbar	$\hbar = h/(2\pi)$
G	Newtonian constant of gravitation
gravitational_constant	Newtonian constant of gravitation
g	standard acceleration of gravity
e	elementary charge
elementary_charge	elementary charge
R	molar gas constant
gas_constant	molar gas constant
alpha	fine-structure constant
fine_structure	fine-structure constant
N_A	Avogadro constant
Avogadro	Avogadro constant
k	Boltzmann constant
Boltzmann	Boltzmann constant
sigma	Stefan-Boltzmann constant σ
Stefan_Boltzmann	Stefan-Boltzmann constant σ
Wien	Wien displacement law constant
Rydberg	Rydberg constant
m_e	electron mass
electron_mass	electron mass
m_p	proton mass
proton_mass	proton mass
m_n	neutron mass
neutron_mass	neutron mass

Constants database

In addition to the above variables, *scipy.constants* also contains the 2018 CODATA recommended values [CODATA2018] database containing more physical constants.

value(key)	Value in physical_constants indexed by key
unit(key)	Unit in physical_constants indexed by key
precision(key)	Relative precision in physical_constants indexed by key
find([sub, disp])	Return list of physical_constant keys containing a given string.

continues on next page

Table 12 – continued from previous page

ConstantWarning	Accessing a constant no longer in current CODATA data set

scipy.constants.value

scipy.constants.**value**(*key*)
Value in physical_constants indexed by key

Parameters

key [Python string or unicode] Key in dictionary *physical_constants*

Returns

value [float] Value in *physical_constants* corresponding to *key*

Examples

```
>>> from scipy import constants
>>> constants.value(u'elementary charge')
1.602176634e-19
```

scipy.constants.unit

scipy.constants.**unit**(*key*)
Unit in physical_constants indexed by key

Parameters

key [Python string or unicode] Key in dictionary *physical_constants*

Returns

unit [Python string] Unit in *physical_constants* corresponding to *key*

Examples

```
>>> from scipy import constants
>>> constants.unit(u'proton mass')
'kg'
```

scipy.constants.precision

scipy.constants.**precision**(*key*)
Relative precision in physical_constants indexed by key

Parameters

key [Python string or unicode] Key in dictionary *physical_constants*

Returns

prec [float] Relative precision in *physical_constants* corresponding to *key*

Examples

```
>>> from scipy import constants
>>> constants.precision(u'proton mass')
5.1e-37
```

scipy.constants.find

scipy.constants.**find**(*sub=None*, *disp=False*)

Return list of physical_constant keys containing a given string.

Parameters

sub [str, unicode] Sub-string to search keys for. By default, return all keys.

disp [bool] If True, print the keys that are found and return None. Otherwise, return the list of keys without printing anything.

Returns

keys [list or None] If *disp* is False, the list of keys is returned. Otherwise, None is returned.

Examples

```
>>> from scipy.constants import find, physical_constants
```

Which keys in the `physical_constants` dictionary contain 'boltzmann'?

```
>>> find('boltzmann')
['Boltzmann constant',
 'Boltzmann constant in Hz/K',
 'Boltzmann constant in eV/K',
 'Boltzmann constant in inverse meter per kelvin',
 'Stefan-Boltzmann constant']
```

Get the constant called 'Boltzmann constant in Hz/K':

```
>>> physical_constants['Boltzmann constant in Hz/K']
(20836619120.0, 'Hz K^-1', 0.0)
```

Find constants with 'radius' in the key:

```
>>> find('radius')
['Bohr radius',
 'classical electron radius',
 'deuteron rms charge radius',
 'proton rms charge radius']
>>> physical_constants['classical electron radius']
(2.8179403262e-15, 'm', 1.3e-24)
```

scipy.constants.ConstantWarning

exception scipy.constants.**ConstantWarning**
Accessing a constant no longer in current CODATA data set

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.constants.**physical_constants**
Dictionary of physical constants, of the format `physical_constants[name] = (value, unit, uncertainty)`.

Available constants:

alpha particle mass	6.6446573357e-27 kg
alpha particle mass energy equivalent	5.9719201914e-10 J
alpha particle mass energy equivalent in MeV	3727.3794066 MeV
alpha particle mass in u	4.001506179127 u
alpha particle molar mass	0.0040015061777 kg mol^-1
alpha particle relative atomic mass	4.001506179127
alpha particle-electron mass ratio	7294.29954142
alpha particle-proton mass ratio	3.97259969009
Angstrom star	1.00001495e-10 m
atomic mass constant	1.6605390666e-27 kg
atomic mass constant energy equivalent	1.4924180856e-10 J
atomic mass constant energy equivalent in MeV	931.49410242 MeV
atomic mass unit-electron volt relationship	931494102.42 eV
atomic mass unit-hartree relationship	34231776.874 E_h
atomic mass unit-hertz relationship	2.25234271871e+23 Hz
atomic mass unit-inverse meter relationship	751300661040000.0 m^-1
atomic mass unit-joule relationship	1.4924180856e-10 J
atomic mass unit-kelvin relationship	10809540191600.0 K
atomic mass unit-kilogram relationship	1.6605390666e-27 kg
atomic unit of 1st hyperpolarizability	3.2063613061e-53 C^3 m^3 J^-2
atomic unit of 2nd hyperpolarizability	6.2353799905e-65 C^4 m^4 J^-3
atomic unit of action	1.054571817e-34 J s
atomic unit of charge	1.602176634e-19 C
atomic unit of charge density	1081202384570.0 C m^-3
atomic unit of current	0.00662361823751 A
atomic unit of electric dipole mom.	8.4783536255e-30 C m
atomic unit of electric field	514220674763.0 V m^-1
atomic unit of electric field gradient	9.7173624292e+21 V m^-2
atomic unit of electric polarizability	1.64877727436e-41 C^2 m^2 J^-1
atomic unit of electric potential	27.211386245988 V
atomic unit of electric quadrupole mom.	4.4865515246e-40 C m^2
atomic unit of energy	4.3597447222071e-18 J
atomic unit of force	8.2387234983e-08 N
atomic unit of length	5.29177210903e-11 m
atomic unit of mag. dipole mom.	1.85480201566e-23 J T^-1
atomic unit of mag. flux density	235051.756758 T
atomic unit of magnetizability	7.8910366008e-29 J T^-2
atomic unit of mass	9.1093837015e-31 kg

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Table 13 – continued from previous page

atomic unit of momentum	1.9928519141e-24 kg m s^-1
atomic unit of permittivity	1.11265005545e-10 F m^-1
atomic unit of time	2.4188843265857e-17 s
atomic unit of velocity	2187691.26364 m s^-1
Avogadro constant	6.02214076e+23 mol^-1
Bohr magneton	9.2740100783e-24 J T^-1
Bohr magneton in eV/T	5.788381806e-05 eV T^-1
Bohr magneton in Hz/T	13996244936.1 Hz T^-1
Bohr magneton in inverse meter per tesla	46.686447783 m^-1 T^-1
Bohr magneton in K/T	0.67171381563 K T^-1
Bohr radius	5.29177210903e-11 m
Boltzmann constant	1.380649e-23 J K^-1
Boltzmann constant in eV/K	8.617333262e-05 eV K^-1
Boltzmann constant in Hz/K	20836619120.0 Hz K^-1
Boltzmann constant in inverse meter per kelvin	69.50348004 m^-1 K^-1
classical electron radius	2.8179403262e-15 m
Compton wavelength	2.42631023867e-12 m
conductance quantum	7.748091729e-05 S
conventional value of ampere-90	1.00000008887 A
conventional value of coulomb-90	1.00000008887 C
conventional value of farad-90	0.9999999822 F
conventional value of henry-90	1.00000001779 H
conventional value of Josephson constant	483597900000000.0 Hz V^-1
conventional value of ohm-90	1.00000001779 ohm
conventional value of volt-90	1.00000010666 V
conventional value of von Klitzing constant	25812.807 ohm
conventional value of watt-90	1.00000019553 W
Cu x unit	1.00207697e-13 m
deuteron g factor	0.8574382338
deuteron mag. mom.	4.330735094e-27 J T^-1
deuteron mag. mom. to Bohr magneton ratio	0.000466975457
deuteron mag. mom. to nuclear magneton ratio	0.8574382338
deuteron mass	3.3435837724e-27 kg
deuteron mass energy equivalent	3.00506323102e-10 J
deuteron mass energy equivalent in MeV	1875.61294257 MeV
deuteron mass in u	2.013553212745 u
deuteron molar mass	0.00201355321205 kg mol^-1
deuteron relative atomic mass	2.013553212745
deuteron rms charge radius	2.12799e-15 m
deuteron-electron mag. mom. ratio	-0.0004664345551
deuteron-electron mass ratio	3670.48296788
deuteron-neutron mag. mom. ratio	-0.44820653
deuteron-proton mag. mom. ratio	0.30701220939
deuteron-proton mass ratio	1.99900750139
electron charge to mass quotient	-175882001076.0 C kg^-1
electron g factor	-2.00231930436256
electron gyromag. ratio	176085963023.0 s^-1 T^-1
electron gyromag. ratio in MHz/T	28024.9514242 MHz T^-1
electron mag. mom.	-9.2847647043e-24 J T^-1
electron mag. mom. anomaly	0.00115965218128

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electron mag. mom. to Bohr magneton ratio	-1.00115965218128
electron mag. mom. to nuclear magneton ratio	-1838.28197188
electron mass	9.1093837015e-31 kg
electron mass energy equivalent	8.1871057769e-14 J
electron mass energy equivalent in MeV	0.51099895 MeV
electron mass in u	0.000548579909065 u
electron molar mass	5.4857990888e-07 kg mol^-1
electron relative atomic mass	0.000548579909065
electron to alpha particle mass ratio	0.0001370933554787
electron to shielded helion mag. mom. ratio	864.058257
electron to shielded proton mag. mom. ratio	-658.2275971
electron volt	1.602176634e-19 J
electron volt-atomic mass unit relationship	1.07354410233e-09 u
electron volt-hartree relationship	0.036749322175655 E_h
electron volt-hertz relationship	241798924200000.0 Hz
electron volt-inverse meter relationship	806554.3937 m^-1
electron volt-joule relationship	1.602176634e-19 J
electron volt-kelvin relationship	11604.51812 K
electron volt-kilogram relationship	1.782661921e-36 kg
electron-deuteron mag. mom. ratio	-2143.9234915
electron-deuteron mass ratio	0.0002724437107462
electron-helion mass ratio	0.0001819543074573
electron-muon mag. mom. ratio	206.7669883
electron-muon mass ratio	0.00483633169
electron-neutron mag. mom. ratio	960.9205
electron-neutron mass ratio	0.00054386734424
electron-proton mag. mom. ratio	-658.21068789
electron-proton mass ratio	0.000544617021487
electron-tau mass ratio	0.000287585
electron-triton mass ratio	0.0001819200062251
elementary charge	1.602176634e-19 C
elementary charge over h-bar	1519267447000000.0 A J^-1
Faraday constant	96485.33212 C mol^-1
Fermi coupling constant	1.1663787e-05 GeV^-2
fine-structure constant	0.0072973525693
first radiation constant	3.741771852e-16 W m^2
first radiation constant for spectral radiance	1.191042972e-16 W m^2 sr^-1
Hartree energy	4.3597447222071e-18 J
Hartree energy in eV	27.211386245988 eV
hartree-atomic mass unit relationship	2.92126232205e-08 u
hartree-electron volt relationship	27.211386245988 eV
hartree-hertz relationship	6579683920502000.0 Hz
hartree-inverse meter relationship	21947463.13632 m^-1
hartree-joule relationship	4.3597447222071e-18 J
hartree-kelvin relationship	315775.02480407 K
hartree-kilogram relationship	4.8508702095432e-35 kg
helion g factor	-4.255250615
helion mag. mom.	-1.074617532e-26 J T^-1
helion mag. mom. to Bohr magneton ratio	-0.001158740958
helion mag. mom. to nuclear magneton ratio	-2.127625307

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helion mass	5.0064127796e-27 kg
helion mass energy equivalent	4.4995394125e-10 J
helion mass energy equivalent in MeV	2808.39160743 MeV
helion mass in u	3.014932247175 u
helion molar mass	0.00301493224613 kg mol^-1
helion relative atomic mass	3.014932247175
helion shielding shift	5.996743e-05
helion-electron mass ratio	5495.88528007
helion-proton mass ratio	2.99315267167
hertz-atomic mass unit relationship	4.4398216652e-24 u
hertz-electron volt relationship	4.135667696e-15 eV
hertz-hartree relationship	1.519829846057e-16 E_h
hertz-inverse meter relationship	3.3356409519815204e-09 m^-1
hertz-joule relationship	6.62607015e-34 J
hertz-kelvin relationship	4.799243073e-11 K
hertz-kilogram relationship	7.372497323e-51 kg
hyperfine transition frequency of Cs-133	9192631770.0 Hz
inverse fine-structure constant	137.035999084
inverse meter-atomic mass unit relationship	1.3310250501e-15 u
inverse meter-electron volt relationship	1.239841984e-06 eV
inverse meter-hartree relationship	4.556335252912e-08 E_h
inverse meter-hertz relationship	299792458.0 Hz
inverse meter-joule relationship	1.986445857e-25 J
inverse meter-kelvin relationship	0.01438776877 K
inverse meter-kilogram relationship	2.210219094e-42 kg
inverse of conductance quantum	12906.40372 ohm
Josephson constant	483597848400000.0 Hz V^-1
joule-atomic mass unit relationship	6700535256.5 u
joule-electron volt relationship	6.241509074e+18 eV
joule-hartree relationship	2.2937122783963e+17 E_h
joule-hertz relationship	1.509190179e+33 Hz
joule-inverse meter relationship	5.034116567e+24 m^-1
joule-kelvin relationship	7.242970516e+22 K
joule-kilogram relationship	1.1126500560536185e-17 kg
kelvin-atomic mass unit relationship	9.2510873014e-14 u
kelvin-electron volt relationship	8.617333262e-05 eV
kelvin-hartree relationship	3.1668115634556e-06 E_h
kelvin-hertz relationship	20836619120.0 Hz
kelvin-inverse meter relationship	69.50348004 m^-1
kelvin-joule relationship	1.380649e-23 J
kelvin-kilogram relationship	1.536179187e-40 kg
kilogram-atomic mass unit relationship	6.0221407621e+26 u
kilogram-electron volt relationship	5.609588603e+35 eV
kilogram-hartree relationship	2.0614857887409e+34 E_h
kilogram-hertz relationship	1.356392489e+50 Hz
kilogram-inverse meter relationship	4.524438335e+41 m^-1
kilogram-joule relationship	8.987551787368176e+16 J
kilogram-kelvin relationship	6.50965726e+39 K
lattice parameter of silicon	5.431020511e-10 m
lattice spacing of ideal Si (220)	1.920155716e-10 m

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Loschmidt constant (273.15 K, 100 kPa)	2.651645804e+25 m^-3
Loschmidt constant (273.15 K, 101.325 kPa)	2.686780111e+25 m^-3
luminous efficacy	683.0 lm W^-1
mag. flux quantum	2.067833848e-15 Wb
Mo x unit	1.00209952e-13 m
molar gas constant	8.314462618 J mol^-1 K^-1
molar mass constant	0.00099999999965 kg mol^-1
molar mass of carbon-12	0.0119999999958 kg mol^-1
molar Planck constant	3.990312712e-10 J Hz^-1 mol^-1
molar volume of ideal gas (273.15 K, 100 kPa)	0.02271095464 m^3 mol^-1
molar volume of ideal gas (273.15 K, 101.325 kPa)	0.02241396954 m^3 mol^-1
molar volume of silicon	1.205883199e-05 m^3 mol^-1
muon Compton wavelength	1.17344411e-14 m
muon g factor	-2.0023318418
muon mag. mom.	-4.4904483e-26 J T^-1
muon mag. mom. anomaly	0.00116592089
muon mag. mom. to Bohr magneton ratio	-0.00484197047
muon mag. mom. to nuclear magneton ratio	-8.89059703
muon mass	1.883531627e-28 kg
muon mass energy equivalent	1.692833804e-11 J
muon mass energy equivalent in MeV	105.6583755 MeV
muon mass in u	0.1134289259 u
muon molar mass	0.0001134289259 kg mol^-1
muon-electron mass ratio	206.768283
muon-neutron mass ratio	0.112454517
muon-proton mag. mom. ratio	-3.183345142
muon-proton mass ratio	0.1126095264
muon-tau mass ratio	0.0594635
natural unit of action	1.054571817e-34 J s
natural unit of action in eV s	6.582119569e-16 eV s
natural unit of energy	8.1871057769e-14 J
natural unit of energy in MeV	0.51099895 MeV
natural unit of length	3.8615926796e-13 m
natural unit of mass	9.1093837015e-31 kg
natural unit of momentum	2.730924488e-22 kg m s^-1
natural unit of momentum in MeV/c	0.5109989461 MeV/c
natural unit of time	1.28808866819e-21 s
natural unit of velocity	299792458.0 m s^-1
neutron Compton wavelength	1.31959090581e-15 m
neutron g factor	-3.82608545
neutron gyromag. ratio	183247171.0 s^-1 T^-1
neutron gyromag. ratio in MHz/T	29.1646931 MHz T^-1
neutron mag. mom.	-9.6623651e-27 J T^-1
neutron mag. mom. to Bohr magneton ratio	-0.00104187563
neutron mag. mom. to nuclear magneton ratio	-1.91304273
neutron mass	1.67492749804e-27 kg
neutron mass energy equivalent	1.50534976287e-10 J
neutron mass energy equivalent in MeV	939.56542052 MeV
neutron mass in u	1.00866491595 u
neutron molar mass	0.0010086649156 kg mol^-1

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neutron relative atomic mass	1.00866491595
neutron to shielded proton mag. mom. ratio	-0.68499694
neutron-electron mag. mom. ratio	0.00104066882
neutron-electron mass ratio	1838.68366173
neutron-muon mass ratio	8.89248406
neutron-proton mag. mom. ratio	-0.68497934
neutron-proton mass difference	2.30557435e-30 kg
neutron-proton mass difference energy equivalent	2.07214689e-13 J
neutron-proton mass difference energy equivalent in MeV	1.29333236 MeV
neutron-proton mass difference in u	0.00138844933 u
neutron-proton mass ratio	1.00137841931
neutron-tau mass ratio	0.528779
Newtonian constant of gravitation	6.6743e-11 m^3 kg^-1 s^-2
Newtonian constant of gravitation over h-bar c	6.70883e-39 (GeV/c^2)^-2
nuclear magneton	5.0507837461e-27 J T^-1
nuclear magneton in eV/T	3.15245125844e-08 eV T^-1
nuclear magneton in inverse meter per tesla	0.0254262341353 m^-1 T^-1
nuclear magneton in K/T	0.00036582677756 K T^-1
nuclear magneton in MHz/T	7.6225932291 MHz T^-1
Planck constant	6.62607015e-34 J Hz^-1
Planck constant in eV/Hz	4.135667696e-15 eV Hz^-1
Planck length	1.616255e-35 m
Planck mass	2.176434e-08 kg
Planck mass energy equivalent in GeV	1.22089e+19 GeV
Planck temperature	1.416784e+32 K
Planck time	5.391247e-44 s
proton charge to mass quotient	95788331.56 C kg^-1
proton Compton wavelength	1.32140985539e-15 m
proton g factor	5.5856946893
proton gyromag. ratio	267522187.44 s^-1 T^-1
proton gyromag. ratio in MHz/T	42.577478518 MHz T^-1
proton mag. mom.	1.41060679736e-26 J T^-1
proton mag. mom. to Bohr magneton ratio	0.0015210322023
proton mag. mom. to nuclear magneton ratio	2.79284734463
proton mag. shielding correction	2.5689e-05
proton mass	1.67262192369e-27 kg
proton mass energy equivalent	1.50327761598e-10 J
proton mass energy equivalent in MeV	938.27208816 MeV
proton mass in u	1.007276466621 u
proton molar mass	0.00100727646627 kg mol^-1
proton relative atomic mass	1.007276466621
proton rms charge radius	8.414e-16 m
proton-electron mass ratio	1836.15267343
proton-muon mass ratio	8.88024337
proton-neutron mag. mom. ratio	-1.45989805
proton-neutron mass ratio	0.99862347812
proton-tau mass ratio	0.528051
quantum of circulation	0.00036369475516 m^2 s^-1
quantum of circulation times 2	0.00072738951032 m^2 s^-1
reduced Compton wavelength	3.8615926796e-13 m

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Table 13 – continued from previous page

reduced muon Compton wavelength	1.867594306e-15 m
reduced neutron Compton wavelength	2.1001941552e-16 m
reduced Planck constant	1.054571817e-34 J s
reduced Planck constant in eV s	6.582119569e-16 eV s
reduced Planck constant times c in MeV fm	197.3269804 MeV fm
reduced proton Compton wavelength	2.10308910336e-16 m
reduced tau Compton wavelength	1.110538e-16 m
Rydberg constant	10973731.56816 m^-1
Rydberg constant times c in Hz	3289841960250800.0 Hz
Rydberg constant times hc in eV	13.605693122994 eV
Rydberg constant times hc in J	2.1798723611035e-18 J
Sackur-Tetrode constant (1 K, 100 kPa)	-1.15170753706
Sackur-Tetrode constant (1 K, 101.325 kPa)	-1.16487052358
second radiation constant	0.01438776877 m K
shielded helion gyromag. ratio	203789456.9 s^-1 T^-1
shielded helion gyromag. ratio in MHz/T	32.43409942 MHz T^-1
shielded helion mag. mom.	-1.07455309e-26 J T^-1
shielded helion mag. mom. to Bohr magneton ratio	-0.001158671471
shielded helion mag. mom. to nuclear magneton ratio	-2.127497719
shielded helion to proton mag. mom. ratio	-0.7617665618
shielded helion to shielded proton mag. mom. ratio	-0.7617861313
shielded proton gyromag. ratio	267515315.1 s^-1 T^-1
shielded proton gyromag. ratio in MHz/T	42.57638474 MHz T^-1
shielded proton mag. mom.	1.41057056e-26 J T^-1
shielded proton mag. mom. to Bohr magneton ratio	0.001520993128
shielded proton mag. mom. to nuclear magneton ratio	2.792775599
shielding difference of d and p in HD	2.02e-08
shielding difference of t and p in HT	2.414e-08
speed of light in vacuum	299792458.0 m s^-1
standard acceleration of gravity	9.80665 m s^-2
standard atmosphere	101325.0 Pa
standard-state pressure	100000.0 Pa
Stefan-Boltzmann constant	5.670374419e-08 W m^-2 K^-4
tau Compton wavelength	6.97771e-16 m
tau energy equivalent	1776.86 MeV
tau mass	3.16754e-27 kg
tau mass energy equivalent	2.84684e-10 J
tau mass in u	1.90754 u
tau molar mass	0.00190754 kg mol^-1
tau-electron mass ratio	3477.23
tau-muon mass ratio	16.817
tau-neutron mass ratio	1.89115
tau-proton mass ratio	1.89376
Thomson cross section	6.6524587321e-29 m^2
triton g factor	5.957924931
triton mag. mom.	1.5046095202e-26 J T^-1
triton mag. mom. to Bohr magneton ratio	0.0016223936651
triton mag. mom. to nuclear magneton ratio	2.9789624656
triton mass	5.0073567446e-27 kg
triton mass energy equivalent	4.500387806e-10 J

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Table 13 – continued from previous page

triton mass energy equivalent in MeV	2808.92113298 MeV
triton mass in u	3.01550071621 u
triton molar mass	0.00301550071517 kg mol^-1
triton relative atomic mass	3.01550071621
triton to proton mag. mom. ratio	1.0666399191
triton-electron mass ratio	5496.92153573
triton-proton mass ratio	2.99371703414
unified atomic mass unit	1.6605390666e-27 kg
vacuum electric permittivity	8.8541878128e-12 F m^-1
vacuum mag. permeability	1.25663706212e-06 N A^-2
von Klitzing constant	25812.80745 ohm
W to Z mass ratio	0.88153
weak mixing angle	0.2229
Wien frequency displacement law constant	58789257570.0 Hz K^-1
Wien wavelength displacement law constant	0.002897771955 m K

Units

SI prefixes

yotta	10^{24}
zetta	10^{21}
exa	10^{18}
peta	10^{15}
tera	10^{12}
giga	10^{9}
mega	10^{6}
kilo	10^{3}
hecto	10^{2}
deka	10^{1}
deci	10^{-1}
centi	10^{-2}
milli	10^{-3}
micro	10^{-6}
nano	10^{-9}
pico	10^{-12}
femto	10^{-15}
atto	10^{-18}
zepto	10^{-21}

Binary prefixes

kibi	2^{10}
mebi	2^{20}
gibi	2^{30}
tebi	2^{40}
pebi	2^{50}
exbi	2^{60}
zebi	2^{70}
yobi	2^{80}

Mass

gram	10^{-3} kg
metric_ton	10^{3} kg
grain	one grain in kg
lb	one pound (avoirdupous) in kg
pound	one pound (avoirdupous) in kg
blob	one inch version of a slug in kg (added in 1.0.0)
slinch	one inch version of a slug in kg (added in 1.0.0)
slug	one slug in kg (added in 1.0.0)
oz	one ounce in kg
ounce	one ounce in kg
stone	one stone in kg
grain	one grain in kg
long_ton	one long ton in kg
short_ton	one short ton in kg
troy_ounce	one Troy ounce in kg
troy_pound	one Troy pound in kg
carat	one carat in kg
m_u	atomic mass constant (in kg)
u	atomic mass constant (in kg)
atomic_mass	atomic mass constant (in kg)

Angle

degree	degree in radians
arcmin	arc minute in radians
arcminute	arc minute in radians
arcsec	arc second in radians
arcsecond	arc second in radians

Time

minute	one minute in seconds
hour	one hour in seconds
day	one day in seconds
week	one week in seconds
year	one year (365 days) in seconds
Julian_year	one Julian year (365.25 days) in seconds

Length

inch	one inch in meters
foot	one foot in meters
yard	one yard in meters
mile	one mile in meters
mil	one mil in meters
pt	one point in meters
point	one point in meters
survey_foot	one survey foot in meters
survey_mile	one survey mile in meters
nautical_mile	one nautical mile in meters
fermi	one Fermi in meters
angstrom	one Angstrom in meters
micron	one micron in meters
au	one astronomical unit in meters
astronomical_unit	one astronomical unit in meters
light_year	one light year in meters
parsec	one parsec in meters

Pressure

atm	standard atmosphere in pascals
atmosphere	standard atmosphere in pascals
bar	one bar in pascals
torr	one torr (mmHg) in pascals
mmHg	one torr (mmHg) in pascals
psi	one psi in pascals

Area

hectare	one hectare in square meters
acre	one acre in square meters

Volume

liter	one liter in cubic meters
litre	one liter in cubic meters
gallon	one gallon (US) in cubic meters
gallon_US	one gallon (US) in cubic meters
gallon_imp	one gallon (UK) in cubic meters
fluid_ounce	one fluid ounce (US) in cubic meters
fluid_ounce_US	one fluid ounce (US) in cubic meters
fluid_ounce_imp	one fluid ounce (UK) in cubic meters
bbl	one barrel in cubic meters
barrel	one barrel in cubic meters

Speed

kmh	kilometers per hour in meters per second
mph	miles per hour in meters per second
mach	one Mach (approx., at 15 C, 1 atm) in meters per second
speed_of_sound	one Mach (approx., at 15 C, 1 atm) in meters per second
knot	one knot in meters per second

Temperature

zero_Celsius	zero of Celsius scale in Kelvin
degree_Fahrenheit	one Fahrenheit (only differences) in Kelvins

convert_temperature(val, old_scale, new_scale)	Convert from a temperature scale to another one among Celsius, Kelvin, Fahrenheit, and Rankine scales.

scipy.constants.convert_temperature

scipy.constants.**convert_temperature**(*val*, *old_scale*, *new_scale*)

Convert from a temperature scale to another one among Celsius, Kelvin, Fahrenheit, and Rankine scales.

Parameters

val [array_like] Value(s) of the temperature(s) to be converted expressed in the original scale.

old_scale: str
Specifies as a string the original scale from which the temperature value(s) will be converted. Supported scales are Celsius ('Celsius', 'celsius', 'C' or 'c'), Kelvin ('Kelvin', 'kelvin', 'K', 'k'), Fahrenheit ('Fahrenheit', 'fahrenheit', 'F' or 'f'), and Rankine ('Rankine', 'rankine', 'R', 'r').

new_scale: str
Specifies as a string the new scale to which the temperature value(s) will be converted. Supported scales are Celsius ('Celsius', 'celsius', 'C' or 'c'), Kelvin ('Kelvin', 'kelvin', 'K', 'k'), Fahrenheit ('Fahrenheit', 'fahrenheit', 'F' or 'f'), and Rankine ('Rankine', 'rankine', 'R', 'r').

Returns

res [float or array of floats] Value(s) of the converted temperature(s) expressed in the new scale.

Notes

New in version 0.18.0.

Examples

```
>>> from scipy.constants import convert_temperature
>>> convert_temperature(np.array([-40, 40]), 'Celsius', 'Kelvin')
array([ 233.15,  313.15])
```

Energy

`eV`	one electron volt in Joules
`electron_volt`	one electron volt in Joules
`calorie`	one calorie (thermochemical) in Joules
`calorie_th`	one calorie (thermochemical) in Joules
`calorie_IT`	one calorie (International Steam Table calorie, 1956) in Joules
`erg`	one erg in Joules
`Btu`	one British thermal unit (International Steam Table) in Joules
`Btu_IT`	one British thermal unit (International Steam Table) in Joules
`Btu_th`	one British thermal unit (thermochemical) in Joules
`ton_TNT`	one ton of TNT in Joules

Power

`hp`	one horsepower in watts
`horsepower`	one horsepower in watts

Force

`dyn`	one dyne in newtons
`dyne`	one dyne in newtons
`lbf`	one pound force in newtons
`pound_force`	one pound force in newtons
`kgf`	one kilogram force in newtons
`kilogram_force`	one kilogram force in newtons

Optics

lambda2nu(lambda_)	Convert wavelength to optical frequency
nu2lambda(nu)	Convert optical frequency to wavelength.

scipy.constants.lambda2nu

scipy.constants.**lambda2nu**(*lambda_*)

Convert wavelength to optical frequency

Parameters

lambda_ [array_like] Wavelength(s) to be converted.

Returns

nu [float or array of floats] Equivalent optical frequency.

Notes

Computes `nu = c / lambda` where c = 299792458.0, i.e., the (vacuum) speed of light in meters/second.

Examples

```
>>> from scipy.constants import lambda2nu, speed_of_light
>>> lambda2nu(np.array((1, speed_of_light)))
array([  2.99792458e+08,   1.00000000e+00])
```

scipy.constants.nu2lambda

scipy.constants.**nu2lambda**(*nu*)

Convert optical frequency to wavelength.

Parameters

nu [array_like] Optical frequency to be converted.

Returns

lambda [float or array of floats] Equivalent wavelength(s).

Notes

Computes `lambda = c / nu` where c = 299792458.0, i.e., the (vacuum) speed of light in meters/second.

Examples

```
>>> from scipy.constants import nu2lambda, speed_of_light
>>> nu2lambda(np.array((1, speed_of_light)))
array([  2.99792458e+08,   1.00000000e+00])
```

References

3.3.5 Discrete Fourier transforms (`scipy.fft`)

Fast Fourier Transforms (FFTs)

fft(x[, n, axis, norm, overwrite_x, …])	Compute the 1-D discrete Fourier Transform.
ifft(x[, n, axis, norm, overwrite_x, …])	Compute the 1-D inverse discrete Fourier Transform.
fft2(x[, s, axes, norm, overwrite_x, …])	Compute the 2-D discrete Fourier Transform
ifft2(x[, s, axes, norm, overwrite_x, …])	Compute the 2-D inverse discrete Fourier Transform.
fftn(x[, s, axes, norm, overwrite_x, …])	Compute the N-D discrete Fourier Transform.
ifftn(x[, s, axes, norm, overwrite_x, …])	Compute the N-D inverse discrete Fourier Transform.
rfft(x[, n, axis, norm, overwrite_x, …])	Compute the 1-D discrete Fourier Transform for real input.
irfft(x[, n, axis, norm, overwrite_x, …])	Computes the inverse of *rfft*.

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Table 16 – continued from previous page

rfft2(x[, s, axes, norm, overwrite_x, …])	Compute the 2-D FFT of a real array.
irfft2(x[, s, axes, norm, overwrite_x, …])	Computes the inverse of *rfft2*
rfftn(x[, s, axes, norm, overwrite_x, …])	Compute the N-D discrete Fourier Transform for real input.
irfftn(x[, s, axes, norm, overwrite_x, …])	Computes the inverse of *rfftn*
hfft(x[, n, axis, norm, overwrite_x, …])	Compute the FFT of a signal that has Hermitian symmetry, i.e., a real spectrum.
ihfft(x[, n, axis, norm, overwrite_x, …])	Compute the inverse FFT of a signal that has Hermitian symmetry.
hfft2(x[, s, axes, norm, overwrite_x, …])	Compute the 2-D FFT of a Hermitian complex array.
ihfft2(x[, s, axes, norm, overwrite_x, …])	Compute the 2-D inverse FFT of a real spectrum.
hfftn(x[, s, axes, norm, overwrite_x, …])	Compute the N-D FFT of Hermitian symmetric complex input, i.e., a signal with a real spectrum.
ihfftn(x[, s, axes, norm, overwrite_x, …])	Compute the N-D inverse discrete Fourier Transform for a real spectrum.

scipy.fft.fft

scipy.fft.**fft**(*x*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*, *workers=None*, *, *plan=None*)

Compute the 1-D discrete Fourier Transform.

This function computes the 1-D *n*-point discrete Fourier Transform (DFT) with the efficient Fast Fourier Transform (FFT) algorithm [1].

Parameters

x [array_like] Input array, can be complex.

n [int, optional] Length of the transformed axis of the output. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode. Default is "backward", meaning no normalization on the forward transforms and scaling by `1/n` on the *ifft*. "forward" instead applies the `1/n` factor on the forward tranform. For `norm="ortho"`, both directions are scaled by `1/sqrt(n)`.
New in version 1.6.0: `norm={"forward", "backward"}` options were added

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See the notes below for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See below for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified.

Raises

IndexError if *axes* is larger than the last axis of *x*.

See also:

ifft

The inverse of *fft*.

fft2

The 2-D FFT.

fftn

The N-D FFT.

rfftn

The N-D FFT of real input.

fftfreq

Frequency bins for given FFT parameters.

next_fast_len

Size to pad input to for most efficient transforms

Notes

FFT (Fast Fourier Transform) refers to a way the discrete Fourier Transform (DFT) can be calculated efficiently, by using symmetries in the calculated terms. The symmetry is highest when *n* is a power of 2, and the transform is therefore most efficient for these sizes. For poorly factorizable sizes, *scipy.fft* uses Bluestein's algorithm [2] and so is never worse than O(*n* log *n*). Further performance improvements may be seen by zero-padding the input using *next_fast_len*.

If `x` is a 1d array, then the *fft* is equivalent to

```
y[k] = np.sum(x * np.exp(-2j * np.pi * k * np.arange(n)/n))
```

The frequency term `f=k/n` is found at `y[k]`. At `y[n/2]` we reach the Nyquist frequency and wrap around to the negative-frequency terms. So, for an 8-point transform, the frequencies of the result are [0, 1, 2, 3, -4, -3, -2, -1]. To rearrange the fft output so that the zero-frequency component is centered, like [-4, -3, -2, -1, 0, 1, 2, 3], use *fftshift*.

Transforms can be done in single, double, or extended precision (long double) floating point. Half precision inputs will be converted to single precision and non-floating-point inputs will be converted to double precision.

If the data type of `x` is real, a "real FFT" algorithm is automatically used, which roughly halves the computation time. To increase efficiency a little further, use *rfft*, which does the same calculation, but only outputs half of the symmetrical spectrum. If the data are both real and symmetrical, the *dct* can again double the efficiency, by generating half of the spectrum from half of the signal.

When `overwrite_x=True` is specified, the memory referenced by `x` may be used by the implementation in any way. This may include reusing the memory for the result, but this is in no way guaranteed. You should not rely on the contents of `x` after the transform as this may change in future without warning.

The `workers` argument specifies the maximum number of parallel jobs to split the FFT computation into. This will execute independent 1-D FFTs within `x`. So, `x` must be at least 2-D and the non-transformed axes must be large enough to split into chunks. If `x` is too small, fewer jobs may be used than requested.

References

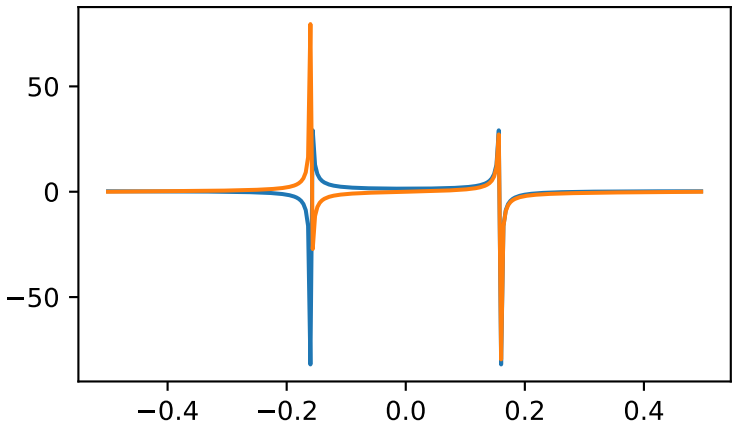
[1], [2]

Examples

```
>>> import scipy.fft
>>> scipy.fft.fft(np.exp(2j * np.pi * np.arange(8) / 8))
array([-2.33486982e-16+1.14423775e-17j,  8.00000000e+00-1.25557246e-15j,
        2.33486982e-16+2.33486982e-16j,  0.00000000e+00+1.22464680e-16j,
       -1.14423775e-17+2.33486982e-16j,  0.00000000e+00+5.20784380e-16j,
        1.14423775e-17+1.14423775e-17j,  0.00000000e+00+1.22464680e-16j])
```

In this example, real input has an FFT which is Hermitian, i.e., symmetric in the real part and anti-symmetric in the imaginary part:

```
>>> from scipy.fft import fft, fftfreq, fftshift
>>> import matplotlib.pyplot as plt
>>> t = np.arange(256)
>>> sp = fftshift(fft(np.sin(t)))
>>> freq = fftshift(fftfreq(t.shape[-1]))
>>> plt.plot(freq, sp.real, freq, sp.imag)
[<matplotlib.lines.Line2D object at 0x...>, <matplotlib.lines.Line2D␣
↪object at 0x...>]
>>> plt.show()
```



scipy.fft.ifft

scipy.fft.**ifft**(*x*, *n=None*, *axis=-1*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the 1-D inverse discrete Fourier Transform.

This function computes the inverse of the 1-D *n*-point discrete Fourier transform computed by `fft`. In other words, `ifft(fft(x)) == x` to within numerical accuracy.

The input should be ordered in the same way as is returned by `fft`, i.e.,

- `x[0]` should contain the zero frequency term,
- `x[1:n//2]` should contain the positive-frequency terms,
- `x[n//2 + 1:]` should contain the negative-frequency terms, in increasing order starting from the most negative frequency.

For an even number of input points, `x[n//2]` represents the sum of the values at the positive and negative Nyquist frequencies, as the two are aliased together. See `fft` for details.

Parameters

x [array_like] Input array, can be complex.

n [int, optional] Length of the transformed axis of the output. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used. See notes about padding issues.

axis [int, optional] Axis over which to compute the inverse DFT. If not given, the last axis is used.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see `fft`). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See `fft` for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See `fft` for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified.

Raises

IndexError If *axes* is larger than the last axis of *x*.

See also:

fft

The 1-D (forward) FFT, of which `ifft` is the inverse.

ifft2

The 2-D inverse FFT.

ifftn

The N-D inverse FFT.

Notes

If the input parameter *n* is larger than the size of the input, the input is padded by appending zeros at the end. Even though this is the common approach, it might lead to surprising results. If a different padding is desired, it must be performed before calling *ifft*.

If `x` is a 1-D array, then the *ifft* is equivalent to

```
y[k] = np.sum(x * np.exp(2j * np.pi * k * np.arange(n)/n)) / len(x)
```

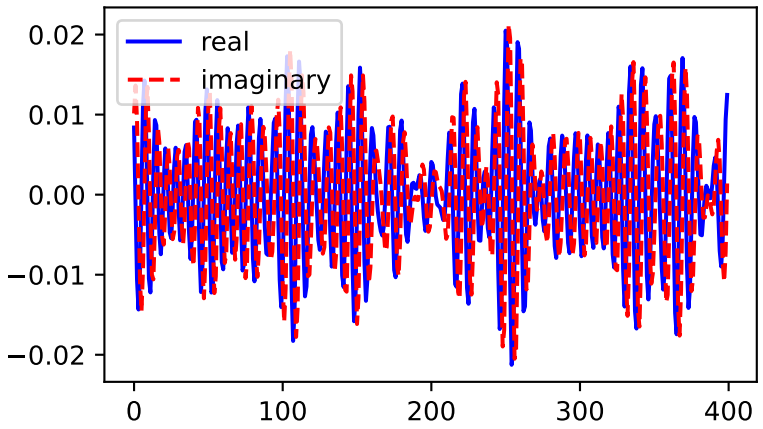
As with *fft*, *ifft* has support for all floating point types and is optimized for real input.

Examples

```
>>> import scipy.fft
>>> scipy.fft.ifft([0, 4, 0, 0])
array([ 1.+0.j,  0.+1.j, -1.+0.j,  0.-1.j]) # may vary
```

Create and plot a band-limited signal with random phases:

```
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> t = np.arange(400)
>>> n = np.zeros((400,), dtype=complex)
>>> n[40:60] = np.exp(1j*rng.uniform(0, 2*np.pi, (20,)))
>>> s = scipy.fft.ifft(n)
>>> plt.plot(t, s.real, 'b-', t, s.imag, 'r--')
[<matplotlib.lines.Line2D object at ...>, <matplotlib.lines.Line2D object␣
↪at ...>]
>>> plt.legend(('real', 'imaginary'))
<matplotlib.legend.Legend object at ...>
>>> plt.show()
```



scipy.fft.fft2

scipy.fft.**fft2**(*x*, *s=None*, *axes=(- 2, - 1)*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the 2-D discrete Fourier Transform

This function computes the N-D discrete Fourier Transform over any axes in an M-D array by means of the Fast Fourier Transform (FFT). By default, the transform is computed over the last two axes of the input array, i.e., a 2-dimensional FFT.

Parameters

x [array_like] Input array, can be complex

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to `n` for `fft(x, n)`. Along each axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last two axes are used.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or the last two axes if *axes* is not given.

Raises

ValueError If *s* and *axes* have different length, or *axes* not given and `len(s) != 2`.

IndexError If an element of *axes* is larger than than the number of axes of *x*.

See also:

ifft2

The inverse 2-D FFT.

fft

The 1-D FFT.

fftn

The N-D FFT.

fftshift

Shifts zero-frequency terms to the center of the array. For 2-D input, swaps first and third quadrants, and second and fourth quadrants.

Notes

fft2 is just *fftn* with a different default for *axes*.

The output, analogously to *fft*, contains the term for zero frequency in the low-order corner of the transformed axes, the positive frequency terms in the first half of these axes, the term for the Nyquist frequency in the middle of the axes and the negative frequency terms in the second half of the axes, in order of decreasingly negative frequency.

See *fftn* for details and a plotting example, and *fft* for definitions and conventions used.

Examples

```
>>> import scipy.fft
>>> x = np.mgrid[:5, :5][0]
>>> scipy.fft.fft2(x)
array([[ 50.  +0.j        ,   0.  +0.j        ,   0.  +0.j        , # may␣
↪vary
          0.  +0.j        ,   0.  +0.j        ],
       [-12.5+17.20477401j,   0.  +0.j        ,   0.  +0.j        ,
          0.  +0.j        ,   0.  +0.j        ],
       [-12.5 +4.0614962j ,   0.  +0.j        ,   0.  +0.j        ,
          0.  +0.j        ,   0.  +0.j        ],
       [-12.5 -4.0614962j ,   0.  +0.j        ,   0.  +0.j        ,
          0.  +0.j        ,   0.  +0.j        ],
       [-12.5-17.20477401j,   0.  +0.j        ,   0.  +0.j        ,
          0.  +0.j        ,   0.  +0.j        ]])
```

scipy.fft.ifft2

scipy.fft.**ifft2**(*x*, *s=None*, *axes=(- 2, - 1)*, *norm=None*, *overwrite_x=False*, *workers=None*, *, *plan=None*)

Compute the 2-D inverse discrete Fourier Transform.

This function computes the inverse of the 2-D discrete Fourier Transform over any number of axes in an M-D array by means of the Fast Fourier Transform (FFT). In other words, `ifft2(fft2(x)) == x` to within numerical accuracy. By default, the inverse transform is computed over the last two axes of the input array.

The input, analogously to *ifft*, should be ordered in the same way as is returned by *fft2*, i.e., it should have the term for zero frequency in the low-order corner of the two axes, the positive frequency terms in the first half of these axes, the term for the Nyquist frequency in the middle of the axes and the negative frequency terms in the second half of both axes, in order of decreasingly negative frequency.

Parameters

x [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to *n* for `ifft(x, n)`. Along each axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used. See notes for issue on *ifft* zero padding.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last two axes are used.

norm [{“backward”, “ortho”, “forward”}, optional] Normalization mode (see *fft*). Default is “backward”.

overwrite_x

[bool, optional] If True, the contents of *x* can be destroyed; the default is False. See `fft` for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See `fft` for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or the last two axes if *axes* is not given.

Raises

ValueError
If *s* and *axes* have different length, or *axes* not given and `len(s) != 2`.

IndexError
If an element of *axes* is larger than than the number of axes of *x*.

See also:

fft2

The forward 2-D FFT, of which `ifft2` is the inverse.

ifftn

The inverse of the N-D FFT.

fft

The 1-D FFT.

ifft

The 1-D inverse FFT.

Notes

`ifft2` is just `ifftn` with a different default for *axes*.

See `ifftn` for details and a plotting example, and `fft` for definition and conventions used.

Zero-padding, analogously with `ifft`, is performed by appending zeros to the input along the specified dimension. Although this is the common approach, it might lead to surprising results. If another form of zero padding is desired, it must be performed before `ifft2` is called.

Examples

```
>>> import scipy.fft
>>> x = 4 * np.eye(4)
>>> scipy.fft.ifft2(x)
array([[1.+0.j,  0.+0.j,  0.+0.j,  0.+0.j], # may vary
       [0.+0.j,  0.+0.j,  0.+0.j,  1.+0.j],
       [0.+0.j,  0.+0.j,  1.+0.j,  0.+0.j],
       [0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j]])
```

scipy.fft.fftn

scipy.fft.**fftn**(*x*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the N-D discrete Fourier Transform.

This function computes the N-D discrete Fourier Transform over any number of axes in an M-D array by means of the Fast Fourier Transform (FFT).

Parameters

x [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to `n` for `fft(x, n)`. Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* and *x*, as explained in the parameters section above.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *x*.

See also:

ifftn

The inverse of *fftn*, the inverse N-D FFT.

fft

The 1-D FFT, with definitions and conventions used.

rfftn

The N-D FFT of real input.

fft2

The 2-D FFT.

fftshift

Shifts zero-frequency terms to centre of array.

Notes

The output, analogously to *fft*, contains the term for zero frequency in the low-order corner of all axes, the positive frequency terms in the first half of all axes, the term for the Nyquist frequency in the middle of all axes and the negative frequency terms in the second half of all axes, in order of decreasingly negative frequency.

Examples

```
>>> import scipy.fft
>>> x = np.mgrid[:3, :3, :3][0]
>>> scipy.fft.fftn(x, axes=(1, 2))
array([[[ 0.+0.j,   0.+0.j,   0.+0.j], # may vary
        [ 0.+0.j,   0.+0.j,   0.+0.j],
        [ 0.+0.j,   0.+0.j,   0.+0.j]],
       [[ 9.+0.j,   0.+0.j,   0.+0.j],
        [ 0.+0.j,   0.+0.j,   0.+0.j],
        [ 0.+0.j,   0.+0.j,   0.+0.j]],
       [[18.+0.j,   0.+0.j,   0.+0.j],
        [ 0.+0.j,   0.+0.j,   0.+0.j],
        [ 0.+0.j,   0.+0.j,   0.+0.j]]])
>>> scipy.fft.fftn(x, (2, 2), axes=(0, 1))
array([[[ 2.+0.j,  2.+0.j,  2.+0.j], # may vary
        [ 0.+0.j,  0.+0.j,  0.+0.j]],
       [[-2.+0.j, -2.+0.j, -2.+0.j],
        [ 0.+0.j,  0.+0.j,  0.+0.j]]])
```

```
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> [X, Y] = np.meshgrid(2 * np.pi * np.arange(200) / 12,
...                      2 * np.pi * np.arange(200) / 34)
>>> S = np.sin(X) + np.cos(Y) + rng.uniform(0, 1, X.shape)
>>> FS = scipy.fft.fftn(S)
>>> plt.imshow(np.log(np.abs(scipy.fft.fftshift(FS))**2))
<matplotlib.image.AxesImage object at 0x...>
>>> plt.show()
```

scipy.fft.ifftn

scipy.fft.**ifftn**(*x*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the N-D inverse discrete Fourier Transform.

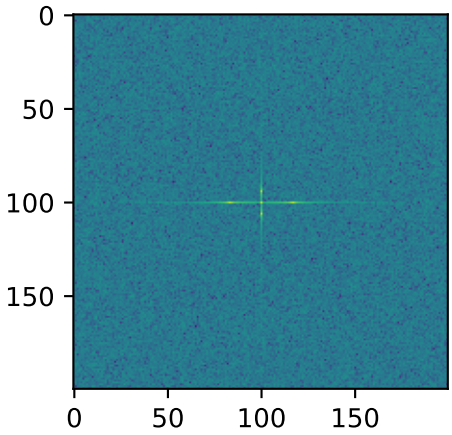
This function computes the inverse of the N-D discrete Fourier Transform over any number of axes in an M-D array by means of the Fast Fourier Transform (FFT). In other words, `ifftn(fftn(x)) == x` to within numerical accuracy.

The input, analogously to *ifft*, should be ordered in the same way as is returned by *fftn*, i.e., it should have the term for zero frequency in all axes in the low-order corner, the positive frequency terms in the first half of all axes, the term for the Nyquist frequency in the middle of all axes and the negative frequency terms in the second half of all axes, in order of decreasingly negative frequency.

Parameters

x [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to `n` for `ifft(x, n)`. Along



any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used. See notes for issue on `ifft` zero padding.

axes [sequence of ints, optional] Axes over which to compute the IFFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see `fft`). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See `fft` for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See `fft` for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* or *x*, as explained in the parameters section above.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *x*.

See also:

`fftn`

The forward N-D FFT, of which `ifftn` is the inverse.

`ifft`

The 1-D inverse FFT.

ifft2

The 2-D inverse FFT.

ifftshift

Undoes *fftshift*, shifts zero-frequency terms to beginning of array.

Notes

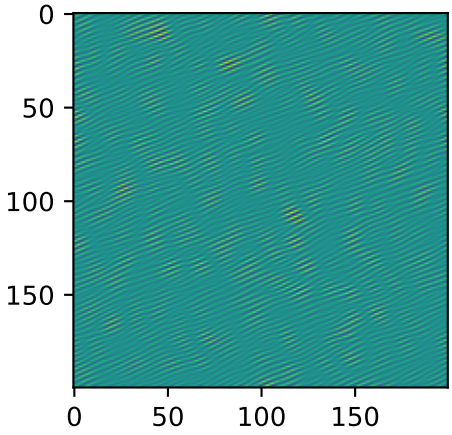
Zero-padding, analogously with *ifft*, is performed by appending zeros to the input along the specified dimension. Although this is the common approach, it might lead to surprising results. If another form of zero padding is desired, it must be performed before *ifftn* is called.

Examples

```
>>> import scipy.fft
>>> x = np.eye(4)
>>> scipy.fft.ifftn(scipy.fft.fftn(x, axes=(0,)), axes=(1,))
array([[1.+0.j,  0.+0.j,  0.+0.j,  0.+0.j], # may vary
       [0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j],
       [0.+0.j,  0.+0.j,  1.+0.j,  0.+0.j],
       [0.+0.j,  0.+0.j,  0.+0.j,  1.+0.j]])
```

Create and plot an image with band-limited frequency content:

```
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> n = np.zeros((200,200), dtype=complex)
>>> n[60:80, 20:40] = np.exp(1j*rng.uniform(0, 2*np.pi, (20, 20)))
>>> im = scipy.fft.ifftn(n).real
>>> plt.imshow(im)
<matplotlib.image.AxesImage object at 0x...>
>>> plt.show()
```



scipy.fft.rfft

scipy.fft.**rfft**(*x*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the 1-D discrete Fourier Transform for real input.

This function computes the 1-D *n*-point discrete Fourier Transform (DFT) of a real-valued array by means of an efficient algorithm called the Fast Fourier Transform (FFT).

Parameters

x [array_like] Input array

n [int, optional] Number of points along transformation axis in the input to use. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. If *n* is even, the length of the transformed axis is `(n/2)+1`. If *n* is odd, the length is `(n+1)/2`.

Raises

IndexError If *axis* is larger than the last axis of *a*.

See also:

irfft

The inverse of *rfft*.

fft

The 1-D FFT of general (complex) input.

fftn

The N-D FFT.

rfft2

The 2-D FFT of real input.

rfftn

The N-D FFT of real input.

Notes

When the DFT is computed for purely real input, the output is Hermitian-symmetric, i.e., the negative frequency terms are just the complex conjugates of the corresponding positive-frequency terms, and the negative-frequency terms are therefore redundant. This function does not compute the negative frequency terms, and the length of the transformed axis of the output is therefore `n//2 + 1`.

When `X = rfft(x)` and fs is the sampling frequency, `X[0]` contains the zero-frequency term 0*fs, which is real due to Hermitian symmetry.

If *n* is even, `A[-1]` contains the term representing both positive and negative Nyquist frequency (+fs/2 and -fs/2), and must also be purely real. If *n* is odd, there is no term at fs/2; `A[-1]` contains the largest positive frequency (fs/2*(n-1)/n), and is complex in the general case.

If the input *a* contains an imaginary part, it is silently discarded.

Examples

```
>>> import scipy.fft
>>> scipy.fft.fft([0, 1, 0, 0])
array([ 1.+0.j,  0.-1.j, -1.+0.j,  0.+1.j]) # may vary
>>> scipy.fft.rfft([0, 1, 0, 0])
array([ 1.+0.j,  0.-1.j, -1.+0.j]) # may vary
```

Notice how the final element of the *fft* output is the complex conjugate of the second element, for real input. For *rfft*, this symmetry is exploited to compute only the non-negative frequency terms.

scipy.fft.irfft

`scipy.fft.`**`irfft`**(*x*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Computes the inverse of *rfft*.

This function computes the inverse of the 1-D *n*-point discrete Fourier Transform of real input computed by *rfft*. In other words, `irfft(rfft(x), len(x)) == x` to within numerical accuracy. (See Notes below for why `len(a)` is necessary here.)

The input is expected to be in the form returned by *rfft*, i.e., the real zero-frequency term followed by the complex positive frequency terms in order of increasing frequency. Since the discrete Fourier Transform of real input is Hermitian-symmetric, the negative frequency terms are taken to be the complex conjugates of the corresponding positive frequency terms.

Parameters

x [array_like] The input array.

n [int, optional] Length of the transformed axis of the output. For *n* output points, `n//2+1` input points are necessary. If the input is longer than this, it is cropped. If it is shorter than this, it is padded with zeros. If *n* is not given, it is taken to be `2*(m-1)`, where `m` is the length of the input along the axis specified by *axis*.

axis [int, optional] Axis over which to compute the inverse FFT. If not given, the last axis is used.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. The length of the transformed axis is *n*, or, if *n* is not given, `2*(m-1)` where `m` is the length of the transformed axis of the input. To get an odd number of output points, *n* must be specified.

Raises

IndexError
If *axis* is larger than the last axis of *x*.

See also:

`rfft`

The 1-D FFT of real input, of which *`irfft`* is inverse.

`fft`

The 1-D FFT.

`irfft2`

The inverse of the 2-D FFT of real input.

`irfftn`

The inverse of the N-D FFT of real input.

Notes

Returns the real valued *n*-point inverse discrete Fourier transform of *x*, where *x* contains the non-negative frequency terms of a Hermitian-symmetric sequence. *n* is the length of the result, not the input.

If you specify an *n* such that *a* must be zero-padded or truncated, the extra/removed values will be added/removed at high frequencies. One can thus resample a series to *m* points via Fourier interpolation by: `a_resamp = irfft(rfft(a), m)`.

The default value of *n* assumes an even output length. By the Hermitian symmetry, the last imaginary component must be 0 and so is ignored. To avoid losing information, the correct length of the real input *must* be given.

Examples

```
>>> import scipy.fft
>>> scipy.fft.ifft([1, -1j, -1, 1j])
array([0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j]) # may vary
>>> scipy.fft.irfft([1, -1j, -1])
array([0.,  1.,  0.,  0.])
```

Notice how the last term in the input to the ordinary *`ifft`* is the complex conjugate of the second term, and the output has zero imaginary part everywhere. When calling *`irfft`*, the negative frequencies are not specified, and the output array is purely real.

scipy.fft.rfft2

scipy.fft.**rfft2**(*x*, *s=None*, *axes=(- 2, - 1)*, *norm=None*, *overwrite_x=False*, *workers=None*, *, plan=None*)

Compute the 2-D FFT of a real array.

Parameters

x [array] Input array, taken to be real.

s [sequence of ints, optional] Shape of the FFT.

axes [sequence of ints, optional] Axes over which to compute the FFT.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [ndarray] The result of the real 2-D FFT.

See also:

irfft2

The inverse of the 2-D FFT of real input.

rfft

The 1-D FFT of real input.

rfftn

Compute the N-D discrete Fourier Transform for real input.

Notes

This is really just *rfftn* with different default behavior. For more details see *rfftn*.

scipy.fft.irfft2

scipy.fft.**irfft2**(*x*, *s=None*, *axes=(- 2, - 1)*, *norm=None*, *overwrite_x=False*, *workers=None*, *, plan=None*)

Computes the inverse of *rfft2*

Parameters

x [array_like] The input array

s [sequence of ints, optional] Shape of the real output to the inverse FFT.

axes [sequence of ints, optional] The axes over which to compute the inverse fft. Default is the last two axes.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [ndarray] The result of the inverse real 2-D FFT.

See also:

rfft2

The 2-D FFT of real input.

irfft

The inverse of the 1-D FFT of real input.

irfftn

The inverse of the N-D FFT of real input.

Notes

This is really *irfftn* with different defaults. For more details see *irfftn*.

scipy.fft.rfftn

`scipy.fft.`**`rfftn`**(*x*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the N-D discrete Fourier Transform for real input.

This function computes the N-D discrete Fourier Transform over any number of axes in an M-D real array by means of the Fast Fourier Transform (FFT). By default, all axes are transformed, with the real transform performed over the last axis, while the remaining transforms are complex.

Parameters

x [array_like] Input array, taken to be real.

s [sequence of ints, optional] Shape (length along each transformed axis) to use from the input. (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). The final element of *s* corresponds to *n* for `rfft(x, n)`, while for the remaining axes, it corresponds to *n* for `fft(x, n)`. Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x
[bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* and *x*, as explained in the parameters section above. The length of the last axis transformed will be `s[-1]//2+1`, while the remaining transformed axes will have lengths according to *s*, or unchanged from the input.

Raises

ValueError
If *s* and *axes* have different length.

IndexError
If an element of *axes* is larger than than the number of axes of *x*.

See also:

irfftn

The inverse of *rfftn*, i.e., the inverse of the N-D FFT of real input.

fft

The 1-D FFT, with definitions and conventions used.

rfft

The 1-D FFT of real input.

fftn

The N-D FFT.

rfft2

The 2-D FFT of real input.

Notes

The transform for real input is performed over the last transformation axis, as by *rfft*, then the transform over the remaining axes is performed as by *fftn*. The order of the output is as for *rfft* for the final transformation axis, and as for *fftn* for the remaining transformation axes.

See *fft* for details, definitions and conventions used.

Examples

```
>>> import scipy.fft
>>> x = np.ones((2, 2, 2))
>>> scipy.fft.rfftn(x)
array([[[8.+0.j,  0.+0.j], # may vary
        [0.+0.j,  0.+0.j]],
       [[0.+0.j,  0.+0.j],
        [0.+0.j,  0.+0.j]]])
```

```
>>> scipy.fft.rfftn(x, axes=(2, 0))
array([[[4.+0.j,  0.+0.j], # may vary
        [4.+0.j,  0.+0.j]],
       [[0.+0.j,  0.+0.j],
        [0.+0.j,  0.+0.j]]])
```

scipy.fft.irfftn

scipy.fft.**irfftn**(*x*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Computes the inverse of *rfftn*

This function computes the inverse of the N-D discrete Fourier Transform for real input over any number of axes in an M-D array by means of the Fast Fourier Transform (FFT). In other words, `irfftn(rfftn(x), x.shape) == x` to within numerical accuracy. (The `a.shape` is necessary like `len(a)` is for *irfft*, and for the same reason.)

The input should be ordered in the same way as is returned by *rfftn*, i.e., as for *irfft* for the final transformation axis, and as for *ifftn* along all the other axes.

Parameters

x [array_like] Input array.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). *s* is also the number of input points used along this axis, except for the last axis, where `s[-1]//2+1` points of the input are used. Along any axis, if the shape indicated by *s* is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. If *s* is not given, the shape of the input along the axes specified by axes is used. Except for the last axis which is taken to be `2*(m-1)`, where `m` is the length of the input along that axis.

axes [sequence of ints, optional] Axes over which to compute the inverse FFT. If not given, the last *len(s)* axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* or *x*, as explained in the parameters section above. The length of each transformed axis is as given by the corresponding element of *s*, or the length of the input in every axis except for the last one if *s* is not given. In the final transformed axis the length of the output when *s* is not given is `2*(m-1)`, where `m` is the length of the final transformed axis of the input. To get an odd number of output points in the final axis, *s* must be specified.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *x*.

See also:

rfftn

The forward N-D FFT of real input, of which *ifftn* is the inverse.

fft

The 1-D FFT, with definitions and conventions used.

irfft

The inverse of the 1-D FFT of real input.

irfft2

The inverse of the 2-D FFT of real input.

Notes

See *fft* for definitions and conventions used.

See *rfft* for definitions and conventions used for real input.

The default value of *s* assumes an even output length in the final transformation axis. When performing the final complex to real transformation, the Hermitian symmetry requires that the last imaginary component along that axis must be 0 and so it is ignored. To avoid losing information, the correct length of the real input *must* be given.

Examples

```
>>> import scipy.fft
>>> x = np.zeros((3, 2, 2))
>>> x[0, 0, 0] = 3 * 2 * 2
>>> scipy.fft.irfftn(x)
array([[[1.,  1.],
        [1.,  1.]],
       [[1.,  1.],
        [1.,  1.]],
       [[1.,  1.],
        [1.,  1.]]])
```

scipy.fft.hfft

scipy.fft.**hfft**(*x*, *n=None*, *axis=-1*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the FFT of a signal that has Hermitian symmetry, i.e., a real spectrum.

Parameters

x [array_like] The input array.

n [int, optional] Length of the transformed axis of the output. For *n* output points, `n//2 + 1` input points are necessary. If the input is longer than this, it is cropped. If it is shorter than this, it is padded with zeros. If *n* is not given, it is taken to be `2*(m-1)`, where `m` is the length of the input along the axis specified by *axis*.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. The length of the transformed axis is *n*, or, if *n* is not given, `2*m - 2`, where `m` is the length of the transformed axis of the input. To get an odd number of output points, *n* must be specified, for instance, as `2*m - 1` in the typical case,

Raises

IndexError
If *axis* is larger than the last axis of *a*.

See also:

rfft

Compute the 1-D FFT for real input.

ihfft

The inverse of *hfft*.

hfftn

Compute the N-D FFT of a Hermitian signal.

Notes

hfft/*ihfft* are a pair analogous to *rfft*/*irfft*, but for the opposite case: here the signal has Hermitian symmetry in the time domain and is real in the frequency domain. So, here, it's *hfft*, for which you must supply the length of the result if it is to be odd. * even: `ihfft(hfft(a, 2*len(a) - 2) == a`, within roundoff error, * odd: `ihfft(hfft(a, 2*len(a) - 1) == a`, within roundoff error.

Examples

```
>>> from scipy.fft import fft, hfft
>>> a = 2 * np.pi * np.arange(10) / 10
>>> signal = np.cos(a) + 3j * np.sin(3 * a)
>>> fft(signal).round(10)
array([ -0.+0.j,   5.+0.j,  -0.+0.j,  15.-0.j,   0.+0.j,   0.+0.j,
        -0.+0.j, -15.-0.j,   0.+0.j,   5.+0.j])
>>> hfft(signal[:6]).round(10) # Input first half of signal
array([  0.,   5.,   0.,  15.,  -0.,   0.,   0., -15.,  -0.,   5.])
>>> hfft(signal, 10)  # Input entire signal and truncate
array([  0.,   5.,   0.,  15.,  -0.,   0.,   0., -15.,  -0.,   5.])
```

scipy.fft.ihfft

scipy.fft.**ihfft**(*x*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the inverse FFT of a signal that has Hermitian symmetry.

Parameters

x [array_like] Input array.

n [int, optional] Length of the inverse FFT, the number of points along transformation axis in the input to use. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the inverse FFT. If not given, the last axis is used.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. The length of the transformed axis is `n//2 + 1`.

See also:

hfft, **irfft**

Notes

hfft/*ihfft* are a pair analogous to *rfft*/*irfft*, but for the opposite case: here, the signal has Hermitian symmetry in the time domain and is real in the frequency domain. So, here, it's *hfft*, for which you must supply the length of the result if it is to be odd: * even: `ihfft(hfft(a, 2*len(a) - 2) == a`, within roundoff error, * odd: `ihfft(hfft(a, 2*len(a) - 1) == a`, within roundoff error.

Examples

```
>>> from scipy.fft import ifft, ihfft
>>> spectrum = np.array([ 15, -4, 0, -1, 0, -4])
>>> ifft(spectrum)
array([1.+0.j,  2.+0.j,  3.+0.j,  4.+0.j,  3.+0.j,  2.+0.j]) # may vary
>>> ihfft(spectrum)
array([ 1.-0.j,  2.-0.j,  3.-0.j,  4.-0.j]) # may vary
```

scipy.fft.hfft2

scipy.fft.**hfft2**(*x*, *s=None*, *axes=(- 2, - 1)*, *norm=None*, *overwrite_x=False*, *workers=None*, *, plan=None*)

Compute the 2-D FFT of a Hermitian complex array.

Parameters

x [array] Input array, taken to be Hermitian complex.

s [sequence of ints, optional] Shape of the real output.

axes [sequence of ints, optional] Axes over which to compute the FFT.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from os.cpu_count(). See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [ndarray] The real result of the 2-D Hermitian complex real FFT.

See also:

hfftn

Compute the N-D discrete Fourier Transform for Hermitian complex input.

Notes

This is really just *hfftn* with different default behavior. For more details see *hfftn*.

scipy.fft.ihfft2

scipy.fft.**ihfft2**(*x*, *s=None*, *axes=(- 2, - 1)*, *norm=None*, *overwrite_x=False*, *workers=None*, *, plan=None*)

Compute the 2-D inverse FFT of a real spectrum.

Parameters

x [array_like] The input array

s [sequence of ints, optional] Shape of the real input to the inverse FFT.

axes [sequence of ints, optional] The axes over which to compute the inverse fft. Default is the last two axes.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from os.cpu_count(). See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [ndarray] The result of the inverse real 2-D FFT.

See also:

ihfftn

Compute the inverse of the N-D FFT of Hermitian input.

Notes

This is really *ihfftn* with different defaults. For more details see *ihfftn*.

scipy.fft.hfftn

scipy.fft.**hfftn**(*x*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*, ***, *plan=None*)

Compute the N-D FFT of Hermitian symmetric complex input, i.e., a signal with a real spectrum.

This function computes the N-D discrete Fourier Transform for a Hermitian symmetric complex input over any number of axes in an M-D array by means of the Fast Fourier Transform (FFT). In other words, `ihfftn(hfftn(x, s)) == x` to within numerical accuracy. (`s` here is `x.shape` with `s[-1] = x.shape[-1] * 2 - 1`, this is necessary for the same reason `x.shape` would be necessary for *irfft*.)

Parameters

x [array_like] Input array.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). *s* is also the number of input points used along this axis, except for the last axis, where `s[-1]//2+1` points of the input are used. Along any axis, if the shape indicated by *s* is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. If *s* is not given, the shape of the input along the axes specified by axes is used. Except for the last axis which is taken to be `2*(m-1)` where `m` is the length of the input along that axis.

axes [sequence of ints, optional] Axes over which to compute the inverse FFT. If not given, the last *len(s)* axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* or *x*, as explained in the parameters section above. The length of each transformed axis is as given by the corresponding element of *s*, or the length of the input in every axis except for the last one if *s* is not given. In the final transformed axis the length of the output when *s* is not given is `2*(m-1)` where `m` is the length of the final transformed axis of the input. To get an odd number of output points in the final axis, *s* must be specified.

Raises

ValueError
If *s* and *axes* have different length.

IndexError
If an element of *axes* is larger than than the number of axes of *x*.

See also:

ihfftn

The inverse N-D FFT with real spectrum. Inverse of *hfftn*.

fft

The 1-D FFT, with definitions and conventions used.

rfft

Forward FFT of real input.

Notes

For a 1-D signal `x` to have a real spectrum, it must satisfy the Hermitian property:

```
x[i] == np.conj(x[-i]) for all i
```

This generalizes into higher dimensions by reflecting over each axis in turn:

```
x[i, j, k, ...] == np.conj(x[-i, -j, -k, ...]) for all i, j, k, ...
```

This should not be confused with a Hermitian matrix, for which the transpose is its own conjugate:

```
x[i, j] == np.conj(x[j, i]) for all i, j
```

The default value of *s* assumes an even output length in the final transformation axis. When performing the final complex to real transformation, the Hermitian symmetry requires that the last imaginary component along that axis must be 0 and so it is ignored. To avoid losing information, the correct length of the real input *must* be given.

Examples

```
>>> import scipy.fft
>>> x = np.ones((3, 2, 2))
>>> scipy.fft.hfftn(x)
array([[[12.,  0.],
        [ 0.,  0.]],
       [[ 0.,  0.],
        [ 0.,  0.]],
       [[ 0.,  0.],
        [ 0.,  0.]]])
```

scipy.fft.ihfftn

scipy.fft.**ihfftn**(*x*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*, **, plan=None*)

Compute the N-D inverse discrete Fourier Transform for a real spectrum.

This function computes the N-D inverse discrete Fourier Transform over any number of axes in an M-D real array by means of the Fast Fourier Transform (FFT). By default, all axes are transformed, with the real transform performed over the last axis, while the remaining transforms are complex.

Parameters

x [array_like] Input array, taken to be real.

s [sequence of ints, optional] Shape (length along each transformed axis) to use from the input. (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see *fft*). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False. See *fft* for more details.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

plan [object, optional] This argument is reserved for passing in a precomputed plan provided by downstream FFT vendors. It is currently not used in SciPy.
New in version 1.5.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* and *x*, as explained in the parameters section above. The length of the last axis transformed will be `s[-1]//2+1`, while the remaining transformed axes will have lengths according to *s*, or unchanged from the input.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *x*.

See also:

hfftn

The forward N-D FFT of Hermitian input.

hfft

The 1-D FFT of Hermitian input.

fft

The 1-D FFT, with definitions and conventions used.

fftn

The N-D FFT.

hfft2

The 2-D FFT of Hermitian input.

Notes

The transform for real input is performed over the last transformation axis, as by *ihfft*, then the transform over the remaining axes is performed as by *ifftn*. The order of the output is the positive part of the Hermitian output signal, in the same format as *rfft*.

Examples

```
>>> import scipy.fft
>>> x = np.ones((2, 2, 2))
>>> scipy.fft.ihfftn(x)
array([[[1.+0.j,  0.+0.j], # may vary
        [0.+0.j,  0.+0.j]],
       [[0.+0.j,  0.+0.j],
        [0.+0.j,  0.+0.j]]])
>>> scipy.fft.ihfftn(x, axes=(2, 0))
array([[[1.+0.j,  0.+0.j], # may vary
        [1.+0.j,  0.+0.j]],
       [[0.+0.j,  0.+0.j],
        [0.+0.j,  0.+0.j]]])
```

Discrete Sin and Cosine Transforms (DST and DCT)

dct(x[, type, n, axis, norm, overwrite_x, …])	Return the Discrete Cosine Transform of arbitrary type sequence x.
idct(x[, type, n, axis, norm, overwrite_x, …])	Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.
dctn(x[, type, s, axes, norm, overwrite_x, …])	Return multidimensional Discrete Cosine Transform along the specified axes.
idctn(x[, type, s, axes, norm, overwrite_x, …])	Return multidimensional Discrete Cosine Transform along the specified axes.
dst(x[, type, n, axis, norm, overwrite_x, …])	Return the Discrete Sine Transform of arbitrary type sequence x.
idst(x[, type, n, axis, norm, overwrite_x, …])	Return the Inverse Discrete Sine Transform of an arbitrary type sequence.
dstn(x[, type, s, axes, norm, overwrite_x, …])	Return multidimensional Discrete Sine Transform along the specified axes.
idstn(x[, type, s, axes, norm, overwrite_x, …])	Return multidimensional Discrete Sine Transform along the specified axes.

scipy.fft.dct

scipy.fft.**dct**(*x*, *type=2*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*, *workers=None*)

Return the Discrete Cosine Transform of arbitrary type sequence x.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.

n [int, optional] Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the dct is computed; the default is over the last axis (i.e., `axis=-1`).

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see Notes). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

Returns

y [ndarray of real] The transformed input array.

See also:

idct

Inverse DCT

Notes

For a single dimension array `x`, `dct(x, norm='ortho')` is equal to MATLAB `dct(x)`.

For `norm="backward"`, there is no scaling on *dct* and the *idct* is scaled by `1/N` where `N` is the "logical" size of the DCT. For `norm="forward"` the `1/N` normalization is applied to the forward *dct* instead and the *idct* is unnormalized. For `norm='ortho'` both directions are scaled by the same factor of `1/sqrt(N)`.

There are, theoretically, 8 types of the DCT, only the first 4 types are implemented in SciPy.'The' DCT generally refers to DCT type 2, and 'the' Inverse DCT generally refers to DCT type 3.

Type I

There are several definitions of the DCT-I; we use the following (for `norm="backward"`)

$$y_k = x_0 + (-1)^k x_{N-1} + 2\sum_{n=1}^{N-2} x_n \cos\left(\frac{\pi k n}{N-1}\right)$$

If `norm='ortho'`, `x[0]` and `x[N-1]` are multiplied by a scaling factor of $\sqrt{2}$, and `y[k]` is multiplied by a scaling factor `f`

$$f = \begin{cases} \frac{1}{2}\sqrt{\frac{1}{N-1}} & \text{if } k = 0 \text{ or } N-1, \\ \frac{1}{2}\sqrt{\frac{2}{N-1}} & \text{otherwise} \end{cases}$$

Note: The DCT-I is only supported for input size > 1.

Type II

There are several definitions of the DCT-II; we use the following (for `norm="backward"`)

$$y_k = 2 \sum_{n=0}^{N-1} x_n \cos\left(\frac{\pi k(2n+1)}{2N}\right)$$

If `norm="ortho"`, `y[k]` is multiplied by a scaling factor `f`

$$f = \begin{cases} \sqrt{\frac{1}{4N}} & \text{if } k = 0, \\ \sqrt{\frac{1}{2N}} & \text{otherwise} \end{cases}$$

which makes the corresponding matrix of coefficients orthonormal (`O @ O.T = np.eye(N)`).

Type III

There are several definitions, we use the following (for `norm="backward"`)

$$y_k = x_0 + 2 \sum_{n=1}^{N-1} x_n \cos\left(\frac{\pi(2k+1)n}{2N}\right)$$

or, for `norm="ortho"`

$$y_k = \frac{x_0}{\sqrt{N}} + \sqrt{\frac{2}{N}} \sum_{n=1}^{N-1} x_n \cos\left(\frac{\pi(2k+1)n}{2N}\right)$$

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor *2N*. The orthonormalized DCT-III is exactly the inverse of the orthonormalized DCT-II.

Type IV

There are several definitions of the DCT-IV; we use the following (for `norm="backward"`)

$$y_k = 2 \sum_{n=0}^{N-1} x_n \cos\left(\frac{\pi(2k+1)(2n+1)}{4N}\right)$$

If `norm="ortho"`, `y[k]` is multiplied by a scaling factor `f`

$$f = \frac{1}{\sqrt{2N}}$$

References

[1], [2]

Examples

The Type 1 DCT is equivalent to the FFT (though faster) for real, even-symmetrical inputs. The output is also real and even-symmetrical. Half of the FFT input is used to generate half of the FFT output:

```
>>> from scipy.fft import fft, dct
>>> fft(np.array([4., 3., 5., 10., 5., 3.])).real
array([ 30.,  -8.,   6.,  -2.,   6.,  -8.])
>>> dct(np.array([4., 3., 5., 10.]), 1)
array([ 30.,  -8.,   6.,  -2.])
```

scipy.fft.idct

scipy.fft.**idct**(*x*, *type=2*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*, *workers=None*)

Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.

n [int, optional] Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the idct is computed; the default is over the last axis (i.e., `axis=-1`).

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see Notes). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

Returns

idct [ndarray of real] The transformed input array.

See also:

dct

Forward DCT

Notes

For a single dimension array *x*, `idct(x, norm='ortho')` is equal to MATLAB `idct(x)`.

'The' IDCT is the IDCT-II, which is the same as the normalized DCT-III.

The IDCT is equivalent to a normal DCT except for the normalization and type. DCT type 1 and 4 are their own inverse and DCTs 2 and 3 are each other's inverses.

Examples

The Type 1 DCT is equivalent to the DFT for real, even-symmetrical inputs. The output is also real and even-symmetrical. Half of the IFFT input is used to generate half of the IFFT output:

```
>>> from scipy.fft import ifft, idct
>>> ifft(np.array([ 30.,  -8.,   6.,  -2.,   6.,  -8.])).real
array([  4.,   3.,   5.,  10.,   5.,   3.])
>>> idct(np.array([ 30.,  -8.,   6.,  -2.]), 1)
array([  4.,   3.,   5.,  10.])
```

scipy.fft.dctn

scipy.fft.**dctn**(*x*, *type=2*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*)

Return multidimensional Discrete Cosine Transform along the specified axes.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.

s [int or array_like of ints or None, optional] The shape of the result. If both *s* and *axes* (see below) are None, *s* is `x.shape`; if *s* is None but *axes* is not None, then *s* is `numpy.take(x.shape, axes, axis=0)`. If `s[i] > x.shape[i]`, the ith dimension is padded with zeros. If `s[i] < x.shape[i]`, the ith dimension is truncated to length `s[i]`. If any element of *s* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] Axes over which the DCT is computed. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see Notes). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

Returns

y [ndarray of real] The transformed input array.

See also:

idctn

Inverse multidimensional DCT

Notes

For full details of the DCT types and normalization modes, as well as references, see *dct*.

Examples

```
>>> from scipy.fft import dctn, idctn
>>> rng = np.random.default_rng()
>>> y = rng.standard_normal((16, 16))
>>> np.allclose(y, idctn(dctn(y)))
True
```

scipy.fft.idctn

scipy.fft.**idctn**(*x*, *type=2*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*)

Return multidimensional Discrete Cosine Transform along the specified axes.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.

s [int or array_like of ints or None, optional] The shape of the result. If both *s* and *axes* (see below) are None, *s* is `x.shape`; if *s* is None but *axes* is not None, then *s* is `numpy.take(x.shape, axes, axis=0)`. If `s[i] > x.shape[i]`, the ith dimension is padded with zeros. If `s[i] < x.shape[i]`, the ith dimension is truncated to length `s[i]`. If any element of *s* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] Axes over which the IDCT is computed. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see Notes). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

Returns

y [ndarray of real] The transformed input array.

See also:

dctn

multidimensional DCT

Notes

For full details of the IDCT types and normalization modes, as well as references, see *idct*.

Examples

```
>>> from scipy.fft import dctn, idctn
>>> rng = np.random.default_rng()
>>> y = rng.standard_normal((16, 16))
>>> np.allclose(y, idctn(dctn(y)))
True
```

scipy.fft.dst

`scipy.fft.`**dst**(*x*, *type=2*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*, *workers=None*)

Return the Discrete Sine Transform of arbitrary type sequence x.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.

n [int, optional] Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the dst is computed; the default is over the last axis (i.e., `axis=-1`).

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see Notes). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

Returns

dst [ndarray of reals] The transformed input array.

See also:

`idst`

Inverse DST

Notes

For a single dimension array `x`.

For `norm="backward"`, there is no scaling on the *`dst`* and the *`idst`* is scaled by `1/N` where `N` is the "logical" size of the DST. For `norm='ortho'` both directions are scaled by the same factor `1/sqrt(N)`.

There are, theoretically, 8 types of the DST for different combinations of even/odd boundary conditions and boundary off sets [1], only the first 4 types are implemented in SciPy.

Type I

There are several definitions of the DST-I; we use the following for `norm="backward"`. DST-I assumes the input is odd around $n=-1$ and $n=N$.

$$y_k = 2\sum_{n=0}^{N-1} x_n \sin\left(\frac{\pi(k+1)(n+1)}{N+1}\right)$$

Note that the DST-I is only supported for input size > 1. The (unnormalized) DST-I is its own inverse, up to a factor $2(N+1)$. The orthonormalized DST-I is exactly its own inverse.

Type II

There are several definitions of the DST-II; we use the following for `norm="backward"`. DST-II assumes the input is odd around $n=-1/2$ and $n=N-1/2$; the output is odd around $k=-1$ and even around $k=N-1$

$$y_k = 2\sum_{n=0}^{N-1} x_n \sin\left(\frac{\pi(k+1)(2n+1)}{2N}\right)$$

if `norm='ortho'`, `y[k]` is multiplied by a scaling factor `f`

$$f = \begin{cases} \sqrt{\frac{1}{4N}} & \text{if } k=0, \\ \sqrt{\frac{1}{2N}} & \text{otherwise} \end{cases}$$

Type III

There are several definitions of the DST-III, we use the following (for `norm="backward"`). DST-III assumes the input is odd around $n=-1$ and even around $n=N-1$

$$y_k = (-1)^k x_{N-1} + 2\sum_{n=0}^{N-2} x_n \sin\left(\frac{\pi(2k+1)(n+1)}{2N}\right)$$

The (unnormalized) DST-III is the inverse of the (unnormalized) DST-II, up to a factor $2N$. The orthonormalized DST-III is exactly the inverse of the orthonormalized DST-II.

Type IV

There are several definitions of the DST-IV, we use the following (for `norm="backward"`). DST-IV assumes the input is odd around $n = -0.5$ and even around $n = N - 0.5$

$$y_k = 2 \sum_{n=0}^{N-1} x_n \sin\left(\frac{\pi(2k+1)(2n+1)}{4N}\right)$$

The (unnormalized) DST-IV is its own inverse, up to a factor $2N$. The orthonormalized DST-IV is exactly its own inverse.

References

[1]

scipy.fft.idst

`scipy.fft.`**`idst`**(*x*, *type=2*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*, *workers=None*)

Return the Inverse Discrete Sine Transform of an arbitrary type sequence.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.

n [int, optional] Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the idst is computed; the default is over the last axis (i.e., `axis=-1`).

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see Notes). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

Returns

idst [ndarray of real] The transformed input array.

See also:

dst

Forward DST

Notes

'The' IDST is the IDST-II, which is the same as the normalized DST-III.

The IDST is equivalent to a normal DST except for the normalization and type. DST type 1 and 4 are their own inverse and DSTs 2 and 3 are each other's inverses.

scipy.fft.dstn

scipy.fft.**dstn**(*x*, *type=2*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*)

Return multidimensional Discrete Sine Transform along the specified axes.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.

s [int or array_like of ints or None, optional] The shape of the result. If both *s* and *axes* (see below) are None, *s* is `x.shape`; if *s* is None but *axes* is not None, then *s* is `numpy.take(x.shape, axes, axis=0)`. If `s[i] > x.shape[i]`, the ith dimension is padded with zeros. If `s[i] < x.shape[i]`, the ith dimension is truncated to length `s[i]`. If any element of *shape* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] Axes over which the DST is computed. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see Notes). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

Returns

y [ndarray of real] The transformed input array.

See also:

idstn

Inverse multidimensional DST

Notes

For full details of the DST types and normalization modes, as well as references, see *dst*.

Examples

```
>>> from scipy.fft import dstn, idstn
>>> rng = np.random.default_rng()
>>> y = rng.standard_normal((16, 16))
>>> np.allclose(y, idstn(dstn(y)))
True
```

scipy.fft.idstn

scipy.fft.**idstn**(*x*, *type=2*, *s=None*, *axes=None*, *norm=None*, *overwrite_x=False*, *workers=None*)

Return multidimensional Discrete Sine Transform along the specified axes.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.

s [int or array_like of ints or None, optional] The shape of the result. If both *s* and *axes* (see below) are None, *s* is `x.shape`; if *s* is None but *axes* is not None, then *s* is `numpy.take(x.shape, axes, axis=0)`. If `s[i] > x.shape[i]`, the ith dimension is padded with zeros. If `s[i] < x.shape[i]`, the ith dimension is truncated to length `s[i]`. If any element of *s* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] Axes over which the IDST is computed. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{"backward", "ortho", "forward"}, optional] Normalization mode (see Notes). Default is "backward".

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

workers [int, optional] Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See *fft* for more details.

Returns

y [ndarray of real] The transformed input array.

See also:

dstn

multidimensional DST

Notes

For full details of the IDST types and normalization modes, as well as references, see *idst*.

Examples

```
>>> from scipy.fft import dstn, idstn
>>> rng = np.random.default_rng()
>>> y = rng.standard_normal((16, 16))
>>> np.allclose(y, idstn(dstn(y)))
True
```

Fast Hankel Transforms

fht(a, dln, mu[, offset, bias])	Compute the fast Hankel transform.
ifht(A, dln, mu[, offset, bias])	Compute the inverse fast Hankel transform.

scipy.fft.fht

`scipy.fft.`**fht**(*a*, *dln*, *mu*, *offset=0.0*, *bias=0.0*)

Compute the fast Hankel transform.

Computes the discrete Hankel transform of a logarithmically spaced periodic sequence using the FFTLog algorithm [1], [2].

Parameters

a [array_like (…, n)] Real periodic input array, uniformly logarithmically spaced. For multi-dimensional input, the transform is performed over the last axis.

dln [float] Uniform logarithmic spacing of the input array.

mu	[float] Order of the Hankel transform, any positive or negative real number.
offset	[float, optional] Offset of the uniform logarithmic spacing of the output array.
bias	[float, optional] Exponent of power law bias, any positive or negative real number.

Returns

A	[array_like (…, n)] The transformed output array, which is real, periodic, uniformly logarithmically spaced, and of the same shape as the input array.

See also:

ifht

The inverse of *fht*.

fhtoffset

Return an optimal offset for *fht*.

Notes

This function computes a discrete version of the Hankel transform

$$A(k) = \int_0^\infty a(r)\, J_\mu(kr)\, k\, dr \;,$$

where J_μ is the Bessel function of order μ. The index μ may be any real number, positive or negative.

The input array *a* is a periodic sequence of length n, uniformly logarithmically spaced with spacing *dln*,

$$a_j = a(r_j) \;, \quad r_j = r_c \exp[(j - j_c)\, \mathtt{dln}]$$

centred about the point r_c. Note that the central index $j_c = (n + 1)/2$ is half-integral if n is even, so that r_c falls between two input elements. Similarly, the output array *A* is a periodic sequence of length n, also uniformly logarithmically spaced with spacing *dln*

$$A_j = A(k_j) \;, \quad k_j = k_c \exp[(j - j_c)\, \mathtt{dln}]$$

centred about the point k_c.

The centre points r_c and k_c of the periodic intervals may be chosen arbitrarily, but it would be usual to choose the product $k_c r_c = k_j r_{n-1-j} = k_{n-1-j} r_j$ to be unity. This can be changed using the *offset* parameter, which controls the logarithmic offset $\log(k_c) = \mathtt{offset} - \log(r_c)$ of the output array. Choosing an optimal value for *offset* may reduce ringing of the discrete Hankel transform.

If the *bias* parameter is nonzero, this function computes a discrete version of the biased Hankel transform

$$A(k) = \int_0^\infty a_q(r)\, (kr)^q\, J_\mu(kr)\, k\, dr$$

where q is the value of *bias*, and a power law bias $a_q(r) = a(r)\, (kr)^{-q}$ is applied to the input sequence. Biasing the transform can help approximate the continuous transform of $a(r)$ if there is a value q such that $a_q(r)$ is close to a periodic sequence, in which case the resulting $A(k)$ will be close to the continuous transform.

References

[1], [2]

scipy.fft.ifht

scipy.fft.**ifht**(*A*, *dln*, *mu*, *offset=0.0*, *bias=0.0*)

Compute the inverse fast Hankel transform.

Computes the discrete inverse Hankel transform of a logarithmically spaced periodic sequence. This is the inverse operation to *fht*.

Parameters

A	[array_like (…, n)] Real periodic input array, uniformly logarithmically spaced. For multi-dimensional input, the transform is performed over the last axis.
dln	[float] Uniform logarithmic spacing of the input array.
mu	[float] Order of the Hankel transform, any positive or negative real number.
offset	[float, optional] Offset of the uniform logarithmic spacing of the output array.
bias	[float, optional] Exponent of power law bias, any positive or negative real number.

Returns

a	[array_like (…, n)] The transformed output array, which is real, periodic, uniformly logarithmically spaced, and of the same shape as the input array.

See also:

fht

Definition of the fast Hankel transform.

fhtoffset

Return an optimal offset for *ifht*.

Notes

This function computes a discrete version of the Hankel transform

$$a(r) = \int_0^\infty A(k)\, J_\mu(kr)\, r\, dk \;,$$

where J_μ is the Bessel function of order μ. The index μ may be any real number, positive or negative.

See *fht* for further details.

Helper functions

fftshift(x[, axes])	Shift the zero-frequency component to the center of the spectrum.
ifftshift(x[, axes])	The inverse of *fftshift*.
fftfreq(n[, d])	Return the Discrete Fourier Transform sample frequencies.
rfftfreq(n[, d])	Return the Discrete Fourier Transform sample frequencies (for usage with rfft, irfft).
fhtoffset(dln, mu[, initial, bias])	Return optimal offset for a fast Hankel transform.

continues on next page

Table 19 – continued from previous page

next_fast_len	Find the next fast size of input data to `fft`, for zero-padding, etc.
set_workers(workers)	Context manager for the default number of workers used in *scipy.fft*
get_workers()	Returns the default number of workers within the current context

scipy.fft.fftshift

`scipy.fft.`**`fftshift`**(*x*, *axes=None*)

Shift the zero-frequency component to the center of the spectrum.

This function swaps half-spaces for all axes listed (defaults to all). Note that `y[0]` is the Nyquist component only if `len(x)` is even.

Parameters

x	[array_like] Input array.
axes	[int or shape tuple, optional] Axes over which to shift. Default is None, which shifts all axes.

Returns

y	[ndarray] The shifted array.

See also:

ifftshift

The inverse of *fftshift*.

Examples

```
>>> freqs = np.fft.fftfreq(10, 0.1)
>>> freqs
array([ 0.,  1.,  2., ..., -3., -2., -1.])
>>> np.fft.fftshift(freqs)
array([-5., -4., -3., -2., -1.,  0.,  1.,  2.,  3.,  4.])
```

Shift the zero-frequency component only along the second axis:

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.fftshift(freqs, axes=(1,))
array([[ 2.,  0.,  1.],
       [-4.,  3.,  4.],
       [-1., -3., -2.]])
```

scipy.fft.ifftshift

scipy.fft.**ifftshift**(*x*, *axes=None*)

The inverse of `fftshift`. Although identical for even-length *x*, the functions differ by one sample for odd-length *x*.

Parameters

x	[array_like] Input array.
axes	[int or shape tuple, optional] Axes over which to calculate. Defaults to None, which shifts all axes.

Returns

y	[ndarray] The shifted array.

See also:

`fftshift`

Shift zero-frequency component to the center of the spectrum.

Examples

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.ifftshift(np.fft.fftshift(freqs))
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
```

scipy.fft.fftfreq

scipy.fft.**fftfreq**(*n*, *d=1.0*)

Return the Discrete Fourier Transform sample frequencies.

The returned float array *f* contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length *n* and a sample spacing *d*:

```
f = [0, 1, ...,   n/2-1,     -n/2, ..., -1] / (d*n)   if n is even
f = [0, 1, ..., (n-1)/2, -(n-1)/2, ..., -1] / (d*n)   if n is odd
```

Parameters

n	[int] Window length.
d	[scalar, optional] Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns

f	[ndarray] Array of length *n* containing the sample frequencies.

Examples

```
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
>>> fourier = np.fft.fft(signal)
>>> n = signal.size
>>> timestep = 0.1
>>> freq = np.fft.fftfreq(n, d=timestep)
>>> freq
array([ 0.  ,  1.25,  2.5 , ..., -3.75, -2.5 , -1.25])
```

scipy.fft.rfftfreq

scipy.fft.**rfftfreq**(*n*, *d=1.0*)

Return the Discrete Fourier Transform sample frequencies (for usage with rfft, irfft).

The returned float array *f* contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length *n* and a sample spacing *d*:

```
f = [0, 1, ...,     n/2-1,     n/2] / (d*n)   if n is even
f = [0, 1, ..., (n-1)/2-1, (n-1)/2] / (d*n)   if n is odd
```

Unlike *fftfreq* (but like *scipy.fftpack.rfftfreq*) the Nyquist frequency component is considered to be positive.

Parameters

n [int] Window length.

d [scalar, optional] Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns

f [ndarray] Array of length `n//2 + 1` containing the sample frequencies.

Examples

```
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5, -3, 4], dtype=float)
>>> fourier = np.fft.rfft(signal)
>>> n = signal.size
>>> sample_rate = 100
>>> freq = np.fft.fftfreq(n, d=1./sample_rate)
>>> freq
array([  0.,  10.,  20., ..., -30., -20., -10.])
>>> freq = np.fft.rfftfreq(n, d=1./sample_rate)
>>> freq
array([  0.,  10.,  20.,  30.,  40.,  50.])
```

scipy.fft.fhtoffset

scipy.fft.**fhtoffset**(*dln*, *mu*, *initial=0.0*, *bias=0.0*)

Return optimal offset for a fast Hankel transform.

Returns an offset close to *initial* that fulfils the low-ringing condition of [1] for the fast Hankel transform `fht` with logarithmic spacing *dln*, order *mu* and bias *bias*.

Parameters

dln	[float] Uniform logarithmic spacing of the transform.
mu	[float] Order of the Hankel transform, any positive or negative real number.
initial	[float, optional] Initial value for the offset. Returns the closest value that fulfils the low-ringing condition.
bias	[float, optional] Exponent of power law bias, any positive or negative real number.

Returns

offset	[float] Optimal offset of the uniform logarithmic spacing of the transform that fulfils a low-ringing condition.

See also:

fht

Definition of the fast Hankel transform.

References

[1]

scipy.fft.next_fast_len

scipy.fft.**next_fast_len**()

Find the next fast size of input data to `fft`, for zero-padding, etc.

SciPy's FFT algorithms gain their speed by a recursive divide and conquer strategy. This relies on efficient functions for small prime factors of the input length. Thus, the transforms are fastest when using composites of the prime factors handled by the fft implementation. If there are efficient functions for all radices <= *n*, then the result will be a number *x* >= `target` with only prime factors < *n*. (Also known as *n*-smooth numbers)

Parameters

target	[int] Length to start searching from. Must be a positive integer.
real	[bool, optional] True if the FFT involves real input or output (e.g., `rfft` or `hfft` but not `fft`). Defaults to False.

Returns

out	[int] The smallest fast length greater than or equal to `target`.

Notes

The result of this function may change in future as performance considerations change, for example, if new prime factors are added.

Calling *fft* or *ifft* with real input data performs an `'R2C'` transform internally.

Examples

On a particular machine, an FFT of prime length takes 11.4 ms:

```
>>> from scipy import fft
>>> rng = np.random.default_rng()
>>> min_len = 93059  # prime length is worst case for speed
>>> a = rng.standard_normal(min_len)
>>> b = fft.fft(a)
```

Zero-padding to the next regular length reduces computation time to 1.6 ms, a speedup of 7.3 times:

```
>>> fft.next_fast_len(min_len, real=True)
93312
>>> b = fft.fft(a, 93312)
```

Rounding up to the next power of 2 is not optimal, taking 3.0 ms to compute; 1.9 times longer than the size given by `next_fast_len`:

```
>>> b = fft.fft(a, 131072)
```

scipy.fft.set_workers

`scipy.fft.`**`set_workers`**(*workers*)

Context manager for the default number of workers used in *scipy.fft*

Parameters

workers [int] The default number of workers to use

Examples

```
>>> from scipy import fft, signal
>>> rng = np.random.default_rng()
>>> x = rng.standard_normal((128, 64))
>>> with fft.set_workers(4):
...     y = signal.fftconvolve(x, x)
```

scipy.fft.get_workers

scipy.fft.**get_workers**()
Returns the default number of workers within the current context

Examples

```
>>> from scipy import fft
>>> fft.get_workers()
1
>>> with fft.set_workers(4):
...     fft.get_workers()
4
```

Backend control

set_backend(backend[, coerce, only])	Context manager to set the backend within a fixed scope.
skip_backend(backend)	Context manager to skip a backend within a fixed scope.
set_global_backend(backend)	Sets the global fft backend
register_backend(backend)	Register a backend for permanent use.

scipy.fft.set_backend

scipy.fft.**set_backend**(*backend*, *coerce=False*, *only=False*)
Context manager to set the backend within a fixed scope.

Upon entering the `with` statement, the given backend will be added to the list of available backends with the highest priority. Upon exit, the backend is reset to the state before entering the scope.

Parameters

backend [{object, 'scipy'}] The backend to use. Can either be a `str` containing the name of a known backend {'scipy'} or an object that implements the uarray protocol.

coerce [bool, optional] Whether to allow expensive conversions for the `x` parameter. e.g., copying a NumPy array to the GPU for a CuPy backend. Implies `only`.

only [bool, optional] If only is `True` and this backend returns `NotImplemented`, then a BackendNotImplemented error will be raised immediately. Ignoring any lower priority backends.

Examples

```
>>> import scipy.fft as fft
>>> with fft.set_backend('scipy', only=True):
...     fft.fft([1])  # Always calls the scipy implementation
array([1.+0.j])
```

scipy.fft.skip_backend

scipy.fft.**skip_backend**(*backend*)

Context manager to skip a backend within a fixed scope.

Within the context of a `with` statement, the given backend will not be called. This covers backends registered both locally and globally. Upon exit, the backend will again be considered.

Parameters

backend [{object, 'scipy'}] The backend to skip. Can either be a `str` containing the name of a known backend {'scipy'} or an object that implements the uarray protocol.

Examples

```
>>> import scipy.fft as fft
>>> fft.fft([1])  # Calls default SciPy backend
array([1.+0.j])
>>> with fft.skip_backend('scipy'):  # We explicitly skip the SciPy␣
↪backend
...     fft.fft([1])                 # leaving no implementation available
Traceback (most recent call last):
    ...
BackendNotImplementedError: No selected backends had an implementation ...
```

scipy.fft.set_global_backend

scipy.fft.**set_global_backend**(*backend*)

Sets the global fft backend

The global backend has higher priority than registered backends, but lower priority than context-specific backends set with *set_backend*.

Parameters

backend [{object, 'scipy'}] The backend to use. Can either be a `str` containing the name of a known backend {'scipy'} or an object that implements the uarray protocol.

Raises

ValueError: If the backend does not implement `numpy.scipy.fft`.

Notes

This will overwrite the previously set global backend, which, by default, is the SciPy implementation.

Examples

We can set the global fft backend:

```
>>> from scipy.fft import fft, set_global_backend
>>> set_global_backend("scipy")  # Sets global backend. "scipy" is the␣
↪default backend.
>>> fft([1])  # Calls the global backend
array([1.+0.j])
```

scipy.fft.register_backend

scipy.fft.**register_backend**(*backend*)

Register a backend for permanent use.

Registered backends have the lowest priority and will be tried after the global backend.

Parameters

backend [{object, 'scipy'}] The backend to use. Can either be a `str` containing the name of a known backend {'scipy'} or an object that implements the uarray protocol.

Raises

ValueError: If the backend does not implement `numpy.scipy.fft`.

Examples

We can register a new fft backend:

```
>>> from scipy.fft import fft, register_backend, set_global_backend
>>> class NoopBackend:  # Define an invalid Backend
...     __ua_domain__ = "numpy.scipy.fft"
...     def __ua_function__(self, func, args, kwargs):
...         return NotImplemented
>>> set_global_backend(NoopBackend())  # Set the invalid backend as global
>>> register_backend("scipy")  # Register a new backend
>>> fft([1])  # The registered backend is called because the global␣
↪backend returns `NotImplemented`
array([1.+0.j])
>>> set_global_backend("scipy")  # Restore global backend to default
```

3.3.6 Legacy discrete Fourier transforms (`scipy.fftpack`)

Warning: This submodule is now considered legacy, new code should use *scipy.fft*.

Fast Fourier Transforms (FFTs)

fft(x[, n, axis, overwrite_x])	Return discrete Fourier transform of real or complex sequence.
ifft(x[, n, axis, overwrite_x])	Return discrete inverse Fourier transform of real or complex sequence.
fft2(x[, shape, axes, overwrite_x])	2-D discrete Fourier transform.
ifft2(x[, shape, axes, overwrite_x])	2-D discrete inverse Fourier transform of real or complex sequence.
fftn(x[, shape, axes, overwrite_x])	Return multidimensional discrete Fourier transform.
ifftn(x[, shape, axes, overwrite_x])	Return inverse multidimensional discrete Fourier transform.
rfft(x[, n, axis, overwrite_x])	Discrete Fourier transform of a real sequence.
irfft(x[, n, axis, overwrite_x])	Return inverse discrete Fourier transform of real sequence x.

continues on next page

Table 21 – continued from previous page

dct(x[, type, n, axis, norm, overwrite_x])	Return the Discrete Cosine Transform of arbitrary type sequence x.
idct(x[, type, n, axis, norm, overwrite_x])	Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.
dctn(x[, type, shape, axes, norm, overwrite_x])	Return multidimensional Discrete Cosine Transform along the specified axes.
idctn(x[, type, shape, axes, norm, overwrite_x])	Return multidimensional Discrete Cosine Transform along the specified axes.
dst(x[, type, n, axis, norm, overwrite_x])	Return the Discrete Sine Transform of arbitrary type sequence x.
idst(x[, type, n, axis, norm, overwrite_x])	Return the Inverse Discrete Sine Transform of an arbitrary type sequence.
dstn(x[, type, shape, axes, norm, overwrite_x])	Return multidimensional Discrete Sine Transform along the specified axes.
idstn(x[, type, shape, axes, norm, overwrite_x])	Return multidimensional Discrete Sine Transform along the specified axes.

scipy.fftpack.fft

scipy.fftpack.**fft**(*x*, *n=None*, *axis=- 1*, *overwrite_x=False*)

Return discrete Fourier transform of real or complex sequence.

The returned complex array contains `y(0), y(1),..., y(n-1)`, where

`y(j) = (x * exp(-2*pi*sqrt(-1)*j*np.arange(n)/n)).sum()`.

Parameters

x [array_like] Array to Fourier transform.

n [int, optional] Length of the Fourier transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the fft's are computed; the default is over the last axis (i.e., `axis=-1`).

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

z [complex ndarray] with the elements:

```
[y(0),y(1),..,y(n/2),y(1-n/2),...,y(-1)]         if n is␣
↪even
[y(0),y(1),..,y((n-1)/2),y(-(n-1)/2),...,y(-1)]  if n is␣
↪odd
```

where:

```
y(j) = sum[k=0..n-1] x[k] * exp(-sqrt(-1)*j*k* 2*pi/n), j␣
↪= 0..n-1
```

See also:

ifft

Inverse FFT

rfft

FFT of a real sequence

Notes

The packing of the result is "standard": If `A = fft(a, n)`, then `A[0]` contains the zero-frequency term, `A[1:n/2]` contains the positive-frequency terms, and `A[n/2:]` contains the negative-frequency terms, in order of decreasingly negative frequency. So ,for an 8-point transform, the frequencies of the result are [0, 1, 2, 3, -4, -3, -2, -1]. To rearrange the fft output so that the zero-frequency component is centered, like [-4, -3, -2, -1, 0, 1, 2, 3], use *fftshift*.

Both single and double precision routines are implemented. Half precision inputs will be converted to single precision. Non-floating-point inputs will be converted to double precision. Long-double precision inputs are not supported.

This function is most efficient when *n* is a power of two, and least efficient when *n* is prime.

Note that if `x` is real-valued, then `A[j] == A[n-j].conjugate()`. If `x` is real-valued and `n` is even, then `A[n/2]` is real.

If the data type of *x* is real, a "real FFT" algorithm is automatically used, which roughly halves the computation time. To increase efficiency a little further, use *rfft*, which does the same calculation, but only outputs half of the symmetrical spectrum. If the data is both real and symmetrical, the *dct* can again double the efficiency by generating half of the spectrum from half of the signal.

Examples

```
>>> from scipy.fftpack import fft, ifft
>>> x = np.arange(5)
>>> np.allclose(fft(ifft(x)), x, atol=1e-15)  # within numerical accuracy.
True
```

scipy.fftpack.ifft

`scipy.fftpack.`**`ifft`**(*x*, *n=None*, *axis=- 1*, *overwrite_x=False*)

Return discrete inverse Fourier transform of real or complex sequence.

The returned complex array contains `y(0), y(1),..., y(n-1)`, where

`y(j) = (x * exp(2*pi*sqrt(-1)*j*np.arange(n)/n)).mean()`.

Parameters

x [array_like] Transformed data to invert.

n [int, optional] Length of the inverse Fourier transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the ifft's are computed; the default is over the last axis (i.e., `axis=-1`).

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

ifft [ndarray of floats] The inverse discrete Fourier transform.

See also:

fft

Forward FFT

Notes

Both single and double precision routines are implemented. Half precision inputs will be converted to single precision. Non-floating-point inputs will be converted to double precision. Long-double precision inputs are not supported.

This function is most efficient when *n* is a power of two, and least efficient when *n* is prime.

If the data type of *x* is real, a "real IFFT" algorithm is automatically used, which roughly halves the computation time.

Examples

```
>>> from scipy.fftpack import fft, ifft
>>> import numpy as np
>>> x = np.arange(5)
>>> np.allclose(ifft(fft(x)), x, atol=1e-15)  # within numerical accuracy.
True
```

scipy.fftpack.fft2

scipy.fftpack.**fft2**(*x*, *shape=None*, *axes=(- 2, - 1)*, *overwrite_x=False*)

2-D discrete Fourier transform.

Return the 2-D discrete Fourier transform of the 2-D argument *x*.

See also:

fftn

for detailed information.

Examples

```
>>> from scipy.fftpack import fft2, ifft2
>>> y = np.mgrid[:5, :5][0]
>>> y
array([[0, 0, 0, 0, 0],
       [1, 1, 1, 1, 1],
       [2, 2, 2, 2, 2],
       [3, 3, 3, 3, 3],
       [4, 4, 4, 4, 4]])
>>> np.allclose(y, ifft2(fft2(y)))
True
```

scipy.fftpack.ifft2

scipy.fftpack.**ifft2**(*x*, *shape=None*, *axes=(- 2, - 1)*, *overwrite_x=False*)

2-D discrete inverse Fourier transform of real or complex sequence.

Return inverse 2-D discrete Fourier transform of arbitrary type sequence x.

See *ifft* for more information.

See also:

fft2, **ifft**

Examples

```
>>> from scipy.fftpack import fft2, ifft2
>>> y = np.mgrid[:5, :5][0]
>>> y
array([[0, 0, 0, 0, 0],
       [1, 1, 1, 1, 1],
       [2, 2, 2, 2, 2],
       [3, 3, 3, 3, 3],
       [4, 4, 4, 4, 4]])
>>> np.allclose(y, fft2(ifft2(y)))
True
```

scipy.fftpack.fftn

scipy.fftpack.**fftn**(*x*, *shape=None*, *axes=None*, *overwrite_x=False*)

Return multidimensional discrete Fourier transform.

The returned array contains:

```
y[j_1,..,j_d] = sum[k_1=0..n_1-1, ..., k_d=0..n_d-1]
   x[k_1,..,k_d] * prod[i=1..d] exp(-sqrt(-1)*2*pi/n_i * j_i * k_i)
```

where d = len(x.shape) and n = x.shape.

Parameters

x [array_like] The (N-D) array to transform.

shape [int or array_like of ints or None, optional] The shape of the result. If both *shape* and *axes* (see below) are None, *shape* is `x.shape`; if *shape* is None but *axes* is not None, then *shape* is `numpy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the ith dimension is padded with zeros. If `shape[i] < x.shape[i]`, the ith dimension is truncated to length `shape[i]`. If any element of *shape* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] The axes of *x* (*y* if *shape* is not None) along which the transform is applied. The default is over all axes.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed. Default is False.

Returns

y [complex-valued N-D NumPy array] The (N-D) DFT of the input array.

See also:

ifftn

Notes

If `x` is real-valued, then `y[..., j_i, ...] == y[..., n_i-j_i, ...].conjugate()`.

Both single and double precision routines are implemented. Half precision inputs will be converted to single precision. Non-floating-point inputs will be converted to double precision. Long-double precision inputs are not supported.

Examples

```
>>> from scipy.fftpack import fftn, ifftn
>>> y = (-np.arange(16), 8 - np.arange(16), np.arange(16))
>>> np.allclose(y, fftn(ifftn(y)))
True
```

scipy.fftpack.ifftn

`scipy.fftpack.`**`ifftn`**(*x*, *shape=None*, *axes=None*, *overwrite_x=False*)

Return inverse multidimensional discrete Fourier transform.

The sequence can be of an arbitrary type.

The returned array contains:

```
y[j_1,..,j_d] = 1/p * sum[k_1=0..n_1-1, ..., k_d=0..n_d-1]
   x[k_1,..,k_d] * prod[i=1..d] exp(sqrt(-1)*2*pi/n_i * j_i * k_i)
```

where `d = len(x.shape)`, `n = x.shape`, and `p = prod[i=1..d] n_i`.

For description of parameters see *fftn*.

See also:

fftn

for detailed information.

Examples

```
>>> from scipy.fftpack import fftn, ifftn
>>> import numpy as np
>>> y = (-np.arange(16), 8 - np.arange(16), np.arange(16))
>>> np.allclose(y, ifftn(fftn(y)))
True
```

scipy.fftpack.rfft

scipy.fftpack.**rfft**(*x*, *n=None*, *axis=- 1*, *overwrite_x=False*)

Discrete Fourier transform of a real sequence.

Parameters

x [array_like, real-valued] The data to transform.

n [int, optional] Defines the length of the Fourier transform. If *n* is not specified (the default) then `n = x.shape[axis]`. If `n < x.shape[axis]`, *x* is truncated, if `n > x.shape[axis]`, *x* is zero-padded.

axis [int, optional] The axis along which the transform is applied. The default is the last axis.

overwrite_x [bool, optional] If set to true, the contents of *x* can be overwritten. Default is False.

Returns

z [real ndarray] The returned real array contains:

```
[y(0),Re(y(1)),Im(y(1)),...,Re(y(n/2))]              if n␣
↪is even
[y(0),Re(y(1)),Im(y(1)),...,Re(y(n/2)),Im(y(n/2))]   if n␣
↪is odd
```

where:

```
y(j) = sum[k=0..n-1] x[k] * exp(-sqrt(-1)*j*k*2*pi/n)
j = 0..n-1
```

See also:

fft, **irfft**, **scipy.fft.rfft**

Notes

Within numerical accuracy, `y == rfft(irfft(y))`.

Both single and double precision routines are implemented. Half precision inputs will be converted to single precision. Non-floating-point inputs will be converted to double precision. Long-double precision inputs are not supported.

To get an output with a complex datatype, consider using the newer function *scipy.fft.rfft*.

Examples

```
>>> from scipy.fftpack import fft, rfft
>>> a = [9, -9, 1, 3]
>>> fft(a)
array([  4. +0.j,   8.+12.j,  16. +0.j,   8.-12.j])
>>> rfft(a)
array([  4.,   8.,  12.,  16.])
```

scipy.fftpack.irfft

scipy.fftpack.**irfft**(*x*, *n=None*, *axis=- 1*, *overwrite_x=False*)

Return inverse discrete Fourier transform of real sequence x.

The contents of *x* are interpreted as the output of the *rfft* function.

Parameters

x [array_like] Transformed data to invert.

n [int, optional] Length of the inverse Fourier transform. If n < x.shape[axis], x is truncated. If n > x.shape[axis], x is zero-padded. The default results in n = x.shape[axis].

axis [int, optional] Axis along which the ifft's are computed; the default is over the last axis (i.e., axis=-1).

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

irfft [ndarray of floats] The inverse discrete Fourier transform.

See also:

rfft, **ifft**, **scipy.fft.irfft**

Notes

The returned real array contains:

```
[y(0),y(1),...,y(n-1)]
```

where for n is even:

```
y(j) = 1/n (sum[k=1..n/2-1] (x[2*k-1]+sqrt(-1)*x[2*k])
                             * exp(sqrt(-1)*j*k* 2*pi/n)
            + c.c. + x[0] + (-1)**(j) x[n-1])
```

and for n is odd:

```
y(j) = 1/n (sum[k=1..(n-1)/2] (x[2*k-1]+sqrt(-1)*x[2*k])
                             * exp(sqrt(-1)*j*k* 2*pi/n)
            + c.c. + x[0])
```

c.c. denotes complex conjugate of preceding expression.

For details on input parameters, see *rfft*.

To process (conjugate-symmetric) frequency-domain data with a complex datatype, consider using the newer function *scipy.fft.irfft*.

Examples

```
>>> from scipy.fftpack import rfft, irfft
>>> a = [1.0, 2.0, 3.0, 4.0, 5.0]
>>> irfft(a)
array([ 2.6       , -3.16405192,  1.24398433, -1.14955713,  1.46962473])
>>> irfft(rfft(a))
array([1., 2., 3., 4., 5.])
```

scipy.fftpack.dct

scipy.fftpack.**dct**(*x*, *type=2*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*)

Return the Discrete Cosine Transform of arbitrary type sequence x.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.

n [int, optional] Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the dct is computed; the default is over the last axis (i.e., `axis=-1`).

norm [{None, 'ortho'}, optional] Normalization mode (see Notes). Default is None.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

y [ndarray of real] The transformed input array.

See also:

`idct`

Inverse DCT

Notes

For a single dimension array `x`, `dct(x, norm='ortho')` is equal to MATLAB `dct(x)`.

There are, theoretically, 8 types of the DCT, only the first 4 types are implemented in scipy. 'The' DCT generally refers to DCT type 2, and 'the' Inverse DCT generally refers to DCT type 3.

Type I

There are several definitions of the DCT-I; we use the following (for `norm=None`)

$$y_k = x_0 + (-1)^k x_{N-1} + 2\sum_{n=1}^{N-2} x_n \cos\left(\frac{\pi k n}{N-1}\right)$$

If `norm='ortho'`, `x[0]` and `x[N-1]` are multiplied by a scaling factor of $\sqrt{2}$, and `y[k]` is multiplied by a scaling factor `f`

$$f = \begin{cases} \frac{1}{2}\sqrt{\frac{1}{N-1}} & \text{if } k = 0 \text{ or } N-1, \\ \frac{1}{2}\sqrt{\frac{2}{N-1}} & \text{otherwise} \end{cases}$$

New in version 1.2.0: Orthonormalization in DCT-I.

Note: The DCT-I is only supported for input size > 1.

Type II

There are several definitions of the DCT-II; we use the following (for `norm=None`)

$$y_k = 2 \sum_{n=0}^{N-1} x_n \cos\left(\frac{\pi k(2n+1)}{2N}\right)$$

If `norm='ortho'`, `y[k]` is multiplied by a scaling factor `f`

$$f = \begin{cases} \sqrt{\frac{1}{4N}} & \text{if } k = 0, \\ \sqrt{\frac{1}{2N}} & \text{otherwise} \end{cases}$$

which makes the corresponding matrix of coefficients orthonormal (`O @ O.T = np.eye(N)`).

Type III

There are several definitions, we use the following (for `norm=None`)

$$y_k = x_0 + 2 \sum_{n=1}^{N-1} x_n \cos\left(\frac{\pi(2k+1)n}{2N}\right)$$

or, for `norm='ortho'`

$$y_k = \frac{x_0}{\sqrt{N}} + \sqrt{\frac{2}{N}} \sum_{n=1}^{N-1} x_n \cos\left(\frac{\pi(2k+1)n}{2N}\right)$$

The (unnormalized) DCT-III is the inverse of the (unnormalized) DCT-II, up to a factor *2N*. The orthonormalized DCT-III is exactly the inverse of the orthonormalized DCT-II.

Type IV

There are several definitions of the DCT-IV; we use the following (for `norm=None`)

$$y_k = 2 \sum_{n=0}^{N-1} x_n \cos\left(\frac{\pi(2k+1)(2n+1)}{4N}\right)$$

If `norm='ortho'`, `y[k]` is multiplied by a scaling factor `f`

$$f = \frac{1}{\sqrt{2N}}$$

New in version 1.2.0: Support for DCT-IV.

References

[1], [2]

Examples

The Type 1 DCT is equivalent to the FFT (though faster) for real, even-symmetrical inputs. The output is also real and even-symmetrical. Half of the FFT input is used to generate half of the FFT output:

```
>>> from scipy.fftpack import fft, dct
>>> fft(np.array([4., 3., 5., 10., 5., 3.])).real
array([ 30.,  -8.,   6.,  -2.,   6.,  -8.])
>>> dct(np.array([4., 3., 5., 10.]), 1)
array([ 30.,  -8.,   6.,  -2.])
```

scipy.fftpack.idct

scipy.fftpack.**idct**(*x*, *type=2*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*)

Return the Inverse Discrete Cosine Transform of an arbitrary type sequence.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.

n [int, optional] Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the idct is computed; the default is over the last axis (i.e., `axis=-1`).

norm [{None, 'ortho'}, optional] Normalization mode (see Notes). Default is None.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

idct [ndarray of real] The transformed input array.

See also:

`dct`

Forward DCT

Notes

For a single dimension array *x*, `idct(x, norm='ortho')` is equal to MATLAB `idct(x)`.

'The' IDCT is the IDCT of type 2, which is the same as DCT of type 3.

IDCT of type 1 is the DCT of type 1, IDCT of type 2 is the DCT of type 3, and IDCT of type 3 is the DCT of type 2. IDCT of type 4 is the DCT of type 4. For the definition of these types, see *dct*.

Examples

The Type 1 DCT is equivalent to the DFT for real, even-symmetrical inputs. The output is also real and even-symmetrical. Half of the IFFT input is used to generate half of the IFFT output:

```
>>> from scipy.fftpack import ifft, idct
>>> ifft(np.array([ 30.,  -8.,   6.,  -2.,   6.,  -8.])).real
array([  4.,   3.,   5.,  10.,   5.,   3.])
>>> idct(np.array([ 30.,  -8.,   6.,  -2.]), 1) / 6
array([  4.,   3.,   5.,  10.])
```

scipy.fftpack.dctn

scipy.fftpack.**dctn**(*x*, *type=2*, *shape=None*, *axes=None*, *norm=None*, *overwrite_x=False*)

Return multidimensional Discrete Cosine Transform along the specified axes.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.

shape [int or array_like of ints or None, optional] The shape of the result. If both *shape* and *axes* (see below) are None, *shape* is `x.shape`; if *shape* is None but *axes* is not None, then *shape* is `numpy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the ith dimension is padded with zeros. If `shape[i] < x.shape[i]`, the ith dimension is truncated to length `shape[i]`. If any element of *shape* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] Axes along which the DCT is computed. The default is over all axes.

norm [{None, 'ortho'}, optional] Normalization mode (see Notes). Default is None.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

y [ndarray of real] The transformed input array.

See also:

`idctn`

Inverse multidimensional DCT

Notes

For full details of the DCT types and normalization modes, as well as references, see *dct*.

Examples

```
>>> from scipy.fftpack import dctn, idctn
>>> rng = np.random.default_rng()
>>> y = rng.standard_normal((16, 16))
>>> np.allclose(y, idctn(dctn(y, norm='ortho'), norm='ortho'))
True
```

scipy.fftpack.idctn

scipy.fftpack.**idctn**(*x*, *type=2*, *shape=None*, *axes=None*, *norm=None*, *overwrite_x=False*)

Return multidimensional Discrete Cosine Transform along the specified axes.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DCT (see Notes). Default type is 2.

shape [int or array_like of ints or None, optional] The shape of the result. If both *shape* and *axes* (see below) are None, *shape* is `x.shape`; if *shape* is None but *axes* is not None, then *shape* is `numpy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the ith dimension is padded with zeros. If `shape[i] < x.shape[i]`, the ith dimension is truncated to length `shape[i]`. If any element of *shape* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] Axes along which the IDCT is computed. The default is over all axes.

norm [{None, 'ortho'}, optional] Normalization mode (see Notes). Default is None.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

y [ndarray of real] The transformed input array.

See also:

`dctn`

multidimensional DCT

Notes

For full details of the IDCT types and normalization modes, as well as references, see *idct*.

Examples

```
>>> from scipy.fftpack import dctn, idctn
>>> rng = np.random.default_rng()
>>> y = rng.standard_normal((16, 16))
>>> np.allclose(y, idctn(dctn(y, norm='ortho'), norm='ortho'))
True
```

scipy.fftpack.dst

scipy.fftpack.**dst**(*x*, *type=2*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*)

Return the Discrete Sine Transform of arbitrary type sequence x.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.

n [int, optional] Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the dst is computed; the default is over the last axis (i.e., `axis=-1`).

norm [{None, 'ortho'}, optional] Normalization mode (see Notes). Default is None.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

dst [ndarray of reals] The transformed input array.

See also:

`idst`

Inverse DST

Notes

For a single dimension array `x`.

There are, theoretically, 8 types of the DST for different combinations of even/odd boundary conditions and boundary off sets [1], only the first 4 types are implemented in scipy.

Type I

There are several definitions of the DST-I; we use the following for `norm=None`. DST-I assumes the input is odd around *n=-1* and *n=N*.

$$y_k = 2 \sum_{n=0}^{N-1} x_n \sin\left(\frac{\pi(k+1)(n+1)}{N+1}\right)$$

Note that the DST-I is only supported for input size > 1. The (unnormalized) DST-I is its own inverse, up to a factor *2(N+1)*. The orthonormalized DST-I is exactly its own inverse.

Type II

There are several definitions of the DST-II; we use the following for `norm=None`. DST-II assumes the input is odd around *n=-1/2* and *n=N-1/2*; the output is odd around $k = -1$ and even around *k=N-1*

$$y_k = 2 \sum_{n=0}^{N-1} x_n \sin\left(\frac{\pi(k+1)(2n+1)}{2N}\right)$$

if `norm='ortho'`, `y[k]` is multiplied by a scaling factor `f`

$$f = \begin{cases} \sqrt{\frac{1}{4N}} & \text{if } k = 0, \\ \sqrt{\frac{1}{2N}} & \text{otherwise} \end{cases}$$

Type III

There are several definitions of the DST-III, we use the following (for `norm=None`). DST-III assumes the input is odd around *n=-1* and even around *n=N-1*

$$y_k = (-1)^k x_{N-1} + 2 \sum_{n=0}^{N-2} x_n \sin\left(\frac{\pi(2k+1)(n+1)}{2N}\right)$$

The (unnormalized) DST-III is the inverse of the (unnormalized) DST-II, up to a factor *2N*. The orthonormalized DST-III is exactly the inverse of the orthonormalized DST-II.

New in version 0.11.0.

Type IV

There are several definitions of the DST-IV, we use the following (for `norm=None`). DST-IV assumes the input is odd around *n=-0.5* and even around *n=N-0.5*

$$y_k = 2 \sum_{n=0}^{N-1} x_n \sin\left(\frac{\pi(2k+1)(2n+1)}{4N}\right)$$

The (unnormalized) DST-IV is its own inverse, up to a factor *2N*. The orthonormalized DST-IV is exactly its own inverse.

New in version 1.2.0: Support for DST-IV.

References

[1]

scipy.fftpack.idst

`scipy.fftpack.`**`idst`**(*x*, *type=2*, *n=None*, *axis=- 1*, *norm=None*, *overwrite_x=False*)

Return the Inverse Discrete Sine Transform of an arbitrary type sequence.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.

n [int, optional] Length of the transform. If `n < x.shape[axis]`, *x* is truncated. If `n > x.shape[axis]`, *x* is zero-padded. The default results in `n = x.shape[axis]`.

axis [int, optional] Axis along which the idst is computed; the default is over the last axis (i.e., `axis=-1`).

norm [{None, 'ortho'}, optional] Normalization mode (see Notes). Default is None.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

idst [ndarray of real] The transformed input array.

See also:

`dst`

Forward DST

Notes

'The' IDST is the IDST of type 2, which is the same as DST of type 3.

IDST of type 1 is the DST of type 1, IDST of type 2 is the DST of type 3, and IDST of type 3 is the DST of type 2. For the definition of these types, see *dst*.

New in version 0.11.0.

scipy.fftpack.dstn

`scipy.fftpack.`**`dstn`**(*x*, *type=2*, *shape=None*, *axes=None*, *norm=None*, *overwrite_x=False*)

Return multidimensional Discrete Sine Transform along the specified axes.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.

shape [int or array_like of ints or None, optional] The shape of the result. If both *shape* and *axes* (see below) are None, *shape* is `x.shape`; if *shape* is None but *axes* is not None, then *shape* is `numpy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the ith dimension is padded with zeros. If `shape[i] < x.shape[i]`, the ith dimension is truncated to length `shape[i]`. If any element of *shape* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] Axes along which the DCT is computed. The default is over all axes.

norm [{None, 'ortho'}, optional] Normalization mode (see Notes). Default is None.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

y [ndarray of real] The transformed input array.

See also:

idstn

Inverse multidimensional DST

Notes

For full details of the DST types and normalization modes, as well as references, see *dst*.

Examples

```
>>> from scipy.fftpack import dstn, idstn
>>> rng = np.random.default_rng()
>>> y = rng.standard_normal((16, 16))
>>> np.allclose(y, idstn(dstn(y, norm='ortho'), norm='ortho'))
True
```

scipy.fftpack.idstn

scipy.fftpack.**idstn**(*x*, *type=2*, *shape=None*, *axes=None*, *norm=None*, *overwrite_x=False*)

Return multidimensional Discrete Sine Transform along the specified axes.

Parameters

x [array_like] The input array.

type [{1, 2, 3, 4}, optional] Type of the DST (see Notes). Default type is 2.

shape [int or array_like of ints or None, optional] The shape of the result. If both *shape* and *axes* (see below) are None, *shape* is `x.shape`; if *shape* is None but *axes* is not None, then *shape* is `numpy.take(x.shape, axes, axis=0)`. If `shape[i] > x.shape[i]`, the ith dimension is padded with zeros. If `shape[i] < x.shape[i]`, the ith dimension is truncated to length `shape[i]`. If any element of *shape* is -1, the size of the corresponding dimension of *x* is used.

axes [int or array_like of ints or None, optional] Axes along which the IDST is computed. The default is over all axes.

norm [{None, 'ortho'}, optional] Normalization mode (see Notes). Default is None.

overwrite_x [bool, optional] If True, the contents of *x* can be destroyed; the default is False.

Returns

y [ndarray of real] The transformed input array.

See also:

dstn

multidimensional DST

Notes

For full details of the IDST types and normalization modes, as well as references, see *idst*.

Examples

```
>>> from scipy.fftpack import dstn, idstn
>>> rng = np.random.default_rng()
>>> y = rng.standard_normal((16, 16))
>>> np.allclose(y, idstn(dstn(y, norm='ortho'), norm='ortho'))
True
```

Differential and pseudo-differential operators

diff(x[, order, period, _cache])	Return kth derivative (or integral) of a periodic sequence x.
tilbert(x, h[, period, _cache])	Return h-Tilbert transform of a periodic sequence x.
itilbert(x, h[, period, _cache])	Return inverse h-Tilbert transform of a periodic sequence x.
hilbert(x[, _cache])	Return Hilbert transform of a periodic sequence x.

continues on next page

Table 22 – continued from previous page

ihilbert(x)	Return inverse Hilbert transform of a periodic sequence x.
cs_diff(x, a, b[, period, _cache])	Return (a,b)-cosh/sinh pseudo-derivative of a periodic sequence.
sc_diff(x, a, b[, period, _cache])	Return (a,b)-sinh/cosh pseudo-derivative of a periodic sequence x.
ss_diff(x, a, b[, period, _cache])	Return (a,b)-sinh/sinh pseudo-derivative of a periodic sequence x.
cc_diff(x, a, b[, period, _cache])	Return (a,b)-cosh/cosh pseudo-derivative of a periodic sequence.
shift(x, a[, period, _cache])	Shift periodic sequence x by a: y(u) = x(u+a).

scipy.fftpack.diff

scipy.fftpack.**diff**(*x*, *order=1*, *period=None*, *_cache={}*)

Return kth derivative (or integral) of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = pow(sqrt(-1)*j*2*pi/period, order) * x_j
y_0 = 0 if order is not 0.
```

Parameters

x	[array_like] Input array.
order	[int, optional] The order of differentiation. Default order is 1. If order is negative, then integration is carried out under the assumption that `x_0 == 0`.
period	[float, optional] The assumed period of the sequence. Default is `2*pi`.

Notes

If `sum(x, axis=0) = 0` then `diff(diff(x, k), -k) == x` (within numerical accuracy).

For odd order and even `len(x)`, the Nyquist mode is taken zero.

scipy.fftpack.tilbert

scipy.fftpack.**tilbert**(*x*, *h*, *period=None*, *_cache={}*)

Return h-Tilbert transform of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = sqrt(-1)*coth(j*h*2*pi/period) * x_j
y_0 = 0
```

Parameters

x	[array_like] The input array to transform.
h	[float] Defines the parameter of the Tilbert transform.
period	[float, optional] The assumed period of the sequence. Default period is `2*pi`.

Returns

tilbert	[ndarray] The result of the transform.

Notes

If `sum(x, axis=0) == 0` and `n = len(x)` is odd, then `tilbert(itilbert(x)) == x`.

If `2 * pi * h / period` is approximately 10 or larger, then numerically `tilbert == hilbert` (theoretically oo-Tilbert == Hilbert).

For even `len(x)`, the Nyquist mode of `x` is taken zero.

scipy.fftpack.itilbert

`scipy.fftpack.`**`itilbert`**(*x*, *h*, *period=None*, *_cache={}*)

Return inverse h-Tilbert transform of a periodic sequence x.

If `x_j` and `y_j` are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = -sqrt(-1)*tanh(j*h*2*pi/period) * x_j
y_0 = 0
```

For more details, see *tilbert*.

scipy.fftpack.hilbert

`scipy.fftpack.`**`hilbert`**(*x*, *_cache={}*)

Return Hilbert transform of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = sqrt(-1)*sign(j) * x_j
y_0 = 0
```

Parameters

x	[array_like] The input array, should be periodic.
_cache	[dict, optional] Dictionary that contains the kernel used to do a convolution with.

Returns

y	[ndarray] The transformed input.

See also:

`scipy.signal.hilbert`

Compute the analytic signal, using the Hilbert transform.

Notes

If `sum(x, axis=0) == 0` then `hilbert(ihilbert(x)) == x`.

For even len(x), the Nyquist mode of x is taken zero.

The sign of the returned transform does not have a factor -1 that is more often than not found in the definition of the Hilbert transform. Note also that *scipy.signal.hilbert* does have an extra -1 factor compared to this function.

scipy.fftpack.ihilbert

scipy.fftpack.**ihilbert**(*x*)

Return inverse Hilbert transform of a periodic sequence x.

If `x_j` and `y_j` are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = -sqrt(-1)*sign(j) * x_j
y_0 = 0
```

scipy.fftpack.cs_diff

scipy.fftpack.**cs_diff**(*x*, *a*, *b*, *period=None*, *_cache={}*)

Return (a,b)-cosh/sinh pseudo-derivative of a periodic sequence.

If `x_j` and `y_j` are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = -sqrt(-1)*cosh(j*a*2*pi/period)/sinh(j*b*2*pi/period) * x_j
y_0 = 0
```

Parameters

x	[array_like] The array to take the pseudo-derivative from.
a, b	[float] Defines the parameters of the cosh/sinh pseudo-differential operator.
period	[float, optional] The period of the sequence. Default period is `2*pi`.

Returns

cs_diff	[ndarray] Pseudo-derivative of periodic sequence *x*.

Notes

For even len(*x*), the Nyquist mode of *x* is taken as zero.

scipy.fftpack.sc_diff

scipy.fftpack.**sc_diff**(*x*, *a*, *b*, *period=None*, *_cache={}*)

Return (a,b)-sinh/cosh pseudo-derivative of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = sqrt(-1)*sinh(j*a*2*pi/period)/cosh(j*b*2*pi/period) * x_j
y_0 = 0
```

Parameters

x	[array_like] Input array.
a,b	[float] Defines the parameters of the sinh/cosh pseudo-differential operator.
period	[float, optional] The period of the sequence x. Default is 2*pi.

Notes

`sc_diff(cs_diff(x,a,b),b,a) == x` For even `len(x)`, the Nyquist mode of x is taken as zero.

scipy.fftpack.ss_diff

scipy.fftpack.**ss_diff**(*x*, *a*, *b*, *period=None*, *_cache={}*)

Return (a,b)-sinh/sinh pseudo-derivative of a periodic sequence x.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = sinh(j*a*2*pi/period)/sinh(j*b*2*pi/period) * x_j
y_0 = a/b * x_0
```

Parameters

x	[array_like] The array to take the pseudo-derivative from.
a,b	Defines the parameters of the sinh/sinh pseudo-differential operator.
period	[float, optional] The period of the sequence x. Default is `2*pi`.

Notes

`ss_diff(ss_diff(x,a,b),b,a) == x`

scipy.fftpack.cc_diff

scipy.fftpack.**cc_diff**(*x*, *a*, *b*, *period=None*, *_cache={}*)

Return (a,b)-cosh/cosh pseudo-derivative of a periodic sequence.

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = cosh(j*a*2*pi/period)/cosh(j*b*2*pi/period) * x_j
```

Parameters

x	[array_like] The array to take the pseudo-derivative from.
a,b	[float] Defines the parameters of the sinh/sinh pseudo-differential operator.
period	[float, optional] The period of the sequence x. Default is `2*pi`.

Returns

cc_diff	[ndarray] Pseudo-derivative of periodic sequence *x*.

Notes

`cc_diff(cc_diff(x,a,b),b,a) == x`

scipy.fftpack.shift

scipy.fftpack.**shift**(*x*, *a*, *period=None*, *_cache={}*)

Shift periodic sequence x by a: y(u) = x(u+a).

If x_j and y_j are Fourier coefficients of periodic functions x and y, respectively, then:

```
y_j = exp(j*a*2*pi/period*sqrt(-1)) * x_f
```

Parameters

x	[array_like] The array to take the pseudo-derivative from.
a	[float] Defines the parameters of the sinh/sinh pseudo-differential
period	[float, optional] The period of the sequences x and y. Default period is `2*pi`.

Helper functions

fftshift(x[, axes])	Shift the zero-frequency component to the center of the spectrum.
ifftshift(x[, axes])	The inverse of *fftshift*.
fftfreq(n[, d])	Return the Discrete Fourier Transform sample frequencies.
rfftfreq(n[, d])	DFT sample frequencies (for usage with rfft, irfft).
next_fast_len(target)	Find the next fast size of input data to *fft*, for zero-padding, etc.

scipy.fftpack.fftshift

scipy.fftpack.**fftshift**(*x*, *axes=None*)

Shift the zero-frequency component to the center of the spectrum.

This function swaps half-spaces for all axes listed (defaults to all). Note that `y[0]` is the Nyquist component only if `len(x)` is even.

Parameters

x	[array_like] Input array.
axes	[int or shape tuple, optional] Axes over which to shift. Default is None, which shifts all axes.

Returns

y	[ndarray] The shifted array.

See also:

ifftshift

The inverse of *fftshift*.

Examples

```
>>> freqs = np.fft.fftfreq(10, 0.1)
>>> freqs
array([ 0.,  1.,  2., ..., -3., -2., -1.])
>>> np.fft.fftshift(freqs)
array([-5., -4., -3., -2., -1.,  0.,  1.,  2.,  3.,  4.])
```

Shift the zero-frequency component only along the second axis:

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.fftshift(freqs, axes=(1,))
array([[ 2.,  0.,  1.],
       [-4.,  3.,  4.],
       [-1., -3., -2.]])
```

scipy.fftpack.ifftshift

scipy.fftpack.**ifftshift**(*x*, *axes=None*)

The inverse of *fftshift*. Although identical for even-length *x*, the functions differ by one sample for odd-length *x*.

Parameters

x	[array_like] Input array.
axes	[int or shape tuple, optional] Axes over which to calculate. Defaults to None, which shifts all axes.

Returns

y	[ndarray] The shifted array.

See also:

fftshift

Shift zero-frequency component to the center of the spectrum.

Examples

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)
>>> freqs
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.ifftshift(np.fft.fftshift(freqs))
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
```

scipy.fftpack.fftfreq

scipy.fftpack.**fftfreq**(*n*, *d=1.0*)

Return the Discrete Fourier Transform sample frequencies.

The returned float array *f* contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length *n* and a sample spacing *d*:

```
f = [0, 1, ...,   n/2-1,     -n/2, ..., -1] / (d*n)   if n is even
f = [0, 1, ..., (n-1)/2, -(n-1)/2, ..., -1] / (d*n)   if n is odd
```

Parameters

n	[int] Window length.
d	[scalar, optional] Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns

f	[ndarray] Array of length *n* containing the sample frequencies.

Examples

```
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
>>> fourier = np.fft.fft(signal)
>>> n = signal.size
>>> timestep = 0.1
>>> freq = np.fft.fftfreq(n, d=timestep)
>>> freq
array([ 0.  ,  1.25,  2.5 , ..., -3.75, -2.5 , -1.25])
```

scipy.fftpack.rfftfreq

scipy.fftpack.**rfftfreq**(*n*, *d=1.0*)

DFT sample frequencies (for usage with rfft, irfft).

The returned float array contains the frequency bins in cycles/unit (with zero at the start) given a window length *n* and a sample spacing *d*:

```
f = [0,1,1,2,2,...,n/2-1,n/2-1,n/2]/(d*n)   if n is even
f = [0,1,1,2,2,...,n/2-1,n/2-1,n/2,n/2]/(d*n)   if n is odd
```

Parameters

n	[int] Window length.
d	[scalar, optional] Sample spacing. Default is 1.

Returns

out	[ndarray] The array of length *n*, containing the sample frequencies.

Examples

```
>>> from scipy import fftpack
>>> sig = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)
>>> sig_fft = fftpack.rfft(sig)
>>> n = sig_fft.size
>>> timestep = 0.1
>>> freq = fftpack.rfftfreq(n, d=timestep)
>>> freq
array([ 0.  ,  1.25,  1.25,  2.5 ,  2.5 ,  3.75,  3.75,  5.  ])
```

scipy.fftpack.next_fast_len

scipy.fftpack.**next_fast_len**(*target*)

Find the next fast size of input data to *fft*, for zero-padding, etc.

SciPy's FFTPACK has efficient functions for radix {2, 3, 4, 5}, so this returns the next composite of the prime factors 2, 3, and 5 which is greater than or equal to *target*. (These are also known as 5-smooth numbers, regular numbers, or Hamming numbers.)

Parameters

target [int] Length to start searching from. Must be a positive integer.

Returns

out [int] The first 5-smooth number greater than or equal to *target*.

Notes

New in version 0.18.0.

Examples

On a particular machine, an FFT of prime length takes 133 ms:

```
>>> from scipy import fftpack
>>> rng = np.random.default_rng()
>>> min_len = 10007  # prime length is worst case for speed
>>> a = rng.standard_normal(min_len)
>>> b = fftpack.fft(a)
```

Zero-padding to the next 5-smooth length reduces computation time to 211 us, a speedup of 630 times:

```
>>> fftpack.helper.next_fast_len(min_len)
10125
>>> b = fftpack.fft(a, 10125)
```

Rounding up to the next power of 2 is not optimal, taking 367 us to compute, 1.7 times as long as the 5-smooth size:

```
>>> b = fftpack.fft(a, 16384)
```

Note that `fftshift`, `ifftshift` and `fftfreq` are numpy functions exposed by `fftpack`; importing them from `numpy` should be preferred.

Convolutions (scipy.fftpack.convolve)

convolve(x,omega,[swap_real_imag,overwrite_x])	Wrapper for convolve.
convolve_z(x,omega_real,omega_imag,[overwrite_x])	Wrapper for convolve_z.
init_convolution_kernel(…)	Wrapper for init_convolution_kernel.
destroy_convolve_cache	

scipy.fftpack.convolve.convolve

scipy.fftpack.convolve.**convolve**(*x*, *omega*[, *swap_real_imag*, *overwrite_x*])

Wrapper for convolve.

Parameters

x [input rank-1 array('d') with bounds (n)]
omega [input rank-1 array('d') with bounds (n)]

Returns

y [rank-1 array('d') with bounds (n) and x storage]

Other Parameters

overwrite_x
[input int, optional] Default: 0
swap_real_imag
[input int, optional] Default: 0

scipy.fftpack.convolve.convolve_z

scipy.fftpack.convolve.**convolve_z**(*x*, *omega_real*, *omega_imag*[, *overwrite_x*])

Wrapper for convolve_z.

Parameters

x [input rank-1 array('d') with bounds (n)]
omega_real
[input rank-1 array('d') with bounds (n)]
omega_imag
[input rank-1 array('d') with bounds (n)]

Returns

y [rank-1 array('d') with bounds (n) and x storage]

Other Parameters

overwrite_x
[input int, optional] Default: 0

scipy.fftpack.convolve.init_convolution_kernel

scipy.fftpack.convolve.**init_convolution_kernel**(*n*, *kernel_func*[, *d*, *zero_nyquist*, *kernel_func_extra_args*])

Wrapper for `init_convolution_kernel`.

Parameters

n [input int]

kernel_func
[call-back function]

Returns

omega [rank-1 array('d') with bounds (n)]

Other Parameters

d [input int, optional] Default: 0

kernel_func_extra_args
[input tuple, optional] Default: ()

zero_nyquist
[input int, optional] Default: d%2

Notes

Call-back functions:

```
def kernel_func(k): return kernel_func
Required arguments:
  k : input int
Return objects:
  kernel_func : float
```

scipy.fftpack.convolve.destroy_convolve_cache

scipy.fftpack.convolve.**destroy_convolve_cache**()

3.3.7 Integration and ODEs (scipy.integrate)

Integrating functions, given function object

quad(func, a, b[, args, full_output, …])	Compute a definite integral.
quad_vec(f, a, b[, epsabs, epsrel, norm, …])	Adaptive integration of a vector-valued function.
dblquad(func, a, b, gfun, hfun[, args, …])	Compute a double integral.
tplquad(func, a, b, gfun, hfun, qfun, rfun)	Compute a triple (definite) integral.
nquad(func, ranges[, args, opts, full_output])	Integration over multiple variables.
fixed_quad(func, a, b[, args, n])	Compute a definite integral using fixed-order Gaussian quadrature.
quadrature(func, a, b[, args, tol, rtol, …])	Compute a definite integral using fixed-tolerance Gaussian quadrature.
romberg(function, a, b[, args, tol, rtol, …])	Romberg integration of a callable function or method.
quad_explain([output])	Print extra information about integrate.quad() parameters and returns.

continues on next page

Table 25 – continued from previous page

newton_cotes(rn[, equal])	Return weights and error coefficient for Newton-Cotes integration.
IntegrationWarning	Warning on issues during integration.
AccuracyWarning	

scipy.integrate.quad

scipy.integrate.**quad**(*func*, *a*, *b*, *args=()*, *full_output=0*, *epsabs=1.49e-08*, *epsrel=1.49e-08*, *limit=50*, *points=None*, *weight=None*, *wvar=None*, *wopts=None*, *maxp1=50*, *limlst=50*)

Compute a definite integral.

Integrate func from *a* to *b* (possibly infinite interval) using a technique from the Fortran library QUADPACK.

Parameters

func [{function, scipy.LowLevelCallable}] A Python function or method to integrate. If *func* takes many arguments, it is integrated along the axis corresponding to the first argument.
If the user desires improved integration performance, then *f* may be a *scipy.LowLevelCallable* with one of the signatures:

```
double func(double x)
double func(double x, void *user_data)
double func(int n, double *xx)
double func(int n, double *xx, void *user_data)
```

The `user_data` is the data contained in the *scipy.LowLevelCallable*. In the call forms with `xx`, `n` is the length of the `xx` array which contains `xx[0] == x` and the rest of the items are numbers contained in the `args` argument of quad.
In addition, certain ctypes call signatures are supported for backward compatibility, but those should not be used in new code.

a [float] Lower limit of integration (use -numpy.inf for -infinity).

b [float] Upper limit of integration (use numpy.inf for +infinity).

args [tuple, optional] Extra arguments to pass to *func*.

full_output [int, optional] Non-zero to return a dictionary of integration information. If non-zero, warning messages are also suppressed and the message is appended to the output tuple.

Returns

y [float] The integral of func from *a* to *b*.

abserr [float] An estimate of the absolute error in the result.

infodict [dict] A dictionary containing additional information. Run scipy.integrate.quad_explain() for more information.

message A convergence message.

explain Appended only with 'cos' or 'sin' weighting and infinite integration limits, it contains an explanation of the codes in infodict['ierlst']

Other Parameters

epsabs [float or int, optional] Absolute error tolerance. Default is 1.49e-8. *quad* tries to obtain an accuracy of `abs(i-result) <= max(epsabs, epsrel*abs(i))` where `i` = integral of *func* from *a* to *b*, and `result` is the numerical approximation. See *epsrel* below.

epsrel [float or int, optional] Relative error tolerance. Default is 1.49e-8. If `epsabs <= 0`, *epsrel* must be greater than both 5e-29 and `50 * (machine epsilon)`. See *epsabs* above.

limit [float or int, optional] An upper bound on the number of subintervals used in the adaptive algorithm.

points [(sequence of floats,ints), optional] A sequence of break points in the bounded integration interval where local difficulties of the integrand may occur (e.g., singularities, discontinuities). The sequence does not have to be sorted. Note that this option cannot be used in conjunction with `weight`.

weight [float or int, optional] String indicating weighting function. Full explanation for this and the remaining arguments can be found below.

wvar [optional] Variables for use with weighting functions.

wopts [optional] Optional input for reusing Chebyshev moments.

maxp1 [float or int, optional] An upper bound on the number of Chebyshev moments.

limlst [int, optional] Upper bound on the number of cycles (>=3) for use with a sinusoidal weighting and an infinite end-point.

See also:

dblquad

double integral

tplquad

triple integral

nquad

n-dimensional integrals (uses *quad* recursively)

fixed_quad

fixed-order Gaussian quadrature

quadrature

adaptive Gaussian quadrature

odeint

ODE integrator

ode

ODE integrator

simpson

integrator for sampled data

romb

integrator for sampled data

scipy.special

for coefficients and roots of orthogonal polynomials

Notes

Extra information for quad() inputs and outputs

If full_output is non-zero, then the third output argument (infodict) is a dictionary with entries as tabulated below. For infinite limits, the range is transformed to (0,1) and the optional outputs are given with respect to this transformed range. Let M be the input argument limit and let K be infodict['last']. The entries are:

'neval'

The number of function evaluations.

'last'

The number, K, of subintervals produced in the subdivision process.

'alist'

A rank-1 array of length M, the first K elements of which are the left end points of the subintervals in the partition of the integration range.

'blist'

A rank-1 array of length M, the first K elements of which are the right end points of the subintervals.

'rlist'

A rank-1 array of length M, the first K elements of which are the integral approximations on the subintervals.

'elist'

A rank-1 array of length M, the first K elements of which are the moduli of the absolute error estimates on the subintervals.

'iord'

A rank-1 integer array of length M, the first L elements of which are pointers to the error estimates over the subintervals with `L=K` if `K<=M/2+2` or `L=M+1-K` otherwise. Let I be the sequence `infodict['iord']` and let E be the sequence `infodict['elist']`. Then `E[I[1]], ..., E[I[L]]` forms a decreasing sequence.

If the input argument points is provided (i.e., it is not None), the following additional outputs are placed in the output dictionary. Assume the points sequence is of length P.

'pts'

A rank-1 array of length P+2 containing the integration limits and the break points of the intervals in ascending order. This is an array giving the subintervals over which integration will occur.

'level'

A rank-1 integer array of length M (=limit), containing the subdivision levels of the subintervals, i.e., if (aa,bb) is a subinterval of `(pts[1], pts[2])` where `pts[0]` and `pts[2]` are adjacent elements of `infodict['pts']`, then (aa,bb) has level l if `|bb-aa| = |pts[2]-pts[1]| * 2**(-l)`.

'ndin'

A rank-1 integer array of length P+2. After the first integration over the intervals (pts[1], pts[2]), the error estimates over some of the intervals may have been increased artificially in order to put their subdivision forward. This array has ones in slots corresponding to the subintervals for which this happens.

Weighting the integrand

The input variables, *weight* and *wvar*, are used to weight the integrand by a select list of functions. Different integration methods are used to compute the integral with these weighting functions, and these do not support specifying break points. The possible values of weight and the corresponding weighting functions are.

weight	Weight function used	wvar
'cos'	cos(w*x)	wvar = w
'sin'	sin(w*x)	wvar = w
'alg'	g(x) = ((x-a)**alpha)*((b-x)**beta)	wvar = (alpha, beta)
'alg-loga'	g(x)*log(x-a)	wvar = (alpha, beta)
'alg-logb'	g(x)*log(b-x)	wvar = (alpha, beta)
'alg-log'	g(x)*log(x-a)*log(b-x)	wvar = (alpha, beta)
'cauchy'	1/(x-c)	wvar = c

wvar holds the parameter w, (alpha, beta), or c depending on the weight selected. In these expressions, a and b are the integration limits.

For the 'cos' and 'sin' weighting, additional inputs and outputs are available.

For finite integration limits, the integration is performed using a Clenshaw-Curtis method which uses Chebyshev moments. For repeated calculations, these moments are saved in the output dictionary:

'momcom'

The maximum level of Chebyshev moments that have been computed, i.e., if `M_c` is `infodict['momcom']` then the moments have been computed for intervals of length `|b-a| * 2**(-l)`, `l=0,1,...,M_c`.

'nnlog'

A rank-1 integer array of length M(=limit), containing the subdivision levels of the subintervals, i.e., an element of this array is equal to l if the corresponding subinterval is `|b-a|* 2**(-l)`.

'chebmo'

A rank-2 array of shape (25, maxp1) containing the computed Chebyshev moments. These can be passed on to an integration over the same interval by passing this array as the second element of the sequence wopts and passing infodict['momcom'] as the first element.

If one of the integration limits is infinite, then a Fourier integral is computed (assuming w neq 0). If full_output is 1 and a numerical error is encountered, besides the error message attached to the output tuple, a dictionary is also appended to the output tuple which translates the error codes in the array `info['ierlst']` to English messages. The output information dictionary contains the following entries instead of 'last', 'alist', 'blist', 'rlist', and 'elist':

'lst'

The number of subintervals needed for the integration (call it `K_f`).

'rslst'

A rank-1 array of length M_f=limlst, whose first `K_f` elements contain the integral contribution over the interval `(a+(k-1)c, a+kc)` where `c = (2*floor(|w|) + 1) * pi / |w|` and `k=1,2,...,K_f`.

'erlst'

A rank-1 array of length `M_f` containing the error estimate corresponding to the interval in the same position in `infodict['rslist']`.

'ierlst'

A rank-1 integer array of length `M_f` containing an error flag corresponding to the interval in the same position in `infodict['rslist']`. See the explanation dictionary (last entry in the output tuple) for the meaning of the codes.

Examples

Calculate $\int_0^4 x^2 dx$ and compare with an analytic result

```
>>> from scipy import integrate
>>> x2 = lambda x: x**2
>>> integrate.quad(x2, 0, 4)
(21.333333333333332, 2.3684757858670003e-13)
>>> print(4**3 / 3.)  # analytical result
21.3333333333
```

Calculate $\int_0^\infty e^{-x} dx$

```
>>> invexp = lambda x: np.exp(-x)
>>> integrate.quad(invexp, 0, np.inf)
(1.0, 5.842605999138044e-11)
```

```
>>> f = lambda x,a : a*x
>>> y, err = integrate.quad(f, 0, 1, args=(1,))
>>> y
0.5
>>> y, err = integrate.quad(f, 0, 1, args=(3,))
>>> y
1.5
```

Calculate $\int_0^1 x^2 + y^2 dx$ with ctypes, holding y parameter as 1:

```
testlib.c =>
    double func(int n, double args[n]){
        return args[0]*args[0] + args[1]*args[1];}
compile to library testlib.*
```

```
from scipy import integrate
import ctypes
lib = ctypes.CDLL('/home/.../testlib.*') #use absolute path
lib.func.restype = ctypes.c_double
lib.func.argtypes = (ctypes.c_int,ctypes.c_double)
integrate.quad(lib.func,0,1,(1))
#(1.3333333333333333, 1.4802973661668752e-14)
print((1.0**3/3.0 + 1.0) - (0.0**3/3.0 + 0.0)) #Analytic result
# 1.3333333333333333
```

Be aware that pulse shapes and other sharp features as compared to the size of the integration interval may not be integrated correctly using this method. A simplified example of this limitation is integrating a y-axis reflected step function with many zero values within the integrals bounds.

```
>>> y = lambda x: 1 if x<=0 else 0
>>> integrate.quad(y, -1, 1)
(1.0, 1.1102230246251565e-14)
>>> integrate.quad(y, -1, 100)
(1.0000000002199108, 1.0189464580163188e-08)
>>> integrate.quad(y, -1, 10000)
(0.0, 0.0)
```

scipy.integrate.quad_vec

scipy.integrate.**quad_vec**(*f*, *a*, *b*, *epsabs=1e-200*, *epsrel=1e-08*, *norm='2'*, *cache_size=100000000.0*, *limit=10000*, *workers=1*, *points=None*, *quadrature=None*, *full_output=False*)

Adaptive integration of a vector-valued function.

Parameters

f [callable] Vector-valued function f(x) to integrate.

a [float] Initial point.

b [float] Final point.

epsabs [float, optional] Absolute tolerance.

epsrel [float, optional] Relative tolerance.

norm [{'max', '2'}, optional] Vector norm to use for error estimation.

cache_size [int, optional] Number of bytes to use for memoization.

workers [int or map-like callable, optional] If *workers* is an integer, part of the computation is done in parallel subdivided to this many tasks (using `multiprocessing.pool.Pool`). Supply *-1* to use all cores available to the Process. Alternatively, supply a map-like callable, such as `multiprocessing.pool.Pool.map` for evaluating the population in parallel. This evaluation is carried out as `workers(func, iterable)`.

points [list, optional] List of additional breakpoints.

quadrature [{'gk21', 'gk15', 'trapezoid'}, optional] Quadrature rule to use on subintervals. Options: 'gk21' (Gauss-Kronrod 21-point rule), 'gk15' (Gauss-Kronrod 15-point rule), 'trapezoid' (composite trapezoid rule). Default: 'gk21' for finite intervals and 'gk15' for (semi-)infinite

full_output [bool, optional] Return an additional `info` dictionary.

Returns

res [{float, array-like}] Estimate for the result

err [float] Error estimate for the result in the given norm

info [dict] Returned only when `full_output=True`. Info dictionary. Is an object with the attributes:

- **success** [bool] Whether integration reached target precision.
- **status** [int] Indicator for convergence, success (0), failure (1), and failure due to rounding error (2).
- **neval** [int] Number of function evaluations.
- **intervals** [ndarray, shape (num_intervals, 2)] Start and end points of subdivision intervals.
- **integrals** [ndarray, shape (num_intervals, …)] Integral for each interval. Note that at most `cache_size` values are recorded, and the array may contains *nan* for missing items.
- **errors** [ndarray, shape (num_intervals,)] Estimated integration error for each interval.

Notes

The algorithm mainly follows the implementation of QUADPACK's DQAG* algorithms, implementing global error control and adaptive subdivision.

The algorithm here has some differences to the QUADPACK approach:

Instead of subdividing one interval at a time, the algorithm subdivides N intervals with largest errors at once. This enables (partial) parallelization of the integration.

The logic of subdividing "next largest" intervals first is then not implemented, and we rely on the above extension to avoid concentrating on "small" intervals only.

The Wynn epsilon table extrapolation is not used (QUADPACK uses it for infinite intervals). This is because the algorithm here is supposed to work on vector-valued functions, in an user-specified norm, and the extension of the epsilon algorithm to this case does not appear to be widely agreed. For max-norm, using elementwise Wynn epsilon could be possible, but we do not do this here with the hope that the epsilon extrapolation is mainly useful in special cases.

References

[1] R. Piessens, E. de Doncker, QUADPACK (1983).

Examples

We can compute integrations of a vector-valued function:

```
>>> from scipy.integrate import quad_vec
>>> import matplotlib.pyplot as plt
>>> alpha = np.linspace(0.0, 2.0, num=30)
>>> f = lambda x: x**alpha
>>> x0, x1 = 0, 2
>>> y, err = quad_vec(f, x0, x1)
>>> plt.plot(alpha, y)
>>> plt.xlabel(r"$\alpha$")
>>> plt.ylabel(r"$\int_{0}^{2} x^\alpha dx$")
>>> plt.show()
```

scipy.integrate.dblquad

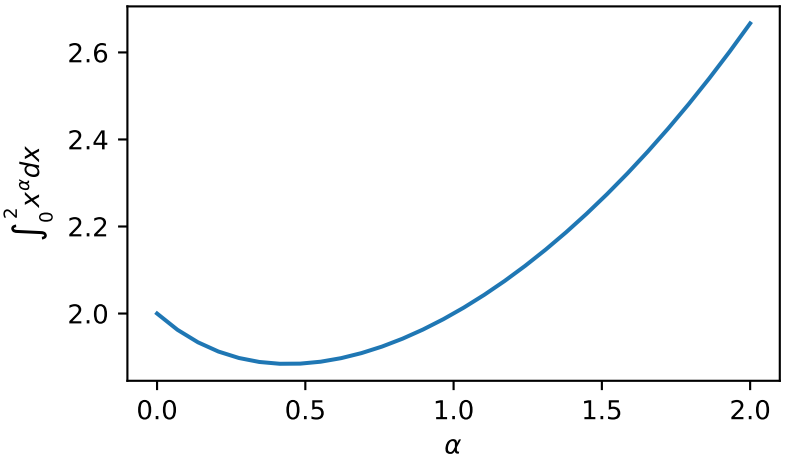
scipy.integrate.**dblquad**(*func*, *a*, *b*, *gfun*, *hfun*, *args=()*, *epsabs=1.49e-08*, *epsrel=1.49e-08*)

Compute a double integral.

Return the double (definite) integral of `func(y, x)` from `x = a..b` and `y = gfun(x)..hfun(x)`.

Parameters

func	[callable] A Python function or method of at least two variables: y must be the first argument and x the second argument.
a, b	[float] The limits of integration in x: $a < b$
gfun	[callable or float] The lower boundary curve in y which is a function taking a single floating point argument (x) and returning a floating point result or a float indicating a constant boundary curve.
hfun	[callable or float] The upper boundary curve in y (same requirements as *gfun*).
args	[sequence, optional] Extra arguments to pass to *func*.



epsabs [float, optional] Absolute tolerance passed directly to the inner 1-D quadrature integration. Default is 1.49e-8. *dblquad*` tries to obtain an accuracy of `abs(i-result) <= max(epsabs, epsrel*abs(i))` where `i` = inner integral of `func(y, x)` from `gfun(x)` to `hfun(x)`, and `result` is the numerical approximation. See *epsrel* below.

epsrel [float, optional] Relative tolerance of the inner 1-D integrals. Default is 1.49e-8. If `epsabs <= 0`, *epsrel* must be greater than both 5e-29 and `50 * (machine epsilon)`. See *epsabs* above.

Returns

y [float] The resultant integral.

abserr [float] An estimate of the error.

See also:

`quad`

single integral

`tplquad`

triple integral

`nquad`

N-dimensional integrals

`fixed_quad`

fixed-order Gaussian quadrature

`quadrature`

adaptive Gaussian quadrature

`odeint`

ODE integrator

`ode`

ODE integrator

simpson

integrator for sampled data

romb

integrator for sampled data

scipy.special

for coefficients and roots of orthogonal polynomials

Examples

Compute the double integral of `x * y**2` over the box `x` ranging from 0 to 2 and `y` ranging from 0 to 1.

```
>>> from scipy import integrate
>>> f = lambda y, x: x*y**2
>>> integrate.dblquad(f, 0, 2, lambda x: 0, lambda x: 1)
    (0.6666666666666667, 7.401486830834377e-15)
```

scipy.integrate.tplquad

scipy.integrate.**tplquad**(*func*, *a*, *b*, *gfun*, *hfun*, *qfun*, *rfun*, *args=()*, *epsabs=1.49e-08*, *epsrel=1.49e-08*)

Compute a triple (definite) integral.

Return the triple integral of `func(z, y, x)` from `x = a..b`, `y = gfun(x)..hfun(x)`, and `z = qfun(x,y)..rfun(x,y)`.

Parameters

func	[function] A Python function or method of at least three variables in the order (z, y, x).
a, b	[float] The limits of integration in x: $a < b$
gfun	[function or float] The lower boundary curve in y which is a function taking a single floating point argument (x) and returning a floating point result or a float indicating a constant boundary curve.
hfun	[function or float] The upper boundary curve in y (same requirements as *gfun*).
qfun	[function or float] The lower boundary surface in z. It must be a function that takes two floats in the order (x, y) and returns a float or a float indicating a constant boundary surface.
rfun	[function or float] The upper boundary surface in z. (Same requirements as *qfun*.)
args	[tuple, optional] Extra arguments to pass to *func*.
epsabs	[float, optional] Absolute tolerance passed directly to the innermost 1-D quadrature integration. Default is 1.49e-8.
epsrel	[float, optional] Relative tolerance of the innermost 1-D integrals. Default is 1.49e-8.

Returns

y	[float] The resultant integral.
abserr	[float] An estimate of the error.

See also:

quad

Adaptive quadrature using QUADPACK

quadrature

Adaptive Gaussian quadrature

fixed_quad

Fixed-order Gaussian quadrature

dblquad

Double integrals

nquad

N-dimensional integrals

romb

Integrators for sampled data

simpson

Integrators for sampled data

ode

ODE integrators

odeint

ODE integrators

scipy.special

For coefficients and roots of orthogonal polynomials

Examples

Compute the triple integral of `x * y * z`, over `x` ranging from 1 to 2, `y` ranging from 2 to 3, `z` ranging from 0 to 1.

```
>>> from scipy import integrate
>>> f = lambda z, y, x: x*y*z
>>> integrate.tplquad(f, 1, 2, lambda x: 2, lambda x: 3,
...                   lambda x, y: 0, lambda x, y: 1)
(1.8750000000000002, 3.324644794257407e-14)
```

scipy.integrate.nquad

scipy.integrate.**nquad**(*func*, *ranges*, *args=None*, *opts=None*, *full_output=False*)

Integration over multiple variables.

Wraps *quad* to enable integration over multiple variables. Various options allow improved integration of discontinuous functions, as well as the use of weighted integration, and generally finer control of the integration process.

Parameters

func [{callable, scipy.LowLevelCallable}] The function to be integrated. Has arguments of `x0, ... xn, t0, ... tm`, where integration is carried out over `x0, ... xn`, which must be floats. Where `` `t0, ... tm` `` are extra arguments passed in args. Function signature should be `func(x0, x1, ..., xn, t0, t1, ..., tm)`. Integration is carried out in order. That is, integration over `x0` is the innermost integral, and `xn` is the outermost. If the user desires improved integration performance, then *f* may be a *scipy.LowLevelCallable* with one of the signatures:

```
double func(int n, double *xx)
double func(int n, double *xx, void *user_data)
```

where `n` is the number of variables and args. The `xx` array contains the coordinates and extra arguments. `user_data` is the data contained in the *scipy.LowLevelCallable*.

ranges [iterable object] Each element of ranges may be either a sequence of 2 numbers, or else a callable that returns such a sequence. `ranges[0]` corresponds to integration over x0, and so on. If an element of ranges is a callable, then it will be called with all of the integration arguments available, as well as any parametric arguments. e.g., if `func = f(x0, x1, x2, t0, t1)`, then `ranges[0]` may be defined as either `(a, b)` or else as `(a, b) = range0(x1, x2, t0, t1)`.

args [iterable object, optional] Additional arguments `t0, ..., tn`, required by *func*, *ranges*, and `opts`.

opts [iterable object or dict, optional] Options to be passed to *quad*. May be empty, a dict, or a sequence of dicts or functions that return a dict. If empty, the default options from scipy.integrate.quad are used. If a dict, the same options are used for all levels of integraion. If a sequence, then each element of the sequence corresponds to a particular integration. e.g., opts[0] corresponds to integration over x0, and so on. If a callable, the signature must be the same as for `ranges`. The available options together with their default values are:

- epsabs = 1.49e-08
- epsrel = 1.49e-08
- limit = 50
- points = None
- weight = None
- wvar = None
- wopts = None

For more information on these options, see *quad* and *quad_explain*.

full_output [bool, optional] Partial implementation of `full_output` from scipy.integrate.quad. The number of integrand function evaluations `neval` can be obtained by setting `full_output=True` when calling nquad.

Returns

result [float] The result of the integration.

abserr [float] The maximum of the estimates of the absolute error in the various integration results.

out_dict [dict, optional] A dict containing additional information on the integration.

See also:

quad

1-D numerical integration

dblquad, **tplquad**

double and triple integrals

fixed_quad

fixed-order Gaussian quadrature

quadrature

adaptive Gaussian quadrature

Examples

```
>>> from scipy import integrate
>>> func = lambda x0,x1,x2,x3 : x0**2 + x1*x2 - x3**3 + np.sin(x0) + (
...                                 1 if (x0-.2*x3-.5-.25*x1>0) else 0)
>>> def opts0(*args, **kwargs):
...     return {'points':[0.2*args[2] + 0.5 + 0.25*args[0]]}
>>> integrate.nquad(func, [[0,1], [-1,1], [.13,.8], [-.15,1]],
...                 opts=[opts0,{},{},{}], full_output=True)
(1.5267454070738633, 2.9437360001402324e-14, {'neval': 388962})
```

```
>>> scale = .1
>>> def func2(x0, x1, x2, x3, t0, t1):
...     return x0*x1*x3**2 + np.sin(x2) + 1 + (1 if x0+t1*x1-t0>0 else 0)
>>> def lim0(x1, x2, x3, t0, t1):
...     return [scale * (x1**2 + x2 + np.cos(x3)*t0*t1 + 1) - 1,
...             scale * (x1**2 + x2 + np.cos(x3)*t0*t1 + 1) + 1]
>>> def lim1(x2, x3, t0, t1):
...     return [scale * (t0*x2 + t1*x3) - 1,
...             scale * (t0*x2 + t1*x3) + 1]
>>> def lim2(x3, t0, t1):
...     return [scale * (x3 + t0**2*t1**3) - 1,
...             scale * (x3 + t0**2*t1**3) + 1]
>>> def lim3(t0, t1):
...     return [scale * (t0+t1) - 1, scale * (t0+t1) + 1]
>>> def opts0(x1, x2, x3, t0, t1):
...     return {'points' : [t0 - t1*x1]}
>>> def opts1(x2, x3, t0, t1):
...     return {}
>>> def opts2(x3, t0, t1):
...     return {}
>>> def opts3(t0, t1):
...     return {}
>>> integrate.nquad(func2, [lim0, lim1, lim2, lim3], args=(0,0),
...                 opts=[opts0, opts1, opts2, opts3])
(25.066666666666666, 2.7829590483937256e-13)
```

scipy.integrate.fixed_quad

scipy.integrate.**fixed_quad**(*func*, *a*, *b*, *args=()*, *n=5*)

Compute a definite integral using fixed-order Gaussian quadrature.

Integrate *func* from *a* to *b* using Gaussian quadrature of order *n*.

Parameters

func	[callable] A Python function or method to integrate (must accept vector inputs). If integrating a vector-valued function, the returned array must have shape `(..., len(x))`.
a	[float] Lower limit of integration.
b	[float] Upper limit of integration.
args	[tuple, optional] Extra arguments to pass to function, if any.
n	[int, optional] Order of quadrature integration. Default is 5.

Returns

val	[float] Gaussian quadrature approximation to the integral

none [None] Statically returned value of None

See also:

quad

adaptive quadrature using QUADPACK

dblquad

double integrals

tplquad

triple integrals

romberg

adaptive Romberg quadrature

quadrature

adaptive Gaussian quadrature

romb

integrators for sampled data

simpson

integrators for sampled data

cumulative_trapezoid

cumulative integration for sampled data

ode

ODE integrator

odeint

ODE integrator

Examples

```
>>> from scipy import integrate
>>> f = lambda x: x**8
>>> integrate.fixed_quad(f, 0.0, 1.0, n=4)
(0.1110884353741496, None)
>>> integrate.fixed_quad(f, 0.0, 1.0, n=5)
(0.1111111111111102, None)
>>> print(1/9.0)  # analytical result
0.1111111111111111
```

```
>>> integrate.fixed_quad(np.cos, 0.0, np.pi/2, n=4)
(0.9999999771971152, None)
>>> integrate.fixed_quad(np.cos, 0.0, np.pi/2, n=5)
(1.000000000039565, None)
>>> np.sin(np.pi/2)-np.sin(0)  # analytical result
1.0
```

scipy.integrate.quadrature

scipy.integrate.**quadrature**(*func*, *a*, *b*, *args=()*, *tol=1.49e-08*, *rtol=1.49e-08*, *maxiter=50*, *vec_func=True*, *miniter=1*)

Compute a definite integral using fixed-tolerance Gaussian quadrature.

Integrate *func* from *a* to *b* using Gaussian quadrature with absolute tolerance *tol*.

Parameters

func	[function] A Python function or method to integrate.
a	[float] Lower limit of integration.
b	[float] Upper limit of integration.
args	[tuple, optional] Extra arguments to pass to function.
tol, rtol	[float, optional] Iteration stops when error between last two iterates is less than *tol* OR the relative change is less than *rtol*.
maxiter	[int, optional] Maximum order of Gaussian quadrature.
vec_func	[bool, optional] True or False if func handles arrays as arguments (is a "vector" function). Default is True.
miniter	[int, optional] Minimum order of Gaussian quadrature.

Returns

val	[float] Gaussian quadrature approximation (within tolerance) to integral.
err	[float] Difference between last two estimates of the integral.

See also:

romberg

adaptive Romberg quadrature

fixed_quad

fixed-order Gaussian quadrature

quad

adaptive quadrature using QUADPACK

dblquad

double integrals

tplquad

triple integrals

romb

integrator for sampled data

simpson

integrator for sampled data

cumulative_trapezoid

cumulative integration for sampled data

ode

ODE integrator

odeint

ODE integrator

Examples

```
>>> from scipy import integrate
>>> f = lambda x: x**8
>>> integrate.quadrature(f, 0.0, 1.0)
(0.1111111111111106, 4.163336342344337e-17)
>>> print(1/9.0)  # analytical result
0.1111111111111111
```

```
>>> integrate.quadrature(np.cos, 0.0, np.pi/2)
(0.9999999999999536, 3.9611425250996035e-11)
>>> np.sin(np.pi/2)-np.sin(0)  # analytical result
1.0
```

scipy.integrate.romberg

scipy.integrate.**romberg**(*function*, *a*, *b*, *args=()*, *tol=1.48e-08*, *rtol=1.48e-08*, *show=False*, *divmax=10*, *vec_func=False*)

Romberg integration of a callable function or method.

Returns the integral of *function* (a function of one variable) over the interval (*a*, *b*).

If *show* is 1, the triangular array of the intermediate results will be printed. If *vec_func* is True (default is False), then *function* is assumed to support vector arguments.

Parameters

function	[callable] Function to be integrated.
a	[float] Lower limit of integration.
b	[float] Upper limit of integration.

Returns

results	[float] Result of the integration.

Other Parameters

args	[tuple, optional] Extra arguments to pass to function. Each element of *args* will be passed as a single argument to *func*. Default is to pass no extra arguments.
tol, rtol	[float, optional] The desired absolute and relative tolerances. Defaults are 1.48e-8.
show	[bool, optional] Whether to print the results. Default is False.
divmax	[int, optional] Maximum order of extrapolation. Default is 10.
vec_func	[bool, optional] Whether *func* handles arrays as arguments (i.e., whether it is a "vector" function). Default is False.

See also:

fixed_quad

Fixed-order Gaussian quadrature.

quad

Adaptive quadrature using QUADPACK.

dblquad

Double integrals.

tplquad

Triple integrals.

romb

Integrators for sampled data.

simpson

Integrators for sampled data.

cumulative_trapezoid

Cumulative integration for sampled data.

ode

ODE integrator.

odeint

ODE integrator.

References

[1]

Examples

Integrate a gaussian from 0 to 1 and compare to the error function.

```
>>> from scipy import integrate
>>> from scipy.special import erf
>>> gaussian = lambda x: 1/np.sqrt(np.pi) * np.exp(-x**2)
>>> result = integrate.romberg(gaussian, 0, 1, show=True)
Romberg integration of <function vfunc at ...> from [0, 1]
```

```
Steps  StepSize  Results
    1  1.000000  0.385872
    2  0.500000  0.412631  0.421551
    4  0.250000  0.419184  0.421368  0.421356
    8  0.125000  0.420810  0.421352  0.421350  0.421350
   16  0.062500  0.421215  0.421350  0.421350  0.421350  0.421350
   32  0.031250  0.421317  0.421350  0.421350  0.421350  0.421350  0.
↪421350
```

The final result is 0.421350396475 after 33 function evaluations.

```
>>> print("%g %g" % (2*result, erf(1)))
0.842701 0.842701
```

scipy.integrate.quad_explain

scipy.integrate.**quad_explain**(*output=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='utf-8'>*)

Print extra information about integrate.quad() parameters and returns.

Parameters

output [instance with "write" method, optional] Information about *quad* is passed to `output.write()`. Default is `sys.stdout`.

Returns

None

Examples

We can show detailed information of the *integrate.quad* function in stdout:

```
>>> from scipy.integrate import quad_explain
>>> quad_explain()
```

scipy.integrate.newton_cotes

scipy.integrate.**newton_cotes**(*rn*, *equal=0*)

Return weights and error coefficient for Newton-Cotes integration.

Suppose we have (N+1) samples of f at the positions x_0, x_1, …, x_N. Then an N-point Newton-Cotes formula for the integral between x_0 and x_N is:

$\int_{x_0}^{x_N} f(x)dx = \Delta x \sum_{i=0}^{N} a_i f(x_i) + B_N (\Delta x)^{N+2} f^{N+1}(\xi)$

where $\xi \in [x_0, x_N]$ and $\Delta x = \frac{x_N - x_0}{N}$ is the average samples spacing.

If the samples are equally-spaced and N is even, then the error term is $B_N (\Delta x)^{N+3} f^{N+2}(\xi)$.

Parameters

rn [int] The integer order for equally-spaced data or the relative positions of the samples with the first sample at 0 and the last at N, where N+1 is the length of *rn*. N is the order of the Newton-Cotes integration.

equal [int, optional] Set to 1 to enforce equally spaced data.

Returns

an [ndarray] 1-D array of weights to apply to the function at the provided sample positions.

B [float] Error coefficient.

Notes

Normally, the Newton-Cotes rules are used on smaller integration regions and a composite rule is used to return the total integral.

Examples

Compute the integral of sin(x) in $[0, \pi]$:

```
>>> from scipy.integrate import newton_cotes
>>> def f(x):
...     return np.sin(x)
>>> a = 0
>>> b = np.pi
>>> exact = 2
>>> for N in [2, 4, 6, 8, 10]:
...     x = np.linspace(a, b, N + 1)
...     an, B = newton_cotes(N, 1)
...     dx = (b - a) / N
...     quad = dx * np.sum(an * f(x))
...     error = abs(quad - exact)
...     print('{:2d}  {:10.9f}  {:.5e}'.format(N, quad, error))
...
 2   2.094395102   9.43951e-02
 4   1.998570732   1.42927e-03
 6   2.000017814   1.78136e-05
 8   1.999999835   1.64725e-07
10   2.000000001   1.14677e-09
```

scipy.integrate.IntegrationWarning

exception scipy.integrate.**IntegrationWarning**

Warning on issues during integration.

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.integrate.AccuracyWarning

exception scipy.integrate.**AccuracyWarning**

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

Integrating functions, given fixed samples

trapezoid(y[, x, dx, axis])	Integrate along the given axis using the composite trapezoidal rule.
cumulative_trapezoid(y[, x, dx, axis, initial])	Cumulatively integrate y(x) using the composite trapezoidal rule.
simpson(y[, x, dx, axis, even])	Integrate y(x) using samples along the given axis and the composite Simpson's rule.
romb(y[, dx, axis, show])	Romberg integration using samples of a function.

scipy.integrate.trapezoid

scipy.integrate.**trapezoid**(*y*, *x=None*, *dx=1.0*, *axis=- 1*)

Integrate along the given axis using the composite trapezoidal rule.

Integrate *y* (*x*) along given axis.

Parameters

y	[array_like] Input array to integrate.
x	[array_like, optional] The sample points corresponding to the *y* values. If *x* is None, the sample points are assumed to be evenly spaced *dx* apart. The default is None.
dx	[scalar, optional] The spacing between sample points when *x* is None. The default is 1.
axis	[int, optional] The axis along which to integrate.

Returns

trapz	[float] Definite integral as approximated by trapezoidal rule.

See also:

numpy.cumsum

Notes

Image [2] illustrates trapezoidal rule – y-axis locations of points will be taken from *y* array, by default x-axis distances between points will be 1.0, alternatively they can be provided with *x* array or with *dx* scalar. Return value will be equal to combined area under the red lines.

References

[1], [2]

Examples

```
>>> np.trapz([1,2,3])
4.0
>>> np.trapz([1,2,3], x=[4,6,8])
8.0
>>> np.trapz([1,2,3], dx=2)
8.0
>>> a = np.arange(6).reshape(2, 3)
>>> a
array([[0, 1, 2],
       [3, 4, 5]])
>>> np.trapz(a, axis=0)
array([1.5, 2.5, 3.5])
>>> np.trapz(a, axis=1)
array([2.,  8.])
```

scipy.integrate.cumulative_trapezoid

scipy.integrate.**cumulative_trapezoid**(*y*, *x=None*, *dx=1.0*, *axis=- 1*, *initial=None*)

Cumulatively integrate y(x) using the composite trapezoidal rule.

Parameters

y	[array_like] Values to integrate.
x	[array_like, optional] The coordinate to integrate along. If None (default), use spacing *dx* between consecutive elements in *y*.
dx	[float, optional] Spacing between elements of *y*. Only used if *x* is None.
axis	[int, optional] Specifies the axis to cumulate. Default is -1 (last axis).
initial	[scalar, optional] If given, insert this value at the beginning of the returned result. Typically this value should be 0. Default is None, which means no value at `x[0]` is returned and *res* has one element less than *y* along the axis of integration.

Returns

res	[ndarray] The result of cumulative integration of *y* along *axis*. If *initial* is None, the shape is such that the axis of integration has one less value than *y*. If *initial* is given, the shape is equal to that of *y*.

See also:

numpy.cumsum*, *numpy.cumprod

quad

adaptive quadrature using QUADPACK

romberg

adaptive Romberg quadrature

quadrature

adaptive Gaussian quadrature

fixed_quad

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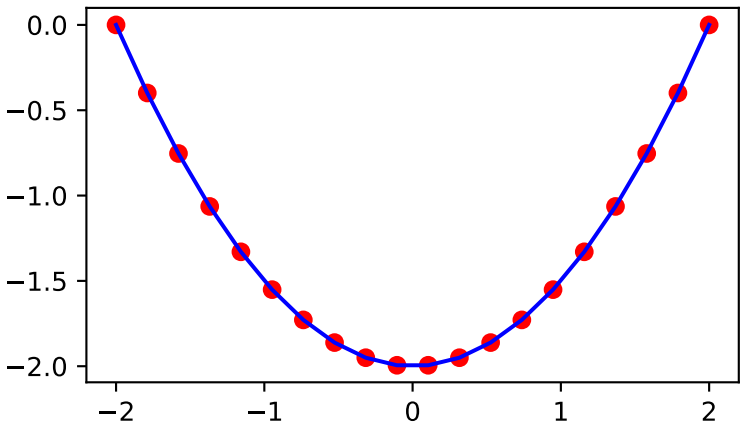
Examples

```
>>> from scipy import integrate
>>> import matplotlib.pyplot as plt
```

```
>>> x = np.linspace(-2, 2, num=20)
>>> y = x
>>> y_int = integrate.cumulative_trapezoid(y, x, initial=0)
>>> plt.plot(x, y_int, 'ro', x, y[0] + 0.5 * x**2, 'b-')
>>> plt.show()
```



scipy.integrate.simpson

scipy.integrate.**simpson**(*y*, *x=None*, *dx=1.0*, *axis=- 1*, *even='avg'*)

Integrate y(x) using samples along the given axis and the composite Simpson's rule. If x is None, spacing of dx is assumed.

If there are an even number of samples, N, then there are an odd number of intervals (N-1), but Simpson's rule requires an even number of intervals. The parameter 'even' controls how this is handled.

Parameters

y [array_like] Array to be integrated.

x [array_like, optional] If given, the points at which *y* is sampled.

dx [float, optional] Spacing of integration points along axis of *x*. Only used when *x* is None. Default is 1.

axis [int, optional] Axis along which to integrate. Default is the last axis.

even [str {'avg', 'first', 'last'}, optional]

- **'avg'** [Average two results:1) use the first N-2 intervals with] a trapezoidal rule on the last interval and 2) use the last N-2 intervals with a trapezoidal rule on the first interval.
- **'first'** [Use Simpson's rule for the first N-2 intervals with] a trapezoidal rule on the last interval.
- **'last'** [Use Simpson's rule for the last N-2 intervals with a] trapezoidal rule on the first interval.

See also:

quad

adaptive quadrature using QUADPACK

romberg

adaptive Romberg quadrature

quadrature

adaptive Gaussian quadrature

fixed_quad

fixed-order Gaussian quadrature

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Notes

For an odd number of samples that are equally spaced the result is exact if the function is a polynomial of order 3 or less. If the samples are not equally spaced, then the result is exact only if the function is a polynomial of order 2 or less.

Examples

```
>>> from scipy import integrate
>>> x = np.arange(0, 10)
>>> y = np.arange(0, 10)
```

```
>>> integrate.simpson(y, x)
40.5
```

```
>>> y = np.power(x, 3)
>>> integrate.simpson(y, x)
1642.5
>>> integrate.quad(lambda x: x**3, 0, 9)[0]
1640.25
```

```
>>> integrate.simpson(y, x, even='first')
1644.5
```

scipy.integrate.romb

scipy.integrate.**romb**(*y*, *dx=1.0*, *axis=- 1*, *show=False*)

Romberg integration using samples of a function.

Parameters

y	[array_like] A vector of `2**k + 1` equally-spaced samples of a function.
dx	[float, optional] The sample spacing. Default is 1.
axis	[int, optional] The axis along which to integrate. Default is -1 (last axis).
show	[bool, optional] When *y* is a single 1-D array, then if this argument is True print the table showing Richardson extrapolation from the samples. Default is False.

Returns

romb	[ndarray] The integrated result for *axis*.

See also:

quad

adaptive quadrature using QUADPACK

romberg

adaptive Romberg quadrature

quadrature

adaptive Gaussian quadrature

fixed_quad

fixed-order Gaussian quadrature

dblquad

double integrals

tplquad

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Examples

```
>>> from scipy import integrate
>>> x = np.arange(10, 14.25, 0.25)
>>> y = np.arange(3, 12)
```

```
>>> integrate.romb(y)
56.0
```

```
>>> y = np.sin(np.power(x, 2.5))
>>> integrate.romb(y)
-0.742561336672229
```

```
>>> integrate.romb(y, show=True)
Richardson Extrapolation Table for Romberg Integration
====================================================================
-0.81576
4.63862  6.45674
-1.10581 -3.02062 -3.65245
-2.57379 -3.06311 -3.06595 -3.05664
-1.34093 -0.92997 -0.78776 -0.75160 -0.74256
====================================================================
-0.742561336672229
```

See also:

scipy.special for orthogonal polynomials (special) for Gaussian quadrature roots and weights for other weighting factors and regions.

Solving initial value problems for ODE systems

The solvers are implemented as individual classes, which can be used directly (low-level usage) or through a convenience function.

solve_ivp(fun, t_span, y0[, method, t_eval, …])	Solve an initial value problem for a system of ODEs.
RK23(fun, t0, y0, t_bound[, max_step, rtol, …])	Explicit Runge-Kutta method of order 3(2).
RK45(fun, t0, y0, t_bound[, max_step, rtol, …])	Explicit Runge-Kutta method of order 5(4).
DOP853(fun, t0, y0, t_bound[, max_step, …])	Explicit Runge-Kutta method of order 8.
Radau(fun, t0, y0, t_bound[, max_step, …])	Implicit Runge-Kutta method of Radau IIA family of order 5.
BDF(fun, t0, y0, t_bound[, max_step, rtol, …])	Implicit method based on backward-differentiation formulas.
LSODA(fun, t0, y0, t_bound[, first_step, …])	Adams/BDF method with automatic stiffness detection and switching.
OdeSolver(fun, t0, y0, t_bound, vectorized)	Base class for ODE solvers.
DenseOutput(t_old, t)	Base class for local interpolant over step made by an ODE solver.

continues on next page

Table 27 – continued from previous page

OdeSolution(ts, interpolants)	Continuous ODE solution.

scipy.integrate.solve_ivp

scipy.integrate.**solve_ivp**(*fun*, *t_span*, *y0*, *method='RK45'*, *t_eval=None*, *dense_output=False*, *events=None*, *vectorized=False*, *args=None*, ***options*)

Solve an initial value problem for a system of ODEs.

This function numerically integrates a system of ordinary differential equations given an initial value:

```
dy / dt = f(t, y)
y(t0) = y0
```

Here t is a 1-D independent variable (time), y(t) is an N-D vector-valued function (state), and an N-D vector-valued function f(t, y) determines the differential equations. The goal is to find y(t) approximately satisfying the differential equations, given an initial value y(t0)=y0.

Some of the solvers support integration in the complex domain, but note that for stiff ODE solvers, the right-hand side must be complex-differentiable (satisfy Cauchy-Riemann equations [11]). To solve a problem in the complex domain, pass y0 with a complex data type. Another option always available is to rewrite your problem for real and imaginary parts separately.

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here *t* is a scalar, and there are two options for the ndarray *y*: It can either have shape (n,); then *fun* must return array_like with shape (n,). Alternatively, it can have shape (n, k); then *fun* must return an array_like with shape (n, k), i.e., each column corresponds to a single column in *y*. The choice between the two options is determined by *vectorized* argument (see below). The vectorized implementation allows a faster approximation of the Jacobian by finite differences (required for stiff solvers).

t_span [2-tuple of floats] Interval of integration (t0, tf). The solver starts with t=t0 and integrates until it reaches t=tf.

y0 [array_like, shape (n,)] Initial state. For problems in the complex domain, pass *y0* with a complex data type (even if the initial value is purely real).

method [string or *OdeSolver*, optional] Integration method to use:

- 'RK45' (default): Explicit Runge-Kutta method of order 5(4) [1]. The error is controlled assuming accuracy of the fourth-order method, but steps are taken using the fifth-order accurate formula (local extrapolation is done). A quartic interpolation polynomial is used for the dense output [2]. Can be applied in the complex domain.
- 'RK23': Explicit Runge-Kutta method of order 3(2) [3]. The error is controlled assuming accuracy of the second-order method, but steps are taken using the third-order accurate formula (local extrapolation is done). A cubic Hermite polynomial is used for the dense output. Can be applied in the complex domain.
- 'DOP853': Explicit Runge-Kutta method of order 8 [13]. Python implementation of the "DOP853" algorithm originally written in Fortran [14]. A 7-th order interpolation polynomial accurate to 7-th order is used for the dense output. Can be applied in the complex domain.
- 'Radau': Implicit Runge-Kutta method of the Radau IIA family of order 5 [4]. The error is controlled with a third-order accurate embedded formula. A cubic polynomial which satisfies the collocation conditions is used for the dense output.
- 'BDF': Implicit multi-step variable-order (1 to 5) method based on a backward differentiation formula for the derivative approximation [5]. The implementation follows the one described in [6]. A quasi-constant step scheme is used and accuracy is enhanced using the NDF modification. Can be applied in the complex domain.

- 'LSODA': Adams/BDF method with automatic stiffness detection and switching [7], [8]. This is a wrapper of the Fortran solver from ODEPACK.

Explicit Runge-Kutta methods ('RK23', 'RK45', 'DOP853') should be used for non-stiff problems and implicit methods ('Radau', 'BDF') for stiff problems [9]. Among Runge-Kutta methods, 'DOP853' is recommended for solving with high precision (low values of *rtol* and *atol*).

If not sure, first try to run 'RK45'. If it makes unusually many iterations, diverges, or fails, your problem is likely to be stiff and you should use 'Radau' or 'BDF'. 'LSODA' can also be a good universal choice, but it might be somewhat less convenient to work with as it wraps old Fortran code.

You can also pass an arbitrary class derived from `OdeSolver` which implements the solver.

t_eval [array_like or None, optional] Times at which to store the computed solution, must be sorted and lie within *t_span*. If None (default), use points selected by the solver.

dense_output
[bool, optional] Whether to compute a continuous solution. Default is False.

events [callable, or list of callables, optional] Events to track. If None (default), no events will be tracked. Each event occurs at the zeros of a continuous function of time and state. Each function must have the signature `event(t, y)` and return a float. The solver will find an accurate value of *t* at which `event(t, y(t)) = 0` using a root-finding algorithm. By default, all zeros will be found. The solver looks for a sign change over each step, so if multiple zero crossings occur within one step, events may be missed. Additionally each *event* function might have the following attributes:

terminal: bool, optional
Whether to terminate integration if this event occurs. Implicitly False if not assigned.

direction: float, optional
Direction of a zero crossing. If *direction* is positive, *event* will only trigger when going from negative to positive, and vice versa if *direction* is negative. If 0, then either direction will trigger event. Implicitly 0 if not assigned.

You can assign attributes like `event.terminal = True` to any function in Python.

vectorized [bool, optional] Whether *fun* is implemented in a vectorized fashion. Default is False.

args [tuple, optional] Additional arguments to pass to the user-defined functions. If given, the additional arguments are passed to all user-defined functions. So if, for example, *fun* has the signature `fun(t, y, a, b, c)`, then *jac* (if given) and any event functions must have the same signature, and *args* must be a tuple of length 3.

options Options passed to a chosen solver. All options available for already implemented solvers are listed below.

first_step [float or None, optional] Initial step size. Default is *None* which means that the algorithm should choose.

max_step [float, optional] Maximum allowed step size. Default is np.inf, i.e., the step size is not bounded and determined solely by the solver.

rtol, atol [float or array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here *rtol* controls a relative accuracy (number of correct digits). But if a component of *y* is approximately below *atol*, the error only needs to fall within the same *atol* threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different *atol* values for different components by passing array_like with shape (n,) for *atol*. Default values are 1e-3 for *rtol* and 1e-6 for *atol*.

jac [array_like, sparse_matrix, callable or None, optional] Jacobian matrix of the right-hand side of the system with respect to y, required by the 'Radau', 'BDF' and 'LSODA' method. The Jacobian matrix has shape (n, n) and its element (i, j) is equal to `d f_i / d y_j`. There are three ways to define the Jacobian:

- If array_like or sparse_matrix, the Jacobian is assumed to be constant. Not supported by 'LSODA'.

- If callable, the Jacobian is assumed to depend on both t and y; it will be called as `jac(t, y)`, as necessary. For 'Radau' and 'BDF' methods, the return value might be a sparse matrix.
- If None (default), the Jacobian will be approximated by finite differences.

It is generally recommended to provide the Jacobian rather than relying on a finite-difference approximation.

jac_sparsity
: [array_like, sparse matrix or None, optional] Defines a sparsity structure of the Jacobian matrix for a finite- difference approximation. Its shape must be (n, n). This argument is ignored if *jac* is not *None*. If the Jacobian has only few non-zero elements in *each* row, providing the sparsity structure will greatly speed up the computations [10]. A zero entry means that a corresponding element in the Jacobian is always zero. If None (default), the Jacobian is assumed to be dense. Not supported by 'LSODA', see *lband* and *uband* instead.

lband, uband
: [int or None, optional] Parameters defining the bandwidth of the Jacobian for the 'LSODA' method, i.e., `jac[i, j] != 0 only for i - lband <= j <= i + uband`. Default is None. Setting these requires your jac routine to return the Jacobian in the packed format: the returned array must have `n` columns and `uband + lband + 1` rows in which Jacobian diagonals are written. Specifically `jac_packed[uband + i - j , j] = jac[i, j]`. The same format is used in *scipy.linalg.solve_banded* (check for an illustration). These parameters can be also used with `jac=None` to reduce the number of Jacobian elements estimated by finite differences.

min_step
: [float, optional] The minimum allowed step size for 'LSODA' method. By default *min_step* is zero.

Returns

Bunch object with the following fields defined:

t
: [ndarray, shape (n_points,)] Time points.

y
: [ndarray, shape (n, n_points)] Values of the solution at *t*.

sol
: [*OdeSolution* or None] Found solution as *OdeSolution* instance; None if *dense_output* was set to False.

t_events
: [list of ndarray or None] Contains for each event type a list of arrays at which an event of that type event was detected. None if *events* was None.

y_events
: [list of ndarray or None] For each value of *t_events*, the corresponding value of the solution. None if *events* was None.

nfev
: [int] Number of evaluations of the right-hand side.

njev
: [int] Number of evaluations of the Jacobian.

nlu
: [int] Number of LU decompositions.

status
: [int] Reason for algorithm termination:
- -1: Integration step failed.
- 0: The solver successfully reached the end of *tspan*.
- 1: A termination event occurred.

message
: [string] Human-readable description of the termination reason.

success
: [bool] True if the solver reached the interval end or a termination event occurred (`status >= 0`).

References

[1], [2], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14]

Examples

Basic exponential decay showing automatically chosen time points.

```
>>> from scipy.integrate import solve_ivp
>>> def exponential_decay(t, y): return -0.5 * y
>>> sol = solve_ivp(exponential_decay, [0, 10], [2, 4, 8])
>>> print(sol.t)
[ 0.          0.11487653  1.26364188  3.06061781  4.81611105  6.57445806
  8.33328988 10.        ]
>>> print(sol.y)
[[2.         1.88836035 1.06327177 0.43319312 0.18017253 0.07483045
  0.03107158 0.01350781]
 [4.         3.7767207  2.12654355 0.86638624 0.36034507 0.14966091
  0.06214316 0.02701561]
 [8.         7.5534414  4.25308709 1.73277247 0.72069014 0.29932181
  0.12428631 0.05403123]]
```

Specifying points where the solution is desired.

```
>>> sol = solve_ivp(exponential_decay, [0, 10], [2, 4, 8],
...                 t_eval=[0, 1, 2, 4, 10])
>>> print(sol.t)
[ 0  1  2  4 10]
>>> print(sol.y)
[[2.         1.21305369 0.73534021 0.27066736 0.01350938]
 [4.         2.42610739 1.47068043 0.54133472 0.02701876]
 [8.         4.85221478 2.94136085 1.08266944 0.05403753]]
```

Cannon fired upward with terminal event upon impact. The `terminal` and `direction` fields of an event are applied by monkey patching a function. Here `y[0]` is position and `y[1]` is velocity. The projectile starts at position 0 with velocity +10. Note that the integration never reaches t=100 because the event is terminal.

```
>>> def upward_cannon(t, y): return [y[1], -0.5]
>>> def hit_ground(t, y): return y[0]
>>> hit_ground.terminal = True
>>> hit_ground.direction = -1
>>> sol = solve_ivp(upward_cannon, [0, 100], [0, 10], events=hit_ground)
>>> print(sol.t_events)
[array([40.])]
>>> print(sol.t)
[0.00000000e+00 9.99900010e-05 1.09989001e-03 1.10988901e-02
 1.11088891e-01 1.11098890e+00 1.11099890e+01 4.00000000e+01]
```

Use *dense_output* and *events* to find position, which is 100, at the apex of the cannonball's trajectory. Apex is not defined as terminal, so both apex and hit_ground are found. There is no information at t=20, so the sol attribute is used to evaluate the solution. The sol attribute is returned by setting `dense_output=True`. Alternatively, the *y_events* attribute can be used to access the solution at the time of the event.

```
>>> def apex(t, y): return y[1]
>>> sol = solve_ivp(upward_cannon, [0, 100], [0, 10],
...                 events=(hit_ground, apex), dense_output=True)
>>> print(sol.t_events)
[array([40.]), array([20.])]
>>> print(sol.t)
[0.00000000e+00 9.99900010e-05 1.09989001e-03 1.10988901e-02
 1.11088891e-01 1.11098890e+00 1.11099890e+01 4.00000000e+01]
>>> print(sol.sol(sol.t_events[1][0]))
[100.   0.]
>>> print(sol.y_events)
[array([[-5.68434189e-14, -1.00000000e+01]]), array([[1.00000000e+02, 1.
↪77635684e-15]])]
```

As an example of a system with additional parameters, we'll implement the Lotka-Volterra equations [12].

```
>>> def lotkavolterra(t, z, a, b, c, d):
...     x, y = z
...     return [a*x - b*x*y, -c*y + d*x*y]
...
```

We pass in the parameter values a=1.5, b=1, c=3 and d=1 with the *args* argument.

```
>>> sol = solve_ivp(lotkavolterra, [0, 15], [10, 5], args=(1.5, 1, 3, 1),
...                 dense_output=True)
```

Compute a dense solution and plot it.

```
>>> t = np.linspace(0, 15, 300)
>>> z = sol.sol(t)
>>> import matplotlib.pyplot as plt
>>> plt.plot(t, z.T)
>>> plt.xlabel('t')
>>> plt.legend(['x', 'y'], shadow=True)
>>> plt.title('Lotka-Volterra System')
>>> plt.show()
```

scipy.integrate.RK23

class scipy.integrate.**RK23**(*fun*, *t0*, *y0*, *t_bound*, *max_step=inf*, *rtol=0.001*, *atol=1e-06*, *vectorized=False*, *first_step=None*, ***extraneous*)

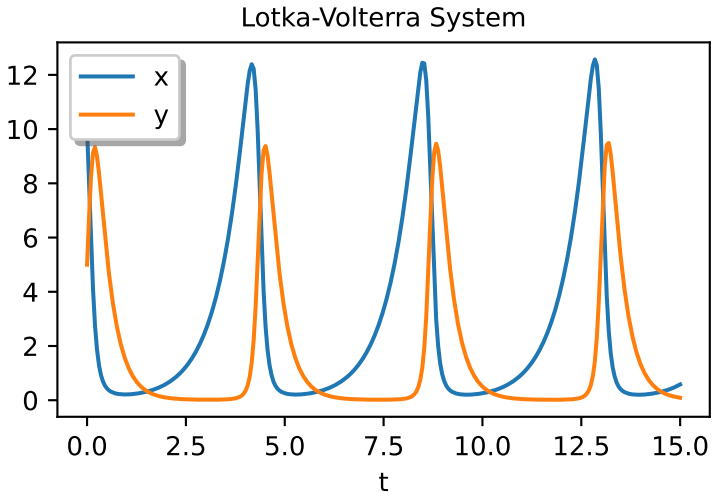
Explicit Runge-Kutta method of order 3(2).

This uses the Bogacki-Shampine pair of formulas [1]. The error is controlled assuming accuracy of the second-order method, but steps are taken using the third-order accurate formula (local extrapolation is done). A cubic Hermite polynomial is used for the dense output.

Can be applied in the complex domain.

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar and there are two options for ndarray `y`. It can either have shape (n,), then `fun` must return array_like with shape (n,). Or alternatively it can have shape (n, k), then `fun` must return array_like with shape (n, k), i.e. each column corresponds to a single column in `y`. The choice between the two options is determined by *vectorized* argument (see below).



t0 [float] Initial time.
y0 [array_like, shape (n,)] Initial state.
t_bound [float] Boundary time - the integration won't continue beyond it. It also determines the direction of the integration.
first_step [float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.
max_step [float, optional] Maximum allowed step size. Default is np.inf, i.e., the step size is not bounded and determined solely by the solver.
rtol, atol [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here, *rtol* controls a relative accuracy (number of correct digits). But if a component of *y* is approximately below *atol*, the error only needs to fall within the same *atol* threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different *atol* values for different components by passing array_like with shape (n,) for *atol*. Default values are 1e-3 for *rtol* and 1e-6 for *atol*.
vectorized [bool, optional] Whether *fun* is implemented in a vectorized fashion. Default is False.

References

[1]

Attributes

n [int] Number of equations.
status [string] Current status of the solver: 'running', 'finished' or 'failed'.
t_bound [float] Boundary time.
direction [float] Integration direction: +1 or -1.
t [float] Current time.
y [ndarray] Current state.
t_old [float] Previous time. None if no steps were made yet.
step_size [float] Size of the last successful step. None if no steps were made yet.
nfev [int] Number evaluations of the system's right-hand side.
njev [int] Number of evaluations of the Jacobian. Is always 0 for this solver as it does not use the Jacobian.

nlu [int] Number of LU decompositions. Is always 0 for this solver.

Methods

dense_output()	Compute a local interpolant over the last successful step.
step()	Perform one integration step.

scipy.integrate.RK23.dense_output

RK23.**dense_output**()
Compute a local interpolant over the last successful step.

Returns

sol [*DenseOutput*] Local interpolant over the last successful step.

scipy.integrate.RK23.step

RK23.**step**()
Perform one integration step.

Returns

message [string or None] Report from the solver. Typically a reason for a failure if *self.status* is 'failed' after the step was taken or None otherwise.

scipy.integrate.RK45

class scipy.integrate.**RK45**(*fun*, *t0*, *y0*, *t_bound*, *max_step=inf*, *rtol=0.001*, *atol=1e-06*, *vectorized=False*, *first_step=None*, ***extraneous*)
Explicit Runge-Kutta method of order 5(4).

This uses the Dormand-Prince pair of formulas [1]. The error is controlled assuming accuracy of the fourth-order method accuracy, but steps are taken using the fifth-order accurate formula (local extrapolation is done). A quartic interpolation polynomial is used for the dense output [2].

Can be applied in the complex domain.

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar, and there are two options for the ndarray `y`: It can either have shape (n,); then `fun` must return array_like with shape (n,). Alternatively it can have shape (n, k); then `fun` must return an array_like with shape (n, k), i.e., each column corresponds to a single column in `y`. The choice between the two options is determined by *vectorized* argument (see below).

t0 [float] Initial time.

y0 [array_like, shape (n,)] Initial state.

t_bound [float] Boundary time - the integration won't continue beyond it. It also determines the direction of the integration.

first_step [float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

max_step [float, optional] Maximum allowed step size. Default is np.inf, i.e., the step size is not bounded and determined solely by the solver.

rtol, atol [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here *rtol* controls a relative accuracy (number of correct digits). But if a component of *y* is approximately below *atol*, the error only needs to fall within the same *atol* threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different *atol* values for different components by passing array_like with shape (n,) for *atol*. Default values are 1e-3 for *rtol* and 1e-6 for *atol*.

vectorized [bool, optional] Whether *fun* is implemented in a vectorized fashion. Default is False.

References

[1], [2]

Attributes

n [int] Number of equations.

status [string] Current status of the solver: 'running', 'finished' or 'failed'.

t_bound [float] Boundary time.

direction [float] Integration direction: +1 or -1.

t [float] Current time.

y [ndarray] Current state.

t_old [float] Previous time. None if no steps were made yet.

step_size [float] Size of the last successful step. None if no steps were made yet.

nfev [int] Number evaluations of the system's right-hand side.

njev [int] Number of evaluations of the Jacobian. Is always 0 for this solver as it does not use the Jacobian.

nlu [int] Number of LU decompositions. Is always 0 for this solver.

Methods

dense_output()	Compute a local interpolant over the last successful step.
step()	Perform one integration step.

scipy.integrate.RK45.dense_output

RK45.**dense_output**()

Compute a local interpolant over the last successful step.

Returns

sol [*DenseOutput*] Local interpolant over the last successful step.

scipy.integrate.RK45.step

RK45.**step**()
Perform one integration step.

Returns

message [string or None] Report from the solver. Typically a reason for a failure if *self.status* is 'failed' after the step was taken or None otherwise.

scipy.integrate.DOP853

class scipy.integrate.**DOP853**(*fun*, *t0*, *y0*, *t_bound*, *max_step=inf*, *rtol=0.001*, *atol=1e-06*, *vectorized=False*, *first_step=None*, ***extraneous*)
Explicit Runge-Kutta method of order 8.

This is a Python implementation of "DOP853" algorithm originally written in Fortran [1], [2]. Note that this is not a literate translation, but the algorithmic core and coefficients are the same.

Can be applied in the complex domain.

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here, `t` is a scalar, and there are two options for the ndarray `y`: It can either have shape (n,); then `fun` must return array_like with shape (n,). Alternatively it can have shape (n, k); then `fun` must return an array_like with shape (n, k), i.e. each column corresponds to a single column in `y`. The choice between the two options is determined by *vectorized* argument (see below).

t0 [float] Initial time.

y0 [array_like, shape (n,)] Initial state.

t_bound [float] Boundary time - the integration won't continue beyond it. It also determines the direction of the integration.

first_step [float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

max_step [float, optional] Maximum allowed step size. Default is np.inf, i.e. the step size is not bounded and determined solely by the solver.

rtol, atol [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here *rtol* controls a relative accuracy (number of correct digits). But if a component of *y* is approximately below *atol*, the error only needs to fall within the same *atol* threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different *atol* values for different components by passing array_like with shape (n,) for *atol*. Default values are 1e-3 for *rtol* and 1e-6 for *atol*.

vectorized [bool, optional] Whether *fun* is implemented in a vectorized fashion. Default is False.

References

[1], [2]

Attributes

n [int] Number of equations.

status [string] Current status of the solver: 'running', 'finished' or 'failed'.

t_bound [float] Boundary time.

direction [float] Integration direction: +1 or -1.

t [float] Current time.

y [ndarray] Current state.

t_old [float] Previous time. None if no steps were made yet.

step_size [float] Size of the last successful step. None if no steps were made yet.
nfev [int] Number evaluations of the system's right-hand side.
njev [int] Number of evaluations of the Jacobian. Is always 0 for this solver as it does not use the Jacobian.
nlu [int] Number of LU decompositions. Is always 0 for this solver.

Methods

dense_output()	Compute a local interpolant over the last successful step.
step()	Perform one integration step.

scipy.integrate.DOP853.dense_output

DOP853.**dense_output**()
Compute a local interpolant over the last successful step.

Returns

sol [*DenseOutput*] Local interpolant over the last successful step.

scipy.integrate.DOP853.step

DOP853.**step**()
Perform one integration step.

Returns

message [string or None] Report from the solver. Typically a reason for a failure if *self.status* is 'failed' after the step was taken or None otherwise.

scipy.integrate.Radau

class scipy.integrate.**Radau**(*fun*, *t0*, *y0*, *t_bound*, *max_step=inf*, *rtol=0.001*, *atol=1e-06*, *jac=None*, *jac_sparsity=None*, *vectorized=False*, *first_step=None*, ***extraneous*)
Implicit Runge-Kutta method of Radau IIA family of order 5.

The implementation follows [1]. The error is controlled with a third-order accurate embedded formula. A cubic polynomial which satisfies the collocation conditions is used for the dense output.

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar, and there are two options for the ndarray `y`: It can either have shape (n,); then `fun` must return array_like with shape (n,). Alternatively it can have shape (n, k); then `fun` must return an array_like with shape (n, k), i.e., each column corresponds to a single column in `y`. The choice between the two options is determined by *vectorized* argument (see below). The vectorized implementation allows a faster approximation of the Jacobian by finite differences (required for this solver).
t0 [float] Initial time.
y0 [array_like, shape (n,)] Initial state.
t_bound [float] Boundary time - the integration won't continue beyond it. It also determines the direction of the integration.

first_step [float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

max_step [float, optional] Maximum allowed step size. Default is np.inf, i.e., the step size is not bounded and determined solely by the solver.

rtol, atol [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here *rtol* controls a relative accuracy (number of correct digits). But if a component of *y* is approximately below *atol*, the error only needs to fall within the same *atol* threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different *atol* values for different components by passing array_like with shape (n,) for *atol*. Default values are 1e-3 for *rtol* and 1e-6 for *atol*.

jac [{None, array_like, sparse_matrix, callable}, optional] Jacobian matrix of the right-hand side of the system with respect to y, required by this method. The Jacobian matrix has shape (n, n) and its element (i, j) is equal to `d f_i / d y_j`. There are three ways to define the Jacobian:

- If array_like or sparse_matrix, the Jacobian is assumed to be constant.
- If callable, the Jacobian is assumed to depend on both t and y; it will be called as `jac(t, y)` as necessary. For the 'Radau' and 'BDF' methods, the return value might be a sparse matrix.
- If None (default), the Jacobian will be approximated by finite differences.

It is generally recommended to provide the Jacobian rather than relying on a finite-difference approximation.

jac_sparsity [{None, array_like, sparse matrix}, optional] Defines a sparsity structure of the Jacobian matrix for a finite-difference approximation. Its shape must be (n, n). This argument is ignored if *jac* is not *None*. If the Jacobian has only few non-zero elements in *each* row, providing the sparsity structure will greatly speed up the computations [2]. A zero entry means that a corresponding element in the Jacobian is always zero. If None (default), the Jacobian is assumed to be dense.

vectorized [bool, optional] Whether *fun* is implemented in a vectorized fashion. Default is False.

References

[1], [2]

Attributes

n [int] Number of equations.

status [string] Current status of the solver: 'running', 'finished' or 'failed'.

t_bound [float] Boundary time.

direction [float] Integration direction: +1 or -1.

t [float] Current time.

y [ndarray] Current state.

t_old [float] Previous time. None if no steps were made yet.

step_size [float] Size of the last successful step. None if no steps were made yet.

nfev [int] Number of evaluations of the right-hand side.

njev [int] Number of evaluations of the Jacobian.

nlu [int] Number of LU decompositions.

Methods

dense_output()	Compute a local interpolant over the last successful step.
step()	Perform one integration step.

scipy.integrate.Radau.dense_output

Radau.**dense_output**()
Compute a local interpolant over the last successful step.

Returns

sol [*DenseOutput*] Local interpolant over the last successful step.

scipy.integrate.Radau.step

Radau.**step**()
Perform one integration step.

Returns

message [string or None] Report from the solver. Typically a reason for a failure if *self.status* is 'failed' after the step was taken or None otherwise.

scipy.integrate.BDF

class scipy.integrate.**BDF**(*fun*, *t0*, *y0*, *t_bound*, *max_step=inf*, *rtol=0.001*, *atol=1e-06*, *jac=None*, *jac_sparsity=None*, *vectorized=False*, *first_step=None*, ***extraneous*)
Implicit method based on backward-differentiation formulas.

This is a variable order method with the order varying automatically from 1 to 5. The general framework of the BDF algorithm is described in [1]. This class implements a quasi-constant step size as explained in [2]. The error estimation strategy for the constant-step BDF is derived in [3]. An accuracy enhancement using modified formulas (NDF) [2] is also implemented.

Can be applied in the complex domain.

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar, and there are two options for the ndarray `y`: It can either have shape (n,); then `fun` must return array_like with shape (n,). Alternatively it can have shape (n, k); then `fun` must return an array_like with shape (n, k), i.e. each column corresponds to a single column in `y`. The choice between the two options is determined by *vectorized* argument (see below). The vectorized implementation allows a faster approximation of the Jacobian by finite differences (required for this solver).

t0 [float] Initial time.

y0 [array_like, shape (n,)] Initial state.

t_bound [float] Boundary time - the integration won't continue beyond it. It also determines the direction of the integration.

first_step [float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

max_step [float, optional] Maximum allowed step size. Default is np.inf, i.e., the step size is not bounded and determined solely by the solver.

rtol, atol [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here *rtol* controls a relative accuracy (number of correct digits). But if a component of *y* is approximately below *atol*, the error only needs to fall within the same *atol* threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different *atol* values for different components by passing array_like with shape (n,) for *atol*. Default values are 1e-3 for *rtol* and 1e-6 for *atol*.

jac [{None, array_like, sparse_matrix, callable}, optional] Jacobian matrix of the right-hand side of the system with respect to y, required by this method. The Jacobian matrix has shape (n, n) and its element (i, j) is equal to `d f_i / d y_j`. There are three ways to define the Jacobian:

- If array_like or sparse_matrix, the Jacobian is assumed to be constant.
- If callable, the Jacobian is assumed to depend on both t and y; it will be called as `jac(t, y)` as necessary. For the 'Radau' and 'BDF' methods, the return value might be a sparse matrix.
- If None (default), the Jacobian will be approximated by finite differences.

It is generally recommended to provide the Jacobian rather than relying on a finite-difference approximation.

jac_sparsity [{None, array_like, sparse matrix}, optional] Defines a sparsity structure of the Jacobian matrix for a finite-difference approximation. Its shape must be (n, n). This argument is ignored if *jac* is not *None*. If the Jacobian has only few non-zero elements in *each* row, providing the sparsity structure will greatly speed up the computations [4]. A zero entry means that a corresponding element in the Jacobian is always zero. If None (default), the Jacobian is assumed to be dense.

vectorized [bool, optional] Whether *fun* is implemented in a vectorized fashion. Default is False.

References

[1], [2], [3], [4]

Attributes

n [int] Number of equations.
status [string] Current status of the solver: 'running', 'finished' or 'failed'.
t_bound [float] Boundary time.
direction [float] Integration direction: +1 or -1.
t [float] Current time.
y [ndarray] Current state.
t_old [float] Previous time. None if no steps were made yet.
step_size [float] Size of the last successful step. None if no steps were made yet.
nfev [int] Number of evaluations of the right-hand side.
njev [int] Number of evaluations of the Jacobian.
nlu [int] Number of LU decompositions.

Methods

dense_output()	Compute a local interpolant over the last successful step.
step()	Perform one integration step.

scipy.integrate.BDF.dense_output

BDF.**dense_output**()
Compute a local interpolant over the last successful step.

Returns

sol [*DenseOutput*] Local interpolant over the last successful step.

scipy.integrate.BDF.step

BDF.**step**()
Perform one integration step.

Returns

message [string or None] Report from the solver. Typically a reason for a failure if *self.status* is 'failed' after the step was taken or None otherwise.

scipy.integrate.LSODA

class scipy.integrate.**LSODA**(*fun*, *t0*, *y0*, *t_bound*, *first_step=None*, *min_step=0.0*, *max_step=inf*, *rtol=0.001*, *atol=1e-06*, *jac=None*, *lband=None*, *uband=None*, *vectorized=False*, ***extraneous*)
Adams/BDF method with automatic stiffness detection and switching.

This is a wrapper to the Fortran solver from ODEPACK [1]. It switches automatically between the nonstiff Adams method and the stiff BDF method. The method was originally detailed in [2].

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar, and there are two options for the ndarray `y`: It can either have shape (n,); then `fun` must return array_like with shape (n,). Alternatively it can have shape (n, k); then `fun` must return an array_like with shape (n, k), i.e. each column corresponds to a single column in `y`. The choice between the two options is determined by *vectorized* argument (see below). The vectorized implementation allows a faster approximation of the Jacobian by finite differences (required for this solver).

t0 [float] Initial time.

y0 [array_like, shape (n,)] Initial state.

t_bound [float] Boundary time - the integration won't continue beyond it. It also determines the direction of the integration.

first_step [float or None, optional] Initial step size. Default is `None` which means that the algorithm should choose.

min_step [float, optional] Minimum allowed step size. Default is 0.0, i.e., the step size is not bounded and determined solely by the solver.

max_step [float, optional] Maximum allowed step size. Default is np.inf, i.e., the step size is not bounded and determined solely by the solver.

rtol, atol [float and array_like, optional] Relative and absolute tolerances. The solver keeps the local error estimates less than `atol + rtol * abs(y)`. Here *rtol* controls a relative accuracy (number of correct digits). But if a component of *y* is approximately below *atol*, the error only needs to fall within the same *atol* threshold, and the number of correct digits is not guaranteed. If components of y have different scales, it might be beneficial to set different *atol* values for different components by passing array_like with shape (n,) for *atol*. Default values are 1e-3 for *rtol* and 1e-6 for *atol*.

jac [None or callable, optional] Jacobian matrix of the right-hand side of the system with respect to `y`. The Jacobian matrix has shape (n, n) and its element (i, j) is equal to `d f_i / d y_j`. The function will be called as `jac(t, y)`. If None (default), the Jacobian will be approximated by finite differences. It is generally recommended to provide the Jacobian rather than relying on a finite-difference approximation.

lband, uband [int or None] Parameters defining the bandwidth of the Jacobian, i.e., `jac[i, j] != 0 only for i - lband <= j <= i + uband`. Setting these requires your jac routine to return the Jacobian in the packed format: the returned array must have `n` columns and `uband + lband + 1` rows in which Jacobian diagonals are written. Specifically `jac_packed[uband + i - j , j] = jac[i, j]`. The same format is used in *scipy.linalg.solve_banded* (check for an illustration). These parameters can be also used with `jac=None` to reduce the number of Jacobian elements estimated by finite differences.

vectorized [bool, optional] Whether *fun* is implemented in a vectorized fashion. A vectorized implementation offers no advantages for this solver. Default is False.

References

[1], [2]

Attributes

n [int] Number of equations.
status [string] Current status of the solver: 'running', 'finished' or 'failed'.
t_bound [float] Boundary time.
direction [float] Integration direction: +1 or -1.
t [float] Current time.
y [ndarray] Current state.
t_old [float] Previous time. None if no steps were made yet.
nfev [int] Number of evaluations of the right-hand side.
njev [int] Number of evaluations of the Jacobian.

Methods

dense_output()	Compute a local interpolant over the last successful step.
step()	Perform one integration step.

scipy.integrate.LSODA.dense_output

LSODA.**dense_output**()
Compute a local interpolant over the last successful step.

Returns

sol [DenseOutput] Local interpolant over the last successful step.

scipy.integrate.LSODA.step

LSODA.**step**()
Perform one integration step.

Returns

message [string or None] Report from the solver. Typically a reason for a failure if *self.status* is 'failed' after the step was taken or None otherwise.

scipy.integrate.OdeSolver

class scipy.integrate.**OdeSolver**(*fun*, *t0*, *y0*, *t_bound*, *vectorized*, *support_complex=False*)
Base class for ODE solvers.

In order to implement a new solver you need to follow the guidelines:

1. A constructor must accept parameters presented in the base class (listed below) along with any other parameters specific to a solver.
2. A constructor must accept arbitrary extraneous arguments `**extraneous`, but warn that these arguments are irrelevant using *common.warn_extraneous* function. Do not pass these arguments to the base class.
3. A solver must implement a private method *_step_impl(self)* which propagates a solver one step further. It must return tuple `(success, message)`, where `success` is a boolean indicating whether a step was successful, and `message` is a string containing description of a failure if a step failed or None otherwise.
4. A solver must implement a private method *_dense_output_impl(self)*, which returns a `DenseOutput` object covering the last successful step.
5. A solver must have attributes listed below in Attributes section. Note that `t_old` and `step_size` are updated automatically.
6. Use *fun(self, t, y)* method for the system rhs evaluation, this way the number of function evaluations (*nfev*) will be tracked automatically.
7. For convenience, a base class provides *fun_single(self, t, y)* and *fun_vectorized(self, t, y)* for evaluating the rhs in non-vectorized and vectorized fashions respectively (regardless of how *fun* from the constructor is implemented). These calls don't increment *nfev*.
8. If a solver uses a Jacobian matrix and LU decompositions, it should track the number of Jacobian evaluations (*njev*) and the number of LU decompositions (*nlu*).
9. By convention, the function evaluations used to compute a finite difference approximation of the Jacobian should not be counted in *nfev*, thus use *fun_single(self, t, y)* or *fun_vectorized(self, t, y)* when computing a finite difference approximation of the Jacobian.

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(t, y)`. Here `t` is a scalar and there are two options for ndarray `y`. It can either have shape (n,), then `fun` must return array_like with shape (n,). Or, alternatively, it can have shape (n, n_points), then `fun` must return array_like with shape (n, n_points) (each column corresponds to a single column in `y`). The choice between the two options is determined by *vectorized* argument (see below).

t0 [float] Initial time.

y0 [array_like, shape (n,)] Initial state.

t_bound [float] Boundary time — the integration won't continue beyond it. It also determines the direction of the integration.

vectorized [bool] Whether *fun* is implemented in a vectorized fashion.

support_complex [bool, optional] Whether integration in a complex domain should be supported. Generally determined by a derived solver class capabilities. Default is False.

Attributes

n [int] Number of equations.

status [string] Current status of the solver: 'running', 'finished' or 'failed'.

t_bound [float] Boundary time.

direction [float] Integration direction: +1 or -1.

t [float] Current time.

y [ndarray] Current state.

t_old [float] Previous time. None if no steps were made yet.

step_size [float] Size of the last successful step. None if no steps were made yet.

nfev [int] Number of the system's rhs evaluations.

njev [int] Number of the Jacobian evaluations.

nlu [int] Number of LU decompositions.

Methods

dense_output()	Compute a local interpolant over the last successful step.
step()	Perform one integration step.

scipy.integrate.OdeSolver.dense_output

OdeSolver.**dense_output**()

Compute a local interpolant over the last successful step.

Returns

sol [*DenseOutput*] Local interpolant over the last successful step.

scipy.integrate.OdeSolver.step

OdeSolver.**step**()
Perform one integration step.

Returns

message [string or None] Report from the solver. Typically a reason for a failure if *self.status* is 'failed' after the step was taken or None otherwise.

scipy.integrate.DenseOutput

class scipy.integrate.**DenseOutput**(*t_old*, *t*)
Base class for local interpolant over step made by an ODE solver.

It interpolates between *t_min* and *t_max* (see Attributes below). Evaluation outside this interval is not forbidden, but the accuracy is not guaranteed.

Attributes

t_min, t_max
[float] Time range of the interpolation.

Methods

__call__(t)	Evaluate the interpolant.

scipy.integrate.DenseOutput.__call__

DenseOutput.**__call__**(*t*)
Evaluate the interpolant.

Parameters

t [float or array_like with shape (n_points,)] Points to evaluate the solution at.

Returns

y [ndarray, shape (n,) or (n, n_points)] Computed values. Shape depends on whether *t* was a scalar or a 1-D array.

scipy.integrate.OdeSolution

class scipy.integrate.**OdeSolution**(*ts*, *interpolants*)
Continuous ODE solution.

It is organized as a collection of *DenseOutput* objects which represent local interpolants. It provides an algorithm to select a right interpolant for each given point.

The interpolants cover the range between *t_min* and *t_max* (see Attributes below). Evaluation outside this interval is not forbidden, but the accuracy is not guaranteed.

When evaluating at a breakpoint (one of the values in *ts*) a segment with the lower index is selected.

Parameters

ts [array_like, shape (n_segments + 1,)] Time instants between which local interpolants are defined. Must be strictly increasing or decreasing (zero segment with two points is also allowed).

interpolants
[list of DenseOutput with n_segments elements] Local interpolants. An i-th interpolant is assumed to be defined between `ts[i]` and `ts[i + 1]`.

Attributes

t_min, t_max
[float] Time range of the interpolation.

Methods

__call__(t)	Evaluate the solution.

scipy.integrate.OdeSolution.__call__

`OdeSolution.`**`__call__`**(*t*)
Evaluate the solution.

Parameters

t [float or array_like with shape (n_points,)] Points to evaluate at.

Returns

y [ndarray, shape (n_states,) or (n_states, n_points)] Computed values. Shape depends on whether *t* is a scalar or a 1-D array.

Old API

These are the routines developed earlier for SciPy. They wrap older solvers implemented in Fortran (mostly ODEPACK). While the interface to them is not particularly convenient and certain features are missing compared to the new API, the solvers themselves are of good quality and work fast as compiled Fortran code. In some cases, it might be worth using this old API.

odeint(func, y0, t[, args, Dfun, col_deriv, …])	Integrate a system of ordinary differential equations.
ode(f[, jac])	A generic interface class to numeric integrators.
complex_ode(f[, jac])	A wrapper of ode for complex systems.

scipy.integrate.odeint

`scipy.integrate.`**`odeint`**(*func*, *y0*, *t*, *args=()*, *Dfun=None*, *col_deriv=0*, *full_output=0*, *ml=None*, *mu=None*, *rtol=None*, *atol=None*, *tcrit=None*, *h0=0.0*, *hmax=0.0*, *hmin=0.0*, *ixpr=0*, *mxstep=0*, *mxhnil=0*, *mxordn=12*, *mxords=5*, *printmessg=0*, *tfirst=False*)
Integrate a system of ordinary differential equations.

Note: For new code, use *scipy.integrate.solve_ivp* to solve a differential equation.

Solve a system of ordinary differential equations using lsoda from the FORTRAN library odepack.

Solves the initial value problem for stiff or non-stiff systems of first order ode-s:

```
dy/dt = func(y, t, ...)  [or func(t, y, ...)]
```

where y can be a vector.

Note: By default, the required order of the first two arguments of *func* are in the opposite order of the arguments in the system definition function used by the *scipy.integrate.ode* class and the function *scipy.integrate.solve_ivp*. To use a function with the signature `func(t, y, ...)`, the argument *tfirst* must be set to `True`.

Parameters

func [callable(y, t, …) or callable(t, y, …)] Computes the derivative of y at t. If the signature is `callable(t, y, ...)`, then the argument *tfirst* must be set `True`.

y0 [array] Initial condition on y (can be a vector).

t [array] A sequence of time points for which to solve for y. The initial value point should be the first element of this sequence. This sequence must be monotonically increasing or monotonically decreasing; repeated values are allowed.

args [tuple, optional] Extra arguments to pass to function.

Dfun [callable(y, t, …) or callable(t, y, …)] Gradient (Jacobian) of *func*. If the signature is `callable(t, y, ...)`, then the argument *tfirst* must be set `True`.

col_deriv [bool, optional] True if *Dfun* defines derivatives down columns (faster), otherwise *Dfun* should define derivatives across rows.

full_output
[bool, optional] True if to return a dictionary of optional outputs as the second output

printmessg
[bool, optional] Whether to print the convergence message

tfirst: bool, optional
If True, the first two arguments of *func* (and *Dfun*, if given) must `t, y` instead of the default `y, t`.
New in version 1.1.0.

Returns

y [array, shape (len(t), len(y0))] Array containing the value of y for each desired time in t, with the initial value *y0* in the first row.

infodict [dict, only returned if full_output == True] Dictionary containing additional output information

key	meaning
'hu'	vector of step sizes successfully used for each time step
'tcur'	vector with the value of t reached for each time step (will always be at least as large as the input times)
'tolsf'	vector of tolerance scale factors, greater than 1.0, computed when a request for too much accuracy was detected
'tsw'	value of t at the time of the last method switch (given for each time step)
'nst'	cumulative number of time steps
'nfe'	cumulative number of function evaluations for each time step
'nje'	cumulative number of jacobian evaluations for each time step
'nqu'	a vector of method orders for each successful step
'imxer'	index of the component of largest magnitude in the weighted local error vector (e / ewt) on an error return, -1 otherwise
'lenrw'	the length of the double work array required
'leniw'	the length of integer work array required
'mused'	a vector of method indicators for each successful time step: 1: adams (nonstiff), 2: bdf (stiff)

Other Parameters

ml, mu [int, optional] If either of these are not None or non-negative, then the Jacobian is assumed to be banded. These give the number of lower and upper non-zero diagonals in this banded matrix. For the banded case, *Dfun* should return a matrix whose rows contain the non-zero bands (starting with the lowest diagonal). Thus, the return matrix *jac* from *Dfun* should have shape `(ml + mu + 1, len(y0))` when `ml >=0` or `mu >=0`. The data in *jac* must be stored such that `jac[i - j + mu, j]` holds the derivative of the *i`th equation with respect to the `j`th state variable. If `col_deriv* is True, the transpose of this *jac* must be returned.

rtol, atol [float, optional] The input parameters *rtol* and *atol* determine the error control performed by the solver. The solver will control the vector, e, of estimated local errors in y, according to an inequality of the form `max-norm of (e / ewt) <= 1`, where ewt is a vector of positive error weights computed as `ewt = rtol * abs(y) + atol`. rtol and atol can be either vectors the same length as y or scalars. Defaults to 1.49012e-8.

tcrit [ndarray, optional] Vector of critical points (e.g., singularities) where integration care should be taken.

h0 [float, (0: solver-determined), optional] The step size to be attempted on the first step.

hmax [float, (0: solver-determined), optional] The maximum absolute step size allowed.

hmin [float, (0: solver-determined), optional] The minimum absolute step size allowed.

ixpr [bool, optional] Whether to generate extra printing at method switches.

mxstep [int, (0: solver-determined), optional] Maximum number of (internally defined) steps allowed for each integration point in t.

mxhnil [int, (0: solver-determined), optional] Maximum number of messages printed.

mxordn [int, (0: solver-determined), optional] Maximum order to be allowed for the non-stiff (Adams) method.

mxords [int, (0: solver-determined), optional] Maximum order to be allowed for the stiff (BDF) method.

See also:

solve_ivp

solve an initial value problem for a system of ODEs

ode

a more object-oriented integrator based on VODE

quad

for finding the area under a curve

Examples

The second order differential equation for the angle *theta* of a pendulum acted on by gravity with friction can be written:

```
theta''(t) + b*theta'(t) + c*sin(theta(t)) = 0
```

where *b* and *c* are positive constants, and a prime (') denotes a derivative. To solve this equation with *odeint*, we must first convert it to a system of first order equations. By defining the angular velocity `omega(t) = theta'(t)`, we obtain the system:

```
theta'(t) = omega(t)
omega'(t) = -b*omega(t) - c*sin(theta(t))
```

Let *y* be the vector [*theta*, *omega*]. We implement this system in Python as:

```
>>> def pend(y, t, b, c):
...     theta, omega = y
...     dydt = [omega, -b*omega - c*np.sin(theta)]
...     return dydt
...
```

We assume the constants are *b* = 0.25 and *c* = 5.0:

```
>>> b = 0.25
>>> c = 5.0
```

For initial conditions, we assume the pendulum is nearly vertical with *theta(0)* = *pi* - 0.1, and is initially at rest, so *omega(0)* = 0. Then the vector of initial conditions is

```
>>> y0 = [np.pi - 0.1, 0.0]
```

We will generate a solution at 101 evenly spaced samples in the interval 0 <= *t* <= 10. So our array of times is:

```
>>> t = np.linspace(0, 10, 101)
```

Call *odeint* to generate the solution. To pass the parameters *b* and *c* to *pend*, we give them to *odeint* using the *args* argument.

```
>>> from scipy.integrate import odeint
>>> sol = odeint(pend, y0, t, args=(b, c))
```

The solution is an array with shape (101, 2). The first column is *theta(t)*, and the second is *omega(t)*. The following code plots both components.

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(t, sol[:, 0], 'b', label='theta(t)')
>>> plt.plot(t, sol[:, 1], 'g', label='omega(t)')
>>> plt.legend(loc='best')
```

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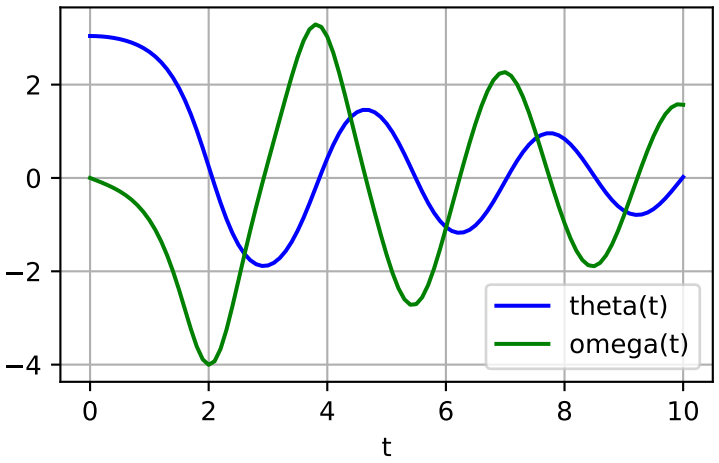
```
>>> plt.xlabel('t')
>>> plt.grid()
>>> plt.show()
```



scipy.integrate.ode

class scipy.integrate.**ode**(*f*, *jac=None*)

A generic interface class to numeric integrators.

Solve an equation system $y'(t) = f(t, y)$ with (optional) `jac = df/dy`.

Note: The first two arguments of `f(t, y, ...)` are in the opposite order of the arguments in the system definition function used by *scipy.integrate.odeint*.

Parameters

f [callable `f(t, y, *f_args)`] Right-hand side of the differential equation. t is a scalar, `y.shape == (n,)`. `f_args` is set by calling `set_f_params(*args)`. *f* should return a scalar, array or list (not a tuple).

jac [callable `jac(t, y, *jac_args)`, optional] Jacobian of the right-hand side, `jac[i, j] = d f[i] / d y[j]`. `jac_args` is set by calling `set_jac_params(*args)`.

See also:

odeint

an integrator with a simpler interface based on lsoda from ODEPACK

quad

for finding the area under a curve

Notes

Available integrators are listed below. They can be selected using the *set_integrator* method.

"vode"

Real-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).
Source: http://www.netlib.org/ode/vode.f

Warning: This integrator is not re-entrant. You cannot have two *ode* instances using the "vode" integrator at the same time.

This integrator accepts the following parameters in *set_integrator* method of the *ode* class:

- atol : float or sequence absolute tolerance for solution
- rtol : float or sequence relative tolerance for solution
- lband : None or int
- uband : None or int Jacobian band width, jac[i,j] != 0 for i-lband <= j <= i+uband. Setting these requires your jac routine to return the jacobian in packed format, jac_packed[i-j+uband, j] = jac[i,j]. The dimension of the matrix must be (lband+uband+1, len(y)).
- method: 'adams' or 'bdf' Which solver to use, Adams (non-stiff) or BDF (stiff)
- with_jacobian : bool This option is only considered when the user has not supplied a Jacobian function and has not indicated (by setting either band) that the Jacobian is banded. In this case, *with_jacobian* specifies whether the iteration method of the ODE solver's correction step is chord iteration with an internally generated full Jacobian or functional iteration with no Jacobian.
- nsteps : int Maximum number of (internally defined) steps allowed during one call to the solver.
- first_step : float
- min_step : float
- max_step : float Limits for the step sizes used by the integrator.
- order : int Maximum order used by the integrator, order <= 12 for Adams, <= 5 for BDF.

"zvode"

Complex-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).
Source: http://www.netlib.org/ode/zvode.f

Warning: This integrator is not re-entrant. You cannot have two *ode* instances using the "zvode" integrator at the same time.

This integrator accepts the same parameters in *set_integrator* as the "vode" solver.

Note: When using ZVODE for a stiff system, it should only be used for the case in which the function f is analytic, that is, when each f(i) is an analytic function of each y(j). Analyticity means that the partial derivative df(i)/dy(j) is a unique complex number, and this fact is critical in the way ZVODE solves the dense or banded linear systems that arise in the stiff case. For a complex stiff ODE system in which f is not analytic, ZVODE is likely to have convergence failures, and for this problem one should instead use DVODE on the equivalent real system (in the real and imaginary parts of y).

"lsoda"

Real-valued Variable-coefficient Ordinary Differential Equation solver, with fixed-leading-coefficient implementation. It provides automatic method switching between implicit Adams method (for non-stiff problems) and a method based on backward differentiation formulas (BDF) (for stiff problems).
Source: http://www.netlib.org/odepack

Warning: This integrator is not re-entrant. You cannot have two `ode` instances using the "lsoda" integrator at the same time.

This integrator accepts the following parameters in `set_integrator` method of the `ode` class:

- atol : float or sequence absolute tolerance for solution
- rtol : float or sequence relative tolerance for solution
- lband : None or int
- uband : None or int Jacobian band width, jac[i,j] != 0 for i-lband <= j <= i+uband. Setting these requires your jac routine to return the jacobian in packed format, jac_packed[i-j+uband, j] = jac[i,j].
- with_jacobian : bool *Not used.*
- nsteps : int Maximum number of (internally defined) steps allowed during one call to the solver.
- first_step : float
- min_step : float
- max_step : float Limits for the step sizes used by the integrator.
- max_order_ns : int Maximum order used in the nonstiff case (default 12).
- max_order_s : int Maximum order used in the stiff case (default 5).
- max_hnil : int Maximum number of messages reporting too small step size (t + h = t) (default 0)
- ixpr : int Whether to generate extra printing at method switches (default False).

"dopri5"

This is an explicit runge-kutta method of order (4)5 due to Dormand & Prince (with stepsize control and dense output).
Authors:

E. Hairer and G. Wanner Universite de Geneve, Dept. de Mathematiques CH-1211 Geneve 24, Switzerland e-mail: ernst.hairer@math.unige.ch, gerhard.wanner@math.unige.ch

This code is described in [HNW93].
This integrator accepts the following parameters in set_integrator() method of the ode class:

- atol : float or sequence absolute tolerance for solution
- rtol : float or sequence relative tolerance for solution
- nsteps : int Maximum number of (internally defined) steps allowed during one call to the solver.
- first_step : float
- max_step : float
- safety : float Safety factor on new step selection (default 0.9)
- ifactor : float
- dfactor : float Maximum factor to increase/decrease step size by in one step
- beta : float Beta parameter for stabilised step size control.
- verbosity : int Switch for printing messages (< 0 for no messages).

"dop853"

This is an explicit runge-kutta method of order 8(5,3) due to Dormand & Prince (with stepsize control and dense output).
Options and references the same as "dopri5".

References

[HNW93]

Examples

A problem to integrate and the corresponding jacobian:

```
>>> from scipy.integrate import ode
>>>
>>> y0, t0 = [1.0j, 2.0], 0
>>>
>>> def f(t, y, arg1):
...     return [1j*arg1*y[0] + y[1], -arg1*y[1]**2]
>>> def jac(t, y, arg1):
...     return [[1j*arg1, 1], [0, -arg1*2*y[1]]]
```

The integration:

```
>>> r = ode(f, jac).set_integrator('zvode', method='bdf')
>>> r.set_initial_value(y0, t0).set_f_params(2.0).set_jac_params(2.0)
>>> t1 = 10
>>> dt = 1
>>> while r.successful() and r.t < t1:
...     print(r.t+dt, r.integrate(r.t+dt))
1 [-0.71038232+0.23749653j  0.40000271+0.j        ]
2.0 [0.19098503-0.52359246j 0.22222356+0.j        ]
3.0 [0.47153208+0.52701229j 0.15384681+0.j        ]
4.0 [-0.61905937+0.30726255j  0.11764744+0.j        ]
5.0 [0.02340997-0.61418799j 0.09523835+0.j        ]
6.0 [0.58643071+0.339819j 0.08000018+0.j      ]
7.0 [-0.52070105+0.44525141j  0.06896565+0.j        ]
8.0 [-0.15986733-0.61234476j  0.06060616+0.j        ]
9.0 [0.64850462+0.15048982j 0.05405414+0.j        ]
10.0 [-0.38404699+0.56382299j  0.04878055+0.j        ]
```

Attributes

t	[float] Current time.
y	[ndarray] Current variable values.

Methods

get_return_code()	Extracts the return code for the integration to enable better control if the integration fails.
integrate(t[, step, relax])	Find y=y(t), set y as an initial condition, and return y.
set_f_params(*args)	Set extra parameters for user-supplied function f.
set_initial_value(y[, t])	Set initial conditions y(t) = y.
set_integrator(name, **integrator_params)	Set integrator by name.
set_jac_params(*args)	Set extra parameters for user-supplied function jac.

continues on next page

Table 38 – continued from previous page

set_solout(solout)	Set callable to be called at every successful integration step.
successful()	Check if integration was successful.

scipy.integrate.ode.get_return_code

ode.**get_return_code**()

Extracts the return code for the integration to enable better control if the integration fails.

In general, a return code > 0 implies success, while a return code < 0 implies failure.

Notes

This section describes possible return codes and their meaning, for available integrators that can be selected by *set_integrator* method.

"vode"

Return Code	Message
2	Integration successful.
-1	Excess work done on this call. (Perhaps wrong MF.)
-2	Excess accuracy requested. (Tolerances too small.)
-3	Illegal input detected. (See printed message.)
-4	Repeated error test failures. (Check all input.)
-5	Repeated convergence failures. (Perhaps bad Jacobian supplied or wrong choice of MF or tolerances.)
-6	Error weight became zero during problem. (Solution component i vanished, and ATOL or ATOL(i) = 0.)

"zvode"

Return Code	Message
2	Integration successful.
-1	Excess work done on this call. (Perhaps wrong MF.)
-2	Excess accuracy requested. (Tolerances too small.)
-3	Illegal input detected. (See printed message.)
-4	Repeated error test failures. (Check all input.)
-5	Repeated convergence failures. (Perhaps bad Jacobian supplied or wrong choice of MF or tolerances.)
-6	Error weight became zero during problem. (Solution component i vanished, and ATOL or ATOL(i) = 0.)

"dopri5"

Return Code	Message
1	Integration successful.
2	Integration successful (interrupted by solout).
-1	Input is not consistent.
-2	Larger nsteps is needed.
-3	Step size becomes too small.
-4	Problem is probably stiff (interrupted).

"dop853"

Return Code	Message
1	Integration successful.
2	Integration successful (interrupted by solout).
-1	Input is not consistent.
-2	Larger nsteps is needed.
-3	Step size becomes too small.
-4	Problem is probably stiff (interrupted).

"lsoda"

Return Code	Message
2	Integration successful.
-1	Excess work done on this call (perhaps wrong Dfun type).
-2	Excess accuracy requested (tolerances too small).
-3	Illegal input detected (internal error).
-4	Repeated error test failures (internal error).
-5	Repeated convergence failures (perhaps bad Jacobian or tolerances).
-6	Error weight became zero during problem.
-7	Internal workspace insufficient to finish (internal error).

scipy.integrate.ode.integrate

`ode.`**`integrate`**(*t*, *step=False*, *relax=False*)

Find y=y(t), set y as an initial condition, and return y.

Parameters

t [float] The endpoint of the integration step.

step [bool] If True, and if the integrator supports the step method, then perform a single integration step and return. This parameter is provided in order to expose internals of the implementation, and should not be changed from its default value in most cases.

relax [bool] If True and if the integrator supports the run_relax method, then integrate until t_1 >= t and return. `relax` is not referenced if `step=True`. This parameter is provided in order to expose internals of the implementation, and should not be changed from its default value in most cases.

Returns

y [float] The integrated value at t

scipy.integrate.ode.set_f_params

ode.**set_f_params**(**args*)
Set extra parameters for user-supplied function f.

scipy.integrate.ode.set_initial_value

ode.**set_initial_value**(*y*, *t=0.0*)
Set initial conditions y(t) = y.

scipy.integrate.ode.set_integrator

ode.**set_integrator**(*name*, ***integrator_params*)
Set integrator by name.

Parameters

name [str] Name of the integrator.
integrator_params
Additional parameters for the integrator.

scipy.integrate.ode.set_jac_params

ode.**set_jac_params**(**args*)
Set extra parameters for user-supplied function jac.

scipy.integrate.ode.set_solout

ode.**set_solout**(*solout*)
Set callable to be called at every successful integration step.

Parameters

solout [callable] `solout(t, y)` is called at each internal integrator step, t is a scalar providing the current independent position y is the current soloution `y.shape == (n,)` solout should return -1 to stop integration otherwise it should return None or 0

scipy.integrate.ode.successful

ode.**successful**()
Check if integration was successful.

scipy.integrate.complex_ode

class scipy.integrate.**complex_ode**(*f*, *jac=None*)

A wrapper of ode for complex systems.

This functions similarly as *ode*, but re-maps a complex-valued equation system to a real-valued one before using the integrators.

Parameters

f [callable `f(t, y, *f_args)`] Rhs of the equation. t is a scalar, `y.shape == (n,)`. `f_args` is set by calling `set_f_params(*args)`.

jac [callable `jac(t, y, *jac_args)`] Jacobian of the rhs, `jac[i,j] = d f[i] / d y[j]`. `jac_args` is set by calling `set_f_params(*args)`.

Examples

For usage examples, see *ode*.

Attributes

t [float] Current time.

y [ndarray] Current variable values.

Methods

get_return_code()	Extracts the return code for the integration to enable better control if the integration fails.
integrate(t[, step, relax])	Find y=y(t), set y as an initial condition, and return y.
set_f_params(*args)	Set extra parameters for user-supplied function f.
set_initial_value(y[, t])	Set initial conditions y(t) = y.
set_integrator(name, **integrator_params)	Set integrator by name.
set_jac_params(*args)	Set extra parameters for user-supplied function jac.
set_solout(solout)	Set callable to be called at every successful integration step.
successful()	Check if integration was successful.

scipy.integrate.complex_ode.get_return_code

complex_ode.**get_return_code**()

Extracts the return code for the integration to enable better control if the integration fails.

In general, a return code > 0 implies success, while a return code < 0 implies failure.

Notes

This section describes possible return codes and their meaning, for available integrators that can be selected by *set_integrator* method.

"vode"

Return Code	Message
2	Integration successful.
-1	Excess work done on this call. (Perhaps wrong MF.)
-2	Excess accuracy requested. (Tolerances too small.)
-3	Illegal input detected. (See printed message.)
-4	Repeated error test failures. (Check all input.)
-5	Repeated convergence failures. (Perhaps bad Jacobian supplied or wrong choice of MF or tolerances.)
-6	Error weight became zero during problem. (Solution component i vanished, and ATOL or ATOL(i) = 0.)

"zvode"

Return Code	Message
2	Integration successful.
-1	Excess work done on this call. (Perhaps wrong MF.)
-2	Excess accuracy requested. (Tolerances too small.)
-3	Illegal input detected. (See printed message.)
-4	Repeated error test failures. (Check all input.)
-5	Repeated convergence failures. (Perhaps bad Jacobian supplied or wrong choice of MF or tolerances.)
-6	Error weight became zero during problem. (Solution component i vanished, and ATOL or ATOL(i) = 0.)

"dopri5"

Return Code	Message
1	Integration successful.
2	Integration successful (interrupted by solout).
-1	Input is not consistent.
-2	Larger nsteps is needed.
-3	Step size becomes too small.
-4	Problem is probably stiff (interrupted).

"dop853"

Return Code	Message
1	Integration successful.
2	Integration successful (interrupted by solout).
-1	Input is not consistent.
-2	Larger nsteps is needed.
-3	Step size becomes too small.
-4	Problem is probably stiff (interrupted).

"lsoda"

Return Code	Message
2	Integration successful.
-1	Excess work done on this call (perhaps wrong Dfun type).
-2	Excess accuracy requested (tolerances too small).
-3	Illegal input detected (internal error).
-4	Repeated error test failures (internal error).
-5	Repeated convergence failures (perhaps bad Jacobian or tolerances).
-6	Error weight became zero during problem.
-7	Internal workspace insufficient to finish (internal error).

scipy.integrate.complex_ode.integrate

`complex_ode.`**`integrate`**(*t*, *step=False*, *relax=False*)

Find y=y(t), set y as an initial condition, and return y.

Parameters

t [float] The endpoint of the integration step.

step [bool] If True, and if the integrator supports the step method, then perform a single integration step and return. This parameter is provided in order to expose internals of the implementation, and should not be changed from its default value in most cases.

relax [bool] If True and if the integrator supports the run_relax method, then integrate until t_1 >= t and return. `relax` is not referenced if `step=True`. This parameter is provided in order to expose internals of the implementation, and should not be changed from its default value in most cases.

Returns

y [float] The integrated value at t

scipy.integrate.complex_ode.set_f_params

`complex_ode.`**`set_f_params`**(**args*)

Set extra parameters for user-supplied function f.

scipy.integrate.complex_ode.set_initial_value

`complex_ode.`**`set_initial_value`**(*y*, *t=0.0*)

Set initial conditions y(t) = y.

scipy.integrate.complex_ode.set_integrator

complex_ode.**set_integrator**(*name*, ***integrator_params*)
Set integrator by name.

Parameters

name [str] Name of the integrator
integrator_params
Additional parameters for the integrator.

scipy.integrate.complex_ode.set_jac_params

complex_ode.**set_jac_params**(**args*)
Set extra parameters for user-supplied function jac.

scipy.integrate.complex_ode.set_solout

complex_ode.**set_solout**(*solout*)
Set callable to be called at every successful integration step.

Parameters

solout [callable] `solout(t, y)` is called at each internal integrator step, t is a scalar providing the current independent position y is the current soloution `y.shape == (n,)` solout should return -1 to stop integration otherwise it should return None or 0

scipy.integrate.complex_ode.successful

complex_ode.**successful**()
Check if integration was successful.

Solving boundary value problems for ODE systems

solve_bvp(fun, bc, x, y[, p, S, fun_jac, …])	Solve a boundary value problem for a system of ODEs.

scipy.integrate.solve_bvp

scipy.integrate.**solve_bvp**(*fun*, *bc*, *x*, *y*, *p=None*, *S=None*, *fun_jac=None*, *bc_jac=None*, *tol=0.001*, *max_nodes=1000*, *verbose=0*, *bc_tol=None*)
Solve a boundary value problem for a system of ODEs.

This function numerically solves a first order system of ODEs subject to two-point boundary conditions:

```
dy / dx = f(x, y, p) + S * y / (x - a), a <= x <= b
bc(y(a), y(b), p) = 0
```

Here x is a 1-D independent variable, y(x) is an N-D vector-valued function and p is a k-D vector of unknown parameters which is to be found along with y(x). For the problem to be determined, there must be n + k boundary conditions, i.e., bc must be an (n + k)-D function.

The last singular term on the right-hand side of the system is optional. It is defined by an n-by-n matrix S, such

that the solution must satisfy S y(a) = 0. This condition will be forced during iterations, so it must not contradict boundary conditions. See [2] for the explanation how this term is handled when solving BVPs numerically.

Problems in a complex domain can be solved as well. In this case, y and p are considered to be complex, and f and bc are assumed to be complex-valued functions, but x stays real. Note that f and bc must be complex differentiable (satisfy Cauchy-Riemann equations [4]), otherwise you should rewrite your problem for real and imaginary parts separately. To solve a problem in a complex domain, pass an initial guess for y with a complex data type (see below).

Parameters

fun [callable] Right-hand side of the system. The calling signature is `fun(x, y)`, or `fun(x, y, p)` if parameters are present. All arguments are ndarray: `x` with shape (m,), `y` with shape (n, m), meaning that `y[:, i]` corresponds to `x[i]`, and `p` with shape (k,). The return value must be an array with shape (n, m) and with the same layout as `y`.

bc [callable] Function evaluating residuals of the boundary conditions. The calling signature is `bc(ya, yb)`, or `bc(ya, yb, p)` if parameters are present. All arguments are ndarray: `ya` and `yb` with shape (n,), and `p` with shape (k,). The return value must be an array with shape (n + k,).

x [array_like, shape (m,)] Initial mesh. Must be a strictly increasing sequence of real numbers with `x[0]=a` and `x[-1]=b`.

y [array_like, shape (n, m)] Initial guess for the function values at the mesh nodes, ith column corresponds to `x[i]`. For problems in a complex domain pass *y* with a complex data type (even if the initial guess is purely real).

p [array_like with shape (k,) or None, optional] Initial guess for the unknown parameters. If None (default), it is assumed that the problem doesn't depend on any parameters.

S [array_like with shape (n, n) or None] Matrix defining the singular term. If None (default), the problem is solved without the singular term.

fun_jac [callable or None, optional] Function computing derivatives of f with respect to y and p. The calling signature is `fun_jac(x, y)`, or `fun_jac(x, y, p)` if parameters are present. The return must contain 1 or 2 elements in the following order:

- df_dy : array_like with shape (n, n, m), where an element (i, j, q) equals to d f_i(x_q, y_q, p) / d (y_q)_j.
- df_dp : array_like with shape (n, k, m), where an element (i, j, q) equals to d f_i(x_q, y_q, p) / d p_j.

Here q numbers nodes at which x and y are defined, whereas i and j number vector components. If the problem is solved without unknown parameters, df_dp should not be returned.
If *fun_jac* is None (default), the derivatives will be estimated by the forward finite differences.

bc_jac [callable or None, optional] Function computing derivatives of bc with respect to ya, yb, and p. The calling signature is `bc_jac(ya, yb)`, or `bc_jac(ya, yb, p)` if parameters are present. The return must contain 2 or 3 elements in the following order:

- dbc_dya : array_like with shape (n, n), where an element (i, j) equals to d bc_i(ya, yb, p) / d ya_j.
- dbc_dyb : array_like with shape (n, n), where an element (i, j) equals to d bc_i(ya, yb, p) / d yb_j.
- dbc_dp : array_like with shape (n, k), where an element (i, j) equals to d bc_i(ya, yb, p) / d p_j.

If the problem is solved without unknown parameters, dbc_dp should not be returned.
If *bc_jac* is None (default), the derivatives will be estimated by the forward finite differences.

tol [float, optional] Desired tolerance of the solution. If we define `r = y' - f(x, y)`, where y is the found solution, then the solver tries to achieve on each mesh interval `norm(r / (1 + abs(f)) < tol`, where `norm` is estimated in a root mean squared sense (using a numerical quadrature formula). Default is 1e-3.

max_nodes

[int, optional] Maximum allowed number of the mesh nodes. If exceeded, the algorithm terminates. Default is 1000.

verbose [{0, 1, 2}, optional] Level of algorithm's verbosity:
- 0 (default) : work silently.
- 1 : display a termination report.
- 2 : display progress during iterations.

bc_tol [float, optional] Desired absolute tolerance for the boundary condition residuals: *bc* value should satisfy `abs(bc) < bc_tol` component-wise. Equals to *tol* by default. Up to 10 iterations are allowed to achieve this tolerance.

Returns

Bunch object with the following fields defined:

sol [PPoly] Found solution for y as *`scipy.interpolate.PPoly`* instance, a C1 continuous cubic spline.

p [ndarray or None, shape (k,)] Found parameters. None, if the parameters were not present in the problem.

x [ndarray, shape (m,)] Nodes of the final mesh.

y [ndarray, shape (n, m)] Solution values at the mesh nodes.

yp [ndarray, shape (n, m)] Solution derivatives at the mesh nodes.

rms_residuals [ndarray, shape (m - 1,)] RMS values of the relative residuals over each mesh interval (see the description of *tol* parameter).

niter [int] Number of completed iterations.

status [int] Reason for algorithm termination:
- 0: The algorithm converged to the desired accuracy.
- 1: The maximum number of mesh nodes is exceeded.
- 2: A singular Jacobian encountered when solving the collocation system.

message [string] Verbal description of the termination reason.

success [bool] True if the algorithm converged to the desired accuracy (`status=0`).

Notes

This function implements a 4th order collocation algorithm with the control of residuals similar to [1]. A collocation system is solved by a damped Newton method with an affine-invariant criterion function as described in [3].

Note that in [1] integral residuals are defined without normalization by interval lengths. So, their definition is different by a multiplier of h**0.5 (h is an interval length) from the definition used here.

New in version 0.18.0.

References

[1], [2], [3], [4]

Examples

In the first example, we solve Bratu's problem:

```
y'' + k * exp(y) = 0
y(0) = y(1) = 0
```

for k = 1.

We rewrite the equation as a first-order system and implement its right-hand side evaluation:

```
y1' = y2
y2' = -exp(y1)
```

```
>>> def fun(x, y):
...     return np.vstack((y[1], -np.exp(y[0])))
```

Implement evaluation of the boundary condition residuals:

```
>>> def bc(ya, yb):
...     return np.array([ya[0], yb[0]])
```

Define the initial mesh with 5 nodes:

```
>>> x = np.linspace(0, 1, 5)
```

This problem is known to have two solutions. To obtain both of them, we use two different initial guesses for y. We denote them by subscripts a and b.

```
>>> y_a = np.zeros((2, x.size))
>>> y_b = np.zeros((2, x.size))
>>> y_b[0] = 3
```

Now we are ready to run the solver.

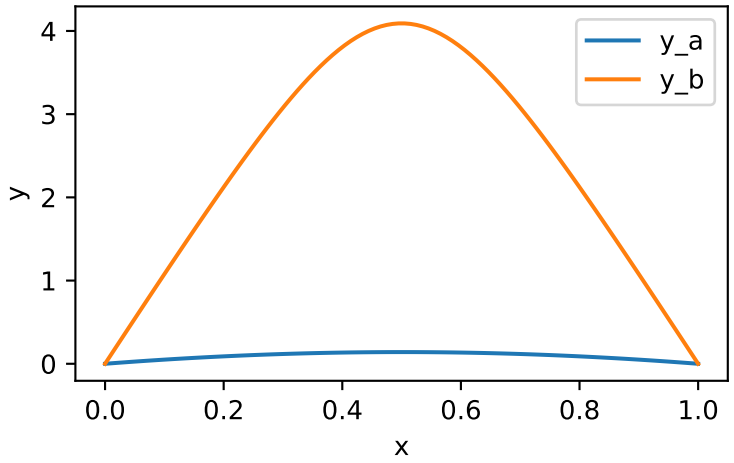
```
>>> from scipy.integrate import solve_bvp
>>> res_a = solve_bvp(fun, bc, x, y_a)
>>> res_b = solve_bvp(fun, bc, x, y_b)
```

Let's plot the two found solutions. We take an advantage of having the solution in a spline form to produce a smooth plot.

```
>>> x_plot = np.linspace(0, 1, 100)
>>> y_plot_a = res_a.sol(x_plot)[0]
>>> y_plot_b = res_b.sol(x_plot)[0]
>>> import matplotlib.pyplot as plt
>>> plt.plot(x_plot, y_plot_a, label='y_a')
>>> plt.plot(x_plot, y_plot_b, label='y_b')
>>> plt.legend()
>>> plt.xlabel("x")
>>> plt.ylabel("y")
>>> plt.show()
```

We see that the two solutions have similar shape, but differ in scale significantly.

In the second example, we solve a simple Sturm-Liouville problem:




```
y'' + k**2 * y = 0
y(0) = y(1) = 0
```

It is known that a non-trivial solution y = A * sin(k * x) is possible for k = pi * n, where n is an integer. To establish the normalization constant A = 1 we add a boundary condition:

```
y'(0) = k
```

Again, we rewrite our equation as a first-order system and implement its right-hand side evaluation:

```
y1' = y2
y2' = -k**2 * y1
```

```
>>> def fun(x, y, p):
...     k = p[0]
...     return np.vstack((y[1], -k**2 * y[0]))
```

Note that parameters p are passed as a vector (with one element in our case).

Implement the boundary conditions:

```
>>> def bc(ya, yb, p):
...     k = p[0]
...     return np.array([ya[0], yb[0], ya[1] - k])
```

Set up the initial mesh and guess for y. We aim to find the solution for k = 2 * pi, to achieve that we set values of y to approximately follow sin(2 * pi * x):

```
>>> x = np.linspace(0, 1, 5)
>>> y = np.zeros((2, x.size))
>>> y[0, 1] = 1
>>> y[0, 3] = -1
```

Run the solver with 6 as an initial guess for k.

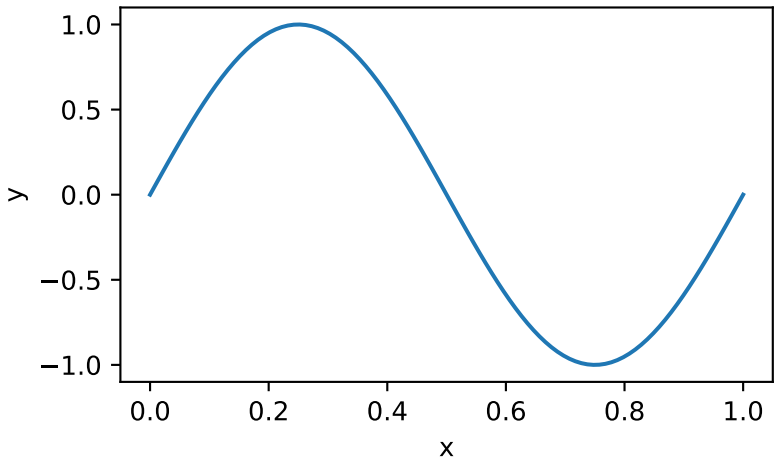
```
>>> sol = solve_bvp(fun, bc, x, y, p=[6])
```

We see that the found k is approximately correct:

```
>>> sol.p[0]
6.28329460046
```

And, finally, plot the solution to see the anticipated sinusoid:

```
>>> x_plot = np.linspace(0, 1, 100)
>>> y_plot = sol.sol(x_plot)[0]
>>> plt.plot(x_plot, y_plot)
>>> plt.xlabel("x")
>>> plt.ylabel("y")
>>> plt.show()
```



3.3.8 Interpolation (`scipy.interpolate`)

Sub-package for objects used in interpolation.

As listed below, this sub-package contains spline functions and classes, 1-D and multidimensional (univariate and multivariate) interpolation classes, Lagrange and Taylor polynomial interpolators, and wrappers for FITPACK and DFITPACK functions.

Univariate interpolation

interp1d(x, y[, kind, axis, copy, …])	Interpolate a 1-D function.
BarycentricInterpolator(xi[, yi, axis])	The interpolating polynomial for a set of points
KroghInterpolator(xi, yi[, axis])	Interpolating polynomial for a set of points.
barycentric_interpolate(xi, yi, x[, axis])	Convenience function for polynomial interpolation.
krogh_interpolate(xi, yi, x[, der, axis])	Convenience function for polynomial interpolation.
pchip_interpolate(xi, yi, x[, der, axis])	Convenience function for pchip interpolation.
CubicHermiteSpline(x, y, dydx[, axis, …])	Piecewise-cubic interpolator matching values and first derivatives.
PchipInterpolator(x, y[, axis, extrapolate])	PCHIP 1-D monotonic cubic interpolation.
Akima1DInterpolator(x, y[, axis])	Akima interpolator
CubicSpline(x, y[, axis, bc_type, extrapolate])	Cubic spline data interpolator.
PPoly(c, x[, extrapolate, axis])	Piecewise polynomial in terms of coefficients and break-points
BPoly(c, x[, extrapolate, axis])	Piecewise polynomial in terms of coefficients and break-points.

scipy.interpolate.interp1d

class scipy.interpolate.**interp1d**(*x*, *y*, *kind='linear'*, *axis=- 1*, *copy=True*, *bounds_error=None*, *fill_value=nan*, *assume_sorted=False*)

Interpolate a 1-D function.

x and *y* are arrays of values used to approximate some function f: `y = f(x)`. This class returns a function whose call method uses interpolation to find the value of new points.

Parameters

x [(N,) array_like] A 1-D array of real values.

y [(…,N,…) array_like] A N-D array of real values. The length of *y* along the interpolation axis must be equal to the length of *x*.

kind [str or int, optional] Specifies the kind of interpolation as a string or as an integer specifying the order of the spline interpolator to use. The string has to be one of 'linear', 'nearest', 'nearest-up', 'zero', 'slinear', 'quadratic', 'cubic', 'previous', or 'next'. 'zero', 'slinear', 'quadratic' and 'cubic' refer to a spline interpolation of zeroth, first, second or third order; 'previous' and 'next' simply return the previous or next value of the point; 'nearest-up' and 'nearest' differ when interpolating half-integers (e.g. 0.5, 1.5) in that 'nearest-up' rounds up and 'nearest' rounds down. Default is 'linear'.

axis [int, optional] Specifies the axis of *y* along which to interpolate. Interpolation defaults to the last axis of *y*.

copy [bool, optional] If True, the class makes internal copies of x and y. If False, references to *x* and *y* are used. The default is to copy.

bounds_error [bool, optional] If True, a ValueError is raised any time interpolation is attempted on a value outside of the range of x (where extrapolation is necessary). If False, out of bounds values are assigned `fill_value`. By default, an error is raised unless `fill_value="extrapolate"`.

fill_value [array-like or (array-like, array_like) or "extrapolate", optional]

- if a ndarray (or float), this value will be used to fill in for requested points outside of the data range. If not provided, then the default is NaN. The array-like must broadcast properly to the dimensions of the non-interpolation axes.
- If a two-element tuple, then the first element is used as a fill value for `x_new < x[0]` and the second element is used for `x_new > x[-1]`. Anything that is not a 2-element tuple

(e.g., list or ndarray, regardless of shape) is taken to be a single array-like argument meant to be used for both bounds as `below, above = fill_value, fill_value`. New in version 0.17.0.

- If "extrapolate", then points outside the data range will be extrapolated. New in version 0.17.0.

assume_sorted
: [bool, optional] If False, values of *x* can be in any order and they are sorted first. If True, *x* has to be an array of monotonically increasing values.

See also:

splrep, **splev**

Spline interpolation/smoothing based on FITPACK.

UnivariateSpline

An object-oriented wrapper of the FITPACK routines.

interp2d

2-D interpolation

Notes

Calling *interp1d* with NaNs present in input values results in undefined behaviour.

Input values *x* and *y* must be convertible to *float* values like *int* or *float*.

If the values in *x* are not unique, the resulting behavior is undefined and specific to the choice of *kind*, i.e., changing *kind* will change the behavior for duplicates.

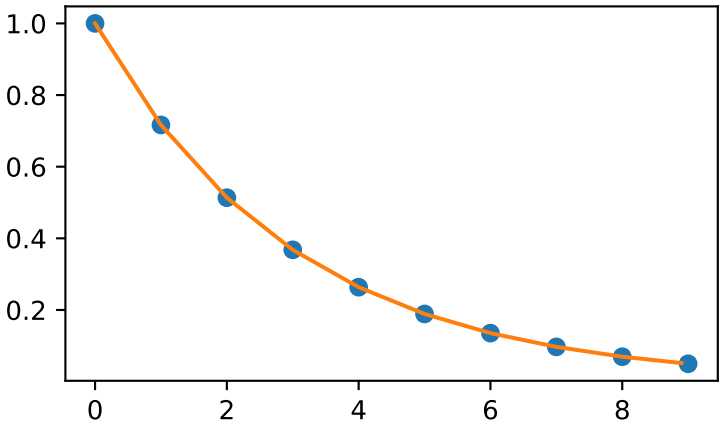
Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy import interpolate
>>> x = np.arange(0, 10)
>>> y = np.exp(-x/3.0)
>>> f = interpolate.interp1d(x, y)
```

```
>>> xnew = np.arange(0, 9, 0.1)
>>> ynew = f(xnew)   # use interpolation function returned by `interp1d`
>>> plt.plot(x, y, 'o', xnew, ynew, '-')
>>> plt.show()
```

Attributes

fill_value
: The fill value.



Methods

`__call__`(x)	Evaluate the interpolant

scipy.interpolate.interp1d.__call__

interp1d.**__call__**(*x*)

Evaluate the interpolant

Parameters

x [array_like] Points to evaluate the interpolant at.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Input values *x* must be convertible to *float* values like *int* or *float*.

scipy.interpolate.BarycentricInterpolator

class scipy.interpolate.**BarycentricInterpolator**(*xi*, *yi=None*, *axis=0*)

The interpolating polynomial for a set of points

Constructs a polynomial that passes through a given set of points. Allows evaluation of the polynomial, efficient changing of the y values to be interpolated, and updating by adding more x values. For reasons of numerical stability, this function does not compute the coefficients of the polynomial.

The values yi need to be provided before the function is evaluated, but none of the preprocessing depends on them, so rapid updates are possible.

Parameters

xi [array_like] 1-D array of x coordinates of the points the polynomial should pass through

yi [array_like, optional] The y coordinates of the points the polynomial should pass through. If None, the y values will be supplied later via the *set_y* method.

axis [int, optional] Axis in the yi array corresponding to the x-coordinate values.

Notes

Methods

__call__(x)	Evaluate the interpolating polynomial at the points x
add_xi(xi[, yi])	Add more x values to the set to be interpolated
set_yi(yi[, axis])	Update the y values to be interpolated

scipy.interpolate.BarycentricInterpolator.__call__

BarycentricInterpolator.**__call__**(*x*)

Evaluate the interpolating polynomial at the points x

Parameters

x [array_like] Points to evaluate the interpolant at.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Currently the code computes an outer product between x and the weights, that is, it constructs an intermediate array of size N by len(x), where N is the degree of the polynomial.

scipy.interpolate.BarycentricInterpolator.add_xi

BarycentricInterpolator.**add_xi**(*xi*, *yi=None*)

Add more x values to the set to be interpolated

The barycentric interpolation algorithm allows easy updating by adding more points for the polynomial to pass through.

Parameters

xi [array_like] The x coordinates of the points that the polynomial should pass through.

yi [array_like, optional] The y coordinates of the points the polynomial should pass through. Should have shape `(xi.size, R)`; if R > 1 then the polynomial is vector-valued. If *yi* is not given, the y values will be supplied later. *yi* should be given if and only if the interpolator has y values specified.

scipy.interpolate.BarycentricInterpolator.set_yi

BarycentricInterpolator.**set_yi**(*yi*, *axis=None*)

Update the y values to be interpolated

The barycentric interpolation algorithm requires the calculation of weights, but these depend only on the xi. The yi can be changed at any time.

Parameters

yi [array_like] The y coordinates of the points the polynomial should pass through. If None, the y values will be supplied later.

axis [int, optional] Axis in the yi array corresponding to the x-coordinate values.

scipy.interpolate.KroghInterpolator

class scipy.interpolate.**KroghInterpolator**(*xi*, *yi*, *axis=0*)

Interpolating polynomial for a set of points.

The polynomial passes through all the pairs (xi,yi). One may additionally specify a number of derivatives at each point xi; this is done by repeating the value xi and specifying the derivatives as successive yi values.

Allows evaluation of the polynomial and all its derivatives. For reasons of numerical stability, this function does not compute the coefficients of the polynomial, although they can be obtained by evaluating all the derivatives.

Parameters

xi	[array_like, length N] Known x-coordinates. Must be sorted in increasing order.
yi	[array_like] Known y-coordinates. When an xi occurs two or more times in a row, the corresponding yi's represent derivative values.
axis	[int, optional] Axis in the yi array corresponding to the x-coordinate values.

Notes

Be aware that the algorithms implemented here are not necessarily the most numerically stable known. Moreover, even in a world of exact computation, unless the x coordinates are chosen very carefully - Chebyshev zeros (e.g., cos(i*pi/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon. In general, even with well-chosen x values, degrees higher than about thirty cause problems with numerical instability in this code.

Based on [1].

References

[1]

Examples

To produce a polynomial that is zero at 0 and 1 and has derivative 2 at 0, call

```
>>> from scipy.interpolate import KroghInterpolator
>>> KroghInterpolator([0,0,1],[0,2,0])
```

This constructs the quadratic 2*X**2-2*X. The derivative condition is indicated by the repeated zero in the xi array; the corresponding yi values are 0, the function value, and 2, the derivative value.

For another example, given xi, yi, and a derivative ypi for each point, appropriate arrays can be constructed as:

```
>>> rng = np.random.default_rng()
>>> xi = np.linspace(0, 1, 5)
>>> yi, ypi = rng.random((2, 5))
>>> xi_k, yi_k = np.repeat(xi, 2), np.ravel(np.dstack((yi,ypi)))
>>> KroghInterpolator(xi_k, yi_k)
```

To produce a vector-valued polynomial, supply a higher-dimensional array for yi:

```
>>> KroghInterpolator([0,1],[[2,3],[4,5]])
```

This constructs a linear polynomial giving (2,3) at 0 and (4,5) at 1.

Attributes

dtype

Methods

__call__(x)	Evaluate the interpolant
derivative(x[, der])	Evaluate one derivative of the polynomial at the point x
derivatives(x[, der])	Evaluate many derivatives of the polynomial at the point x

scipy.interpolate.KroghInterpolator.__call__

KroghInterpolator.**__call__**(*x*)

Evaluate the interpolant

Parameters

x [array_like] Points to evaluate the interpolant at.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Input values *x* must be convertible to *float* values like *int* or *float*.

scipy.interpolate.KroghInterpolator.derivative

KroghInterpolator.**derivative**(*x*, *der=1*)

Evaluate one derivative of the polynomial at the point x

Parameters

x [array_like] Point or points at which to evaluate the derivatives

der [integer, optional] Which derivative to extract. This number includes the function value as 0th derivative.

Returns

d [ndarray] Derivative interpolated at the x-points. Shape of d is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

This is computed by evaluating all derivatives up to the desired one (using self.derivatives()) and then discarding the rest.

scipy.interpolate.KroghInterpolator.derivatives

KroghInterpolator.**derivatives**(*x*, *der=None*)

Evaluate many derivatives of the polynomial at the point x

Produce an array of all derivative values at the point x.

Parameters

x	[array_like] Point or points at which to evaluate the derivatives
der	[int or None, optional] How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points). This number includes the function value as 0th derivative.

Returns

d	[ndarray] Array with derivatives; d[j] contains the jth derivative. Shape of d[j] is determined by replacing the interpolation axis in the original array with the shape of x.

Examples

```
>>> from scipy.interpolate import KroghInterpolator
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives(0)
array([1.0,2.0,3.0])
>>> KroghInterpolator([0,0,0],[1,2,3]).derivatives([0,0])
array([[1.0,1.0],
       [2.0,2.0],
       [3.0,3.0]])
```

scipy.interpolate.barycentric_interpolate

scipy.interpolate.**barycentric_interpolate**(*xi*, *yi*, *x*, *axis=0*)

Convenience function for polynomial interpolation.

Constructs a polynomial that passes through a given set of points, then evaluates the polynomial. For reasons of numerical stability, this function does not compute the coefficients of the polynomial.

This function uses a "barycentric interpolation" method that treats the problem as a special case of rational function interpolation. This algorithm is quite stable, numerically, but even in a world of exact computation, unless the *x* coordinates are chosen very carefully - Chebyshev zeros (e.g., cos(i*pi/n)) are a good choice - polynomial interpolation itself is a very ill-conditioned process due to the Runge phenomenon.

Parameters

xi	[array_like] 1-D array of x coordinates of the points the polynomial should pass through
yi	[array_like] The y coordinates of the points the polynomial should pass through.
x	[scalar or array_like] Points to evaluate the interpolator at.
axis	[int, optional] Axis in the yi array corresponding to the x-coordinate values.

Returns

y [scalar or array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

See also:

BarycentricInterpolator

Bary centric interpolator

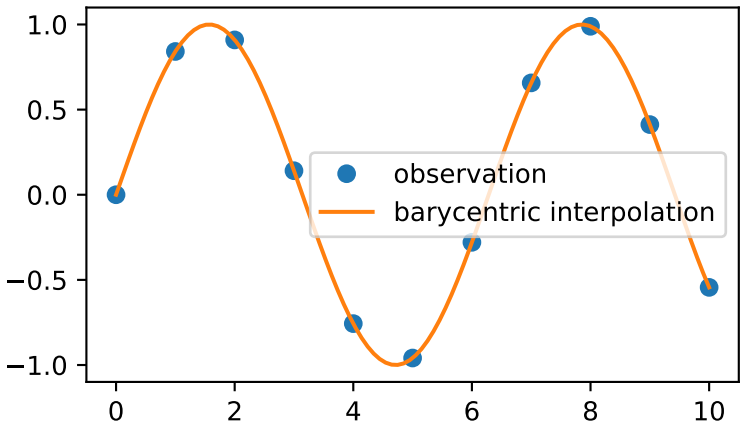
Notes

Construction of the interpolation weights is a relatively slow process. If you want to call this many times with the same xi (but possibly varying yi or x) you should use the class *BarycentricInterpolator*. This is what this function uses internally.

Examples

We can interpolate 2D observed data using barycentric interpolation:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import barycentric_interpolate
>>> x_observed = np.linspace(0.0, 10.0, 11)
>>> y_observed = np.sin(x_observed)
>>> x = np.linspace(min(x_observed), max(x_observed), num=100)
>>> y = barycentric_interpolate(x_observed, y_observed, x)
>>> plt.plot(x_observed, y_observed, "o", label="observation")
>>> plt.plot(x, y, label="barycentric interpolation")
>>> plt.legend()
>>> plt.show()
```



scipy.interpolate.krogh_interpolate

scipy.interpolate.**krogh_interpolate**(*xi*, *yi*, *x*, *der=0*, *axis=0*)

Convenience function for polynomial interpolation.

See *KroghInterpolator* for more details.

Parameters

xi	[array_like] Known x-coordinates.
yi	[array_like] Known y-coordinates, of shape `(xi.size, R)`. Interpreted as vectors of length R, or scalars if R=1.
x	[array_like] Point or points at which to evaluate the derivatives.
der	[int or list, optional] How many derivatives to extract; None for all potentially nonzero derivatives (that is a number equal to the number of points), or a list of derivatives to extract. This number includes the function value as 0th derivative.
axis	[int, optional] Axis in the yi array corresponding to the x-coordinate values.

Returns

d	[ndarray] If the interpolator's values are R-D then the returned array will be the number of derivatives by N by R. If *x* is a scalar, the middle dimension will be dropped; if the *yi* are scalars then the last dimension will be dropped.

See also:

KroghInterpolator

Krogh interpolator

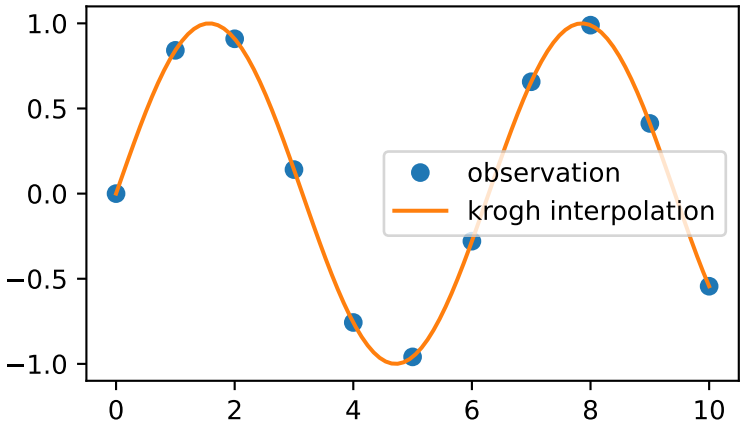
Notes

Construction of the interpolating polynomial is a relatively expensive process. If you want to evaluate it repeatedly consider using the class KroghInterpolator (which is what this function uses).

Examples

We can interpolate 2D observed data using krogh interpolation:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import krogh_interpolate
>>> x_observed = np.linspace(0.0, 10.0, 11)
>>> y_observed = np.sin(x_observed)
>>> x = np.linspace(min(x_observed), max(x_observed), num=100)
>>> y = krogh_interpolate(x_observed, y_observed, x)
>>> plt.plot(x_observed, y_observed, "o", label="observation")
>>> plt.plot(x, y, label="krogh interpolation")
>>> plt.legend()
>>> plt.show()
```



scipy.interpolate.pchip_interpolate

`scipy.interpolate.`**`pchip_interpolate`**(*xi*, *yi*, *x*, *der=0*, *axis=0*)

Convenience function for pchip interpolation.

xi and yi are arrays of values used to approximate some function f, with `yi = f(xi)`. The interpolant uses monotonic cubic splines to find the value of new points x and the derivatives there.

See *`scipy.interpolate.PchipInterpolator`* for details.

Parameters

xi	[array_like] A sorted list of x-coordinates, of length N.
yi	[array_like] A 1-D array of real values. *yi*'s length along the interpolation axis must be equal to the length of *xi*. If N-D array, use axis parameter to select correct axis.
x	[scalar or array_like] Of length M.
der	[int or list, optional] Derivatives to extract. The 0th derivative can be included to return the function value.
axis	[int, optional] Axis in the yi array corresponding to the x-coordinate values.

Returns

y	[scalar or array_like] The result, of length R or length M or M by R,

See also:

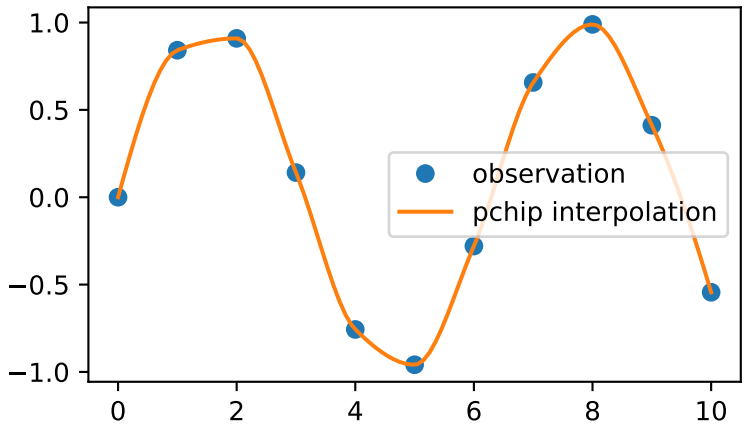
`PchipInterpolator`

PCHIP 1-D monotonic cubic interpolator.

Examples

We can interpolate 2D observed data using pchip interpolation:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import pchip_interpolate
>>> x_observed = np.linspace(0.0, 10.0, 11)
>>> y_observed = np.sin(x_observed)
>>> x = np.linspace(min(x_observed), max(x_observed), num=100)
>>> y = pchip_interpolate(x_observed, y_observed, x)
>>> plt.plot(x_observed, y_observed, "o", label="observation")
>>> plt.plot(x, y, label="pchip interpolation")
>>> plt.legend()
>>> plt.show()
```



scipy.interpolate.CubicHermiteSpline

class scipy.interpolate.**CubicHermiteSpline**(*x*, *y*, *dydx*, *axis=0*, *extrapolate=None*)

Piecewise-cubic interpolator matching values and first derivatives.

The result is represented as a *PPoly* instance.

Parameters

x [array_like, shape (n,)] 1-D array containing values of the independent variable. Values must be real, finite and in strictly increasing order.

y [array_like] Array containing values of the dependent variable. It can have arbitrary number of dimensions, but the length along `axis` (see below) must match the length of `x`. Values must be finite.

dydx [array_like] Array containing derivatives of the dependent variable. It can have arbitrary number of dimensions, but the length along `axis` (see below) must match the length of `x`. Values must be finite.

axis [int, optional] Axis along which *y* is assumed to be varying. Meaning that for `x[i]` the corresponding values are `np.take(y, i, axis=axis)`. Default is 0.

extrapolate

[{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), it is set to True.

See also:

Akima1DInterpolator

Akima 1D interpolator.

PchipInterpolator

PCHIP 1-D monotonic cubic interpolator.

CubicSpline

Cubic spline data interpolator.

PPoly

Piecewise polynomial in terms of coefficients and breakpoints

Notes

If you want to create a higher-order spline matching higher-order derivatives, use *BPoly.from_derivatives*.

References

[1]

Attributes

x [ndarray, shape (n,)] Breakpoints. The same `x` which was passed to the constructor.

c [ndarray, shape (4, n-1, ...)] Coefficients of the polynomials on each segment. The trailing dimensions match the dimensions of *y*, excluding `axis`. For example, if *y* is 1-D, then `c[k, i]` is a coefficient for `(x-x[i])**(3-k)` on the segment between `x[i]` and `x[i+1]`.

axis [int] Interpolation axis. The same axis which was passed to the constructor.

Methods

__call__(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative.
derivative([nu])	Construct a new piecewise polynomial representing the derivative.
antiderivative([nu])	Construct a new piecewise polynomial representing the antiderivative.
integrate(a, b[, extrapolate])	Compute a definite integral over a piecewise polynomial.
roots([discontinuity, extrapolate])	Find real roots of the the piecewise polynomial.

scipy.interpolate.CubicHermiteSpline.__call__

CubicHermiteSpline.**__call__**(*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative.

Parameters

x [array_like] Points to evaluate the interpolant at.

nu [int, optional] Order of derivative to evaluate. Must be non-negative.

extrapolate [{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.CubicHermiteSpline.derivative

CubicHermiteSpline.**derivative**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu [int, optional] Order of derivative to evaluate. Default is 1, i.e., compute the first derivative. If negative, the antiderivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.CubicHermiteSpline.antiderivative

CubicHermiteSpline.**antiderivative**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters

nu [int, optional] Order of antiderivative to evaluate. Default is 1, i.e., compute the first integral. If negative, the derivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

scipy.interpolate.CubicHermiteSpline.integrate

CubicHermiteSpline.**integrate**(*a*, *b*, *extrapolate=None*)

Compute a definite integral over a piecewise polynomial.

Parameters

a [float] Lower integration bound

b [float] Upper integration bound

extrapolate

[{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

ig [array_like] Definite integral of the piecewise polynomial over [a, b]

scipy.interpolate.CubicHermiteSpline.roots

CubicHermiteSpline.**roots**(*discontinuity=True*, *extrapolate=None*)

Find real roots of the the piecewise polynomial.

Parameters

discontinuity

[bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.

extrapolate
[{bool, 'periodic', None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, 'periodic' works the same as False. If None (default), use *self.extrapolate*.

Returns

roots [ndarray] Roots of the polynomial(s).
If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

See also:

`PPoly.solve`

scipy.interpolate.PchipInterpolator

class scipy.interpolate.**PchipInterpolator**(*x*, *y*, *axis=0*, *extrapolate=None*)
PCHIP 1-D monotonic cubic interpolation.

`x` and `y` are arrays of values used to approximate some function f, with `y = f(x)`. The interpolant uses monotonic cubic splines to find the value of new points. (PCHIP stands for Piecewise Cubic Hermite Interpolating Polynomial).

Parameters

x [ndarray] A 1-D array of monotonically increasing real values. `x` cannot include duplicate values (otherwise f is overspecified)
y [ndarray] A 1-D array of real values. `y`'s length along the interpolation axis must be equal to the length of `x`. If N-D array, use `axis` parameter to select correct axis.
axis [int, optional] Axis in the y array corresponding to the x-coordinate values.
extrapolate
[bool, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs.

See also:

`CubicHermiteSpline`

Piecewise-cubic interpolator.

`Akima1DInterpolator`

Akima 1D interpolator.

`CubicSpline`

Cubic spline data interpolator.

`PPoly`

Piecewise polynomial in terms of coefficients and breakpoints.

Notes

The interpolator preserves monotonicity in the interpolation data and does not overshoot if the data is not smooth.

The first derivatives are guaranteed to be continuous, but the second derivatives may jump at x_k.

Determines the derivatives at the points x_k, f'_k, by using PCHIP algorithm [1].

Let $h_k = x_{k+1} - x_k$, and $d_k = (y_{k+1} - y_k)/h_k$ are the slopes at internal points x_k. If the signs of d_k and d_{k-1} are different or either of them equals zero, then $f'_k = 0$. Otherwise, it is given by the weighted harmonic mean

$$\frac{w_1 + w_2}{f'_k} = \frac{w_1}{d_{k-1}} + \frac{w_2}{d_k}$$

where $w_1 = 2h_k + h_{k-1}$ and $w_2 = h_k + 2h_{k-1}$.

The end slopes are set using a one-sided scheme [2].

References

[1], [2]

Attributes

axis
c
extrapolate
x

Methods

__call__(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative.
derivative([nu])	Construct a new piecewise polynomial representing the derivative.
antiderivative([nu])	Construct a new piecewise polynomial representing the antiderivative.
roots([discontinuity, extrapolate])	Find real roots of the the piecewise polynomial.

scipy.interpolate.PchipInterpolator.__call__

PchipInterpolator.**__call__**(*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative.

Parameters

x [array_like] Points to evaluate the interpolant at.
nu [int, optional] Order of derivative to evaluate. Must be non-negative.
extrapolate [{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.PchipInterpolator.derivative

`PchipInterpolator.`**`derivative`**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu [int, optional] Order of derivative to evaluate. Default is 1, i.e., compute the first derivative. If negative, the antiderivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.PchipInterpolator.antiderivative

`PchipInterpolator.`**`antiderivative`**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters

nu [int, optional] Order of antiderivative to evaluate. Default is 1, i.e., compute the first integral. If negative, the derivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

scipy.interpolate.PchipInterpolator.roots

`PchipInterpolator.`**`roots`**(*discontinuity=True*, *extrapolate=None*)

Find real roots of the the piecewise polynomial.

Parameters

discontinuity
: [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.

extrapolate
: [{bool, 'periodic', None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, 'periodic' works the same as False. If None (default), use *self.extrapolate*.

Returns

roots
: [ndarray] Roots of the polynomial(s).
If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

See also:

`PPoly.solve`

scipy.interpolate.Akima1DInterpolator

`class` `scipy.interpolate.`**`Akima1DInterpolator`**(*x*, *y*, *axis=0*)

Akima interpolator

Fit piecewise cubic polynomials, given vectors x and y. The interpolation method by Akima uses a continuously differentiable sub-spline built from piecewise cubic polynomials. The resultant curve passes through the given data points and will appear smooth and natural.

Parameters

x
: [ndarray, shape (m,)] 1-D array of monotonically increasing real values.

y
: [ndarray, shape (m, …)] N-D array of real values. The length of `y` along the first axis must be equal to the length of `x`.

axis
: [int, optional] Specifies the axis of `y` along which to interpolate. Interpolation defaults to the first axis of `y`.

See also:

`PchipInterpolator`

PCHIP 1-D monotonic cubic interpolator.

`CubicSpline`

Cubic spline data interpolator.

`PPoly`

Piecewise polynomial in terms of coefficients and breakpoints

Notes

New in version 0.14.

Use only for precise data, as the fitted curve passes through the given points exactly. This routine is useful for plotting a pleasingly smooth curve through a few given points for purposes of plotting.

References

[1] A new method of interpolation and smooth curve fitting based

on local procedures. Hiroshi Akima, J. ACM, October 1970, 17(4), 589-602.

Attributes

axis
c
extrapolate
x

Methods

`__call__`(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative.
`derivative`([nu])	Construct a new piecewise polynomial representing the derivative.
`antiderivative`([nu])	Construct a new piecewise polynomial representing the antiderivative.
`roots`([discontinuity, extrapolate])	Find real roots of the the piecewise polynomial.

scipy.interpolate.Akima1DInterpolator.__call__

`Akima1DInterpolator.__call__` (*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative.

Parameters

x [array_like] Points to evaluate the interpolant at.
nu [int, optional] Order of derivative to evaluate. Must be non-negative.
extrapolate [{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.Akima1DInterpolator.derivative

`Akima1DInterpolator.`**`derivative`**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu [int, optional] Order of derivative to evaluate. Default is 1, i.e., compute the first derivative. If negative, the antiderivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.Akima1DInterpolator.antiderivative

`Akima1DInterpolator.`**`antiderivative`**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters

nu [int, optional] Order of antiderivative to evaluate. Default is 1, i.e., compute the first integral. If negative, the derivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

scipy.interpolate.Akima1DInterpolator.roots

Akima1DInterpolator.**roots**(*discontinuity=True*, *extrapolate=None*)

Find real roots of the the piecewise polynomial.

Parameters

discontinuity
: [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.

extrapolate
: [{bool, 'periodic', None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, 'periodic' works the same as False. If None (default), use *self.extrapolate*.

Returns

roots
: [ndarray] Roots of the polynomial(s).
If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

See also:

`PPoly.solve`

scipy.interpolate.CubicSpline

class scipy.interpolate.**CubicSpline**(*x*, *y*, *axis=0*, *bc_type='not-a-knot'*, *extrapolate=None*)

Cubic spline data interpolator.

Interpolate data with a piecewise cubic polynomial which is twice continuously differentiable [1]. The result is represented as a *PPoly* instance with breakpoints matching the given data.

Parameters

x
: [array_like, shape (n,)] 1-D array containing values of the independent variable. Values must be real, finite and in strictly increasing order.

y
: [array_like] Array containing values of the dependent variable. It can have arbitrary number of dimensions, but the length along `axis` (see below) must match the length of `x`. Values must be finite.

axis
: [int, optional] Axis along which *y* is assumed to be varying. Meaning that for `x[i]` the corresponding values are `np.take(y, i, axis=axis)`. Default is 0.

bc_type
: [string or 2-tuple, optional] Boundary condition type. Two additional equations, given by the boundary conditions, are required to determine all coefficients of polynomials on each segment [2].
If *bc_type* is a string, then the specified condition will be applied at both ends of a spline. Available conditions are:
- 'not-a-knot' (default): The first and second segment at a curve end are the same polynomial. It is a good default when there is no information on boundary conditions.
- 'periodic': The interpolated functions is assumed to be periodic of period `x[-1] - x[0]`. The first and last value of *y* must be identical: `y[0] == y[-1]`. This boundary condition will result in `y'[0] == y'[-1]` and `y''[0] == y''[-1]`.
- 'clamped': The first derivative at curves ends are zero. Assuming a 1D *y*, `bc_type=((1, 0.0), (1, 0.0))` is the same condition.
- 'natural': The second derivative at curve ends are zero. Assuming a 1D *y*, `bc_type=((2, 0.0), (2, 0.0))` is the same condition.

If *bc_type* is a 2-tuple, the first and the second value will be applied at the curve start and end respectively. The tuple values can be one of the previously mentioned strings (except 'periodic') or a tuple *(order, deriv_values)* allowing to specify arbitrary derivatives at curve ends:

- *order*: the derivative order, 1 or 2.
- *deriv_value*: array_like containing derivative values, shape must be the same as *y*, excluding `axis` dimension. For example, if *y* is 1-D, then *deriv_value* must be a scalar. If *y* is 3-D with the shape (n0, n1, n2) and axis=2, then *deriv_value* must be 2-D and have the shape (n0, n1).

extrapolate

[{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), `extrapolate` is set to 'periodic' for `bc_type='periodic'` and to True otherwise.

See also:

Akima1DInterpolator

Akima 1D interpolator.

PchipInterpolator

PCHIP 1-D monotonic cubic interpolator.

PPoly

Piecewise polynomial in terms of coefficients and breakpoints.

Notes

Parameters *bc_type* and `interpolate` work independently, i.e. the former controls only construction of a spline, and the latter only evaluation.

When a boundary condition is 'not-a-knot' and n = 2, it is replaced by a condition that the first derivative is equal to the linear interpolant slope. When both boundary conditions are 'not-a-knot' and n = 3, the solution is sought as a parabola passing through given points.

When 'not-a-knot' boundary conditions is applied to both ends, the resulting spline will be the same as returned by *splrep* (with `s=0`) and *InterpolatedUnivariateSpline*, but these two methods use a representation in B-spline basis.

New in version 0.18.0.

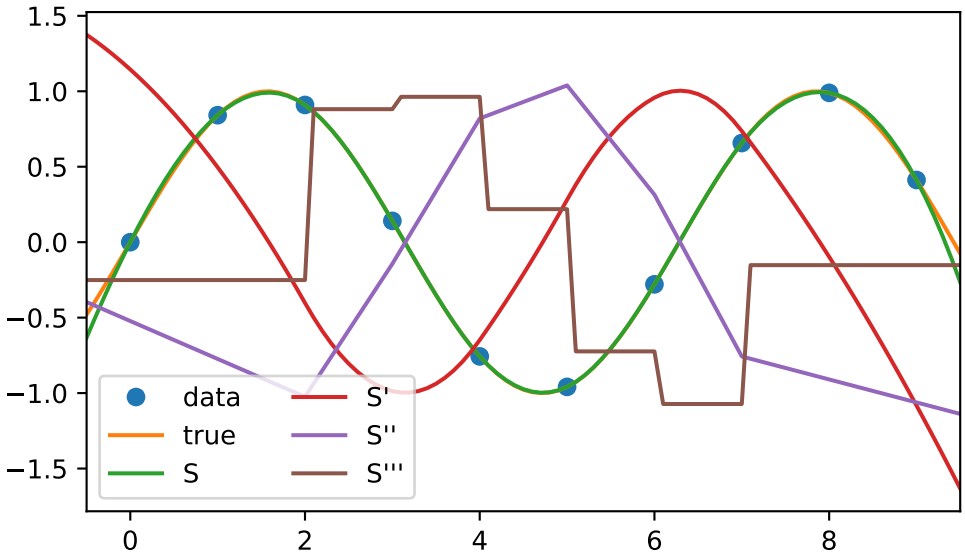
References

[1], [2]

Examples

In this example the cubic spline is used to interpolate a sampled sinusoid. You can see that the spline continuity property holds for the first and second derivatives and violates only for the third derivative.

```
>>> from scipy.interpolate import CubicSpline
>>> import matplotlib.pyplot as plt
>>> x = np.arange(10)
>>> y = np.sin(x)
>>> cs = CubicSpline(x, y)
>>> xs = np.arange(-0.5, 9.6, 0.1)
>>> fig, ax = plt.subplots(figsize=(6.5, 4))
>>> ax.plot(x, y, 'o', label='data')
>>> ax.plot(xs, np.sin(xs), label='true')
>>> ax.plot(xs, cs(xs), label="S")
>>> ax.plot(xs, cs(xs, 1), label="S'")
>>> ax.plot(xs, cs(xs, 2), label="S''")
>>> ax.plot(xs, cs(xs, 3), label="S'''")
>>> ax.set_xlim(-0.5, 9.5)
>>> ax.legend(loc='lower left', ncol=2)
>>> plt.show()
```



In the second example, the unit circle is interpolated with a spline. A periodic boundary condition is used. You can see that the first derivative values, ds/dx=0, ds/dy=1 at the periodic point (1, 0) are correctly computed. Note that a circle cannot be exactly represented by a cubic spline. To increase precision, more breakpoints would be required.

```
>>> theta = 2 * np.pi * np.linspace(0, 1, 5)
>>> y = np.c_[np.cos(theta), np.sin(theta)]
```

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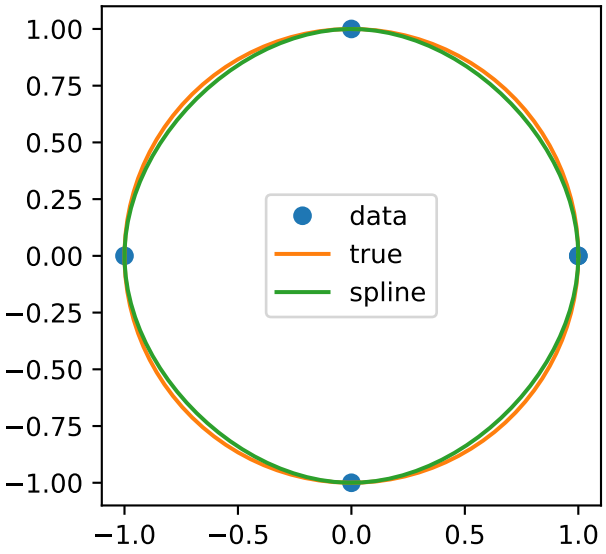
```
>>> cs = CubicSpline(theta, y, bc_type='periodic')
>>> print("ds/dx={:.1f} ds/dy={:.1f}".format(cs(0, 1)[0], cs(0, 1)[1]))
ds/dx=0.0 ds/dy=1.0
>>> xs = 2 * np.pi * np.linspace(0, 1, 100)
>>> fig, ax = plt.subplots(figsize=(6.5, 4))
>>> ax.plot(y[:, 0], y[:, 1], 'o', label='data')
>>> ax.plot(np.cos(xs), np.sin(xs), label='true')
>>> ax.plot(cs(xs)[:, 0], cs(xs)[:, 1], label='spline')
>>> ax.axes.set_aspect('equal')
>>> ax.legend(loc='center')
>>> plt.show()
```



The third example is the interpolation of a polynomial y = x**3 on the interval 0 <= x<= 1. A cubic spline can represent this function exactly. To achieve that we need to specify values and first derivatives at endpoints of the interval. Note that y' = 3 * x**2 and thus y'(0) = 0 and y'(1) = 3.

```
>>> cs = CubicSpline([0, 1], [0, 1], bc_type=((1, 0), (1, 3)))
>>> x = np.linspace(0, 1)
>>> np.allclose(x**3, cs(x))
True
```

Attributes

x	[ndarray, shape (n,)] Breakpoints. The same `x` which was passed to the constructor.
c	[ndarray, shape (4, n-1, …)] Coefficients of the polynomials on each segment. The trailing dimensions match the dimensions of *y*, excluding `axis`. For example, if *y* is 1-d, then `c[k, i]` is a coefficient for `(x-x[i])**(3-k)` on the segment between `x[i]` and `x[i+1]`.

axis [int] Interpolation axis. The same axis which was passed to the constructor.

Methods

`__call__`(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative.
`derivative`([nu])	Construct a new piecewise polynomial representing the derivative.
`antiderivative`([nu])	Construct a new piecewise polynomial representing the antiderivative.
`integrate`(a, b[, extrapolate])	Compute a definite integral over a piecewise polynomial.
`roots`([discontinuity, extrapolate])	Find real roots of the the piecewise polynomial.

scipy.interpolate.CubicSpline.__call__

CubicSpline.**__call__**(*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative.

Parameters

x [array_like] Points to evaluate the interpolant at.

nu [int, optional] Order of derivative to evaluate. Must be non-negative.

extrapolate

[{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.CubicSpline.derivative

CubicSpline.**derivative**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu [int, optional] Order of derivative to evaluate. Default is 1, i.e., compute the first derivative. If negative, the antiderivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.CubicSpline.antiderivative

`CubicSpline.`**`antiderivative`**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters

nu [int, optional] Order of antiderivative to evaluate. Default is 1, i.e., compute the first integral. If negative, the derivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

scipy.interpolate.CubicSpline.integrate

`CubicSpline.`**`integrate`**(*a*, *b*, *extrapolate=None*)

Compute a definite integral over a piecewise polynomial.

Parameters

a [float] Lower integration bound

b [float] Upper integration bound

extrapolate [{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

ig [array_like] Definite integral of the piecewise polynomial over [a, b]

scipy.interpolate.CubicSpline.roots

CubicSpline.**roots**(*discontinuity=True*, *extrapolate=None*)

Find real roots of the the piecewise polynomial.

Parameters

discontinuity
: [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.

extrapolate
: [{bool, 'periodic', None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, 'periodic' works the same as False. If None (default), use *self.extrapolate*.

Returns

roots
: [ndarray] Roots of the polynomial(s).
If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

See also:

PPoly.solve

scipy.interpolate.PPoly

class scipy.interpolate.**PPoly**(*c*, *x*, *extrapolate=None*, *axis=0*)

Piecewise polynomial in terms of coefficients and breakpoints

The polynomial between `x[i]` and `x[i + 1]` is written in the local power basis:

```
S = sum(c[m, i] * (xp - x[i])**(k-m) for m in range(k+1))
```

where `k` is the degree of the polynomial.

Parameters

c
: [ndarray, shape (k, m, …)] Polynomial coefficients, order *k* and *m* intervals.

x
: [ndarray, shape (m+1,)] Polynomial breakpoints. Must be sorted in either increasing or decreasing order.

extrapolate
: [bool or 'periodic', optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. Default is True.

axis
: [int, optional] Interpolation axis. Default is zero.

See also:

BPoly

piecewise polynomials in the Bernstein basis

Notes

High-order polynomials in the power basis can be numerically unstable. Precision problems can start to appear for orders larger than 20-30.

Attributes

x	[ndarray] Breakpoints.
c	[ndarray] Coefficients of the polynomials. They are reshaped to a 3-D array with the last dimension representing the trailing dimensions of the original coefficient array.
axis	[int] Interpolation axis.

Methods

__call__(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative.
derivative([nu])	Construct a new piecewise polynomial representing the derivative.
antiderivative([nu])	Construct a new piecewise polynomial representing the antiderivative.
integrate(a, b[, extrapolate])	Compute a definite integral over a piecewise polynomial.
solve([y, discontinuity, extrapolate])	Find real solutions of the the equation `pp(x) == y`.
roots([discontinuity, extrapolate])	Find real roots of the the piecewise polynomial.
extend(c, x[, right])	Add additional breakpoints and coefficients to the polynomial.
from_spline(tck[, extrapolate])	Construct a piecewise polynomial from a spline
from_bernstein_basis(bp[, extrapolate])	Construct a piecewise polynomial in the power basis from a polynomial in Bernstein basis.
construct_fast(c, x[, extrapolate, axis])	Construct the piecewise polynomial without making checks.

scipy.interpolate.PPoly.__call__

PPoly.**__call__**(*x*, *nu=0*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative.

Parameters

x	[array_like] Points to evaluate the interpolant at.
nu	[int, optional] Order of derivative to evaluate. Must be non-negative.
extrapolate	[{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

y	[array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.PPoly.derivative

`PPoly.`**`derivative`**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu [int, optional] Order of derivative to evaluate. Default is 1, i.e., compute the first derivative. If negative, the antiderivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k - n representing the derivative of this polynomial.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.PPoly.antiderivative

`PPoly.`**`antiderivative`**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters

nu [int, optional] Order of antiderivative to evaluate. Default is 1, i.e., compute the first integral. If negative, the derivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

scipy.interpolate.PPoly.integrate

PPoly.**integrate**(*a*, *b*, *extrapolate=None*)

Compute a definite integral over a piecewise polynomial.

Parameters

a [float] Lower integration bound

b [float] Upper integration bound

extrapolate [{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

ig [array_like] Definite integral of the piecewise polynomial over [a, b]

scipy.interpolate.PPoly.solve

PPoly.**solve**(*y=0.0*, *discontinuity=True*, *extrapolate=None*)

Find real solutions of the the equation `pp(x) == y`.

Parameters

y [float, optional] Right-hand side. Default is zero.

discontinuity [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.

extrapolate [{bool, 'periodic', None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, 'periodic' works the same as False. If None (default), use *self.extrapolate*.

Returns

roots [ndarray] Roots of the polynomial(s).
If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

Notes

This routine works only on real-valued polynomials.

If the piecewise polynomial contains sections that are identically zero, the root list will contain the start point of the corresponding interval, followed by a `nan` value.

If the polynomial is discontinuous across a breakpoint, and there is a sign change across the breakpoint, this is reported if the *discont* parameter is True.

Examples

Finding roots of `[x**2 - 1, (x - 1)**2]` defined on intervals `[-2, 1], [1, 2]`:

```
>>> from scipy.interpolate import PPoly
>>> pp = PPoly(np.array([[1, -4, 3], [1, 0, 0]]).T, [-2, 1, 2])
>>> pp.solve()
array([-1.,  1.])
```

scipy.interpolate.PPoly.roots

`PPoly.`**`roots`**(*discontinuity=True*, *extrapolate=None*)

Find real roots of the the piecewise polynomial.

Parameters

discontinuity
: [bool, optional] Whether to report sign changes across discontinuities at breakpoints as roots.

extrapolate
: [{bool, 'periodic', None}, optional] If bool, determines whether to return roots from the polynomial extrapolated based on first and last intervals, 'periodic' works the same as False. If None (default), use *self.extrapolate*.

Returns

roots
: [ndarray] Roots of the polynomial(s).
If the PPoly object describes multiple polynomials, the return value is an object array whose each element is an ndarray containing the roots.

See also:

`PPoly.solve`

scipy.interpolate.PPoly.extend

`PPoly.`**`extend`**(*c*, *x*, *right=None*)

Add additional breakpoints and coefficients to the polynomial.

Parameters

c
: [ndarray, size (k, m, …)] Additional coefficients for polynomials in intervals. Note that the first additional interval will be formed using one of the `self.x` end points.

x
: [ndarray, size (m,)] Additional breakpoints. Must be sorted in the same order as `self.x` and either to the right or to the left of the current breakpoints.

right
: Deprecated argument. Has no effect.
Deprecated since version 0.19.

scipy.interpolate.PPoly.from_spline

classmethod PPoly.**from_spline**(*tck*, *extrapolate=None*)
Construct a piecewise polynomial from a spline

Parameters

tck A spline, as returned by *splrep* or a BSpline object.

extrapolate [bool or 'periodic', optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. Default is True.

scipy.interpolate.PPoly.from_bernstein_basis

classmethod PPoly.**from_bernstein_basis**(*bp*, *extrapolate=None*)
Construct a piecewise polynomial in the power basis from a polynomial in Bernstein basis.

Parameters

bp [BPoly] A Bernstein basis polynomial, as created by BPoly

extrapolate [bool or 'periodic', optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. Default is True.

scipy.interpolate.PPoly.construct_fast

classmethod PPoly.**construct_fast**(*c*, *x*, *extrapolate=None*, *axis=0*)
Construct the piecewise polynomial without making checks.

Takes the same parameters as the constructor. Input arguments `c` and `x` must be arrays of the correct shape and type. The `c` array can only be of dtypes float and complex, and `x` array must have dtype float.

scipy.interpolate.BPoly

class scipy.interpolate.**BPoly**(*c*, *x*, *extrapolate=None*, *axis=0*)
Piecewise polynomial in terms of coefficients and breakpoints.

The polynomial between `x[i]` and `x[i + 1]` is written in the Bernstein polynomial basis:

```
S = sum(c[a, i] * b(a, k; x) for a in range(k+1)),
```

where `k` is the degree of the polynomial, and:

```
b(a, k; x) = binom(k, a) * t**a * (1 - t)**(k - a),
```

with `t = (x - x[i]) / (x[i+1] - x[i])` and `binom` is the binomial coefficient.

Parameters

c [ndarray, shape (k, m, …)] Polynomial coefficients, order *k* and *m* intervals

x [ndarray, shape (m+1,)] Polynomial breakpoints. Must be sorted in either increasing or decreasing order.

extrapolate
: [bool, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. Default is True.

axis
: [int, optional] Interpolation axis. Default is zero.

See also:

`PPoly`

piecewise polynomials in the power basis

Notes

Properties of Bernstein polynomials are well documented in the literature, see for example [1] [2] [3].

References

[1], [2], [3]

Examples

```
>>> from scipy.interpolate import BPoly
>>> x = [0, 1]
>>> c = [[1], [2], [3]]
>>> bp = BPoly(c, x)
```

This creates a 2nd order polynomial

$$B(x) = 1 \times b_{0,2}(x) + 2 \times b_{1,2}(x) + 3 \times b_{2,2}(x)$$
$$= 1 \times (1-x)^2 + 2 \times 2x(1-x) + 3 \times x^2$$

Attributes

x
: [ndarray] Breakpoints.

c
: [ndarray] Coefficients of the polynomials. They are reshaped to a 3-D array with the last dimension representing the trailing dimensions of the original coefficient array.

axis
: [int] Interpolation axis.

Methods

__call__(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative.
extend(c, x[, right])	Add additional breakpoints and coefficients to the polynomial.
derivative([nu])	Construct a new piecewise polynomial representing the derivative.
antiderivative([nu])	Construct a new piecewise polynomial representing the antiderivative.
integrate(a, b[, extrapolate])	Compute a definite integral over a piecewise polynomial.

continues on next page

Table 50 – continued from previous page

construct_fast(c, x[, extrapolate, axis])	Construct the piecewise polynomial without making checks.
from_power_basis(pp[, extrapolate])	Construct a piecewise polynomial in Bernstein basis from a power basis polynomial.
from_derivatives(xi, yi[, orders, extrapolate])	Construct a piecewise polynomial in the Bernstein basis, compatible with the specified values and derivatives at breakpoints.

scipy.interpolate.BPoly.__call__

BPoly.**__call__**(*x*, *nu=0*, *extrapolate=None*)
Evaluate the piecewise polynomial or its derivative.

Parameters

x [array_like] Points to evaluate the interpolant at.
nu [int, optional] Order of derivative to evaluate. Must be non-negative.
extrapolate [{bool, 'periodic', None}, optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

y [array_like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.BPoly.extend

BPoly.**extend**(*c*, *x*, *right=None*)
Add additional breakpoints and coefficients to the polynomial.

Parameters

c [ndarray, size (k, m, …)] Additional coefficients for polynomials in intervals. Note that the first additional interval will be formed using one of the `self.x` end points.
x [ndarray, size (m,)] Additional breakpoints. Must be sorted in the same order as `self.x` and either to the right or to the left of the current breakpoints.
right Deprecated argument. Has no effect.
Deprecated since version 0.19.

scipy.interpolate.BPoly.derivative

BPoly.**derivative**(*nu=1*)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu [int, optional] Order of derivative to evaluate. Default is 1, i.e., compute the first derivative. If negative, the antiderivative is returned.

Returns

bp [BPoly] Piecewise polynomial of order k - nu representing the derivative of this polynomial.

scipy.interpolate.BPoly.antiderivative

BPoly.**antiderivative**(*nu=1*)

Construct a new piecewise polynomial representing the antiderivative.

Parameters

nu [int, optional] Order of antiderivative to evaluate. Default is 1, i.e., compute the first integral. If negative, the derivative is returned.

Returns

bp [BPoly] Piecewise polynomial of order k + nu representing the antiderivative of this polynomial.

Notes

If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

scipy.interpolate.BPoly.integrate

BPoly.**integrate**(*a*, *b*, *extrapolate=None*)

Compute a definite integral over a piecewise polynomial.

Parameters

a [float] Lower integration bound

b [float] Upper integration bound

extrapolate

[{bool, 'periodic', None}, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

array_like Definite integral of the piecewise polynomial over [a, b]

scipy.interpolate.BPoly.construct_fast

classmethod BPoly.**construct_fast**(*c*, *x*, *extrapolate=None*, *axis=0*)
Construct the piecewise polynomial without making checks.

Takes the same parameters as the constructor. Input arguments `c` and `x` must be arrays of the correct shape and type. The `c` array can only be of dtypes float and complex, and `x` array must have dtype float.

scipy.interpolate.BPoly.from_power_basis

classmethod BPoly.**from_power_basis**(*pp*, *extrapolate=None*)
Construct a piecewise polynomial in Bernstein basis from a power basis polynomial.

Parameters

pp [PPoly] A piecewise polynomial in the power basis

extrapolate
[bool or 'periodic', optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. Default is True.

scipy.interpolate.BPoly.from_derivatives

classmethod BPoly.**from_derivatives**(*xi*, *yi*, *orders=None*, *extrapolate=None*)
Construct a piecewise polynomial in the Bernstein basis, compatible with the specified values and derivatives at breakpoints.

Parameters

xi [array_like] sorted 1-D array of x-coordinates

yi [array_like or list of array_likes] `yi[i][j]` is the `j``th derivative known at ``xi[i]`

orders [None or int or array_like of ints. Default: None.] Specifies the degree of local polynomials. If not None, some derivatives are ignored.

extrapolate
[bool or 'periodic', optional] If bool, determines whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. If 'periodic', periodic extrapolation is used. Default is True.

Notes

If `k` derivatives are specified at a breakpoint `x`, the constructed polynomial is exactly `k` times continuously differentiable at `x`, unless the `order` is provided explicitly. In the latter case, the smoothness of the polynomial at the breakpoint is controlled by the `order`.

Deduces the number of derivatives to match at each end from `order` and the number of derivatives available. If possible it uses the same number of derivatives from each end; if the number is odd it tries to take the extra one from y2. In any case if not enough derivatives are available at one end or another it draws enough to make up the total from the other end.

If the order is too high and not enough derivatives are available, an exception is raised.

Examples

```
>>> from scipy.interpolate import BPoly
>>> BPoly.from_derivatives([0, 1], [[1, 2], [3, 4]])
```

Creates a polynomial *f(x)* of degree 3, defined on *[0, 1]* such that *f(0) = 1, df/dx(0) = 2, f(1) = 3, df/dx(1) = 4*

```
>>> BPoly.from_derivatives([0, 1, 2], [[0, 1], [0], [2]])
```

Creates a piecewise polynomial *f(x)*, such that *f(0) = f(1) = 0*, *f(2) = 2*, and *df/dx(0) = 1*. Based on the number of derivatives provided, the order of the local polynomials is 2 on *[0, 1]* and 1 on *[1, 2]*. Notice that no restriction is imposed on the derivatives at `x = 1` and `x = 2`.

Indeed, the explicit form of the polynomial is:

```
f(x) = | x * (1 - x),  0 <= x < 1
       | 2 * (x - 1),  1 <= x <= 2
```

So that f'(1-0) = -1 and f'(1+0) = 2

Multivariate interpolation

Unstructured data:

griddata(points, values, xi[, method, …])	Interpolate unstructured D-D data.
LinearNDInterpolator(points, values[, …])	Piecewise linear interpolant in N > 1 dimensions.
NearestNDInterpolator(x, y[, rescale, …])	NearestNDInterpolator(x, y).
CloughTocher2DInterpolator(points, values[, …])	CloughTocher2DInterpolator(points, values, tol=1e-6).
RBFInterpolator(y, d[, neighbors, …])	Radial basis function (RBF) interpolation in N dimensions.
Rbf(*args)	A class for radial basis function interpolation of functions from N-D scattered data to an M-D domain.
interp2d(x, y, z[, kind, copy, …])	Interpolate over a 2-D grid.

scipy.interpolate.griddata

scipy.interpolate.**griddata**(*points*, *values*, *xi*, *method='linear'*, *fill_value=nan*, *rescale=False*)

Interpolate unstructured D-D data.

Parameters

points [2-D ndarray of floats with shape (n, D), or length D tuple of 1-D ndarrays with shape (n,).] Data point coordinates.

values [ndarray of float or complex, shape (n,)] Data values.

xi [2-D ndarray of floats with shape (m, D), or length D tuple of ndarrays broadcastable to the same shape.] Points at which to interpolate data.

method [{'linear', 'nearest', 'cubic'}, optional] Method of interpolation. One of

- **nearest** return the value at the data point closest to the point of interpolation. See *NearestNDInterpolator* for more details.
- **linear** tessellate the input point set to N-D simplices, and interpolate linearly on each simplex. See *LinearNDInterpolator* for more details.
- **cubic (1-D)**

return the value determined from a cubic spline.

cubic (2-D)
return the value determined from a piecewise cubic, continuously differentiable (C1), and approximately curvature-minimizing polynomial surface. See *CloughTocher2DInterpolator* for more details.

fill_value [float, optional] Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is `nan`. This option has no effect for the 'nearest' method.

rescale [bool, optional] Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.
New in version 0.14.0.

Returns

ndarray Array of interpolated values.

See also:

LinearNDInterpolator

Piecewise linear interpolant in N dimensions.

NearestNDInterpolator

Nearest-neighbor interpolation in N dimensions.

CloughTocher2DInterpolator

Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.

Notes

New in version 0.9.

Examples

Suppose we want to interpolate the 2-D function

```
>>> def func(x, y):
...     return x*(1-x)*np.cos(4*np.pi*x) * np.sin(4*np.pi*y**2)**2
```

on a grid in [0, 1]x[0, 1]

```
>>> grid_x, grid_y = np.mgrid[0:1:100j, 0:1:200j]
```

but we only know its values at 1000 data points:

```
>>> rng = np.random.default_rng()
>>> points = rng.random((1000, 2))
>>> values = func(points[:,0], points[:,1])
```

This can be done with *griddata* – below we try out all of the interpolation methods:

```
>>> from scipy.interpolate import griddata
>>> grid_z0 = griddata(points, values, (grid_x, grid_y), method='nearest')
>>> grid_z1 = griddata(points, values, (grid_x, grid_y), method='linear')
>>> grid_z2 = griddata(points, values, (grid_x, grid_y), method='cubic')
```

One can see that the exact result is reproduced by all of the methods to some degree, but for this smooth function the piecewise cubic interpolant gives the best results:

```
>>> import matplotlib.pyplot as plt
>>> plt.subplot(221)
>>> plt.imshow(func(grid_x, grid_y).T, extent=(0,1,0,1), origin='lower')
>>> plt.plot(points[:,0], points[:,1], 'k.', ms=1)
>>> plt.title('Original')
>>> plt.subplot(222)
>>> plt.imshow(grid_z0.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Nearest')
>>> plt.subplot(223)
>>> plt.imshow(grid_z1.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Linear')
>>> plt.subplot(224)
>>> plt.imshow(grid_z2.T, extent=(0,1,0,1), origin='lower')
>>> plt.title('Cubic')
>>> plt.gcf().set_size_inches(6, 6)
>>> plt.show()
```

scipy.interpolate.LinearNDInterpolator

class scipy.interpolate.**LinearNDInterpolator**(*points*, *values*, *fill_value=np.nan*, *rescale=False*)

Piecewise linear interpolant in N > 1 dimensions.

New in version 0.9.

Parameters

points : [ndarray of floats, shape (npoints, ndims); or Delaunay] Data point coordinates, or a precomputed Delaunay triangulation.

values : [ndarray of float or complex, shape (npoints, ...)] Data values.

fill_value : [float, optional] Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is `nan`.

rescale : [bool, optional] Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.

See also:

griddata

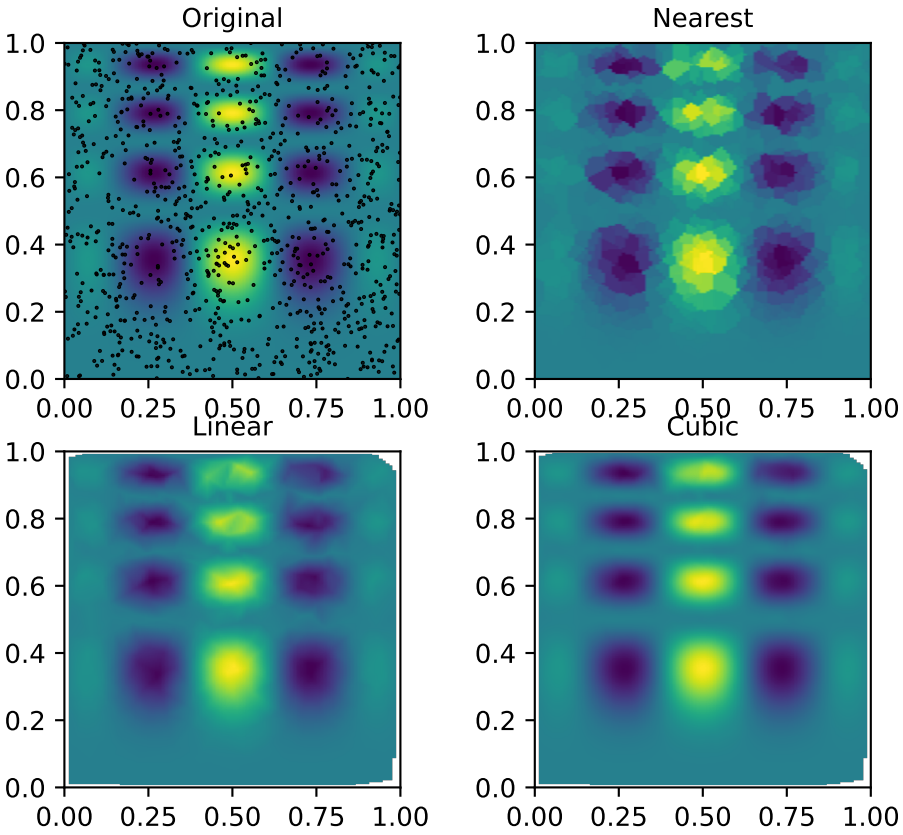
Interpolate unstructured D-D data.

NearestNDInterpolator

Nearest-neighbor interpolation in N dimensions.

CloughTocher2DInterpolator

Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.


Original
Nearest
Linear
Cubic
1.0
0.8
0.6
0.4
0.2
0.0
0.00
0.25
0.50
0.75
1.00

Notes

The interpolant is constructed by triangulating the input data with Qhull [1], and on each triangle performing linear barycentric interpolation.

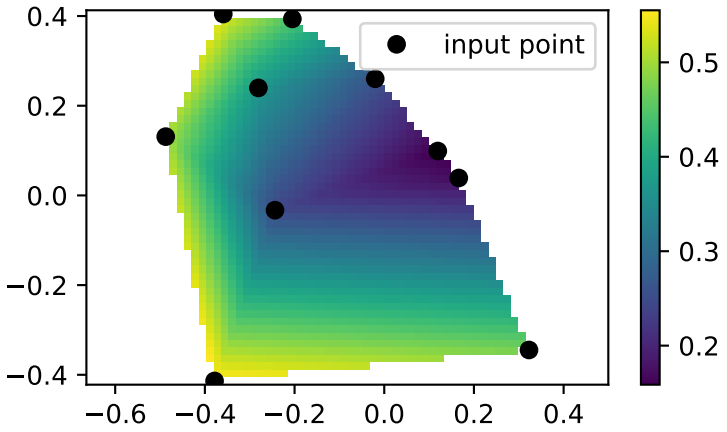
References

[1]

Examples

We can interpolate values on a 2D plane:

```
>>> from scipy.interpolate import LinearNDInterpolator
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> x = rng.random(10) - 0.5
>>> y = rng.random(10) - 0.5
>>> z = np.hypot(x, y)
>>> X = np.linspace(min(x), max(x))
>>> Y = np.linspace(min(y), max(y))
>>> X, Y = np.meshgrid(X, Y)  # 2D grid for interpolation
>>> interp = LinearNDInterpolator(list(zip(x, y)), z)
>>> Z = interp(X, Y)
>>> plt.pcolormesh(X, Y, Z, shading='auto')
>>> plt.plot(x, y, "ok", label="input point")
>>> plt.legend()
>>> plt.colorbar()
>>> plt.axis("equal")
>>> plt.show()
```



Methods

`__call__`(xi)	Evaluate interpolator at given points.

scipy.interpolate.LinearNDInterpolator.__call__

LinearNDInterpolator.**__call__**(*xi*)

Evaluate interpolator at given points.

Parameters

x1, x2, … xn: array-like of float

Points where to interpolate data at. x1, x2, … xn can be array-like of float with broadcastable shape. or x1 can be array-like of float with shape `(..., ndim)`

scipy.interpolate.NearestNDInterpolator

class scipy.interpolate.**NearestNDInterpolator**(*x*, *y*, *rescale=False*, *tree_options=None*)

NearestNDInterpolator(x, y).

Nearest-neighbor interpolation in N > 1 dimensions.

New in version 0.9.

Parameters

x [(Npoints, Ndims) ndarray of floats] Data point coordinates.

y [(Npoints,) ndarray of float or complex] Data values.

rescale [boolean, optional] Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.
New in version 0.14.0.

tree_options

[dict, optional] Options passed to the underlying `cKDTree`.
New in version 0.17.0.

See also:

griddata

Interpolate unstructured D-D data.

LinearNDInterpolator

Piecewise linear interpolant in N dimensions.

CloughTocher2DInterpolator

Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.

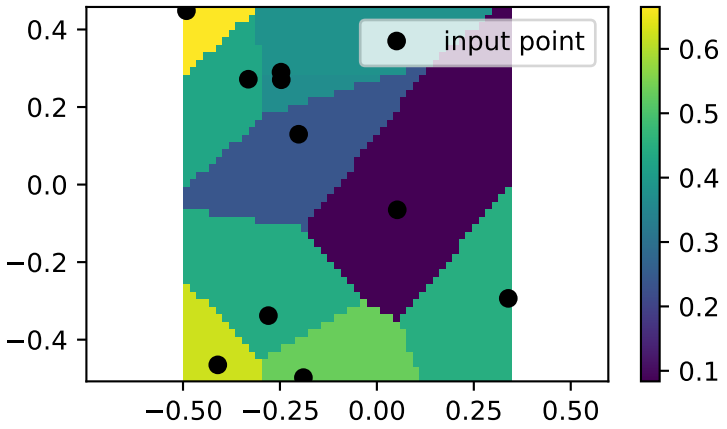
Notes

Uses `scipy.spatial.cKDTree`

Examples

We can interpolate values on a 2D plane:

```
>>> from scipy.interpolate import NearestNDInterpolator
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> x = rng.random(10) - 0.5
>>> y = rng.random(10) - 0.5
>>> z = np.hypot(x, y)
>>> X = np.linspace(min(x), max(x))
>>> Y = np.linspace(min(y), max(y))
>>> X, Y = np.meshgrid(X, Y)  # 2D grid for interpolation
>>> interp = NearestNDInterpolator(list(zip(x, y)), z)
>>> Z = interp(X, Y)
>>> plt.pcolormesh(X, Y, Z, shading='auto')
>>> plt.plot(x, y, "ok", label="input point")
>>> plt.legend()
>>> plt.colorbar()
>>> plt.axis("equal")
>>> plt.show()
```



Methods

`__call__`(*args)	Evaluate interpolator at given points.

scipy.interpolate.NearestNDInterpolator.__call__

NearestNDInterpolator.**__call__**(**args*)

Evaluate interpolator at given points.

Parameters

x1, x2, … xn: array-like of float

Points where to interpolate data at. x1, x2, … xn can be array-like of float with broadcastable shape. or x1 can be array-like of float with shape `(..., ndim)`

scipy.interpolate.CloughTocher2DInterpolator

class scipy.interpolate.**CloughTocher2DInterpolator**(*points*, *values*, *fill_value=nan*, *tol=1e-06*, *maxiter=400*, *rescale=False*)

CloughTocher2DInterpolator(points, values, tol=1e-6).

Piecewise cubic, C1 smooth, curvature-minimizing interpolant in 2D.

New in version 0.9.

Parameters

points	[ndarray of floats, shape (npoints, ndims); or Delaunay] Data point coordinates, or a precomputed Delaunay triangulation.
values	[ndarray of float or complex, shape (npoints, …)] Data values.
fill_value	[float, optional] Value used to fill in for requested points outside of the convex hull of the input points. If not provided, then the default is `nan`.
tol	[float, optional] Absolute/relative tolerance for gradient estimation.
maxiter	[int, optional] Maximum number of iterations in gradient estimation.
rescale	[bool, optional] Rescale points to unit cube before performing interpolation. This is useful if some of the input dimensions have incommensurable units and differ by many orders of magnitude.

See also:

griddata

Interpolate unstructured D-D data.

LinearNDInterpolator

Piecewise linear interpolant in N > 1 dimensions.

NearestNDInterpolator

Nearest-neighbor interpolation in N > 1 dimensions.

Notes

The interpolant is constructed by triangulating the input data with Qhull [1], and constructing a piecewise cubic interpolating Bezier polynomial on each triangle, using a Clough-Tocher scheme [CT]. The interpolant is guaranteed to be continuously differentiable.

The gradients of the interpolant are chosen so that the curvature of the interpolating surface is approximatively minimized. The gradients necessary for this are estimated using the global algorithm described in [Nielson83] and [Renka84].

References

[1], [CT], [Nielson83], [Renka84]

Examples

We can interpolate values on a 2D plane:

```
>>> from scipy.interpolate import CloughTocher2DInterpolator
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> x = rng.random(10) - 0.5
>>> y = rng.random(10) - 0.5
>>> z = np.hypot(x, y)
>>> X = np.linspace(min(x), max(x))
>>> Y = np.linspace(min(y), max(y))
>>> X, Y = np.meshgrid(X, Y)  # 2D grid for interpolation
>>> interp = CloughTocher2DInterpolator(list(zip(x, y)), z)
>>> Z = interp(X, Y)
>>> plt.pcolormesh(X, Y, Z, shading='auto')
>>> plt.plot(x, y, "ok", label="input point")
>>> plt.legend()
>>> plt.colorbar()
>>> plt.axis("equal")
>>> plt.show()
```

Methods

__call__(xi)	Evaluate interpolator at given points.

scipy.interpolate.CloughTocher2DInterpolator.__call__

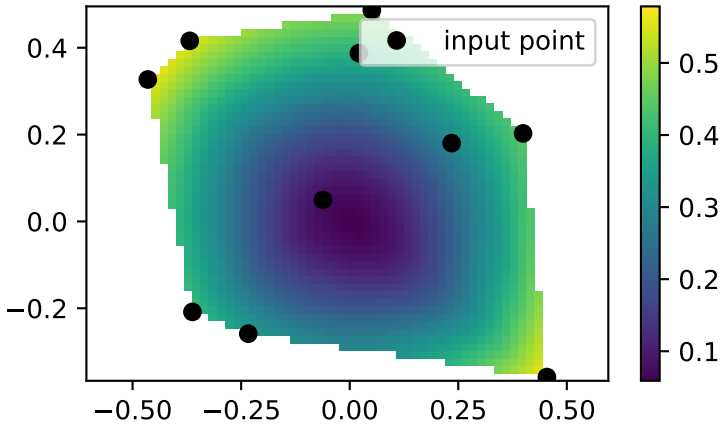
CloughTocher2DInterpolator.**__call__**(*xi*)

Evaluate interpolator at given points.

Parameters

x1, x2, … xn: array-like of float

Points where to interpolate data at. x1, x2, … xn can be array-like of float with broadcastable shape. or x1 can be array-like of float with shape `(..., ndim)`



scipy.interpolate.RBFInterpolator

class scipy.interpolate.**RBFInterpolator**(*y*, *d*, *neighbors=None*, *smoothing=0.0*, *kernel='thin_plate_spline'*, *epsilon=None*, *degree=None*)

Radial basis function (RBF) interpolation in N dimensions.

Parameters

y [(P, N) array_like] Data point coordinates.

d [(P, …) array_like] Data values at *y*.

neighbors [int, optional] If specified, the value of the interpolant at each evaluation point will be computed using only this many nearest data points. All the data points are used by default.

smoothing [float or (P,) array_like, optional] Smoothing parameter. The interpolant perfectly fits the data when this is set to 0. For large values, the interpolant approaches a least squares fit of a polynomial with the specified degree. Default is 0.

kernel [str, optional] Type of RBF. This should be one of

- 'linear' : `-r`
- 'thin_plate_spline' : `r**2 * log(r)`
- 'cubic' : `r**3`
- 'quintic' : `-r**5`
- 'multiquadric' : `-sqrt(1 + r**2)`
- 'inverse_multiquadric' : `1/sqrt(1 + r**2)`
- 'inverse_quadratic' : `1/(1 + r**2)`
- 'gaussian' : `exp(-r**2)`

Default is 'thin_plate_spline'.

epsilon [float, optional] Shape parameter that scales the input to the RBF. If *kernel* is 'linear', 'thin_plate_spline', 'cubic', or 'quintic', this defaults to 1 and can be ignored because it has the same effect as scaling the smoothing parameter. Otherwise, this must be specified.

degree [int, optional] Degree of the added polynomial. For some RBFs the interpolant may not be well-posed if the polynomial degree is too small. Those RBFs and their corresponding minimum degrees are

- 'multiquadric' : 0
- 'linear' : 0
- 'thin_plate_spline' : 1
- 'cubic' : 1

- 'quintic' : 2

The default value is the minimum degree for *kernel* or 0 if there is no minimum degree. Set this to -1 for no added polynomial.

See also:

`NearestNDInterpolator`

`LinearNDInterpolator`

`CloughTocher2DInterpolator`

Notes

An RBF is a scalar valued function in N-dimensional space whose value at x can be expressed in terms of $r = ||x - c||$, where c is the center of the RBF.

An RBF interpolant for the vector of data values d, which are from locations y, is a linear combination of RBFs centered at y plus a polynomial with a specified degree. The RBF interpolant is written as

$$f(x) = K(x, y)a + P(x)b,$$

where $K(x, y)$ is a matrix of RBFs with centers at y evaluated at the points x, and $P(x)$ is a matrix of monomials, which span polynomials with the specified degree, evaluated at x. The coefficients a and b are the solution to the linear equations

$$(K(y, y) + \lambda I)a + P(y)b = d$$

and

$$P(y)^T a = 0,$$

where λ is a non-negative smoothing parameter that controls how well we want to fit the data. The data are fit exactly when the smoothing parameter is 0.

The above system is uniquely solvable if the following requirements are met:

- $P(y)$ must have full column rank. $P(y)$ always has full column rank when *degree* is -1 or 0. When *degree* is 1, $P(y)$ has full column rank if the data point locations are not all collinear (N=2), coplanar (N=3), etc.
- If *kernel* is 'multiquadric', 'linear', 'thin_plate_spline', 'cubic', or 'quintic', then *degree* must not be lower than the minimum value listed above.
- If *smoothing* is 0, then each data point location must be distinct.

When using an RBF that is not scale invariant ('multiquadric', 'inverse_multiquadric', 'inverse_quadratic', or 'gaussian'), an appropriate shape parameter must be chosen (e.g., through cross validation). Smaller values for the shape parameter correspond to wider RBFs. The problem can become ill-conditioned or singular when the shape parameter is too small.

The memory required to solve for the RBF interpolation coefficients increases quadratically with the number of data points, which can become impractical when interpolating more than about a thousand data points. To overcome memory limitations for large interpolation problems, the *neighbors* argument can be specified to compute an RBF interpolant for each evaluation point using only the nearest data points.

New in version 1.7.0.

References

[1], [2], [3], [4]

Examples

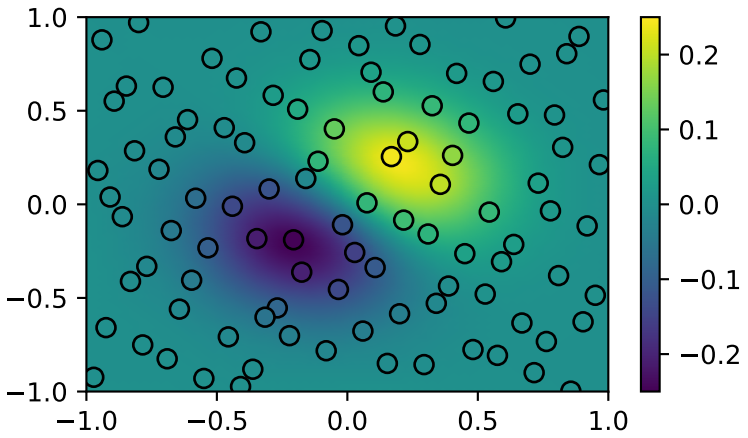
Demonstrate interpolating scattered data to a grid in 2-D.

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import RBFInterpolator
>>> from scipy.stats.qmc import Halton
```

```
>>> rng = np.random.default_rng()
>>> xobs = 2*Halton(2, seed=rng).random(100) - 1
>>> yobs = np.sum(xobs, axis=1)*np.exp(-6*np.sum(xobs**2, axis=1))
```

```
>>> xgrid = np.mgrid[-1:1:50j, -1:1:50j]
>>> xflat = xgrid.reshape(2, -1).T
>>> yflat = RBFInterpolator(xobs, yobs)(xflat)
>>> ygrid = yflat.reshape(50, 50)
```

```
>>> fig, ax = plt.subplots()
>>> ax.pcolormesh(*xgrid, ygrid, vmin=-0.25, vmax=0.25, shading='gouraud')
>>> p = ax.scatter(*xobs.T, c=yobs, s=50, ec='k', vmin=-0.25, vmax=0.25)
>>> fig.colorbar(p)
>>> plt.show()
```



Methods

__call__(x)	Evaluate the interpolant at *x*.

scipy.interpolate.RBFInterpolator.__call__

RBFInterpolator.**__call__**(*x*)

Evaluate the interpolant at *x*.

Parameters

x [(Q, N) array_like] Evaluation point coordinates.

Returns

(Q, …) ndarray
Values of the interpolant at *x*.

scipy.interpolate.Rbf

class scipy.interpolate.**Rbf**(**args*)

A class for radial basis function interpolation of functions from N-D scattered data to an M-D domain.

Note: *Rbf* is legacy code, for new usage please use *RBFInterpolator* instead.

Parameters

***args** [arrays] x, y, z, …, d, where x, y, z, … are the coordinates of the nodes and d is the array of values at the nodes

function [str or callable, optional] The radial basis function, based on the radius, r, given by the norm (default is Euclidean distance); the default is 'multiquadric':

```
'multiquadric': sqrt((r/self.epsilon)**2 + 1)
'inverse': 1.0/sqrt((r/self.epsilon)**2 + 1)
'gaussian': exp(-(r/self.epsilon)**2)
'linear': r
'cubic': r**3
'quintic': r**5
'thin_plate': r**2 * log(r)
```

If callable, then it must take 2 arguments (self, r). The epsilon parameter will be available as self.epsilon. Other keyword arguments passed in will be available as well.

epsilon [float, optional] Adjustable constant for gaussian or multiquadrics functions - defaults to approximate average distance between nodes (which is a good start).

smooth [float, optional] Values greater than zero increase the smoothness of the approximation. 0 is for interpolation (default), the function will always go through the nodal points in this case.

norm [str, callable, optional] A function that returns the 'distance' between two points, with inputs as arrays of positions (x, y, z, …), and an output as an array of distance. E.g., the default: 'euclidean', such that the result is a matrix of the distances from each point in `x1` to each point in `x2`. For more options, see documentation of *scipy.spatial.distances.cdist*.

mode [str, optional] Mode of the interpolation, can be '1-D' (default) or 'N-D'. When it is '1-D' the data *d* will be considered as 1-D and flattened internally. When it is 'N-D' the data *d* is assumed to be an array of shape (n_samples, m), where m is the dimension of the target domain.

See also:

`RBFInterpolator`

Examples

```
>>> from scipy.interpolate import Rbf
>>> rng = np.random.default_rng()
>>> x, y, z, d = rng.random((4, 50))
>>> rbfi = Rbf(x, y, z, d)  # radial basis function interpolator instance
>>> xi = yi = zi = np.linspace(0, 1, 20)
>>> di = rbfi(xi, yi, zi)   # interpolated values
>>> di.shape
(20,)
```

Attributes

N	[int] The number of data points (as determined by the input arrays).
di	[ndarray] The 1-D array of data values at each of the data coordinates *xi*.
xi	[ndarray] The 2-D array of data coordinates.
function	[str or callable] The radial basis function. See description under Parameters.
epsilon	[float] Parameter used by gaussian or multiquadrics functions. See Parameters.
smooth	[float] Smoothing parameter. See description under Parameters.
norm	[str or callable] The distance function. See description under Parameters.
mode	[str] Mode of the interpolation. See description under Parameters.
nodes	[ndarray] A 1-D array of node values for the interpolation.
A	[internal property, do not use]

Methods

__call__(*args)	Call self as a function.

scipy.interpolate.Rbf.__call__

Rbf.**__call__**(**args*)
Call self as a function.

scipy.interpolate.interp2d

class scipy.interpolate.**interp2d**(*x*, *y*, *z*, *kind='linear'*, *copy=True*, *bounds_error=False*, *fill_value=None*)

Interpolate over a 2-D grid.

x, *y* and *z* are arrays of values used to approximate some function f: `z = f(x, y)` which returns a scalar value *z*. This class returns a function whose call method uses spline interpolation to find the value of new points.

If *x* and *y* represent a regular grid, consider using *RectBivariateSpline*.

If *z* is a vector value, consider using *interpn*.

Note that calling *interp2d* with NaNs present in input values results in undefined behaviour.

Parameters

x, y [array_like] Arrays defining the data point coordinates.
If the points lie on a regular grid, *x* can specify the column coordinates and *y* the row coordinates, for example:

```
>>> x = [0,1,2];  y = [0,3]; z = [[1,2,3], [4,5,6]]
```

Otherwise, *x* and *y* must specify the full coordinates for each point, for example:

```
>>> x = [0,1,2,0,1,2];  y = [0,0,0,3,3,3]; z = [1,2,3,4,5,
↪6]
```

If *x* and *y* are multidimensional, they are flattened before use.

z [array_like] The values of the function to interpolate at the data points. If *z* is a multidimensional array, it is flattened before use. The length of a flattened *z* array is either len(*x*)*len(*y*) if *x* and *y* specify the column and row coordinates or `len(z) == len(x) == len(y)` if *x* and *y* specify coordinates for each point.

kind [{'linear', 'cubic', 'quintic'}, optional] The kind of spline interpolation to use. Default is 'linear'.

copy [bool, optional] If True, the class makes internal copies of x, y and z. If False, references may be used. The default is to copy.

bounds_error [bool, optional] If True, when interpolated values are requested outside of the domain of the input data (x,y), a ValueError is raised. If False, then *fill_value* is used.

fill_value [number, optional] If provided, the value to use for points outside of the interpolation domain. If omitted (None), values outside the domain are extrapolated via nearest-neighbor extrapolation.

See also:

RectBivariateSpline

Much faster 2-D interpolation if your input data is on a grid

bisplrep, **bisplev**

Spline interpolation based on FITPACK

BivariateSpline

a more recent wrapper of the FITPACK routines

interp1d

1-D version of this function

Notes

The minimum number of data points required along the interpolation axis is `(k+1)**2`, with k=1 for linear, k=3 for cubic and k=5 for quintic interpolation.

The interpolator is constructed by *bisplrep*, with a smoothing factor of 0. If more control over smoothing is needed, *bisplrep* should be used directly.

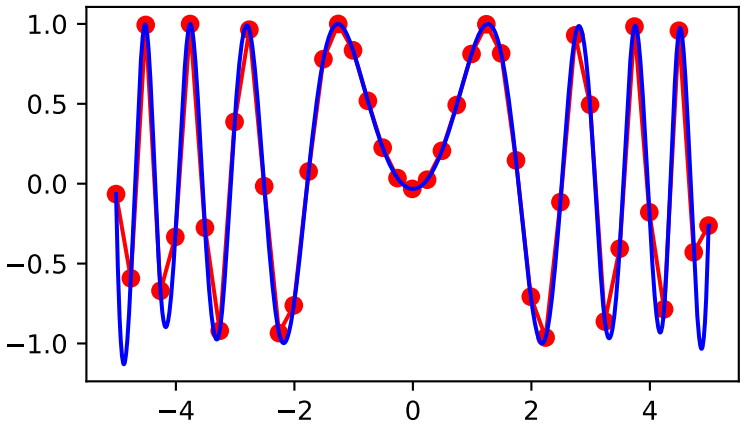
Examples

Construct a 2-D grid and interpolate on it:

```
>>> from scipy import interpolate
>>> x = np.arange(-5.01, 5.01, 0.25)
>>> y = np.arange(-5.01, 5.01, 0.25)
>>> xx, yy = np.meshgrid(x, y)
>>> z = np.sin(xx**2+yy**2)
>>> f = interpolate.interp2d(x, y, z, kind='cubic')
```

Now use the obtained interpolation function and plot the result:

```
>>> import matplotlib.pyplot as plt
>>> xnew = np.arange(-5.01, 5.01, 1e-2)
>>> ynew = np.arange(-5.01, 5.01, 1e-2)
>>> znew = f(xnew, ynew)
>>> plt.plot(x, z[0, :], 'ro-', xnew, znew[0, :], 'b-')
>>> plt.show()
```



Methods

__call__(x, y[, dx, dy, assume_sorted])	Interpolate the function.

scipy.interpolate.interp2d.__call__

interp2d.**__call__**(*x*, *y*, *dx=0*, *dy=0*, *assume_sorted=False*)

Interpolate the function.

Parameters

x [1-D array] x-coordinates of the mesh on which to interpolate.

y [1-D array] y-coordinates of the mesh on which to interpolate.

dx [int >= 0, < kx] Order of partial derivatives in x.

dy [int >= 0, < ky] Order of partial derivatives in y.

assume_sorted [bool, optional] If False, values of *x* and *y* can be in any order and they are sorted first. If True, *x* and *y* have to be arrays of monotonically increasing values.

Returns

z [2-D array with shape (len(y), len(x))] The interpolated values.

For data on a grid:

interpn(points, values, xi[, method, …])	Multidimensional interpolation on regular grids.
RegularGridInterpolator(points, values[, …])	Interpolation on a regular grid in arbitrary dimensions
RectBivariateSpline(x, y, z[, bbox, kx, ky, s])	Bivariate spline approximation over a rectangular mesh.

scipy.interpolate.interpn

scipy.interpolate.**interpn**(*points*, *values*, *xi*, *method='linear'*, *bounds_error=True*, *fill_value=nan*)

Multidimensional interpolation on regular grids.

Parameters

points [tuple of ndarray of float, with shapes (m1,), …, (mn,)] The points defining the regular grid in n dimensions.

values [array_like, shape (m1, …, mn, …)] The data on the regular grid in n dimensions.

xi [ndarray of shape (…, ndim)] The coordinates to sample the gridded data at

method [str, optional] The method of interpolation to perform. Supported are “linear” and “nearest”, and “splinef2d”. “splinef2d” is only supported for 2-dimensional data.

bounds_error [bool, optional] If True, when interpolated values are requested outside of the domain of the input data, a ValueError is raised. If False, then *fill_value* is used.

fill_value [number, optional] If provided, the value to use for points outside of the interpolation domain. If None, values outside the domain are extrapolated. Extrapolation is not supported by method “splinef2d”.

Returns

values_x [ndarray, shape xi.shape[:-1] + values.shape[ndim:]] Interpolated values at input coordinates.

See also:

NearestNDInterpolator

Nearest neighbor interpolation on unstructured data in N dimensions

LinearNDInterpolator

Piecewise linear interpolant on unstructured data in N dimensions

RegularGridInterpolator

Linear and nearest-neighbor Interpolation on a regular grid in arbitrary dimensions

RectBivariateSpline

Bivariate spline approximation over a rectangular mesh

Notes

New in version 0.14.

Examples

Evaluate a simple example function on the points of a regular 3-D grid:

```
>>> from scipy.interpolate import interpn
>>> def value_func_3d(x, y, z):
...     return 2 * x + 3 * y - z
>>> x = np.linspace(0, 4, 5)
>>> y = np.linspace(0, 5, 6)
>>> z = np.linspace(0, 6, 7)
>>> points = (x, y, z)
>>> values = value_func_3d(*np.meshgrid(*points, indexing='ij'))
```

Evaluate the interpolating function at a point

```
>>> point = np.array([2.21, 3.12, 1.15])
>>> print(interpn(points, values, point))
[12.63]
```

scipy.interpolate.RegularGridInterpolator

class scipy.interpolate.**RegularGridInterpolator**(*points*, *values*, *method='linear'*, *bounds_error=True*, *fill_value=nan*)

Interpolation on a regular grid in arbitrary dimensions

The data must be defined on a regular grid; the grid spacing however may be uneven. Linear and nearest-neighbor interpolation are supported. After setting up the interpolator object, the interpolation method (*linear* or *nearest*) may be chosen at each evaluation.

Parameters

points [tuple of ndarray of float, with shapes (m1,), …, (mn,)] The points defining the regular grid in n dimensions.

values [array_like, shape (m1, …, mn, …)] The data on the regular grid in n dimensions.

method [str, optional] The method of interpolation to perform. Supported are “linear” and “nearest”. This parameter will become the default for the object’s `__call__` method. Default is “linear”.

bounds_error
[bool, optional] If True, when interpolated values are requested outside of the domain of the input data, a ValueError is raised. If False, then *fill_value* is used.

fill_value [number, optional] If provided, the value to use for points outside of the interpolation domain. If None, values outside the domain are extrapolated.

See also:

NearestNDInterpolator

Nearest neighbor interpolation on unstructured data in N dimensions

LinearNDInterpolator

Piecewise linear interpolant on unstructured data in N dimensions

Notes

Contrary to LinearNDInterpolator and NearestNDInterpolator, this class avoids expensive triangulation of the input data by taking advantage of the regular grid structure.

If any of *points* have a dimension of size 1, linear interpolation will return an array of *nan* values. Nearest-neighbor interpolation will work as usual in this case.

New in version 0.14.

References

[1], [2], [3]

Examples

Evaluate a simple example function on the points of a 3-D grid:

```
>>> from scipy.interpolate import RegularGridInterpolator
>>> def f(x, y, z):
...     return 2 * x**3 + 3 * y**2 - z
>>> x = np.linspace(1, 4, 11)
>>> y = np.linspace(4, 7, 22)
>>> z = np.linspace(7, 9, 33)
>>> xg, yg ,zg = np.meshgrid(x, y, z, indexing='ij', sparse=True)
>>> data = f(xg, yg, zg)
```

`data` is now a 3-D array with `data[i,j,k] = f(x[i], y[j], z[k])`. Next, define an interpolating function from this data:

```
>>> my_interpolating_function = RegularGridInterpolator((x, y, z), data)
```

Evaluate the interpolating function at the two points `(x,y,z) = (2.1, 6.2, 8.3)` and `(3.3, 5.2, 7.1)`:

```
>>> pts = np.array([[2.1, 6.2, 8.3], [3.3, 5.2, 7.1]])
>>> my_interpolating_function(pts)
array([ 125.80469388,  146.30069388])
```

which is indeed a close approximation to `[f(2.1, 6.2, 8.3), f(3.3, 5.2, 7.1)]`.

Methods

`__call__`(xi[, method])	Interpolation at coordinates

scipy.interpolate.RegularGridInterpolator.__call__

RegularGridInterpolator.**__call__**(*xi*, *method=None*)

Interpolation at coordinates

Parameters

xi [ndarray of shape (…, ndim)] The coordinates to sample the gridded data at

method [str] The method of interpolation to perform. Supported are "linear" and "nearest".

scipy.interpolate.RectBivariateSpline

class scipy.interpolate.**RectBivariateSpline**(*x*, *y*, *z*, *bbox=[None, None, None, None]*, *kx=3*, *ky=3*, *s=0*)

Bivariate spline approximation over a rectangular mesh.

Can be used for both smoothing and interpolating data.

Parameters

x,y [array_like] 1-D arrays of coordinates in strictly ascending order.

z [array_like] 2-D array of data with shape (x.size,y.size).

bbox [array_like, optional] Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, `bbox=[min(x), max(x), min(y), max(y)]`.

kx, ky [ints, optional] Degrees of the bivariate spline. Default is 3.

s [float, optional] Positive smoothing factor defined for estimation condition: `sum((z[i]-f(x[i], y[i]))**2, axis=0) <= s` where f is a spline function. Default is `s=0`, which is for interpolation.

See also:

BivariateSpline

a base class for bivariate splines.

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

SmoothBivariateSpline

a smoothing bivariate spline through the given points

LSQBivariateSpline

a bivariate spline using weighted least-squares fitting

RectSphereBivariateSpline

a bivariate spline over a rectangular mesh on a sphere

SmoothSphereBivariateSpline

a smoothing bivariate spline in spherical coordinates

LSQSphereBivariateSpline

a bivariate spline in spherical coordinates using weighted least-squares fitting

bisplrep

a function to find a bivariate B-spline representation of a surface

bisplev

a function to evaluate a bivariate B-spline and its derivatives

Methods

__call__(x, y[, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
ev(xi, yi[, dx, dy])	Evaluate the spline at points
get_coeffs()	Return spline coefficients.
get_knots()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
get_residual()	Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)
integral(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

scipy.interpolate.RectBivariateSpline.__call__

RectBivariateSpline.**__call__**(*x*, *y*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

x, y : [array_like] Input coordinates.
If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.
Note that the axis ordering is inverted relative to the output of meshgrid.

dx : [int] Order of x-derivative
New in version 0.14.0.

dy : [int] Order of y-derivative
New in version 0.14.0.

grid : [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

scipy.interpolate.RectBivariateSpline.ev

RectBivariateSpline.**ev**(*xi*, *yi*, *dx=0*, *dy=0*)

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters

xi, yi	[array_like] Input coordinates. Standard Numpy broadcasting is obeyed.
dx	[int, optional] Order of x-derivative New in version 0.14.0.
dy	[int, optional] Order of y-derivative New in version 0.14.0.

scipy.interpolate.RectBivariateSpline.get_coeffs

RectBivariateSpline.**get_coeffs**()

Return spline coefficients.

scipy.interpolate.RectBivariateSpline.get_knots

RectBivariateSpline.**get_knots**()

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.RectBivariateSpline.get_residual

RectBivariateSpline.**get_residual**()

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

scipy.interpolate.RectBivariateSpline.integral

RectBivariateSpline.**integral**(*xa*, *xb*, *ya*, *yb*)

Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters

xa, xb	[float] The end-points of the x integration interval.
ya, yb	[float] The end-points of the y integration interval.

Returns

integ	[float] The value of the resulting integral.

See also:

scipy.ndimage.map_coordinates

Tensor product polynomials:

NdPPoly(c, x[, extrapolate])	Piecewise tensor product polynomial

scipy.interpolate.NdPPoly

class scipy.interpolate.**NdPPoly**(*c*, *x*, *extrapolate=None*)

Piecewise tensor product polynomial

The value at point `xp = (x', y', z', ...)` is evaluated by first computing the interval indices *i* such that:

```
x[0][i[0]] <= x' < x[0][i[0]+1]
x[1][i[1]] <= y' < x[1][i[1]+1]
...
```

and then computing:

```
S = sum(c[k0-m0-1,...,kn-mn-1,i[0],...,i[n]]
        * (xp[0] - x[0][i[0]])**m0
        * ...
        * (xp[n] - x[n][i[n]])**mn
        for m0 in range(k[0]+1)
        ...
        for mn in range(k[n]+1))
```

where `k[j]` is the degree of the polynomial in dimension j. This representation is the piecewise multivariate power basis.

Parameters

c [ndarray, shape (k0, …, kn, m0, …, mn, …)] Polynomial coefficients, with polynomial order *kj* and *mj+1* intervals for each dimension *j*.

x [ndim-tuple of ndarrays, shapes (mj+1,)] Polynomial breakpoints for each dimension. These must be sorted in increasing order.

extrapolate [bool, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs. Default: True.

See also:

PPoly

piecewise polynomials in 1D

Notes

High-order polynomials in the power basis can be numerically unstable.

Attributes

x [tuple of ndarrays] Breakpoints.

c [ndarray] Coefficients of the polynomials.

Methods

__call__(x[, nu, extrapolate])	Evaluate the piecewise polynomial or its derivative
derivative(nu)	Construct a new piecewise polynomial representing the derivative.
antiderivative(nu)	Construct a new piecewise polynomial representing the antiderivative.
integrate(ranges[, extrapolate])	Compute a definite integral over a piecewise polynomial.
integrate_1d(a, b, axis[, extrapolate])	Compute NdPPoly representation for one dimensional definite integral
construct_fast(c, x[, extrapolate])	Construct the piecewise polynomial without making checks.

scipy.interpolate.NdPPoly.__call__

NdPPoly.**__call__**(*x*, *nu=None*, *extrapolate=None*)

Evaluate the piecewise polynomial or its derivative

Parameters

x [array-like] Points to evaluate the interpolant at.

nu [tuple, optional] Orders of derivatives to evaluate. Each must be non-negative.

extrapolate [bool, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs.

Returns

y [array-like] Interpolated values. Shape is determined by replacing the interpolation axis in the original array with the shape of x.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.NdPPoly.derivative

NdPPoly.**derivative**(*nu*)

Construct a new piecewise polynomial representing the derivative.

Parameters

nu [ndim-tuple of int] Order of derivatives to evaluate for each dimension. If negative, the antiderivative is returned.

Returns

pp [NdPPoly] Piecewise polynomial of orders (k[0] - nu[0], …, k[n] - nu[n]) representing the derivative of this polynomial.

Notes

Derivatives are evaluated piecewise for each polynomial segment, even if the polynomial is not differentiable at the breakpoints. The polynomial intervals in each dimension are considered half-open, `[a, b)`, except for the last interval which is closed `[a, b]`.

scipy.interpolate.NdPPoly.antiderivative

`NdPPoly.`**`antiderivative`**(*nu*)

Construct a new piecewise polynomial representing the antiderivative.

Antiderivative is also the indefinite integral of the function, and derivative is its inverse operation.

Parameters

nu [ndim-tuple of int] Order of derivatives to evaluate for each dimension. If negative, the derivative is returned.

Returns

pp [PPoly] Piecewise polynomial of order k2 = k + n representing the antiderivative of this polynomial.

Notes

The antiderivative returned by this function is continuous and continuously differentiable to order n-1, up to floating point rounding error.

scipy.interpolate.NdPPoly.integrate

`NdPPoly.`**`integrate`**(*ranges*, *extrapolate=None*)

Compute a definite integral over a piecewise polynomial.

Parameters

ranges [ndim-tuple of 2-tuples float] Sequence of lower and upper bounds for each dimension, `[(a[0], b[0]), ..., (a[ndim-1], b[ndim-1])]`

extrapolate

[bool, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs.

Returns

ig [array_like] Definite integral of the piecewise polynomial over [a[0], b[0]] x … x [a[ndim-1], b[ndim-1]]

scipy.interpolate.NdPPoly.integrate_1d

NdPPoly.**integrate_1d**(*a*, *b*, *axis*, *extrapolate=None*)

Compute NdPPoly representation for one dimensional definite integral

The result is a piecewise polynomial representing the integral:

$$p(y, z, ...) = \int_a^b dx\, p(x, y, z, ...)$$

where the dimension integrated over is specified with the *axis* parameter.

Parameters

a, b [float] Lower and upper bound for integration.

axis [int] Dimension over which to compute the 1-D integrals

extrapolate [bool, optional] Whether to extrapolate to out-of-bounds points based on first and last intervals, or to return NaNs.

Returns

ig [NdPPoly or array-like] Definite integral of the piecewise polynomial over [a, b]. If the polynomial was 1D, an array is returned, otherwise, an NdPPoly object.

scipy.interpolate.NdPPoly.construct_fast

classmethod NdPPoly.**construct_fast**(*c*, *x*, *extrapolate=None*)

Construct the piecewise polynomial without making checks.

Takes the same parameters as the constructor. Input arguments `c` and `x` must be arrays of the correct shape and type. The `c` array can only be of dtypes float and complex, and `x` array must have dtype float.

1-D Splines

BSpline(t, c, k[, extrapolate, axis])	Univariate spline in the B-spline basis.
make_interp_spline(x, y[, k, t, bc_type, …])	Compute the (coefficients of) interpolating B-spline.
make_lsq_spline(x, y, t[, k, w, axis, …])	Compute the (coefficients of) an LSQ B-spline.

scipy.interpolate.BSpline

class scipy.interpolate.**BSpline**(*t*, *c*, *k*, *extrapolate=True*, *axis=0*)

Univariate spline in the B-spline basis.

$$S(x) = \sum_{j=0}^{n-1} c_j B_{j,k;t}(x)$$

where $B_{j,k;t}$ are B-spline basis functions of degree *k* and knots *t*.

Parameters

t [ndarray, shape (n+k+1,)] knots

c [ndarray, shape (>=n, …)] spline coefficients

k [int] B-spline degree

extrapolate

[bool or 'periodic', optional] whether to extrapolate beyond the base interval, `t[k] .. t[n]`, or to return nans. If True, extrapolates the first and last polynomial pieces of b-spline functions active on the base interval. If 'periodic', periodic extrapolation is used. Default is True.

axis [int, optional] Interpolation axis. Default is zero.

Notes

B-spline basis elements are defined via

$$B_{i,0}(x) = 1, \text{if } t_i \le x < t_{i+1}, \text{otherwise } 0,$$
$$B_{i,k}(x) = \frac{x - t_i}{t_{i+k} - t_i} B_{i,k-1}(x) + \frac{t_{i+k+1} - x}{t_{i+k+1} - t_{i+1}} B_{i+1,k-1}(x)$$

Implementation details

- At least `k+1` coefficients are required for a spline of degree *k*, so that `n >= k+1`. Additional coefficients, `c[j]` with `j > n`, are ignored.
- B-spline basis elements of degree *k* form a partition of unity on the *base interval*, `t[k] <= x <= t[n]`.

References

[1], [2]

Examples

Translating the recursive definition of B-splines into Python code, we have:

```
>>> def B(x, k, i, t):
...    if k == 0:
...       return 1.0 if t[i] <= x < t[i+1] else 0.0
...    if t[i+k] == t[i]:
...       c1 = 0.0
...    else:
...       c1 = (x - t[i])/(t[i+k] - t[i]) * B(x, k-1, i, t)
...    if t[i+k+1] == t[i+1]:
...       c2 = 0.0
...    else:
...       c2 = (t[i+k+1] - x)/(t[i+k+1] - t[i+1]) * B(x, k-1, i+1, t)
...    return c1 + c2
```

```
>>> def bspline(x, t, c, k):
...    n = len(t) - k - 1
...    assert (n >= k+1) and (len(c) >= n)
...    return sum(c[i] * B(x, k, i, t) for i in range(n))
```

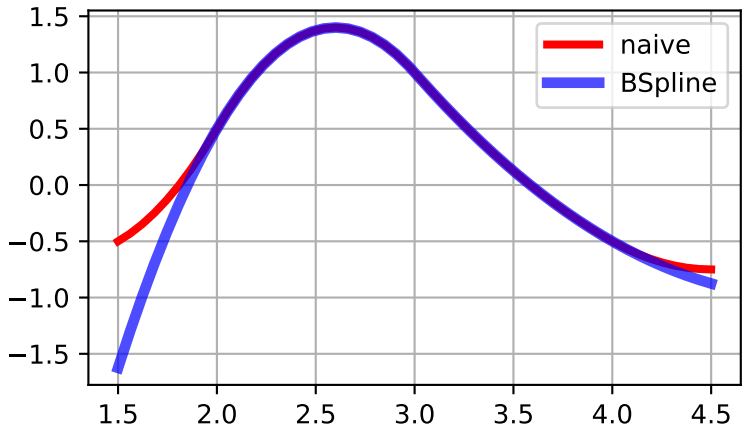
Note that this is an inefficient (if straightforward) way to evaluate B-splines — this spline class does it in an equivalent, but much more efficient way.

Here we construct a quadratic spline function on the base interval `2 <= x <= 4` and compare with the naive way of evaluating the spline:

```
>>> from scipy.interpolate import BSpline
>>> k = 2
>>> t = [0, 1, 2, 3, 4, 5, 6]
>>> c = [-1, 2, 0, -1]
>>> spl = BSpline(t, c, k)
>>> spl(2.5)
array(1.375)
>>> bspline(2.5, t, c, k)
1.375
```

Note that outside of the base interval results differ. This is because *BSpline* extrapolates the first and last polynomial pieces of B-spline functions active on the base interval.

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> xx = np.linspace(1.5, 4.5, 50)
>>> ax.plot(xx, [bspline(x, t, c ,k) for x in xx], 'r-', lw=3, label=
↪'naive')
>>> ax.plot(xx, spl(xx), 'b-', lw=4, alpha=0.7, label='BSpline')
>>> ax.grid(True)
>>> ax.legend(loc='best')
>>> plt.show()
```



Attributes

t	[ndarray] knot vector
c	[ndarray] spline coefficients
k	[int] spline degree
extrapolate	[bool] If True, extrapolates the first and last polynomial pieces of b-spline functions active on the base interval.
axis	[int] Interpolation axis.
tck	[tuple] Equivalent to `(self.t, self.c, self.k)` (read-only).

Methods

__call__(x[, nu, extrapolate])	Evaluate a spline function.
basis_element(t[, extrapolate])	Return a B-spline basis element `B(x | t[0], .. ., t[k+1])`.
derivative([nu])	Return a B-spline representing the derivative.
antiderivative([nu])	Return a B-spline representing the antiderivative.
integrate(a, b[, extrapolate])	Compute a definite integral of the spline.
construct_fast(t, c, k[, extrapolate, axis])	Construct a spline without making checks.

scipy.interpolate.BSpline.__call__

`BSpline.`**`__call__`**(*x*, *nu=0*, *extrapolate=None*)

Evaluate a spline function.

Parameters

x [array_like] points to evaluate the spline at.

nu: int, optional

derivative to evaluate (default is 0).

extrapolate

[bool or 'periodic', optional] whether to extrapolate based on the first and last intervals or return nans. If 'periodic', periodic extrapolation is used. Default is *self.extrapolate*.

Returns

y [array_like] Shape is determined by replacing the interpolation axis in the coefficient array with the shape of *x*.

scipy.interpolate.BSpline.basis_element

`classmethod` `BSpline.`**`basis_element`**(*t*, *extrapolate=True*)

Return a B-spline basis element `B(x | t[0], ..., t[k+1])`.

Parameters

t [ndarray, shape (k+1,)] internal knots

extrapolate

[bool or 'periodic', optional] whether to extrapolate beyond the base interval, `t[0] .. t[k+1]`, or to return nans. If 'periodic', periodic extrapolation is used. Default is True.

Returns

basis_element

[callable] A callable representing a B-spline basis element for the knot vector *t*.

Notes

The degree of the B-spline, *k*, is inferred from the length of *t* as `len(t)-2`. The knot vector is constructed by appending and prepending `k+1` elements to internal knots *t*.

Examples

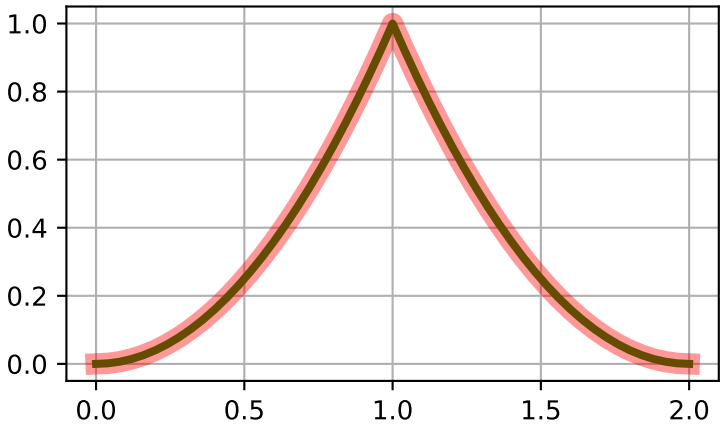
Construct a cubic B-spline:

```
>>> from scipy.interpolate import BSpline
>>> b = BSpline.basis_element([0, 1, 2, 3, 4])
>>> k = b.k
>>> b.t[k:-k]
array([ 0.,  1.,  2.,  3.,  4.])
>>> k
3
```

Construct a quadratic B-spline on `[0, 1, 1, 2]`, and compare to its explicit form:

```
>>> t = [-1, 0, 1, 1, 2]
>>> b = BSpline.basis_element(t[1:])
>>> def f(x):
...     return np.where(x < 1, x*x, (2. - x)**2)
```

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> x = np.linspace(0, 2, 51)
>>> ax.plot(x, b(x), 'g', lw=3)
>>> ax.plot(x, f(x), 'r', lw=8, alpha=0.4)
>>> ax.grid(True)
>>> plt.show()
```



scipy.interpolate.BSpline.derivative

BSpline.**derivative**(*nu=1*)

Return a B-spline representing the derivative.

Parameters

nu [int, optional] Derivative order. Default is 1.

Returns

b [BSpline object] A new instance representing the derivative.

See also:

splder, **splantider**

scipy.interpolate.BSpline.antiderivative

BSpline.**antiderivative**(*nu=1*)

Return a B-spline representing the antiderivative.

Parameters

nu [int, optional] Antiderivative order. Default is 1.

Returns

b [BSpline object] A new instance representing the antiderivative.

See also:

splder, **splantider**

Notes

If antiderivative is computed and `self.extrapolate='periodic'`, it will be set to False for the returned instance. This is done because the antiderivative is no longer periodic and its correct evaluation outside of the initially given x interval is difficult.

scipy.interpolate.BSpline.integrate

BSpline.**integrate**(*a*, *b*, *extrapolate=None*)

Compute a definite integral of the spline.

Parameters

a [float] Lower limit of integration.

b [float] Upper limit of integration.

extrapolate [bool or 'periodic', optional] whether to extrapolate beyond the base interval, `t[k] . . t[-k-1]`, or take the spline to be zero outside of the base interval. If 'periodic', periodic extrapolation is used. If None (default), use *self.extrapolate*.

Returns

I [array_like] Definite integral of the spline over the interval `[a, b]`.

Examples

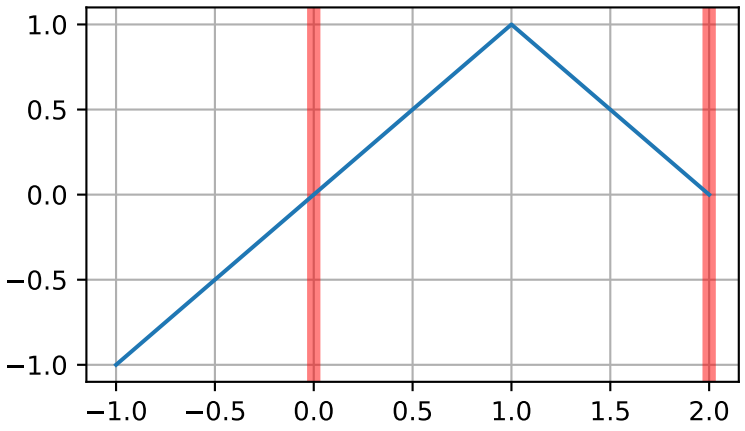
Construct the linear spline `x if x < 1 else 2 - x` on the base interval $[0, 2]$, and integrate it

```
>>> from scipy.interpolate import BSpline
>>> b = BSpline.basis_element([0, 1, 2])
>>> b.integrate(0, 1)
array(0.5)
```

If the integration limits are outside of the base interval, the result is controlled by the *extrapolate* parameter

```
>>> b.integrate(-1, 1)
array(0.0)
>>> b.integrate(-1, 1, extrapolate=False)
array(0.5)
```

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.grid(True)
>>> ax.axvline(0, c='r', lw=5, alpha=0.5)  # base interval
>>> ax.axvline(2, c='r', lw=5, alpha=0.5)
>>> xx = [-1, 1, 2]
>>> ax.plot(xx, b(xx))
>>> plt.show()
```



scipy.interpolate.BSpline.construct_fast

classmethod BSpline.**construct_fast**(*t*, *c*, *k*, *extrapolate=True*, *axis=0*)

Construct a spline without making checks.

Accepts same parameters as the regular constructor. Input arrays *t* and *c* must of correct shape and dtype.

scipy.interpolate.make_interp_spline

scipy.interpolate.**make_interp_spline**(*x*, *y*, *k=3*, *t=None*, *bc_type=None*, *axis=0*, *check_finite=True*)

Compute the (coefficients of) interpolating B-spline.

Parameters

x [array_like, shape (n,)] Abscissas.

y [array_like, shape (n, …)] Ordinates.

k [int, optional] B-spline degree. Default is cubic, k=3.

t [array_like, shape (nt + k + 1,), optional.] Knots. The number of knots needs to agree with the number of datapoints and the number of derivatives at the edges. Specifically, `nt - n` must equal `len(deriv_l) + len(deriv_r)`.

bc_type [2-tuple or None] Boundary conditions. Default is None, which means choosing the boundary conditions automatically. Otherwise, it must be a length-two tuple where the first element sets the boundary conditions at `x[0]` and the second element sets the boundary conditions at `x[-1]`. Each of these must be an iterable of pairs `(order, value)` which gives the values of derivatives of specified orders at the given edge of the interpolation interval. Alternatively, the following string aliases are recognized:

- **`"clamped"`: The first derivatives at the ends are zero. This is** equivalent to `bc_type=([(1, 0.0)], [(1, 0.0)])`.
- `"natural"`: The second derivatives at ends are zero. This is equivalent to `bc_type=([(2, 0.0)], [(2, 0.0)])`.
- `"not-a-knot"` (default): The first and second segments are the same polynomial. This is equivalent to having `bc_type=None`.
- `"periodic"`: The values and the first `k-1` derivatives at the ends are equivalent.

axis [int, optional] Interpolation axis. Default is 0.

check_finite [bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

b [a BSpline object of the degree `k` and with knots `t`.]

See also:

BSpline

base class representing the B-spline objects

CubicSpline

a cubic spline in the polynomial basis

make_lsq_spline

a similar factory function for spline fitting

UnivariateSpline

a wrapper over FITPACK spline fitting routines

splrep

a wrapper over FITPACK spline fitting routines

Examples

Use cubic interpolation on Chebyshev nodes:

```
>>> def cheb_nodes(N):
...     jj = 2.*np.arange(N) + 1
...     x = np.cos(np.pi * jj / 2 / N)[::-1]
...     return x
```

```
>>> x = cheb_nodes(20)
>>> y = np.sqrt(1 - x**2)
```

```
>>> from scipy.interpolate import BSpline, make_interp_spline
>>> b = make_interp_spline(x, y)
>>> np.allclose(b(x), y)
True
```

Note that the default is a cubic spline with a not-a-knot boundary condition

```
>>> b.k
3
```

Here we use a 'natural' spline, with zero 2nd derivatives at edges:

```
>>> l, r = [(2, 0.0)], [(2, 0.0)]
>>> b_n = make_interp_spline(x, y, bc_type=(l, r))  # or, bc_type="natural
↪"
>>> np.allclose(b_n(x), y)
True
>>> x0, x1 = x[0], x[-1]
>>> np.allclose([b_n(x0, 2), b_n(x1, 2)], [0, 0])
True
```

Interpolation of parametric curves is also supported. As an example, we compute a discretization of a snail curve in polar coordinates

```
>>> phi = np.linspace(0, 2.*np.pi, 40)
>>> r = 0.3 + np.cos(phi)
>>> x, y = r*np.cos(phi), r*np.sin(phi)  # convert to Cartesian␣
↪coordinates
```

Build an interpolating curve, parameterizing it by the angle

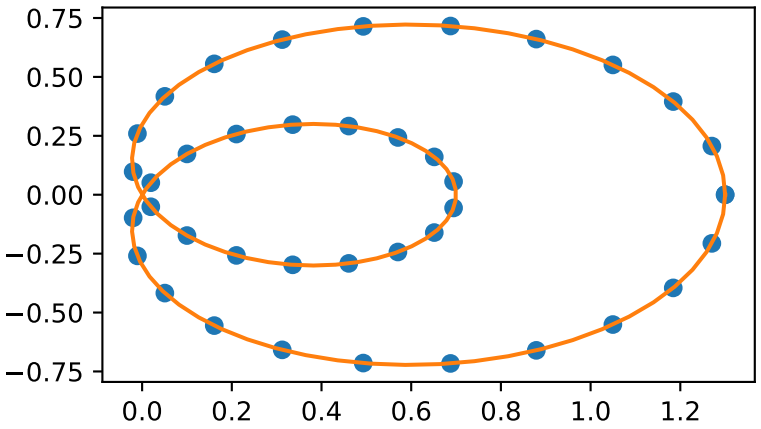
```
>>> from scipy.interpolate import make_interp_spline
>>> spl = make_interp_spline(phi, np.c_[x, y])
```

Evaluate the interpolant on a finer grid (note that we transpose the result to unpack it into a pair of x- and y-arrays)

```
>>> phi_new = np.linspace(0, 2.*np.pi, 100)
>>> x_new, y_new = spl(phi_new).T
```

Plot the result

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'o')
>>> plt.plot(x_new, y_new, '-')
>>> plt.show()
```



Build a B-spline curve with 2 dimensional y

```
>>> x = np.linspace(0, 2*np.pi, 10)
>>> y = np.array([np.sin(x), np.cos(x)])
```

Periodic condition is satisfied because y coordinates of points on the ends are equivalent

```
>>> ax = plt.axes(projection='3d')
>>> xx = np.linspace(0, 2*np.pi, 100)
>>> bspl = make_interp_spline(x, y, k=5, bc_type='periodic', axis=1)
>>> ax.plot3D(xx, *bspl(xx))
>>> ax.scatter3D(x, *y, color='red')
>>> plt.show()
```

scipy.interpolate.make_lsq_spline

scipy.interpolate.**make_lsq_spline**(*x*, *y*, *t*, *k=3*, *w=None*, *axis=0*, *check_finite=True*)

Compute the (coefficients of) an LSQ B-spline.

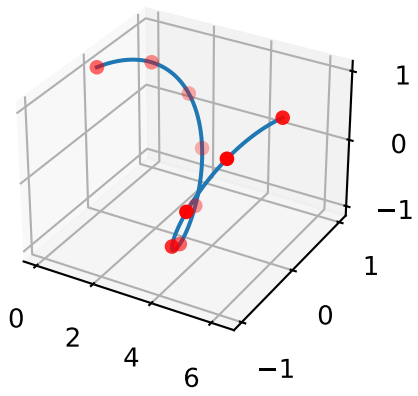
The result is a linear combination

$$S(x) = \sum_j c_j B_j(x; t)$$

of the B-spline basis elements, $B_j(x; t)$, which minimizes

$$\sum_j \left(w_j \times (S(x_j) - y_j) \right)^2$$

Parameters



x	[array_like, shape (m,)] Abscissas.
y	[array_like, shape (m, …)] Ordinates.
t	[array_like, shape (n + k + 1,).] Knots. Knots and data points must satisfy Schoenberg-Whitney conditions.
k	[int, optional] B-spline degree. Default is cubic, k=3.
w	[array_like, shape (n,), optional] Weights for spline fitting. Must be positive. If `None`, then weights are all equal. Default is `None`.
axis	[int, optional] Interpolation axis. Default is zero.
check_finite	[bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

b	[a BSpline object of the degree *k* with knots *t*.]

See also:

`BSpline`

base class representing the B-spline objects

`make_interp_spline`

a similar factory function for interpolating splines

`LSQUnivariateSpline`

a FITPACK-based spline fitting routine

`splrep`

a FITPACK-based fitting routine

Notes

The number of data points must be larger than the spline degree *k*.

Knots *t* must satisfy the Schoenberg-Whitney conditions, i.e., there must be a subset of data points `x[j]` such that `t[j] < x[j] < t[j+k+1]`, for `j=0, 1,...,n-k-2`.

Examples

Generate some noisy data:

```
>>> rng = np.random.default_rng()
>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * rng.standard_normal(50)
```

Now fit a smoothing cubic spline with a pre-defined internal knots. Here we make the knot vector (k+1)-regular by adding boundary knots:

```
>>> from scipy.interpolate import make_lsq_spline, BSpline
>>> t = [-1, 0, 1]
>>> k = 3
>>> t = np.r_[(x[0],)*(k+1),
...           t,
...           (x[-1],)*(k+1)]
>>> spl = make_lsq_spline(x, y, t, k)
```

For comparison, we also construct an interpolating spline for the same set of data:

```
>>> from scipy.interpolate import make_interp_spline
>>> spl_i = make_interp_spline(x, y)
```

Plot both:

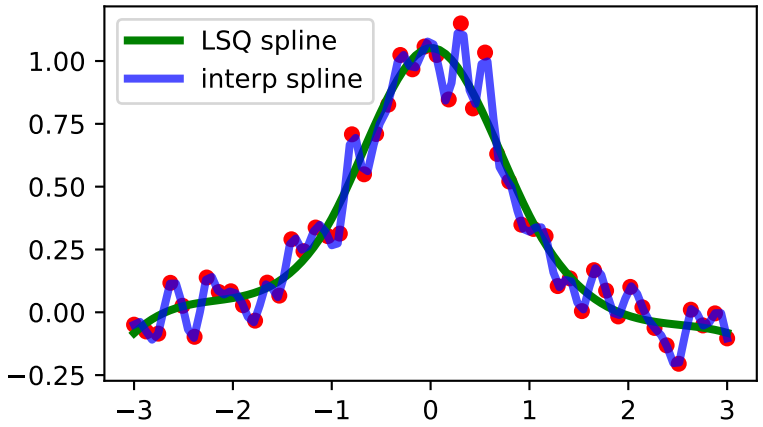
```
>>> import matplotlib.pyplot as plt
>>> xs = np.linspace(-3, 3, 100)
>>> plt.plot(x, y, 'ro', ms=5)
>>> plt.plot(xs, spl(xs), 'g-', lw=3, label='LSQ spline')
>>> plt.plot(xs, spl_i(xs), 'b-', lw=3, alpha=0.7, label='interp spline')
>>> plt.legend(loc='best')
>>> plt.show()
```

NaN handling: If the input arrays contain `nan` values, the result is not useful since the underlying spline fitting routines cannot deal with `nan`. A workaround is to use zero weights for not-a-number data points:

```
>>> y[8] = np.nan
>>> w = np.isnan(y)
>>> y[w] = 0.
>>> tck = make_lsq_spline(x, y, t, w=~w)
```

Notice the need to replace a `nan` by a numerical value (precise value does not matter as long as the corresponding weight is zero.)

Functional interface to FITPACK routines:



splrep(x, y[, w, xb, xe, k, task, s, t, …])	Find the B-spline representation of a 1-D curve.
splprep(x[, w, u, ub, ue, k, task, s, t, …])	Find the B-spline representation of an N-D curve.
splev(x, tck[, der, ext])	Evaluate a B-spline or its derivatives.
splint(a, b, tck[, full_output])	Evaluate the definite integral of a B-spline between two given points.
sproot(tck[, mest])	Find the roots of a cubic B-spline.
spalde(x, tck)	Evaluate all derivatives of a B-spline.
splder(tck[, n])	Compute the spline representation of the derivative of a given spline
splantider(tck[, n])	Compute the spline for the antiderivative (integral) of a given spline.
insert(x, tck[, m, per])	Insert knots into a B-spline.

scipy.interpolate.splrep

scipy.interpolate.**splrep**(*x*, *y*, *w=None*, *xb=None*, *xe=None*, *k=3*, *task=0*, *s=None*, *t=None*, *full_output=0*, *per=0*, *quiet=1*)

Find the B-spline representation of a 1-D curve.

Given the set of data points `(x[i], y[i])` determine a smooth spline approximation of degree k on the interval `xb <= x <= xe`.

Parameters

x, y [array_like] The data points defining a curve y = f(x).

w [array_like, optional] Strictly positive rank-1 array of weights the same length as x and y. The weights are used in computing the weighted least-squares spline fit. If the errors in the y values have standard-deviation given by the vector d, then w should be 1/d. Default is ones(len(x)).

xb, xe [float, optional] The interval to fit. If None, these default to x[0] and x[-1] respectively.

k [int, optional] The degree of the spline fit. It is recommended to use cubic splines. Even values of k should be avoided especially with small s values. 1 <= k <= 5

task [{1, 0, -1}, optional] If task==0 find t and c for a given smoothing factor, s.
If task==1 find t and c for another value of the smoothing factor, s. There must have been a previous call with task=0 or task=1 for the same set of data (t will be stored an used internally)
If task=-1 find the weighted least square spline for a given set of knots, t. These should be interior knots as knots on the ends will be added automatically.

s [float, optional] A smoothing condition. The amount of smoothness is determined by satisfying the conditions: sum((w * (y - g))**2,axis=0) <= s where g(x) is the smoothed interpolation of (x,y). The user can use s to control the tradeoff between closeness and smoothness of fit. Larger s means more smoothing while smaller values of s indicate less smoothing. Recommended values of s depend on the weights, w. If the weights represent the

Returns

tck	[tuple] A tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and the degree of the spline.
fp	[array, optional] The weighted sum of squared residuals of the spline approximation.
ier	[int, optional] An integer flag about splrep success. Success is indicated if ier<=0. If ier in [1,2,3] an error occurred but was not raised. Otherwise an error is raised.
msg	[str, optional] A message corresponding to the integer flag, ier.

See also:

UnivariateSpline, **BivariateSpline**

splprep, **splev**, **sproot**, **spalde**, **splint**

bisplrep, **bisplev**

BSpline

make_interp_spline

Notes

See *splev* for evaluation of the spline and its derivatives. Uses the FORTRAN routine `curfit` from FITPACK.

The user is responsible for assuring that the values of *x* are unique. Otherwise, *splrep* will not return sensible results.

If provided, knots *t* must satisfy the Schoenberg-Whitney conditions, i.e., there must be a subset of data points `x[j]` such that `t[j] < x[j] < t[j+k+1]`, for `j=0, 1,...,n-k-2`.

This routine zero-pads the coefficients array `c` to have the same length as the array of knots `t` (the trailing `k + 1` coefficients are ignored by the evaluation routines, *splev* and *BSpline*.) This is in contrast with *splprep*, which does not zero-pad the coefficients.

References

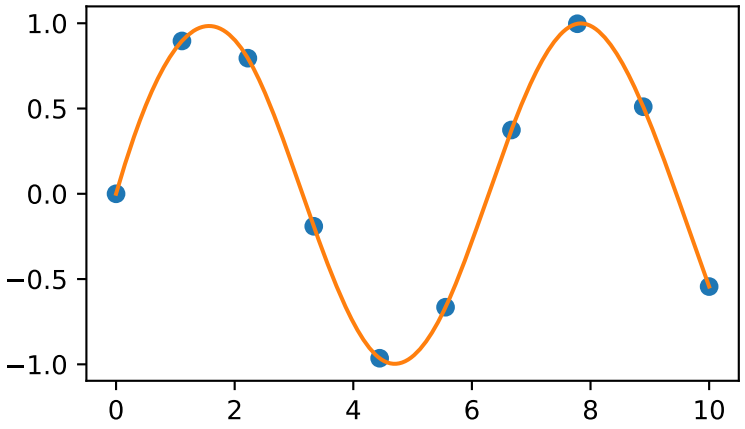
Based on algorithms described in [1], [2], [3], and [4]:

[1], [2], [3], [4]

Examples

You can interpolate 1-D points with a B-spline curve. Further examples are given in *in the tutorial*.

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import splev, splrep
>>> x = np.linspace(0, 10, 10)
>>> y = np.sin(x)
>>> spl = splrep(x, y)
>>> x2 = np.linspace(0, 10, 200)
>>> y2 = splev(x2, spl)
>>> plt.plot(x, y, 'o', x2, y2)
>>> plt.show()
```



scipy.interpolate.splprep

scipy.interpolate.**splprep**(*x*, *w=None*, *u=None*, *ub=None*, *ue=None*, *k=3*, *task=0*, *s=None*, *t=None*, *full_output=0*, *nest=None*, *per=0*, *quiet=1*)

Find the B-spline representation of an N-D curve.

Given a list of N rank-1 arrays, *x*, which represent a curve in N-D space parametrized by *u*, find a smooth approximating spline curve g(*u*). Uses the FORTRAN routine parcur from FITPACK.

Parameters

x [array_like] A list of sample vector arrays representing the curve.

w [array_like, optional] Strictly positive rank-1 array of weights the same length as *x[0]*. The weights are used in computing the weighted least-squares spline fit. If the errors in the *x* values have standard-deviation given by the vector d, then *w* should be 1/d. Default is `ones(len(x[0]))`.

u [array_like, optional] An array of parameter values. If not given, these values are calculated automatically as `M = len(x[0])`, where

v[0] = 0
v[i] = v[i-1] + distance(*x[i]*, *x[i-1]*)
u[i] = v[i] / v[M-1]

ub, ue [int, optional] The end-points of the parameters interval. Defaults to u[0] and u[-1].

k [int, optional] Degree of the spline. Cubic splines are recommended. Even values of *k* should be avoided especially with a small s-value. `1 <= k <= 5`, default is 3.

task [int, optional] If task==0 (default), find t and c for a given smoothing factor, s. If task==1, find t and c for another value of the smoothing factor, s. There must have been a previous call with task=0 or task=1 for the same set of data. If task=-1 find the weighted least square spline for a given set of knots, t.

s [float, optional] A smoothing condition. The amount of smoothness is determined by satisfying the conditions: `sum((w * (y - g))**2,axis=0) <= s`, where g(x) is the smoothed interpolation of (x,y). The user can use *s* to control the trade-off between closeness and smoothness of fit. Larger *s* means more smoothing while smaller values of *s* indicate less smoothing. Recommended values of *s* depend on the weights, w. If the weights represent the inverse of the standard-deviation of y, then a good *s* value should be found in the range `(m-sqrt(2*m),m+sqrt(2*m))`, where m is the number of data points in x, y, and w.

t [int, optional] The knots needed for task=-1.

full_output
: [int, optional] If non-zero, then return optional outputs.

nest
: [int, optional] An over-estimate of the total number of knots of the spline to help in determining the storage space. By default nest=m/2. Always large enough is nest=m+k+1.

per
: [int, optional] If non-zero, data points are considered periodic with period `x[m-1] - x[0]` and a smooth periodic spline approximation is returned. Values of `y[m-1]` and `w[m-1]` are not used.

quiet
: [int, optional] Non-zero to suppress messages. This parameter is deprecated; use standard Python warning filters instead.

Returns

tck
: [tuple] (t,c,k) a tuple containing the vector of knots, the B-spline coefficients, and the degree of the spline.

u
: [array] An array of the values of the parameter.

fp
: [float] The weighted sum of squared residuals of the spline approximation.

ier
: [int] An integer flag about splrep success. Success is indicated if ier<=0. If ier in [1,2,3] an error occurred but was not raised. Otherwise an error is raised.

msg
: [str] A message corresponding to the integer flag, ier.

See also:

splrep, **splev**, **sproot**, **spalde**, **splint**

bisplrep, **bisplev**

UnivariateSpline, **BivariateSpline**

BSpline

make_interp_spline

Notes

See *splev* for evaluation of the spline and its derivatives. The number of dimensions N must be smaller than 11.

The number of coefficients in the *c* array is `k+1` less then the number of knots, `len(t)`. This is in contrast with *splrep*, which zero-pads the array of coefficients to have the same length as the array of knots. These additional coefficients are ignored by evaluation routines, *splev* and *BSpline*.

References

[1], [2], [3]

Examples

Generate a discretization of a limacon curve in the polar coordinates:

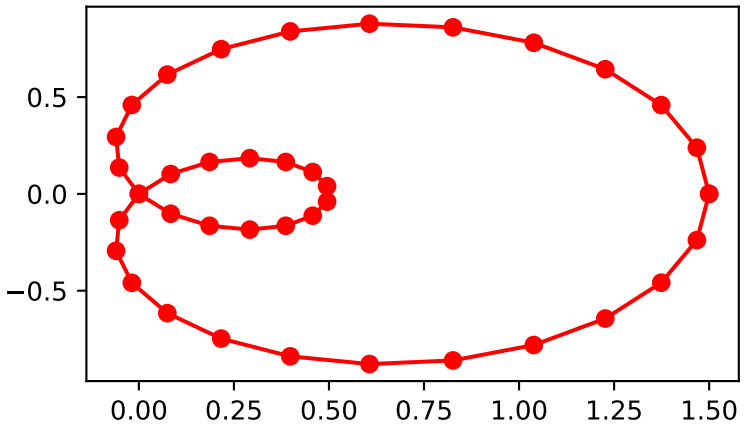
```
>>> phi = np.linspace(0, 2.*np.pi, 40)
>>> r = 0.5 + np.cos(phi)          # polar coords
>>> x, y = r * np.cos(phi), r * np.sin(phi)    # convert to cartesian
```

And interpolate:

```
>>> from scipy.interpolate import splprep, splev
>>> tck, u = splprep([x, y], s=0)
>>> new_points = splev(u, tck)
```

Notice that (i) we force interpolation by using *s=0*, (ii) the parameterization, `u`, is generated automatically. Now plot the result:

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.plot(x, y, 'ro')
>>> ax.plot(new_points[0], new_points[1], 'r-')
>>> plt.show()
```



scipy.interpolate.splev

`scipy.interpolate.`**splev**(*x*, *tck*, *der=0*, *ext=0*)

Evaluate a B-spline or its derivatives.

Given the knots and coefficients of a B-spline representation, evaluate the value of the smoothing polynomial and its derivatives. This is a wrapper around the FORTRAN routines splev and splder of FITPACK.

Parameters

x [array_like] An array of points at which to return the value of the smoothed spline or its derivatives. If *tck* was returned from *splprep*, then the parameter values, u should be given.

tck [3-tuple or a BSpline object] If a tuple, then it should be a sequence of length 3 returned by *splrep* or *splprep* containing the knots, coefficients, and degree of the spline. (Also see Notes.)

der [int, optional] The order of derivative of the spline to compute (must be less than or equal to k, the degree of the spline).

ext [int, optional] Controls the value returned for elements of `x` not in the interval defined by the knot sequence.

- if ext=0, return the extrapolated value.
- if ext=1, return 0
- if ext=2, raise a ValueError

- if ext=3, return the boundary value.

The default value is 0.

Returns

y [ndarray or list of ndarrays] An array of values representing the spline function evaluated at the points in *x*. If *tck* was returned from `splprep`, then this is a list of arrays representing the curve in an N-D space.

See also:

splprep, **splrep**, **sproot**, **spalde**, **splint**

bisplrep, **bisplev**

BSpline

Notes

Manipulating the tck-tuples directly is not recommended. In new code, prefer using `BSpline` objects.

References

[1], [2], [3]

Examples

Examples are given *in the tutorial*.

scipy.interpolate.splint

scipy.interpolate.**splint**(*a*, *b*, *tck*, *full_output=0*)

Evaluate the definite integral of a B-spline between two given points.

Parameters

a, b [float] The end-points of the integration interval.

tck [tuple or a BSpline instance] If a tuple, then it should be a sequence of length 3, containing the vector of knots, the B-spline coefficients, and the degree of the spline (see `splev`).

full_output [int, optional] Non-zero to return optional output.

Returns

integral [float] The resulting integral.

wrk [ndarray] An array containing the integrals of the normalized B-splines defined on the set of knots. (Only returned if *full_output* is non-zero)

See also:

splprep, **splrep**, **sproot**, **spalde**, **splev**

bisplrep, **bisplev**

BSpline

Notes

splint silently assumes that the spline function is zero outside the data interval (*a*, *b*).

Manipulating the tck-tuples directly is not recommended. In new code, prefer using the *BSpline* objects.

References

[1], [2]

Examples

Examples are given *in the tutorial*.

scipy.interpolate.sproot

scipy.interpolate.**sproot**(*tck*, *mest=10*)

Find the roots of a cubic B-spline.

Given the knots (>=8) and coefficients of a cubic B-spline return the roots of the spline.

Parameters

tck [tuple or a BSpline object] If a tuple, then it should be a sequence of length 3, containing the vector of knots, the B-spline coefficients, and the degree of the spline. The number of knots must be >= 8, and the degree must be 3. The knots must be a montonically increasing sequence.

mest [int, optional] An estimate of the number of zeros (Default is 10).

Returns

zeros [ndarray] An array giving the roots of the spline.

See also:

splprep, **splrep**, **splint**, **spalde**, **splev**

bisplrep, **bisplev**

BSpline

Notes

Manipulating the tck-tuples directly is not recommended. In new code, prefer using the *BSpline* objects.

References

[1], [2], [3]

Examples

Examples are given *in the tutorial*.

scipy.interpolate.spalde

scipy.interpolate.**spalde**(*x*, *tck*)

Evaluate all derivatives of a B-spline.

Given the knots and coefficients of a cubic B-spline compute all derivatives up to order k at a point (or set of points).

Parameters

x [array_like] A point or a set of points at which to evaluate the derivatives. Note that `t(k) <= x <= t(n-k+1)` must hold for each *x*.

tck [tuple] A tuple `(t, c, k)`, containing the vector of knots, the B-spline coefficients, and the degree of the spline (see *splev*).

Returns

results [{ndarray, list of ndarrays}] An array (or a list of arrays) containing all derivatives up to order k inclusive for each point *x*.

See also:

splprep, **splrep**, **splint**, **sproot**, **splev**, **bisplrep**, **bisplev**

BSpline

References

[1], [2], [3]

Examples

Examples are given *in the tutorial*.

scipy.interpolate.splder

scipy.interpolate.**splder**(*tck*, *n=1*)

Compute the spline representation of the derivative of a given spline

Parameters

tck [BSpline instance or a tuple of (t, c, k)] Spline whose derivative to compute

n [int, optional] Order of derivative to evaluate. Default: 1

Returns

***BSpline* instance or tuple**

Spline of order k2=k-n representing the derivative of the input spline. A tuple is returned iff the input argument *tck* is a tuple, otherwise a BSpline object is constructed and returned.

See also:

splantider, **splev**, **spalde**

BSpline

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```
>>> from scipy.interpolate import splrep, splder, sproot
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = splrep(x, y, k=4)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: *sproot* only works for order 3 splines, so we fit an order 4 spline):

```
>>> dspl = splder(spl)
>>> sproot(dspl) / np.pi
array([ 0.50000001,  1.5       ,  2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of $\cos(x) = \sin'(x)$.

scipy.interpolate.splantider

scipy.interpolate.**splantider**(*tck*, *n=1*)

Compute the spline for the antiderivative (integral) of a given spline.

Parameters

tck : [BSpline instance or a tuple of (t, c, k)] Spline whose antiderivative to compute

n : [int, optional] Order of antiderivative to evaluate. Default: 1

Returns

BSpline instance or a tuple of (t2, c2, k2)

Spline of order k2=k+n representing the antiderivative of the input spline. A tuple is returned iff the input argument *tck* is a tuple, otherwise a BSpline object is constructed and returned.

See also:

splder, **splev**, **spalde**

BSpline

Notes

The *splder* function is the inverse operation of this function. Namely, `splder(splantider(tck))` is identical to *tck*, modulo rounding error.

New in version 0.13.0.

Examples

```
>>> from scipy.interpolate import splrep, splder, splantider, splev
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = splrep(x, y)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> splev(1.7, spl), splev(1.7, splder(splantider(spl)))
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = splantider(spl)
>>> splev(np.pi/2, ispl) - splev(0, ispl)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2} [1 - m \sin^2 x]^{-1/2} dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

scipy.interpolate.insert

scipy.interpolate.**insert**(*x*, *tck*, *m=1*, *per=0*)

Insert knots into a B-spline.

Given the knots and coefficients of a B-spline representation, create a new B-spline with a knot inserted *m* times at point *x*. This is a wrapper around the FORTRAN routine insert of FITPACK.

Parameters

x (u) [array_like] A 1-D point at which to insert a new knot(s). If *tck* was returned from `splprep`, then the parameter values, u should be given.

tck [a *BSpline* instance or a tuple] If tuple, then it is expected to be a tuple (t,c,k) containing the vector of knots, the B-spline coefficients, and the degree of the spline.

m [int, optional] The number of times to insert the given knot (its multiplicity). Default is 1.

per [int, optional] If non-zero, the input spline is considered periodic.

Returns

BSpline instance or a tuple

A new B-spline with knots t, coefficients c, and degree k. `t(k+1) <= x <= t(n-k)`, where k is the degree of the spline. In case of a periodic spline (`per != 0`) there must be either at least k interior knots t(j) satisfying `t(k+1)<t(j)<=x` or at least k interior knots t(j) satisfying `x<=t(j)<t(n-k)`. A tuple is returned iff the input argument *tck* is a tuple, otherwise a BSpline object is constructed and returned.

Notes

Based on algorithms from [1] and [2].

Manipulating the tck-tuples directly is not recommended. In new code, prefer using the *BSpline* objects.

References

[1], [2]

Examples

You can insert knots into a B-spline.

```
>>> from scipy.interpolate import splrep, insert
>>> x = np.linspace(0, 10, 5)
>>> y = np.sin(x)
>>> tck = splrep(x, y)
>>> tck[0]
array([ 0.,  0.,  0.,  0.,  5., 10., 10., 10., 10.])
```

A knot is inserted:

```
>>> tck_inserted = insert(3, tck)
>>> tck_inserted[0]
array([ 0.,  0.,  0.,  0.,  3.,  5., 10., 10., 10., 10.])
```

Some knots are inserted:

```
>>> tck_inserted2 = insert(8, tck, m=3)
>>> tck_inserted2[0]
array([ 0.,  0.,  0.,  0.,  5.,  8.,  8.,  8., 10., 10., 10., 10.])
```

Object-oriented FITPACK interface:

UnivariateSpline(x, y[, w, bbox, k, s, ext, …])	1-D smoothing spline fit to a given set of data points.
InterpolatedUnivariateSpline(x, y[, w, …])	1-D interpolating spline for a given set of data points.
LSQUnivariateSpline(x, y, t[, w, bbox, k, …])	1-D spline with explicit internal knots.

scipy.interpolate.UnivariateSpline

class scipy.interpolate.**UnivariateSpline**(*x*, *y*, *w=None*, *bbox=[None, None]*, *k=3*, *s=None*, *ext=0*, *check_finite=False*)

1-D smoothing spline fit to a given set of data points.

Fits a spline y = spl(x) of degree *k* to the provided *x*, *y* data. *s* specifies the number of knots by specifying a smoothing condition.

Parameters

x [(N,) array_like] 1-D array of independent input data. Must be increasing; must be strictly increasing if *s* is 0.

y [(N,) array_like] 1-D array of dependent input data, of the same length as *x*.

w [(N,) array_like, optional] Weights for spline fitting. Must be positive. If *w* is None, weights are all equal. Default is None.

bbox [(2,) array_like, optional] 2-sequence specifying the boundary of the approximation interval. If *bbox* is None, `bbox=[x[0], x[-1]]`. Default is None.

k [int, optional] Degree of the smoothing spline. Must be 1 <= *k* <= 5. `k = 3` is a cubic spline. Default is 3.

s [float or None, optional] Positive smoothing factor used to choose the number of knots. Number of knots will be increased until the smoothing condition is satisfied:

```
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0) <= s
```

If *s* is None, `s = len(w)` which should be a good value if `1/w[i]` is an estimate of the standard deviation of `y[i]`. If 0, spline will interpolate through all data points. Default is None.

ext [int or str, optional] Controls the extrapolation mode for elements not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 of 'const', return the boundary value.

Default is 0.

check_finite [bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination or non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

See also:

BivariateSpline

a base class for bivariate splines.

SmoothBivariateSpline

a smoothing bivariate spline through the given points

LSQBivariateSpline

a bivariate spline using weighted least-squares fitting

RectSphereBivariateSpline

a bivariate spline over a rectangular mesh on a sphere

SmoothSphereBivariateSpline

a smoothing bivariate spline in spherical coordinates

LSQSphereBivariateSpline

a bivariate spline in spherical coordinates using weighted least-squares fitting

RectBivariateSpline

a bivariate spline over a rectangular mesh

InterpolatedUnivariateSpline

a interpolating univariate spline for a given set of data points.

bisplrep

a function to find a bivariate B-spline representation of a surface

bisplev

a function to evaluate a bivariate B-spline and its derivatives

splrep

a function to find the B-spline representation of a 1-D curve

splev

a function to evaluate a B-spline or its derivatives

sproot

a function to find the roots of a cubic B-spline

splint

a function to evaluate the definite integral of a B-spline between two given points

spalde

a function to evaluate all derivatives of a B-spline

Notes

The number of data points must be larger than the spline degree k.

NaN handling: If the input arrays contain `nan` values, the result is not useful, since the underlying spline fitting routines cannot deal with `nan`. A workaround is to use zero weights for not-a-number data points:

```
>>> from scipy.interpolate import UnivariateSpline
>>> x, y = np.array([1, 2, 3, 4]), np.array([1, np.nan, 3, 4])
>>> w = np.isnan(y)
>>> y[w] = 0.
>>> spl = UnivariateSpline(x, y, w=~w)
```

Notice the need to replace a `nan` by a numerical value (precise value does not matter as long as the corresponding weight is zero.)

Examples

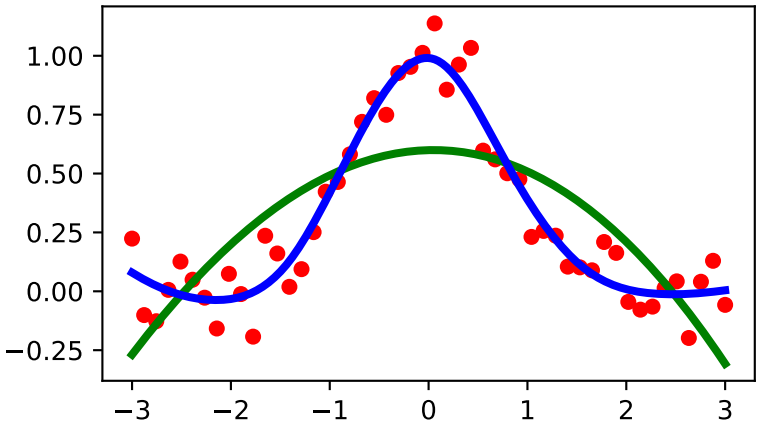
```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import UnivariateSpline
>>> rng = np.random.default_rng()
>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * rng.standard_normal(50)
>>> plt.plot(x, y, 'ro', ms=5)
```

Use the default value for the smoothing parameter:

```
>>> spl = UnivariateSpline(x, y)
>>> xs = np.linspace(-3, 3, 1000)
>>> plt.plot(xs, spl(xs), 'g', lw=3)
```

Manually change the amount of smoothing:

```
>>> spl.set_smoothing_factor(0.5)
>>> plt.plot(xs, spl(xs), 'b', lw=3)
>>> plt.show()
```



Methods

__call__(x[, nu, ext])	Evaluate spline (or its nu-th derivative) at positions x.
antiderivative([n])	Construct a new spline representing the antiderivative of this spline.
derivative([n])	Construct a new spline representing the derivative of this spline.
derivatives(x)	Return all derivatives of the spline at the point x.
get_coeffs()	Return spline coefficients.
get_knots()	Return positions of interior knots of the spline.
get_residual()	Return weighted sum of squared residuals of the spline approximation.
integral(a, b)	Return definite integral of the spline between two given points.
roots()	Return the zeros of the spline.
set_smoothing_factor(s)	Continue spline computation with the given smoothing factor s and with the knots found at the last call.

scipy.interpolate.UnivariateSpline.__call__

UnivariateSpline.**__call__**(*x*, *nu=0*, *ext=None*)

Evaluate spline (or its nu-th derivative) at positions x.

Parameters

x [array_like] A 1-D array of points at which to return the value of the smoothed spline or its derivatives. Note: *x* can be unordered but the evaluation is more efficient if *x* is (partially) ordered.

nu [int] The order of derivative of the spline to compute.

ext [int] Controls the value returned for elements of *x* not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 or 'const', return the boundary value.

The default value is 0, passed from the initialization of UnivariateSpline.

scipy.interpolate.UnivariateSpline.antiderivative

Notes

New in version 0.13.0.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2}[1 - m\sin^2 x]^{-1/2}dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

scipy.interpolate.UnivariateSpline.derivative

UnivariateSpline.**derivative**(*n=1*)

Construct a new spline representing the derivative of this spline.

Parameters

n [int, optional] Order of derivative to evaluate. Default: 1

Returns

spline [UnivariateSpline] Spline of order k2=k-n representing the derivative of this spline.

See also:

splder, **antiderivative**

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: *sproot* only works for order 3 splines, so we fit an order 4 spline):

```
>>> spl.derivative().roots() / np.pi
array([ 0.50000001,  1.5       ,  2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of $\cos(x) = \sin'(x)$.

scipy.interpolate.UnivariateSpline.derivatives

UnivariateSpline.**derivatives**(*x*)

Return all derivatives of the spline at the point x.

Parameters

x [float] The point to evaluate the derivatives at.

Returns

der [ndarray, shape(k+1,)] Derivatives of the orders 0 to k.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

scipy.interpolate.UnivariateSpline.get_coeffs

UnivariateSpline.**get_coeffs**()
Return spline coefficients.

scipy.interpolate.UnivariateSpline.get_knots

UnivariateSpline.**get_knots**()
Return positions of interior knots of the spline.

Internally, the knot vector contains `2*k` additional boundary knots.

scipy.interpolate.UnivariateSpline.get_residual

UnivariateSpline.**get_residual**()
Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

```
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0)
```

scipy.interpolate.UnivariateSpline.integral

UnivariateSpline.**integral**(*a*, *b*)
Return definite integral of the spline between two given points.

Parameters

a [float] Lower limit of integration.
b [float] Upper limit of integration.

Returns

integral [float] The value of the definite integral of the spline between limits.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
```

which agrees with $\int x^2 dx = x^3/3$ between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

scipy.interpolate.UnivariateSpline.roots

UnivariateSpline.**roots**()
Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

scipy.interpolate.UnivariateSpline.set_smoothing_factor

UnivariateSpline.**set_smoothing_factor**(*s*)
Continue spline computation with the given smoothing factor s and with the knots found at the last call.

This routine modifies the spline in place.

validate_input	

scipy.interpolate.InterpolatedUnivariateSpline

class scipy.interpolate.**InterpolatedUnivariateSpline**(*x*, *y*, *w=None*, *bbox=[None, None]*, *k=3*, *ext=0*, *check_finite=False*)

1-D interpolating spline for a given set of data points.

Fits a spline y = spl(x) of degree *k* to the provided *x*, *y* data. Spline function passes through all provided points. Equivalent to *UnivariateSpline* with s=0.

Parameters

x [(N,) array_like] Input dimension of data points – must be strictly increasing

y [(N,) array_like] input dimension of data points

w [(N,) array_like, optional] Weights for spline fitting. Must be positive. If None (default), weights are all equal.

bbox [(2,) array_like, optional] 2-sequence specifying the boundary of the approximation interval. If None (default), `bbox=[x[0], x[-1]]`.

k [int, optional] Degree of the smoothing spline. Must be 1 <= *k* <= 5.

ext [int or str, optional] Controls the extrapolation mode for elements not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 of 'const', return the boundary value.

The default value is 0.

check_finite [bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination or non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

See also:

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

LSQUnivariateSpline

a spline for which knots are user-selected

SmoothBivariateSpline

a smoothing bivariate spline through the given points

LSQBivariateSpline

a bivariate spline using weighted least-squares fitting

splrep

a function to find the B-spline representation of a 1-D curve

splev

a function to evaluate a B-spline or its derivatives

sproot

a function to find the roots of a cubic B-spline

splint

a function to evaluate the definite integral of a B-spline between two given points

spalde

a function to evaluate all derivatives of a B-spline

Notes

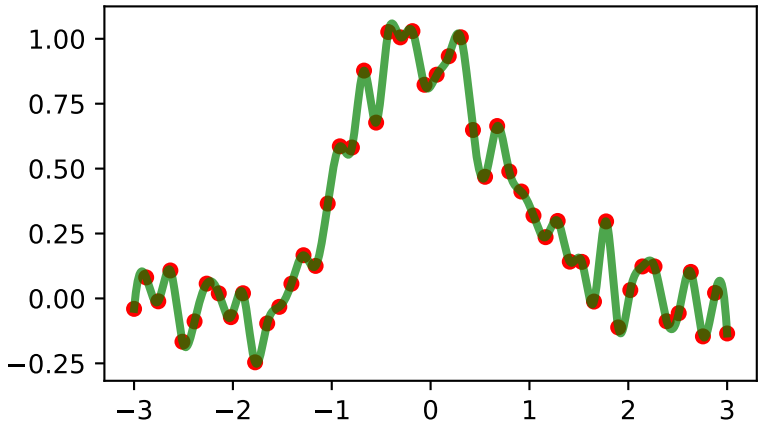
The number of data points must be larger than the spline degree k.

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import InterpolatedUnivariateSpline
>>> rng = np.random.default_rng()
>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * rng.standard_normal(50)
>>> spl = InterpolatedUnivariateSpline(x, y)
>>> plt.plot(x, y, 'ro', ms=5)
>>> xs = np.linspace(-3, 3, 1000)
>>> plt.plot(xs, spl(xs), 'g', lw=3, alpha=0.7)
>>> plt.show()
```

Notice that the `spl(x)` interpolates *y*:

```
>>> spl.get_residual()
0.0
```



Methods

__call__(x[, nu, ext])	Evaluate spline (or its nu-th derivative) at positions x.
antiderivative([n])	Construct a new spline representing the antiderivative of this spline.
derivative([n])	Construct a new spline representing the derivative of this spline.
derivatives(x)	Return all derivatives of the spline at the point x.
get_coeffs()	Return spline coefficients.
get_knots()	Return positions of interior knots of the spline.
get_residual()	Return weighted sum of squared residuals of the spline approximation.
integral(a, b)	Return definite integral of the spline between two given points.
roots()	Return the zeros of the spline.
set_smoothing_factor(s)	Continue spline computation with the given smoothing factor s and with the knots found at the last call.

scipy.interpolate.InterpolatedUnivariateSpline.__call__

InterpolatedUnivariateSpline.**__call__**(*x*, *nu=0*, *ext=None*)

Evaluate spline (or its nu-th derivative) at positions x.

Parameters

x [array_like] A 1-D array of points at which to return the value of the smoothed spline or its derivatives. Note: *x* can be unordered but the evaluation is more efficient if *x* is (partially) ordered.

nu [int] The order of derivative of the spline to compute.

ext [int] Controls the value returned for elements of *x* not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 or 'const', return the boundary value.

The default value is 0, passed from the initialization of UnivariateSpline.

scipy.interpolate.InterpolatedUnivariateSpline.antiderivative

Notes

New in version 0.13.0.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2}[1 - m\sin^2 x]^{-1/2}dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

scipy.interpolate.InterpolatedUnivariateSpline.derivative

InterpolatedUnivariateSpline.**derivative**(*n=1*)

Construct a new spline representing the derivative of this spline.

Parameters

n [int, optional] Order of derivative to evaluate. Default: 1

Returns

spline [UnivariateSpline] Spline of order k2=k-n representing the derivative of this spline.

See also:

splder, **antiderivative**

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: *sproot* only works for order 3 splines, so we fit an order 4 spline):

```
>>> spl.derivative().roots() / np.pi
array([ 0.50000001,  1.5       ,  2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of $\cos(x) = \sin'(x)$.

scipy.interpolate.InterpolatedUnivariateSpline.derivatives

InterpolatedUnivariateSpline.**derivatives**(*x*)

Return all derivatives of the spline at the point x.

Parameters

x [float] The point to evaluate the derivatives at.

Returns

der [ndarray, shape(k+1,)] Derivatives of the orders 0 to k.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

scipy.interpolate.InterpolatedUnivariateSpline.get_coeffs

InterpolatedUnivariateSpline.**get_coeffs**()
Return spline coefficients.

scipy.interpolate.InterpolatedUnivariateSpline.get_knots

InterpolatedUnivariateSpline.**get_knots**()
Return positions of interior knots of the spline.

Internally, the knot vector contains `2*k` additional boundary knots.

scipy.interpolate.InterpolatedUnivariateSpline.get_residual

InterpolatedUnivariateSpline.**get_residual**()
Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

```
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0)
```

scipy.interpolate.InterpolatedUnivariateSpline.integral

InterpolatedUnivariateSpline.**integral**(*a*, *b*)
Return definite integral of the spline between two given points.

Parameters

a [float] Lower limit of integration.
b [float] Upper limit of integration.

Returns

integral [float] The value of the definite integral of the spline between limits.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
```

which agrees with $\int x^2 dx = x^3/3$ between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

scipy.interpolate.InterpolatedUnivariateSpline.roots

InterpolatedUnivariateSpline.**roots**()

Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

scipy.interpolate.InterpolatedUnivariateSpline.set_smoothing_factor

InterpolatedUnivariateSpline.**set_smoothing_factor**(*s*)

Continue spline computation with the given smoothing factor s and with the knots found at the last call.

This routine modifies the spline in place.

validate_input	

scipy.interpolate.LSQUnivariateSpline

class scipy.interpolate.**LSQUnivariateSpline**(*x*, *y*, *t*, *w=None*, *bbox=[None, None]*, *k=3*, *ext=0*, *check_finite=False*)

1-D spline with explicit internal knots.

Fits a spline y = spl(x) of degree *k* to the provided *x*, *y* data. *t* specifies the internal knots of the spline

Parameters

x [(N,) array_like] Input dimension of data points – must be increasing

y [(N,) array_like] Input dimension of data points

t [(M,) array_like] interior knots of the spline. Must be in ascending order and:

```
bbox[0] < t[0] < ... < t[-1] < bbox[-1]
```

w [(N,) array_like, optional] weights for spline fitting. Must be positive. If None (default), weights are all equal.

bbox [(2,) array_like, optional] 2-sequence specifying the boundary of the approximation interval. If None (default), `bbox = [x[0], x[-1]]`.

k [int, optional] Degree of the smoothing spline. Must be 1 <= *k* <= 5. Default is *k* = 3, a cubic spline.

ext [int or str, optional] Controls the extrapolation mode for elements not in the interval defined by the knot sequence.

- if ext=0 or 'extrapolate', return the extrapolated value.
- if ext=1 or 'zeros', return 0
- if ext=2 or 'raise', raise a ValueError
- if ext=3 of 'const', return the boundary value.

The default value is 0.

check_finite

[bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination or non-sensical results) if the inputs do contain infinities or NaNs. Default is False.

Raises

ValueError

If the interior knots do not satisfy the Schoenberg-Whitney conditions

See also:

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

InterpolatedUnivariateSpline

a interpolating univariate spline for a given set of data points.

splrep

a function to find the B-spline representation of a 1-D curve

splev

a function to evaluate a B-spline or its derivatives

sproot

a function to find the roots of a cubic B-spline

splint

a function to evaluate the definite integral of a B-spline between two given points

spalde

a function to evaluate all derivatives of a B-spline

Notes

The number of data points must be larger than the spline degree *k*.

Knots *t* must satisfy the Schoenberg-Whitney conditions, i.e., there must be a subset of data points `x[j]` such that `t[j] < x[j] < t[j+k+1]`, for `j=0, 1,...,n-k-2`.

Examples

```
>>> from scipy.interpolate import LSQUnivariateSpline, UnivariateSpline
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> x = np.linspace(-3, 3, 50)
>>> y = np.exp(-x**2) + 0.1 * rng.standard_normal(50)
```

Fit a smoothing spline with a pre-defined internal knots:

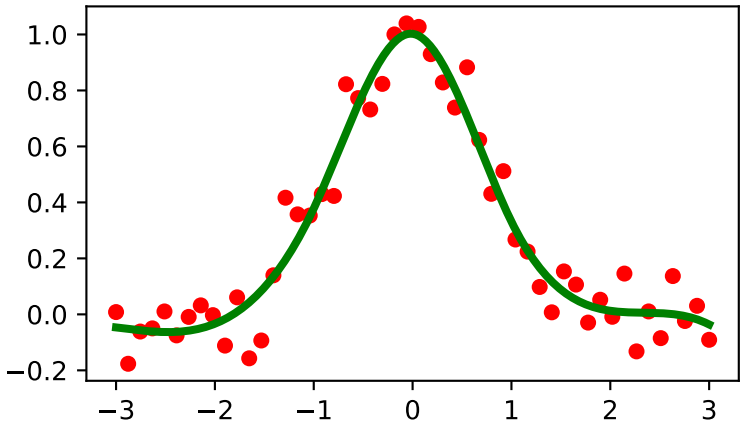
```
>>> t = [-1, 0, 1]
>>> spl = LSQUnivariateSpline(x, y, t)
```

```
>>> xs = np.linspace(-3, 3, 1000)
>>> plt.plot(x, y, 'ro', ms=5)
>>> plt.plot(xs, spl(xs), 'g-', lw=3)
>>> plt.show()
```

Check the knot vector:

```
>>> spl.get_knots()
array([-3., -1., 0., 1., 3.])
```

Constructing lsq spline using the knots from another spline:




```
>>> x = np.arange(10)
>>> s = UnivariateSpline(x, x, s=0)
>>> s.get_knots()
array([ 0.,  2.,  3.,  4.,  5.,  6.,  7.,  9.])
>>> knt = s.get_knots()
>>> s1 = LSQUnivariateSpline(x, x, knt[1:-1])    # Chop 1st and last knot
>>> s1.get_knots()
array([ 0.,  2.,  3.,  4.,  5.,  6.,  7.,  9.])
```

Methods

__call__(x[, nu, ext])	Evaluate spline (or its nu-th derivative) at positions x.
antiderivative([n])	Construct a new spline representing the antiderivative of this spline.
derivative([n])	Construct a new spline representing the derivative of this spline.
derivatives(x)	Return all derivatives of the spline at the point x.
get_coeffs()	Return spline coefficients.
get_knots()	Return positions of interior knots of the spline.
get_residual()	Return weighted sum of squared residuals of the spline approximation.
integral(a, b)	Return definite integral of the spline between two given points.
roots()	Return the zeros of the spline.
set_smoothing_factor(s)	Continue spline computation with the given smoothing factor s and with the knots found at the last call.

scipy.interpolate.LSQUnivariateSpline.__call__

LSQUnivariateSpline.**__call__**(*x*, *nu=0*, *ext=None*)

Evaluate spline (or its nu-th derivative) at positions x.

Parameters

x [array_like] A 1-D array of points at which to return the value of the smoothed spline or its derivatives. Note: *x* can be unordered but the evaluation is more efficient if *x* is (partially) ordered.

nu [int] The order of derivative of the spline to compute.

scipy.interpolate.LSQUnivariateSpline.antiderivative

LSQUnivariateSpline.**antiderivative**(*n=1*)

Construct a new spline representing the antiderivative of this spline.

Parameters

n [int, optional] Order of antiderivative to evaluate. Default: 1

Returns

spline [UnivariateSpline] Spline of order k2=k+n representing the antiderivative of this spline.

See also:

splantider, **derivative**

Notes

New in version 0.13.0.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, np.pi/2, 70)
>>> y = 1 / np.sqrt(1 - 0.8*np.sin(x)**2)
>>> spl = UnivariateSpline(x, y, s=0)
```

The derivative is the inverse operation of the antiderivative, although some floating point error accumulates:

```
>>> spl(1.7), spl.antiderivative().derivative()(1.7)
(array(2.1565429877197317), array(2.1565429877201865))
```

Antiderivative can be used to evaluate definite integrals:

```
>>> ispl = spl.antiderivative()
>>> ispl(np.pi/2) - ispl(0)
2.2572053588768486
```

This is indeed an approximation to the complete elliptic integral $K(m) = \int_0^{\pi/2}[1 - m\sin^2 x]^{-1/2}dx$:

```
>>> from scipy.special import ellipk
>>> ellipk(0.8)
2.2572053268208538
```

scipy.interpolate.LSQUnivariateSpline.derivative

LSQUnivariateSpline.**derivative**(*n=1*)

Construct a new spline representing the derivative of this spline.

Parameters

n [int, optional] Order of derivative to evaluate. Default: 1

Returns

spline [UnivariateSpline] Spline of order k2=k-n representing the derivative of this spline.

See also:

splder, **antiderivative**

Notes

New in version 0.13.0.

Examples

This can be used for finding maxima of a curve:

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 10, 70)
>>> y = np.sin(x)
>>> spl = UnivariateSpline(x, y, k=4, s=0)
```

Now, differentiate the spline and find the zeros of the derivative. (NB: *sproot* only works for order 3 splines, so we fit an order 4 spline):

```
>>> spl.derivative().roots() / np.pi
array([ 0.50000001,  1.5       ,  2.49999998])
```

This agrees well with roots $\pi/2 + n\pi$ of $\cos(x) = \sin'(x)$.

scipy.interpolate.LSQUnivariateSpline.derivatives

LSQUnivariateSpline.**derivatives**(*x*)

Return all derivatives of the spline at the point x.

Parameters

x [float] The point to evaluate the derivatives at.

Returns

der [ndarray, shape(k+1,)] Derivatives of the orders 0 to k.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.derivatives(1.5)
array([2.25, 3.0, 2.0, 0])
```

scipy.interpolate.LSQUnivariateSpline.get_coeffs

LSQUnivariateSpline.**get_coeffs**()
Return spline coefficients.

scipy.interpolate.LSQUnivariateSpline.get_knots

LSQUnivariateSpline.**get_knots**()
Return positions of interior knots of the spline.

Internally, the knot vector contains `2*k` additional boundary knots.

scipy.interpolate.LSQUnivariateSpline.get_residual

LSQUnivariateSpline.**get_residual**()
Return weighted sum of squared residuals of the spline approximation.

This is equivalent to:

```
sum((w[i] * (y[i]-spl(x[i])))**2, axis=0)
```

scipy.interpolate.LSQUnivariateSpline.integral

LSQUnivariateSpline.**integral**(*a*, *b*)
Return definite integral of the spline between two given points.

Parameters

a [float] Lower limit of integration.
b [float] Upper limit of integration.

Returns

integral [float] The value of the definite integral of the spline between limits.

Examples

```
>>> from scipy.interpolate import UnivariateSpline
>>> x = np.linspace(0, 3, 11)
>>> y = x**2
>>> spl = UnivariateSpline(x, y)
>>> spl.integral(0, 3)
9.0
```

which agrees with $\int x^2 dx = x^3/3$ between the limits of 0 and 3.

A caveat is that this routine assumes the spline to be zero outside of the data limits:

```
>>> spl.integral(-1, 4)
9.0
>>> spl.integral(-1, 0)
0.0
```

scipy.interpolate.LSQUnivariateSpline.roots

LSQUnivariateSpline.**roots**()
Return the zeros of the spline.

Restriction: only cubic splines are supported by fitpack.

scipy.interpolate.LSQUnivariateSpline.set_smoothing_factor

LSQUnivariateSpline.**set_smoothing_factor**(*s*)
Continue spline computation with the given smoothing factor s and with the knots found at the last call.

This routine modifies the spline in place.

validate_input	

2-D Splines

For data on a grid:

RectBivariateSpline(x, y, z[, bbox, kx, ky, s])	Bivariate spline approximation over a rectangular mesh.
RectSphereBivariateSpline(u, v, r[, s, …])	Bivariate spline approximation over a rectangular mesh on a sphere.

scipy.interpolate.RectSphereBivariateSpline

class scipy.interpolate.**RectSphereBivariateSpline**(*u*, *v*, *r*, *s=0.0*, *pole_continuity=False*, *pole_values=None*, *pole_exact=False*, *pole_flat=False*)

Bivariate spline approximation over a rectangular mesh on a sphere.

Can be used for smoothing data.

New in version 0.11.0.

Parameters

u [array_like] 1-D array of colatitude coordinates in strictly ascending order. Coordinates must be given in radians and lie within the open interval `(0, pi)`.

v [array_like] 1-D array of longitude coordinates in strictly ascending order. Coordinates must be given in radians. First element (`v[0]`) must lie within the interval `[-pi, pi)`. Last element (`v[-1]`) must satisfy `v[-1] <= v[0] + 2*pi`.

r [array_like] 2-D array of data with shape `(u.size, v.size)`.

s [float, optional] Positive smoothing factor defined for estimation condition (`s=0` is for interpolation).

pole_continuity
[bool or (bool, bool), optional] Order of continuity at the poles `u=0` (`pole_continuity[0]`) and `u=pi` (`pole_continuity[1]`). The order of continuity at the pole will be 1 or 0 when this is True or False, respectively. Defaults to False.

pole_values
[float or (float, float), optional] Data values at the poles `u=0` and `u=pi`. Either the whole parameter or each individual element can be None. Defaults to None.

pole_exact [bool or (bool, bool), optional] Data value exactness at the poles `u=0` and `u=pi`. If True, the value is considered to be the right function value, and it will be fitted exactly. If False, the value will be considered to be a data value just like the other data values. Defaults to False.

pole_flat [bool or (bool, bool), optional] For the poles at `u=0` and `u=pi`, specify whether or not the approximation has vanishing derivatives. Defaults to False.

See also:

BivariateSpline

a base class for bivariate splines.

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

SmoothBivariateSpline

a smoothing bivariate spline through the given points

LSQBivariateSpline

a bivariate spline using weighted least-squares fitting

SmoothSphereBivariateSpline

a smoothing bivariate spline in spherical coordinates

LSQSphereBivariateSpline

a bivariate spline in spherical coordinates using weighted least-squares fitting

RectBivariateSpline

a bivariate spline over a rectangular mesh.

bisplrep

a function to find a bivariate B-spline representation of a surface

bisplev

a function to evaluate a bivariate B-spline and its derivatives

Notes

Currently, only the smoothing spline approximation (`iopt[0] = 0` and `iopt[0] = 1` in the FITPACK routine) is supported. The exact least-squares spline approximation is not implemented yet.

When actually performing the interpolation, the requested *v* values must lie within the same length 2pi interval that the original *v* values were chosen from.

For more information, see the FITPACK site about this function.

Examples

Suppose we have global data on a coarse grid

```
>>> lats = np.linspace(10, 170, 9) * np.pi / 180.
>>> lons = np.linspace(0, 350, 18) * np.pi / 180.
>>> data = np.dot(np.atleast_2d(90. - np.linspace(-80., 80., 18)).T,
...               np.atleast_2d(180. - np.abs(np.linspace(0., 350., 9)))).
 ↪T
```

We want to interpolate it to a global one-degree grid

```
>>> new_lats = np.linspace(1, 180, 180) * np.pi / 180
>>> new_lons = np.linspace(1, 360, 360) * np.pi / 180
>>> new_lats, new_lons = np.meshgrid(new_lats, new_lons)
```

We need to set up the interpolator object

```
>>> from scipy.interpolate import RectSphereBivariateSpline
>>> lut = RectSphereBivariateSpline(lats, lons, data)
```

Finally we interpolate the data. The *RectSphereBivariateSpline* object only takes 1-D arrays as input, therefore we need to do some reshaping.

```
>>> data_interp = lut.ev(new_lats.ravel(),
...                      new_lons.ravel()).reshape((360, 180)).T
```

Looking at the original and the interpolated data, one can see that the interpolant reproduces the original data very well:

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(211)
>>> ax1.imshow(data, interpolation='nearest')
```

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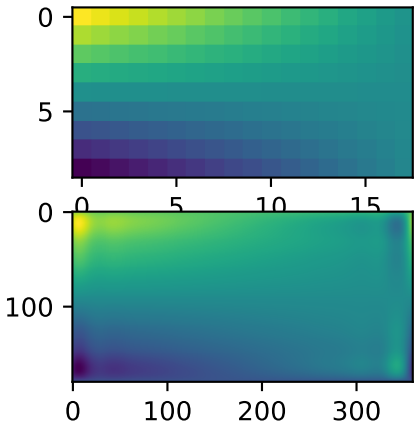
```
>>> ax2 = fig.add_subplot(212)
>>> ax2.imshow(data_interp, interpolation='nearest')
>>> plt.show()
```

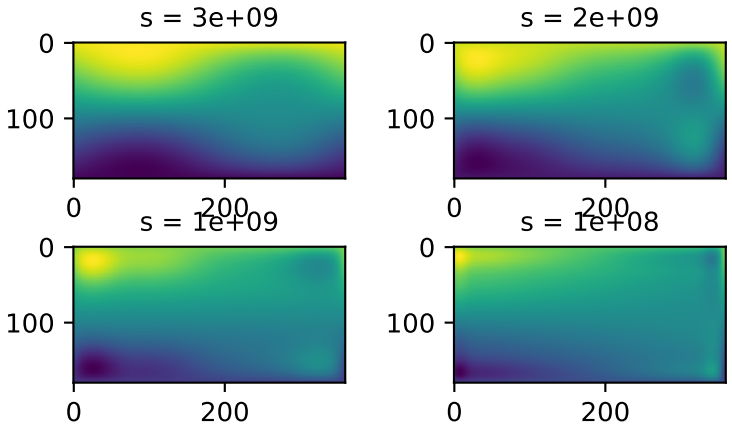


Choosing the optimal value of `s` can be a delicate task. Recommended values for `s` depend on the accuracy of the data values. If the user has an idea of the statistical errors on the data, she can also find a proper estimate for `s`. By assuming that, if she specifies the right `s`, the interpolator will use a spline `f(u,v)` which exactly reproduces the function underlying the data, she can evaluate `sum((r(i,j)-s(u(i),v(j)))**2)` to find a good estimate for this `s`. For example, if she knows that the statistical errors on her `r(i,j)`-values are not greater than 0.1, she may expect that a good `s` should have a value not larger than `u.size * v.size * (0.1)**2`.

If nothing is known about the statistical error in `r(i,j)`, `s` must be determined by trial and error. The best is then to start with a very large value of `s` (to determine the least-squares polynomial and the corresponding upper bound `fp0` for `s`) and then to progressively decrease the value of `s` (say by a factor 10 in the beginning, i.e. `s = fp0 / 10, fp0 / 100, ...` and more carefully as the approximation shows more detail) to obtain closer fits.

The interpolation results for different values of `s` give some insight into this process:

```
>>> fig2 = plt.figure()
>>> s = [3e9, 2e9, 1e9, 1e8]
>>> for ii in range(len(s)):
...     lut = RectSphereBivariateSpline(lats, lons, data, s=s[ii])
...     data_interp = lut.ev(new_lats.ravel(),
...                          new_lons.ravel()).reshape((360, 180)).T
...     ax = fig2.add_subplot(2, 2, ii+1)
...     ax.imshow(data_interp, interpolation='nearest')
...     ax.set_title("s = %g" % s[ii])
>>> plt.show()
```



Methods

__call__(theta, phi[, dtheta, dphi, grid])	Evaluate the spline or its derivatives at given positions.
ev(theta, phi[, dtheta, dphi])	Evaluate the spline at points
get_coeffs()	Return spline coefficients.
get_knots()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
get_residual()	Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

scipy.interpolate.RectSphereBivariateSpline.__call__

RectSphereBivariateSpline.**__call__**(*theta*, *phi*, *dtheta=0*, *dphi=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

theta, phi [array_like] Input coordinates.
If *grid* is False, evaluate the spline at points `(theta[i], phi[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays theta, phi. The arrays must be sorted to increasing order.

dtheta [int, optional] Order of theta-derivative
New in version 0.14.0.

dphi [int] Order of phi-derivative
New in version 0.14.0.

grid [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

scipy.interpolate.RectSphereBivariateSpline.ev

 RectSphereBivariateSpline.**ev**(*theta*, *phi*, *dtheta=0*, *dphi=0*)

Evaluate the spline at points

Returns the interpolated value at `(theta[i], phi[i]), i=0,...,len(theta)-1`.

Parameters

scipy.interpolate.RectSphereBivariateSpline.get_coeffs

RectSphereBivariateSpline.**get_coeffs**()
Return spline coefficients.

scipy.interpolate.RectSphereBivariateSpline.get_knots

RectSphereBivariateSpline.**get_knots**()
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.RectSphereBivariateSpline.get_residual

RectSphereBivariateSpline.**get_residual**()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

For unstructured data:

BivariateSpline()	Base class for bivariate splines.
SmoothBivariateSpline(x, y, z[, w, bbox, …])	Smooth bivariate spline approximation.
SmoothSphereBivariateSpline(theta, phi, r[, …])	Smooth bivariate spline approximation in spherical coordinates.
LSQBivariateSpline(x, y, z, tx, ty[, w, …])	Weighted least-squares bivariate spline approximation.
LSQSphereBivariateSpline(theta, phi, r, tt, tp)	Weighted least-squares bivariate spline approximation in spherical coordinates.

scipy.interpolate.BivariateSpline

class scipy.interpolate.**BivariateSpline**
Base class for bivariate splines.

This describes a spline `s(x, y)` of degrees `kx` and `ky` on the rectangle `[xb, xe] * [yb, ye]` calculated from a given set of data points `(x, y, z)`.

This class is meant to be subclassed, not instantiated directly. To construct these splines, call either *SmoothBivariateSpline* or *LSQBivariateSpline* or *RectBivariateSpline*.

See also:

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

SmoothBivariateSpline

a smoothing bivariate spline through the given points

LSQBivariateSpline

a bivariate spline using weighted least-squares fitting

RectSphereBivariateSpline

a bivariate spline over a rectangular mesh on a sphere

SmoothSphereBivariateSpline

a smoothing bivariate spline in spherical coordinates

LSQSphereBivariateSpline

a bivariate spline in spherical coordinates using weighted least-squares fitting

RectBivariateSpline

a bivariate spline over a rectangular mesh.

bisplrep

a function to find a bivariate B-spline representation of a surface

bisplev

a function to evaluate a bivariate B-spline and its derivatives

Methods

__call__(x, y[, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
ev(xi, yi[, dx, dy])	Evaluate the spline at points
get_coeffs()	Return spline coefficients.
get_knots()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
get_residual()	Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)
integral(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

scipy.interpolate.BivariateSpline.__call__

BivariateSpline.**__call__**(*x*, *y*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

x, y [array_like] Input coordinates.
If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.
Note that the axis ordering is inverted relative to the output of meshgrid.

dx [int] Order of x-derivative
New in version 0.14.0.

dy [int] Order of y-derivative
New in version 0.14.0.

grid [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

scipy.interpolate.BivariateSpline.ev

BivariateSpline.**ev**(*xi*, *yi*, *dx=0*, *dy=0*)

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters

xi, yi	[array_like] Input coordinates. Standard Numpy broadcasting is obeyed.
dx	[int, optional] Order of x-derivative New in version 0.14.0.
dy	[int, optional] Order of y-derivative New in version 0.14.0.

scipy.interpolate.BivariateSpline.get_coeffs

BivariateSpline.**get_coeffs**()

Return spline coefficients.

scipy.interpolate.BivariateSpline.get_knots

BivariateSpline.**get_knots**()

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.BivariateSpline.get_residual

BivariateSpline.**get_residual**()

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

scipy.interpolate.BivariateSpline.integral

BivariateSpline.**integral**(*xa*, *xb*, *ya*, *yb*)

Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters

xa, xb	[float] The end-points of the x integration interval.
ya, yb	[float] The end-points of the y integration interval.

Returns

integ	[float] The value of the resulting integral.

scipy.interpolate.SmoothBivariateSpline

class scipy.interpolate.**SmoothBivariateSpline**(*x*, *y*, *z*, *w=None*, *bbox=[None, None, None, None]*, *kx=3*, *ky=3*, *s=None*, *eps=1e-16*)

Smooth bivariate spline approximation.

Parameters

x, y, z	[array_like] 1-D sequences of data points (order is not important).
w	[array_like, optional] Positive 1-D sequence of weights, of same length as *x*, *y* and *z*.
bbox	[array_like, optional] Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, `bbox=[min(x), max(x), min(y), max(y)]`.
kx, ky	[ints, optional] Degrees of the bivariate spline. Default is 3.
s	[float, optional] Positive smoothing factor defined for estimation condition: `sum((w[i]*(z[i]-s(x[i], y[i])))**2, axis=0) <= s` Default `s=len(w)` which should be a good value if `1/w[i]` is an estimate of the standard deviation of `z[i]`.
eps	[float, optional] A threshold for determining the effective rank of an over-determined linear system of equations. *eps* should have a value within the open interval `(0, 1)`, the default is 1e-16.

See also:

BivariateSpline

a base class for bivariate splines.

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

LSQBivariateSpline

a bivariate spline using weighted least-squares fitting

RectSphereBivariateSpline

a bivariate spline over a rectangular mesh on a sphere

SmoothSphereBivariateSpline

a smoothing bivariate spline in spherical coordinates

LSQSphereBivariateSpline

a bivariate spline in spherical coordinates using weighted least-squares fitting

RectBivariateSpline

a bivariate spline over a rectangular mesh

bisplrep

a function to find a bivariate B-spline representation of a surface

bisplev

a function to evaluate a bivariate B-spline and its derivatives

Notes

The length of *x*, *y* and *z* should be at least `(kx+1) * (ky+1)`.

Methods

__call__(x, y[, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
ev(xi, yi[, dx, dy])	Evaluate the spline at points
get_coeffs()	Return spline coefficients.
get_knots()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
get_residual()	Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)
integral(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

scipy.interpolate.SmoothBivariateSpline.__call__

`SmoothBivariateSpline.`**`__call__`**(*x*, *y*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

x, y [array_like] Input coordinates.
If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.
Note that the axis ordering is inverted relative to the output of meshgrid.

dx [int] Order of x-derivative
New in version 0.14.0.

dy [int] Order of y-derivative
New in version 0.14.0.

grid [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

scipy.interpolate.SmoothBivariateSpline.ev

`SmoothBivariateSpline.`**`ev`**(*xi*, *yi*, *dx=0*, *dy=0*)

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters

xi, yi [array_like] Input coordinates. Standard Numpy broadcasting is obeyed.

dx [int, optional] Order of x-derivative
New in version 0.14.0.

dy [int, optional] Order of y-derivative
New in version 0.14.0.

scipy.interpolate.SmoothBivariateSpline.get_coeffs

`SmoothBivariateSpline.`**`get_coeffs`**`()`
Return spline coefficients.

scipy.interpolate.SmoothBivariateSpline.get_knots

`SmoothBivariateSpline.`**`get_knots`**`()`
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.SmoothBivariateSpline.get_residual

`SmoothBivariateSpline.`**`get_residual`**`()`
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

scipy.interpolate.SmoothBivariateSpline.integral

`SmoothBivariateSpline.`**`integral`**`(`*xa*, *xb*, *ya*, *yb*`)`
Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters

xa, xb [float] The end-points of the x integration interval.
ya, yb [float] The end-points of the y integration interval.

Returns

integ [float] The value of the resulting integral.

scipy.interpolate.SmoothSphereBivariateSpline

`class` `scipy.interpolate.`**`SmoothSphereBivariateSpline`**`(`*theta*, *phi*, *r*, *w=None*, *s=0.0*, *eps=1e-16*`)`
Smooth bivariate spline approximation in spherical coordinates.

New in version 0.11.0.

Parameters

theta, phi, r
[array_like] 1-D sequences of data points (order is not important). Coordinates must be given in radians. Theta must lie within the interval `[0, pi]`, and phi must lie within the interval `[0, 2pi]`.
w [array_like, optional] Positive 1-D sequence of weights.
s [float, optional] Positive smoothing factor defined for estimation condition: `sum((w(i)*(r(i) - s(theta(i), phi(i))))**2, axis=0) <= s` Default `s=len(w)` which should be a good value if `1/w[i]` is an estimate of the standard deviation of `r[i]`.

eps [float, optional] A threshold for determining the effective rank of an over-determined linear system of equations. *eps* should have a value within the open interval `(0, 1)`, the default is 1e-16.

See also:

BivariateSpline

a base class for bivariate splines.

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

SmoothBivariateSpline

a smoothing bivariate spline through the given points

LSQBivariateSpline

a bivariate spline using weighted least-squares fitting

RectSphereBivariateSpline

a bivariate spline over a rectangular mesh on a sphere

LSQSphereBivariateSpline

a bivariate spline in spherical coordinates using weighted least-squares fitting

RectBivariateSpline

a bivariate spline over a rectangular mesh.

bisplrep

a function to find a bivariate B-spline representation of a surface

bisplev

a function to evaluate a bivariate B-spline and its derivatives

Notes

For more information, see the FITPACK site about this function.

Examples

Suppose we have global data on a coarse grid (the input data does not have to be on a grid):

```
>>> theta = np.linspace(0., np.pi, 7)
>>> phi = np.linspace(0., 2*np.pi, 9)
>>> data = np.empty((theta.shape[0], phi.shape[0]))
>>> data[:,0], data[0,:], data[-1,:] = 0., 0., 0.
>>> data[1:-1,1], data[1:-1,-1] = 1., 1.
>>> data[1,1:-1], data[-2,1:-1] = 1., 1.
>>> data[2:-2,2], data[2:-2,-2] = 2., 2.
>>> data[2,2:-2], data[-3,2:-2] = 2., 2.
>>> data[3,3:-2] = 3.
>>> data = np.roll(data, 4, 1)
```

We need to set up the interpolator object

```
>>> lats, lons = np.meshgrid(theta, phi)
>>> from scipy.interpolate import SmoothSphereBivariateSpline
>>> lut = SmoothSphereBivariateSpline(lats.ravel(), lons.ravel(),
...                                   data.T.ravel(), s=3.5)
```

As a first test, we'll see what the algorithm returns when run on the input coordinates

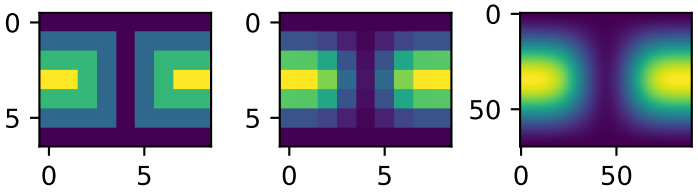
```
>>> data_orig = lut(theta, phi)
```

Finally we interpolate the data to a finer grid

```
>>> fine_lats = np.linspace(0., np.pi, 70)
>>> fine_lons = np.linspace(0., 2 * np.pi, 90)
```

```
>>> data_smth = lut(fine_lats, fine_lons)
```

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(131)
>>> ax1.imshow(data, interpolation='nearest')
>>> ax2 = fig.add_subplot(132)
>>> ax2.imshow(data_orig, interpolation='nearest')
>>> ax3 = fig.add_subplot(133)
>>> ax3.imshow(data_smth, interpolation='nearest')
>>> plt.show()
```



Methods

`__call__`(theta, phi[, dtheta, dphi, grid])	Evaluate the spline or its derivatives at given positions.
`ev`(theta, phi[, dtheta, dphi])	Evaluate the spline at points
`get_coeffs`()	Return spline coefficients.
`get_knots`()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
`get_residual`()	Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

scipy.interpolate.SmoothSphereBivariateSpline.__call__

SmoothSphereBivariateSpline.**__call__**(*theta*, *phi*, *dtheta=0*, *dphi=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

theta, phi [array_like] Input coordinates.
If *grid* is False, evaluate the spline at points `(theta[i], phi[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays theta, phi. The arrays must be sorted to increasing order.

dtheta [int, optional] Order of theta-derivative
New in version 0.14.0.

dphi [int] Order of phi-derivative
New in version 0.14.0.

grid [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

scipy.interpolate.SmoothSphereBivariateSpline.ev

SmoothSphereBivariateSpline.**ev**(*theta*, *phi*, *dtheta=0*, *dphi=0*)

Evaluate the spline at points

Returns the interpolated value at `(theta[i], phi[i]), i=0,...,len(theta)-1`.

Parameters

theta, phi [array_like] Input coordinates. Standard Numpy broadcasting is obeyed.

dtheta [int, optional] Order of theta-derivative
New in version 0.14.0.

dphi [int, optional] Order of phi-derivative
New in version 0.14.0.

scipy.interpolate.SmoothSphereBivariateSpline.get_coeffs

SmoothSphereBivariateSpline.**get_coeffs**()
Return spline coefficients.

scipy.interpolate.SmoothSphereBivariateSpline.get_knots

SmoothSphereBivariateSpline.**get_knots**()
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.SmoothSphereBivariateSpline.get_residual

SmoothSphereBivariateSpline.**get_residual**()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

scipy.interpolate.LSQBivariateSpline

class scipy.interpolate.**LSQBivariateSpline**(*x*, *y*, *z*, *tx*, *ty*, *w=None*, *bbox=[None, None, None, None]*, *kx=3*, *ky=3*, *eps=None*)

Weighted least-squares bivariate spline approximation.

Parameters

x, y, z	[array_like] 1-D sequences of data points (order is not important).
tx, ty	[array_like] Strictly ordered 1-D sequences of knots coordinates.
w	[array_like, optional] Positive 1-D array of weights, of the same length as *x*, *y* and *z*.
bbox	[(4,) array_like, optional] Sequence of length 4 specifying the boundary of the rectangular approximation domain. By default, `bbox=[min(x,tx),max(x,tx), min(y,ty), max(y,ty)]`.
kx, ky	[ints, optional] Degrees of the bivariate spline. Default is 3.
eps	[float, optional] A threshold for determining the effective rank of an over-determined linear system of equations. *eps* should have a value within the open interval `(0, 1)`, the default is 1e-16.

See also:

BivariateSpline

a base class for bivariate splines.

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

SmoothBivariateSpline

a smoothing bivariate spline through the given points

RectSphereBivariateSpline

a bivariate spline over a rectangular mesh on a sphere

SmoothSphereBivariateSpline

a smoothing bivariate spline in spherical coordinates

LSQSphereBivariateSpline

a bivariate spline in spherical coordinates using weighted least-squares fitting

RectBivariateSpline

a bivariate spline over a rectangular mesh.

bisplrep

a function to find a bivariate B-spline representation of a surface

bisplev

a function to evaluate a bivariate B-spline and its derivatives

Notes

The length of *x*, *y* and *z* should be at least `(kx+1) * (ky+1)`.

Methods

__call__(x, y[, dx, dy, grid])	Evaluate the spline or its derivatives at given positions.
ev(xi, yi[, dx, dy])	Evaluate the spline at points
get_coeffs()	Return spline coefficients.
get_knots()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
get_residual()	Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)
integral(xa, xb, ya, yb)	Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

scipy.interpolate.LSQBivariateSpline.__call__

LSQBivariateSpline.**__call__**(*x*, *y*, *dx=0*, *dy=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

x, y [array_like] Input coordinates.
If *grid* is False, evaluate the spline at points `(x[i], y[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays x, y. The arrays must be sorted to increasing order.
Note that the axis ordering is inverted relative to the output of meshgrid.

dx [int] Order of x-derivative
New in version 0.14.0.

dy [int] Order of y-derivative
New in version 0.14.0.

grid [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

scipy.interpolate.LSQBivariateSpline.ev

LSQBivariateSpline.**ev**(*xi*, *yi*, *dx=0*, *dy=0*)

Evaluate the spline at points

Returns the interpolated value at `(xi[i], yi[i]), i=0,...,len(xi)-1`.

Parameters

xi, yi	[array_like] Input coordinates. Standard Numpy broadcasting is obeyed.
dx	[int, optional] Order of x-derivative New in version 0.14.0.
dy	[int, optional] Order of y-derivative New in version 0.14.0.

scipy.interpolate.LSQBivariateSpline.get_coeffs

LSQBivariateSpline.**get_coeffs**()

Return spline coefficients.

scipy.interpolate.LSQBivariateSpline.get_knots

LSQBivariateSpline.**get_knots**()

Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.LSQBivariateSpline.get_residual

LSQBivariateSpline.**get_residual**()

Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

scipy.interpolate.LSQBivariateSpline.integral

LSQBivariateSpline.**integral**(*xa*, *xb*, *ya*, *yb*)

Evaluate the integral of the spline over area [xa,xb] x [ya,yb].

Parameters

xa, xb	[float] The end-points of the x integration interval.
ya, yb	[float] The end-points of the y integration interval.

Returns

integ	[float] The value of the resulting integral.

scipy.interpolate.LSQSphereBivariateSpline

class scipy.interpolate.**LSQSphereBivariateSpline**(*theta*, *phi*, *r*, *tt*, *tp*, *w=None*, *eps=1e-16*)

Weighted least-squares bivariate spline approximation in spherical coordinates.

Determines a smoothing bicubic spline according to a given set of knots in the *theta* and *phi* directions.

New in version 0.11.0.

Parameters

theta, phi, r
: [array_like] 1-D sequences of data points (order is not important). Coordinates must be given in radians. Theta must lie within the interval `[0, pi]`, and phi must lie within the interval `[0, 2pi]`.

tt, tp
: [array_like] Strictly ordered 1-D sequences of knots coordinates. Coordinates must satisfy `0 < tt[i] < pi`, `0 < tp[i] < 2*pi`.

w
: [array_like, optional] Positive 1-D sequence of weights, of the same length as *theta*, *phi* and *r*.

eps
: [float, optional] A threshold for determining the effective rank of an over-determined linear system of equations. *eps* should have a value within the open interval `(0, 1)`, the default is 1e-16.

See also:

BivariateSpline

a base class for bivariate splines.

UnivariateSpline

a smooth univariate spline to fit a given set of data points.

SmoothBivariateSpline

a smoothing bivariate spline through the given points

LSQBivariateSpline

a bivariate spline using weighted least-squares fitting

RectSphereBivariateSpline

a bivariate spline over a rectangular mesh on a sphere

SmoothSphereBivariateSpline

a smoothing bivariate spline in spherical coordinates

RectBivariateSpline

a bivariate spline over a rectangular mesh.

bisplrep

a function to find a bivariate B-spline representation of a surface

bisplev

a function to evaluate a bivariate B-spline and its derivatives

Notes

For more information, see the FITPACK site about this function.

Examples

Suppose we have global data on a coarse grid (the input data does not have to be on a grid):

```
>>> from scipy.interpolate import LSQSphereBivariateSpline
>>> import matplotlib.pyplot as plt
```

```
>>> theta = np.linspace(0, np.pi, num=7)
>>> phi = np.linspace(0, 2*np.pi, num=9)
>>> data = np.empty((theta.shape[0], phi.shape[0]))
>>> data[:,0], data[0,:], data[-1,:] = 0., 0., 0.
>>> data[1:-1,1], data[1:-1,-1] = 1., 1.
>>> data[1,1:-1], data[-2,1:-1] = 1., 1.
>>> data[2:-2,2], data[2:-2,-2] = 2., 2.
>>> data[2,2:-2], data[-3,2:-2] = 2., 2.
>>> data[3,3:-2] = 3.
>>> data = np.roll(data, 4, 1)
```

We need to set up the interpolator object. Here, we must also specify the coordinates of the knots to use.

```
>>> lats, lons = np.meshgrid(theta, phi)
>>> knotst, knotsp = theta.copy(), phi.copy()
>>> knotst[0] += .0001
>>> knotst[-1] -= .0001
>>> knotsp[0] += .0001
>>> knotsp[-1] -= .0001
>>> lut = LSQSphereBivariateSpline(lats.ravel(), lons.ravel(),
...                                data.T.ravel(), knotst, knotsp)
```

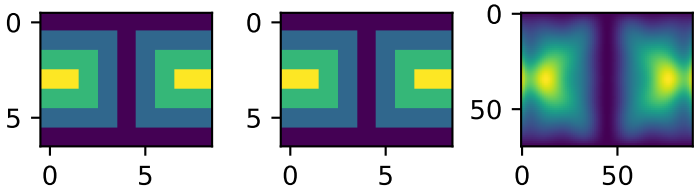
As a first test, we'll see what the algorithm returns when run on the input coordinates

```
>>> data_orig = lut(theta, phi)
```

Finally we interpolate the data to a finer grid

```
>>> fine_lats = np.linspace(0., np.pi, 70)
>>> fine_lons = np.linspace(0., 2*np.pi, 90)
>>> data_lsq = lut(fine_lats, fine_lons)
```

```
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(131)
>>> ax1.imshow(data, interpolation='nearest')
>>> ax2 = fig.add_subplot(132)
>>> ax2.imshow(data_orig, interpolation='nearest')
>>> ax3 = fig.add_subplot(133)
>>> ax3.imshow(data_lsq, interpolation='nearest')
>>> plt.show()
```



Methods

__call__(theta, phi[, dtheta, dphi, grid])	Evaluate the spline or its derivatives at given positions.
ev(theta, phi[, dtheta, dphi])	Evaluate the spline at points
get_coeffs()	Return spline coefficients.
get_knots()	Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively.
get_residual()	Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

scipy.interpolate.LSQSphereBivariateSpline.__call__

LSQSphereBivariateSpline.**__call__**(*theta*, *phi*, *dtheta=0*, *dphi=0*, *grid=True*)

Evaluate the spline or its derivatives at given positions.

Parameters

theta, phi [array_like] Input coordinates.
If *grid* is False, evaluate the spline at points `(theta[i], phi[i]), i=0, ..., len(x)-1`. Standard Numpy broadcasting is obeyed.
If *grid* is True: evaluate spline at the grid points defined by the coordinate arrays theta, phi. The arrays must be sorted to increasing order.

dtheta [int, optional] Order of theta-derivative
New in version 0.14.0.

dphi [int] Order of phi-derivative
New in version 0.14.0.

grid [bool] Whether to evaluate the results on a grid spanned by the input arrays, or at points specified by the input arrays.
New in version 0.14.0.

scipy.interpolate.LSQSphereBivariateSpline.ev

LSQSphereBivariateSpline.**ev**(*theta*, *phi*, *dtheta=0*, *dphi=0*)

Evaluate the spline at points

Returns the interpolated value at `(theta[i], phi[i]), i=0,...,len(theta)-1`.

Parameters

scipy.interpolate.LSQSphereBivariateSpline.get_coeffs

LSQSphereBivariateSpline.**get_coeffs**()
Return spline coefficients.

scipy.interpolate.LSQSphereBivariateSpline.get_knots

LSQSphereBivariateSpline.**get_knots**()
Return a tuple (tx,ty) where tx,ty contain knots positions of the spline with respect to x-, y-variable, respectively. The position of interior and additional knots are given as t[k+1:-k-1] and t[:k+1]=b, t[-k-1:]=e, respectively.

scipy.interpolate.LSQSphereBivariateSpline.get_residual

LSQSphereBivariateSpline.**get_residual**()
Return weighted sum of squared residuals of the spline approximation: sum ((w[i]*(z[i]-s(x[i],y[i])))**2,axis=0)

Low-level interface to FITPACK functions:

bisplrep(x, y, z[, w, xb, xe, yb, ye, kx, …])	Find a bivariate B-spline representation of a surface.
bisplev(x, y, tck[, dx, dy])	Evaluate a bivariate B-spline and its derivatives.

scipy.interpolate.bisplrep

scipy.interpolate.**bisplrep**(*x*, *y*, *z*, *w=None*, *xb=None*, *xe=None*, *yb=None*, *ye=None*, *kx=3*, *ky=3*, *task=0*, *s=None*, *eps=1e-16*, *tx=None*, *ty=None*, *full_output=0*, *nxest=None*, *nyest=None*, *quiet=1*)
Find a bivariate B-spline representation of a surface.

Given a set of data points (x[i], y[i], z[i]) representing a surface z=f(x,y), compute a B-spline representation of the surface. Based on the routine SURFIT from FITPACK.

Parameters

x, y, z [ndarray] Rank-1 arrays of data points.
w [ndarray, optional] Rank-1 array of weights. By default `w=np.ones(len(x))`.
xb, xe [float, optional] End points of approximation interval in *x*. By default `xb = x.min(), xe=x.max()`.
yb, ye [float, optional] End points of approximation interval in *y*. By default `yb=y.min(), ye = y.max()`.
kx, ky [int, optional] The degrees of the spline (1 <= kx, ky <= 5). Third order (kx=ky=3) is recommended.
task [int, optional] If task=0, find knots in x and y and coefficients for a given smoothing factor, s. If task=1, find knots and coefficients for another value of the smoothing factor, s. bisplrep must have been previously called with task=0 or task=1. If task=-1, find coefficients for a given set of knots tx, ty.
s [float, optional] A non-negative smoothing factor. If weights correspond to the inverse of the standard-deviation of the errors in z, then a good s-value should be found in the range `(m-sqrt(2*m),m+sqrt(2*m))` where m=len(x).
eps [float, optional] A threshold for determining the effective rank of an over-determined linear system of equations (0 < eps < 1). *eps* is not likely to need changing.
tx, ty [ndarray, optional] Rank-1 arrays of the knots of the spline for task=-1

full_output
: [int, optional] Non-zero to return optional outputs.

nxest, nyest
: [int, optional] Over-estimates of the total number of knots. If None then `nxest = max(kx+sqrt(m/2),2*kx+3)`, `nyest = max(ky+sqrt(m/2),2*ky+3)`.

quiet
: [int, optional] Non-zero to suppress printing of messages. This parameter is deprecated; use standard Python warning filters instead.

Returns

tck
: [array_like] A list [tx, ty, c, kx, ky] containing the knots (tx, ty) and coefficients (c) of the bivariate B-spline representation of the surface along with the degree of the spline.

fp
: [ndarray] The weighted sum of squared residuals of the spline approximation.

ier
: [int] An integer flag about splrep success. Success is indicated if ier<=0. If ier in [1,2,3] an error occurred but was not raised. Otherwise an error is raised.

msg
: [str] A message corresponding to the integer flag, ier.

See also:

splprep, **splrep**, **splint**, **sproot**, **splev**

UnivariateSpline, **BivariateSpline**

Notes

See *bisplev* to evaluate the value of the B-spline given its tck representation.

References

[1], [2], [3]

Examples

Examples are given *in the tutorial*.

scipy.interpolate.bisplev

scipy.interpolate.**bisplev**(*x*, *y*, *tck*, *dx=0*, *dy=0*)

Evaluate a bivariate B-spline and its derivatives.

Return a rank-2 array of spline function values (or spline derivative values) at points given by the cross-product of the rank-1 arrays *x* and *y*. In special cases, return an array or just a float if either *x* or *y* or both are floats. Based on BISPEV from FITPACK.

Parameters

x, y
: [ndarray] Rank-1 arrays specifying the domain over which to evaluate the spline or its derivative.

tck
: [tuple] A sequence of length 5 returned by *bisplrep* containing the knot locations, the coefficients, and the degree of the spline: [tx, ty, c, kx, ky].

dx, dy
: [int, optional] The orders of the partial derivatives in *x* and *y* respectively.

Returns

vals
: [ndarray] The B-spline or its derivative evaluated over the set formed by the cross-product of *x* and *y*.

See also:

splprep, **splrep**, **splint**, **sproot**, **splev**

UnivariateSpline, **BivariateSpline**

Notes

See *bisplrep* to generate the *tck* representation.

References

[1], [2], [3]

Examples

Examples are given *in the tutorial*.

Additional tools

lagrange(x, w)	Return a Lagrange interpolating polynomial.
approximate_taylor_polynomial(f, x, degree, …)	Estimate the Taylor polynomial of f at x by polynomial fitting.
pade(an, m[, n])	Return Pade approximation to a polynomial as the ratio of two polynomials.

scipy.interpolate.lagrange

scipy.interpolate.**lagrange**(*x*, *w*)

Return a Lagrange interpolating polynomial.

Given two 1-D arrays *x* and *w,* returns the Lagrange interpolating polynomial through the points `(x, w)`.

Warning: This implementation is numerically unstable. Do not expect to be able to use more than about 20 points even if they are chosen optimally.

Parameters

x [array_like] *x* represents the x-coordinates of a set of datapoints.

w [array_like] *w* represents the y-coordinates of a set of datapoints, i.e., f(*x*).

Returns

lagrange [`numpy.poly1d` instance] The Lagrange interpolating polynomial.

Examples

Interpolate $f(x) = x^3$ by 3 points.

```
>>> from scipy.interpolate import lagrange
>>> x = np.array([0, 1, 2])
>>> y = x**3
>>> poly = lagrange(x, y)
```

Since there are only 3 points, Lagrange polynomial has degree 2. Explicitly, it is given by

$$\begin{aligned} L(x) &= 1 \times \frac{x(x-2)}{-1} + 8 \times \frac{x(x-1)}{2} \\ &= x(-2+3x) \end{aligned}$$

```
>>> from numpy.polynomial.polynomial import Polynomial
>>> Polynomial(poly).coef
array([ 3., -2.,  0.])
```

scipy.interpolate.approximate_taylor_polynomial

scipy.interpolate.**approximate_taylor_polynomial**(*f*, *x*, *degree*, *scale*, *order=None*)

Estimate the Taylor polynomial of f at x by polynomial fitting.

Parameters

f	[callable] The function whose Taylor polynomial is sought. Should accept a vector of *x* values.
x	[scalar] The point at which the polynomial is to be evaluated.
degree	[int] The degree of the Taylor polynomial
scale	[scalar] The width of the interval to use to evaluate the Taylor polynomial. Function values spread over a range this wide are used to fit the polynomial. Must be chosen carefully.
order	[int or None, optional] The order of the polynomial to be used in the fitting; *f* will be evaluated `order+1` times. If None, use *degree*.

Returns

p	[poly1d instance] The Taylor polynomial (translated to the origin, so that for example p(0)=f(x)).

Notes

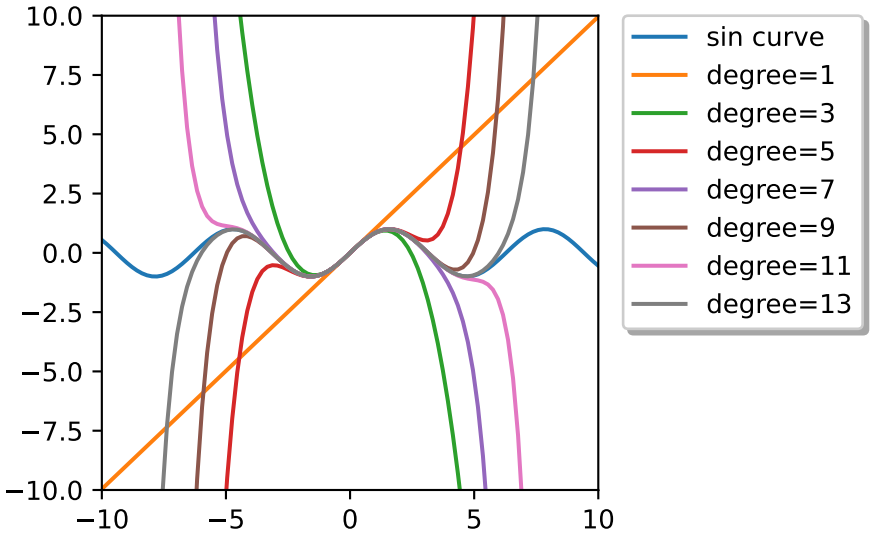
The appropriate choice of "scale" is a trade-off; too large and the function differs from its Taylor polynomial too much to get a good answer, too small and round-off errors overwhelm the higher-order terms. The algorithm used becomes numerically unstable around order 30 even under ideal circumstances.

Choosing order somewhat larger than degree may improve the higher-order terms.

Examples

We can calculate Taylor approximation polynomials of sin function with various degrees:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.interpolate import approximate_taylor_polynomial
>>> x = np.linspace(-10.0, 10.0, num=100)
>>> plt.plot(x, np.sin(x), label="sin curve")
>>> for degree in np.arange(1, 15, step=2):
...     sin_taylor = approximate_taylor_polynomial(np.sin, 0, degree, 1,
...                                                order=degree + 2)
...     plt.plot(x, sin_taylor(x), label=f"degree={degree}")
>>> plt.legend(bbox_to_anchor=(1.05, 1), loc='upper left',
...            borderaxespad=0.0, shadow=True)
>>> plt.tight_layout()
>>> plt.axis([-10, 10, -10, 10])
>>> plt.show()
```



scipy.interpolate.pade

`scipy.interpolate.`**pade**(*an*, *m*, *n=None*)

Return Pade approximation to a polynomial as the ratio of two polynomials.

Parameters

an	[(N,) array_like] Taylor series coefficients.
m	[int] The order of the returned approximating polynomial *q*.
n	[int, optional] The order of the returned approximating polynomial *p*. By default, the order is `len(an)-m`.

Returns

p, q	[Polynomial class] The Pade approximation of the polynomial defined by *an* is `p(x)/q(x)`.

Examples

```
>>> from scipy.interpolate import pade
>>> e_exp = [1.0, 1.0, 1.0/2.0, 1.0/6.0, 1.0/24.0, 1.0/120.0]
>>> p, q = pade(e_exp, 2)
```

```
>>> e_exp.reverse()
>>> e_poly = np.poly1d(e_exp)
```

Compare `e_poly(x)` and the Pade approximation `p(x)/q(x)`

```
>>> e_poly(1)
2.7166666666666668
```

```
>>> p(1)/q(1)
2.7179487179487181
```

See also:

scipy.ndimage.map_coordinates, *scipy.ndimage.spline_filter*, *scipy.signal.resample*, *scipy.signal.bspline*, *scipy.signal.gauss_spline*, *scipy.signal.qspline1d*, *scipy.signal.cspline1d*, *scipy.signal.qspline1d_eval*, *scipy.signal.cspline1d_eval*, *scipy.signal.qspline2d*, *scipy.signal.cspline2d*.

`pchip` is an alias of *PchipInterpolator* for backward compatibility (should not be used in new code).

3.3.9 Input and output (`scipy.io`)

SciPy has many modules, classes, and functions available to read data from and write data to a variety of file formats.

See also:

NumPy IO routines

MATLAB® files

loadmat(file_name[, mdict, appendmat])	Load MATLAB file.
savemat(file_name, mdict[, appendmat, …])	Save a dictionary of names and arrays into a MATLAB-style .mat file.
whosmat(file_name[, appendmat])	List variables inside a MATLAB file.

scipy.io.loadmat

`scipy.io.`**`loadmat`**(*file_name*, *mdict=None*, *appendmat=True*, ***kwargs*)

Load MATLAB file.

Parameters

file_name [str] Name of the mat file (do not need .mat extension if appendmat==True). Can also pass open file-like object.

mdict [dict, optional] Dictionary in which to insert matfile variables.

appendmat [bool, optional] True to append the .mat extension to the end of the given filename, if not already present.

byte_order
: [str or None, optional] None by default, implying byte order guessed from mat file. Otherwise can be one of ('native', '=', 'little', '<', 'BIG', '>').

mat_dtype
: [bool, optional] If True, return arrays in same dtype as would be loaded into MATLAB (instead of the dtype with which they are saved).

squeeze_me
: [bool, optional] Whether to squeeze unit matrix dimensions or not.

chars_as_strings
: [bool, optional] Whether to convert char arrays to string arrays.

matlab_compatible
: [bool, optional] Returns matrices as would be loaded by MATLAB (implies squeeze_me=False, chars_as_strings=False, mat_dtype=True, struct_as_record=True).

struct_as_record
: [bool, optional] Whether to load MATLAB structs as NumPy record arrays, or as old-style NumPy arrays with dtype=object. Setting this flag to False replicates the behavior of scipy version 0.7.x (returning NumPy object arrays). The default setting is True, because it allows easier round-trip load and save of MATLAB files.

verify_compressed_data_integrity
: [bool, optional] Whether the length of compressed sequences in the MATLAB file should be checked, to ensure that they are not longer than we expect. It is advisable to enable this (the default) because overlong compressed sequences in MATLAB files generally indicate that the files have experienced some sort of corruption.

variable_names
: [None or sequence] If None (the default) - read all variables in file. Otherwise, *variable_names* should be a sequence of strings, giving names of the MATLAB variables to read from the file. The reader will skip any variable with a name not in this sequence, possibly saving some read processing.

simplify_cells
: [False, optional] If True, return a simplified dict structure (which is useful if the mat file contains cell arrays). Note that this only affects the structure of the result and not its contents (which is identical for both output structures). If True, this automatically sets *struct_as_record* to False and *squeeze_me* to True, which is required to simplify cells.

Returns

mat_dict [dict] dictionary with variable names as keys, and loaded matrices as values.

Notes

v4 (Level 1.0), v6 and v7 to 7.2 matfiles are supported.

You will need an HDF5 Python library to read MATLAB 7.3 format mat files. Because SciPy does not supply one, we do not implement the HDF5 / 7.3 interface here.

Examples

```
>>> from os.path import dirname, join as pjoin
>>> import scipy.io as sio
```

Get the filename for an example .mat file from the tests/data directory.

```
>>> data_dir = pjoin(dirname(sio.__file__), 'matlab', 'tests', 'data')
>>> mat_fname = pjoin(data_dir, 'testdouble_7.4_GLNX86.mat')
```

Load the .mat file contents.

```
>>> mat_contents = sio.loadmat(mat_fname)
```

The result is a dictionary, one key/value pair for each variable:

```
>>> sorted(mat_contents.keys())
['__globals__', '__header__', '__version__', 'testdouble']
>>> mat_contents['testdouble']
array([[0.        , 0.78539816, 1.57079633, 2.35619449, 3.14159265,
        3.92699082, 4.71238898, 5.49778714, 6.28318531]])
```

By default SciPy reads MATLAB structs as structured NumPy arrays where the dtype fields are of type *object* and the names correspond to the MATLAB struct field names. This can be disabled by setting the optional argument *struct_as_record=False*.

Get the filename for an example .mat file that contains a MATLAB struct called *teststruct* and load the contents.

```
>>> matstruct_fname = pjoin(data_dir, 'teststruct_7.4_GLNX86.mat')
>>> matstruct_contents = sio.loadmat(matstruct_fname)
>>> teststruct = matstruct_contents['teststruct']
>>> teststruct.dtype
dtype([('stringfield', 'O'), ('doublefield', 'O'), ('complexfield', 'O')])
```

The size of the structured array is the size of the MATLAB struct, not the number of elements in any particular field. The shape defaults to 2-D unless the optional argument *squeeze_me=True*, in which case all length 1 dimensions are removed.

```
>>> teststruct.size
1
>>> teststruct.shape
(1, 1)
```

Get the 'stringfield' of the first element in the MATLAB struct.

```
>>> teststruct[0, 0]['stringfield']
array(['Rats live on no evil star.'],
  dtype='<U26')
```

Get the first element of the 'doublefield'.

```
>>> teststruct['doublefield'][0, 0]
array([[ 1.41421356,  2.71828183,  3.14159265]])
```

Load the MATLAB struct, squeezing out length 1 dimensions, and get the item from the 'complexfield'.

```
>>> matstruct_squeezed = sio.loadmat(matstruct_fname, squeeze_me=True)
>>> matstruct_squeezed['teststruct'].shape
()
>>> matstruct_squeezed['teststruct']['complexfield'].shape
()
>>> matstruct_squeezed['teststruct']['complexfield'].item()
array([ 1.41421356+1.41421356j,  2.71828183+2.71828183j,
    3.14159265+3.14159265j])
```

scipy.io.savemat

scipy.io.**savemat**(*file_name*, *mdict*, *appendmat=True*, *format='5'*, *long_field_names=False*, *do_compression=False*, *oned_as='row'*)

Save a dictionary of names and arrays into a MATLAB-style .mat file.

This saves the array objects in the given dictionary to a MATLAB- style .mat file.

Parameters

file_name [str or file-like object] Name of the .mat file (.mat extension not needed if `appendmat == True`). Can also pass open file_like object.

mdict [dict] Dictionary from which to save matfile variables.

appendmat [bool, optional] True (the default) to append the .mat extension to the end of the given filename, if not already present.

format [{'5', '4'}, string, optional] '5' (the default) for MATLAB 5 and up (to 7.2), '4' for MATLAB 4 .mat files.

long_field_names [bool, optional] False (the default) - maximum field name length in a structure is 31 characters which is the documented maximum length. True - maximum field name length in a structure is 63 characters which works for MATLAB 7.6+.

do_compression [bool, optional] Whether or not to compress matrices on write. Default is False.

oned_as [{'row', 'column'}, optional] If 'column', write 1-D NumPy arrays as column vectors. If 'row', write 1-D NumPy arrays as row vectors.

Examples

```
>>> from scipy.io import savemat
>>> a = np.arange(20)
>>> mdic = {"a": a, "label": "experiment"}
>>> mdic
{'a': array([ 0,  1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12, 13, 14,␣
↪15, 16,
    17, 18, 19]),
'label': 'experiment'}
>>> savemat("matlab_matrix.mat", mdic)
```

scipy.io.whosmat

scipy.io.**whosmat**(*file_name*, *appendmat=True*, ***kwargs*)

List variables inside a MATLAB file.

Parameters

file_name [str] Name of the mat file (do not need .mat extension if appendmat==True) Can also pass open file-like object.

appendmat [bool, optional] True to append the .mat extension to the end of the given filename, if not already present.

byte_order [str or None, optional] None by default, implying byte order guessed from mat file. Otherwise can be one of ('native', '=', 'little', '<', 'BIG', '>').

mat_dtype [bool, optional] If True, return arrays in same dtype as would be loaded into MATLAB (instead of the dtype with which they are saved).

squeeze_me [bool, optional] Whether to squeeze unit matrix dimensions or not.

chars_as_strings [bool, optional] Whether to convert char arrays to string arrays.

matlab_compatible [bool, optional] Returns matrices as would be loaded by MATLAB (implies squeeze_me=False, chars_as_strings=False, mat_dtype=True, struct_as_record=True).

struct_as_record [bool, optional] Whether to load MATLAB structs as NumPy record arrays, or as old-style NumPy arrays with dtype=object. Setting this flag to False replicates the behavior of SciPy version 0.7.x (returning numpy object arrays). The default setting is True, because it allows easier round-trip load and save of MATLAB files.

Returns

variables [list of tuples] A list of tuples, where each tuple holds the matrix name (a string), its shape (tuple of ints), and its data class (a string). Possible data classes are: int8, uint8, int16, uint16, int32, uint32, int64, uint64, single, double, cell, struct, object, char, sparse, function, opaque, logical, unknown.

Notes

v4 (Level 1.0), v6 and v7 to 7.2 matfiles are supported.

You will need an HDF5 python library to read matlab 7.3 format mat files. Because SciPy does not supply one, we do not implement the HDF5 / 7.3 interface here.

New in version 0.12.0.

IDL® files

readsav(file_name[, idict, python_dict, …])	Read an IDL .sav file.

scipy.io.readsav

scipy.io.**readsav**(*file_name*, *idict=None*, *python_dict=False*, *uncompressed_file_name=None*, *verbose=False*)

Read an IDL .sav file.

Parameters

file_name [str] Name of the IDL save file.

idict [dict, optional] Dictionary in which to insert .sav file variables.

python_dict [bool, optional] By default, the object return is not a Python dictionary, but a case-insensitive dictionary with item, attribute, and call access to variables. To get a standard Python dictionary, set this option to True.

uncompressed_file_name [str, optional] This option only has an effect for .sav files written with the /compress option. If a file name is specified, compressed .sav files are uncompressed to this file. Otherwise, readsav will use the `tempfile` module to determine a temporary filename automatically, and will remove the temporary file upon successfully reading it in.

verbose [bool, optional] Whether to print out information about the save file, including the records read, and available variables.

Returns

idl_dict [AttrDict or dict] If *python_dict* is set to False (default), this function returns a case-insensitive dictionary with item, attribute, and call access to variables. If *python_dict* is set to True, this function returns a Python dictionary with all variable names in lowercase. If *idict* was specified, then variables are written to the dictionary specified, and the updated dictionary is returned.

Examples

```
>>> from os.path import dirname, join as pjoin
>>> import scipy.io as sio
>>> from scipy.io import readsav
```

Get the filename for an example .sav file from the tests/data directory.

```
>>> data_dir = pjoin(dirname(sio.__file__), 'tests', 'data')
>>> sav_fname = pjoin(data_dir, 'array_float32_1d.sav')
```

Load the .sav file contents.

```
>>> sav_data = readsav(sav_fname)
```

Get keys of the .sav file contents.

```
>>> print(sav_data.keys())
dict_keys(['array1d'])
```

Access a content with a key.

```
>>> print(sav_data['array1d'])
[0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.
 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.
 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.
 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.
 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.
 0. 0. 0.]
```

Matrix Market files

mminfo(source)	Return size and storage parameters from Matrix Market file-like 'source'.
mmread(source)	Reads the contents of a Matrix Market file-like 'source' into a matrix.
mmwrite(target, a[, comment, field, …])	Writes the sparse or dense array *a* to Matrix Market file-like *target*.

scipy.io.mminfo

scipy.io.**mminfo**(*source*)

Return size and storage parameters from Matrix Market file-like 'source'.

Parameters

source [str or file-like] Matrix Market filename (extension .mtx) or open file-like object

Returns

rows [int] Number of matrix rows.
cols [int] Number of matrix columns.
entries [int] Number of non-zero entries of a sparse matrix or rows*cols for a dense matrix.
format [str] Either 'coordinate' or 'array'.
field [str] Either 'real', 'complex', 'pattern', or 'integer'.
symmetry [str] Either 'general', 'symmetric', 'skew-symmetric', or 'hermitian'.

scipy.io.mmread

scipy.io.**mmread**(*source*)

Reads the contents of a Matrix Market file-like 'source' into a matrix.

Parameters

source [str or file-like] Matrix Market filename (extensions .mtx, .mtz.gz) or open file-like object.

Returns

a [ndarray or coo_matrix] Dense or sparse matrix depending on the matrix format in the Matrix Market file.

scipy.io.mmwrite

scipy.io.**mmwrite**(*target*, *a*, *comment=''*, *field=None*, *precision=None*, *symmetry=None*)

Writes the sparse or dense array *a* to Matrix Market file-like *target*.

Parameters

target [str or file-like] Matrix Market filename (extension .mtx) or open file-like object.
a [array like] Sparse or dense 2-D array.
comment [str, optional] Comments to be prepended to the Matrix Market file.
field [None or str, optional] Either 'real', 'complex', 'pattern', or 'integer'.
precision [None or int, optional] Number of digits to display for real or complex values.
symmetry [None or str, optional] Either 'general', 'symmetric', 'skew-symmetric', or 'hermitian'. If symmetry is None the symmetry type of 'a' is determined by its values.

Unformatted Fortran files

FortranFile(filename[, mode, header_dtype])	A file object for unformatted sequential files from Fortran code.
FortranEOFError	Indicates that the file ended properly.
FortranFormattingError	Indicates that the file ended mid-record.

scipy.io.FortranFile

class scipy.io.**FortranFile**(*filename*, *mode='r'*, *header_dtype=<class 'numpy.uint32'>*)

A file object for unformatted sequential files from Fortran code.

Parameters

filename [file or str] Open file object or filename.
mode [{'r', 'w'}, optional] Read-write mode, default is 'r'.
header_dtype
[dtype, optional] Data type of the header. Size and endiness must match the input/output file.

Notes

These files are broken up into records of unspecified types. The size of each record is given at the start (although the size of this header is not standard) and the data is written onto disk without any formatting. Fortran compilers supporting the BACKSPACE statement will write a second copy of the size to facilitate backwards seeking.

This class only supports files written with both sizes for the record. It also does not support the subrecords used in Intel and gfortran compilers for records which are greater than 2GB with a 4-byte header.

An example of an unformatted sequential file in Fortran would be written as:

```
OPEN(1, FILE=myfilename, FORM='unformatted')

WRITE(1) myvariable
```

Since this is a non-standard file format, whose contents depend on the compiler and the endianness of the machine, caution is advised. Files from gfortran 4.8.0 and gfortran 4.1.2 on x86_64 are known to work.

Consider using Fortran direct-access files or files from the newer Stream I/O, which can be easily read by numpy.fromfile.

Examples

To create an unformatted sequential Fortran file:

```
>>> from scipy.io import FortranFile
>>> f = FortranFile('test.unf', 'w')
>>> f.write_record(np.array([1,2,3,4,5], dtype=np.int32))
>>> f.write_record(np.linspace(0,1,20).reshape((5,4)).T)
>>> f.close()
```

To read this file:

```
>>> f = FortranFile('test.unf', 'r')
>>> print(f.read_ints(np.int32))
[1 2 3 4 5]
>>> print(f.read_reals(float).reshape((5,4), order="F"))
[[0.         0.05263158 0.10526316 0.15789474]
 [0.21052632 0.26315789 0.31578947 0.36842105]
 [0.42105263 0.47368421 0.52631579 0.57894737]
 [0.63157895 0.68421053 0.73684211 0.78947368]
 [0.84210526 0.89473684 0.94736842 1.        ]]
>>> f.close()
```

Or, in Fortran:

```
integer :: a(5), i
double precision :: b(5,4)
open(1, file='test.unf', form='unformatted')
read(1) a
read(1) b
close(1)
write(*,*) a
do i = 1, 5
    write(*,*) b(i,:)
end do
```

Methods

close()	Closes the file.
read_ints([dtype])	Reads a record of a given type from the file, defaulting to an integer type (`INTEGER*4` in Fortran).
read_reals([dtype])	Reads a record of a given type from the file, defaulting to a floating point number (`real*8` in Fortran).
read_record(*dtypes, **kwargs)	Reads a record of a given type from the file.
write_record(*items)	Write a record (including sizes) to the file.

scipy.io.FortranFile.close

FortranFile.**close**()
Closes the file. It is unsupported to call any other methods off this object after closing it. Note that this class supports the 'with' statement in modern versions of Python, to call this automatically

scipy.io.FortranFile.read_ints

FortranFile.**read_ints**(*dtype='i4'*)
Reads a record of a given type from the file, defaulting to an integer type (`INTEGER*4` in Fortran).

Parameters

dtype [dtype, optional] Data type specifying the size and endiness of the data.

Returns

data [ndarray] A 1-D array object.

See also:

read_reals

read_record

scipy.io.FortranFile.read_reals

FortranFile.**read_reals**(*dtype='f8'*)
Reads a record of a given type from the file, defaulting to a floating point number (`real*8` in Fortran).

Parameters

dtype [dtype, optional] Data type specifying the size and endiness of the data.

Returns

data [ndarray] A 1-D array object.

See also:

read_ints

read_record

scipy.io.FortranFile.read_record

FortranFile.**read_record**(**dtypes*, ***kwargs*)
Reads a record of a given type from the file.

Parameters

***dtypes** [dtypes, optional] Data type(s) specifying the size and endiness of the data.

Returns

data [ndarray] A 1-D array object.

Raises

FortranEOFError
To signal that no further records are available
FortranFormattingError
To signal that the end of the file was encountered part-way through a record

See also:

`read_reals`

`read_ints`

Notes

If the record contains a multidimensional array, you can specify the size in the dtype. For example:

```
INTEGER var(5,4)
```

can be read with:

```
read_record('(4,5)i4').T
```

Note that this function does **not** assume the file data is in Fortran column major order, so you need to (i) swap the order of dimensions when reading and (ii) transpose the resulting array.

Alternatively, you can read the data as a 1-D array and handle the ordering yourself. For example:

```
read_record('i4').reshape(5, 4, order='F')
```

For records that contain several variables or mixed types (as opposed to single scalar or array types), give them as separate arguments:

```
double precision :: a
integer :: b
write(1) a, b

record = f.read_record('<f4', '<i4')
a = record[0]  # first number
b = record[1]  # second number
```

and if any of the variables are arrays, the shape can be specified as the third item in the relevant dtype:

```
double precision :: a
integer :: b(3,4)
write(1) a, b

record = f.read_record('<f4', np.dtype(('<i4', (4, 3))))
a = record[0]
b = record[1].T
```

NumPy also supports a short syntax for this kind of type:

```
record = f.read_record('<f4', '(3,3)<i4')
```

scipy.io.FortranFile.write_record

FortranFile.**write_record**(**items*)
Write a record (including sizes) to the file.

Parameters

***items** [array_like] The data arrays to write.

Notes

Writes data items to a file:

```
write_record(a.T, b.T, c.T, ...)

write(1) a, b, c, ...
```

Note that data in multidimensional arrays is written in row-major order — to make them read correctly by Fortran programs, you need to transpose the arrays yourself when writing them.

scipy.io.FortranEOFError

exception scipy.io.**FortranEOFError**
Indicates that the file ended properly.

This error descends from TypeError because the code used to raise TypeError (and this was the only way to know that the file had ended) so users might have `except TypeError:`.

errno
POSIX exception code

filename
exception filename

filename2
second exception filename

strerror
exception strerror

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.io.FortranFormattingError

exception scipy.io.**FortranFormattingError**
Indicates that the file ended mid-record.

Descends from TypeError for backward compatibility.

errno
POSIX exception code

filename
exception filename

filename2
second exception filename

strerror
exception strerror

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

Netcdf

netcdf_file(filename[, mode, mmap, version, …])	A file object for NetCDF data.
netcdf_variable(data, typecode, size, shape, …)	A data object for netcdf files.

scipy.io.netcdf_file

class scipy.io.**netcdf_file**(*filename*, *mode='r'*, *mmap=None*, *version=1*, *maskandscale=False*)
A file object for NetCDF data.

A *netcdf_file* object has two standard attributes: *dimensions* and *variables*. The values of both are dictionaries, mapping dimension names to their associated lengths and variable names to variables, respectively. Application programs should never modify these dictionaries.

All other attributes correspond to global attributes defined in the NetCDF file. Global file attributes are created by assigning to an attribute of the *netcdf_file* object.

Parameters

filename [string or file-like] string -> filename
mode [{'r', 'w', 'a'}, optional] read-write-append mode, default is 'r'
mmap [None or bool, optional] Whether to mmap *filename* when reading. Default is True when *filename* is a file name, False when *filename* is a file-like object. Note that when mmap is in use, data arrays returned refer directly to the mmapped data on disk, and the file cannot be closed as long as references to it exist.
version [{1, 2}, optional] version of netcdf to read / write, where 1 means *Classic format* and 2 means *64-bit offset format*. Default is 1. See here for more info.
maskandscale
[bool, optional] Whether to automatically scale and/or mask data based on attributes. Default is False.

Notes

The major advantage of this module over other modules is that it doesn't require the code to be linked to the NetCDF libraries. This module is derived from pupynere.

NetCDF files are a self-describing binary data format. The file contains metadata that describes the dimensions and variables in the file. More details about NetCDF files can be found here. There are three main sections to a NetCDF data structure:

1. Dimensions
2. Variables
3. Attributes

The dimensions section records the name and length of each dimension used by the variables. The variables would then indicate which dimensions it uses and any attributes such as data units, along with containing the data values for the variable. It is good practice to include a variable that is the same name as a dimension to provide the values for that axes. Lastly, the attributes section would contain additional information such as the name of the file creator or the instrument used to collect the data.

When writing data to a NetCDF file, there is often the need to indicate the 'record dimension'. A record dimension is the unbounded dimension for a variable. For example, a temperature variable may have dimensions of latitude,

longitude and time. If one wants to add more temperature data to the NetCDF file as time progresses, then the temperature variable should have the time dimension flagged as the record dimension.

In addition, the NetCDF file header contains the position of the data in the file, so access can be done in an efficient manner without loading unnecessary data into memory. It uses the `mmap` module to create Numpy arrays mapped to the data on disk, for the same purpose.

Note that when *`netcdf_file`* is used to open a file with mmap=True (default for read-only), arrays returned by it refer to data directly on the disk. The file should not be closed, and cannot be cleanly closed when asked, if such arrays are alive. You may want to copy data arrays obtained from mmapped Netcdf file if they are to be processed after the file is closed, see the example below.

Examples

To create a NetCDF file:

```
>>> from scipy.io import netcdf
>>> f = netcdf.netcdf_file('simple.nc', 'w')
>>> f.history = 'Created for a test'
>>> f.createDimension('time', 10)
>>> time = f.createVariable('time', 'i', ('time',))
>>> time[:] = np.arange(10)
>>> time.units = 'days since 2008-01-01'
>>> f.close()
```

Note the assignment of `arange(10)` to `time[:]`. Exposing the slice of the time variable allows for the data to be set in the object, rather than letting `arange(10)` overwrite the `time` variable.

To read the NetCDF file we just created:

```
>>> from scipy.io import netcdf
>>> f = netcdf.netcdf_file('simple.nc', 'r')
>>> print(f.history)
b'Created for a test'
>>> time = f.variables['time']
>>> print(time.units)
b'days since 2008-01-01'
>>> print(time.shape)
(10,)
>>> print(time[-1])
9
```

NetCDF files, when opened read-only, return arrays that refer directly to memory-mapped data on disk:

```
>>> data = time[:]
>>> data.base.base
<mmap.mmap object at 0x7fe753763180>
```

If the data is to be processed after the file is closed, it needs to be copied to main memory:

```
>>> data = time[:].copy()
>>> f.close()
>>> data.mean()
4.5
```

A NetCDF file can also be used as context manager:

```
>>> from scipy.io import netcdf
>>> with netcdf.netcdf_file('simple.nc', 'r') as f:
...     print(f.history)
b'Created for a test'
```

Methods

close()	Closes the NetCDF file.
createDimension(name, length)	Adds a dimension to the Dimension section of the NetCDF data structure.
createVariable(name, type, dimensions)	Create an empty variable for the *netcdf_file* object, specifying its data type and the dimensions it uses.
flush()	Perform a sync-to-disk flush if the *netcdf_file* object is in write mode.
sync()	Perform a sync-to-disk flush if the *netcdf_file* object is in write mode.

scipy.io.netcdf_file.close

netcdf_file.**close**()
Closes the NetCDF file.

scipy.io.netcdf_file.createDimension

netcdf_file.**createDimension**(*name*, *length*)
Adds a dimension to the Dimension section of the NetCDF data structure.

Note that this function merely adds a new dimension that the variables can reference. The values for the dimension, if desired, should be added as a variable using *createVariable*, referring to this dimension.

Parameters

name [str] Name of the dimension (Eg, 'lat' or 'time').
length [int] Length of the dimension.

See also:

createVariable

scipy.io.netcdf_file.createVariable

netcdf_file.**createVariable**(*name*, *type*, *dimensions*)
Create an empty variable for the *netcdf_file* object, specifying its data type and the dimensions it uses.

Parameters

name [str] Name of the new variable.
type [dtype or str] Data type of the variable.
dimensions
[sequence of str] List of the dimension names used by the variable, in the desired order.

Returns

variable [netcdf_variable] The newly created `netcdf_variable` object. This object has also been added to the *netcdf_file* object as well.

See also:

createDimension

Notes

Any dimensions to be used by the variable should already exist in the NetCDF data structure or should be created by *createDimension* prior to creating the NetCDF variable.

scipy.io.netcdf_file.flush

`netcdf_file.`**flush**`()`

Perform a sync-to-disk flush if the *netcdf_file* object is in write mode.

See also:

sync

Identical function

scipy.io.netcdf_file.sync

`netcdf_file.`**sync**`()`

Perform a sync-to-disk flush if the *netcdf_file* object is in write mode.

See also:

sync

Identical function

scipy.io.netcdf_variable

class `scipy.io.`**netcdf_variable**(*data*, *typecode*, *size*, *shape*, *dimensions*, *attributes=None*, *maskandscale=False*)

A data object for netcdf files.

netcdf_variable objects are constructed by calling the method *netcdf_file.createVariable* on the *netcdf_file* object. *netcdf_variable* objects behave much like array objects defined in numpy, except that their data resides in a file. Data is read by indexing and written by assigning to an indexed subset; the entire array can be accessed by the index `[:]` or (for scalars) by using the methods *getValue* and *assignValue*. *netcdf_variable* objects also have attribute `shape` with the same meaning as for arrays, but the shape cannot be modified. There is another read-only attribute *dimensions*, whose value is the tuple of dimension names.

All other attributes correspond to variable attributes defined in the NetCDF file. Variable attributes are created by assigning to an attribute of the *netcdf_variable* object.

Parameters

data [array_like] The data array that holds the values for the variable. Typically, this is initialized as empty, but with the proper shape.

typecode [dtype character code] Desired data-type for the data array.
size [int] Desired element size for the data array.
shape [sequence of ints] The shape of the array. This should match the lengths of the variable's dimensions.
dimensions
[sequence of strings] The names of the dimensions used by the variable. Must be in the same order of the dimension lengths given by `shape`.
attributes [dict, optional] Attribute values (any type) keyed by string names. These attributes become attributes for the netcdf_variable object.
maskandscale
[bool, optional] Whether to automatically scale and/or mask data based on attributes. Default is False.

See also:

isrec*, *shape

Attributes

dimensions
[list of str] List of names of dimensions used by the variable object.
isrec, shape
Properties

Methods

assignValue(value)	Assign a scalar value to a *netcdf_variable* of length one.
getValue()	Retrieve a scalar value from a *netcdf_variable* of length one.
itemsize()	Return the itemsize of the variable.
typecode()	Return the typecode of the variable.

scipy.io.netcdf_variable.assignValue

netcdf_variable.**assignValue**(*value*)
Assign a scalar value to a *netcdf_variable* of length one.

Parameters

value [scalar] Scalar value (of compatible type) to assign to a length-one netcdf variable. This value will be written to file.

Raises

ValueError
If the input is not a scalar, or if the destination is not a length-one netcdf variable.

scipy.io.netcdf_variable.getValue

netcdf_variable.**getValue**()
Retrieve a scalar value from a *netcdf_variable* of length one.

Raises

ValueError
If the netcdf variable is an array of length greater than one, this exception will be raised.

scipy.io.netcdf_variable.itemsize

netcdf_variable.**itemsize**()
Return the itemsize of the variable.

Returns

itemsize [int] The element size of the variable (e.g., 8 for float64).

scipy.io.netcdf_variable.typecode

netcdf_variable.**typecode**()
Return the typecode of the variable.

Returns

typecode [char] The character typecode of the variable (e.g., 'i' for int).

__getitem__	

Harwell-Boeing files

hb_read(path_or_open_file)	Read HB-format file.
hb_write(path_or_open_file, m[, hb_info])	Write HB-format file.

scipy.io.hb_read

scipy.io.**hb_read**(*path_or_open_file*)
Read HB-format file.

Parameters

path_or_open_file
[path-like or file-like] If a file-like object, it is used as-is. Otherwise, it is opened before reading.

Returns

data [scipy.sparse.csc_matrix instance] The data read from the HB file as a sparse matrix.

Notes

At the moment not the full Harwell-Boeing format is supported. Supported features are:

- assembled, non-symmetric, real matrices
- integer for pointer/indices
- exponential format for float values, and int format

Examples

We can read and write a harwell-boeing format file:

```
>>> from scipy.io.harwell_boeing import hb_read, hb_write
>>> from scipy.sparse import csr_matrix, eye
>>> data = csr_matrix(eye(3))  # create a sparse matrix
>>> hb_write("data.hb", data)  # write a hb file
>>> print(hb_read("data.hb"))  # read a hb file
  (0, 0)    1.0
  (1, 1)    1.0
  (2, 2)    1.0
```

scipy.io.hb_write

scipy.io.**hb_write**(*path_or_open_file*, *m*, *hb_info=None*)

Write HB-format file.

Parameters

path_or_open_file
: [path-like or file-like] If a file-like object, it is used as-is. Otherwise, it is opened before writing.

m
: [sparse-matrix] the sparse matrix to write

hb_info
: [HBInfo] contains the meta-data for write

Returns

None

Notes

At the moment not the full Harwell-Boeing format is supported. Supported features are:

- assembled, non-symmetric, real matrices
- integer for pointer/indices
- exponential format for float values, and int format

Examples

We can read and write a harwell-boeing format file:

```
>>> from scipy.io.harwell_boeing import hb_read, hb_write
>>> from scipy.sparse import csr_matrix, eye
>>> data = csr_matrix(eye(3))  # create a sparse matrix
>>> hb_write("data.hb", data)  # write a hb file
>>> print(hb_read("data.hb"))  # read a hb file
  (0, 0)    1.0
  (1, 1)    1.0
  (2, 2)    1.0
```

Wav sound files (`scipy.io.wavfile`)

read(filename[, mmap])	Open a WAV file.
write(filename, rate, data)	Write a NumPy array as a WAV file.
WavFileWarning	

scipy.io.wavfile.read

scipy.io.wavfile.**read**(*filename*, *mmap=False*)

Open a WAV file.

Return the sample rate (in samples/sec) and data from an LPCM WAV file.

Parameters

filename [string or open file handle] Input WAV file.

mmap [bool, optional] Whether to read data as memory-mapped (default: False). Not compatible with some bit depths; see Notes. Only to be used on real files.
New in version 0.12.0.

Returns

rate [int] Sample rate of WAV file.

data [numpy array] Data read from WAV file. Data-type is determined from the file; see Notes. Data is 1-D for 1-channel WAV, or 2-D of shape (Nsamples, Nchannels) otherwise. If a file-like input without a C-like file descriptor (e.g., `io.BytesIO`) is passed, this will not be writeable.

Notes

Common data types: [1]

WAV format	Min	Max	NumPy dtype
32-bit floating-point	-1.0	+1.0	float32
32-bit integer PCM	-2147483648	+2147483647	int32
24-bit integer PCM	-2147483648	+2147483392	int32
16-bit integer PCM	-32768	+32767	int16
8-bit integer PCM	0	255	uint8

WAV files can specify arbitrary bit depth, and this function supports reading any integer PCM depth from 1 to 64 bits. Data is returned in the smallest compatible numpy int type, in left-justified format. 8-bit and lower is unsigned, while 9-bit and higher is signed.

For example, 24-bit data will be stored as int32, with the MSB of the 24-bit data stored at the MSB of the int32, and typically the least significant byte is 0x00. (However, if a file actually contains data past its specified bit depth, those bits will be read and output, too. [2])

This bit justification and sign matches WAV's native internal format, which allows memory mapping of WAV files that use 1, 2, 4, or 8 bytes per sample (so 24-bit files cannot be memory-mapped, but 32-bit can).

IEEE float PCM in 32- or 64-bit format is supported, with or without mmap. Values exceeding [-1, +1] are not clipped.

Non-linear PCM (mu-law, A-law) is not supported.

References

[1], [2]

Examples

```
>>> from os.path import dirname, join as pjoin
>>> from scipy.io import wavfile
>>> import scipy.io
```

Get the filename for an example .wav file from the tests/data directory.

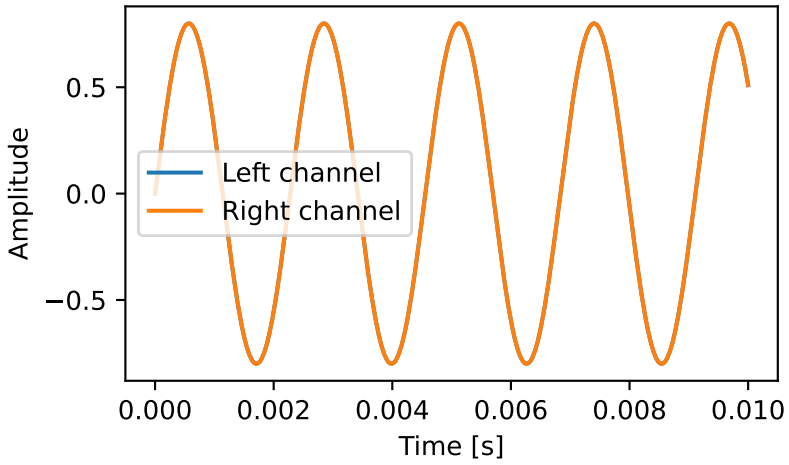
```
>>> data_dir = pjoin(dirname(scipy.io.__file__), 'tests', 'data')
>>> wav_fname = pjoin(data_dir, 'test-44100Hz-2ch-32bit-float-be.wav')
```

Load the .wav file contents.

```
>>> samplerate, data = wavfile.read(wav_fname)
>>> print(f"number of channels = {data.shape[1]}")
number of channels = 2
>>> length = data.shape[0] / samplerate
>>> print(f"length = {length}s")
length = 0.01s
```

Plot the waveform.

```
>>> import matplotlib.pyplot as plt
>>> import numpy as np
>>> time = np.linspace(0., length, data.shape[0])
>>> plt.plot(time, data[:, 0], label="Left channel")
>>> plt.plot(time, data[:, 1], label="Right channel")
>>> plt.legend()
>>> plt.xlabel("Time [s]")
>>> plt.ylabel("Amplitude")
>>> plt.show()
```



scipy.io.wavfile.write

scipy.io.wavfile.**write**(*filename*, *rate*, *data*)

Write a NumPy array as a WAV file.

Parameters

filename [string or open file handle] Output wav file.
rate [int] The sample rate (in samples/sec).
data [ndarray] A 1-D or 2-D NumPy array of either integer or float data-type.

Notes

- Writes a simple uncompressed WAV file.
- To write multiple-channels, use a 2-D array of shape (Nsamples, Nchannels).
- The bits-per-sample and PCM/float will be determined by the data-type.

Common data types: [1]

WAV format	Min	Max	NumPy dtype
32-bit floating-point	-1.0	+1.0	float32
32-bit PCM	-2147483648	+2147483647	int32
16-bit PCM	-32768	+32767	int16
8-bit PCM	0	255	uint8

Note that 8-bit PCM is unsigned.

References

[1]

Examples

Create a 100Hz sine wave, sampled at 44100Hz. Write to 16-bit PCM, Mono.

```
>>> from scipy.io.wavfile import write
>>> samplerate = 44100; fs = 100
>>> t = np.linspace(0., 1., samplerate)
>>> amplitude = np.iinfo(np.int16).max
>>> data = amplitude * np.sin(2. * np.pi * fs * t)
>>> write("example.wav", samplerate, data.astype(np.int16))
```

scipy.io.wavfile.WavFileWarning

exception scipy.io.wavfile.**WavFileWarning**

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

Arff files (scipy.io.arff)

loadarff(f)	Read an arff file.
MetaData(rel, attr)	Small container to keep useful information on a ARFF dataset.
ArffError	
ParseArffError	

scipy.io.arff.loadarff

scipy.io.arff.**loadarff**(*f*)
Read an arff file.

The data is returned as a record array, which can be accessed much like a dictionary of NumPy arrays. For example, if one of the attributes is called 'pressure', then its first 10 data points can be accessed from the `data` record array like so: `data['pressure'][0:10]`

Parameters

f [file-like or str] File-like object to read from, or filename to open.

Returns

data [record array] The data of the arff file, accessible by attribute names.
meta [*MetaData*] Contains information about the arff file such as name and type of attributes, the relation (name of the dataset), etc.

Raises

ParseArffError
This is raised if the given file is not ARFF-formatted.

NotImplementedError
The ARFF file has an attribute which is not supported yet.

Notes

This function should be able to read most arff files. Not implemented functionality include:

- date type attributes
- string type attributes

It can read files with numeric and nominal attributes. It cannot read files with sparse data ({} in the file). However, this function can read files with missing data (? in the file), representing the data points as NaNs.

Examples

```
>>> from scipy.io import arff
>>> from io import StringIO
>>> content = """
... @relation foo
... @attribute width  numeric
... @attribute height numeric
... @attribute color  {red,green,blue,yellow,black}
... @data
... 5.0,3.25,blue
... 4.5,3.75,green
... 3.0,4.00,red
... """
>>> f = StringIO(content)
>>> data, meta = arff.loadarff(f)
>>> data
array([(5.0, 3.25, 'blue'), (4.5, 3.75, 'green'), (3.0, 4.0, 'red')],
      dtype=[('width', '<f8'), ('height', '<f8'), ('color', '|S6')])
>>> meta
Dataset: foo
    width's type is numeric
    height's type is numeric
    color's type is nominal, range is ('red', 'green', 'blue', 'yellow',
 ↪'black')
```

scipy.io.arff.MetaData

class scipy.io.arff.**MetaData**(*rel*, *attr*)
Small container to keep useful information on a ARFF dataset.

Knows about attributes names and types.

Notes

Also maintains the list of attributes in order, i.e., doing for i in meta, where meta is an instance of MetaData, will return the different attribute names in the order they were defined.

Examples

```
data, meta = loadarff('iris.arff')
# This will print the attributes names of the iris.arff dataset
for i in meta:
    print(i)
# This works too
meta.names()
# Getting attribute type
types = meta.types()
```

Methods

names()	Return the list of attribute names.
types()	Return the list of attribute types.

scipy.io.arff.MetaData.names

MetaData.**names**()
Return the list of attribute names.

Returns

attrnames [list of str] The attribute names.

scipy.io.arff.MetaData.types

MetaData.**types**()
Return the list of attribute types.

Returns

attr_types [list of str] The attribute types.

scipy.io.arff.ArffError

exception scipy.io.arff.**ArffError**

errno
POSIX exception code

filename
exception filename

filename2
second exception filename

strerror
exception strerror

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.io.arff.ParseArffError

exception scipy.io.arff.**ParseArffError**

errno
POSIX exception code

filename
exception filename

filename2
second exception filename

strerror
exception strerror

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

3.3.10 Linear algebra (scipy.linalg)

Linear algebra functions.

See also:

numpy.linalg for more linear algebra functions. Note that although *scipy.linalg* imports most of them, identically named functions from *scipy.linalg* may offer more or slightly differing functionality.

Basics

inv(a[, overwrite_a, check_finite])	Compute the inverse of a matrix.
solve(a, b[, sym_pos, lower, overwrite_a, …])	Solves the linear equation set `a * x = b` for the unknown `x` for square `a` matrix.
solve_banded(l_and_u, ab, b[, overwrite_ab, …])	Solve the equation a x = b for x, assuming a is banded matrix.
solveh_banded(ab, b[, overwrite_ab, …])	Solve equation a x = b.
solve_circulant(c, b[, singular, tol, …])	Solve C x = b for x, where C is a circulant matrix.
solve_triangular(a, b[, trans, lower, …])	Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.
solve_toeplitz(c_or_cr, b[, check_finite])	Solve a Toeplitz system using Levinson Recursion
matmul_toeplitz(c_or_cr, x[, check_finite, …])	Efficient Toeplitz Matrix-Matrix Multiplication using FFT
det(a[, overwrite_a, check_finite])	Compute the determinant of a matrix
norm(a[, ord, axis, keepdims, check_finite])	Matrix or vector norm.
lstsq(a, b[, cond, overwrite_a, …])	Compute least-squares solution to equation Ax = b.
pinv(a[, atol, rtol, return_rank, …])	Compute the (Moore-Penrose) pseudo-inverse of a matrix.

continues on next page

Table 92 – continued from previous page

pinv2(a[, cond, rcond, return_rank, …])	Compute the (Moore-Penrose) pseudo-inverse of a matrix.
pinvh(a[, atol, rtol, lower, return_rank, …])	Compute the (Moore-Penrose) pseudo-inverse of a Hermitian matrix.
kron(a, b)	Kronecker product.
khatri_rao(a, b)	Khatri-rao product
tril(m[, k])	Make a copy of a matrix with elements above the kth diagonal zeroed.
triu(m[, k])	Make a copy of a matrix with elements below the kth diagonal zeroed.
orthogonal_procrustes(A, B[, check_finite])	Compute the matrix solution of the orthogonal Procrustes problem.
matrix_balance(A[, permute, scale, …])	Compute a diagonal similarity transformation for row/column balancing.
subspace_angles(A, B)	Compute the subspace angles between two matrices.
LinAlgError	Generic Python-exception-derived object raised by linalg functions.
LinAlgWarning	The warning emitted when a linear algebra related operation is close to fail conditions of the algorithm or loss of accuracy is expected.

scipy.linalg.inv

scipy.linalg.**inv**(*a*, *overwrite_a=False*, *check_finite=True*)

Compute the inverse of a matrix.

Parameters

a [array_like] Square matrix to be inverted.

overwrite_a
[bool, optional] Discard data in *a* (may improve performance). Default is False.

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

ainv [ndarray] Inverse of the matrix *a*.

Raises

LinAlgError
If *a* is singular.

ValueError
If *a* is not square, or not 2D.

Examples

```
>>> from scipy import linalg
>>> a = np.array([[1., 2.], [3., 4.]])
>>> linalg.inv(a)
array([[-2. ,  1. ],
       [ 1.5, -0.5]])
>>> np.dot(a, linalg.inv(a))
array([[ 1.,  0.],
       [ 0.,  1.]])
```

scipy.linalg.solve

scipy.linalg.**solve**(*a*, *b*, *sym_pos=False*, *lower=False*, *overwrite_a=False*, *overwrite_b=False*, *debug=None*, *check_finite=True*, *assume_a='gen'*, *transposed=False*)

Solves the linear equation set `a * x = b` for the unknown `x` for square `a` matrix.

If the data matrix is known to be a particular type then supplying the corresponding string to `assume_a` key chooses the dedicated solver. The available options are

generic matrix	'gen'
symmetric	'sym'
hermitian	'her'
positive definite	'pos'

If omitted, `'gen'` is the default structure.

The datatype of the arrays define which solver is called regardless of the values. In other words, even when the complex array entries have precisely zero imaginary parts, the complex solver will be called based on the data type of the array.

Parameters

a [(N, N) array_like] Square input data

b [(N, NRHS) array_like] Input data for the right hand side.

sym_pos [bool, optional] Assume *a* is symmetric and positive definite. This key is deprecated and assume_a = 'pos' keyword is recommended instead. The functionality is the same. It will be removed in the future.

lower [bool, optional] If True, only the data contained in the lower triangle of *a*. Default is to use upper triangle. (ignored for `'gen'`)

overwrite_a [bool, optional] Allow overwriting data in *a* (may enhance performance). Default is False.

overwrite_b [bool, optional] Allow overwriting data in *b* (may enhance performance). Default is False.

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

assume_a [str, optional] Valid entries are explained above.

transposed: bool, optional If True, `a^T x = b` for real matrices, raises *NotImplementedError* for complex matrices (only for True).

Returns

x [(N, NRHS) ndarray] The solution array.

Raises

ValueError
: If size mismatches detected or input a is not square.

LinAlgError
: If the matrix is singular.

LinAlgWarning
: If an ill-conditioned input a is detected.

NotImplementedError
: If transposed is True and input a is a complex matrix.

Notes

If the input b matrix is a 1-D array with N elements, when supplied together with an NxN input a, it is assumed as a valid column vector despite the apparent size mismatch. This is compatible with the numpy.dot() behavior and the returned result is still 1-D array.

The generic, symmetric, Hermitian and positive definite solutions are obtained via calling ?GESV, ?SYSV, ?HESV, and ?POSV routines of LAPACK respectively.

Examples

Given *a* and *b*, solve for *x*:

```
>>> a = np.array([[3, 2, 0], [1, -1, 0], [0, 5, 1]])
>>> b = np.array([2, 4, -1])
>>> from scipy import linalg
>>> x = linalg.solve(a, b)
>>> x
array([ 2., -2.,  9.])
>>> np.dot(a, x) == b
array([ True,  True,  True], dtype=bool)
```

scipy.linalg.solve_banded

scipy.linalg.**solve_banded**(*l_and_u*, *ab*, *b*, *overwrite_ab=False*, *overwrite_b=False*, *debug=None*, *check_finite=True*)

Solve the equation a x = b for x, assuming a is banded matrix.

The matrix a is stored in *ab* using the matrix diagonal ordered form:

```
ab[u + i - j, j] == a[i,j]
```

Example of *ab* (shape of a is (6,6), u =1, l =2):

```
*    a01  a12  a23  a34  a45
a00  a11  a22  a33  a44  a55
a10  a21  a32  a43  a54   *
a20  a31  a42  a53   *    *
```

Parameters

(l, u) [(integer, integer)] Number of non-zero lower and upper diagonals

ab [(l + u + 1, M) array_like] Banded matrix

b [(M,) or (M, K) array_like] Right-hand side

overwrite_ab
: [bool, optional] Discard data in *ab* (may enhance performance)

overwrite_b
: [bool, optional] Discard data in *b* (may enhance performance)

check_finite
: [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x
: [(M,) or (M, K) ndarray] The solution to the system a x = b. Returned shape depends on the shape of *b*.

Examples

Solve the banded system a x = b, where:

```
    [5  2 -1  0  0]       [0]
    [1  4  2 -1  0]       [1]
a = [0  1  3  2 -1]   b = [2]
    [0  0  1  2  2]       [2]
    [0  0  0  1  1]       [3]
```

There is one nonzero diagonal below the main diagonal (l = 1), and two above (u = 2). The diagonal banded form of the matrix is:

```
     [*  * -1 -1 -1]
ab = [*  2  2  2  2]
     [5  4  3  2  1]
     [1  1  1  1  *]
```

```
>>> from scipy.linalg import solve_banded
>>> ab = np.array([[0,  0, -1, -1, -1],
...                [0,  2,  2,  2,  2],
...                [5,  4,  3,  2,  1],
...                [1,  1,  1,  1,  0]])
>>> b = np.array([0, 1, 2, 2, 3])
>>> x = solve_banded((1, 2), ab, b)
>>> x
array([-2.37288136,  3.93220339, -4.        ,  4.3559322 , -1.3559322 ])
```

scipy.linalg.solveh_banded

`scipy.linalg.`**`solveh_banded`**(*ab*, *b*, *overwrite_ab=False*, *overwrite_b=False*, *lower=False*, *check_finite=True*)

Solve equation a x = b. a is Hermitian positive-definite banded matrix.

The matrix a is stored in *ab* either in lower diagonal or upper diagonal ordered form:

ab[u + i - j, j] == a[i,j] (if upper form; i <= j) ab[i - j, j] == a[i,j] (if lower form; i >= j)

Example of *ab* (shape of a is (6, 6), *u* =2):

```
upper form:
*   *   a02 a13 a24 a35
*   a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *   *
```

Cells marked with * are not used.

Parameters

ab [(*u* + 1, M) array_like] Banded matrix

b [(M,) or (M, K) array_like] Right-hand side

overwrite_ab
[bool, optional] Discard data in *ab* (may enhance performance)

overwrite_b
[bool, optional] Discard data in *b* (may enhance performance)

lower [bool, optional] Is the matrix in the lower form. (Default is upper form)

check_finite
[bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x [(M,) or (M, K) ndarray] The solution to the system a x = b. Shape of return matches shape of *b*.

Examples

Solve the banded system A x = b, where:

```
    [ 4  2 -1  0  0  0]        [1]
    [ 2  5  2 -1  0  0]        [2]
A = [-1  2  6  2 -1  0]    b = [2]
    [ 0 -1  2  7  2 -1]        [3]
    [ 0  0 -1  2  8  2]        [3]
    [ 0  0  0 -1  2  9]        [3]
```

```
>>> from scipy.linalg import solveh_banded
```

ab contains the main diagonal and the nonzero diagonals below the main diagonal. That is, we use the lower form:

```
>>> ab = np.array([[ 4,  5,  6,  7, 8, 9],
...                [ 2,  2,  2,  2, 2, 0],
...                [-1, -1, -1, -1, 0, 0]])
>>> b = np.array([1, 2, 2, 3, 3, 3])
>>> x = solveh_banded(ab, b, lower=True)
>>> x
array([ 0.03431373,  0.45938375,  0.05602241,  0.47759104,  0.17577031,
        0.34733894])
```

Solve the Hermitian banded system H x = b, where:

```
    [ 8   2-1j    0      0  ]         [ 1   ]
H = [2+1j  5      1j     0  ]     b = [1+1j]
    [ 0   -1j     9   -2-1j]         [1-2j]
    [ 0    0   -2+1j    6  ]         [ 0   ]
```

In this example, we put the upper diagonals in the array *hb*:

```
>>> hb = np.array([[0, 2-1j, 1j, -2-1j],
...                [8,  5,    9,   6  ]])
>>> b = np.array([1, 1+1j, 1-2j, 0])
>>> x = solveh_banded(hb, b)
>>> x
array([ 0.07318536-0.02939412j,  0.11877624+0.17696461j,
        0.10077984-0.23035393j, -0.00479904-0.09358128j])
```

scipy.linalg.solve_circulant

scipy.linalg.**solve_circulant**(*c*, *b*, *singular='raise'*, *tol=None*, *caxis=- 1*, *baxis=0*, *outaxis=0*)

Solve C x = b for x, where C is a circulant matrix.

C is the circulant matrix associated with the vector *c*.

The system is solved by doing division in Fourier space. The calculation is:

```
x = ifft(fft(b) / fft(c))
```

where *fft* and *ifft* are the fast Fourier transform and its inverse, respectively. For a large vector *c*, this is *much* faster than solving the system with the full circulant matrix.

Parameters

c [array_like] The coefficients of the circulant matrix.

b [array_like] Right-hand side matrix in `a x = b`.

singular [str, optional] This argument controls how a near singular circulant matrix is handled. If *singular* is "raise" and the circulant matrix is near singular, a *LinAlgError* is raised. If *singular* is "lstsq", the least squares solution is returned. Default is "raise".

tol [float, optional] If any eigenvalue of the circulant matrix has an absolute value that is less than or equal to *tol*, the matrix is considered to be near singular. If not given, *tol* is set to:

```
tol = abs_eigs.max() * abs_eigs.size * np.finfo(np.
↪float64).eps
```

where *abs_eigs* is the array of absolute values of the eigenvalues of the circulant matrix.

caxis [int] When *c* has dimension greater than 1, it is viewed as a collection of circulant vectors. In this case, *caxis* is the axis of *c* that holds the vectors of circulant coefficients.

baxis [int] When *b* has dimension greater than 1, it is viewed as a collection of vectors. In this case, *baxis* is the axis of *b* that holds the right-hand side vectors.

outaxis [int] When *c* or *b* are multidimensional, the value returned by *solve_circulant* is multidimensional. In this case, *outaxis* is the axis of the result that holds the solution vectors.

Returns

x [ndarray] Solution to the system `C x = b`.

Raises

LinAlgError
If the circulant matrix associated with *c* is near singular.

See also:

`circulant`
circulant matrix

Notes

For a 1-D vector *c* with length *m*, and an array *b* with shape `(m, ...)`,

solve_circulant(c, b)

returns the same result as

solve(circulant(c), b)

where *solve* and *circulant* are from *scipy.linalg*.

New in version 0.16.0.

Examples

```
>>> from scipy.linalg import solve_circulant, solve, circulant, lstsq
```

```
>>> c = np.array([2, 2, 4])
>>> b = np.array([1, 2, 3])
>>> solve_circulant(c, b)
array([ 0.75, -0.25,  0.25])
```

Compare that result to solving the system with *scipy.linalg.solve*:

```
>>> solve(circulant(c), b)
array([ 0.75, -0.25,  0.25])
```

A singular example:

```
>>> c = np.array([1, 1, 0, 0])
>>> b = np.array([1, 2, 3, 4])
```

Calling `solve_circulant(c, b)` will raise a *LinAlgError*. For the least square solution, use the option `singular='lstsq'`:

```
>>> solve_circulant(c, b, singular='lstsq')
array([ 0.25,  1.25,  2.25,  1.25])
```

Compare to *scipy.linalg.lstsq*:

```
>>> x, resid, rnk, s = lstsq(circulant(c), b)
>>> x
array([ 0.25,  1.25,  2.25,  1.25])
```

A broadcasting example:

Suppose we have the vectors of two circulant matrices stored in an array with shape (2, 5), and three *b* vectors stored in an array with shape (3, 5). For example,

```
>>> c = np.array([[1.5, 2, 3, 0, 0], [1, 1, 4, 3, 2]])
>>> b = np.arange(15).reshape(-1, 5)
```

We want to solve all combinations of circulant matrices and *b* vectors, with the result stored in an array with shape (2, 3, 5). When we disregard the axes of *c* and *b* that hold the vectors of coefficients, the shapes of the collections are (2,) and (3,), respectively, which are not compatible for broadcasting. To have a broadcast result with shape (2, 3), we add a trivial dimension to *c*: `c[:, np.newaxis, :]` has shape (2, 1, 5). The last dimension holds the coefficients of the circulant matrices, so when we call *solve_circulant*, we can use the default `caxis=-1`. The coefficients of the *b* vectors are in the last dimension of the array *b*, so we use `baxis=-1`. If we use the default *outaxis*, the result will have shape (5, 2, 3), so we'll use `outaxis=-1` to put the solution vectors in the last dimension.

```
>>> x = solve_circulant(c[:, np.newaxis, :], b, baxis=-1, outaxis=-1)
>>> x.shape
(2, 3, 5)
>>> np.set_printoptions(precision=3)  # For compact output of numbers.
>>> x
array([[[-0.118,  0.22 ,  1.277, -0.142,  0.302],
        [ 0.651,  0.989,  2.046,  0.627,  1.072],
        [ 1.42 ,  1.758,  2.816,  1.396,  1.841]],
       [[ 0.401,  0.304,  0.694, -0.867,  0.377],
        [ 0.856,  0.758,  1.149, -0.412,  0.831],
        [ 1.31 ,  1.213,  1.603,  0.042,  1.286]]])
```

Check by solving one pair of *c* and *b* vectors (cf. `x[1, 1, :]`):

```
>>> solve_circulant(c[1], b[1, :])
array([ 0.856,  0.758,  1.149, -0.412,  0.831])
```

scipy.linalg.solve_triangular

scipy.linalg.**solve_triangular**(*a*, *b*, *trans=0*, *lower=False*, *unit_diagonal=False*, *overwrite_b=False*, *debug=None*, *check_finite=True*)

Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.

Parameters

a [(M, M) array_like] A triangular matrix

b [(M,) or (M, N) array_like] Right-hand side matrix in *a x = b*

lower [bool, optional] Use only data contained in the lower triangle of *a*. Default is to use upper triangle.

trans [{0, 1, 2, 'N', 'T', 'C'}, optional] Type of system to solve:

trans	system
0 or 'N'	a x = b
1 or 'T'	a^T x = b
2 or 'C'	a^H x = b

unit_diagonal

[bool, optional] If True, diagonal elements of *a* are assumed to be 1 and will not be referenced.

overwrite_b
: [bool, optional] Allow overwriting data in *b* (may enhance performance)

check_finite
: [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x
: [(M,) or (M, N) ndarray] Solution to the system *a x = b*. Shape of return matches *b*.

Raises

LinAlgError
: If *a* is singular

Notes

New in version 0.9.0.

Examples

Solve the lower triangular system a x = b, where:

```
     [3  0  0  0]       [4]
a =  [2  1  0  0]   b = [2]
     [1  0  1  0]       [4]
     [1  1  1  1]       [2]
```

```
>>> from scipy.linalg import solve_triangular
>>> a = np.array([[3, 0, 0, 0], [2, 1, 0, 0], [1, 0, 1, 0], [1, 1, 1, 1]])
>>> b = np.array([4, 2, 4, 2])
>>> x = solve_triangular(a, b, lower=True)
>>> x
array([ 1.33333333, -0.66666667,  2.66666667, -1.33333333])
>>> a.dot(x)  # Check the result
array([ 4.,  2.,  4.,  2.])
```

scipy.linalg.solve_toeplitz

`scipy.linalg.`**`solve_toeplitz`**(*c_or_cr*, *b*, *check_finite=True*)
Solve a Toeplitz system using Levinson Recursion

The Toeplitz matrix has constant diagonals, with c as its first column and r as its first row. If r is not given, `r == conjugate(c)` is assumed.

Parameters

c_or_cr
: [array_like or tuple of (array_like, array_like)] The vector `c`, or a tuple of arrays (`c`, `r`). Whatever the actual shape of `c`, it will be converted to a 1-D array. If not supplied, `r = conjugate(c)` is assumed; in this case, if c[0] is real, the Toeplitz matrix is Hermitian. r[0] is ignored; the first row of the Toeplitz matrix is `[c[0], r[1:]]`. Whatever the actual shape of `r`, it will be converted to a 1-D array.

b
: [(M,) or (M, K) array_like] Right-hand side in `T x = b`.

check_finite
: [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (result entirely NaNs) if the inputs do contain infinities or NaNs.

Returns

x
: [(M,) or (M, K) ndarray] The solution to the system `T x = b`. Shape of return matches shape of *b*.

See also:

`toeplitz`

Toeplitz matrix

Notes

The solution is computed using Levinson-Durbin recursion, which is faster than generic least-squares methods, but can be less numerically stable.

Examples

Solve the Toeplitz system T x = b, where:

```
     [ 1 -1 -2 -3]       [1]
T =  [ 3  1 -1 -2]   b = [2]
     [ 6  3  1 -1]       [2]
     [10  6  3  1]       [5]
```

To specify the Toeplitz matrix, only the first column and the first row are needed.

```
>>> c = np.array([1, 3, 6, 10])    # First column of T
>>> r = np.array([1, -1, -2, -3])  # First row of T
>>> b = np.array([1, 2, 2, 5])
```

```
>>> from scipy.linalg import solve_toeplitz, toeplitz
>>> x = solve_toeplitz((c, r), b)
>>> x
array([ 1.66666667, -1.        , -2.66666667,  2.33333333])
```

Check the result by creating the full Toeplitz matrix and multiplying it by *x*. We should get *b*.

```
>>> T = toeplitz(c, r)
>>> T.dot(x)
array([ 1.,  2.,  2.,  5.])
```

scipy.linalg.matmul_toeplitz

scipy.linalg.**matmul_toeplitz**(*c_or_cr*, *x*, *check_finite=False*, *workers=None*)

Efficient Toeplitz Matrix-Matrix Multiplication using FFT

This function returns the matrix multiplication between a Toeplitz matrix and a dense matrix.

The Toeplitz matrix has constant diagonals, with c as its first column and r as its first row. If r is not given, `r == conjugate(c)` is assumed.

Parameters

c_or_cr [array_like or tuple of (array_like, array_like)] The vector `c`, or a tuple of arrays (`c`, `r`). Whatever the actual shape of `c`, it will be converted to a 1-D array. If not supplied, `r = conjugate(c)` is assumed; in this case, if c[0] is real, the Toeplitz matrix is Hermitian. r[0] is ignored; the first row of the Toeplitz matrix is `[c[0], r[1:]]`. Whatever the actual shape of `r`, it will be converted to a 1-D array.

x [(M,) or (M, K) array_like] Matrix with which to multiply.

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (result entirely NaNs) if the inputs do contain infinities or NaNs.

workers [int, optional] To pass to scipy.fft.fft and ifft. Maximum number of workers to use for parallel computation. If negative, the value wraps around from `os.cpu_count()`. See scipy.fft.fft for more details.

Returns

T @ x [(M,) or (M, K) ndarray] The result of the matrix multiplication `T @ x`. Shape of return matches shape of *x*.

See also:

toeplitz

Toeplitz matrix

solve_toeplitz

Solve a Toeplitz system using Levinson Recursion

Notes

The Toeplitz matrix is embedded in a circulant matrix and the FFT is used to efficiently calculate the matrix-matrix product.

Because the computation is based on the FFT, integer inputs will result in floating point outputs. This is unlike NumPy's *matmul*, which preserves the data type of the input.

This is partly based on the implementation that can be found in [1], licensed under the MIT license. More information about the method can be found in reference [2]. References [3] and [4] have more reference implementations in Python.

New in version 1.6.0.

References

[1], [2], [3], [4]

Examples

Multiply the Toeplitz matrix T with matrix x:

```
    [ 1 -1 -2 -3]       [1 10]
T = [ 3  1 -1 -2]   x = [2 11]
    [ 6  3  1 -1]       [2 11]
    [10  6  3  1]       [5 19]
```

To specify the Toeplitz matrix, only the first column and the first row are needed.

```
>>> c = np.array([1, 3, 6, 10])    # First column of T
>>> r = np.array([1, -1, -2, -3])  # First row of T
>>> x = np.array([[1, 10], [2, 11], [2, 11], [5, 19]])
```

```
>>> from scipy.linalg import toeplitz, matmul_toeplitz
>>> matmul_toeplitz((c, r), x)
array([[-20., -80.],
       [ -7.,  -8.],
       [  9.,  85.],
       [ 33., 218.]])
```

Check the result by creating the full Toeplitz matrix and multiplying it by `x`.

```
>>> toeplitz(c, r) @ x
array([[-20, -80],
       [ -7,  -8],
       [  9,  85],
       [ 33, 218]])
```

The full matrix is never formed explicitly, so this routine is suitable for very large Toeplitz matrices.

```
>>> n = 1000000
>>> matmul_toeplitz([1] + [0]*(n-1), np.ones(n))
array([1., 1., 1., ..., 1., 1., 1.])
```

scipy.linalg.det

`scipy.linalg.`**`det`**(*a*, *overwrite_a=False*, *check_finite=True*)

Compute the determinant of a matrix

The determinant of a square matrix is a value derived arithmetically from the coefficients of the matrix.

The determinant for a 3x3 matrix, for example, is computed as follows:

```
a    b    c
d    e    f = A
g    h    i

det(A) = a*e*i + b*f*g + c*d*h - c*e*g - b*d*i - a*f*h
```

Parameters

a [(M, M) array_like] A square matrix.

overwrite_a [bool, optional] Allow overwriting data in a (may enhance performance).

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

det [float or complex] Determinant of *a*.

Notes

The determinant is computed via LU factorization, LAPACK routine z/dgetrf.

Examples

```
>>> from scipy import linalg
>>> a = np.array([[1,2,3], [4,5,6], [7,8,9]])
>>> linalg.det(a)
0.0
>>> a = np.array([[0,2,3], [4,5,6], [7,8,9]])
>>> linalg.det(a)
3.0
```

scipy.linalg.norm

scipy.linalg.**norm**(*a*, *ord=None*, *axis=None*, *keepdims=False*, *check_finite=True*)

Matrix or vector norm.

This function is able to return one of eight different matrix norms, or one of an infinite number of vector norms (described below), depending on the value of the `ord` parameter. For tensors with rank different from 1 or 2, only *ord=None* is supported.

Parameters

a [array_like] Input array. If *axis* is None, *a* must be 1-D or 2-D, unless *ord* is None. If both *axis* and *ord* are None, the 2-norm of `a.ravel` will be returned.

ord [{int, inf, -inf, 'fro', 'nuc', None}, optional] Order of the norm (see table under `Notes`). inf means NumPy's *inf* object.

axis [{int, 2-tuple of ints, None}, optional] If *axis* is an integer, it specifies the axis of *a* along which to compute the vector norms. If *axis* is a 2-tuple, it specifies the axes that hold 2-D matrices, and the matrix norms of these matrices are computed. If *axis* is None then either a vector norm (when *a* is 1-D) or a matrix norm (when *a* is 2-D) is returned.

keepdims [bool, optional] If this is set to True, the axes which are normed over are left in the result as dimensions with size one. With this option the result will broadcast correctly against the original *a*.

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

n [float or ndarray] Norm of the matrix or vector(s).

Notes

For values of `ord <= 0`, the result is, strictly speaking, not a mathematical 'norm', but it may still be useful for various numerical purposes.

The following norms can be calculated:

ord	norm for matrices	norm for vectors
None	Frobenius norm	2-norm
'fro'	Frobenius norm	–
'nuc'	nuclear norm	–
inf	max(sum(abs(a), axis=1))	max(abs(a))
-inf	min(sum(abs(a), axis=1))	min(abs(a))
0	–	sum(a != 0)
1	max(sum(abs(a), axis=0))	as below
-1	min(sum(abs(a), axis=0))	as below
2	2-norm (largest sing. value)	as below
-2	smallest singular value	as below
other	–	sum(abs(a)**ord)**(1./ord)

The Frobenius norm is given by [1]:

$||A||_F = [\sum_{i,j} abs(a_{i,j})^2]^{1/2}$

The nuclear norm is the sum of the singular values.

Both the Frobenius and nuclear norm orders are only defined for matrices.

References

[1]

Examples

```
>>> from scipy.linalg import norm
>>> a = np.arange(9) - 4.0
>>> a
array([-4., -3., -2., -1.,  0.,  1.,  2.,  3.,  4.])
>>> b = a.reshape((3, 3))
>>> b
array([[-4., -3., -2.],
       [-1.,  0.,  1.],
       [ 2.,  3.,  4.]])
```

```
>>> norm(a)
7.745966692414834
>>> norm(b)
7.745966692414834
>>> norm(b, 'fro')
```

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```
7.745966692414834
>>> norm(a, np.inf)
4
>>> norm(b, np.inf)
9
>>> norm(a, -np.inf)
0
>>> norm(b, -np.inf)
2
```

```
>>> norm(a, 1)
20
>>> norm(b, 1)
7
>>> norm(a, -1)
-4.6566128774142013e-010
>>> norm(b, -1)
6
>>> norm(a, 2)
7.745966692414834
>>> norm(b, 2)
7.3484692283495345
```

```
>>> norm(a, -2)
0
>>> norm(b, -2)
1.8570331885190563e-016
>>> norm(a, 3)
5.8480354764257312
>>> norm(a, -3)
0
```

scipy.linalg.lstsq

scipy.linalg.**lstsq**(*a*, *b*, *cond=None*, *overwrite_a=False*, *overwrite_b=False*, *check_finite=True*, *lapack_driver=None*)

Compute least-squares solution to equation Ax = b.

Compute a vector x such that the 2-norm `|b - A x|` is minimized.

Parameters

a [(M, N) array_like] Left-hand side array

b [(M,) or (M, K) array_like] Right hand side array

cond [float, optional] Cutoff for 'small' singular values; used to determine effective rank of a. Singular values smaller than `rcond * largest_singular_value` are considered zero.

overwrite_a [bool, optional] Discard data in *a* (may enhance performance). Default is False.

overwrite_b [bool, optional] Discard data in *b* (may enhance performance). Default is False.

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination)

if the inputs do contain infinities or NaNs.

lapack_driver
: [str, optional] Which LAPACK driver is used to solve the least-squares problem. Options are `'gelsd'`, `'gelsy'`, `'gelss'`. Default (`'gelsd'`) is a good choice. However, `'gelsy'` can be slightly faster on many problems. `'gelss'` was used historically. It is generally slow but uses less memory.
New in version 0.17.0.

Returns

x
: [(N,) or (N, K) ndarray] Least-squares solution. Return shape matches shape of *b*.

residues
: [(K,) ndarray or float] Square of the 2-norm for each column in `b - a x`, if `M > N` and `ndim(A) == n` (returns a scalar if b is 1-D). Otherwise a (0,)-shaped array is returned.

rank
: [int] Effective rank of *a*.

s
: [(min(M, N),) ndarray or None] Singular values of *a*. The condition number of a is `abs(s[0] / s[-1])`.

Raises

LinAlgError
: If computation does not converge.

ValueError
: When parameters are not compatible.

See also:

`scipy.optimize.nnls`

linear least squares with non-negativity constraint

Notes

When `'gelsy'` is used as a driver, *residues* is set to a (0,)-shaped array and *s* is always `None`.

Examples

```
>>> from scipy.linalg import lstsq
>>> import matplotlib.pyplot as plt
```

Suppose we have the following data:

```
>>> x = np.array([1, 2.5, 3.5, 4, 5, 7, 8.5])
>>> y = np.array([0.3, 1.1, 1.5, 2.0, 3.2, 6.6, 8.6])
```

We want to fit a quadratic polynomial of the form `y = a + b*x**2` to this data. We first form the "design matrix" M, with a constant column of 1s and a column containing `x**2`:

```
>>> M = x[:, np.newaxis]**[0, 2]
>>> M
array([[  1.  ,   1.  ],
       [  1.  ,   6.25],
       [  1.  ,  12.25],
       [  1.  ,  16.  ],
       [  1.  ,  25.  ],
```

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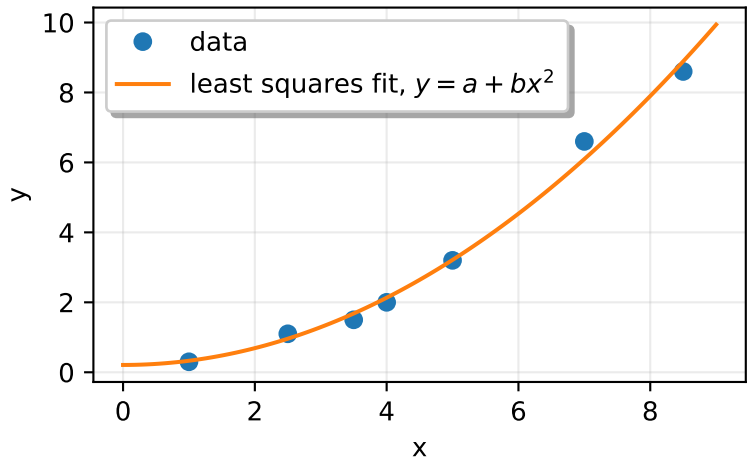
```
       [  1.  ,  49.  ],
       [  1.  ,  72.25]])
```

We want to find the least-squares solution to `M.dot(p) = y`, where `p` is a vector with length 2 that holds the parameters `a` and `b`.

```
>>> p, res, rnk, s = lstsq(M, y)
>>> p
array([ 0.20925829,  0.12013861])
```

Plot the data and the fitted curve.

```
>>> plt.plot(x, y, 'o', label='data')
>>> xx = np.linspace(0, 9, 101)
>>> yy = p[0] + p[1]*xx**2
>>> plt.plot(xx, yy, label='least squares fit, $y = a + bx^2$')
>>> plt.xlabel('x')
>>> plt.ylabel('y')
>>> plt.legend(framealpha=1, shadow=True)
>>> plt.grid(alpha=0.25)
>>> plt.show()
```



scipy.linalg.pinv

`scipy.linalg.`**`pinv`**(*a*, *atol=None*, *rtol=None*, *return_rank=False*, *check_finite=True*, *cond=None*, *rcond=None*)

Compute the (Moore-Penrose) pseudo-inverse of a matrix.

Calculate a generalized inverse of a matrix using its singular-value decomposition `U @ S @ V` in the economy mode and picking up only the columns/rows that are associated with significant singular values.

If `s` is the maximum singular value of `a`, then the significance cut-off value is determined by `atol + rtol * s`. Any singular value below this value is assumed insignificant.

Parameters

a [(M, N) array_like] Matrix to be pseudo-inverted.

atol: float, optional
Absolute threshold term, default value is 0.
New in version 1.7.0.

rtol: float, optional
Relative threshold term, default value is `max(M, N) * eps` where `eps` is the machine precision value of the datatype of `a`.
New in version 1.7.0.

return_rank
[bool, optional] If True, return the effective rank of the matrix.

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

cond, rcond
[float, optional] In older versions, these values were meant to be used as `atol` with `rtol=0`. If both were given `rcond` overwrote `cond` and hence the code was not correct. Thus using these are strongly discouraged and the tolerances above are recommended instead. In fact, if provided, atol, rtol takes precedence over these keywords.
Changed in version 1.7.0: Deprecated in favor of `rtol` and `atol` parameters above and will be removed in future versions of SciPy.
Changed in version 1.3.0: Previously the default cutoff value was just `eps*f` where `f` was `1e3` for single precision and `1e6` for double precision.

Returns

B [(N, M) ndarray] The pseudo-inverse of matrix *a*.

rank [int] The effective rank of the matrix. Returned if *return_rank* is True.

Raises

LinAlgError
If SVD computation does not converge.

Examples

```
>>> from scipy import linalg
>>> rng = np.random.default_rng()
>>> a = rng.standard_normal((9, 6))
>>> B = linalg.pinv(a)
>>> np.allclose(a, a @ B @ a)
True
>>> np.allclose(B, B @ a @ B)
True
```

scipy.linalg.pinv2

scipy.linalg.**pinv2**(*a*, *cond=None*, *rcond=None*, *return_rank=False*, *check_finite=True*)

Compute the (Moore-Penrose) pseudo-inverse of a matrix.

scipy.linalg.pinv2 is deprecated since SciPy 1.7.0, use *scipy.linalg.pinv* instead for better tolerance control.

Calculate a generalized inverse of a matrix using its singular-value decomposition and including all 'large' singular values.

Parameters

a [(M, N) array_like] Matrix to be pseudo-inverted.

cond, rcond
[float or None] Cutoff for 'small' singular values; singular values smaller than this value are considered as zero. If both are omitted, the default value `max(M, N)*largest_singular_value*eps` is used where `eps` is the machine precision value of the datatype of `a`.
Changed in version 1.3.0: Previously the default cutoff value was just `eps*f` where `f` was `1e3` for single precision and `1e6` for double precision.

return_rank
[bool, optional] If True, return the effective rank of the matrix.

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

B [(N, M) ndarray] The pseudo-inverse of matrix *a*.

rank [int] The effective rank of the matrix. Returned if *return_rank* is True.

Raises

LinAlgError
If SVD computation does not converge.

scipy.linalg.pinvh

scipy.linalg.**pinvh**(*a*, *atol=None*, *rtol=None*, *lower=True*, *return_rank=False*, *check_finite=True*, *cond=None*, *rcond=None*)

Compute the (Moore-Penrose) pseudo-inverse of a Hermitian matrix.

Calculate a generalized inverse of a copmlex Hermitian/real symmetric matrix using its eigenvalue decomposition and including all eigenvalues with 'large' absolute value.

Parameters

a [(N, N) array_like] Real symmetric or complex hermetian matrix to be pseudo-inverted

atol: float, optional
Absolute threshold term, default value is 0.
New in version 1.7.0.

rtol: float, optional
Relative threshold term, default value is `N * eps` where `eps` is the machine precision value of the datatype of `a`.
New in version 1.7.0.

lower [bool, optional] Whether the pertinent array data is taken from the lower or upper triangle of *a*. (Default: lower)

return_rank
[bool, optional] If True, return the effective rank of the matrix.

check_finite
: [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

cond, rcond
: [float, optional] In older versions, these values were meant to be used as `atol` with `rtol=0`. If both were given `rcond` overwrote `cond` and hence the code was not correct. Thus using these are strongly discouraged and the tolerances above are recommended instead. In fact, if provided, atol, rtol takes precedence over these keywords.
Changed in version 1.7.0: Deprecated in favor of `rtol` and `atol` parameters above and will be removed in future versions of SciPy.
Changed in version 1.3.0: Previously the default cutoff value was just `eps*f` where `f` was `1e3` for single precision and `1e6` for double precision.

Returns

B [(N, N) ndarray] The pseudo-inverse of matrix *a*.
rank [int] The effective rank of the matrix. Returned if *return_rank* is True.

Raises

LinAlgError
: If eigenvalue algorithm does not converge.

Examples

```
>>> from scipy.linalg import pinvh
>>> rng = np.random.default_rng()
>>> a = rng.standard_normal((9, 6))
>>> a = np.dot(a, a.T)
>>> B = pinvh(a)
>>> np.allclose(a, a @ B @ a)
True
>>> np.allclose(B, B @ a @ B)
True
```

scipy.linalg.kron

`scipy.linalg.`**`kron`**(*a*, *b*)
Kronecker product.

The result is the block matrix:

```
a[0,0]*b    a[0,1]*b  ... a[0,-1]*b
a[1,0]*b    a[1,1]*b  ... a[1,-1]*b
...
a[-1,0]*b   a[-1,1]*b ... a[-1,-1]*b
```

Parameters

a [(M, N) ndarray] Input array
b [(P, Q) ndarray] Input array

Returns

A [(M*P, N*Q) ndarray] Kronecker product of *a* and *b*.

Examples

```
>>> from numpy import array
>>> from scipy.linalg import kron
>>> kron(array([[1,2],[3,4]]), array([[1,1,1]]))
array([[1, 1, 1, 2, 2, 2],
       [3, 3, 3, 4, 4, 4]])
```

scipy.linalg.khatri_rao

scipy.linalg.**khatri_rao**(*a*, *b*)

Khatri-rao product

A column-wise Kronecker product of two matrices

Parameters

a: (n, k) array_like
Input array

b: (m, k) array_like
Input array

Returns

c: (n*m, k) ndarray
Khatri-rao product of *a* and *b*.

See also:

kron

Kronecker product

Notes

The mathematical definition of the Khatri-Rao product is:

$$(A_{ij} \bigotimes B_{ij})_{ij}$$

which is the Kronecker product of every column of A and B, e.g.:

```
c = np.vstack([np.kron(a[:, k], b[:, k]) for k in range(b.shape[1])]).T
```

Examples

```
>>> from scipy import linalg
>>> a = np.array([[1, 2, 3], [4, 5, 6]])
>>> b = np.array([[3, 4, 5], [6, 7, 8], [2, 3, 9]])
>>> linalg.khatri_rao(a, b)
array([[ 3,  8, 15],
       [ 6, 14, 24],
       [ 2,  6, 27],
       [12, 20, 30],
       [24, 35, 48],
       [ 8, 15, 54]])
```

scipy.linalg.tril

scipy.linalg.**tril**(*m*, *k=0*)

Make a copy of a matrix with elements above the kth diagonal zeroed.

Parameters

m	[array_like] Matrix whose elements to return
k	[int, optional] Diagonal above which to zero elements. $k == 0$ is the main diagonal, $k < 0$ subdiagonal and $k > 0$ superdiagonal.

Returns

tril	[ndarray] Return is the same shape and type as *m*.

Examples

```
>>> from scipy.linalg import tril
>>> tril([[1,2,3],[4,5,6],[7,8,9],[10,11,12]], -1)
array([[ 0,  0,  0],
       [ 4,  0,  0],
       [ 7,  8,  0],
       [10, 11, 12]])
```

scipy.linalg.triu

scipy.linalg.**triu**(*m*, *k=0*)

Make a copy of a matrix with elements below the kth diagonal zeroed.

Parameters

m	[array_like] Matrix whose elements to return
k	[int, optional] Diagonal below which to zero elements. $k == 0$ is the main diagonal, $k < 0$ subdiagonal and $k > 0$ superdiagonal.

Returns

triu	[ndarray] Return matrix with zeroed elements below the kth diagonal and has same shape and type as *m*.

Examples

```
>>> from scipy.linalg import triu
>>> triu([[1,2,3],[4,5,6],[7,8,9],[10,11,12]], -1)
array([[ 1,  2,  3],
       [ 4,  5,  6],
       [ 0,  8,  9],
       [ 0,  0, 12]])
```

scipy.linalg.orthogonal_procrustes

scipy.linalg.**orthogonal_procrustes**(*A*, *B*, *check_finite=True*)

Compute the matrix solution of the orthogonal Procrustes problem.

Given matrices A and B of equal shape, find an orthogonal matrix R that most closely maps A to B using the algorithm given in [1].

Parameters

A [(M, N) array_like] Matrix to be mapped.

B [(M, N) array_like] Target matrix.

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

R [(N, N) ndarray] The matrix solution of the orthogonal Procrustes problem. Minimizes the Frobenius norm of `(A @ R) - B`, subject to `R.T @ R = I`.

scale [float] Sum of the singular values of `A.T @ B`.

Raises

ValueError If the input array shapes don't match or if check_finite is True and the arrays contain Inf or NaN.

Notes

Note that unlike higher level Procrustes analyses of spatial data, this function only uses orthogonal transformations like rotations and reflections, and it does not use scaling or translation.

New in version 0.15.0.

References

[1]

Examples

```
>>> from scipy.linalg import orthogonal_procrustes
>>> A = np.array([[ 2,  0,  1], [-2,  0,  0]])
```

Flip the order of columns and check for the anti-diagonal mapping

```
>>> R, sca = orthogonal_procrustes(A, np.fliplr(A))
>>> R
array([[-5.34384992e-17,  0.00000000e+00,  1.00000000e+00],
       [ 0.00000000e+00,  1.00000000e+00,  0.00000000e+00],
       [ 1.00000000e+00,  0.00000000e+00, -7.85941422e-17]])
>>> sca
9.0
```

scipy.linalg.matrix_balance

scipy.linalg.**matrix_balance**(*A*, *permute=True*, *scale=True*, *separate=False*, *overwrite_a=False*)

Compute a diagonal similarity transformation for row/column balancing.

The balancing tries to equalize the row and column 1-norms by applying a similarity transformation such that the magnitude variation of the matrix entries is reflected to the scaling matrices.

Moreover, if enabled, the matrix is first permuted to isolate the upper triangular parts of the matrix and, again if scaling is also enabled, only the remaining subblocks are subjected to scaling.

The balanced matrix satisfies the following equality

$$B = T^{-1}AT$$

The scaling coefficients are approximated to the nearest power of 2 to avoid round-off errors.

Parameters

A [(n, n) array_like] Square data matrix for the balancing.

permute [bool, optional] The selector to define whether permutation of A is also performed prior to scaling.

scale [bool, optional] The selector to turn on and off the scaling. If False, the matrix will not be scaled.

separate [bool, optional] This switches from returning a full matrix of the transformation to a tuple of two separate 1-D permutation and scaling arrays.

overwrite_a [bool, optional] This is passed to xGEBAL directly. Essentially, overwrites the result to the data. It might increase the space efficiency. See LAPACK manual for details. This is False by default.

Returns

B [(n, n) ndarray] Balanced matrix

T [(n, n) ndarray] A possibly permuted diagonal matrix whose nonzero entries are integer powers of 2 to avoid numerical truncation errors.

scale, perm [(n,) ndarray] If `separate` keyword is set to True then instead of the array `T` above, the scaling and the permutation vectors are given separately as a tuple without allocating the full array `T`.

Notes

This algorithm is particularly useful for eigenvalue and matrix decompositions and in many cases it is already called by various LAPACK routines.

The algorithm is based on the well-known technique of [1] and has been modified to account for special cases. See [2] for details which have been implemented since LAPACK v3.5.0. Before this version there are corner cases where balancing can actually worsen the conditioning. See [3] for such examples.

The code is a wrapper around LAPACK's xGEBAL routine family for matrix balancing.

New in version 0.19.0.

References

[1], [2], [3]

Examples

```
>>> from scipy import linalg
>>> x = np.array([[1,2,0], [9,1,0.01], [1,2,10*np.pi]])
```

```
>>> y, permscale = linalg.matrix_balance(x)
>>> np.abs(x).sum(axis=0) / np.abs(x).sum(axis=1)
array([ 3.66666667,  0.4995005 ,  0.91312162])
```

```
>>> np.abs(y).sum(axis=0) / np.abs(y).sum(axis=1)
array([ 1.2       ,  1.27041742,  0.92658316])  # may vary
```

```
>>> permscale  # only powers of 2 (0.5 == 2^(-1))
array([[  0.5,   0. ,  0. ],  # may vary
       [  0. ,   1. ,  0. ],
       [  0. ,   0. ,  1. ]])
```

scipy.linalg.subspace_angles

scipy.linalg.**subspace_angles**(*A*, *B*)

Compute the subspace angles between two matrices.

Parameters

A [(M, N) array_like] The first input array.

B [(M, K) array_like] The second input array.

Returns

angles [ndarray, shape (min(N, K),)] The subspace angles between the column spaces of *A* and *B* in descending order.

See also:

orth

svd

Notes

This computes the subspace angles according to the formula provided in [1]. For equivalence with MATLAB and Octave behavior, use `angles[0]`.

New in version 1.0.

References

[1]

Examples

An Hadamard matrix, which has orthogonal columns, so we expect that the suspace angle to be $\frac{\pi}{2}$:

```
>>> from numpy.random import default_rng
>>> from scipy.linalg import hadamard, subspace_angles
>>> rng = default_rng()
>>> H = hadamard(4)
>>> print(H)
[[ 1  1  1  1]
 [ 1 -1  1 -1]
 [ 1  1 -1 -1]
 [ 1 -1 -1  1]]
>>> np.rad2deg(subspace_angles(H[:, :2], H[:, 2:]))
array([ 90.,  90.])
```

And the subspace angle of a matrix to itself should be zero:

```
>>> subspace_angles(H[:, :2], H[:, :2]) <= 2 * np.finfo(float).eps
array([ True,  True], dtype=bool)
```

The angles between non-orthogonal subspaces are in between these extremes:

```
>>> x = rng.standard_normal((4, 3))
>>> np.rad2deg(subspace_angles(x[:, :2], x[:, [2]]))
array([ 55.832])  # random
```

scipy.linalg.LinAlgError

exception scipy.linalg.**LinAlgError**

Generic Python-exception-derived object raised by linalg functions.

General purpose exception class, derived from Python's exception.Exception class, programmatically raised in linalg functions when a Linear Algebra-related condition would prevent further correct execution of the function.

Parameters

None

Examples

```
>>> from numpy import linalg as LA
>>> LA.inv(np.zeros((2,2)))
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
  File "...linalg.py", line 350,
    in inv return wrap(solve(a, identity(a.shape[0], dtype=a.dtype)))
  File "...linalg.py", line 249,
    in solve
```

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```
    raise LinAlgError('Singular matrix')
numpy.linalg.LinAlgError: Singular matrix
```

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.linalg.LinAlgWarning

exception scipy.linalg.**LinAlgWarning**
The warning emitted when a linear algebra related operation is close to fail conditions of the algorithm or loss of accuracy is expected.

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

Eigenvalue Problems

eig(a[, b, left, right, overwrite_a, …])	Solve an ordinary or generalized eigenvalue problem of a square matrix.
eigvals(a[, b, overwrite_a, check_finite, …])	Compute eigenvalues from an ordinary or generalized eigenvalue problem.
eigh(a[, b, lower, eigvals_only, …])	Solve a standard or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.
eigvalsh(a[, b, lower, overwrite_a, …])	Solves a standard or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.
eig_banded(a_band[, lower, eigvals_only, …])	Solve real symmetric or complex Hermitian band matrix eigenvalue problem.
eigvals_banded(a_band[, lower, …])	Solve real symmetric or complex Hermitian band matrix eigenvalue problem.
eigh_tridiagonal(d, e[, eigvals_only, …])	Solve eigenvalue problem for a real symmetric tridiagonal matrix.
eigvalsh_tridiagonal(d, e[, select, …])	Solve eigenvalue problem for a real symmetric tridiagonal matrix.

scipy.linalg.eig

scipy.linalg.**eig**(*a*, *b=None*, *left=False*, *right=True*, *overwrite_a=False*, *overwrite_b=False*, *check_finite=True*, *homogeneous_eigvals=False*)
Solve an ordinary or generalized eigenvalue problem of a square matrix.

Find eigenvalues w and right or left eigenvectors of a general matrix:

```
a   vr[:,i] = w[i]        b   vr[:,i]
a.H vl[:,i] = w[i].conj() b.H vl[:,i]
```

where `.H` is the Hermitian conjugation.

Parameters

a [(M, M) array_like] A complex or real matrix whose eigenvalues and eigenvectors will be computed.

b [(M, M) array_like, optional] Right-hand side matrix in a generalized eigenvalue problem. Default is None, identity matrix is assumed.

left [bool, optional] Whether to calculate and return left eigenvectors. Default is False.

right [bool, optional] Whether to calculate and return right eigenvectors. Default is True.

overwrite_a [bool, optional] Whether to overwrite *a*; may improve performance. Default is False.

overwrite_b [bool, optional] Whether to overwrite *b*; may improve performance. Default is False.

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

homogeneous_eigvals [bool, optional] If True, return the eigenvalues in homogeneous coordinates. In this case `w` is a (2, M) array so that:

```
w[1,i] a vr[:,i] = w[0,i] b vr[:,i]
```

Default is False.

Returns

w [(M,) or (2, M) double or complex ndarray] The eigenvalues, each repeated according to its multiplicity. The shape is (M,) unless `homogeneous_eigvals=True`.

vl [(M, M) double or complex ndarray] The normalized left eigenvector corresponding to the eigenvalue `w[i]` is the column vl[:,i]. Only returned if `left=True`.

vr [(M, M) double or complex ndarray] The normalized right eigenvector corresponding to the eigenvalue `w[i]` is the column `vr[:,i]`. Only returned if `right=True`.

Raises

LinAlgError If eigenvalue computation does not converge.

See also:

eigvals

eigenvalues of general arrays

eigh

Eigenvalues and right eigenvectors for symmetric/Hermitian arrays.

eig_banded

eigenvalues and right eigenvectors for symmetric/Hermitian band matrices

eigh_tridiagonal

eigenvalues and right eiegenvectors for symmetric/Hermitian tridiagonal matrices

Examples

```
>>> from scipy import linalg
>>> a = np.array([[0., -1.], [1., 0.]])
>>> linalg.eigvals(a)
array([0.+1.j, 0.-1.j])
```

```
>>> b = np.array([[0., 1.], [1., 1.]])
>>> linalg.eigvals(a, b)
array([ 1.+0.j, -1.+0.j])
```

```
>>> a = np.array([[3., 0., 0.], [0., 8., 0.], [0., 0., 7.]])
>>> linalg.eigvals(a, homogeneous_eigvals=True)
array([[3.+0.j, 8.+0.j, 7.+0.j],
       [1.+0.j, 1.+0.j, 1.+0.j]])
```

```
>>> a = np.array([[0., -1.], [1., 0.]])
>>> linalg.eigvals(a) == linalg.eig(a)[0]
array([ True,  True])
>>> linalg.eig(a, left=True, right=False)[1] # normalized left eigenvector
array([[-0.70710678+0.j        , -0.70710678-0.j        ],
       [-0.        +0.70710678j, -0.        -0.70710678j]])
>>> linalg.eig(a, left=False, right=True)[1] # normalized right␣
↪eigenvector
array([[0.70710678+0.j        , 0.70710678-0.j        ],
       [0.        -0.70710678j, 0.        +0.70710678j]])
```

scipy.linalg.eigvals

scipy.linalg.**eigvals**(*a*, *b=None*, *overwrite_a=False*, *check_finite=True*, *homogeneous_eigvals=False*)

Compute eigenvalues from an ordinary or generalized eigenvalue problem.

Find eigenvalues of a general matrix:

```
a   vr[:,i] = w[i]        b   vr[:,i]
```

Parameters

a [(M, M) array_like] A complex or real matrix whose eigenvalues and eigenvectors will be computed.

b [(M, M) array_like, optional] Right-hand side matrix in a generalized eigenvalue problem. If omitted, identity matrix is assumed.

overwrite_a [bool, optional] Whether to overwrite data in a (may improve performance)

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

homogeneous_eigvals [bool, optional] If True, return the eigenvalues in homogeneous coordinates. In this case `w` is a (2, M) array so that:

```
w[1,i] a vr[:,i] = w[0,i] b vr[:,i]
```

Default is False.

Returns

w [(M,) or (2, M) double or complex ndarray] The eigenvalues, each repeated according to its multiplicity but not in any specific order. The shape is (M,) unless `homogeneous_eigvals=True`.

Raises

LinAlgError If eigenvalue computation does not converge

See also:

eig

eigenvalues and right eigenvectors of general arrays.

eigvalsh

eigenvalues of symmetric or Hermitian arrays

eigvals_banded

eigenvalues for symmetric/Hermitian band matrices

eigvalsh_tridiagonal

eigenvalues of symmetric/Hermitian tridiagonal matrices

Examples

```
>>> from scipy import linalg
>>> a = np.array([[0., -1.], [1., 0.]])
>>> linalg.eigvals(a)
array([0.+1.j, 0.-1.j])
```

```
>>> b = np.array([[0., 1.], [1., 1.]])
>>> linalg.eigvals(a, b)
array([ 1.+0.j, -1.+0.j])
```

```
>>> a = np.array([[3., 0., 0.], [0., 8., 0.], [0., 0., 7.]])
>>> linalg.eigvals(a, homogeneous_eigvals=True)
array([[3.+0.j, 8.+0.j, 7.+0.j],
       [1.+0.j, 1.+0.j, 1.+0.j]])
```

scipy.linalg.eigh

scipy.linalg.**eigh**(*a*, *b=None*, *lower=True*, *eigvals_only=False*, *overwrite_a=False*, *overwrite_b=False*, *turbo=True*, *eigvals=None*, *type=1*, *check_finite=True*, *subset_by_index=None*, *subset_by_value=None*, *driver=None*)

Solve a standard or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.

Find eigenvalues array `w` and optionally eigenvectors array `v` of array `a`, where `b` is positive definite such that for every eigenvalue λ (i-th entry of w) and its eigenvector `vi` (i-th column of `v`) satisfies:

```
                a @ vi = λ * b @ vi
vi.conj().T @ a @ vi = λ
vi.conj().T @ b @ vi = 1
```

In the standard problem, `b` is assumed to be the identity matrix.

Parameters

a [(M, M) array_like] A complex Hermitian or real symmetric matrix whose eigenvalues and eigenvectors will be computed.

b [(M, M) array_like, optional] A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

lower [bool, optional] Whether the pertinent array data is taken from the lower or upper triangle of `a` and, if applicable, `b`. (Default: lower)

eigvals_only
: [bool, optional] Whether to calculate only eigenvalues and no eigenvectors. (Default: both are calculated)

subset_by_index
: [iterable, optional] If provided, this two-element iterable defines the start and the end indices of the desired eigenvalues (ascending order and 0-indexed). To return only the second smallest to fifth smallest eigenvalues, `[1, 4]` is used. `[n-3, n-1]` returns the largest three. Only available with "evr", "evx", and "gvx" drivers. The entries are directly converted to integers via `int()`.

subset_by_value
: [iterable, optional] If provided, this two-element iterable defines the half-open interval `(a, b]` that, if any, only the eigenvalues between these values are returned. Only available with "evr", "evx", and "gvx" drivers. Use `np.inf` for the unconstrained ends.

driver: str, optional
: Defines which LAPACK driver should be used. Valid options are "ev", "evd", "evr", "evx" for standard problems and "gv", "gvd", "gvx" for generalized (where b is not None) problems. See the Notes section.

type
: [int, optional] For the generalized problems, this keyword specifies the problem type to be solved for `w` and `v` (only takes 1, 2, 3 as possible inputs):

```
1 =>     a @ v = w @ b @ v
2 => a @ b @ v = w @ v
3 => b @ a @ v = w @ v
```

This keyword is ignored for standard problems.

overwrite_a
: [bool, optional] Whether to overwrite data in `a` (may improve performance). Default is False.

overwrite_b
: [bool, optional] Whether to overwrite data in `b` (may improve performance). Default is False.

check_finite
: [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

turbo
: [bool, optional] *Deprecated since v1.5.0, use ``driver=gvd`` keyword instead.* Use divide and conquer algorithm (faster but expensive in memory, only for generalized eigenvalue problem and if full set of eigenvalues are requested.). Has no significant effect if eigenvectors are not requested.

eigvals
: [tuple (lo, hi), optional] *Deprecated since v1.5.0, use ``subset_by_index`` keyword instead.* Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: 0 <= lo <= hi <= M-1. If omitted, all eigenvalues and eigenvectors are returned.

Returns

w
: [(N,) ndarray] The N (1<=N<=M) selected eigenvalues, in ascending order, each repeated according to its multiplicity.

v
: [(M, N) ndarray] (if `eigvals_only == False`)

Raises

LinAlgError
: If eigenvalue computation does not converge, an error occurred, or b matrix is not definite positive. Note that if input matrices are not symmetric or Hermitian, no error will be reported but results will be wrong.

See also:

eigvalsh

eigenvalues of symmetric or Hermitian arrays

eig

eigenvalues and right eigenvectors for non-symmetric arrays

eigh_tridiagonal

eigenvalues and right eiegenvectors for symmetric/Hermitian tridiagonal matrices

Notes

This function does not check the input array for being Hermitian/symmetric in order to allow for representing arrays with only their upper/lower triangular parts. Also, note that even though not taken into account, finiteness check applies to the whole array and unaffected by "lower" keyword.

This function uses LAPACK drivers for computations in all possible keyword combinations, prefixed with `sy` if arrays are real and `he` if complex, e.g., a float array with "evr" driver is solved via "syevr", complex arrays with "gvx" driver problem is solved via "hegvx" etc.

As a brief summary, the slowest and the most robust driver is the classical `<sy/he>ev` which uses symmetric QR. `<sy/he>evr` is seen as the optimal choice for the most general cases. However, there are certain occasions that `<sy/he>evd` computes faster at the expense of more memory usage. `<sy/he>evx`, while still being faster than `<sy/he>ev`, often performs worse than the rest except when very few eigenvalues are requested for large arrays though there is still no performance guarantee.

For the generalized problem, normalization with respect to the given type argument:

```
type 1 and 3 :      v.conj().T @ a @ v = w
type 2       : inv(v).conj().T @ a @ inv(v) = w

type 1 or 2  :      v.conj().T @ b @ v  = I
type 3       : v.conj().T @ inv(b) @ v  = I
```

Examples

```
>>> from scipy.linalg import eigh
>>> A = np.array([[6, 3, 1, 5], [3, 0, 5, 1], [1, 5, 6, 2], [5, 1, 2, 2]])
>>> w, v = eigh(A)
>>> np.allclose(A @ v - v @ np.diag(w), np.zeros((4, 4)))
True
```

Request only the eigenvalues

```
>>> w = eigh(A, eigvals_only=True)
```

Request eigenvalues that are less than 10.

```
>>> A = np.array([[34, -4, -10, -7, 2],
...               [-4, 7, 2, 12, 0],
...               [-10, 2, 44, 2, -19],
...               [-7, 12, 2, 79, -34],
...               [2, 0, -19, -34, 29]])
```

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```
>>> eigh(A, eigvals_only=True, subset_by_value=[-np.inf, 10])
array([6.69199443e-07, 9.11938152e+00])
```

Request the largest second eigenvalue and its eigenvector

```
>>> w, v = eigh(A, subset_by_index=[1, 1])
>>> w
array([9.11938152])
>>> v.shape  # only a single column is returned
(5, 1)
```

scipy.linalg.eigvalsh

scipy.linalg.**eigvalsh**(*a*, *b=None*, *lower=True*, *overwrite_a=False*, *overwrite_b=False*, *turbo=True*, *eigvals=None*, *type=1*, *check_finite=True*, *subset_by_index=None*, *subset_by_value=None*, *driver=None*)

Solves a standard or generalized eigenvalue problem for a complex Hermitian or real symmetric matrix.

Find eigenvalues array `w` of array `a`, where `b` is positive definite such that for every eigenvalue λ (i-th entry of w) and its eigenvector vi (i-th column of v) satisfies:

```
                a @ vi = λ * b @ vi
vi.conj().T @ a @ vi = λ
vi.conj().T @ b @ vi = 1
```

In the standard problem, b is assumed to be the identity matrix.

Parameters

a [(M, M) array_like] A complex Hermitian or real symmetric matrix whose eigenvalues will be computed.

b [(M, M) array_like, optional] A complex Hermitian or real symmetric definite positive matrix in. If omitted, identity matrix is assumed.

lower [bool, optional] Whether the pertinent array data is taken from the lower or upper triangle of `a` and, if applicable, `b`. (Default: lower)

overwrite_a

[bool, optional] Whether to overwrite data in `a` (may improve performance). Default is False.

overwrite_b

[bool, optional] Whether to overwrite data in `b` (may improve performance). Default is False.

type [int, optional] For the generalized problems, this keyword specifies the problem type to be solved for `w` and `v` (only takes 1, 2, 3 as possible inputs):

```
1 =>     a @ v = w @ b @ v
2 => a @ b @ v = w @ v
3 => b @ a @ v = w @ v
```

This keyword is ignored for standard problems.

check_finite

[bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

subset_by_index

[iterable, optional] If provided, this two-element iterable defines the start and the end indices of the desired eigenvalues (ascending order and 0-indexed). To return only the second smallest to fifth smallest eigenvalues, `[1, 4]` is used. `[n-3, n-1]` returns the largest

three. Only available with “evr”, “evx”, and “gvx” drivers. The entries are directly converted to integers via `int()`.

subset_by_value
: [iterable, optional] If provided, this two-element iterable defines the half-open interval `(a, b]` that, if any, only the eigenvalues between these values are returned. Only available with “evr”, “evx”, and “gvx” drivers. Use `np.inf` for the unconstrained ends.

driver: str, optional
: Defines which LAPACK driver should be used. Valid options are “ev”, “evd”, “evr”, “evx” for standard problems and “gv”, “gvd”, “gvx” for generalized (where b is not None) problems. See the Notes section of *scipy.linalg.eigh*.

turbo
: [bool, optional] *Deprecated by ``driver=gvd`` option*. Has no significant effect for eigenvalue computations since no eigenvectors are requested.
Deprecated since version 1.5.0.

eigvals
: [tuple (lo, hi), optional] *Deprecated by ``subset_by_index`` keyword*. Indexes of the smallest and largest (in ascending order) eigenvalues and corresponding eigenvectors to be returned: 0 <= lo <= hi <= M-1. If omitted, all eigenvalues and eigenvectors are returned.
Deprecated since version 1.5.0.

Returns

w
: [(N,) ndarray] The `N` (`1<=N<=M`) selected eigenvalues, in ascending order, each repeated according to its multiplicity.

Raises

LinAlgError
: If eigenvalue computation does not converge, an error occurred, or b matrix is not definite positive. Note that if input matrices are not symmetric or Hermitian, no error will be reported but results will be wrong.

See also:

eigh

eigenvalues and right eigenvectors for symmetric/Hermitian arrays

eigvals

eigenvalues of general arrays

eigvals_banded

eigenvalues for symmetric/Hermitian band matrices

eigvalsh_tridiagonal

eigenvalues of symmetric/Hermitian tridiagonal matrices

Notes

This function does not check the input array for being Hermitian/symmetric in order to allow for representing arrays with only their upper/lower triangular parts.

This function serves as a one-liner shorthand for *scipy.linalg.eigh* with the option `eigvals_only=True` to get the eigenvalues and not the eigenvectors. Here it is kept as a legacy convenience. It might be beneficial to use the main function to have full control and to be a bit more pythonic.

Examples

For more examples see *scipy.linalg.eigh*.

```
>>> from scipy.linalg import eigvalsh
>>> A = np.array([[6, 3, 1, 5], [3, 0, 5, 1], [1, 5, 6, 2], [5, 1, 2, 2]])
>>> w = eigvalsh(A)
>>> w
array([-3.74637491, -0.76263923,  6.08502336, 12.42399079])
```

scipy.linalg.eig_banded

scipy.linalg.**eig_banded**(*a_band*, *lower=False*, *eigvals_only=False*, *overwrite_a_band=False*, *select='a'*, *select_range=None*, *max_ev=0*, *check_finite=True*)

Solve real symmetric or complex Hermitian band matrix eigenvalue problem.

Find eigenvalues w and optionally right eigenvectors v of a:

```
a v[:,i] = w[i] v[:,i]
v.H v    = identity
```

The matrix a is stored in a_band either in lower diagonal or upper diagonal ordered form:

a_band[u + i - j, j] == a[i,j] (if upper form; i <= j) a_band[i - j, j] == a[i,j] (if lower form; i >= j)

where u is the number of bands above the diagonal.

Example of a_band (shape of a is (6,6), u=2):

```
upper form:
*   *   a02 a13 a24 a35
*   a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *   *
```

Cells marked with * are not used.

Parameters

a_band [(u+1, M) array_like] The bands of the M by M matrix a.

lower [bool, optional] Is the matrix in the lower form. (Default is upper form)

eigvals_only [bool, optional] Compute only the eigenvalues and no eigenvectors. (Default: calculate also eigenvectors)

overwrite_a_band [bool, optional] Discard data in a_band (may enhance performance)

select [{'a', 'v', 'i'}, optional] Which eigenvalues to calculate

select	calculated
'a'	All eigenvalues
'v'	Eigenvalues in the interval (min, max]
'i'	Eigenvalues with indices min <= i <= max

select_range
: [(min, max), optional] Range of selected eigenvalues

max_ev
: [int, optional] For select=='v', maximum number of eigenvalues expected. For other values of select, has no meaning.
In doubt, leave this parameter untouched.

check_finite
: [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

w
: [(M,) ndarray] The eigenvalues, in ascending order, each repeated according to its multiplicity.

v
: [(M, M) float or complex ndarray] The normalized eigenvector corresponding to the eigenvalue w[i] is the column v[:,i].

Raises

LinAlgError
: If eigenvalue computation does not converge.

See also:

eigvals_banded

eigenvalues for symmetric/Hermitian band matrices

eig

eigenvalues and right eigenvectors of general arrays.

eigh

eigenvalues and right eigenvectors for symmetric/Hermitian arrays

eigh_tridiagonal

eigenvalues and right eigenvectors for symmetric/Hermitian tridiagonal matrices

Examples

```
>>> from scipy.linalg import eig_banded
>>> A = np.array([[1, 5, 2, 0], [5, 2, 5, 2], [2, 5, 3, 5], [0, 2, 5, 4]])
>>> Ab = np.array([[1, 2, 3, 4], [5, 5, 5, 0], [2, 2, 0, 0]])
>>> w, v = eig_banded(Ab, lower=True)
>>> np.allclose(A @ v - v @ np.diag(w), np.zeros((4, 4)))
True
>>> w = eig_banded(Ab, lower=True, eigvals_only=True)
>>> w
array([-4.26200532, -2.22987175,  3.95222349, 12.53965359])
```

Request only the eigenvalues between `[-3, 4]`

```
>>> w, v = eig_banded(Ab, lower=True, select='v', select_range=[-3, 4])
>>> w
array([-2.22987175,  3.95222349])
```

scipy.linalg.eigvals_banded

scipy.linalg.**eigvals_banded**(*a_band*, *lower=False*, *overwrite_a_band=False*, *select='a'*, *select_range=None*, *check_finite=True*)

Solve real symmetric or complex Hermitian band matrix eigenvalue problem.

Find eigenvalues w of a:

```
a v[:,i] = w[i] v[:,i]
v.H v    = identity
```

The matrix a is stored in a_band either in lower diagonal or upper diagonal ordered form:

a_band[u + i - j, j] == a[i,j] (if upper form; i <= j) a_band[i - j, j] == a[i,j] (if lower form; i >= j)

where u is the number of bands above the diagonal.

Example of a_band (shape of a is (6,6), u=2):

```
upper form:
*   *   a02 a13 a24 a35
*   a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *   *
```

Cells marked with * are not used.

Parameters

a_band [(u+1, M) array_like] The bands of the M by M matrix a.

lower [bool, optional] Is the matrix in the lower form. (Default is upper form)

overwrite_a_band
[bool, optional] Discard data in a_band (may enhance performance)

select [{'a', 'v', 'i'}, optional] Which eigenvalues to calculate

select	calculated
'a'	All eigenvalues
'v'	Eigenvalues in the interval (min, max]
'i'	Eigenvalues with indices min <= i <= max

select_range
[(min, max), optional] Range of selected eigenvalues

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

w [(M,) ndarray] The eigenvalues, in ascending order, each repeated according to its multiplicity.

Raises

LinAlgError
If eigenvalue computation does not converge.

See also:

eig_banded

eigenvalues and right eigenvectors for symmetric/Hermitian band matrices

eigvalsh_tridiagonal

eigenvalues of symmetric/Hermitian tridiagonal matrices

eigvals

eigenvalues of general arrays

eigh

eigenvalues and right eigenvectors for symmetric/Hermitian arrays

eig

eigenvalues and right eigenvectors for non-symmetric arrays

Examples

```
>>> from scipy.linalg import eigvals_banded
>>> A = np.array([[1, 5, 2, 0], [5, 2, 5, 2], [2, 5, 3, 5], [0, 2, 5, 4]])
>>> Ab = np.array([[1, 2, 3, 4], [5, 5, 5, 0], [2, 2, 0, 0]])
>>> w = eigvals_banded(Ab, lower=True)
>>> w
array([-4.26200532, -2.22987175,  3.95222349, 12.53965359])
```

scipy.linalg.eigh_tridiagonal

scipy.linalg.**eigh_tridiagonal**(*d*, *e*, *eigvals_only=False*, *select='a'*, *select_range=None*, *check_finite=True*, *tol=0.0*, *lapack_driver='auto'*)

Solve eigenvalue problem for a real symmetric tridiagonal matrix.

Find eigenvalues *w* and optionally right eigenvectors *v* of `a`:

```
a v[:,i] = w[i] v[:,i]
v.H v    = identity
```

For a real symmetric matrix `a` with diagonal elements *d* and off-diagonal elements *e*.

Parameters

d [ndarray, shape (ndim,)] The diagonal elements of the array.

e [ndarray, shape (ndim-1,)] The off-diagonal elements of the array.

select [{'a', 'v', 'i'}, optional] Which eigenvalues to calculate

select	calculated
'a'	All eigenvalues
'v'	Eigenvalues in the interval (min, max]
'i'	Eigenvalues with indices min <= i <= max

select_range

[(min, max), optional] Range of selected eigenvalues

check_finite
: [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

tol
: [float] The absolute tolerance to which each eigenvalue is required (only used when 'stebz' is the *lapack_driver*). An eigenvalue (or cluster) is considered to have converged if it lies in an interval of this width. If <= 0. (default), the value `eps*|a|` is used where eps is the machine precision, and `|a|` is the 1-norm of the matrix `a`.

lapack_driver
: [str] LAPACK function to use, can be 'auto', 'stemr', 'stebz', 'sterf', or 'stev'. When 'auto' (default), it will use 'stemr' if `select='a'` and 'stebz' otherwise. When 'stebz' is used to find the eigenvalues and `eigvals_only=False`, then a second LAPACK call (to `?STEIN`) is used to find the corresponding eigenvectors. 'sterf' can only be used when `eigvals_only=True` and `select='a'`. 'stev' can only be used when `select='a'`.

Returns

w
: [(M,) ndarray] The eigenvalues, in ascending order, each repeated according to its multiplicity.

v
: [(M, M) ndarray] The normalized eigenvector corresponding to the eigenvalue `w[i]` is the column `v[:,i]`.

Raises

LinAlgError
: If eigenvalue computation does not converge.

See also:

eigvalsh_tridiagonal

eigenvalues of symmetric/Hermitian tridiagonal matrices

eig

eigenvalues and right eigenvectors for non-symmetric arrays

eigh

eigenvalues and right eigenvectors for symmetric/Hermitian arrays

eig_banded

eigenvalues and right eigenvectors for symmetric/Hermitian band matrices

Notes

This function makes use of LAPACK `S/DSTEMR` routines.

Examples

```
>>> from scipy.linalg import eigh_tridiagonal
>>> d = 3*np.ones(4)
>>> e = -1*np.ones(3)
>>> w, v = eigh_tridiagonal(d, e)
>>> A = np.diag(d) + np.diag(e, k=1) + np.diag(e, k=-1)
>>> np.allclose(A @ v - v @ np.diag(w), np.zeros((4, 4)))
True
```

scipy.linalg.eigvalsh_tridiagonal

scipy.linalg.**eigvalsh_tridiagonal**(*d*, *e*, *select='a'*, *select_range=None*, *check_finite=True*, *tol=0.0*, *lapack_driver='auto'*)

Solve eigenvalue problem for a real symmetric tridiagonal matrix.

Find eigenvalues *w* of `a`:

```
a v[:,i] = w[i] v[:,i]
v.H v    = identity
```

For a real symmetric matrix `a` with diagonal elements *d* and off-diagonal elements *e*.

Parameters

d [ndarray, shape (ndim,)] The diagonal elements of the array.

e [ndarray, shape (ndim-1,)] The off-diagonal elements of the array.

select [{'a', 'v', 'i'}, optional] Which eigenvalues to calculate

select	calculated
'a'	All eigenvalues
'v'	Eigenvalues in the interval (min, max]
'i'	Eigenvalues with indices min <= i <= max

select_range
[(min, max), optional] Range of selected eigenvalues

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

tol [float] The absolute tolerance to which each eigenvalue is required (only used when `lapack_driver='stebz'`). An eigenvalue (or cluster) is considered to have converged if it lies in an interval of this width. If <= 0. (default), the value `eps*|a|` is used where eps is the machine precision, and `|a|` is the 1-norm of the matrix `a`.

lapack_driver
[str] LAPACK function to use, can be 'auto', 'stemr', 'stebz', 'sterf', or 'stev'. When 'auto' (default), it will use 'stemr' if `select='a'` and 'stebz' otherwise. 'sterf' and 'stev' can only be used when `select='a'`.

Returns

w [(M,) ndarray] The eigenvalues, in ascending order, each repeated according to its multiplicity.

Raises

LinAlgError
If eigenvalue computation does not converge.

See also:

eigh_tridiagonal

eigenvalues and right eiegenvectors for symmetric/Hermitian tridiagonal matrices

Examples

```
>>> from scipy.linalg import eigvalsh_tridiagonal, eigvalsh
>>> d = 3*np.ones(4)
>>> e = -1*np.ones(3)
>>> w = eigvalsh_tridiagonal(d, e)
>>> A = np.diag(d) + np.diag(e, k=1) + np.diag(e, k=-1)
>>> w2 = eigvalsh(A)  # Verify with other eigenvalue routines
>>> np.allclose(w - w2, np.zeros(4))
True
```

Decompositions

lu(a[, permute_l, overwrite_a, check_finite])	Compute pivoted LU decomposition of a matrix.
lu_factor(a[, overwrite_a, check_finite])	Compute pivoted LU decomposition of a matrix.
lu_solve(lu_and_piv, b[, trans, …])	Solve an equation system, a x = b, given the LU factorization of a
svd(a[, full_matrices, compute_uv, …])	Singular Value Decomposition.
svdvals(a[, overwrite_a, check_finite])	Compute singular values of a matrix.
diagsvd(s, M, N)	Construct the sigma matrix in SVD from singular values and size M, N.
orth(A[, rcond])	Construct an orthonormal basis for the range of A using SVD
null_space(A[, rcond])	Construct an orthonormal basis for the null space of A using SVD
ldl(A[, lower, hermitian, overwrite_a, …])	Computes the LDLt or Bunch-Kaufman factorization of a symmetric/ hermitian matrix.
cholesky(a[, lower, overwrite_a, check_finite])	Compute the Cholesky decomposition of a matrix.
cholesky_banded(ab[, overwrite_ab, lower, …])	Cholesky decompose a banded Hermitian positive-definite matrix
cho_factor(a[, lower, overwrite_a, check_finite])	Compute the Cholesky decomposition of a matrix, to use in cho_solve
cho_solve(c_and_lower, b[, overwrite_b, …])	Solve the linear equations A x = b, given the Cholesky factorization of A.
cho_solve_banded(cb_and_lower, b[, …])	Solve the linear equations `A x = b`, given the Cholesky factorization of the banded Hermitian `A`.
polar(a[, side])	Compute the polar decomposition.
qr(a[, overwrite_a, lwork, mode, pivoting, …])	Compute QR decomposition of a matrix.
qr_multiply(a, c[, mode, pivoting, …])	Calculate the QR decomposition and multiply Q with a matrix.
qr_update(Q, R, u, v[, overwrite_qruv, …])	Rank-k QR update
qr_delete(Q, R, k, int p=1[, which, …])	QR downdate on row or column deletions
qr_insert(Q, R, u, k[, which, rcond, …])	QR update on row or column insertions
rq(a[, overwrite_a, lwork, mode, check_finite])	Compute RQ decomposition of a matrix.

continues on next page

Table 94 – continued from previous page

qz(A, B[, output, lwork, sort, overwrite_a, …])	QZ decomposition for generalized eigenvalues of a pair of matrices.
ordqz(A, B[, sort, output, overwrite_a, …])	QZ decomposition for a pair of matrices with reordering.
schur(a[, output, lwork, overwrite_a, sort, …])	Compute Schur decomposition of a matrix.
rsf2csf(T, Z[, check_finite])	Convert real Schur form to complex Schur form.
hessenberg(a[, calc_q, overwrite_a, …])	Compute Hessenberg form of a matrix.
cdf2rdf(w, v)	Converts complex eigenvalues `w` and eigenvectors `v` to real eigenvalues in a block diagonal form `wr` and the associated real eigenvectors `vr`, such that.
cossin(X[, p, q, separate, swap_sign, …])	Compute the cosine-sine (CS) decomposition of an orthogonal/unitary matrix.

scipy.linalg.lu

scipy.linalg.**lu**(*a*, *permute_l=False*, *overwrite_a=False*, *check_finite=True*)

Compute pivoted LU decomposition of a matrix.

The decomposition is:

```
A = P L U
```

where P is a permutation matrix, L lower triangular with unit diagonal elements, and U upper triangular.

Parameters

a [(M, N) array_like] Array to decompose

permute_l [bool, optional] Perform the multiplication P*L (Default: do not permute)

overwrite_a
[bool, optional] Whether to overwrite data in a (may improve performance)

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

(If permute_l == False)

p [(M, M) ndarray] Permutation matrix

l [(M, K) ndarray] Lower triangular or trapezoidal matrix with unit diagonal. K = min(M, N)

u [(K, N) ndarray] Upper triangular or trapezoidal matrix

(If permute_l == True)

pl [(M, K) ndarray] Permuted L matrix. K = min(M, N)

u [(K, N) ndarray] Upper triangular or trapezoidal matrix

Notes

This is a LU factorization routine written for SciPy.

Examples

```
>>> from scipy.linalg import lu
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> p, l, u = lu(A)
>>> np.allclose(A - p @ l @ u, np.zeros((4, 4)))
True
```

scipy.linalg.lu_factor

scipy.linalg.**lu_factor**(*a*, *overwrite_a=False*, *check_finite=True*)

Compute pivoted LU decomposition of a matrix.

The decomposition is:

```
A = P L U
```

where P is a permutation matrix, L lower triangular with unit diagonal elements, and U upper triangular.

Parameters

a [(M, M) array_like] Matrix to decompose

overwrite_a [bool, optional] Whether to overwrite data in A (may increase performance)

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

lu [(N, N) ndarray] Matrix containing U in its upper triangle, and L in its lower triangle. The unit diagonal elements of L are not stored.

piv [(N,) ndarray] Pivot indices representing the permutation matrix P: row i of matrix was interchanged with row piv[i].

See also:

lu_solve

solve an equation system using the LU factorization of a matrix

Notes

This is a wrapper to the *GETRF routines from LAPACK.

Examples

```
>>> from scipy.linalg import lu_factor
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> lu, piv = lu_factor(A)
>>> piv
array([2, 2, 3, 3], dtype=int32)
```

Convert LAPACK's piv array to NumPy index and test the permutation

```
>>> piv_py = [2, 0, 3, 1]
>>> L, U = np.tril(lu, k=-1) + np.eye(4), np.triu(lu)
>>> np.allclose(A[piv_py] - L @ U, np.zeros((4, 4)))
True
```

scipy.linalg.lu_solve

scipy.linalg.**lu_solve**(*lu_and_piv*, *b*, *trans=0*, *overwrite_b=False*, *check_finite=True*)

Solve an equation system, a x = b, given the LU factorization of a

Parameters

(lu, piv) Factorization of the coefficient matrix a, as given by lu_factor

b [array] Right-hand side

trans [{0, 1, 2}, optional] Type of system to solve:

trans	system
0	a x = b
1	a^T x = b
2	a^H x = b

overwrite_b
[bool, optional] Whether to overwrite data in b (may increase performance)

check_finite
[bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x [array] Solution to the system

See also:

lu_factor

LU factorize a matrix

Examples

```
>>> from scipy.linalg import lu_factor, lu_solve
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> b = np.array([1, 1, 1, 1])
>>> lu, piv = lu_factor(A)
>>> x = lu_solve((lu, piv), b)
>>> np.allclose(A @ x - b, np.zeros((4,)))
True
```

scipy.linalg.svd

scipy.linalg.**svd**(*a*, *full_matrices=True*, *compute_uv=True*, *overwrite_a=False*, *check_finite=True*, *lapack_driver='gesdd'*)

Singular Value Decomposition.

Factorizes the matrix *a* into two unitary matrices `U` and `Vh`, and a 1-D array `s` of singular values (real, non-negative) such that `a == U @ S @ Vh`, where `S` is a suitably shaped matrix of zeros with main diagonal `s`.

Parameters

a [(M, N) array_like] Matrix to decompose.

full_matrices [bool, optional] If True (default), *U* and *Vh* are of shape `(M, M)`, `(N, N)`. If False, the shapes are `(M, K)` and `(K, N)`, where `K = min(M, N)`.

compute_uv [bool, optional] Whether to compute also `U` and `Vh` in addition to `s`. Default is True.

overwrite_a [bool, optional] Whether to overwrite *a*; may improve performance. Default is False.

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

lapack_driver [{'gesdd', 'gesvd'}, optional] Whether to use the more efficient divide-and-conquer approach (`'gesdd'`) or general rectangular approach (`'gesvd'`) to compute the SVD. MATLAB and Octave use the `'gesvd'` approach. Default is `'gesdd'`.
New in version 0.18.

Returns

U [ndarray] Unitary matrix having left singular vectors as columns. Of shape `(M, M)` or `(M, K)`, depending on *full_matrices*.

s [ndarray] The singular values, sorted in non-increasing order. Of shape (K,), with `K = min(M, N)`.

Vh [ndarray] Unitary matrix having right singular vectors as rows. Of shape `(N, N)` or `(K, N)` depending on *full_matrices*.

For `compute_uv=False`, only `s` is returned.

Raises

LinAlgError If SVD computation does not converge.

See also:

`svdvals`

Compute singular values of a matrix.

`diagsvd`

Construct the Sigma matrix, given the vector s.

Examples

```
>>> from scipy import linalg
>>> from numpy.random import default_rng
>>> rng = default_rng()
>>> m, n = 9, 6
>>> a = rng.standard_normal((m, n)) + 1.j*rng.standard_normal((m, n))
>>> U, s, Vh = linalg.svd(a)
>>> U.shape,  s.shape, Vh.shape
((9, 9), (6,), (6, 6))
```

Reconstruct the original matrix from the decomposition:

```
>>> sigma = np.zeros((m, n))
>>> for i in range(min(m, n)):
...     sigma[i, i] = s[i]
>>> a1 = np.dot(U, np.dot(sigma, Vh))
>>> np.allclose(a, a1)
True
```

Alternatively, use `full_matrices=False` (notice that the shape of `U` is then `(m, n)` instead of `(m, m)`):

```
>>> U, s, Vh = linalg.svd(a, full_matrices=False)
>>> U.shape, s.shape, Vh.shape
((9, 6), (6,), (6, 6))
>>> S = np.diag(s)
>>> np.allclose(a, np.dot(U, np.dot(S, Vh)))
True
```

```
>>> s2 = linalg.svd(a, compute_uv=False)
>>> np.allclose(s, s2)
True
```

scipy.linalg.svdvals

scipy.linalg.**svdvals**(*a*, *overwrite_a=False*, *check_finite=True*)

Compute singular values of a matrix.

Parameters

a [(M, N) array_like] Matrix to decompose.

overwrite_a
[bool, optional] Whether to overwrite *a*; may improve performance. Default is False.

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

s [(min(M, N),) ndarray] The singular values, sorted in decreasing order.

Raises

LinAlgError
If SVD computation does not converge.

See also:

svd

Compute the full singular value decomposition of a matrix.

diagsvd

Construct the Sigma matrix, given the vector s.

Notes

`svdvals(a)` only differs from `svd(a, compute_uv=False)` by its handling of the edge case of empty `a`, where it returns an empty sequence:

```
>>> a = np.empty((0, 2))
>>> from scipy.linalg import svdvals
>>> svdvals(a)
array([], dtype=float64)
```

Examples

```
>>> from scipy.linalg import svdvals
>>> m = np.array([[1.0, 0.0],
...               [2.0, 3.0],
...               [1.0, 1.0],
...               [0.0, 2.0],
...               [1.0, 0.0]])
>>> svdvals(m)
array([ 4.28091555,  1.63516424])
```

We can verify the maximum singular value of *m* by computing the maximum length of *m.dot(u)* over all the unit vectors *u* in the (x,y) plane. We approximate "all" the unit vectors with a large sample. Because of linearity, we only need the unit vectors with angles in [0, pi].

```
>>> t = np.linspace(0, np.pi, 2000)
>>> u = np.array([np.cos(t), np.sin(t)])
>>> np.linalg.norm(m.dot(u), axis=0).max()
4.2809152422538475
```

p is a projection matrix with rank 1. With exact arithmetic, its singular values would be [1, 0, 0, 0].

```
>>> v = np.array([0.1, 0.3, 0.9, 0.3])
>>> p = np.outer(v, v)
>>> svdvals(p)
array([  1.00000000e+00,   2.02021698e-17,   1.56692500e-17,
         8.15115104e-34])
```

The singular values of an orthogonal matrix are all 1. Here, we create a random orthogonal matrix by using the *rvs()* method of *scipy.stats.ortho_group*.

```
>>> from scipy.stats import ortho_group
>>> orth = ortho_group.rvs(4)
```

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```
>>> svdvals(orth)
array([ 1.,  1.,  1.,  1.])
```

scipy.linalg.diagsvd

scipy.linalg.**diagsvd**(*s*, *M*, *N*)

Construct the sigma matrix in SVD from singular values and size M, N.

Parameters

s	[(M,) or (N,) array_like] Singular values
M	[int] Size of the matrix whose singular values are *s*.
N	[int] Size of the matrix whose singular values are *s*.

Returns

S	[(M, N) ndarray] The S-matrix in the singular value decomposition

See also:

svd

Singular value decomposition of a matrix

svdvals

Compute singular values of a matrix.

Examples

```
>>> from scipy.linalg import diagsvd
>>> vals = np.array([1, 2, 3])  # The array representing the computed svd
>>> diagsvd(vals, 3, 4)
array([[1, 0, 0, 0],
       [0, 2, 0, 0],
       [0, 0, 3, 0]])
>>> diagsvd(vals, 4, 3)
array([[1, 0, 0],
       [0, 2, 0],
       [0, 0, 3],
       [0, 0, 0]])
```

scipy.linalg.orth

scipy.linalg.**orth**(*A*, *rcond=None*)

Construct an orthonormal basis for the range of A using SVD

Parameters

A	[(M, N) array_like] Input array
rcond	[float, optional] Relative condition number. Singular values `s` smaller than `rcond * max(s)` are considered zero. Default: floating point eps * max(M,N).

Returns

Q	[(M, K) ndarray] Orthonormal basis for the range of A. K = effective rank of A, as determined by rcond

See also:

svd

Singular value decomposition of a matrix

null_space

Matrix null space

Examples

```
>>> from scipy.linalg import orth
>>> A = np.array([[2, 0, 0], [0, 5, 0]])  # rank 2 array
>>> orth(A)
array([[0., 1.],
       [1., 0.]])
>>> orth(A.T)
array([[0., 1.],
       [1., 0.],
       [0., 0.]])
```

scipy.linalg.null_space

scipy.linalg.**null_space**(*A*, *rcond=None*)

Construct an orthonormal basis for the null space of A using SVD

Parameters

A [(M, N) array_like] Input array

rcond [float, optional] Relative condition number. Singular values `s` smaller than `rcond * max(s)` are considered zero. Default: floating point eps * max(M,N).

Returns

Z [(N, K) ndarray] Orthonormal basis for the null space of A. K = dimension of effective null space, as determined by rcond

See also:

svd

Singular value decomposition of a matrix

orth

Matrix range

Examples

1-D null space:

```
>>> from scipy.linalg import null_space
>>> A = np.array([[1, 1], [1, 1]])
>>> ns = null_space(A)
>>> ns * np.sign(ns[0,0])  # Remove the sign ambiguity of the vector
array([[ 0.70710678],
       [-0.70710678]])
```

2-D null space:

```
>>> from numpy.random import default_rng
>>> rng = default_rng()
>>> B = rng.random((3, 5))
>>> Z = null_space(B)
>>> Z.shape
(5, 2)
>>> np.allclose(B.dot(Z), 0)
True
```

The basis vectors are orthonormal (up to rounding error):

```
>>> Z.T.dot(Z)
array([[  1.00000000e+00,   6.92087741e-17],
       [  6.92087741e-17,   1.00000000e+00]])
```

scipy.linalg.ldl

scipy.linalg.**ldl**(*A*, *lower=True*, *hermitian=True*, *overwrite_a=False*, *check_finite=True*)

Computes the LDLt or Bunch-Kaufman factorization of a symmetric/ hermitian matrix.

This function returns a block diagonal matrix D consisting blocks of size at most 2x2 and also a possibly permuted unit lower triangular matrix `L` such that the factorization `A = L D L^H` or `A = L D L^T` holds. If *lower* is False then (again possibly permuted) upper triangular matrices are returned as outer factors.

The permutation array can be used to triangularize the outer factors simply by a row shuffle, i.e., `lu[perm, :]` is an upper/lower triangular matrix. This is also equivalent to multiplication with a permutation matrix `P.dot(lu)`, where `P` is a column-permuted identity matrix `I[:, perm]`.

Depending on the value of the boolean *lower*, only upper or lower triangular part of the input array is referenced. Hence, a triangular matrix on entry would give the same result as if the full matrix is supplied.

Parameters

A [array_like] Square input array

lower [bool, optional] This switches between the lower and upper triangular outer factors of the factorization. Lower triangular (`lower=True`) is the default.

hermitian [bool, optional] For complex-valued arrays, this defines whether `A = A.conj().T` or `A = A.T` is assumed. For real-valued arrays, this switch has no effect.

overwrite_a

[bool, optional] Allow overwriting data in *A* (may enhance performance). The default is False.

check_finite

[bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

lu [ndarray] The (possibly) permuted upper/lower triangular outer factor of the factorization.
d [ndarray] The block diagonal multiplier of the factorization.
perm [ndarray] The row-permutation index array that brings lu into triangular form.

Raises

ValueError
If input array is not square.
ComplexWarning
If a complex-valued array with nonzero imaginary parts on the diagonal is given and hermitian is set to True.

See also:

`cholesky`, `lu`

Notes

This function uses `?SYTRF` routines for symmetric matrices and `?HETRF` routines for Hermitian matrices from LAPACK. See [1] for the algorithm details.

Depending on the *lower* keyword value, only lower or upper triangular part of the input array is referenced. Moreover, this keyword also defines the structure of the outer factors of the factorization.

New in version 1.1.0.

References

[1]

Examples

Given an upper triangular array `a` that represents the full symmetric array with its entries, obtain `l`, 'd' and the permutation vector *perm*:

```
>>> import numpy as np
>>> from scipy.linalg import ldl
>>> a = np.array([[2, -1, 3], [0, 2, 0], [0, 0, 1]])
>>> lu, d, perm = ldl(a, lower=0) # Use the upper part
>>> lu
array([[ 0. ,  0. ,  1. ],
       [ 0. ,  1. , -0.5],
       [ 1. ,  1. ,  1.5]])
>>> d
array([[-5. ,  0. ,  0. ],
       [ 0. ,  1.5,  0. ],
       [ 0. ,  0. ,  2. ]])
>>> perm
```

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```
array([2, 1, 0])
>>> lu[perm, :]
array([[ 1. ,  1. ,  1.5],
       [ 0. ,  1. , -0.5],
       [ 0. ,  0. ,  1. ]])
>>> lu.dot(d).dot(lu.T)
array([[ 2., -1.,  3.],
       [-1.,  2.,  0.],
       [ 3.,  0.,  1.]])
```

scipy.linalg.cholesky

scipy.linalg.**cholesky**(*a*, *lower=False*, *overwrite_a=False*, *check_finite=True*)

Compute the Cholesky decomposition of a matrix.

Returns the Cholesky decomposition, $A = LL^*$ or $A = U^*U$ of a Hermitian positive-definite matrix A.

Parameters

a [(M, M) array_like] Matrix to be decomposed

lower [bool, optional] Whether to compute the upper- or lower-triangular Cholesky factorization. Default is upper-triangular.

overwrite_a [bool, optional] Whether to overwrite data in *a* (may improve performance).

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

c [(M, M) ndarray] Upper- or lower-triangular Cholesky factor of *a*.

Raises

LinAlgError [if decomposition fails.]

Examples

```
>>> from scipy.linalg import cholesky
>>> a = np.array([[1,-2j],[2j,5]])
>>> L = cholesky(a, lower=True)
>>> L
array([[ 1.+0.j,  0.+0.j],
       [ 0.+2.j,  1.+0.j]])
>>> L @ L.T.conj()
array([[ 1.+0.j,  0.-2.j],
       [ 0.+2.j,  5.+0.j]])
```

scipy.linalg.cholesky_banded

scipy.linalg.**cholesky_banded**(*ab*, *overwrite_ab=False*, *lower=False*, *check_finite=True*)

Cholesky decompose a banded Hermitian positive-definite matrix

The matrix a is stored in ab either in lower-diagonal or upper- diagonal ordered form:

```
ab[u + i - j, j] == a[i,j]          (if upper form; i <= j)
ab[    i - j, j] == a[i,j]          (if lower form; i >= j)
```

Example of ab (shape of a is (6,6), u=2):

```
upper form:
*   *   a02 a13 a24 a35
*   a01 a12 a23 a34 a45
a00 a11 a22 a33 a44 a55

lower form:
a00 a11 a22 a33 a44 a55
a10 a21 a32 a43 a54 *
a20 a31 a42 a53 *   *
```

Parameters

ab [(u + 1, M) array_like] Banded matrix

overwrite_ab [bool, optional] Discard data in ab (may enhance performance)

lower [bool, optional] Is the matrix in the lower form. (Default is upper form)

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

c [(u + 1, M) ndarray] Cholesky factorization of a, in the same banded format as ab

See also:

cho_solve_banded

Solve a linear set equations, given the Cholesky factorization of a banded Hermitian.

Examples

```
>>> from scipy.linalg import cholesky_banded
>>> from numpy import allclose, zeros, diag
>>> Ab = np.array([[0, 0, 1j, 2, 3j], [0, -1, -2, 3, 4], [9, 8, 7, 6, 9]])
>>> A = np.diag(Ab[0,2:], k=2) + np.diag(Ab[1,1:], k=1)
>>> A = A + A.conj().T + np.diag(Ab[2, :])
>>> c = cholesky_banded(Ab)
>>> C = np.diag(c[0, 2:], k=2) + np.diag(c[1, 1:], k=1) + np.diag(c[2, :])
>>> np.allclose(C.conj().T @ C - A, np.zeros((5, 5)))
True
```

scipy.linalg.cho_factor

scipy.linalg.**cho_factor**(*a*, *lower=False*, *overwrite_a=False*, *check_finite=True*)

Compute the Cholesky decomposition of a matrix, to use in cho_solve

Returns a matrix containing the Cholesky decomposition, `A = L L*` or `A = U* U` of a Hermitian positive-definite matrix *a*. The return value can be directly used as the first parameter to cho_solve.

Warning: The returned matrix also contains random data in the entries not used by the Cholesky decomposition. If you need to zero these entries, use the function *cholesky* instead.

Parameters

a [(M, M) array_like] Matrix to be decomposed

lower [bool, optional] Whether to compute the upper or lower triangular Cholesky factorization (Default: upper-triangular)

overwrite_a [bool, optional] Whether to overwrite data in a (may improve performance)

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

c [(M, M) ndarray] Matrix whose upper or lower triangle contains the Cholesky factor of *a*. Other parts of the matrix contain random data.

lower [bool] Flag indicating whether the factor is in the lower or upper triangle

Raises

LinAlgError Raised if decomposition fails.

See also:

cho_solve

Solve a linear set equations using the Cholesky factorization of a matrix.

Examples

```
>>> from scipy.linalg import cho_factor
>>> A = np.array([[9, 3, 1, 5], [3, 7, 5, 1], [1, 5, 9, 2], [5, 1, 2, 6]])
>>> c, low = cho_factor(A)
>>> c
array([[3.        , 1.        , 0.33333333, 1.66666667],
       [3.        , 2.44948974, 1.90515869, -0.27216553],
       [1.        , 5.        , 2.29330749, 0.8559528 ],
       [5.        , 1.        , 2.        , 1.55418563]])
>>> np.allclose(np.triu(c).T @ np. triu(c) - A, np.zeros((4, 4)))
True
```

scipy.linalg.cho_solve

scipy.linalg.**cho_solve**(*c_and_lower*, *b*, *overwrite_b=False*, *check_finite=True*)

Solve the linear equations A x = b, given the Cholesky factorization of A.

Parameters

(c, lower) [tuple, (array, bool)] Cholesky factorization of a, as given by cho_factor

b [array] Right-hand side

overwrite_b [bool, optional] Whether to overwrite data in b (may improve performance)

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x [array] The solution to the system A x = b

See also:

`cho_factor`

Cholesky factorization of a matrix

Examples

```
>>> from scipy.linalg import cho_factor, cho_solve
>>> A = np.array([[9, 3, 1, 5], [3, 7, 5, 1], [1, 5, 9, 2], [5, 1, 2, 6]])
>>> c, low = cho_factor(A)
>>> x = cho_solve((c, low), [1, 1, 1, 1])
>>> np.allclose(A @ x - [1, 1, 1, 1], np.zeros(4))
True
```

scipy.linalg.cho_solve_banded

scipy.linalg.**cho_solve_banded**(*cb_and_lower*, *b*, *overwrite_b=False*, *check_finite=True*)

Solve the linear equations `A x = b`, given the Cholesky factorization of the banded Hermitian `A`.

Parameters

(cb, lower) [tuple, (ndarray, bool)] *cb* is the Cholesky factorization of A, as given by cholesky_banded. *lower* must be the same value that was given to cholesky_banded.

b [array_like] Right-hand side

overwrite_b [bool, optional] If True, the function will overwrite the values in *b*.

check_finite [bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

x [array] The solution to the system A x = b

See also:

cholesky_banded

Cholesky factorization of a banded matrix

Notes

New in version 0.8.0.

Examples

```
>>> from scipy.linalg import cholesky_banded, cho_solve_banded
>>> Ab = np.array([[0, 0, 1j, 2, 3j], [0, -1, -2, 3, 4], [9, 8, 7, 6, 9]])
>>> A = np.diag(Ab[0,2:], k=2) + np.diag(Ab[1,1:], k=1)
>>> A = A + A.conj().T + np.diag(Ab[2, :])
>>> c = cholesky_banded(Ab)
>>> x = cho_solve_banded((c, False), np.ones(5))
>>> np.allclose(A @ x - np.ones(5), np.zeros(5))
True
```

scipy.linalg.polar

scipy.linalg.**polar**(*a*, *side='right'*)

Compute the polar decomposition.

Returns the factors of the polar decomposition [1] *u* and *p* such that `a = up` (if *side* is "right") or `a = pu` (if *side* is "left"), where *p* is positive semidefinite. Depending on the shape of *a*, either the rows or columns of *u* are orthonormal. When *a* is a square array, *u* is a square unitary array. When *a* is not square, the "canonical polar decomposition" [2] is computed.

Parameters

a [(m, n) array_like] The array to be factored.

side [{'left', 'right'}, optional] Determines whether a right or left polar decomposition is computed. If *side* is "right", then `a = up`. If *side* is "left", then `a = pu`. The default is "right".

Returns

u [(m, n) ndarray] If *a* is square, then *u* is unitary. If m > n, then the columns of *a* are orthonormal, and if m < n, then the rows of *u* are orthonormal.

p [ndarray] *p* is Hermitian positive semidefinite. If *a* is nonsingular, *p* is positive definite. The shape of *p* is (n, n) or (m, m), depending on whether *side* is "right" or "left", respectively.

References

[1], [2]

Examples

```
>>> from scipy.linalg import polar
>>> a = np.array([[1, -1], [2, 4]])
>>> u, p = polar(a)
>>> u
array([[ 0.85749293, -0.51449576],
       [ 0.51449576,  0.85749293]])
>>> p
array([[ 1.88648444,  1.2004901 ],
       [ 1.2004901 ,  3.94446746]])
```

A non-square example, with m < n:

```
>>> b = np.array([[0.5, 1, 2], [1.5, 3, 4]])
>>> u, p = polar(b)
>>> u
array([[-0.21196618, -0.42393237,  0.88054056],
       [ 0.39378971,  0.78757942,  0.4739708 ]])
>>> p
array([[ 0.48470147,  0.96940295,  1.15122648],
       [ 0.96940295,  1.9388059 ,  2.30245295],
       [ 1.15122648,  2.30245295,  3.65696431]])
>>> u.dot(p)    # Verify the decomposition.
array([[ 0.5,  1. ,  2. ],
       [ 1.5,  3. ,  4. ]])
>>> u.dot(u.T)    # The rows of u are orthonormal.
array([[  1.00000000e+00,  -2.07353665e-17],
       [ -2.07353665e-17,   1.00000000e+00]])
```

Another non-square example, with m > n:

```
>>> c = b.T
>>> u, p = polar(c)
>>> u
array([[-0.21196618,  0.39378971],
       [-0.42393237,  0.78757942],
       [ 0.88054056,  0.4739708 ]])
>>> p
array([[ 1.23116567,  1.93241587],
       [ 1.93241587,  4.84930602]])
>>> u.dot(p)    # Verify the decomposition.
array([[ 0.5,  1.5],
       [ 1. ,  3. ],
       [ 2. ,  4. ]])
>>> u.T.dot(u)  # The columns of u are orthonormal.
array([[  1.00000000e+00,  -1.26363763e-16],
       [ -1.26363763e-16,   1.00000000e+00]])
```

scipy.linalg.qr

scipy.linalg.**qr**(*a*, *overwrite_a=False*, *lwork=None*, *mode='full'*, *pivoting=False*, *check_finite=True*)

Compute QR decomposition of a matrix.

Calculate the decomposition `A = Q R` where Q is unitary/orthogonal and R upper triangular.

Parameters

a [(M, N) array_like] Matrix to be decomposed

overwrite_a [bool, optional] Whether data in *a* is overwritten (may improve performance if *overwrite_a* is set to True by reusing the existing input data structure rather than creating a new one.)

lwork [int, optional] Work array size, lwork >= a.shape[1]. If None or -1, an optimal size is computed.

mode [{'full', 'r', 'economic', 'raw'}, optional] Determines what information is to be returned: either both Q and R ('full', default), only R ('r') or both Q and R but computed in economy-size ('economic', see Notes). The final option 'raw' (added in SciPy 0.11) makes the function return two matrices (Q, TAU) in the internal format used by LAPACK.

pivoting [bool, optional] Whether or not factorization should include pivoting for rank-revealing qr decomposition. If pivoting, compute the decomposition `A P = Q R` as above, but where P is chosen such that the diagonal of R is non-increasing.

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

Q [float or complex ndarray] Of shape (M, M), or (M, K) for `mode='economic'`. Not returned if `mode='r'`.

R [float or complex ndarray] Of shape (M, N), or (K, N) for `mode='economic'`. `K = min(M, N)`.

P [int ndarray] Of shape (N,) for `pivoting=True`. Not returned if `pivoting=False`.

Raises

LinAlgError Raised if decomposition fails

Notes

This is an interface to the LAPACK routines dgeqrf, zgeqrf, dorgqr, zungqr, dgeqp3, and zgeqp3.

If `mode=economic`, the shapes of Q and R are (M, K) and (K, N) instead of (M,M) and (M,N), with `K=min(M, N)`.

Examples

```
>>> from scipy import linalg
>>> rng = np.random.default_rng()
>>> a = rng.standard_normal((9, 6))
```

```
>>> q, r = linalg.qr(a)
>>> np.allclose(a, np.dot(q, r))
True
>>> q.shape, r.shape
((9, 9), (9, 6))
```

```
>>> r2 = linalg.qr(a, mode='r')
>>> np.allclose(r, r2)
True
```

```
>>> q3, r3 = linalg.qr(a, mode='economic')
>>> q3.shape, r3.shape
((9, 6), (6, 6))
```

```
>>> q4, r4, p4 = linalg.qr(a, pivoting=True)
>>> d = np.abs(np.diag(r4))
>>> np.all(d[1:] <= d[:-1])
True
>>> np.allclose(a[:, p4], np.dot(q4, r4))
True
>>> q4.shape, r4.shape, p4.shape
((9, 9), (9, 6), (6,))
```

```
>>> q5, r5, p5 = linalg.qr(a, mode='economic', pivoting=True)
>>> q5.shape, r5.shape, p5.shape
((9, 6), (6, 6), (6,))
```

scipy.linalg.qr_multiply

scipy.linalg.**qr_multiply**(*a*, *c*, *mode='right'*, *pivoting=False*, *conjugate=False*, *overwrite_a=False*, *overwrite_c=False*)

Calculate the QR decomposition and multiply Q with a matrix.

Calculate the decomposition `A = Q R` where Q is unitary/orthogonal and R upper triangular. Multiply Q with a vector or a matrix c.

Parameters

a [(M, N), array_like] Input array

c [array_like] Input array to be multiplied by `q`.

mode [{'left', 'right'}, optional] `Q @ c` is returned if mode is 'left', `c @ Q` is returned if mode is 'right'. The shape of c must be appropriate for the matrix multiplications, if mode is 'left', `min(a.shape) == c.shape[0]`, if mode is 'right', `a.shape[0] == c.shape[1]`.

pivoting [bool, optional] Whether or not factorization should include pivoting for rank-revealing qr decomposition, see the documentation of qr.

conjugate [bool, optional] Whether Q should be complex-conjugated. This might be faster than explicit conjugation.

overwrite_a [bool, optional] Whether data in a is overwritten (may improve performance)

overwrite_c [bool, optional] Whether data in c is overwritten (may improve performance). If this is used, c must be big enough to keep the result, i.e. `c.shape[0] = a.shape[0]` if mode is 'left'.

Returns

CQ [ndarray] The product of `Q` and `c`.
R [(K, N), ndarray] R array of the resulting QR factorization where `K = min(M, N)`.
P [(N,) ndarray] Integer pivot array. Only returned when `pivoting=True`.

Raises

LinAlgError
Raised if QR decomposition fails.

Notes

This is an interface to the LAPACK routines `?GEQRF`, `?ORMQR`, `?UNMQR`, and `?GEQP3`.

New in version 0.11.0.

Examples

```
>>> from scipy.linalg import qr_multiply, qr
>>> A = np.array([[1, 3, 3], [2, 3, 2], [2, 3, 3], [1, 3, 2]])
>>> qc, r1, piv1 = qr_multiply(A, 2*np.eye(4), pivoting=1)
>>> qc
array([[-1.,  1., -1.],
       [-1., -1.,  1.],
       [-1., -1., -1.],
       [-1.,  1.,  1.]])
>>> r1
array([[-6., -3., -5.            ],
       [ 0., -1., -1.11022302e-16],
       [ 0.,  0., -1.            ]])
>>> piv1
array([1, 0, 2], dtype=int32)
>>> q2, r2, piv2 = qr(A, mode='economic', pivoting=1)
>>> np.allclose(2*q2 - qc, np.zeros((4, 3)))
True
```

scipy.linalg.qr_update

`scipy.linalg.`**`qr_update`**(*Q*, *R*, *u*, *v*, *overwrite_qruv=False*, *check_finite=True*)
Rank-k QR update

If `A = Q R` is the QR factorization of `A`, return the QR factorization of `A + u v**T` for real `A` or `A + u v**H` for complex `A`.

Parameters

Q [(M, M) or (M, N) array_like] Unitary/orthogonal matrix from the qr decomposition of A.
R [(M, N) or (N, N) array_like] Upper triangular matrix from the qr decomposition of A.
u [(M,) or (M, k) array_like] Left update vector
v [(N,) or (N, k) array_like] Right update vector
overwrite_qruv
[bool, optional] If True, consume Q, R, u, and v, if possible, while performing the update, otherwise make copies as necessary. Defaults to False.

check_finite
: [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

Q1 [ndarray] Updated unitary/orthogonal factor
R1 [ndarray] Updated upper triangular factor

See also:

qr, **qr_multiply**, **qr_delete**, **qr_insert**

Notes

This routine does not guarantee that the diagonal entries of *R1* are real or positive.

New in version 0.16.0.

References

[1], [2], [3]

Examples

```
>>> from scipy import linalg
>>> a = np.array([[  3.,  -2.,  -2.],
...               [  6.,  -9.,  -3.],
...               [ -3.,  10.,   1.],
...               [  6.,  -7.,   4.],
...               [  7.,   8.,  -6.]])
>>> q, r = linalg.qr(a)
```

Given this q, r decomposition, perform a rank 1 update.

```
>>> u = np.array([7., -2., 4., 3., 5.])
>>> v = np.array([1., 3., -5.])
>>> q_up, r_up = linalg.qr_update(q, r, u, v, False)
>>> q_up
array([[ 0.54073807,  0.18645997,  0.81707661, -0.02136616,  0.06902409],␣
 ↪ # may vary (signs)
       [ 0.21629523, -0.63257324,  0.06567893,  0.34125904, -0.65749222],
       [ 0.05407381,  0.64757787, -0.12781284, -0.20031219, -0.72198188],
       [ 0.48666426, -0.30466718, -0.27487277, -0.77079214,  0.0256951 ],
       [ 0.64888568,  0.23001   , -0.4859845 ,  0.49883891,  0.20253783]])
>>> r_up
array([[ 18.49324201,  24.11691794, -44.98940746],  # may vary (signs)
       [  0.        ,  31.95894662, -27.40998201],
       [  0.        ,   0.        ,  -9.25451794],
       [  0.        ,   0.        ,   0.        ],
       [  0.        ,   0.        ,   0.        ]])
```

The update is equivalent, but faster than the following.

```
>>> a_up = a + np.outer(u, v)
>>> q_direct, r_direct = linalg.qr(a_up)
```

Check that we have equivalent results:

```
>>> np.allclose(np.dot(q_up, r_up), a_up)
True
```

And the updated Q is still unitary:

```
>>> np.allclose(np.dot(q_up.T, q_up), np.eye(5))
True
```

Updating economic (reduced, thin) decompositions is also possible:

```
>>> qe, re = linalg.qr(a, mode='economic')
>>> qe_up, re_up = linalg.qr_update(qe, re, u, v, False)
>>> qe_up
array([[ 0.54073807,  0.18645997,  0.81707661],  # may vary (signs)
       [ 0.21629523, -0.63257324,  0.06567893],
       [ 0.05407381,  0.64757787, -0.12781284],
       [ 0.48666426, -0.30466718, -0.27487277],
       [ 0.64888568,  0.23001   , -0.4859845 ]])
>>> re_up
array([[ 18.49324201,  24.11691794, -44.98940746],  # may vary (signs)
       [  0.        ,  31.95894662, -27.40998201],
       [  0.        ,   0.        ,  -9.25451794]])
>>> np.allclose(np.dot(qe_up, re_up), a_up)
True
>>> np.allclose(np.dot(qe_up.T, qe_up), np.eye(3))
True
```

Similarly to the above, perform a rank 2 update.

```
>>> u2 = np.array([[ 7., -1,],
...                [-2.,  4.],
...                [ 4.,  2.],
...                [ 3., -6.],
...                [ 5.,  3.]])
>>> v2 = np.array([[ 1., 2.],
...                [ 3., 4.],
...                [-5., 2]])
>>> q_up2, r_up2 = linalg.qr_update(q, r, u2, v2, False)
>>> q_up2
array([[-0.33626508, -0.03477253,  0.61956287, -0.64352987, -0.29618884],␣
 ↪ # may vary (signs)
       [-0.50439762,  0.58319694, -0.43010077, -0.33395279,  0.33008064],
       [-0.21016568, -0.63123106,  0.0582249 , -0.13675572,  0.73163206],
       [ 0.12609941,  0.49694436,  0.64590024,  0.31191919,  0.47187344],
       [-0.75659643, -0.11517748,  0.10284903,  0.5986227 , -0.21299983]])
>>> r_up2
array([[-23.79075451, -41.1084062 ,  24.71548348],  # may vary (signs)
       [  0.        , -33.83931057,  11.02226551],
```

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```
       [  0.        ,   0.        ,  48.91476811],
       [  0.        ,   0.        ,   0.        ],
       [  0.        ,   0.        ,   0.        ]])
```

This update is also a valid qr decomposition of `A + U V**T`.

```
>>> a_up2 = a + np.dot(u2, v2.T)
>>> np.allclose(a_up2, np.dot(q_up2, r_up2))
True
>>> np.allclose(np.dot(q_up2.T, q_up2), np.eye(5))
True
```

scipy.linalg.qr_delete

scipy.linalg.**qr_delete**(*Q*, *R*, *k*, *int p=1*, *which=u'row'*, *overwrite_qr=False*, *check_finite=True*)

QR downdate on row or column deletions

If `A = Q R` is the QR factorization of `A`, return the QR factorization of `A` where `p` rows or columns have been removed starting at row or column `k`.

Parameters

Q [(M, M) or (M, N) array_like] Unitary/orthogonal matrix from QR decomposition.

R [(M, N) or (N, N) array_like] Upper triangular matrix from QR decomposition.

k [int] Index of the first row or column to delete.

p [int, optional] Number of rows or columns to delete, defaults to 1.

which: {'row', 'col'}, optional
Determines if rows or columns will be deleted, defaults to 'row'

overwrite_qr
[bool, optional] If True, consume Q and R, overwriting their contents with their downdated versions, and returning approriately sized views. Defaults to False.

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

Q1 [ndarray] Updated unitary/orthogonal factor

R1 [ndarray] Updated upper triangular factor

See also:

qr, **qr_multiply**, **qr_insert**, **qr_update**

Notes

This routine does not guarantee that the diagonal entries of `R1` are positive.

New in version 0.16.0.

References

[1], [2], [3]

Examples

```
>>> from scipy import linalg
>>> a = np.array([[  3.,  -2.,  -2.],
...               [  6.,  -9.,  -3.],
...               [ -3.,  10.,   1.],
...               [  6.,  -7.,   4.],
...               [  7.,   8.,  -6.]])
>>> q, r = linalg.qr(a)
```

Given this QR decomposition, update q and r when 2 rows are removed.

```
>>> q1, r1 = linalg.qr_delete(q, r, 2, 2, 'row', False)
>>> q1
array([[ 0.30942637,  0.15347579,  0.93845645],  # may vary (signs)
       [ 0.61885275,  0.71680171, -0.32127338],
       [ 0.72199487, -0.68017681, -0.12681844]])
>>> r1
array([[  9.69535971,  -0.4125685 ,  -6.80738023],  # may vary (signs)
       [  0.        , -12.19958144,   1.62370412],
       [  0.        ,   0.        ,  -0.15218213]])
```

The update is equivalent, but faster than the following.

```
>>> a1 = np.delete(a, slice(2,4), 0)
>>> a1
array([[ 3., -2., -2.],
       [ 6., -9., -3.],
       [ 7.,  8., -6.]])
>>> q_direct, r_direct = linalg.qr(a1)
```

Check that we have equivalent results:

```
>>> np.dot(q1, r1)
array([[ 3., -2., -2.],
       [ 6., -9., -3.],
       [ 7.,  8., -6.]])
>>> np.allclose(np.dot(q1, r1), a1)
True
```

And the updated Q is still unitary:

```
>>> np.allclose(np.dot(q1.T, q1), np.eye(3))
True
```

scipy.linalg.qr_insert

scipy.linalg.**qr_insert**(*Q*, *R*, *u*, *k*, *which='row'*, *rcond=None*, *overwrite_qru=False*, *check_finite=True*)

QR update on row or column insertions

If `A = Q R` is the QR factorization of `A`, return the QR factorization of `A` where rows or columns have been inserted starting at row or column `k`.

Parameters

Q [(M, M) array_like] Unitary/orthogonal matrix from the QR decomposition of A.

R [(M, N) array_like] Upper triangular matrix from the QR decomposition of A.

u [(N,), (p, N), (M,), or (M, p) array_like] Rows or columns to insert

k [int] Index before which *u* is to be inserted.

which: {'row', 'col'}, optional
Determines if rows or columns will be inserted, defaults to 'row'

rcond [float] Lower bound on the reciprocal condition number of `Q` augmented with `u/||u||` Only used when updating economic mode (thin, (M,N) (N,N)) decompositions. If None, machine precision is used. Defaults to None.

overwrite_qru
[bool, optional] If True, consume Q, R, and u, if possible, while performing the update, otherwise make copies as necessary. Defaults to False.

check_finite
[bool, optional] Whether to check that the input matrices contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs. Default is True.

Returns

Q1 [ndarray] Updated unitary/orthogonal factor

R1 [ndarray] Updated upper triangular factor

Raises

LinAlgError :
If updating a (M,N) (N,N) factorization and the reciprocal condition number of Q augmented with u/||u|| is smaller than rcond.

See also:

qr, **qr_multiply**, **qr_delete**, **qr_update**

Notes

This routine does not guarantee that the diagonal entries of `R1` are positive.

New in version 0.16.0.

References

[1], [2], [3]

Examples

```
>>> from scipy import linalg
>>> a = np.array([[  3.,  -2.,  -2.],
...               [  6.,  -7.,   4.],
...               [  7.,   8.,  -6.]])
>>> q, r = linalg.qr(a)
```

Given this QR decomposition, update q and r when 2 rows are inserted.

```
>>> u = np.array([[  6.,  -9.,  -3.],
...               [ -3.,  10.,   1.]])
>>> q1, r1 = linalg.qr_insert(q, r, u, 2, 'row')
>>> q1
array([[-0.25445668,  0.02246245,  0.18146236, -0.72798806,  0.60979671],␣
 ↪ # may vary (signs)
       [-0.50891336,  0.23226178, -0.82836478, -0.02837033, -0.00828114],
       [-0.50891336,  0.35715302,  0.38937158,  0.58110733,  0.35235345],
       [ 0.25445668, -0.52202743, -0.32165498,  0.36263239,  0.65404509],
       [-0.59373225, -0.73856549,  0.16065817, -0.0063658 , -0.27595554]])
>>> r1
array([[-11.78982612,   6.44623587,   3.81685018],  # may vary (signs)
       [  0.        , -16.01393278,   3.72202865],
       [  0.        ,   0.        ,  -6.13010256],
       [  0.        ,   0.        ,   0.        ],
       [  0.        ,   0.        ,   0.        ]])
```

The update is equivalent, but faster than the following.

```
>>> a1 = np.insert(a, 2, u, 0)
>>> a1
array([[  3.,  -2.,  -2.],
       [  6.,  -7.,   4.],
       [  6.,  -9.,  -3.],
       [ -3.,  10.,   1.],
       [  7.,   8.,  -6.]])
>>> q_direct, r_direct = linalg.qr(a1)
```

Check that we have equivalent results:

```
>>> np.dot(q1, r1)
array([[  3.,  -2.,  -2.],
       [  6.,  -7.,   4.],
       [  6.,  -9.,  -3.],
       [ -3.,  10.,   1.],
       [  7.,   8.,  -6.]])
```

```
>>> np.allclose(np.dot(q1, r1), a1)
True
```

And the updated Q is still unitary:

```
>>> np.allclose(np.dot(q1.T, q1), np.eye(5))
True
```

scipy.linalg.rq

scipy.linalg.**rq**(*a*, *overwrite_a=False*, *lwork=None*, *mode='full'*, *check_finite=True*)

Compute RQ decomposition of a matrix.

Calculate the decomposition `A = R Q` where Q is unitary/orthogonal and R upper triangular.

Parameters

a [(M, N) array_like] Matrix to be decomposed

overwrite_a [bool, optional] Whether data in a is overwritten (may improve performance)

lwork [int, optional] Work array size, lwork >= a.shape[1]. If None or -1, an optimal size is computed.

mode [{'full', 'r', 'economic'}, optional] Determines what information is to be returned: either both Q and R ('full', default), only R ('r') or both Q and R but computed in economy-size ('economic', see Notes).

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

R [float or complex ndarray] Of shape (M, N) or (M, K) for `mode='economic'`. `K = min(M, N)`.

Q [float or complex ndarray] Of shape (N, N) or (K, N) for `mode='economic'`. Not returned if `mode='r'`.

Raises

LinAlgError If decomposition fails.

Notes

This is an interface to the LAPACK routines sgerqf, dgerqf, cgerqf, zgerqf, sorgrq, dorgrq, cungrq and zungrq.

If `mode=economic`, the shapes of Q and R are (K, N) and (M, K) instead of (N,N) and (M,N), with `K=min(M, N)`.

Examples

```
>>> from scipy import linalg
>>> rng = np.random.default_rng()
>>> a = rng.standard_normal((6, 9))
>>> r, q = linalg.rq(a)
>>> np.allclose(a, r @ q)
True
>>> r.shape, q.shape
((6, 9), (9, 9))
```

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```
>>> r2 = linalg.rq(a, mode='r')
>>> np.allclose(r, r2)
True
>>> r3, q3 = linalg.rq(a, mode='economic')
>>> r3.shape, q3.shape
((6, 6), (6, 9))
```

scipy.linalg.qz

scipy.linalg.**qz**(*A*, *B*, *output='real'*, *lwork=None*, *sort=None*, *overwrite_a=False*, *overwrite_b=False*, *check_finite=True*)

QZ decomposition for generalized eigenvalues of a pair of matrices.

The QZ, or generalized Schur, decomposition for a pair of n-by-n matrices (A,B) is:

```
(A,B) = (Q @ AA @ Z*, Q @ BB @ Z*)
```

where AA, BB is in generalized Schur form if BB is upper-triangular with non-negative diagonal and AA is upper-triangular, or for real QZ decomposition (`output='real'`) block upper triangular with 1x1 and 2x2 blocks. In this case, the 1x1 blocks correspond to real generalized eigenvalues and 2x2 blocks are 'standardized' by making the corresponding elements of BB have the form:

```
[ a 0 ]
[ 0 b ]
```

and the pair of corresponding 2x2 blocks in AA and BB will have a complex conjugate pair of generalized eigenvalues. If (`output='complex'`) or A and B are complex matrices, Z' denotes the conjugate-transpose of Z. Q and Z are unitary matrices.

Parameters

A [(N, N) array_like] 2-D array to decompose

B [(N, N) array_like] 2-D array to decompose

output [{'real', 'complex'}, optional] Construct the real or complex QZ decomposition for real matrices. Default is 'real'.

lwork [int, optional] Work array size. If None or -1, it is automatically computed.

sort [{None, callable, 'lhp', 'rhp', 'iuc', 'ouc'}, optional] NOTE: THIS INPUT IS DISABLED FOR NOW. Use ordqz instead.

Specifies whether the upper eigenvalues should be sorted. A callable may be passed that, given a eigenvalue, returns a boolean denoting whether the eigenvalue should be sorted to the top-left (True). For real matrix pairs, the sort function takes three real arguments (alphar, alphai, beta). The eigenvalue `x = (alphar + alphai*1j)/beta`. For complex matrix pairs or output='complex', the sort function takes two complex arguments (alpha, beta). The eigenvalue `x = (alpha/beta)`. Alternatively, string parameters may be used:

- 'lhp' Left-hand plane (x.real < 0.0)
- 'rhp' Right-hand plane (x.real > 0.0)
- 'iuc' Inside the unit circle (x*x.conjugate() < 1.0)
- 'ouc' Outside the unit circle (x*x.conjugate() > 1.0)

Defaults to None (no sorting).

overwrite_a [bool, optional] Whether to overwrite data in a (may improve performance)

overwrite_b [bool, optional] Whether to overwrite data in b (may improve performance)

check_finite
: [bool, optional] If true checks the elements of *A* and *B* are finite numbers. If false does no checking and passes matrix through to underlying algorithm.

Returns

AA [(N, N) ndarray] Generalized Schur form of A.
BB [(N, N) ndarray] Generalized Schur form of B.
Q [(N, N) ndarray] The left Schur vectors.
Z [(N, N) ndarray] The right Schur vectors.

See also:

`ordqz`

Notes

Q is transposed versus the equivalent function in Matlab.

New in version 0.11.0.

Examples

```
>>> from scipy import linalg
>>> rng = np.random.default_rng()
>>> A = np.arange(9).reshape((3, 3))
>>> B = rng.standard_normal((3, 3))
```

```
>>> AA, BB, Q, Z = linalg.qz(A, B)
>>> AA
array([[ 8.99591445e+00, -1.07917902e+01, -2.18309912e+00],
       [ 0.00000000e+00, -8.60837546e-01,  1.05063006e+00],
       [ 0.00000000e+00,  0.00000000e+00, -1.40584278e-15]])
>>> BB
array([[ 0.2058989 , -0.6007898 , -0.5771396 ],
       [ 0.        ,  1.6997737 , -1.12160842],
       [ 0.        ,  0.        ,  1.76304656]])
>>> Q
array([[ 0.10356118,  0.90697763, -0.40824829],
       [ 0.48575095,  0.31205664,  0.81649658],
       [ 0.86794072, -0.28286434, -0.40824829]])
>>> Z
array([[ 0.78900531,  0.16010775, -0.59315776],
       [-0.21754047, -0.83009894, -0.51343148],
       [ 0.57458399, -0.53413598,  0.62012256]])
```

scipy.linalg.ordqz

scipy.linalg.**ordqz**(*A*, *B*, *sort='lhp'*, *output='real'*, *overwrite_a=False*, *overwrite_b=False*, *check_finite=True*)

QZ decomposition for a pair of matrices with reordering.

Parameters

A [(N, N) array_like] 2-D array to decompose

B [(N, N) array_like] 2-D array to decompose

sort [{callable, 'lhp', 'rhp', 'iuc', 'ouc'}, optional] Specifies whether the upper eigenvalues should be sorted. A callable may be passed that, given an ordered pair `(alpha, beta)` representing the eigenvalue `x = (alpha/beta)`, returns a boolean denoting whether the eigenvalue should be sorted to the top-left (True). For the real matrix pairs `beta` is real while `alpha` can be complex, and for complex matrix pairs both `alpha` and `beta` can be complex. The callable must be able to accept a NumPy array. Alternatively, string parameters may be used:

- 'lhp' Left-hand plane (x.real < 0.0)
- 'rhp' Right-hand plane (x.real > 0.0)
- 'iuc' Inside the unit circle (x*x.conjugate() < 1.0)
- 'ouc' Outside the unit circle (x*x.conjugate() > 1.0)

With the predefined sorting functions, an infinite eigenvalue (i.e., `alpha != 0` and `beta = 0`) is considered to lie in neither the left-hand nor the right-hand plane, but it is considered to lie outside the unit circle. For the eigenvalue `(alpha, beta) = (0, 0)`, the predefined sorting functions all return *False*.

output [str {'real','complex'}, optional] Construct the real or complex QZ decomposition for real matrices. Default is 'real'.

overwrite_a
[bool, optional] If True, the contents of A are overwritten.

overwrite_b
[bool, optional] If True, the contents of B are overwritten.

check_finite
[bool, optional] If true checks the elements of *A* and *B* are finite numbers. If false does no checking and passes matrix through to underlying algorithm.

Returns

AA [(N, N) ndarray] Generalized Schur form of A.

BB [(N, N) ndarray] Generalized Schur form of B.

alpha [(N,) ndarray] alpha = alphar + alphai * 1j. See notes.

beta [(N,) ndarray] See notes.

Q [(N, N) ndarray] The left Schur vectors.

Z [(N, N) ndarray] The right Schur vectors.

See also:

qz

Notes

On exit, `(ALPHAR(j) + ALPHAI(j)*i)/BETA(j), j=1,...,N`, will be the generalized eigenvalues. `ALPHAR(j) + ALPHAI(j)*i` and `BETA(j),j=1,...,N` are the diagonals of the complex Schur form (S,T) that would result if the 2-by-2 diagonal blocks of the real generalized Schur form of (A,B) were further reduced to triangular form using complex unitary transformations. If ALPHAI(j) is zero, then the jth eigenvalue is real; if positive, then the `j``th and ``(j+1)``st eigenvalues are a complex conjugate pair, with ``ALPHAI(j+1)` negative.

New in version 0.17.0.

Examples

```
>>> from scipy.linalg import ordqz
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> B = np.array([[0, 6, 0, 0], [5, 0, 2, 1], [5, 2, 6, 6], [4, 7, 7, 7]])
>>> AA, BB, alpha, beta, Q, Z = ordqz(A, B, sort='lhp')
```

Since we have sorted for left half plane eigenvalues, negatives come first

```
>>> (alpha/beta).real < 0
array([ True,  True, False, False], dtype=bool)
```

scipy.linalg.schur

scipy.linalg.**schur**(*a*, *output='real'*, *lwork=None*, *overwrite_a=False*, *sort=None*, *check_finite=True*)

Compute Schur decomposition of a matrix.

The Schur decomposition is:

```
A = Z T Z^H
```

where Z is unitary and T is either upper-triangular, or for real Schur decomposition (output='real'), quasi-upper triangular. In the quasi-triangular form, 2x2 blocks describing complex-valued eigenvalue pairs may extrude from the diagonal.

Parameters

a [(M, M) array_like] Matrix to decompose

output [{'real', 'complex'}, optional] Construct the real or complex Schur decomposition (for real matrices).

lwork [int, optional] Work array size. If None or -1, it is automatically computed.

overwrite_a [bool, optional] Whether to overwrite data in a (may improve performance).

sort [{None, callable, 'lhp', 'rhp', 'iuc', 'ouc'}, optional] Specifies whether the upper eigenvalues should be sorted. A callable may be passed that, given a eigenvalue, returns a boolean denoting whether the eigenvalue should be sorted to the top-left (True). Alternatively, string parameters may be used:

```
'lhp'   Left-hand plane (x.real < 0.0)
'rhp'   Right-hand plane (x.real > 0.0)
'iuc'   Inside the unit circle (x*x.conjugate() <= 1.0)
'ouc'   Outside the unit circle (x*x.conjugate() > 1.0)
```

Defaults to None (no sorting).

check_finite
: [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

T
: [(M, M) ndarray] Schur form of A. It is real-valued for the real Schur decomposition.

Z
: [(M, M) ndarray] An unitary Schur transformation matrix for A. It is real-valued for the real Schur decomposition.

sdim
: [int] If and only if sorting was requested, a third return value will contain the number of eigenvalues satisfying the sort condition.

Raises

LinAlgError
: Error raised under three conditions:
1. The algorithm failed due to a failure of the QR algorithm to compute all eigenvalues.
2. If eigenvalue sorting was requested, the eigenvalues could not be reordered due to a failure to separate eigenvalues, usually because of poor conditioning.
3. If eigenvalue sorting was requested, roundoff errors caused the leading eigenvalues to no longer satisfy the sorting condition.

See also:

`rsf2csf`

Convert real Schur form to complex Schur form

Examples

```
>>> from scipy.linalg import schur, eigvals
>>> A = np.array([[0, 2, 2], [0, 1, 2], [1, 0, 1]])
>>> T, Z = schur(A)
>>> T
array([[ 2.65896708,  1.42440458, -1.92933439],
       [ 0.        , -0.32948354, -0.49063704],
       [ 0.        ,  1.31178921, -0.32948354]])
>>> Z
array([[0.72711591, -0.60156188, 0.33079564],
       [0.52839428, 0.79801892, 0.28976765],
       [0.43829436, 0.03590414, -0.89811411]])
```

```
>>> T2, Z2 = schur(A, output='complex')
>>> T2
array([[ 2.65896708, -1.22839825+1.32378589j,  0.42590089+1.51937378j],
       [ 0.        , -0.32948354+0.80225456j, -0.59877807+0.56192146j],
       [ 0.        ,  0.                    , -0.32948354-0.80225456j]])
>>> eigvals(T2)
array([2.65896708, -0.32948354+0.80225456j, -0.32948354-0.80225456j])
```

An arbitrary custom eig-sorting condition, having positive imaginary part, which is satisfied by only one eigenvalue

```
>>> T3, Z3, sdim = schur(A, output='complex', sort=lambda x: x.imag > 0)
>>> sdim
1
```

scipy.linalg.rsf2csf

scipy.linalg.**rsf2csf**(*T*, *Z*, *check_finite=True*)

Convert real Schur form to complex Schur form.

Convert a quasi-diagonal real-valued Schur form to the upper-triangular complex-valued Schur form.

Parameters

T [(M, M) array_like] Real Schur form of the original array

Z [(M, M) array_like] Schur transformation matrix

check_finite

[bool, optional] Whether to check that the input arrays contain only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

T [(M, M) ndarray] Complex Schur form of the original array

Z [(M, M) ndarray] Schur transformation matrix corresponding to the complex form

See also:

schur

Schur decomposition of an array

Examples

```
>>> from scipy.linalg import schur, rsf2csf
>>> A = np.array([[0, 2, 2], [0, 1, 2], [1, 0, 1]])
>>> T, Z = schur(A)
>>> T
array([[ 2.65896708,  1.42440458, -1.92933439],
       [ 0.        , -0.32948354, -0.49063704],
       [ 0.        ,  1.31178921, -0.32948354]])
>>> Z
array([[0.72711591, -0.60156188, 0.33079564],
       [0.52839428, 0.79801892, 0.28976765],
       [0.43829436, 0.03590414, -0.89811411]])
>>> T2 , Z2 = rsf2csf(T, Z)
>>> T2
array([[2.65896708+0.j, -1.64592781+0.743164187j, -1.21516887+1.
↪00660462j],
       [0.+0.j , -0.32948354+8.02254558e-01j, -0.82115218-2.77555756e-
↪17j],
       [0.+0.j , 0.+0.j, -0.32948354-0.802254558j]])
>>> Z2
array([[0.72711591+0.j,  0.28220393-0.31385693j,  0.51319638-0.17258824j],
       [0.52839428+0.j,  0.24720268+0.41635578j, -0.68079517-0.15118243j],
       [0.43829436+0.j, -0.76618703+0.01873251j, -0.03063006+0.
↪46857912j]])
```

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scipy.linalg.hessenberg

scipy.linalg.**hessenberg**(*a*, *calc_q=False*, *overwrite_a=False*, *check_finite=True*)

Compute Hessenberg form of a matrix.

The Hessenberg decomposition is:

```
A = Q H Q^H
```

where *Q* is unitary/orthogonal and *H* has only zero elements below the first sub-diagonal.

Parameters

a [(M, M) array_like] Matrix to bring into Hessenberg form.

calc_q [bool, optional] Whether to compute the transformation matrix. Default is False.

overwrite_a [bool, optional] Whether to overwrite *a*; may improve performance. Default is False.

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

H [(M, M) ndarray] Hessenberg form of *a*.

Q [(M, M) ndarray] Unitary/orthogonal similarity transformation matrix `A = Q H Q^H`. Only returned if `calc_q=True`.

Examples

```
>>> from scipy.linalg import hessenberg
>>> A = np.array([[2, 5, 8, 7], [5, 2, 2, 8], [7, 5, 6, 6], [5, 4, 4, 8]])
>>> H, Q = hessenberg(A, calc_q=True)
>>> H
array([[  2.        , -11.65843866,   1.42005301,   0.25349066],
       [ -9.94987437,  14.53535354,  -5.31022304,   2.43081618],
       [  0.        ,  -1.83299243,   0.38969961,  -0.51527034],
       [  0.        ,   0.        ,  -3.83189513,   1.07494686]])
>>> np.allclose(Q @ H @ Q.conj().T - A, np.zeros((4, 4)))
True
```

scipy.linalg.cdf2rdf

scipy.linalg.**cdf2rdf**(*w*, *v*)

Converts complex eigenvalues `w` and eigenvectors `v` to real eigenvalues in a block diagonal form `wr` and the associated real eigenvectors `vr`, such that:

```
vr @ wr = X @ vr
```

continues to hold, where `X` is the original array for which `w` and `v` are the eigenvalues and eigenvectors.

New in version 1.1.0.

Parameters

w [(…, M) array_like] Complex or real eigenvalues, an array or stack of arrays
Conjugate pairs must not be interleaved, else the wrong result will be produced. So `[1+1j, 1, 1-1j]` will give a correct result, but `[1+1j, 2+1j, 1-1j, 2-1j]` will not.

v [(…, M, M) array_like] Complex or real eigenvectors, a square array or stack of square arrays.

Returns

wr [(…, M, M) ndarray] Real diagonal block form of eigenvalues

vr [(…, M, M) ndarray] Real eigenvectors associated with `wr`

See also:

`eig`

Eigenvalues and right eigenvectors for non-symmetric arrays

`rsf2csf`

Convert real Schur form to complex Schur form

Notes

`w`, `v` must be the eigenstructure for some *real* matrix `X`. For example, obtained by `w, v = scipy.linalg.eig(X)` or `w, v = numpy.linalg.eig(X)` in which case `X` can also represent stacked arrays.

New in version 1.1.0.

Examples

```
>>> X = np.array([[1, 2, 3], [0, 4, 5], [0, -5, 4]])
>>> X
array([[ 1,  2,  3],
       [ 0,  4,  5],
       [ 0, -5,  4]])
```

```
>>> from scipy import linalg
>>> w, v = linalg.eig(X)
>>> w
array([ 1.+0.j,  4.+5.j,  4.-5.j])
>>> v
array([[ 1.00000+0.j     , -0.01906-0.40016j, -0.01906+0.40016j],
       [ 0.00000+0.j     ,  0.00000-0.64788j,  0.00000+0.64788j],
       [ 0.00000+0.j     ,  0.64788+0.j     ,  0.64788-0.j     ]])
```

```
>>> wr, vr = linalg.cdf2rdf(w, v)
>>> wr
array([[ 1.,  0.,  0.],
       [ 0.,  4.,  5.],
       [ 0., -5.,  4.]])
>>> vr
array([[ 1.     ,  0.40016, -0.01906],
       [ 0.     ,  0.64788,  0.     ],
       [ 0.     ,  0.     ,  0.64788]])
```

```
>>> vr @ wr
array([[ 1.     ,  1.69593,  1.9246 ],
       [ 0.     ,  2.59153,  3.23942],
       [ 0.     , -3.23942,  2.59153]])
>>> X @ vr
array([[ 1.     ,  1.69593,  1.9246 ],
       [ 0.     ,  2.59153,  3.23942],
       [ 0.     , -3.23942,  2.59153]])
```

scipy.linalg.cossin

scipy.linalg.**cossin**(*X*, *p=None*, *q=None*, *separate=False*, *swap_sign=False*, *compute_u=True*, *compute_vh=True*)

Compute the cosine-sine (CS) decomposition of an orthogonal/unitary matrix.

X is an `(m, m)` orthogonal/unitary matrix, partitioned as the following where upper left block has the shape of `(p, q)`:

```
                                ┌                   ┐
                                │ I  0  0 │ 0  0  0 │
┌         ┐    ┌         ┐     │ 0  C  0 │ 0 -S  0 │┌         ┐*
│ X11 │ X12 │    │ U1 │    │     │ 0  0  0 │ 0  0 -I ││ V1 │    │
│ ────┼──── │ = │────┼────│└─────────┼─────────┘└────┼────┘
│ X21 │ X22 │    │    │ U2 │     │ 0  0  0 │ I  0  0 │     │ V2 │
└         ┘    └         ┘     │ 0  S  0 │ 0  C  0 │└         ┘
                                │ 0  0  I │ 0  0  0 │
                                └                   ┘
```

`U1`, `U2`, `V1`, `V2` are square orthogonal/unitary matrices of dimensions `(p,p)`, `(m-p,m-p)`, `(q,q)`, and `(m-q,m-q)` respectively, and `C` and `S` are `(r, r)` nonnegative diagonal matrices satisfying `C^2 + S^2 = I` where `r = min(p, m-p, q, m-q)`.

Moreover, the rank of the identity matrices are `min(p, q) - r`, `min(p, m - q) - r`, `min(m - p, q) - r`, and `min(m - p, m - q) - r` respectively.

X can be supplied either by itself and block specifications p, q or its subblocks in an iterable from which the shapes would be derived. See the examples below.

Parameters

X [array_like, iterable] complex unitary or real orthogonal matrix to be decomposed, or iterable of subblocks `X11`, `X12`, `X21`, `X22`, when `p`, `q` are omitted.

p [int, optional] Number of rows of the upper left block `X11`, used only when X is given as an array.

q [int, optional] Number of columns of the upper left block `X11`, used only when X is given as an array.

separate [bool, optional] if `True`, the low level components are returned instead of the matrix factors, i.e. `(u1,u2)`, `theta`, `(v1h,v2h)` instead of `u`, `cs`, `vh`.

swap_sign [bool, optional] if `True`, the `-S`, `-I` block will be the bottom left, otherwise (by default) they will be in the upper right block.

compute_u [bool, optional] if `False`, `u` won't be computed and an empty array is returned.

compute_vh [bool, optional] if `False`, `vh` won't be computed and an empty array is returned.

Returns

u [ndarray] When `compute_u=True`, contains the block diagonal orthogonal/unitary matrix consisting of the blocks `U1` (`p` x `p`) and `U2` (`m-p` x `m-p`) orthogonal/unitary matrices. If `separate=True`, this contains the tuple of `(U1, U2)`.

cs [ndarray]
The cosine-sine factor with the structure described above.
If `separate=True`, this contains the `theta` array containing the angles in radians.

vh [ndarray] When `compute_vh=True`, contains the block diagonal orthogonal/unitary matrix consisting of the blocks ``V1H`` (`q` x `q`) and `V2H` (`m-q` x `m-q`) orthogonal/unitary matrices. If `separate=True`, this contains the tuple of `(V1H, V2H)`.

References

[1]

Examples

```
>>> from scipy.linalg import cossin
>>> from scipy.stats import unitary_group
>>> x = unitary_group.rvs(4)
>>> u, cs, vdh = cossin(x, p=2, q=2)
>>> np.allclose(x, u @ cs @ vdh)
True
```

Same can be entered via subblocks without the need of `p` and `q`. Also let's skip the computation of `u`

```
>>> ue, cs, vdh = cossin((x[:2, :2], x[:2, 2:], x[2:, :2], x[2:, 2:]),
...                      compute_u=False)
>>> print(ue)
[]
>>> np.allclose(x, u @ cs @ vdh)
True
```

See also:

scipy.linalg.interpolative – Interpolative matrix decompositions

Matrix Functions

expm(A)	Compute the matrix exponential using Pade approximation.
logm(A[, disp])	Compute matrix logarithm.
cosm(A)	Compute the matrix cosine.
sinm(A)	Compute the matrix sine.
tanm(A)	Compute the matrix tangent.
coshm(A)	Compute the hyperbolic matrix cosine.
sinhm(A)	Compute the hyperbolic matrix sine.
tanhm(A)	Compute the hyperbolic matrix tangent.
signm(A[, disp])	Matrix sign function.

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Table 95 – continued from previous page

sqrtm(A[, disp, blocksize])	Matrix square root.
funm(A, func[, disp])	Evaluate a matrix function specified by a callable.
expm_frechet(A, E[, method, compute_expm, …])	Frechet derivative of the matrix exponential of A in the direction E.
expm_cond(A[, check_finite])	Relative condition number of the matrix exponential in the Frobenius norm.
fractional_matrix_power(A, t)	Compute the fractional power of a matrix.

scipy.linalg.expm

scipy.linalg.**expm**(*A*)

Compute the matrix exponential using Pade approximation.

Parameters

A [(N, N) array_like or sparse matrix] Matrix to be exponentiated.

Returns

expm [(N, N) ndarray] Matrix exponential of *A*.

References

[1]

Examples

```
>>> from scipy.linalg import expm, sinm, cosm
```

Matrix version of the formula exp(0) = 1:

```
>>> expm(np.zeros((2,2)))
array([[ 1.,  0.],
       [ 0.,  1.]])
```

Euler's identity (exp(i*theta) = cos(theta) + i*sin(theta)) applied to a matrix:

```
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
>>> cosm(a) + 1j*sinm(a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```

scipy.linalg.logm

scipy.linalg.**logm**(*A*, *disp=True*)

Compute matrix logarithm.

The matrix logarithm is the inverse of expm: expm(logm(*A*)) == *A*

Parameters

A	[(N, N) array_like] Matrix whose logarithm to evaluate
disp	[bool, optional] Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns

logm	[(N, N) ndarray] Matrix logarithm of *A*
errest	[float] (if disp == False) 1-norm of the estimated error, ||err||_1 / ||A||_1

References

[1], [2], [3]

Examples

```
>>> from scipy.linalg import logm, expm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> b = logm(a)
>>> b
array([[-1.02571087,  2.05142174],
       [ 0.68380725,  1.02571087]])
>>> expm(b)          # Verify expm(logm(a)) returns a
array([[ 1.,  3.],
       [ 1.,  4.]])
```

scipy.linalg.cosm

scipy.linalg.**cosm**(*A*)

Compute the matrix cosine.

This routine uses expm to compute the matrix exponentials.

Parameters

A	[(N, N) array_like] Input array

Returns

cosm	[(N, N) ndarray] Matrix cosine of A

Examples

```
>>> from scipy.linalg import expm, sinm, cosm
```

Euler's identity (exp(i*theta) = cos(theta) + i*sin(theta)) applied to a matrix:

```
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
>>> cosm(a) + 1j*sinm(a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```

scipy.linalg.sinm

scipy.linalg.**sinm**(*A*)

Compute the matrix sine.

This routine uses expm to compute the matrix exponentials.

Parameters

A [(N, N) array_like] Input array.

Returns

sinm [(N, N) ndarray] Matrix sine of *A*

Examples

```
>>> from scipy.linalg import expm, sinm, cosm
```

Euler's identity (exp(i*theta) = cos(theta) + i*sin(theta)) applied to a matrix:

```
>>> a = np.array([[1.0, 2.0], [-1.0, 3.0]])
>>> expm(1j*a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
>>> cosm(a) + 1j*sinm(a)
array([[ 0.42645930+1.89217551j, -2.13721484-0.97811252j],
       [ 1.06860742+0.48905626j, -1.71075555+0.91406299j]])
```

scipy.linalg.tanm

scipy.linalg.**tanm**(*A*)

Compute the matrix tangent.

This routine uses expm to compute the matrix exponentials.

Parameters

A [(N, N) array_like] Input array.

Returns

tanm [(N, N) ndarray] Matrix tangent of *A*

Examples

```
>>> from scipy.linalg import tanm, sinm, cosm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> t = tanm(a)
>>> t
array([[ -2.00876993,  -8.41880636],
       [ -2.80626879, -10.42757629]])
```

Verify tanm(a) = sinm(a).dot(inv(cosm(a)))

```
>>> s = sinm(a)
>>> c = cosm(a)
>>> s.dot(np.linalg.inv(c))
array([[ -2.00876993,  -8.41880636],
       [ -2.80626879, -10.42757629]])
```

scipy.linalg.coshm

scipy.linalg.**coshm**(*A*)

Compute the hyperbolic matrix cosine.

This routine uses expm to compute the matrix exponentials.

Parameters

A [(N, N) array_like] Input array.

Returns

coshm [(N, N) ndarray] Hyperbolic matrix cosine of *A*

Examples

```
>>> from scipy.linalg import tanhm, sinhm, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> c = coshm(a)
>>> c
array([[ 11.24592233,  38.76236492],
       [ 12.92078831,  50.00828725]])
```

Verify tanhm(a) = sinhm(a).dot(inv(coshm(a)))

```
>>> t = tanhm(a)
>>> s = sinhm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[  2.72004641e-15,   4.55191440e-15],
       [  0.00000000e+00,  -5.55111512e-16]])
```

scipy.linalg.sinhm

scipy.linalg.**sinhm**(*A*)

Compute the hyperbolic matrix sine.

This routine uses expm to compute the matrix exponentials.

Parameters

A [(N, N) array_like] Input array.

Returns

sinhm [(N, N) ndarray] Hyperbolic matrix sine of *A*

Examples

```
>>> from scipy.linalg import tanhm, sinhm, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> s = sinhm(a)
>>> s
array([[ 10.57300653,  39.28826594],
       [ 13.09608865,  49.86127247]])
```

Verify tanhm(a) = sinhm(a).dot(inv(coshm(a)))

```
>>> t = tanhm(a)
>>> c = coshm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[  2.72004641e-15,   4.55191440e-15],
       [  0.00000000e+00,  -5.55111512e-16]])
```

scipy.linalg.tanhm

scipy.linalg.**tanhm**(*A*)

Compute the hyperbolic matrix tangent.

This routine uses expm to compute the matrix exponentials.

Parameters

A [(N, N) array_like] Input array

Returns

tanhm [(N, N) ndarray] Hyperbolic matrix tangent of *A*

Examples

```
>>> from scipy.linalg import tanhm, sinhm, coshm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> t = tanhm(a)
>>> t
array([[ 0.3428582 ,  0.51987926],
       [ 0.17329309,  0.86273746]])
```

Verify tanhm(a) = sinhm(a).dot(inv(coshm(a)))

```
>>> s = sinhm(a)
>>> c = coshm(a)
>>> t - s.dot(np.linalg.inv(c))
array([[  2.72004641e-15,   4.55191440e-15],
       [  0.00000000e+00,  -5.55111512e-16]])
```

scipy.linalg.signm

scipy.linalg.**signm**(*A*, *disp=True*)

Matrix sign function.

Extension of the scalar sign(x) to matrices.

Parameters

A	[(N, N) array_like] Matrix at which to evaluate the sign function
disp	[bool, optional] Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns

signm	[(N, N) ndarray] Value of the sign function at *A*
errest	[float] (if disp == False) 1-norm of the estimated error, ||err||_1 / ||A||_1

Examples

```
>>> from scipy.linalg import signm, eigvals
>>> a = [[1,2,3], [1,2,1], [1,1,1]]
>>> eigvals(a)
array([ 4.12488542+0.j, -0.76155718+0.j,  0.63667176+0.j])
>>> eigvals(signm(a))
array([-1.+0.j,  1.+0.j,  1.+0.j])
```

scipy.linalg.sqrtm

scipy.linalg.**sqrtm**(*A*, *disp=True*, *blocksize=64*)

Matrix square root.

Parameters

A	[(N, N) array_like] Matrix whose square root to evaluate
disp	[bool, optional] Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)
blocksize	[integer, optional] If the blocksize is not degenerate with respect to the size of the input array, then use a blocked algorithm. (Default: 64)

Returns

sqrtm	[(N, N) ndarray] Value of the sqrt function at *A*
errest	[float] (if disp == False) Frobenius norm of the estimated error, ||err||_F / ||A||_F

References

[1]

Examples

```
>>> from scipy.linalg import sqrtm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> r = sqrtm(a)
>>> r
array([[ 0.75592895,  1.13389342],
       [ 0.37796447,  1.88982237]])
>>> r.dot(r)
array([[ 1.,  3.],
       [ 1.,  4.]])
```

scipy.linalg.funm

scipy.linalg.**funm**(*A*, *func*, *disp=True*)

Evaluate a matrix function specified by a callable.

Returns the value of matrix-valued function `f` at *A*. The function `f` is an extension of the scalar-valued function *func* to matrices.

Parameters

A	[(N, N) array_like] Matrix at which to evaluate the function
func	[callable] Callable object that evaluates a scalar function f. Must be vectorized (eg. using vectorize).
disp	[bool, optional] Print warning if error in the result is estimated large instead of returning estimated error. (Default: True)

Returns

funm	[(N, N) ndarray] Value of the matrix function specified by func evaluated at *A*
errest	[float] (if disp == False) 1-norm of the estimated error, ||err||_1 / ||A||_1

Notes

This function implements the general algorithm based on Schur decomposition (Algorithm 9.1.1. in [1]).

If the input matrix is known to be diagonalizable, then relying on the eigendecomposition is likely to be faster. For example, if your matrix is Hermitian, you can do

```
>>> from scipy.linalg import eigh
>>> def funm_herm(a, func, check_finite=False):
...     w, v = eigh(a, check_finite=check_finite)
...     ## if you further know that your matrix is positive semidefinite,
...     ## you can optionally guard against precision errors by doing
...     # w = np.maximum(w, 0)
...     w = func(w)
...     return (v * w).dot(v.conj().T)
```

References

[1]

Examples

```
>>> from scipy.linalg import funm
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> funm(a, lambda x: x*x)
array([[  4.,  15.],
       [  5.,  19.]])
>>> a.dot(a)
array([[  4.,  15.],
       [  5.,  19.]])
```

scipy.linalg.expm_frechet

scipy.linalg.**expm_frechet**(*A*, *E*, *method=None*, *compute_expm=True*, *check_finite=True*)

Frechet derivative of the matrix exponential of A in the direction E.

Parameters

A [(N, N) array_like] Matrix of which to take the matrix exponential.

E [(N, N) array_like] Matrix direction in which to take the Frechet derivative.

method [str, optional] Choice of algorithm. Should be one of

- *SPS* (default)
- *blockEnlarge*

compute_expm
[bool, optional] Whether to compute also *expm_A* in addition to *expm_frechet_AE*. Default is True.

check_finite
[bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

expm_A [ndarray] Matrix exponential of A.

expm_frechet_AE
[ndarray] Frechet derivative of the matrix exponential of A in the direction E.

For `compute_expm = False`, only *expm_frechet_AE* is returned.

See also:

expm

Compute the exponential of a matrix.

Notes

This section describes the available implementations that can be selected by the *method* parameter. The default method is *SPS*.

Method *blockEnlarge* is a naive algorithm.

Method *SPS* is Scaling-Pade-Squaring [1]. It is a sophisticated implementation which should take only about 3/8 as much time as the naive implementation. The asymptotics are the same.

New in version 0.13.0.

References

[1]

Examples

```
>>> import scipy.linalg
>>> rng = np.random.default_rng()
>>> A = rng.standard_normal((3, 3))
>>> E = rng.standard_normal((3, 3))
>>> expm_A, expm_frechet_AE = scipy.linalg.expm_frechet(A, E)
>>> expm_A.shape, expm_frechet_AE.shape
((3, 3), (3, 3))
```

```
>>> import scipy.linalg
>>> rng = np.random.default_rng()
>>> A = rng.standard_normal((3, 3))
>>> E = rng.standard_normal((3, 3))
>>> expm_A, expm_frechet_AE = scipy.linalg.expm_frechet(A, E)
>>> M = np.zeros((6, 6))
>>> M[:3, :3] = A; M[:3, 3:] = E; M[3:, 3:] = A
>>> expm_M = scipy.linalg.expm(M)
>>> np.allclose(expm_A, expm_M[:3, :3])
True
>>> np.allclose(expm_frechet_AE, expm_M[:3, 3:])
True
```

scipy.linalg.expm_cond

scipy.linalg.**expm_cond**(*A*, *check_finite=True*)

Relative condition number of the matrix exponential in the Frobenius norm.

Parameters

A [2-D array_like] Square input matrix with shape (N, N).

check_finite [bool, optional] Whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

Returns

kappa [float] The relative condition number of the matrix exponential in the Frobenius norm

See also:

expm

Compute the exponential of a matrix.

expm_frechet

Compute the Frechet derivative of the matrix exponential.

Notes

A faster estimate for the condition number in the 1-norm has been published but is not yet implemented in SciPy.

New in version 0.14.0.

Examples

```
>>> from scipy.linalg import expm_cond
>>> A = np.array([[-0.3, 0.2, 0.6], [0.6, 0.3, -0.1], [-0.7, 1.2, 0.9]])
>>> k = expm_cond(A)
>>> k
1.7787805864469866
```

scipy.linalg.fractional_matrix_power

scipy.linalg.**fractional_matrix_power**(*A*, *t*)

Compute the fractional power of a matrix.

Proceeds according to the discussion in section (6) of [1].

Parameters

A [(N, N) array_like] Matrix whose fractional power to evaluate.

t [float] Fractional power.

Returns

X [(N, N) array_like] The fractional power of the matrix.

References

[1]

Examples

```
>>> from scipy.linalg import fractional_matrix_power
>>> a = np.array([[1.0, 3.0], [1.0, 4.0]])
>>> b = fractional_matrix_power(a, 0.5)
>>> b
array([[ 0.75592895,  1.13389342],
       [ 0.37796447,  1.88982237]])
>>> np.dot(b, b)      # Verify square root
array([[ 1.,  3.],
       [ 1.,  4.]])
```

Matrix Equation Solvers

solve_sylvester(a, b, q)	Computes a solution (X) to the Sylvester equation $AX + XB = Q$.
solve_continuous_are(a, b, q, r[, e, s, …])	Solves the continuous-time algebraic Riccati equation (CARE).
solve_discrete_are(a, b, q, r[, e, s, balanced])	Solves the discrete-time algebraic Riccati equation (DARE).
solve_continuous_lyapunov(a, q)	Solves the continuous Lyapunov equation $AX+XA^H = Q$.
solve_discrete_lyapunov(a, q[, method])	Solves the discrete Lyapunov equation $AXA^H - X + Q = 0$.

scipy.linalg.solve_sylvester

scipy.linalg.**solve_sylvester**(*a*, *b*, *q*)

Computes a solution (X) to the Sylvester equation $AX + XB = Q$.

Parameters

a [(M, M) array_like] Leading matrix of the Sylvester equation
b [(N, N) array_like] Trailing matrix of the Sylvester equation
q [(M, N) array_like] Right-hand side

Returns

x [(M, N) ndarray] The solution to the Sylvester equation.

Raises

LinAlgError
If solution was not found

Notes

Computes a solution to the Sylvester matrix equation via the Bartels- Stewart algorithm. The A and B matrices first undergo Schur decompositions. The resulting matrices are used to construct an alternative Sylvester equation (`RY + YS^T = F`) where the R and S matrices are in quasi-triangular form (or, when R, S or F are complex, triangular form). The simplified equation is then solved using `*TRSYL` from LAPACK directly.

New in version 0.11.0.

Examples

Given *a*, *b*, and *q* solve for *x*:

```
>>> from scipy import linalg
>>> a = np.array([[-3, -2, 0], [-1, -1, 3], [3, -5, -1]])
>>> b = np.array([[1]])
>>> q = np.array([[1],[2],[3]])
>>> x = linalg.solve_sylvester(a, b, q)
>>> x
array([[ 0.0625],
       [-0.5625],
       [ 0.6875]])
```

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```
>>> np.allclose(a.dot(x) + x.dot(b), q)
True
```

scipy.linalg.solve_continuous_are

scipy.linalg.**solve_continuous_are**(*a*, *b*, *q*, *r*, *e=None*, *s=None*, *balanced=True*)

Solves the continuous-time algebraic Riccati equation (CARE).

The CARE is defined as

$$XA + A^H X - XBR^{-1}B^H X + Q = 0$$

The limitations for a solution to exist are :

- All eigenvalues of A on the right half plane, should be controllable.
- The associated hamiltonian pencil (See Notes), should have eigenvalues sufficiently away from the imaginary axis.

Moreover, if `e` or `s` is not precisely `None`, then the generalized version of CARE

$$E^H XA + A^H XE - (E^H XB + S)R^{-1}(B^H XE + S^H) + Q = 0$$

is solved. When omitted, `e` is assumed to be the identity and `s` is assumed to be the zero matrix with sizes compatible with `a` and `b`, respectively.

Parameters

a	[(M, M) array_like] Square matrix
b	[(M, N) array_like] Input
q	[(M, M) array_like] Input
r	[(N, N) array_like] Nonsingular square matrix
e	[(M, M) array_like, optional] Nonsingular square matrix
s	[(M, N) array_like, optional] Input
balanced	[bool, optional] The boolean that indicates whether a balancing step is performed on the data. The default is set to True.

Returns

x	[(M, M) ndarray] Solution to the continuous-time algebraic Riccati equation.

Raises

LinAlgError
: For cases where the stable subspace of the pencil could not be isolated. See Notes section and the references for details.

See also:

`solve_discrete_are`

Solves the discrete-time algebraic Riccati equation

Notes

The equation is solved by forming the extended hamiltonian matrix pencil, as described in [1], $H - \lambda J$ given by the block matrices

```
[ A    0    B ]             [ E   0    0 ]
[-Q  -A^H  -S ] - \lambda * [ 0  E^H   0 ]
[ S^H B^H   R ]             [ 0   0    0 ]
```

and using a QZ decomposition method.

In this algorithm, the fail conditions are linked to the symmetry of the product $U_2 U_1^{-1}$ and condition number of U_1. Here, U is the 2m-by-m matrix that holds the eigenvectors spanning the stable subspace with 2-m rows and partitioned into two m-row matrices. See [1] and [2] for more details.

In order to improve the QZ decomposition accuracy, the pencil goes through a balancing step where the sum of absolute values of H and J entries (after removing the diagonal entries of the sum) is balanced following the recipe given in [3].

New in version 0.11.0.

References

[1], [2], [3]

Examples

Given *a*, *b*, *q*, and *r* solve for *x*:

```
>>> from scipy import linalg
>>> a = np.array([[4, 3], [-4.5, -3.5]])
>>> b = np.array([[1], [-1]])
>>> q = np.array([[9, 6], [6, 4.]])
>>> r = 1
>>> x = linalg.solve_continuous_are(a, b, q, r)
>>> x
array([[ 21.72792206,  14.48528137],
       [ 14.48528137,   9.65685425]])
>>> np.allclose(a.T.dot(x) + x.dot(a)-x.dot(b).dot(b.T).dot(x), -q)
True
```

scipy.linalg.solve_discrete_are

scipy.linalg.**solve_discrete_are**(*a*, *b*, *q*, *r*, *e=None*, *s=None*, *balanced=True*)

Solves the discrete-time algebraic Riccati equation (DARE).

The DARE is defined as

$$A^H X A - X - (A^H X B)(R + B^H X B)^{-1}(B^H X A) + Q = 0$$

The limitations for a solution to exist are :

- All eigenvalues of A outside the unit disc, should be controllable.
- The associated symplectic pencil (See Notes), should have eigenvalues sufficiently away from the unit circle.

Moreover, if `e` and `s` are not both precisely `None`, then the generalized version of DARE

$$A^H X A - E^H X E - (A^H X B + S)(R + B^H X B)^{-1}(B^H X A + S^H) + Q = 0$$

is solved. When omitted, `e` is assumed to be the identity and `s` is assumed to be the zero matrix.

Parameters

a	[(M, M) array_like] Square matrix
b	[(M, N) array_like] Input
q	[(M, M) array_like] Input
r	[(N, N) array_like] Square matrix
e	[(M, M) array_like, optional] Nonsingular square matrix
s	[(M, N) array_like, optional] Input
balanced	[bool] The boolean that indicates whether a balancing step is performed on the data. The default is set to True.

Returns

x	[(M, M) ndarray] Solution to the discrete algebraic Riccati equation.

Raises

LinAlgError
: For cases where the stable subspace of the pencil could not be isolated. See Notes section and the references for details.

See also:

`solve_continuous_are`

Solves the continuous algebraic Riccati equation

Notes

The equation is solved by forming the extended symplectic matrix pencil, as described in [1], $H - \lambda J$ given by the block matrices

```
[  A   0   B ]             [ E   0   B ]
[ -Q  E^H -S ] - \lambda * [ 0  A^H  0 ]
[ S^H  0   R ]             [ 0 -B^H  0 ]
```

and using a QZ decomposition method.

In this algorithm, the fail conditions are linked to the symmetry of the product $U_2 U_1^{-1}$ and condition number of U_1. Here, U is the 2m-by-m matrix that holds the eigenvectors spanning the stable subspace with 2-m rows and partitioned into two m-row matrices. See [1] and [2] for more details.

In order to improve the QZ decomposition accuracy, the pencil goes through a balancing step where the sum of absolute values of H and J rows/cols (after removing the diagonal entries) is balanced following the recipe given in [3]. If the data has small numerical noise, balancing may amplify their effects and some clean up is required.

New in version 0.11.0.

References

[1], [2], [3]

Examples

Given a, b, q, and r solve for x:

```
>>> from scipy import linalg as la
>>> a = np.array([[0, 1], [0, -1]])
>>> b = np.array([[1, 0], [2, 1]])
>>> q = np.array([[-4, -4], [-4, 7]])
>>> r = np.array([[9, 3], [3, 1]])
>>> x = la.solve_discrete_are(a, b, q, r)
>>> x
array([[-4., -4.],
       [-4.,  7.]])
>>> R = la.solve(r + b.T.dot(x).dot(b), b.T.dot(x).dot(a))
>>> np.allclose(a.T.dot(x).dot(a) - x - a.T.dot(x).dot(b).dot(R), -q)
True
```

scipy.linalg.solve_continuous_lyapunov

scipy.linalg.**solve_continuous_lyapunov**(*a*, *q*)

Solves the continuous Lyapunov equation $AX + XA^H = Q$.

Uses the Bartels-Stewart algorithm to find X.

Parameters

a	[array_like] A square matrix
q	[array_like] Right-hand side square matrix

Returns

x	[ndarray] Solution to the continuous Lyapunov equation

See also:

solve_discrete_lyapunov

computes the solution to the discrete-time Lyapunov equation

solve_sylvester

computes the solution to the Sylvester equation

Notes

The continuous Lyapunov equation is a special form of the Sylvester equation, hence this solver relies on LAPACK routine ?TRSYL.

New in version 0.11.0.

Examples

Given a and q solve for x:

```
>>> from scipy import linalg
>>> a = np.array([[-3, -2, 0], [-1, -1, 0], [0, -5, -1]])
>>> b = np.array([2, 4, -1])
>>> q = np.eye(3)
>>> x = linalg.solve_continuous_lyapunov(a, q)
>>> x
array([[ -0.75  ,   0.875 ,  -3.75  ],
       [  0.875 ,  -1.375 ,   5.3125],
       [ -3.75  ,   5.3125, -27.0625]])
>>> np.allclose(a.dot(x) + x.dot(a.T), q)
True
```

scipy.linalg.solve_discrete_lyapunov

scipy.linalg.**solve_discrete_lyapunov**(*a*, *q*, *method=None*)

Solves the discrete Lyapunov equation $AXA^H - X + Q = 0$.

Parameters

a, q : [(M, M) array_like] Square matrices corresponding to A and Q in the equation above respectively. Must have the same shape.

method : [{'direct', 'bilinear'}, optional] Type of solver.
If not given, chosen to be `direct` if `M` is less than 10 and `bilinear` otherwise.

Returns

x : [ndarray] Solution to the discrete Lyapunov equation

See also:

solve_continuous_lyapunov

computes the solution to the continuous-time Lyapunov equation

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *direct* if `M` is less than 10 and `bilinear` otherwise.

Method *direct* uses a direct analytical solution to the discrete Lyapunov equation. The algorithm is given in, for example, [1]. However, it requires the linear solution of a system with dimension M^2 so that performance degrades rapidly for even moderately sized matrices.

Method *bilinear* uses a bilinear transformation to convert the discrete Lyapunov equation to a continuous Lyapunov equation $(BX + XB' = -C)$ where $B = (A-I)(A+I)^{-1}$ and $C = 2(A'+I)^{-1}Q(A+I)^{-1}$. The continuous equation can be efficiently solved since it is a special case of a Sylvester equation. The transformation algorithm is from Popov (1964) as described in [2].

New in version 0.11.0.

References

[1], [2]

Examples

Given a and q solve for x:

```
>>> from scipy import linalg
>>> a = np.array([[0.2, 0.5],[0.7, -0.9]])
>>> q = np.eye(2)
>>> x = linalg.solve_discrete_lyapunov(a, q)
>>> x
array([[ 0.70872893,  1.43518822],
       [ 1.43518822, -2.4266315 ]])
>>> np.allclose(a.dot(x).dot(a.T)-x, -q)
True
```

Sketches and Random Projections

clarkson_woodruff_transform(input_matrix, …)	Applies a Clarkson-Woodruff Transform/sketch to the input matrix.

scipy.linalg.clarkson_woodruff_transform

scipy.linalg.**clarkson_woodruff_transform**(*input_matrix*, *sketch_size*, *seed=None*)

Applies a Clarkson-Woodruff Transform/sketch to the input matrix.

Given an input_matrix `A` of size `(n, d)`, compute a matrix `A'` of size (sketch_size, d) so that

$$\|Ax\| \approx \|A'x\|$$

with high probability via the Clarkson-Woodruff Transform, otherwise known as the CountSketch matrix.

Parameters

input_matrix: array_like
: Input matrix, of shape `(n, d)`.

sketch_size: int
: Number of rows for the sketch.

seed
: [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Returns

A'
: [array_like] Sketch of the input matrix `A`, of size `(sketch_size, d)`.

Notes

To make the statement

$$\|Ax\| \approx \|A'x\|$$

precise, observe the following result which is adapted from the proof of Theorem 14 of [2] via Markov's Inequality. If we have a sketch size `sketch_size=k` which is at least

$$k \geq \frac{2}{\epsilon^2 \delta}$$

Then for any fixed vector `x`,

$$\|Ax\| = (1 \pm \epsilon)\|A'x\|$$

with probability at least one minus delta.

This implementation takes advantage of sparsity: computing a sketch takes time proportional to `A.nnz`. Data `A` which is in `scipy.sparse.csc_matrix` format gives the quickest computation time for sparse input.

```
>>> from scipy import linalg
>>> from scipy import sparse
>>> rng = np.random.default_rng()
>>> n_rows, n_columns, density, sketch_n_rows = 15000, 100, 0.01, 200
>>> A = sparse.rand(n_rows, n_columns, density=density, format='csc')
>>> B = sparse.rand(n_rows, n_columns, density=density, format='csr')
>>> C = sparse.rand(n_rows, n_columns, density=density, format='coo')
>>> D = rng.standard_normal((n_rows, n_columns))
>>> SA = linalg.clarkson_woodruff_transform(A, sketch_n_rows) # fastest
>>> SB = linalg.clarkson_woodruff_transform(B, sketch_n_rows) # fast
>>> SC = linalg.clarkson_woodruff_transform(C, sketch_n_rows) # slower
>>> SD = linalg.clarkson_woodruff_transform(D, sketch_n_rows) # slowest
```

That said, this method does perform well on dense inputs, just slower on a relative scale.

References

[1], [2]

Examples

Given a big dense matrix `A`:

```
>>> from scipy import linalg
>>> n_rows, n_columns, sketch_n_rows = 15000, 100, 200
>>> rng = np.random.default_rng()
>>> A = rng.standard_normal((n_rows, n_columns))
>>> sketch = linalg.clarkson_woodruff_transform(A, sketch_n_rows)
>>> sketch.shape
(200, 100)
>>> norm_A = np.linalg.norm(A)
>>> norm_sketch = np.linalg.norm(sketch)
```

Now with high probability, the true norm `norm_A` is close to the sketched norm `norm_sketch` in absolute value.

Similarly, applying our sketch preserves the solution to a linear regression of $\min \|Ax - b\|$.

```
>>> from scipy import linalg
>>> n_rows, n_columns, sketch_n_rows = 15000, 100, 200
>>> rng = np.random.default_rng()
>>> A = rng.standard_normal((n_rows, n_columns))
>>> b = rng.standard_normal(n_rows)
>>> x = np.linalg.lstsq(A, b, rcond=None)
>>> Ab = np.hstack((A, b.reshape(-1,1)))
>>> SAb = linalg.clarkson_woodruff_transform(Ab, sketch_n_rows)
>>> SA, Sb = SAb[:,:-1], SAb[:,-1]
>>> x_sketched = np.linalg.lstsq(SA, Sb, rcond=None)
```

As with the matrix norm example, `np.linalg.norm(A @ x - b)` is close to `np.linalg.norm(A @ x_sketched - b)` with high probability.

Special Matrices

block_diag(*arrs)	Create a block diagonal matrix from provided arrays.
circulant(c)	Construct a circulant matrix.
companion(a)	Create a companion matrix.
convolution_matrix(a, n[, mode])	Construct a convolution matrix.
dft(n[, scale])	Discrete Fourier transform matrix.
fiedler(a)	Returns a symmetric Fiedler matrix
fiedler_companion(a)	Returns a Fiedler companion matrix
hadamard(n[, dtype])	Construct an Hadamard matrix.
hankel(c[, r])	Construct a Hankel matrix.
helmert(n[, full])	Create an Helmert matrix of order *n*.
hilbert(n)	Create a Hilbert matrix of order *n*.
invhilbert(n[, exact])	Compute the inverse of the Hilbert matrix of order *n*.
leslie(f, s)	Create a Leslie matrix.
pascal(n[, kind, exact])	Returns the n x n Pascal matrix.
invpascal(n[, kind, exact])	Returns the inverse of the n x n Pascal matrix.
toeplitz(c[, r])	Construct a Toeplitz matrix.
tri(N[, M, k, dtype])	Construct (N, M) matrix filled with ones at and below the kth diagonal.

scipy.linalg.block_diag

scipy.linalg.**block_diag**(**arrs*)

Create a block diagonal matrix from provided arrays.

Given the inputs *A*, *B* and *C*, the output will have these arrays arranged on the diagonal:

```
[[A, 0, 0],
 [0, B, 0],
 [0, 0, C]]
```

Parameters

A, B, C, …

[array_like, up to 2-D] Input arrays. A 1-D array or array_like sequence of length *n* is treated as a 2-D array with shape `(1,n)`.

Returns

D [ndarray] Array with *A*, *B*, *C*, … on the diagonal. *D* has the same dtype as *A*.

Notes

If all the input arrays are square, the output is known as a block diagonal matrix.

Empty sequences (i.e., array-likes of zero size) will not be ignored. Noteworthy, both [] and [[]] are treated as matrices with shape `(1,0)`.

Examples

```
>>> from scipy.linalg import block_diag
>>> A = [[1, 0],
...      [0, 1]]
>>> B = [[3, 4, 5],
...      [6, 7, 8]]
>>> C = [[7]]
>>> P = np.zeros((2, 0), dtype='int32')
>>> block_diag(A, B, C)
array([[1, 0, 0, 0, 0, 0],
       [0, 1, 0, 0, 0, 0],
       [0, 0, 3, 4, 5, 0],
       [0, 0, 6, 7, 8, 0],
       [0, 0, 0, 0, 0, 7]])
>>> block_diag(A, P, B, C)
array([[1, 0, 0, 0, 0, 0],
       [0, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 3, 4, 5, 0],
       [0, 0, 6, 7, 8, 0],
       [0, 0, 0, 0, 0, 7]])
>>> block_diag(1.0, [2, 3], [[4, 5], [6, 7]])
array([[ 1.,  0.,  0.,  0.,  0.],
       [ 0.,  2.,  3.,  0.,  0.],
       [ 0.,  0.,  0.,  4.,  5.],
       [ 0.,  0.,  0.,  6.,  7.]])
```

scipy.linalg.circulant

`scipy.linalg.`**`circulant`**(*c*)

Construct a circulant matrix.

Parameters

c [(N,) array_like] 1-D array, the first column of the matrix.

Returns

A [(N, N) ndarray] A circulant matrix whose first column is *c*.

See also:

`toeplitz`

Toeplitz matrix

`hankel`

Hankel matrix

`solve_circulant`

Solve a circulant system.

Notes

New in version 0.8.0.

Examples

```
>>> from scipy.linalg import circulant
>>> circulant([1, 2, 3])
array([[1, 3, 2],
       [2, 1, 3],
       [3, 2, 1]])
```

scipy.linalg.companion

scipy.linalg.**companion**(*a*)

Create a companion matrix.

Create the companion matrix [1] associated with the polynomial whose coefficients are given in *a*.

Parameters

a [(N,) array_like] 1-D array of polynomial coefficients. The length of *a* must be at least two, and `a[0]` must not be zero.

Returns

c [(N-1, N-1) ndarray] The first row of *c* is `-a[1:]/a[0]`, and the first sub-diagonal is all ones. The data-type of the array is the same as the data-type of `1.0*a[0]`.

Raises

ValueError

If any of the following are true: a) `a.ndim != 1`; b) `a.size < 2`; c) `a[0] == 0`.

Notes

New in version 0.8.0.

References

[1]

Examples

```
>>> from scipy.linalg import companion
>>> companion([1, -10, 31, -30])
array([[ 10., -31.,  30.],
       [  1.,   0.,   0.],
       [  0.,   1.,   0.]])
```

scipy.linalg.convolution_matrix

scipy.linalg.**convolution_matrix**(*a*, *n*, *mode='full'*)

Construct a convolution matrix.

Constructs the Toeplitz matrix representing one-dimensional convolution [1]. See the notes below for details.

Parameters

a [(m,) array_like] The 1-D array to convolve.

n [int] The number of columns in the resulting matrix. It gives the length of the input to be convolved with *a*. This is analogous to the length of *v* in `numpy.convolve(a, v)`.

mode [str] This is analogous to *mode* in `numpy.convolve(v, a, mode)`. It must be one of ('full', 'valid', 'same'). See below for how *mode* determines the shape of the result.

Returns

A [(k, n) ndarray] The convolution matrix whose row count *k* depends on *mode*:

```
=======  =========================
 mode    k
=======  =========================
'full'   m + n -1
'same'   max(m, n)
'valid'  max(m, n) - min(m, n) + 1
=======  =========================
```

See also:

toeplitz

Toeplitz matrix

Notes

The code:

```
A = convolution_matrix(a, n, mode)
```

creates a Toeplitz matrix *A* such that `A @ v` is equivalent to using `convolve(a, v, mode)`. The returned array always has *n* columns. The number of rows depends on the specified *mode*, as explained above.

In the default 'full' mode, the entries of *A* are given by:

```
A[i, j] == (a[i-j] if (0 <= (i-j) < m) else 0)
```

where `m = len(a)`. Suppose, for example, the input array is `[x, y, z]`. The convolution matrix has the form:

```
[x, 0, 0, ..., 0, 0]
[y, x, 0, ..., 0, 0]
[z, y, x, ..., 0, 0]
...
[0, 0, 0, ..., x, 0]
[0, 0, 0, ..., y, x]
[0, 0, 0, ..., z, y]
[0, 0, 0, ..., 0, z]
```

In 'valid' mode, the entries of *A* are given by:

```
A[i, j] == (a[i-j+m-1] if (0 <= (i-j+m-1) < m) else 0)
```

This corresponds to a matrix whose rows are the subset of those from the 'full' case where all the coefficients in *a* are contained in the row. For input `[x, y, z]`, this array looks like:

```
[z, y, x, 0, 0, ..., 0, 0, 0]
[0, z, y, x, 0, ..., 0, 0, 0]
[0, 0, z, y, x, ..., 0, 0, 0]
...
[0, 0, 0, 0, 0, ..., x, 0, 0]
[0, 0, 0, 0, 0, ..., y, x, 0]
[0, 0, 0, 0, 0, ..., z, y, x]
```

In the 'same' mode, the entries of *A* are given by:

```
d = (m - 1) // 2
A[i, j] == (a[i-j+d] if (0 <= (i-j+d) < m) else 0)
```

The typical application of the 'same' mode is when one has a signal of length *n* (with *n* greater than `len(a)`), and the desired output is a filtered signal that is still of length *n*.

For input `[x, y, z]`, this array looks like:

```
[y, x, 0, 0, ..., 0, 0, 0]
[z, y, x, 0, ..., 0, 0, 0]
[0, z, y, x, ..., 0, 0, 0]
[0, 0, z, y, ..., 0, 0, 0]
...
```

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```
[0, 0, 0, 0, ..., y, x, 0]
[0, 0, 0, 0, ..., z, y, x]
[0, 0, 0, 0, ..., 0, z, y]
```

New in version 1.5.0.

References

[1]

Examples

```
>>> from scipy.linalg import convolution_matrix
>>> A = convolution_matrix([-1, 4, -2], 5, mode='same')
>>> A
array([[ 4, -1,  0,  0,  0],
       [-2,  4, -1,  0,  0],
       [ 0, -2,  4, -1,  0],
       [ 0,  0, -2,  4, -1],
       [ 0,  0,  0, -2,  4]])
```

Compare multiplication by *A* with the use of `numpy.convolve`.

```
>>> x = np.array([1, 2, 0, -3, 0.5])
>>> A @ x
array([  2. ,   6. ,  -1. , -12.5,   8. ])
```

Verify that `A @ x` produced the same result as applying the convolution function.

```
>>> np.convolve([-1, 4, -2], x, mode='same')
array([  2. ,   6. ,  -1. , -12.5,   8. ])
```

For comparison to the case `mode='same'` shown above, here are the matrices produced by `mode='full'` and `mode='valid'` for the same coefficients and size.

```
>>> convolution_matrix([-1, 4, -2], 5, mode='full')
array([[-1,  0,  0,  0,  0],
       [ 4, -1,  0,  0,  0],
       [-2,  4, -1,  0,  0],
       [ 0, -2,  4, -1,  0],
       [ 0,  0, -2,  4, -1],
       [ 0,  0,  0, -2,  4],
       [ 0,  0,  0,  0, -2]])
```

```
>>> convolution_matrix([-1, 4, -2], 5, mode='valid')
array([[-2,  4, -1,  0,  0],
       [ 0, -2,  4, -1,  0],
       [ 0,  0, -2,  4, -1]])
```

scipy.linalg.dft

scipy.linalg.**dft**(*n*, *scale=None*)

Discrete Fourier transform matrix.

Create the matrix that computes the discrete Fourier transform of a sequence [1]. The nth primitive root of unity used to generate the matrix is exp(-2*pi*i/n), where i = sqrt(-1).

Parameters

n	[int] Size the matrix to create.
scale	[str, optional] Must be None, 'sqrtn', or 'n'. If *scale* is 'sqrtn', the matrix is divided by *sqrt(n)*. If *scale* is 'n', the matrix is divided by *n*. If *scale* is None (the default), the matrix is not normalized, and the return value is simply the Vandermonde matrix of the roots of unity.

Returns

m	[(n, n) ndarray] The DFT matrix.

Notes

When *scale* is None, multiplying a vector by the matrix returned by *dft* is mathematically equivalent to (but much less efficient than) the calculation performed by *scipy.fft.fft*.

New in version 0.14.0.

References

[1]

Examples

```
>>> from scipy.linalg import dft
>>> np.set_printoptions(precision=2, suppress=True)  # for compact output
>>> m = dft(5)
>>> m
array([[ 1.  +0.j  ,  1.  +0.j  ,  1.  +0.j  ,  1.  +0.j  ,  1.  +0.j  ],
       [ 1.  +0.j  ,  0.31-0.95j, -0.81-0.59j, -0.81+0.59j,  0.31+0.95j],
       [ 1.  +0.j  , -0.81-0.59j,  0.31+0.95j,  0.31-0.95j, -0.81+0.59j],
       [ 1.  +0.j  , -0.81+0.59j,  0.31-0.95j,  0.31+0.95j, -0.81-0.59j],
       [ 1.  +0.j  ,  0.31+0.95j, -0.81+0.59j, -0.81-0.59j,  0.31-0.95j]])
>>> x = np.array([1, 2, 3, 0, 3])
>>> m @ x  # Compute the DFT of x
array([ 9.  +0.j  ,  0.12-0.81j, -2.12+3.44j, -2.12-3.44j,  0.12+0.81j])
```

Verify that `m @ x` is the same as `fft(x)`.

```
>>> from scipy.fft import fft
>>> fft(x)      # Same result as m @ x
array([ 9.  +0.j  ,  0.12-0.81j, -2.12+3.44j, -2.12-3.44j,  0.12+0.81j])
```

scipy.linalg.fiedler

scipy.linalg.**fiedler**(*a*)

Returns a symmetric Fiedler matrix

Given an sequence of numbers *a*, Fiedler matrices have the structure `F[i, j] = np.abs(a[i] - a[j])`, and hence zero diagonals and nonnegative entries. A Fiedler matrix has a dominant positive eigenvalue and other eigenvalues are negative. Although not valid generally, for certain inputs, the inverse and the determinant can be derived explicitly as given in [1].

Parameters

a [(n,) array_like] coefficient array

Returns

F [(n, n) ndarray]

See also:

circulant, **toeplitz**

Notes

New in version 1.3.0.

References

[1]

Examples

```
>>> from scipy.linalg import det, inv, fiedler
>>> a = [1, 4, 12, 45, 77]
>>> n = len(a)
>>> A = fiedler(a)
>>> A
array([[ 0,  3, 11, 44, 76],
       [ 3,  0,  8, 41, 73],
       [11,  8,  0, 33, 65],
       [44, 41, 33,  0, 32],
       [76, 73, 65, 32,  0]])
```

The explicit formulas for determinant and inverse seem to hold only for monotonically increasing/decreasing arrays. Note the tridiagonal structure and the corners.

```
>>> Ai = inv(A)
>>> Ai[np.abs(Ai) < 1e-12] = 0.  # cleanup the numerical noise for display
>>> Ai
array([[-0.16008772,  0.16666667,  0.        ,  0.        ,  0.00657895],
       [ 0.16666667, -0.22916667,  0.0625    ,  0.        ,  0.        ],
       [ 0.        ,  0.0625    , -0.07765152,  0.01515152,  0.        ],
       [ 0.        ,  0.        ,  0.01515152, -0.03077652,  0.015625  ],
       [ 0.00657895,  0.        ,  0.        ,  0.015625  , -0.00904605]])
```

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```
>>> det(A)
15409151.999999998
>>> (-1)**(n-1) * 2**(n-2) * np.diff(a).prod() * (a[-1] - a[0])
15409152
```

scipy.linalg.fiedler_companion

scipy.linalg.**fiedler_companion**(*a*)

Returns a Fiedler companion matrix

Given a polynomial coefficient array `a`, this function forms a pentadiagonal matrix with a special structure whose eigenvalues coincides with the roots of `a`.

Parameters

a [(N,) array_like] 1-D array of polynomial coefficients in descending order with a nonzero leading coefficient. For `N < 2`, an empty array is returned.

Returns

c [(N-1, N-1) ndarray] Resulting companion matrix

See also:

`companion`

Notes

Similar to *companion* the leading coefficient should be nonzero. In the case the leading coefficient is not 1, other coefficients are rescaled before the array generation. To avoid numerical issues, it is best to provide a monic polynomial.

New in version 1.3.0.

References

[1]

Examples

```
>>> from scipy.linalg import fiedler_companion, eigvals
>>> p = np.poly(np.arange(1, 9, 2))  # [1., -16., 86., -176., 105.]
>>> fc = fiedler_companion(p)
>>> fc
array([[  16.,  -86.,    1.,    0.],
       [   1.,    0.,    0.,    0.],
       [   0.,  176.,    0., -105.],
       [   0.,    1.,    0.,    0.]])
>>> eigvals(fc)
array([7.+0.j, 5.+0.j, 3.+0.j, 1.+0.j])
```

scipy.linalg.hadamard

scipy.linalg.**hadamard**(*n*, *dtype=<class 'int'>*)

Construct an Hadamard matrix.

Constructs an n-by-n Hadamard matrix, using Sylvester's construction. *n* must be a power of 2.

Parameters

n	[int] The order of the matrix. *n* must be a power of 2.
dtype	[dtype, optional] The data type of the array to be constructed.

Returns

H	[(n, n) ndarray] The Hadamard matrix.

Notes

New in version 0.8.0.

Examples

```
>>> from scipy.linalg import hadamard
>>> hadamard(2, dtype=complex)
array([[ 1.+0.j,  1.+0.j],
       [ 1.+0.j, -1.-0.j]])
>>> hadamard(4)
array([[ 1,  1,  1,  1],
       [ 1, -1,  1, -1],
       [ 1,  1, -1, -1],
       [ 1, -1, -1,  1]])
```

scipy.linalg.hankel

scipy.linalg.**hankel**(*c*, *r=None*)

Construct a Hankel matrix.

The Hankel matrix has constant anti-diagonals, with *c* as its first column and *r* as its last row. If *r* is not given, then *r = zeros_like(c)* is assumed.

Parameters

c	[array_like] First column of the matrix. Whatever the actual shape of *c*, it will be converted to a 1-D array.
r	[array_like, optional] Last row of the matrix. If None, `r = zeros_like(c)` is assumed. r[0] is ignored; the last row of the returned matrix is `[c[-1], r[1:]]`. Whatever the actual shape of *r*, it will be converted to a 1-D array.

Returns

A	[(len(c), len(r)) ndarray] The Hankel matrix. Dtype is the same as `(c[0] + r[0]).dtype`.

See also:

toeplitz

Toeplitz matrix

circulant

circulant matrix

Examples

```
>>> from scipy.linalg import hankel
>>> hankel([1, 17, 99])
array([[ 1, 17, 99],
       [17, 99,  0],
       [99,  0,  0]])
>>> hankel([1,2,3,4], [4,7,7,8,9])
array([[1, 2, 3, 4, 7],
       [2, 3, 4, 7, 7],
       [3, 4, 7, 7, 8],
       [4, 7, 7, 8, 9]])
```

scipy.linalg.helmert

scipy.linalg.**helmert**(*n*, *full=False*)

Create an Helmert matrix of order *n*.

This has applications in statistics, compositional or simplicial analysis, and in Aitchison geometry.

Parameters

n [int] The size of the array to create.

full [bool, optional] If True the (n, n) ndarray will be returned. Otherwise the submatrix that does not include the first row will be returned. Default: False.

Returns

M [ndarray] The Helmert matrix. The shape is (n, n) or (n-1, n) depending on the *full* argument.

Examples

```
>>> from scipy.linalg import helmert
>>> helmert(5, full=True)
array([[ 0.4472136 ,  0.4472136 ,  0.4472136 ,  0.4472136 ,  0.4472136 ],
       [ 0.70710678, -0.70710678,  0.        ,  0.        ,  0.        ],
       [ 0.40824829,  0.40824829, -0.81649658,  0.        ,  0.        ],
       [ 0.28867513,  0.28867513,  0.28867513, -0.8660254 ,  0.        ],
       [ 0.2236068 ,  0.2236068 ,  0.2236068 ,  0.2236068 , -0.89442719]])
```

scipy.linalg.hilbert

scipy.linalg.**hilbert**(*n*)

Create a Hilbert matrix of order *n*.

Returns the *n* by *n* array with entries *h[i,j] = 1 / (i + j + 1)*.

Parameters

n [int] The size of the array to create.

Returns

h [(n, n) ndarray] The Hilbert matrix.

See also:

`invhilbert`

Compute the inverse of a Hilbert matrix.

Notes

New in version 0.10.0.

Examples

```
>>> from scipy.linalg import hilbert
>>> hilbert(3)
array([[ 1.        ,  0.5       ,  0.33333333],
       [ 0.5       ,  0.33333333,  0.25      ],
       [ 0.33333333,  0.25      ,  0.2       ]])
```

scipy.linalg.invhilbert

`scipy.linalg.`**`invhilbert`**(*n*, *exact=False*)

Compute the inverse of the Hilbert matrix of order *n*.

The entries in the inverse of a Hilbert matrix are integers. When *n* is greater than 14, some entries in the inverse exceed the upper limit of 64 bit integers. The *exact* argument provides two options for dealing with these large integers.

Parameters

n [int] The order of the Hilbert matrix.

exact [bool, optional] If False, the data type of the array that is returned is np.float64, and the array is an approximation of the inverse. If True, the array is the exact integer inverse array. To represent the exact inverse when n > 14, the returned array is an object array of long integers. For n <= 14, the exact inverse is returned as an array with data type np.int64.

Returns

invh [(n, n) ndarray] The data type of the array is np.float64 if *exact* is False. If *exact* is True, the data type is either np.int64 (for n <= 14) or object (for n > 14). In the latter case, the objects in the array will be long integers.

See also:

`hilbert`

Create a Hilbert matrix.

Notes

New in version 0.10.0.

Examples

```
>>> from scipy.linalg import invhilbert
>>> invhilbert(4)
array([[   16.,  -120.,   240.,  -140.],
       [ -120.,  1200., -2700.,  1680.],
       [  240., -2700.,  6480., -4200.],
       [ -140.,  1680., -4200.,  2800.]])
>>> invhilbert(4, exact=True)
array([[   16,  -120,   240,  -140],
       [ -120,  1200, -2700,  1680],
       [  240, -2700,  6480, -4200],
       [ -140,  1680, -4200,  2800]], dtype=int64)
>>> invhilbert(16)[7,7]
4.2475099528537506e+19
>>> invhilbert(16, exact=True)[7,7]
42475099528537378560
```

scipy.linalg.leslie

scipy.linalg.**leslie**(*f*, *s*)

Create a Leslie matrix.

Given the length n array of fecundity coefficients *f* and the length n-1 array of survival coefficients *s*, return the associated Leslie matrix.

Parameters

f	[(N,) array_like] The "fecundity" coefficients.
s	[(N-1,) array_like] The "survival" coefficients, has to be 1-D. The length of *s* must be one less than the length of *f*, and it must be at least 1.

Returns

L	[(N, N) ndarray] The array is zero except for the first row, which is *f*, and the first sub-diagonal, which is *s*. The data-type of the array will be the data-type of `f[0]+s[0]`.

Notes

New in version 0.8.0.

The Leslie matrix is used to model discrete-time, age-structured population growth [1] [2]. In a population with *n* age classes, two sets of parameters define a Leslie matrix: the *n* "fecundity coefficients", which give the number of offspring per-capita produced by each age class, and the *n* - 1 "survival coefficients", which give the per-capita survival rate of each age class.

References

[1], [2]

Examples

```
>>> from scipy.linalg import leslie
>>> leslie([0.1, 2.0, 1.0, 0.1], [0.2, 0.8, 0.7])
array([[ 0.1,  2. ,  1. ,  0.1],
       [ 0.2,  0. ,  0. ,  0. ],
       [ 0. ,  0.8,  0. ,  0. ],
       [ 0. ,  0. ,  0.7,  0. ]])
```

scipy.linalg.pascal

scipy.linalg.**pascal**(*n*, *kind='symmetric'*, *exact=True*)

Returns the n x n Pascal matrix.

The Pascal matrix is a matrix containing the binomial coefficients as its elements.

Parameters

n	[int] The size of the matrix to create; that is, the result is an n x n matrix.
kind	[str, optional] Must be one of 'symmetric', 'lower', or 'upper'. Default is 'symmetric'.
exact	[bool, optional] If *exact* is True, the result is either an array of type numpy.uint64 (if n < 35) or an object array of Python long integers. If *exact* is False, the coefficients in the matrix are computed using *scipy.special.comb* with *exact=False*. The result will be a floating point array, and the values in the array will not be the exact coefficients, but this version is much faster than *exact=True*.

Returns

p	[(n, n) ndarray] The Pascal matrix.

See also:

invpascal

Notes

See https://en.wikipedia.org/wiki/Pascal_matrix for more information about Pascal matrices.

New in version 0.11.0.

Examples

```
>>> from scipy.linalg import pascal
>>> pascal(4)
array([[ 1,  1,  1,  1],
       [ 1,  2,  3,  4],
       [ 1,  3,  6, 10],
       [ 1,  4, 10, 20]], dtype=uint64)
>>> pascal(4, kind='lower')
array([[1, 0, 0, 0],
```

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```
       [1, 1, 0, 0],
       [1, 2, 1, 0],
       [1, 3, 3, 1]], dtype=uint64)
>>> pascal(50)[-1, -1]
25477612258980856902730428600
>>> from scipy.special import comb
>>> comb(98, 49, exact=True)
25477612258980856902730428600
```

scipy.linalg.invpascal

scipy.linalg.**invpascal**(*n*, *kind='symmetric'*, *exact=True*)

Returns the inverse of the n x n Pascal matrix.

The Pascal matrix is a matrix containing the binomial coefficients as its elements.

Parameters

n	[int] The size of the matrix to create; that is, the result is an n x n matrix.
kind	[str, optional] Must be one of 'symmetric', 'lower', or 'upper'. Default is 'symmetric'.
exact	[bool, optional] If *exact* is True, the result is either an array of type `numpy.int64` (if $n <= 35$) or an object array of Python integers. If *exact* is False, the coefficients in the matrix are computed using *scipy.special.comb* with *exact=False*. The result will be a floating point array, and for large *n*, the values in the array will not be the exact coefficients.

Returns

invp	[(n, n) ndarray] The inverse of the Pascal matrix.

See also:

pascal

Notes

New in version 0.16.0.

References

[1], [2]

Examples

```
>>> from scipy.linalg import invpascal, pascal
>>> invp = invpascal(5)
>>> invp
array([[  5, -10,  10,  -5,   1],
       [-10,  30, -35,  19,  -4],
       [ 10, -35,  46, -27,   6],
       [ -5,  19, -27,  17,  -4],
       [  1,  -4,   6,  -4,   1]])
```

```
>>> p = pascal(5)
>>> p.dot(invp)
array([[ 1.,  0.,  0.,  0.,  0.],
       [ 0.,  1.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  1.,  0.],
       [ 0.,  0.,  0.,  0.,  1.]])
```

An example of the use of *kind* and *exact*:

```
>>> invpascal(5, kind='lower', exact=False)
array([[ 1., -0.,  0., -0.,  0.],
       [-1.,  1., -0.,  0., -0.],
       [ 1., -2.,  1., -0.,  0.],
       [-1.,  3., -3.,  1., -0.],
       [ 1., -4.,  6., -4.,  1.]])
```

scipy.linalg.toeplitz

scipy.linalg.**toeplitz**(*c*, *r=None*)

Construct a Toeplitz matrix.

The Toeplitz matrix has constant diagonals, with c as its first column and r as its first row. If r is not given, `r == conjugate(c)` is assumed.

Parameters

c : [array_like] First column of the matrix. Whatever the actual shape of *c*, it will be converted to a 1-D array.

r : [array_like, optional] First row of the matrix. If None, `r = conjugate(c)` is assumed; in this case, if c[0] is real, the result is a Hermitian matrix. r[0] is ignored; the first row of the returned matrix is `[c[0], r[1:]]`. Whatever the actual shape of *r*, it will be converted to a 1-D array.

Returns

A : [(len(c), len(r)) ndarray] The Toeplitz matrix. Dtype is the same as `(c[0] + r[0]).dtype`.

See also:

circulant

circulant matrix

hankel

Hankel matrix

solve_toeplitz

Solve a Toeplitz system.

Notes

The behavior when *c* or *r* is a scalar, or when *c* is complex and *r* is None, was changed in version 0.8.0. The behavior in previous versions was undocumented and is no longer supported.

Examples

```
>>> from scipy.linalg import toeplitz
>>> toeplitz([1,2,3], [1,4,5,6])
array([[1, 4, 5, 6],
       [2, 1, 4, 5],
       [3, 2, 1, 4]])
>>> toeplitz([1.0, 2+3j, 4-1j])
array([[ 1.+0.j,  2.-3.j,  4.+1.j],
       [ 2.+3.j,  1.+0.j,  2.-3.j],
       [ 4.-1.j,  2.+3.j,  1.+0.j]])
```

scipy.linalg.tri

scipy.linalg.**tri**(*N*, *M=None*, *k=0*, *dtype=None*)

Construct (N, M) matrix filled with ones at and below the kth diagonal.

The matrix has A[i,j] == 1 for i <= j + k

Parameters

N	[int] The size of the first dimension of the matrix.
M	[int or None, optional] The size of the second dimension of the matrix. If *M* is None, *M* = *N* is assumed.
k	[int, optional] Number of subdiagonal below which matrix is filled with ones. *k* = 0 is the main diagonal, *k* < 0 subdiagonal and *k* > 0 superdiagonal.
dtype	[dtype, optional] Data type of the matrix.

Returns

tri	[(N, M) ndarray] Tri matrix.

Examples

```
>>> from scipy.linalg import tri
>>> tri(3, 5, 2, dtype=int)
array([[1, 1, 1, 0, 0],
       [1, 1, 1, 1, 0],
       [1, 1, 1, 1, 1]])
>>> tri(3, 5, -1, dtype=int)
array([[0, 0, 0, 0, 0],
       [1, 0, 0, 0, 0],
       [1, 1, 0, 0, 0]])
```

Low-level routines

get_blas_funcs(names[, arrays, dtype, ilp64])	Return available BLAS function objects from names.
get_lapack_funcs(names[, arrays, dtype, ilp64])	Return available LAPACK function objects from names.
find_best_blas_type([arrays, dtype])	Find best-matching BLAS/LAPACK type.

scipy.linalg.get_blas_funcs

scipy.linalg.**get_blas_funcs**(*names*, *arrays=()*, *dtype=None*, *ilp64=False*)

Return available BLAS function objects from names.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters

names [str or sequence of str] Name(s) of BLAS functions without type prefix.

arrays [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype [str or dtype, optional] Data-type specifier. Not used if *arrays* is non-empty.

ilp64 [{True, False, 'preferred'}, optional] Whether to return ILP64 routine variant. Choosing 'preferred' returns ILP64 routine if available, and otherwise the 32-bit routine. Default: False

Returns

funcs [list] List containing the found function(s).

Notes

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In BLAS, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the NumPy types {float32, float64, complex64, complex128} respectively. The code and the dtype are stored in attributes *typecode* and *dtype* of the returned functions.

Examples

```
>>> import scipy.linalg as LA
>>> rng = np.random.default_rng()
>>> a = rng.random((3,2))
>>> x_gemv = LA.get_blas_funcs('gemv', (a,))
>>> x_gemv.typecode
'd'
>>> x_gemv = LA.get_blas_funcs('gemv',(a*1j,))
>>> x_gemv.typecode
'z'
```

scipy.linalg.get_lapack_funcs

scipy.linalg.**get_lapack_funcs**(*names*, *arrays=()*, *dtype=None*, *ilp64=False*)

Return available LAPACK function objects from names.

Arrays are used to determine the optimal prefix of LAPACK routines.

Parameters

names [str or sequence of str] Name(s) of LAPACK functions without type prefix.

arrays [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of LAPACK routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype [str or dtype, optional] Data-type specifier. Not used if *arrays* is non-empty.

ilp64 [{True, False, 'preferred'}, optional] Whether to return ILP64 routine variant. Choosing 'preferred' returns ILP64 routine if available, and otherwise the 32-bit routine. Default: False

Returns

funcs [list] List containing the found function(s).

Notes

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In LAPACK, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the NumPy types {float32, float64, complex64, complex128} respectively, and are stored in attribute `typecode` of the returned functions.

Examples

Suppose we would like to use '?lange' routine which computes the selected norm of an array. We pass our array in order to get the correct 'lange' flavor.

```
>>> import scipy.linalg as LA
>>> rng = np.random.default_rng()
>>> a = rng.random((3,2))
>>> x_lange = LA.get_lapack_funcs('lange', (a,))
>>> x_lange.typecode
'd'
>>> x_lange = LA.get_lapack_funcs('lange',(a*1j,))
>>> x_lange.typecode
'z'
```

Several LAPACK routines work best when its internal WORK array has the optimal size (big enough for fast computation and small enough to avoid waste of memory). This size is determined also by a dedicated query to the function which is often wrapped as a standalone function and commonly denoted as `###_lwork`. Below is an example for `?sysv`

```
>>> import scipy.linalg as LA
>>> rng = np.random.default_rng()
>>> a = rng.random((1000, 1000))
>>> b = rng.random((1000, 1)) * 1j
```

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```
>>> # We pick up zsysv and zsysv_lwork due to b array
... xsysv, xlwork = LA.get_lapack_funcs(('sysv', 'sysv_lwork'), (a, b))
>>> opt_lwork, _ = xlwork(a.shape[0])  # returns a complex for 'z' prefix
>>> udut, ipiv, x, info = xsysv(a, b, lwork=int(opt_lwork.real))
```

scipy.linalg.find_best_blas_type

scipy.linalg.**find_best_blas_type**(*arrays=()*, *dtype=None*)

Find best-matching BLAS/LAPACK type.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters

arrays [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype [str or dtype, optional] Data-type specifier. Not used if *arrays* is non-empty.

Returns

prefix [str] BLAS/LAPACK prefix character.

dtype [dtype] Inferred Numpy data type.

prefer_fortran [bool] Whether to prefer Fortran order routines over C order.

Examples

```
>>> import scipy.linalg.blas as bla
>>> rng = np.random.default_rng()
>>> a = rng.random((10,15))
>>> b = np.asfortranarray(a)  # Change the memory layout order
>>> bla.find_best_blas_type((a,))
('d', dtype('float64'), False)
>>> bla.find_best_blas_type((a*1j,))
('z', dtype('complex128'), False)
>>> bla.find_best_blas_type((b,))
('d', dtype('float64'), True)
```

See also:

scipy.linalg.blas – Low-level BLAS functions

scipy.linalg.lapack – Low-level LAPACK functions

scipy.linalg.cython_blas – Low-level BLAS functions for Cython

scipy.linalg.cython_lapack – Low-level LAPACK functions for Cython

3.3.11 Low-level BLAS functions (`scipy.linalg.blas`)

This module contains low-level functions from the BLAS library.

New in version 0.12.0.

Note: The common `overwrite_<>` option in many routines, allows the input arrays to be overwritten to avoid extra memory allocation. However this requires the array to satisfy two conditions which are memory order and the data type to match exactly the order and the type expected by the routine.

As an example, if you pass a double precision float array to any `S....` routine which expects single precision arguments, f2py will create an intermediate array to match the argument types and overwriting will be performed on that intermediate array.

Similarly, if a C-contiguous array is passed, f2py will pass a FORTRAN-contiguous array internally. Please make sure that these details are satisfied. More information can be found in the f2py documentation.

Warning: These functions do little to no error checking. It is possible to cause crashes by mis-using them, so prefer using the higher-level routines in *scipy.linalg*.

Finding functions

get_blas_funcs(names[, arrays, dtype, ilp64])	Return available BLAS function objects from names.
find_best_blas_type([arrays, dtype])	Find best-matching BLAS/LAPACK type.

scipy.linalg.blas.get_blas_funcs

scipy.linalg.blas.**get_blas_funcs**(*names*, *arrays=()*, *dtype=None*, *ilp64=False*)

Return available BLAS function objects from names.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters

names [str or sequence of str] Name(s) of BLAS functions without type prefix.

arrays [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype [str or dtype, optional] Data-type specifier. Not used if *arrays* is non-empty.

ilp64 [{True, False, 'preferred'}, optional] Whether to return ILP64 routine variant. Choosing 'preferred' returns ILP64 routine if available, and otherwise the 32-bit routine. Default: False

Returns

funcs [list] List containing the found function(s).

Notes

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In BLAS, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the NumPy types {float32, float64, complex64, complex128} respectively. The code and the dtype are stored in attributes *typecode* and *dtype* of the returned functions.

Examples

```
>>> import scipy.linalg as LA
>>> rng = np.random.default_rng()
>>> a = rng.random((3,2))
>>> x_gemv = LA.get_blas_funcs('gemv', (a,))
>>> x_gemv.typecode
'd'
>>> x_gemv = LA.get_blas_funcs('gemv',(a*1j,))
>>> x_gemv.typecode
'z'
```

scipy.linalg.blas.find_best_blas_type

scipy.linalg.blas.**find_best_blas_type**(*arrays=()*, *dtype=None*)

Find best-matching BLAS/LAPACK type.

Arrays are used to determine the optimal prefix of BLAS routines.

Parameters

arrays [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of BLAS routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype [str or dtype, optional] Data-type specifier. Not used if *arrays* is non-empty.

Returns

prefix [str] BLAS/LAPACK prefix character.

dtype [dtype] Inferred Numpy data type.

prefer_fortran [bool] Whether to prefer Fortran order routines over C order.

Examples

```
>>> import scipy.linalg.blas as bla
>>> rng = np.random.default_rng()
>>> a = rng.random((10,15))
>>> b = np.asfortranarray(a)  # Change the memory layout order
>>> bla.find_best_blas_type((a,))
('d', dtype('float64'), False)
>>> bla.find_best_blas_type((a*1j,))
('z', dtype('complex128'), False)
>>> bla.find_best_blas_type((b,))
('d', dtype('float64'), True)
```

BLAS Level 1 functions

caxpy(x,y,[n,a,offx,incx,offy,incy])	Wrapper for caxpy.
ccopy(x,y,[n,offx,incx,offy,incy])	Wrapper for ccopy.
cdotc(x,y,[n,offx,incx,offy,incy])	Wrapper for cdotc.
cdotu(x,y,[n,offx,incx,offy,incy])	Wrapper for cdotu.
crotg(a,b)	Wrapper for crotg.
cscal(a,x,[n,offx,incx])	Wrapper for cscal.
csrot(...)	Wrapper for csrot.
csscal(a,x,[n,offx,incx,overwrite_x])	Wrapper for csscal.
cswap(x,y,[n,offx,incx,offy,incy])	Wrapper for cswap.
dasum(x,[n,offx,incx])	Wrapper for dasum.
daxpy(x,y,[n,a,offx,incx,offy,incy])	Wrapper for daxpy.
dcopy(x,y,[n,offx,incx,offy,incy])	Wrapper for dcopy.
ddot(x,y,[n,offx,incx,offy,incy])	Wrapper for ddot.
dnrm2(x,[n,offx,incx])	Wrapper for dnrm2.
drot(...)	Wrapper for drot.
drotg(a,b)	Wrapper for drotg.
drotm(...)	Wrapper for drotm.
drotmg(d1,d2,x1,y1)	Wrapper for drotmg.
dscal(a,x,[n,offx,incx])	Wrapper for dscal.
dswap(x,y,[n,offx,incx,offy,incy])	Wrapper for dswap.
dzasum(x,[n,offx,incx])	Wrapper for dzasum.
dznrm2(x,[n,offx,incx])	Wrapper for dznrm2.
icamax(x,[n,offx,incx])	Wrapper for icamax.
idamax(x,[n,offx,incx])	Wrapper for idamax.
isamax(x,[n,offx,incx])	Wrapper for isamax.
izamax(x,[n,offx,incx])	Wrapper for izamax.
sasum(x,[n,offx,incx])	Wrapper for sasum.
saxpy(x,y,[n,a,offx,incx,offy,incy])	Wrapper for saxpy.
scasum(x,[n,offx,incx])	Wrapper for scasum.
scnrm2(x,[n,offx,incx])	Wrapper for scnrm2.
scopy(x,y,[n,offx,incx,offy,incy])	Wrapper for scopy.
sdot(x,y,[n,offx,incx,offy,incy])	Wrapper for sdot.
snrm2(x,[n,offx,incx])	Wrapper for snrm2.
srot(...)	Wrapper for srot.
srotg(a,b)	Wrapper for srotg.
srotm(...)	Wrapper for srotm.
srotmg(d1,d2,x1,y1)	Wrapper for srotmg.
sscal(a,x,[n,offx,incx])	Wrapper for sscal.
sswap(x,y,[n,offx,incx,offy,incy])	Wrapper for sswap.
zaxpy(x,y,[n,a,offx,incx,offy,incy])	Wrapper for zaxpy.
zcopy(x,y,[n,offx,incx,offy,incy])	Wrapper for zcopy.
zdotc(x,y,[n,offx,incx,offy,incy])	Wrapper for zdotc.
zdotu(x,y,[n,offx,incx,offy,incy])	Wrapper for zdotu.
zdrot(...)	Wrapper for zdrot.
zdscal(a,x,[n,offx,incx,overwrite_x])	Wrapper for zdscal.
zrotg(a,b)	Wrapper for zrotg.
zscal(a,x,[n,offx,incx])	Wrapper for zscal.
zswap(x,y,[n,offx,incx,offy,incy])	Wrapper for zswap.

scipy.linalg.blas.caxpy

scipy.linalg.blas.**caxpy**(*x*, *y*[, *n*, *a*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for caxpy.

Parameters

x [input rank-1 array('F') with bounds (*)]
y [input rank-1 array('F') with bounds (*)]

Returns

z [rank-1 array('F') with bounds (*) and y storage]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
a [input complex, optional] Default: (1.0, 0.0)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.ccopy

scipy.linalg.blas.**ccopy**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for ccopy.

Parameters

x [input rank-1 array('F') with bounds (*)]
y [input rank-1 array('F') with bounds (*)]

Returns

y [rank-1 array('F') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.cdotc

scipy.linalg.blas.**cdotc**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran cdotc>**

Wrapper for cdotc.

Parameters

x [input rank-1 array('F') with bounds (*)]
y [input rank-1 array('F') with bounds (*)]

Returns

xy [complex]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.cdotu

scipy.linalg.blas.**cdotu**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran cdotu>**
Wrapper for cdotu.

Parameters

x [input rank-1 array('F') with bounds (*)]
y [input rank-1 array('F') with bounds (*)]

Returns

xy [complex]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.crotg

scipy.linalg.blas.**crotg**(*a*, *b*) **= <fortran object>**
Wrapper for crotg.

Parameters

a [input complex]
b [input complex]

Returns

c [complex]
s [complex]

scipy.linalg.blas.cscal

scipy.linalg.blas.**cscal**(*a*, *x*[, *n*, *offx*, *incx*]) **= <fortran object>**
Wrapper for cscal.

Parameters

a [input complex]
x [input rank-1 array('F') with bounds (*)]

Returns

x [rank-1 array('F') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.csrot

scipy.linalg.blas.**csrot**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for csrot.

Parameters

x [input rank-1 array('F') with bounds (*)]
y [input rank-1 array('F') with bounds (*)]
c [input float]
s [input float]

Returns

x [rank-1 array('F') with bounds (*)]
y [rank-1 array('F') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y [input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.csscal

scipy.linalg.blas.**csscal**(*a*, *x*[, *n*, *offx*, *incx*, *overwrite_x*]) **= <fortran object>**

Wrapper for csscal.

Parameters

a [input float]
x [input rank-1 array('F') with bounds (*)]

Returns

x [rank-1 array('F') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
overwrite_x [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.cswap

scipy.linalg.blas.**cswap**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for cswap.

Parameters

x	[input rank-1 array('F') with bounds (*)]
y	[input rank-1 array('F') with bounds (*)]

Returns

x	[rank-1 array('F') with bounds (*)]
y	[rank-1 array('F') with bounds (*)]

Other Parameters

n	[input int, optional] Default: (len(x)-offx)/abs(incx)
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
offy	[input int, optional] Default: 0
incy	[input int, optional] Default: 1

scipy.linalg.blas.dasum

scipy.linalg.blas.**dasum**(*x*[, *n*, *offx*, *incx*]) **= <fortran dasum>**

Wrapper for dasum.

Parameters

x	[input rank-1 array('d') with bounds (*)]

Returns

s	[float]

Other Parameters

n	[input int, optional] Default: (len(x)-offx)/abs(incx)
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1

scipy.linalg.blas.daxpy

scipy.linalg.blas.**daxpy**(*x*, *y*[, *n*, *a*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for daxpy.

Parameters

x	[input rank-1 array('d') with bounds (*)]
y	[input rank-1 array('d') with bounds (*)]

Returns

z	[rank-1 array('d') with bounds (*) and y storage]

Other Parameters

n	[input int, optional] Default: (len(x)-offx)/abs(incx)
a	[input float, optional] Default: 1.0
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
offy	[input int, optional] Default: 0
incy	[input int, optional] Default: 1

scipy.linalg.blas.dcopy

scipy.linalg.blas.**dcopy**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for dcopy.

Parameters

x	[input rank-1 array('d') with bounds (*)]
y	[input rank-1 array('d') with bounds (*)]

Returns

y	[rank-1 array('d') with bounds (*)]

Other Parameters

n	[input int, optional] Default: (len(x)-offx)/abs(incx)
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
offy	[input int, optional] Default: 0
incy	[input int, optional] Default: 1

scipy.linalg.blas.ddot

scipy.linalg.blas.**ddot**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran ddot>**

Wrapper for ddot.

Parameters

x	[input rank-1 array('d') with bounds (*)]
y	[input rank-1 array('d') with bounds (*)]

Returns

xy	[float]

Other Parameters

n	[input int, optional] Default: (len(x)-offx)/abs(incx)
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
offy	[input int, optional] Default: 0
incy	[input int, optional] Default: 1

scipy.linalg.blas.dnrm2

scipy.linalg.blas.**dnrm2**(*x*[, *n*, *offx*, *incx*]) **= <fortran dnrm2>**

Wrapper for dnrm2.

Parameters

x	[input rank-1 array('d') with bounds (*)]

Returns

n2	[float]

Other Parameters

n	[input int, optional] Default: (len(x)-offx)/abs(incx)
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1

scipy.linalg.blas.drot

scipy.linalg.blas.**drot**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for drot.

Parameters

x [input rank-1 array('d') with bounds (*)]
y [input rank-1 array('d') with bounds (*)]
c [input float]
s [input float]

Returns

x [rank-1 array('d') with bounds (*)]
y [rank-1 array('d') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y [input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.drotg

scipy.linalg.blas.**drotg**(*a*, *b*) **= <fortran object>**

Wrapper for drotg.

Parameters

a [input float]
b [input float]

Returns

c [float]
s [float]

scipy.linalg.blas.drotm

scipy.linalg.blas.**drotm**(*x*, *y*, *param*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for drotm.

Parameters

x [input rank-1 array('d') with bounds (*)]
y [input rank-1 array('d') with bounds (*)]
param [input rank-1 array('d') with bounds (5)]

Returns

x [rank-1 array('d') with bounds (*)]
y [rank-1 array('d') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
overwrite_x
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y
[input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.drotmg

scipy.linalg.blas.**drotmg**(*d1*, *d2*, *x1*, *y1*) **= <fortran object>**
Wrapper for drotmg.

Parameters

d1 [input float]
d2 [input float]
x1 [input float]
y1 [input float]

Returns

param [rank-1 array('d') with bounds (5)]

scipy.linalg.blas.dscal

scipy.linalg.blas.**dscal**(*a*, *x*[, *n*, *offx*, *incx*]) **= <fortran object>**
Wrapper for dscal.

Parameters

a [input float]
x [input rank-1 array('d') with bounds (*)]

Returns

x [rank-1 array('d') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.dswap

scipy.linalg.blas.**dswap**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**
Wrapper for dswap.

Parameters

x [input rank-1 array('d') with bounds (*)]
y [input rank-1 array('d') with bounds (*)]

Returns

x [rank-1 array('d') with bounds (*)]
y [rank-1 array('d') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.dzasum

scipy.linalg.blas.**dzasum**(*x*[, *n*, *offx*, *incx*]) **= <fortran dzasum>**

Wrapper for dzasum.

Parameters

x [input rank-1 array('D') with bounds (*)]

Returns

s [float]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.dznrm2

scipy.linalg.blas.**dznrm2**(*x*[, *n*, *offx*, *incx*]) **= <fortran dznrm2>**

Wrapper for dznrm2.

Parameters

x [input rank-1 array('D') with bounds (*)]

Returns

n2 [float]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.icamax

scipy.linalg.blas.**icamax**(*x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for icamax.

Parameters

x [input rank-1 array('F') with bounds (*)]

Returns

k [int]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.idamax

scipy.linalg.blas.**idamax**(*x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for idamax.

Parameters

x [input rank-1 array('d') with bounds (*)]

Returns

k [int]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.isamax

scipy.linalg.blas.**isamax**(*x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for isamax.

Parameters

x [input rank-1 array('f') with bounds (*)]

Returns

k [int]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.izamax

scipy.linalg.blas.**izamax**(*x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for izamax.

Parameters

x [input rank-1 array('D') with bounds (*)]

Returns

k [int]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.sasum

scipy.linalg.blas.**sasum**(*x*[, *n*, *offx*, *incx*]) **= <fortran sasum>**

Wrapper for sasum.

Parameters

x [input rank-1 array('f') with bounds (*)]

Returns

s [float]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.saxpy

scipy.linalg.blas.**saxpy**(*x*, *y*[, *n*, *a*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for saxpy.

Parameters

x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]

Returns

z [rank-1 array('f') with bounds (*) and y storage]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
a [input float, optional] Default: 1.0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.scasum

scipy.linalg.blas.**scasum**(*x*[, *n*, *offx*, *incx*]) **= <fortran scasum>**

Wrapper for scasum.

Parameters

x [input rank-1 array('F') with bounds (*)]

Returns

s [float]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.scnrm2

scipy.linalg.blas.**scnrm2**(*x*[, *n*, *offx*, *incx*]) **= <fortran scnrm2>**

Wrapper for scnrm2.

Parameters

x [input rank-1 array('F') with bounds (*)]

Returns

n2 [float]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.scopy

scipy.linalg.blas.**scopy**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for scopy.

Parameters

x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]

Returns

y [rank-1 array('f') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.sdot

scipy.linalg.blas.**sdot**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran sdot>**

Wrapper for sdot.

Parameters

x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]

Returns

xy [float]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.snrm2

scipy.linalg.blas.**snrm2**(*x*[, *n*, *offx*, *incx*]) **= <fortran snrm2>**

Wrapper for snrm2.

Parameters

x [input rank-1 array('f') with bounds (*)]

Returns

n2 [float]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.srot

scipy.linalg.blas.**srot**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for srot.

Parameters

x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]
c [input float]
s [input float]

Returns

x [rank-1 array('f') with bounds (*)]
y [rank-1 array('f') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y
[input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.srotg

scipy.linalg.blas.**srotg**(*a*, *b*) **= <fortran object>**

Wrapper for srotg.

Parameters

a [input float]
b [input float]

Returns

c [float]
s [float]

scipy.linalg.blas.srotm

scipy.linalg.blas.**srotm**(*x*, *y*, *param*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) = **<fortran object>**

Wrapper for `srotm`.

Parameters

x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]
param [input rank-1 array('f') with bounds (5)]

Returns

x [rank-1 array('f') with bounds (*)]
y [rank-1 array('f') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
overwrite_x [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y [input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.srotmg

scipy.linalg.blas.**srotmg**(*d1*, *d2*, *x1*, *y1*) = **<fortran object>**

Wrapper for `srotmg`.

Parameters

d1 [input float]
d2 [input float]
x1 [input float]
y1 [input float]

Returns

param [rank-1 array('f') with bounds (5)]

scipy.linalg.blas.sscal

scipy.linalg.blas.**sscal**(*a*, *x*[, *n*, *offx*, *incx*]) = **<fortran object>**

Wrapper for `sscal`.

Parameters

a [input float]
x [input rank-1 array('f') with bounds (*)]

Returns

x [rank-1 array('f') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0

incx [input int, optional] Default: 1

scipy.linalg.blas.sswap

scipy.linalg.blas.**sswap**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for sswap.

Parameters

x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]

Returns

x [rank-1 array('f') with bounds (*)]
y [rank-1 array('f') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.zaxpy

scipy.linalg.blas.**zaxpy**(*x*, *y*[, *n*, *a*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for zaxpy.

Parameters

x [input rank-1 array('D') with bounds (*)]
y [input rank-1 array('D') with bounds (*)]

Returns

z [rank-1 array('D') with bounds (*) and y storage]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
a [input complex, optional] Default: (1.0, 0.0)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.zcopy

scipy.linalg.blas.**zcopy**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for zcopy.

Parameters

x [input rank-1 array('D') with bounds (*)]
y [input rank-1 array('D') with bounds (*)]

Returns

y [rank-1 array('D') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.zdotc

scipy.linalg.blas.**zdotc**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran zdotc>**

Wrapper for zdotc.

Parameters

x [input rank-1 array('D') with bounds (*)]
y [input rank-1 array('D') with bounds (*)]

Returns

xy [complex]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.zdotu

scipy.linalg.blas.**zdotu**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran zdotu>**

Wrapper for zdotu.

Parameters

x [input rank-1 array('D') with bounds (*)]
y [input rank-1 array('D') with bounds (*)]

Returns

xy [complex]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.zdrot

scipy.linalg.blas.**zdrot**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) **= <fortran object>**

Wrapper for zdrot.

Parameters

x [input rank-1 array('D') with bounds (*)]
y [input rank-1 array('D') with bounds (*)]
c [input float]
s [input float]

Returns

x [rank-1 array('D') with bounds (*)]
y [rank-1 array('D') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
overwrite_x
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y
[input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.blas.zdscal

scipy.linalg.blas.**zdscal**(*a*, *x*[, *n*, *offx*, *incx*, *overwrite_x*]) **= <fortran object>**
Wrapper for zdscal.

Parameters

a [input float]
x [input rank-1 array('D') with bounds (*)]

Returns

x [rank-1 array('D') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
overwrite_x
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.zrotg

scipy.linalg.blas.**zrotg**(*a*, *b*) **= <fortran object>**
Wrapper for zrotg.

Parameters

a [input complex]
b [input complex]

Returns

c [complex]
s [complex]

scipy.linalg.blas.zscal

scipy.linalg.blas.**zscal**(*a*, *x*[, *n*, *offx*, *incx*]) **= <fortran object>**

Wrapper for zscal.

Parameters

a [input complex]
x [input rank-1 array('D') with bounds (*)]

Returns

x [rank-1 array('D') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.blas.zswap

scipy.linalg.blas.**zswap**(*x*, *y*[, *n*, *offx*, *incx*, *offy*, *incy*]) **= <fortran object>**

Wrapper for zswap.

Parameters

x [input rank-1 array('D') with bounds (*)]
y [input rank-1 array('D') with bounds (*)]

Returns

x [rank-1 array('D') with bounds (*)]
y [rank-1 array('D') with bounds (*)]

Other Parameters

n [input int, optional] Default: (len(x)-offx)/abs(incx)
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

BLAS Level 2 functions

sgbmv(...)	Wrapper for sgbmv.
sgemv(...)	Wrapper for sgemv.
sger(...)	Wrapper for sger.
ssbmv(...)	Wrapper for ssbmv.
sspr(n,alpha,x,ap,[incx,offx,lower,overwrite_ap])	Wrapper for sspr.
sspr2(...)	Wrapper for sspr2.
ssymv(...)	Wrapper for ssymv.
ssyr(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for ssyr.
ssyr2(...)	Wrapper for ssyr2.
stbmv(...)	Wrapper for stbmv.
stpsv(...)	Wrapper for stpsv.
strmv(...)	Wrapper for strmv.
strsv(...)	Wrapper for strsv.

continues on next page

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dgbmv(...)	Wrapper for dgbmv.
dgemv(...)	Wrapper for dgemv.
dger(...)	Wrapper for dger.
dsbmv(...)	Wrapper for dsbmv.
dspr(n,alpha,x,ap,[incx,offx,lower,overwrite_ap])	Wrapper for dspr.
dspr2(...)	Wrapper for dspr2.
dsymv(...)	Wrapper for dsymv.
dsyr(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for dsyr.
dsyr2(...)	Wrapper for dsyr2.
dtbmv(...)	Wrapper for dtbmv.
dtpsv(...)	Wrapper for dtpsv.
dtrmv(...)	Wrapper for dtrmv.
dtrsv(...)	Wrapper for dtrsv.
cgbmv(...)	Wrapper for cgbmv.
cgemv(...)	Wrapper for cgemv.
cgerc(...)	Wrapper for cgerc.
cgeru(...)	Wrapper for cgeru.
chbmv(...)	Wrapper for chbmv.
chemv(...)	Wrapper for chemv.
cher(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for cher.
cher2(...)	Wrapper for cher2.
chpmv(...)	Wrapper for chpmv.
chpr(n,alpha,x,ap,[incx,offx,lower,overwrite_ap])	Wrapper for chpr.
chpr2(...)	Wrapper for chpr2.
ctbmv(...)	Wrapper for ctbmv.
ctbsv(...)	Wrapper for ctbsv.
ctpmv(...)	Wrapper for ctpmv.
ctpsv(...)	Wrapper for ctpsv.
ctrmv(...)	Wrapper for ctrmv.
ctrsv(...)	Wrapper for ctrsv.
csyr(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for csyr.
zgbmv(...)	Wrapper for zgbmv.
zgemv(...)	Wrapper for zgemv.
zgerc(...)	Wrapper for zgerc.
zgeru(...)	Wrapper for zgeru.
zhbmv(...)	Wrapper for zhbmv.
zhemv(...)	Wrapper for zhemv.
zher(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for zher.
zher2(...)	Wrapper for zher2.
zhpmv(...)	Wrapper for zhpmv.
zhpr(n,alpha,x,ap,[incx,offx,lower,overwrite_ap])	Wrapper for zhpr.
zhpr2(...)	Wrapper for zhpr2.
ztbmv(...)	Wrapper for ztbmv.
ztbsv(...)	Wrapper for ztbsv.
ztpmv(...)	Wrapper for ztpmv.
ztrmv(...)	Wrapper for ztrmv.
ztrsv(...)	Wrapper for ztrsv.
zsyr(alpha,x,[lower,incx,offx,n,a,overwrite_a])	Wrapper for zsyr.

scipy.linalg.blas.sgbmv

scipy.linalg.blas.**sgbmv**(*m*, *n*, *kl*, *ku*, *alpha*, *a*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *trans*, *overwrite_y*])
= <fortran object>

Wrapper for sgbmv.

Parameters

m [input int]
n [input int]
kl [input int]
ku [input int]
alpha [input float]
a [input rank-2 array('f') with bounds (lda,n)]
x [input rank-1 array('f') with bounds (*)]

Returns

yout [rank-1 array('f') with bounds (ly) and y storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input float, optional] Default: 0.0
y [input rank-1 array('f') with bounds (ly)]
overwrite_y
[input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
trans [input int, optional] Default: 0

scipy.linalg.blas.sgemv

scipy.linalg.blas.**sgemv**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *trans*, *overwrite_y*]) **=**
<fortran object>

Wrapper for sgemv.

Parameters

alpha [input float]
a [input rank-2 array('f') with bounds (m,n)]
x [input rank-1 array('f') with bounds (*)]

Returns

y [rank-1 array('f') with bounds (ly)]

Other Parameters

beta [input float, optional] Default: 0.0
y [input rank-1 array('f') with bounds (ly)]
overwrite_y
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1
trans [input int, optional] Default: 0

scipy.linalg.blas.sger

scipy.linalg.blas.**sger**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) = **<fortran object>**

Wrapper for `sger`.

Parameters

alpha [input float]
x [input rank-1 array('f') with bounds (m)]
y [input rank-1 array('f') with bounds (n)]

Returns

a [rank-2 array('f') with bounds (m,n)]

Other Parameters

overwrite_x
[input int, optional] Default: 1
incx [input int, optional] Default: 1
overwrite_y
[input int, optional] Default: 1
incy [input int, optional] Default: 1
a [input rank-2 array('f') with bounds (m,n), optional] Default: 0.0
overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.ssbmv

scipy.linalg.blas.**ssbmv**(*k*, *alpha*, *a*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for `ssbmv`.

Parameters

k [input int]
alpha [input float]
a [input rank-2 array('f') with bounds (lda,n)]
x [input rank-1 array('f') with bounds (*)]

Returns

yout [rank-1 array('f') with bounds (ly) and y storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input float, optional] Default: 0.0
y [input rank-1 array('f') with bounds (ly)]
overwrite_y
[input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.sspr

scipy.linalg.blas.**sspr**(*n*, *alpha*, *x*, *ap*[, *incx*, *offx*, *lower*, *overwrite_ap*]) **= <fortran object>**

Wrapper for sspr.

Parameters

n	[input int]
alpha	[input float]
x	[input rank-1 array('f') with bounds (*)]
ap	[input rank-1 array('f') with bounds (*)]

Returns

apu	[rank-1 array('f') with bounds (*) and ap storage]

Other Parameters

incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
overwrite_ap	[input int, optional] Default: 0
lower	[input int, optional] Default: 0

scipy.linalg.blas.sspr2

scipy.linalg.blas.**sspr2**(*n*, *alpha*, *x*, *y*, *ap*[, *incx*, *offx*, *incy*, *offy*, *lower*, *overwrite_ap*]) **= <fortran object>**

Wrapper for sspr2.

Parameters

n	[input int]
alpha	[input float]
x	[input rank-1 array('f') with bounds (*)]
y	[input rank-1 array('f') with bounds (*)]
ap	[input rank-1 array('f') with bounds (*)]

Returns

apu	[rank-1 array('f') with bounds (*) and ap storage]

Other Parameters

incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
incy	[input int, optional] Default: 1
offy	[input int, optional] Default: 0
overwrite_ap	[input int, optional] Default: 0
lower	[input int, optional] Default: 0

scipy.linalg.blas.ssymv

scipy.linalg.blas.**ssymv**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for ssymv.

Parameters

alpha [input float]
a [input rank-2 array('f') with bounds (n,n)]
x [input rank-1 array('f') with bounds (*)]

Returns

y [rank-1 array('f') with bounds (ly)]

Other Parameters

beta [input float, optional] Default: 0.0
y [input rank-1 array('f') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.blas.ssyr

scipy.linalg.blas.**ssyr**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) = **<fortran object>**

Wrapper for ssyr.

Parameters

alpha [input float]
x [input rank-1 array('f') with bounds (*)]

Returns

a [rank-2 array('f') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
a [input rank-2 array('f') with bounds (n,n)]
overwrite_a [input int, optional] Default: 0

scipy.linalg.blas.ssyr2

scipy.linalg.blas.**ssyr2**(*alpha*, *x*, *y*[, *lower*, *incx*, *offx*, *incy*, *offy*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for ssyr2.

Parameters

alpha [input float]
x [input rank-1 array('f') with bounds (*)]
y [input rank-1 array('f') with bounds (*)]

Returns

a [rank-2 array('f') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
n [input int, optional] Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)
a [input rank-2 array('f') with bounds (n,n)]
overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.stbmv

scipy.linalg.blas.**stbmv**(*k*, *a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for stbmv.

Parameters

k [input int]
a [input rank-2 array('f') with bounds (lda,n)]
x [input rank-1 array('f') with bounds (*)]

Returns

xout [rank-1 array('f') with bounds (*) and x storage]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.stpsv

scipy.linalg.blas.**stpsv**(*n*, *ap*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for stpsv.

Parameters

n	[input int]
ap	[input rank-1 array('f') with bounds (*)]
x	[input rank-1 array('f') with bounds (*)]

Returns

xout	[rank-1 array('f') with bounds (*) and x storage]

Other Parameters

overwrite_x	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
lower	[input int, optional] Default: 0
trans	[input int, optional] Default: 0
diag	[input int, optional] Default: 0

scipy.linalg.blas.strmv

scipy.linalg.blas.**strmv**(*a*, *x*[, *offx*, *incx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for strmv.

Parameters

a	[input rank-2 array('f') with bounds (n,n)]
x	[input rank-1 array('f') with bounds (*)]

Returns

x	[rank-1 array('f') with bounds (*)]

Other Parameters

overwrite_x	[input int, optional] Default: 0
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
lower	[input int, optional] Default: 0
trans	[input int, optional] Default: 0
diag	[input int, optional] Default: 0

scipy.linalg.blas.strsv

scipy.linalg.blas.**strsv**(*a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for strsv.

Parameters

a	[input rank-2 array('f') with bounds (n,n)]
x	[input rank-1 array('f') with bounds (*)]

Returns

xout	[rank-1 array('f') with bounds (*) and x storage]

Other Parameters

overwrite_x
: [input int, optional] Default: 0

incx
: [input int, optional] Default: 1

offx
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

trans
: [input int, optional] Default: 0

diag
: [input int, optional] Default: 0

scipy.linalg.blas.dgbmv

scipy.linalg.blas.**dgbmv**(*m*, *n*, *kl*, *ku*, *alpha*, *a*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *trans*, *overwrite_y*])
= <fortran object>

Wrapper for dgbmv.

Parameters

m
: [input int]

n
: [input int]

kl
: [input int]

ku
: [input int]

alpha
: [input float]

a
: [input rank-2 array('d') with bounds (lda,n)]

x
: [input rank-1 array('d') with bounds (*)]

Returns

yout
: [rank-1 array('d') with bounds (ly) and y storage]

Other Parameters

incx
: [input int, optional] Default: 1

offx
: [input int, optional] Default: 0

beta
: [input float, optional] Default: 0.0

y
: [input rank-1 array('d') with bounds (ly)]

overwrite_y
: [input int, optional] Default: 0

incy
: [input int, optional] Default: 1

offy
: [input int, optional] Default: 0

trans
: [input int, optional] Default: 0

scipy.linalg.blas.dgemv

scipy.linalg.blas.**dgemv**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *trans*, *overwrite_y*]) **=**
<fortran object>

Wrapper for dgemv.

Parameters

alpha
: [input float]

a
: [input rank-2 array('d') with bounds (m,n)]

x
: [input rank-1 array('d') with bounds (*)]

Returns

y
: [rank-1 array('d') with bounds (ly)]

Other Parameters

beta
: [input float, optional] Default: 0.0

y
: [input rank-1 array('d') with bounds (ly)]

overwrite_y
: [input int, optional] Default: 0

offx
: [input int, optional] Default: 0

incx
: [input int, optional] Default: 1

offy
: [input int, optional] Default: 0

incy
: [input int, optional] Default: 1

trans
: [input int, optional] Default: 0

scipy.linalg.blas.dger

scipy.linalg.blas.**dger**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) = **<fortran object>**

Wrapper for `dger`.

Parameters

alpha
: [input float]

x
: [input rank-1 array('d') with bounds (m)]

y
: [input rank-1 array('d') with bounds (n)]

Returns

a
: [rank-2 array('d') with bounds (m,n)]

Other Parameters

overwrite_x
: [input int, optional] Default: 1

incx
: [input int, optional] Default: 1

overwrite_y
: [input int, optional] Default: 1

incy
: [input int, optional] Default: 1

a
: [input rank-2 array('d') with bounds (m,n), optional] Default: 0.0

overwrite_a
: [input int, optional] Default: 0

scipy.linalg.blas.dsbmv

scipy.linalg.blas.**dsbmv**(*k*, *alpha*, *a*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for `dsbmv`.

Parameters

k
: [input int]

alpha
: [input float]

a
: [input rank-2 array('d') with bounds (lda,n)]

x
: [input rank-1 array('d') with bounds (*)]

Returns

yout
: [rank-1 array('d') with bounds (ly) and y storage]

Other Parameters

incx
: [input int, optional] Default: 1

offx
: [input int, optional] Default: 0

beta
: [input float, optional] Default: 0.0

y
: [input rank-1 array('d') with bounds (ly)]

overwrite_y
: [input int, optional] Default: 0

incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.dspr

scipy.linalg.blas.**dspr**(*n*, *alpha*, *x*, *ap*[, *incx*, *offx*, *lower*, *overwrite_ap*]) **= <fortran object>**

Wrapper for dspr.

Parameters

n [input int]
alpha [input float]
x [input rank-1 array('d') with bounds (*)]
ap [input rank-1 array('d') with bounds (*)]

Returns

apu [rank-1 array('d') with bounds (*) and ap storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
overwrite_ap
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.dspr2

scipy.linalg.blas.**dspr2**(*n*, *alpha*, *x*, *y*, *ap*[, *incx*, *offx*, *incy*, *offy*, *lower*, *overwrite_ap*]) **= <fortran object>**

Wrapper for dspr2.

Parameters

n [input int]
alpha [input float]
x [input rank-1 array('d') with bounds (*)]
y [input rank-1 array('d') with bounds (*)]
ap [input rank-1 array('d') with bounds (*)]

Returns

apu [rank-1 array('d') with bounds (*) and ap storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
overwrite_ap
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.dsymv

scipy.linalg.blas.**dsymv**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for dsymv.

Parameters

alpha [input float]
a [input rank-2 array('d') with bounds (n,n)]
x [input rank-1 array('d') with bounds (*)]

Returns

y [rank-1 array('d') with bounds (ly)]

Other Parameters

beta [input float, optional] Default: 0.0
y [input rank-1 array('d') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.blas.dsyr

scipy.linalg.blas.**dsyr**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) = **<fortran object>**

Wrapper for dsyr.

Parameters

alpha [input float]
x [input rank-1 array('d') with bounds (*)]

Returns

a [rank-2 array('d') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
a [input rank-2 array('d') with bounds (n,n)]
overwrite_a [input int, optional] Default: 0

scipy.linalg.blas.dsyr2

scipy.linalg.blas.**dsyr2**(*alpha*, *x*, *y*[, *lower*, *incx*, *offx*, *incy*, *offy*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for dsyr2.

Parameters

alpha [input float]
x [input rank-1 array('d') with bounds (*)]
y [input rank-1 array('d') with bounds (*)]

Returns

a [rank-2 array('d') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
n [input int, optional] Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)
a [input rank-2 array('d') with bounds (n,n)]
overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.dtbmv

scipy.linalg.blas.**dtbmv**(*k*, *a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for dtbmv.

Parameters

k [input int]
a [input rank-2 array('d') with bounds (lda,n)]
x [input rank-1 array('d') with bounds (*)]

Returns

xout [rank-1 array('d') with bounds (*) and x storage]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.dtpsv

scipy.linalg.blas.**dtpsv**(*n*, *ap*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for dtpsv.

Parameters

n	[input int]
ap	[input rank-1 array('d') with bounds (*)]
x	[input rank-1 array('d') with bounds (*)]

Returns

xout	[rank-1 array('d') with bounds (*) and x storage]

Other Parameters

overwrite_x	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
lower	[input int, optional] Default: 0
trans	[input int, optional] Default: 0
diag	[input int, optional] Default: 0

scipy.linalg.blas.dtrmv

scipy.linalg.blas.**dtrmv**(*a*, *x*[, *offx*, *incx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for dtrmv.

Parameters

a	[input rank-2 array('d') with bounds (n,n)]
x	[input rank-1 array('d') with bounds (*)]

Returns

x	[rank-1 array('d') with bounds (*)]

Other Parameters

overwrite_x	[input int, optional] Default: 0
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
lower	[input int, optional] Default: 0
trans	[input int, optional] Default: 0
diag	[input int, optional] Default: 0

scipy.linalg.blas.dtrsv

scipy.linalg.blas.**dtrsv**(*a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for dtrsv.

Parameters

a	[input rank-2 array('d') with bounds (n,n)]
x	[input rank-1 array('d') with bounds (*)]

Returns

xout	[rank-1 array('d') with bounds (*) and x storage]

Other Parameters

overwrite_x
: [input int, optional] Default: 0

incx
: [input int, optional] Default: 1

offx
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

trans
: [input int, optional] Default: 0

diag
: [input int, optional] Default: 0

scipy.linalg.blas.cgbmv

scipy.linalg.blas.**cgbmv**(*m*, *n*, *kl*, *ku*, *alpha*, *a*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *trans*, *overwrite_y*]) **= <fortran object>**

Wrapper for cgbmv.

Parameters

m
: [input int]

n
: [input int]

kl
: [input int]

ku
: [input int]

alpha
: [input complex]

a
: [input rank-2 array('F') with bounds (lda,n)]

x
: [input rank-1 array('F') with bounds (*)]

Returns

yout
: [rank-1 array('F') with bounds (ly) and y storage]

Other Parameters

incx
: [input int, optional] Default: 1

offx
: [input int, optional] Default: 0

beta
: [input complex, optional] Default: (0.0, 0.0)

y
: [input rank-1 array('F') with bounds (ly)]

overwrite_y
: [input int, optional] Default: 0

incy
: [input int, optional] Default: 1

offy
: [input int, optional] Default: 0

trans
: [input int, optional] Default: 0

scipy.linalg.blas.cgemv

scipy.linalg.blas.**cgemv**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *trans*, *overwrite_y*]) **= <fortran object>**

Wrapper for cgemv.

Parameters

alpha
: [input complex]

a
: [input rank-2 array('F') with bounds (m,n)]

x
: [input rank-1 array('F') with bounds (*)]

Returns

y
: [rank-1 array('F') with bounds (ly)]

Other Parameters

beta
: [input complex, optional] Default: (0.0, 0.0)

y
: [input rank-1 array('F') with bounds (ly)]

overwrite_y
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1
trans [input int, optional] Default: 0

scipy.linalg.blas.cgerc

scipy.linalg.blas.**cgerc**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) = **<fortran object>**

Wrapper for cgerc.

Parameters

alpha [input complex]
x [input rank-1 array('F') with bounds (m)]
y [input rank-1 array('F') with bounds (n)]

Returns

a [rank-2 array('F') with bounds (m,n)]

Other Parameters

overwrite_x
[input int, optional] Default: 1
incx [input int, optional] Default: 1
overwrite_y
[input int, optional] Default: 1
incy [input int, optional] Default: 1
a [input rank-2 array('F') with bounds (m,n), optional] Default: (0.0,0.0)
overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.cgeru

scipy.linalg.blas.**cgeru**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) = **<fortran object>**

Wrapper for cgeru.

Parameters

alpha [input complex]
x [input rank-1 array('F') with bounds (m)]
y [input rank-1 array('F') with bounds (n)]

Returns

a [rank-2 array('F') with bounds (m,n)]

Other Parameters

overwrite_x
[input int, optional] Default: 1
incx [input int, optional] Default: 1
overwrite_y
[input int, optional] Default: 1
incy [input int, optional] Default: 1
a [input rank-2 array('F') with bounds (m,n), optional] Default: (0.0,0.0)

overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.chbmv

scipy.linalg.blas.**chbmv**(*k*, *alpha*, *a*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for chbmv.

Parameters

k [input int]
alpha [input complex]
a [input rank-2 array('F') with bounds (lda,n)]
x [input rank-1 array('F') with bounds (*)]

Returns

yout [rank-1 array('F') with bounds (ly) and y storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array('F') with bounds (ly)]
overwrite_y
[input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.chemv

scipy.linalg.blas.**chemv**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for chemv.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (n,n)]
x [input rank-1 array('F') with bounds (*)]

Returns

y [rank-1 array('F') with bounds (ly)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array('F') with bounds (ly)]
overwrite_y
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.blas.cher

scipy.linalg.blas.**cher**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for cher.

Parameters

alpha [input complex]
x [input rank-1 array('F') with bounds (*)]

Returns

a [rank-2 array('F') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
a [input rank-2 array('F') with bounds (n,n)]
overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.cher2

scipy.linalg.blas.**cher2**(*alpha*, *x*, *y*[, *lower*, *incx*, *offx*, *incy*, *offy*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for cher2.

Parameters

alpha [input complex]
x [input rank-1 array('F') with bounds (*)]
y [input rank-1 array('F') with bounds (*)]

Returns

a [rank-2 array('F') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
n [input int, optional] Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)
a [input rank-2 array('F') with bounds (n,n)]
overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.chpmv

scipy.linalg.blas.**chpmv**(*n*, *alpha*, *ap*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for chpmv.

Parameters

n	[input int]
alpha	[input complex]
ap	[input rank-1 array('F') with bounds (*)]
x	[input rank-1 array('F') with bounds (*)]

Returns

yout	[rank-1 array('F') with bounds (ly) and y storage]

Other Parameters

incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
beta	[input complex, optional] Default: (0.0, 0.0)
y	[input rank-1 array('F') with bounds (ly)]
overwrite_y	[input int, optional] Default: 0
incy	[input int, optional] Default: 1
offy	[input int, optional] Default: 0
lower	[input int, optional] Default: 0

scipy.linalg.blas.chpr

scipy.linalg.blas.**chpr**(*n*, *alpha*, *x*, *ap*[, *incx*, *offx*, *lower*, *overwrite_ap*]) = **<fortran object>**

Wrapper for chpr.

Parameters

n	[input int]
alpha	[input float]
x	[input rank-1 array('F') with bounds (*)]
ap	[input rank-1 array('F') with bounds (*)]

Returns

apu	[rank-1 array('F') with bounds (*) and ap storage]

Other Parameters

incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
overwrite_ap	[input int, optional] Default: 0
lower	[input int, optional] Default: 0

scipy.linalg.blas.chpr2

scipy.linalg.blas.**chpr2**(*n*, *alpha*, *x*, *y*, *ap*[, *incx*, *offx*, *incy*, *offy*, *lower*, *overwrite_ap*]) = **<fortran object>**

Wrapper for chpr2.

Parameters

n [input int]
alpha [input complex]
x [input rank-1 array('F') with bounds (*)]
y [input rank-1 array('F') with bounds (*)]
ap [input rank-1 array('F') with bounds (*)]

Returns

apu [rank-1 array('F') with bounds (*) and ap storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
overwrite_ap [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.ctbmv

scipy.linalg.blas.**ctbmv**(*k*, *a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) = **<fortran object>**

Wrapper for ctbmv.

Parameters

k [input int]
a [input rank-2 array('F') with bounds (lda,n)]
x [input rank-1 array('F') with bounds (*)]

Returns

xout [rank-1 array('F') with bounds (*) and x storage]

Other Parameters

overwrite_x [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ctbsv

scipy.linalg.blas.**ctbsv**(*k*, *a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ctbsv.

Parameters

k [input int]
a [input rank-2 array('F') with bounds (lda,n)]
x [input rank-1 array('F') with bounds (*)]

Returns

xout [rank-1 array('F') with bounds (*) and x storage]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ctpmv

scipy.linalg.blas.**ctpmv**(*n*, *ap*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ctpmv.

Parameters

n [input int]
ap [input rank-1 array('F') with bounds (*)]
x [input rank-1 array('F') with bounds (*)]

Returns

xout [rank-1 array('F') with bounds (*) and x storage]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ctpsv

scipy.linalg.blas.**ctpsv**(*n*, *ap*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ctpsv.

Parameters

n	[input int]
ap	[input rank-1 array('F') with bounds (*)]
x	[input rank-1 array('F') with bounds (*)]

Returns

xout	[rank-1 array('F') with bounds (*) and x storage]

Other Parameters

overwrite_x	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
lower	[input int, optional] Default: 0
trans	[input int, optional] Default: 0
diag	[input int, optional] Default: 0

scipy.linalg.blas.ctrmv

scipy.linalg.blas.**ctrmv**(*a*, *x*[, *offx*, *incx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ctrmv.

Parameters

a	[input rank-2 array('F') with bounds (n,n)]
x	[input rank-1 array('F') with bounds (*)]

Returns

x	[rank-1 array('F') with bounds (*)]

Other Parameters

overwrite_x	[input int, optional] Default: 0
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
lower	[input int, optional] Default: 0
trans	[input int, optional] Default: 0
diag	[input int, optional] Default: 0

scipy.linalg.blas.ctrsv

scipy.linalg.blas.**ctrsv**(*a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ctrsv.

Parameters

a	[input rank-2 array('F') with bounds (n,n)]
x	[input rank-1 array('F') with bounds (*)]

Returns

xout	[rank-1 array('F') with bounds (*) and x storage]

Other Parameters

overwrite_x
: [input int, optional] Default: 0

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.csyr

scipy.linalg.blas.**csyr**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for csyr.

Parameters

alpha [input complex]
x [input rank-1 array('F') with bounds (*)]

Returns

a [rank-2 array('F') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
a [input rank-2 array('F') with bounds (n,n)]
overwrite_a
: [input int, optional] Default: 0

scipy.linalg.blas.zgbmv

scipy.linalg.blas.**zgbmv**(*m*, *n*, *kl*, *ku*, *alpha*, *a*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *trans*, *overwrite_y*]) **= <fortran object>**

Wrapper for zgbmv.

Parameters

m [input int]
n [input int]
kl [input int]
ku [input int]
alpha [input complex]
a [input rank-2 array('D') with bounds (lda,n)]
x [input rank-1 array('D') with bounds (*)]

Returns

yout [rank-1 array('D') with bounds (ly) and y storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array('D') with bounds (ly)]

overwrite_y
: [input int, optional] Default: 0

incy [input int, optional] Default: 1

offy [input int, optional] Default: 0

trans [input int, optional] Default: 0

scipy.linalg.blas.zgemv

scipy.linalg.blas.**zgemv**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *trans*, *overwrite_y*]) = **<fortran object>**

Wrapper for zgemv.

Parameters

alpha [input complex]

a [input rank-2 array('D') with bounds (m,n)]

x [input rank-1 array('D') with bounds (*)]

Returns

y [rank-1 array('D') with bounds (ly)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)

y [input rank-1 array('D') with bounds (ly)]

overwrite_y
: [input int, optional] Default: 0

offx [input int, optional] Default: 0

incx [input int, optional] Default: 1

offy [input int, optional] Default: 0

incy [input int, optional] Default: 1

trans [input int, optional] Default: 0

scipy.linalg.blas.zgerc

scipy.linalg.blas.**zgerc**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) = **<fortran object>**

Wrapper for zgerc.

Parameters

alpha [input complex]

x [input rank-1 array('D') with bounds (m)]

y [input rank-1 array('D') with bounds (n)]

Returns

a [rank-2 array('D') with bounds (m,n)]

Other Parameters

overwrite_x
: [input int, optional] Default: 1

incx [input int, optional] Default: 1

overwrite_y
: [input int, optional] Default: 1

incy [input int, optional] Default: 1

a [input rank-2 array('D') with bounds (m,n), optional] Default: (0.0,0.0)

overwrite_a
: [input int, optional] Default: 0

scipy.linalg.blas.zgeru

scipy.linalg.blas.**zgeru**(*alpha*, *x*, *y*[, *incx*, *incy*, *a*, *overwrite_x*, *overwrite_y*, *overwrite_a*]) = **<fortran object>**

Wrapper for zgeru.

Parameters

alpha [input complex]
x [input rank-1 array('D') with bounds (m)]
y [input rank-1 array('D') with bounds (n)]

Returns

a [rank-2 array('D') with bounds (m,n)]

Other Parameters

overwrite_x
[input int, optional] Default: 1
incx [input int, optional] Default: 1
overwrite_y
[input int, optional] Default: 1
incy [input int, optional] Default: 1
a [input rank-2 array('D') with bounds (m,n), optional] Default: (0.0,0.0)
overwrite_a
[input int, optional] Default: 0

scipy.linalg.blas.zhbmv

scipy.linalg.blas.**zhbmv**(*k*, *alpha*, *a*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for zhbmv.

Parameters

k [input int]
alpha [input complex]
a [input rank-2 array('D') with bounds (lda,n)]
x [input rank-1 array('D') with bounds (*)]

Returns

yout [rank-1 array('D') with bounds (ly) and y storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array('D') with bounds (ly)]
overwrite_y
[input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zhemv

scipy.linalg.blas.**zhemv**(*alpha*, *a*, *x*[, *beta*, *y*, *offx*, *incx*, *offy*, *incy*, *lower*, *overwrite_y*]) = **<fortran object>**

Wrapper for zhemv.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (n,n)]
x [input rank-1 array('D') with bounds (*)]

Returns

y [rank-1 array('D') with bounds (ly)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array('D') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.blas.zher

scipy.linalg.blas.**zher**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) = **<fortran object>**

Wrapper for zher.

Parameters

alpha [input complex]
x [input rank-1 array('D') with bounds (*)]

Returns

a [rank-2 array('D') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1
a [input rank-2 array('D') with bounds (n,n)]
overwrite_a [input int, optional] Default: 0

scipy.linalg.blas.zher2

scipy.linalg.blas.**zher2**(*alpha*, *x*, *y*[, *lower*, *incx*, *offx*, *incy*, *offy*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for zher2.

Parameters

alpha [input complex]
x [input rank-1 array('D') with bounds (*)]
y [input rank-1 array('D') with bounds (*)]

Returns

a [rank-2 array('D') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
n [input int, optional] Default: ((len(x)-1-offx)/abs(incx)+1 <=(len(y)-1-offy)/abs(incy)+1 ?(len(x)-1-offx)/abs(incx)+1 :(len(y)-1-offy)/abs(incy)+1)
a [input rank-2 array('D') with bounds (n,n)]
overwrite_a [input int, optional] Default: 0

scipy.linalg.blas.zhpmv

scipy.linalg.blas.**zhpmv**(*n*, *alpha*, *ap*, *x*[, *incx*, *offx*, *beta*, *y*, *incy*, *offy*, *lower*, *overwrite_y*]) **= <fortran object>**

Wrapper for zhpmv.

Parameters

n [input int]
alpha [input complex]
ap [input rank-1 array('D') with bounds (*)]
x [input rank-1 array('D') with bounds (*)]

Returns

yout [rank-1 array('D') with bounds (ly) and y storage]

Other Parameters

incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
beta [input complex, optional] Default: (0.0, 0.0)
y [input rank-1 array('D') with bounds (ly)]
overwrite_y [input int, optional] Default: 0
incy [input int, optional] Default: 1
offy [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zhpr

scipy.linalg.blas.**zhpr**(*n*, *alpha*, *x*, *ap*[, *incx*, *offx*, *lower*, *overwrite_ap*]) **= <fortran object>**

Wrapper for zhpr.

Parameters

n	[input int]
alpha	[input float]
x	[input rank-1 array('D') with bounds (*)]
ap	[input rank-1 array('D') with bounds (*)]

Returns

apu	[rank-1 array('D') with bounds (*) and ap storage]

Other Parameters

incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
overwrite_ap	[input int, optional] Default: 0
lower	[input int, optional] Default: 0

scipy.linalg.blas.zhpr2

scipy.linalg.blas.**zhpr2**(*n*, *alpha*, *x*, *y*, *ap*[, *incx*, *offx*, *incy*, *offy*, *lower*, *overwrite_ap*]) **= <fortran object>**

Wrapper for zhpr2.

Parameters

n	[input int]
alpha	[input complex]
x	[input rank-1 array('D') with bounds (*)]
y	[input rank-1 array('D') with bounds (*)]
ap	[input rank-1 array('D') with bounds (*)]

Returns

apu	[rank-1 array('D') with bounds (*) and ap storage]

Other Parameters

incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
incy	[input int, optional] Default: 1
offy	[input int, optional] Default: 0
overwrite_ap	[input int, optional] Default: 0
lower	[input int, optional] Default: 0

scipy.linalg.blas.ztbmv

scipy.linalg.blas.**ztbmv**(*k*, *a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ztbmv.

Parameters

k [input int]
a [input rank-2 array('D') with bounds (lda,n)]
x [input rank-1 array('D') with bounds (*)]

Returns

xout [rank-1 array('D') with bounds (*) and x storage]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ztbsv

scipy.linalg.blas.**ztbsv**(*k*, *a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ztbsv.

Parameters

k [input int]
a [input rank-2 array('D') with bounds (lda,n)]
x [input rank-1 array('D') with bounds (*)]

Returns

xout [rank-1 array('D') with bounds (*) and x storage]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1
offx [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ztpmv

scipy.linalg.blas.**ztpmv**(*n*, *ap*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ztpmv.

Parameters

n	[input int]
ap	[input rank-1 array('D') with bounds (*)]
x	[input rank-1 array('D') with bounds (*)]

Returns

xout	[rank-1 array('D') with bounds (*) and x storage]

Other Parameters

overwrite_x	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
offx	[input int, optional] Default: 0
lower	[input int, optional] Default: 0
trans	[input int, optional] Default: 0
diag	[input int, optional] Default: 0

scipy.linalg.blas.ztrmv

scipy.linalg.blas.**ztrmv**(*a*, *x*[, *offx*, *incx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ztrmv.

Parameters

a	[input rank-2 array('D') with bounds (n,n)]
x	[input rank-1 array('D') with bounds (*)]

Returns

x	[rank-1 array('D') with bounds (*)]

Other Parameters

overwrite_x	[input int, optional] Default: 0
offx	[input int, optional] Default: 0
incx	[input int, optional] Default: 1
lower	[input int, optional] Default: 0
trans	[input int, optional] Default: 0
diag	[input int, optional] Default: 0

scipy.linalg.blas.ztrsv

scipy.linalg.blas.**ztrsv**(*a*, *x*[, *incx*, *offx*, *lower*, *trans*, *diag*, *overwrite_x*]) **= <fortran object>**

Wrapper for ztrsv.

Parameters

a	[input rank-2 array('D') with bounds (n,n)]
x	[input rank-1 array('D') with bounds (*)]

Returns

xout	[rank-1 array('D') with bounds (*) and x storage]

Other Parameters

overwrite_x
: [input int, optional] Default: 0

incx [input int, optional] Default: 1

offx [input int, optional] Default: 0

lower [input int, optional] Default: 0

trans [input int, optional] Default: 0

diag [input int, optional] Default: 0

scipy.linalg.blas.zsyr

scipy.linalg.blas.**zsyr**(*alpha*, *x*[, *lower*, *incx*, *offx*, *n*, *a*, *overwrite_a*]) **= <fortran object>**

Wrapper for zsyr.

Parameters

alpha [input complex]

x [input rank-1 array('D') with bounds (*)]

Returns

a [rank-2 array('D') with bounds (n,n)]

Other Parameters

lower [input int, optional] Default: 0

incx [input int, optional] Default: 1

offx [input int, optional] Default: 0

n [input int, optional] Default: (len(x)-1-offx)/abs(incx)+1

a [input rank-2 array('D') with bounds (n,n)]

overwrite_a
: [input int, optional] Default: 0

BLAS Level 3 functions

sgemm(...)	Wrapper for sgemm.
ssymm(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for ssymm.
ssyr2k(...)	Wrapper for ssyr2k.
ssyrk(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for ssyrk.
strmm(...)	Wrapper for strmm.
strsm(...)	Wrapper for strsm.
dgemm(...)	Wrapper for dgemm.
dsymm(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for dsymm.
dsyr2k(...)	Wrapper for dsyr2k.
dsyrk(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for dsyrk.
dtrmm(...)	Wrapper for dtrmm.
dtrsm(...)	Wrapper for dtrsm.
cgemm(...)	Wrapper for cgemm.
chemm(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for chemm.
cher2k(...)	Wrapper for cher2k.
cherk(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for cherk.
csymm(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for csymm.
csyr2k(...)	Wrapper for csyr2k.
csyrk(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for csyrk.

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Table 103 – continued from previous page

ctrmm(...)	Wrapper for ctrmm.
ctrsm(...)	Wrapper for ctrsm.
zgemm(...)	Wrapper for zgemm.
zhemm(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for zhemm.
zher2k(...)	Wrapper for zher2k.
zherk(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for zherk.
zsymm(alpha,a,b,[beta,c,side,lower,overwrite_c])	Wrapper for zsymm.
zsyr2k(...)	Wrapper for zsyr2k.
zsyrk(alpha,a,[beta,c,trans,lower,overwrite_c])	Wrapper for zsyrk.
ztrmm(...)	Wrapper for ztrmm.
ztrsm(...)	Wrapper for ztrsm.

scipy.linalg.blas.sgemm

scipy.linalg.blas.**sgemm**(*alpha*, *a*, *b*[, *beta*, *c*, *trans_a*, *trans_b*, *overwrite_c*]) **= <fortran object>**

Wrapper for sgemm.

Parameters

alpha [input float]
a [input rank-2 array('f') with bounds (lda,ka)]
b [input rank-2 array('f') with bounds (ldb,kb)]

Returns

c [rank-2 array('f') with bounds (m,n)]

Other Parameters

beta [input float, optional] Default: 0.0
c [input rank-2 array('f') with bounds (m,n)]
overwrite_c [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
trans_b [input int, optional] Default: 0

scipy.linalg.blas.ssymm

scipy.linalg.blas.**ssymm**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for ssymm.

Parameters

alpha [input float]
a [input rank-2 array('f') with bounds (lda,ka)]
b [input rank-2 array('f') with bounds (ldb,kb)]

Returns

c [rank-2 array('f') with bounds (m,n)]

Other Parameters

beta [input float, optional] Default: 0.0
c [input rank-2 array('f') with bounds (m,n)]
overwrite_c [input int, optional] Default: 0
side [input int, optional] Default: 0

lower [input int, optional] Default: 0

scipy.linalg.blas.ssyr2k

scipy.linalg.blas.**ssyr2k**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for ssyr2k.

Parameters

alpha [input float]
a [input rank-2 array('f') with bounds (lda,ka)]
b [input rank-2 array('f') with bounds (ldb,kb)]

Returns

c [rank-2 array('f') with bounds (n,n)]

Other Parameters

beta [input float, optional] Default: 0.0
c [input rank-2 array('f') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.ssyrk

scipy.linalg.blas.**ssyrk**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for ssyrk.

Parameters

alpha [input float]
a [input rank-2 array('f') with bounds (lda,ka)]

Returns

c [rank-2 array('f') with bounds (n,n)]

Other Parameters

beta [input float, optional] Default: 0.0
c [input rank-2 array('f') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.strmm

scipy.linalg.blas.**strmm**(*alpha*, *a*, *b*[, *side*, *lower*, *trans_a*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for strmm.

Parameters

alpha [input float]
a [input rank-2 array('f') with bounds (lda,k)]
b [input rank-2 array('f') with bounds (ldb,n)]

Returns

b [rank-2 array('f') with bounds (ldb,n)]

Other Parameters

overwrite_b
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.strsm

scipy.linalg.blas.**strsm**(*alpha*, *a*, *b*[, *side*, *lower*, *trans_a*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for strsm.

Parameters

alpha [input float]
a [input rank-2 array('f') with bounds (lda,*)]
b [input rank-2 array('f') with bounds (ldb,n)]

Returns

x [rank-2 array('f') with bounds (ldb,n) and b storage]

Other Parameters

overwrite_b
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.dgemm

scipy.linalg.blas.**dgemm**(*alpha*, *a*, *b*[, *beta*, *c*, *trans_a*, *trans_b*, *overwrite_c*]) **= <fortran object>**

Wrapper for dgemm.

Parameters

alpha [input float]
a [input rank-2 array('d') with bounds (lda,ka)]
b [input rank-2 array('d') with bounds (ldb,kb)]

Returns

c [rank-2 array('d') with bounds (m,n)]

Other Parameters

beta [input float, optional] Default: 0.0
c [input rank-2 array('d') with bounds (m,n)]
overwrite_c
[input int, optional] Default: 0
trans_a [input int, optional] Default: 0
trans_b [input int, optional] Default: 0

scipy.linalg.blas.dsymm

scipy.linalg.blas.**dsymm**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for dsymm.

Parameters

alpha [input float]
a [input rank-2 array('d') with bounds (lda,ka)]
b [input rank-2 array('d') with bounds (ldb,kb)]

Returns

c [rank-2 array('d') with bounds (m,n)]

Other Parameters

beta [input float, optional] Default: 0.0
c [input rank-2 array('d') with bounds (m,n)]
overwrite_c
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.dsyr2k

scipy.linalg.blas.**dsyr2k**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for dsyr2k.

Parameters

alpha [input float]
a [input rank-2 array('d') with bounds (lda,ka)]
b [input rank-2 array('d') with bounds (ldb,kb)]

Returns

c [rank-2 array('d') with bounds (n,n)]

Other Parameters

beta [input float, optional] Default: 0.0
c [input rank-2 array('d') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.dsyrk

scipy.linalg.blas.**dsyrk**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for dsyrk.

Parameters

alpha [input float]
a [input rank-2 array('d') with bounds (lda,ka)]

Returns

c [rank-2 array('d') with bounds (n,n)]

Other Parameters

beta [input float, optional] Default: 0.0
c [input rank-2 array('d') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.dtrmm

scipy.linalg.blas.**dtrmm**(*alpha*, *a*, *b*[, *side*, *lower*, *trans_a*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for dtrmm.

Parameters

alpha [input float]
a [input rank-2 array('d') with bounds (lda,k)]
b [input rank-2 array('d') with bounds (ldb,n)]

Returns

b [rank-2 array('d') with bounds (ldb,n)]

Other Parameters

overwrite_b
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.dtrsm

scipy.linalg.blas.**dtrsm**(*alpha*, *a*, *b*[, *side*, *lower*, *trans_a*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for dtrsm.

Parameters

alpha [input float]
a [input rank-2 array('d') with bounds (lda,*)]
b [input rank-2 array('d') with bounds (ldb,n)]

Returns

x [rank-2 array('d') with bounds (ldb,n) and b storage]

Other Parameters

overwrite_b
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.cgemm

scipy.linalg.blas.**cgemm**(*alpha*, *a*, *b*[, *beta*, *c*, *trans_a*, *trans_b*, *overwrite_c*]) **= <fortran object>**

Wrapper for cgemm.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]
b [input rank-2 array('F') with bounds (ldb,kb)]

Returns

c [rank-2 array('F') with bounds (m,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (m,n)]
overwrite_c [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
trans_b [input int, optional] Default: 0

scipy.linalg.blas.chemm

scipy.linalg.blas.**chemm**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for chemm.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]
b [input rank-2 array('F') with bounds (ldb,kb)]

Returns

c [rank-2 array('F') with bounds (m,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (m,n)]
overwrite_c [input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.cher2k

scipy.linalg.blas.**cher2k**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for cher2k.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]
b [input rank-2 array('F') with bounds (ldb,kb)]

Returns

c [rank-2 array('F') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.cherk

scipy.linalg.blas.**cherk**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for cherk.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]

Returns

c [rank-2 array('F') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.csymm

scipy.linalg.blas.**csymm**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for csymm.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]
b [input rank-2 array('F') with bounds (ldb,kb)]

Returns

c [rank-2 array('F') with bounds (m,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (m,n)]
overwrite_c
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.csyr2k

scipy.linalg.blas.**csyr2k**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for csyr2k.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]
b [input rank-2 array('F') with bounds (ldb,kb)]

Returns

c [rank-2 array('F') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.csyrk

scipy.linalg.blas.**csyrk**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for csyrk.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,ka)]

Returns

c [rank-2 array('F') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('F') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.ctrmm

scipy.linalg.blas.**ctrmm**(*alpha*, *a*, *b*[, *side*, *lower*, *trans_a*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for ctrmm.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,k)]
b [input rank-2 array('F') with bounds (ldb,n)]

Returns

b [rank-2 array('F') with bounds (ldb,n)]

Other Parameters

overwrite_b
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ctrsm

scipy.linalg.blas.**ctrsm**(*alpha*, *a*, *b*[, *side*, *lower*, *trans_a*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for ctrsm.

Parameters

alpha [input complex]
a [input rank-2 array('F') with bounds (lda,*)]
b [input rank-2 array('F') with bounds (ldb,n)]

Returns

x [rank-2 array('F') with bounds (ldb,n) and b storage]

Other Parameters

overwrite_b
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.zgemm

scipy.linalg.blas.**zgemm**(*alpha*, *a*, *b*[, *beta*, *c*, *trans_a*, *trans_b*, *overwrite_c*]) **= <fortran object>**

Wrapper for zgemm.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]
b [input rank-2 array('D') with bounds (ldb,kb)]

Returns

c [rank-2 array('D') with bounds (m,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (m,n)]
overwrite_c
[input int, optional] Default: 0
trans_a [input int, optional] Default: 0
trans_b [input int, optional] Default: 0

scipy.linalg.blas.zhemm

scipy.linalg.blas.**zhemm**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for zhemm.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]
b [input rank-2 array('D') with bounds (ldb,kb)]

Returns

c [rank-2 array('D') with bounds (m,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (m,n)]
overwrite_c
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zher2k

scipy.linalg.blas.**zher2k**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for zher2k.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]
b [input rank-2 array('D') with bounds (ldb,kb)]

Returns

c [rank-2 array('D') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zherk

scipy.linalg.blas.**zherk**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for zherk.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]

Returns

c [rank-2 array('D') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zsymm

scipy.linalg.blas.**zsymm**(*alpha*, *a*, *b*[, *beta*, *c*, *side*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for zsymm.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]
b [input rank-2 array('D') with bounds (ldb,kb)]

Returns

c [rank-2 array('D') with bounds (m,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (m,n)]
overwrite_c
[input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zsyr2k

scipy.linalg.blas.**zsyr2k**(*alpha*, *a*, *b*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for zsyr2k.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]
b [input rank-2 array('D') with bounds (ldb,kb)]

Returns

c [rank-2 array('D') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (n,n)]
overwrite_c
[input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.zsyrk

scipy.linalg.blas.**zsyrk**(*alpha*, *a*[, *beta*, *c*, *trans*, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for zsyrk.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,ka)]

Returns

c [rank-2 array('D') with bounds (n,n)]

Other Parameters

beta [input complex, optional] Default: (0.0, 0.0)
c [input rank-2 array('D') with bounds (n,n)]
overwrite_c [input int, optional] Default: 0
trans [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.blas.ztrmm

scipy.linalg.blas.**ztrmm**(*alpha*, *a*, *b*[, *side*, *lower*, *trans_a*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for ztrmm.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,k)]
b [input rank-2 array('D') with bounds (ldb,n)]

Returns

b [rank-2 array('D') with bounds (ldb,n)]

Other Parameters

overwrite_b [input int, optional] Default: 0
side [input int, optional] Default: 0
lower [input int, optional] Default: 0
trans_a [input int, optional] Default: 0
diag [input int, optional] Default: 0

scipy.linalg.blas.ztrsm

scipy.linalg.blas.**ztrsm**(*alpha*, *a*, *b*[, *side*, *lower*, *trans_a*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for ztrsm.

Parameters

alpha [input complex]
a [input rank-2 array('D') with bounds (lda,*)]
b [input rank-2 array('D') with bounds (ldb,n)]

Returns

x [rank-2 array('D') with bounds (ldb,n) and b storage]

Other Parameters

overwrite_b
: [input int, optional] Default: 0

side
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

trans_a
: [input int, optional] Default: 0

diag
: [input int, optional] Default: 0

3.3.12 Low-level LAPACK functions (`scipy.linalg.lapack`)

This module contains low-level functions from the LAPACK library.

The **gegv* family of routines have been removed from LAPACK 3.6.0 and have been deprecated in SciPy 0.17.0. They will be removed in a future release.

New in version 0.12.0.

Note: The common `overwrite_<>` option in many routines, allows the input arrays to be overwritten to avoid extra memory allocation. However this requires the array to satisfy two conditions which are memory order and the data type to match exactly the order and the type expected by the routine.

As an example, if you pass a double precision float array to any `S....` routine which expects single precision arguments, f2py will create an intermediate array to match the argument types and overwriting will be performed on that intermediate array.

Similarly, if a C-contiguous array is passed, f2py will pass a FORTRAN-contiguous array internally. Please make sure that these details are satisfied. More information can be found in the f2py documentation.

Warning: These functions do little to no error checking. It is possible to cause crashes by mis-using them, so prefer using the higher-level routines in *scipy.linalg*.

Finding functions

get_lapack_funcs(names[, arrays, dtype, ilp64])	Return available LAPACK function objects from names.

scipy.linalg.lapack.get_lapack_funcs

scipy.linalg.lapack.**get_lapack_funcs**(*names*, *arrays=()*, *dtype=None*, *ilp64=False*)

Return available LAPACK function objects from names.

Arrays are used to determine the optimal prefix of LAPACK routines.

Parameters

names
: [str or sequence of str] Name(s) of LAPACK functions without type prefix.

arrays
: [sequence of ndarrays, optional] Arrays can be given to determine optimal prefix of LAPACK routines. If not given, double-precision routines will be used, otherwise the most generic type in arrays will be used.

dtype
: [str or dtype, optional] Data-type specifier. Not used if *arrays* is non-empty.

ilp64
: [{True, False, 'preferred'}, optional] Whether to return ILP64 routine variant. Choosing 'preferred' returns ILP64 routine if available, and otherwise the 32-bit routine. Default: False

Returns

funcs [list] List containing the found function(s).

Notes

This routine automatically chooses between Fortran/C interfaces. Fortran code is used whenever possible for arrays with column major order. In all other cases, C code is preferred.

In LAPACK, the naming convention is that all functions start with a type prefix, which depends on the type of the principal matrix. These can be one of {'s', 'd', 'c', 'z'} for the NumPy types {float32, float64, complex64, complex128} respectively, and are stored in attribute `typecode` of the returned functions.

Examples

Suppose we would like to use '?lange' routine which computes the selected norm of an array. We pass our array in order to get the correct 'lange' flavor.

```
>>> import scipy.linalg as LA
>>> rng = np.random.default_rng()
>>> a = rng.random((3,2))
>>> x_lange = LA.get_lapack_funcs('lange', (a,))
>>> x_lange.typecode
'd'
>>> x_lange = LA.get_lapack_funcs('lange',(a*1j,))
>>> x_lange.typecode
'z'
```

Several LAPACK routines work best when its internal WORK array has the optimal size (big enough for fast computation and small enough to avoid waste of memory). This size is determined also by a dedicated query to the function which is often wrapped as a standalone function and commonly denoted as `###_lwork`. Below is an example for `?sysv`

```
>>> import scipy.linalg as LA
>>> rng = np.random.default_rng()
>>> a = rng.random((1000, 1000))
>>> b = rng.random((1000, 1)) * 1j
>>> # We pick up zsysv and zsysv_lwork due to b array
... xsysv, xlwork = LA.get_lapack_funcs(('sysv', 'sysv_lwork'), (a, b))
>>> opt_lwork, _ = xlwork(a.shape[0])  # returns a complex for 'z' prefix
>>> udut, ipiv, x, info = xsysv(a, b, lwork=int(opt_lwork.real))
```

All functions

sgbsv(kl,ku,ab,b,[overwrite_ab,overwrite_b])	Wrapper for `sgbsv`.
dgbsv(kl,ku,ab,b,[overwrite_ab,overwrite_b])	Wrapper for `dgbsv`.
cgbsv(kl,ku,ab,b,[overwrite_ab,overwrite_b])	Wrapper for `cgbsv`.
zgbsv(kl,ku,ab,b,[overwrite_ab,overwrite_b])	Wrapper for `zgbsv`.
sgbtrf(ab,kl,ku,[m,n,ldab,overwrite_ab])	Wrapper for `sgbtrf`.
dgbtrf(ab,kl,ku,[m,n,ldab,overwrite_ab])	Wrapper for `dgbtrf`.
cgbtrf(ab,kl,ku,[m,n,ldab,overwrite_ab])	Wrapper for `cgbtrf`.

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Table 105 – continued from previous page

zgbtrf(ab,kl,ku,[m,n,ldab,overwrite_ab])	Wrapper for zgbtrf.
sgbtrs(…)	Wrapper for sgbtrs.
dgbtrs(…)	Wrapper for dgbtrs.
cgbtrs(…)	Wrapper for cgbtrs.
zgbtrs(…)	Wrapper for zgbtrs.
sgebal(a,[scale,permute,overwrite_a])	Wrapper for sgebal.
dgebal(a,[scale,permute,overwrite_a])	Wrapper for dgebal.
cgebal(a,[scale,permute,overwrite_a])	Wrapper for cgebal.
zgebal(a,[scale,permute,overwrite_a])	Wrapper for zgebal.
sgecon(a,anorm,[norm])	Wrapper for sgecon.
dgecon(a,anorm,[norm])	Wrapper for dgecon.
cgecon(a,anorm,[norm])	Wrapper for cgecon.
zgecon(a,anorm,[norm])	Wrapper for zgecon.
sgeequ(a)	Wrapper for sgeequ.
dgeequ(a)	Wrapper for dgeequ.
cgeequ(a)	Wrapper for cgeequ.
zgeequ(a)	Wrapper for zgeequ.
sgeequb(a)	Wrapper for sgeequb.
dgeequb(a)	Wrapper for dgeequb.
cgeequb(a)	Wrapper for cgeequb.
zgeequb(a)	Wrapper for zgeequb.
sgees(…)	Wrapper for sgees.
dgees(…)	Wrapper for dgees.
cgees(…)	Wrapper for cgees.
zgees(…)	Wrapper for zgees.
sgeev(…)	Wrapper for sgeev.
dgeev(…)	Wrapper for dgeev.
cgeev(…)	Wrapper for cgeev.
zgeev(…)	Wrapper for zgeev.
sgeev_lwork(n,[compute_vl,compute_vr])	Wrapper for sgeev_lwork.
dgeev_lwork(n,[compute_vl,compute_vr])	Wrapper for dgeev_lwork.
cgeev_lwork(n,[compute_vl,compute_vr])	Wrapper for cgeev_lwork.
zgeev_lwork(n,[compute_vl,compute_vr])	Wrapper for zgeev_lwork.
sgegv(*args, **kwds)	sgegv is deprecated! The *gegv family of routines has been deprecated in LAPACK 3.6.0 in favor of the *ggev family of routines.
dgegv(*args, **kwds)	dgegv is deprecated! The *gegv family of routines has been deprecated in LAPACK 3.6.0 in favor of the *ggev family of routines.
cgegv(*args, **kwds)	cgegv is deprecated! The *gegv family of routines has been deprecated in LAPACK 3.6.0 in favor of the *ggev family of routines.
zgegv(*args, **kwds)	zgegv is deprecated! The *gegv family of routines has been deprecated in LAPACK 3.6.0 in favor of the *ggev family of routines.
sgehrd(a,[lo,hi,lwork,overwrite_a])	Wrapper for sgehrd.
dgehrd(a,[lo,hi,lwork,overwrite_a])	Wrapper for dgehrd.
cgehrd(a,[lo,hi,lwork,overwrite_a])	Wrapper for cgehrd.
zgehrd(a,[lo,hi,lwork,overwrite_a])	Wrapper for zgehrd.
sgehrd_lwork(n,[lo,hi])	Wrapper for sgehrd_lwork.
dgehrd_lwork(n,[lo,hi])	Wrapper for dgehrd_lwork.

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Table 105 – continued from previous page

cgehrd_lwork(n,[lo,hi])	Wrapper for cgehrd_lwork.
zgehrd_lwork(n,[lo,hi])	Wrapper for zgehrd_lwork.
sgejsv(…)	Wrapper for sgejsv.
dgejsv(…)	Wrapper for dgejsv.
sgels(a,b,[trans,lwork,overwrite_a,overwrite_b])	Wrapper for sgels.
dgels(a,b,[trans,lwork,overwrite_a,overwrite_b])	Wrapper for dgels.
cgels(a,b,[trans,lwork,overwrite_a,overwrite_b])	Wrapper for cgels.
zgels(a,b,[trans,lwork,overwrite_a,overwrite_b])	Wrapper for zgels.
sgels_lwork(m,n,nrhs,[trans])	Wrapper for sgels_lwork.
dgels_lwork(m,n,nrhs,[trans])	Wrapper for dgels_lwork.
cgels_lwork(m,n,nrhs,[trans])	Wrapper for cgels_lwork.
zgels_lwork(m,n,nrhs,[trans])	Wrapper for zgels_lwork.
sgelsd(…)	Wrapper for sgelsd.
dgelsd(…)	Wrapper for dgelsd.
cgelsd(…)	Wrapper for cgelsd.
zgelsd(…)	Wrapper for zgelsd.
sgelsd_lwork(m,n,nrhs,[cond,lwork])	Wrapper for sgelsd_lwork.
dgelsd_lwork(m,n,nrhs,[cond,lwork])	Wrapper for dgelsd_lwork.
cgelsd_lwork(m,n,nrhs,[cond,lwork])	Wrapper for cgelsd_lwork.
zgelsd_lwork(m,n,nrhs,[cond,lwork])	Wrapper for zgelsd_lwork.
sgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])	Wrapper for sgelss.
dgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])	Wrapper for dgelss.
cgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])	Wrapper for cgelss.
zgelss(a,b,[cond,lwork,overwrite_a,overwrite_b])	Wrapper for zgelss.
sgelss_lwork(m,n,nrhs,[cond,lwork])	Wrapper for sgelss_lwork.
dgelss_lwork(m,n,nrhs,[cond,lwork])	Wrapper for dgelss_lwork.
cgelss_lwork(m,n,nrhs,[cond,lwork])	Wrapper for cgelss_lwork.
zgelss_lwork(m,n,nrhs,[cond,lwork])	Wrapper for zgelss_lwork.
sgelsy(…)	Wrapper for sgelsy.
dgelsy(…)	Wrapper for dgelsy.
cgelsy(…)	Wrapper for cgelsy.
zgelsy(…)	Wrapper for zgelsy.
sgelsy_lwork(m,n,nrhs,cond,[lwork])	Wrapper for sgelsy_lwork.
dgelsy_lwork(m,n,nrhs,cond,[lwork])	Wrapper for dgelsy_lwork.
cgelsy_lwork(m,n,nrhs,cond,[lwork])	Wrapper for cgelsy_lwork.
zgelsy_lwork(m,n,nrhs,cond,[lwork])	Wrapper for zgelsy_lwork.
sgeqp3(a,[lwork,overwrite_a])	Wrapper for sgeqp3.
dgeqp3(a,[lwork,overwrite_a])	Wrapper for dgeqp3.
cgeqp3(a,[lwork,overwrite_a])	Wrapper for cgeqp3.
zgeqp3(a,[lwork,overwrite_a])	Wrapper for zgeqp3.
sgeqrf(a,[lwork,overwrite_a])	Wrapper for sgeqrf.
dgeqrf(a,[lwork,overwrite_a])	Wrapper for dgeqrf.
cgeqrf(a,[lwork,overwrite_a])	Wrapper for cgeqrf.
zgeqrf(a,[lwork,overwrite_a])	Wrapper for zgeqrf.
sgeqrf_lwork(m,n)	Wrapper for sgeqrf_lwork.
dgeqrf_lwork(m,n)	Wrapper for dgeqrf_lwork.
cgeqrf_lwork(m,n)	Wrapper for cgeqrf_lwork.
zgeqrf_lwork(m,n)	Wrapper for zgeqrf_lwork.
sgeqrfp(a,[lwork,overwrite_a])	Wrapper for sgeqrfp.
dgeqrfp(a,[lwork,overwrite_a])	Wrapper for dgeqrfp.

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cgeqrfp(a,[lwork,overwrite_a])	Wrapper for cgeqrfp.
zgeqrfp(a,[lwork,overwrite_a])	Wrapper for zgeqrfp.
sgeqrfp_lwork(m,n)	Wrapper for sgeqrfp_lwork.
dgeqrfp_lwork(m,n)	Wrapper for dgeqrfp_lwork.
cgeqrfp_lwork(m,n)	Wrapper for cgeqrfp_lwork.
zgeqrfp_lwork(m,n)	Wrapper for zgeqrfp_lwork.
sgerqf(a,[lwork,overwrite_a])	Wrapper for sgerqf.
dgerqf(a,[lwork,overwrite_a])	Wrapper for dgerqf.
cgerqf(a,[lwork,overwrite_a])	Wrapper for cgerqf.
zgerqf(a,[lwork,overwrite_a])	Wrapper for zgerqf.
sgesdd(…)	Wrapper for sgesdd.
dgesdd(…)	Wrapper for dgesdd.
cgesdd(…)	Wrapper for cgesdd.
zgesdd(…)	Wrapper for zgesdd.
sgesdd_lwork(m,n,[compute_uv,full_matrices])	Wrapper for sgesdd_lwork.
dgesdd_lwork(m,n,[compute_uv,full_matrices])	Wrapper for dgesdd_lwork.
cgesdd_lwork(m,n,[compute_uv,full_matrices])	Wrapper for cgesdd_lwork.
zgesdd_lwork(m,n,[compute_uv,full_matrices])	Wrapper for zgesdd_lwork.
sgesv(a,b,[overwrite_a,overwrite_b])	Wrapper for sgesv.
dgesv(a,b,[overwrite_a,overwrite_b])	Wrapper for dgesv.
cgesv(a,b,[overwrite_a,overwrite_b])	Wrapper for cgesv.
zgesv(a,b,[overwrite_a,overwrite_b])	Wrapper for zgesv.
sgesvd(…)	Wrapper for sgesvd.
dgesvd(…)	Wrapper for dgesvd.
cgesvd(…)	Wrapper for cgesvd.
zgesvd(…)	Wrapper for zgesvd.
sgesvd_lwork(m,n,[compute_uv,full_matrices])	Wrapper for sgesvd_lwork.
dgesvd_lwork(m,n,[compute_uv,full_matrices])	Wrapper for dgesvd_lwork.
cgesvd_lwork(m,n,[compute_uv,full_matrices])	Wrapper for cgesvd_lwork.
zgesvd_lwork(m,n,[compute_uv,full_matrices])	Wrapper for zgesvd_lwork.
sgesvx(…)	Wrapper for sgesvx.
dgesvx(…)	Wrapper for dgesvx.
cgesvx(…)	Wrapper for cgesvx.
zgesvx(…)	Wrapper for zgesvx.
sgetrf(a,[overwrite_a])	Wrapper for sgetrf.
dgetrf(a,[overwrite_a])	Wrapper for dgetrf.
cgetrf(a,[overwrite_a])	Wrapper for cgetrf.
zgetrf(a,[overwrite_a])	Wrapper for zgetrf.
sgetc2(a,[overwrite_a])	Wrapper for sgetc2.
dgetc2(a,[overwrite_a])	Wrapper for dgetc2.
cgetc2(a,[overwrite_a])	Wrapper for cgetc2.
zgetc2(a,[overwrite_a])	Wrapper for zgetc2.
sgetri(lu,piv,[lwork,overwrite_lu])	Wrapper for sgetri.
dgetri(lu,piv,[lwork,overwrite_lu])	Wrapper for dgetri.
cgetri(lu,piv,[lwork,overwrite_lu])	Wrapper for cgetri.
zgetri(lu,piv,[lwork,overwrite_lu])	Wrapper for zgetri.
sgetri_lwork(n)	Wrapper for sgetri_lwork.
dgetri_lwork(n)	Wrapper for dgetri_lwork.
cgetri_lwork(n)	Wrapper for cgetri_lwork.
zgetri_lwork(n)	Wrapper for zgetri_lwork.

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sgetrs(lu,piv,b,[trans,overwrite_b])	Wrapper for sgetrs.
dgetrs(lu,piv,b,[trans,overwrite_b])	Wrapper for dgetrs.
cgetrs(lu,piv,b,[trans,overwrite_b])	Wrapper for cgetrs.
zgetrs(lu,piv,b,[trans,overwrite_b])	Wrapper for zgetrs.
sgesc2(lu,rhs,ipiv,jpiv,[overwrite_rhs])	Wrapper for sgesc2.
dgesc2(lu,rhs,ipiv,jpiv,[overwrite_rhs])	Wrapper for dgesc2.
cgesc2(lu,rhs,ipiv,jpiv,[overwrite_rhs])	Wrapper for cgesc2.
zgesc2(lu,rhs,ipiv,jpiv,[overwrite_rhs])	Wrapper for zgesc2.
sgges(…)	Wrapper for sgges.
dgges(…)	Wrapper for dgges.
cgges(…)	Wrapper for cgges.
zgges(…)	Wrapper for zgges.
sggev(…)	Wrapper for sggev.
dggev(…)	Wrapper for dggev.
cggev(…)	Wrapper for cggev.
zggev(…)	Wrapper for zggev.
sgglse(…)	Wrapper for sgglse.
dgglse(…)	Wrapper for dgglse.
cgglse(…)	Wrapper for cgglse.
zgglse(…)	Wrapper for zgglse.
sgglse_lwork(m,n,p)	Wrapper for sgglse_lwork.
dgglse_lwork(m,n,p)	Wrapper for dgglse_lwork.
cgglse_lwork(m,n,p)	Wrapper for cgglse_lwork.
zgglse_lwork(m,n,p)	Wrapper for zgglse_lwork.
sgtsv(…)	Wrapper for sgtsv.
dgtsv(…)	Wrapper for dgtsv.
cgtsv(…)	Wrapper for cgtsv.
zgtsv(…)	Wrapper for zgtsv.
sgtsvx(…)	Wrapper for sgtsvx.
dgtsvx(…)	Wrapper for dgtsvx.
cgtsvx(…)	Wrapper for cgtsvx.
zgtsvx(…)	Wrapper for zgtsvx.
chbevd(…)	Wrapper for chbevd.
zhbevd(…)	Wrapper for zhbevd.
chbevx(…)	Wrapper for chbevx.
zhbevx(…)	Wrapper for zhbevx.
checon(a,ipiv,anorm,[lower])	Wrapper for checon.
zhecon(a,ipiv,anorm,[lower])	Wrapper for zhecon.
cheequb(a,[lower])	Wrapper for cheequb.
zheequb(a,[lower])	Wrapper for zheequb.
cheev(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for cheev.
zheev(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for zheev.
cheev_lwork(n,[lower])	Wrapper for cheev_lwork.
zheev_lwork(n,[lower])	Wrapper for zheev_lwork.
cheevd(…)	Wrapper for cheevd.
zheevd(…)	Wrapper for zheevd.
cheevd_lwork(n,[compute_v,lower])	Wrapper for cheevd_lwork.
zheevd_lwork(n,[compute_v,lower])	Wrapper for zheevd_lwork.
cheevr(…)	Wrapper for cheevr.
zheevr(…)	Wrapper for zheevr.

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cheevr_lwork(n,[lower])	Wrapper for cheevr_lwork.
zheevr_lwork(n,[lower])	Wrapper for zheevr_lwork.
cheevx(…)	Wrapper for cheevx.
zheevx(…)	Wrapper for zheevx.
cheevx_lwork(n,[lower])	Wrapper for cheevx_lwork.
zheevx_lwork(n,[lower])	Wrapper for zheevx_lwork.
chegst(a,b,[itype,lower,overwrite_a])	Wrapper for chegst.
zhegst(a,b,[itype,lower,overwrite_a])	Wrapper for zhegst.
chegv(…)	Wrapper for chegv.
zhegv(…)	Wrapper for zhegv.
chegv_lwork(n,[uplo])	Wrapper for chegv_lwork.
zhegv_lwork(n,[uplo])	Wrapper for zhegv_lwork.
chegvd(…)	Wrapper for chegvd.
zhegvd(…)	Wrapper for zhegvd.
chegvx(…)	Wrapper for chegvx.
zhegvx(…)	Wrapper for zhegvx.
chegvx_lwork(n,[uplo])	Wrapper for chegvx_lwork.
zhegvx_lwork(n,[uplo])	Wrapper for zhegvx_lwork.
chesv(a,b,[lwork,lower,overwrite_a,overwrite_b])	Wrapper for chesv.
zhesv(a,b,[lwork,lower,overwrite_a,overwrite_b])	Wrapper for zhesv.
chesv_lwork(n,[lower])	Wrapper for chesv_lwork.
zhesv_lwork(n,[lower])	Wrapper for zhesv_lwork.
chesvx(…)	Wrapper for chesvx.
zhesvx(…)	Wrapper for zhesvx.
chesvx_lwork(n,[lower])	Wrapper for chesvx_lwork.
zhesvx_lwork(n,[lower])	Wrapper for zhesvx_lwork.
chetrd(a,[lower,lwork,overwrite_a])	Wrapper for chetrd.
zhetrd(a,[lower,lwork,overwrite_a])	Wrapper for zhetrd.
chetrd_lwork(n,[lower])	Wrapper for chetrd_lwork.
zhetrd_lwork(n,[lower])	Wrapper for zhetrd_lwork.
chetrf(a,[lower,lwork,overwrite_a])	Wrapper for chetrf.
zhetrf(a,[lower,lwork,overwrite_a])	Wrapper for zhetrf.
chetrf_lwork(n,[lower])	Wrapper for chetrf_lwork.
zhetrf_lwork(n,[lower])	Wrapper for zhetrf_lwork.
chfrk(…)	Wrapper for chfrk.
zhfrk(…)	Wrapper for zhfrk.
slamch(cmach)	Wrapper for slamch.
dlamch(cmach)	Wrapper for dlamch.
slange(norm,a)	Wrapper for slange.
dlange(norm,a)	Wrapper for dlange.
clange(norm,a)	Wrapper for clange.
zlange(norm,a)	Wrapper for zlange.
slarf(v,tau,c,work,[side,incv,overwrite_c])	Wrapper for slarf.
dlarf(v,tau,c,work,[side,incv,overwrite_c])	Wrapper for dlarf.
clarf(v,tau,c,work,[side,incv,overwrite_c])	Wrapper for clarf.
zlarf(v,tau,c,work,[side,incv,overwrite_c])	Wrapper for zlarf.
slarfg(n,alpha,x,[incx,overwrite_x])	Wrapper for slarfg.
dlarfg(n,alpha,x,[incx,overwrite_x])	Wrapper for dlarfg.
clarfg(n,alpha,x,[incx,overwrite_x])	Wrapper for clarfg.
zlarfg(n,alpha,x,[incx,overwrite_x])	Wrapper for zlarfg.

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slartg(f,g)	Wrapper for slartg.
dlartg(f,g)	Wrapper for dlartg.
clartg(f,g)	Wrapper for clartg.
zlartg(f,g)	Wrapper for zlartg.
slasd4(i,d,z,[rho])	Wrapper for slasd4.
dlasd4(i,d,z,[rho])	Wrapper for dlasd4.
slaswp(a,piv,[k1,k2,off,inc,overwrite_a])	Wrapper for slaswp.
dlaswp(a,piv,[k1,k2,off,inc,overwrite_a])	Wrapper for dlaswp.
claswp(a,piv,[k1,k2,off,inc,overwrite_a])	Wrapper for claswp.
zlaswp(a,piv,[k1,k2,off,inc,overwrite_a])	Wrapper for zlaswp.
slauum(c,[lower,overwrite_c])	Wrapper for slauum.
dlauum(c,[lower,overwrite_c])	Wrapper for dlauum.
clauum(c,[lower,overwrite_c])	Wrapper for clauum.
zlauum(c,[lower,overwrite_c])	Wrapper for zlauum.
sorcsd(…)	Wrapper for sorcsd.
dorcsd(…)	Wrapper for dorcsd.
sorcsd_lwork(m,p,q)	Wrapper for sorcsd_lwork.
dorcsd_lwork(m,p,q)	Wrapper for dorcsd_lwork.
sorghr(a,tau,[lo,hi,lwork,overwrite_a])	Wrapper for sorghr.
dorghr(a,tau,[lo,hi,lwork,overwrite_a])	Wrapper for dorghr.
sorghr_lwork(n,[lo,hi])	Wrapper for sorghr_lwork.
dorghr_lwork(n,[lo,hi])	Wrapper for dorghr_lwork.
sorgqr(a,tau,[lwork,overwrite_a])	Wrapper for sorgqr.
dorgqr(a,tau,[lwork,overwrite_a])	Wrapper for dorgqr.
sorgrq(a,tau,[lwork,overwrite_a])	Wrapper for sorgrq.
dorgrq(a,tau,[lwork,overwrite_a])	Wrapper for dorgrq.
sormqr(side,trans,a,tau,c,lwork,[overwrite_c])	Wrapper for sormqr.
dormqr(side,trans,a,tau,c,lwork,[overwrite_c])	Wrapper for dormqr.
sormrz(a,tau,c,[side,trans,lwork,overwrite_c])	Wrapper for sormrz.
dormrz(a,tau,c,[side,trans,lwork,overwrite_c])	Wrapper for dormrz.
sormrz_lwork(m,n,[side,trans])	Wrapper for sormrz_lwork.
dormrz_lwork(m,n,[side,trans])	Wrapper for dormrz_lwork.
spbsv(ab,b,[lower,ldab,overwrite_ab,overwrite_b])	Wrapper for spbsv.
dpbsv(ab,b,[lower,ldab,overwrite_ab,overwrite_b])	Wrapper for dpbsv.
cpbsv(ab,b,[lower,ldab,overwrite_ab,overwrite_b])	Wrapper for cpbsv.
zpbsv(ab,b,[lower,ldab,overwrite_ab,overwrite_b])	Wrapper for zpbsv.
spbtrf(ab,[lower,ldab,overwrite_ab])	Wrapper for spbtrf.
dpbtrf(ab,[lower,ldab,overwrite_ab])	Wrapper for dpbtrf.
cpbtrf(ab,[lower,ldab,overwrite_ab])	Wrapper for cpbtrf.
zpbtrf(ab,[lower,ldab,overwrite_ab])	Wrapper for zpbtrf.
spbtrs(ab,b,[lower,ldab,overwrite_b])	Wrapper for spbtrs.
dpbtrs(ab,b,[lower,ldab,overwrite_b])	Wrapper for dpbtrs.
cpbtrs(ab,b,[lower,ldab,overwrite_b])	Wrapper for cpbtrs.
zpbtrs(ab,b,[lower,ldab,overwrite_b])	Wrapper for zpbtrs.
spftrf(n,a,[transr,uplo,overwrite_a])	Wrapper for spftrf.
dpftrf(n,a,[transr,uplo,overwrite_a])	Wrapper for dpftrf.
cpftrf(n,a,[transr,uplo,overwrite_a])	Wrapper for cpftrf.
zpftrf(n,a,[transr,uplo,overwrite_a])	Wrapper for zpftrf.
spftri(n,a,[transr,uplo,overwrite_a])	Wrapper for spftri.
dpftri(n,a,[transr,uplo,overwrite_a])	Wrapper for dpftri.

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cpftri(n,a,[transr,uplo,overwrite_a])	Wrapper for cpftri.
zpftri(n,a,[transr,uplo,overwrite_a])	Wrapper for zpftri.
spftrs(n,a,b,[transr,uplo,overwrite_b])	Wrapper for spftrs.
dpftrs(n,a,b,[transr,uplo,overwrite_b])	Wrapper for dpftrs.
cpftrs(n,a,b,[transr,uplo,overwrite_b])	Wrapper for cpftrs.
zpftrs(n,a,b,[transr,uplo,overwrite_b])	Wrapper for zpftrs.
spocon(a,anorm,[uplo])	Wrapper for spocon.
dpocon(a,anorm,[uplo])	Wrapper for dpocon.
cpocon(a,anorm,[uplo])	Wrapper for cpocon.
zpocon(a,anorm,[uplo])	Wrapper for zpocon.
spstrf(a,[tol,lower,overwrite_a])	Wrapper for spstrf.
dpstrf(a,[tol,lower,overwrite_a])	Wrapper for dpstrf.
cpstrf(a,[tol,lower,overwrite_a])	Wrapper for cpstrf.
zpstrf(a,[tol,lower,overwrite_a])	Wrapper for zpstrf.
spstf2(a,[tol,lower,overwrite_a])	Wrapper for spstf2.
dpstf2(a,[tol,lower,overwrite_a])	Wrapper for dpstf2.
cpstf2(a,[tol,lower,overwrite_a])	Wrapper for cpstf2.
zpstf2(a,[tol,lower,overwrite_a])	Wrapper for zpstf2.
sposv(a,b,[lower,overwrite_a,overwrite_b])	Wrapper for sposv.
dposv(a,b,[lower,overwrite_a,overwrite_b])	Wrapper for dposv.
cposv(a,b,[lower,overwrite_a,overwrite_b])	Wrapper for cposv.
zposv(a,b,[lower,overwrite_a,overwrite_b])	Wrapper for zposv.
sposvx(…)	Wrapper for sposvx.
dposvx(…)	Wrapper for dposvx.
cposvx(…)	Wrapper for cposvx.
zposvx(…)	Wrapper for zposvx.
spotrf(a,[lower,clean,overwrite_a])	Wrapper for spotrf.
dpotrf(a,[lower,clean,overwrite_a])	Wrapper for dpotrf.
cpotrf(a,[lower,clean,overwrite_a])	Wrapper for cpotrf.
zpotrf(a,[lower,clean,overwrite_a])	Wrapper for zpotrf.
spotri(c,[lower,overwrite_c])	Wrapper for spotri.
dpotri(c,[lower,overwrite_c])	Wrapper for dpotri.
cpotri(c,[lower,overwrite_c])	Wrapper for cpotri.
zpotri(c,[lower,overwrite_c])	Wrapper for zpotri.
spotrs(c,b,[lower,overwrite_b])	Wrapper for spotrs.
dpotrs(c,b,[lower,overwrite_b])	Wrapper for dpotrs.
cpotrs(c,b,[lower,overwrite_b])	Wrapper for cpotrs.
zpotrs(c,b,[lower,overwrite_b])	Wrapper for zpotrs.
sppcon(n,ap,anorm,[lower])	Wrapper for sppcon.
dppcon(n,ap,anorm,[lower])	Wrapper for dppcon.
cppcon(n,ap,anorm,[lower])	Wrapper for cppcon.
zppcon(n,ap,anorm,[lower])	Wrapper for zppcon.
sppsv(n,ap,b,[lower,overwrite_b])	Wrapper for sppsv.
dppsv(n,ap,b,[lower,overwrite_b])	Wrapper for dppsv.
cppsv(n,ap,b,[lower,overwrite_b])	Wrapper for cppsv.
zppsv(n,ap,b,[lower,overwrite_b])	Wrapper for zppsv.
spptrf(n,ap,[lower,overwrite_ap])	Wrapper for spptrf.
dpptrf(n,ap,[lower,overwrite_ap])	Wrapper for dpptrf.
cpptrf(n,ap,[lower,overwrite_ap])	Wrapper for cpptrf.
zpptrf(n,ap,[lower,overwrite_ap])	Wrapper for zpptrf.

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spptri(n,ap,[lower,overwrite_ap])	Wrapper for spptri.
dpptri(n,ap,[lower,overwrite_ap])	Wrapper for dpptri.
cpptri(n,ap,[lower,overwrite_ap])	Wrapper for cpptri.
zpptri(n,ap,[lower,overwrite_ap])	Wrapper for zpptri.
spptrs(n,ap,b,[lower,overwrite_b])	Wrapper for spptrs.
dpptrs(n,ap,b,[lower,overwrite_b])	Wrapper for dpptrs.
cpptrs(n,ap,b,[lower,overwrite_b])	Wrapper for cpptrs.
zpptrs(n,ap,b,[lower,overwrite_b])	Wrapper for zpptrs.
sptsv(…)	Wrapper for sptsv.
dptsv(…)	Wrapper for dptsv.
cptsv(…)	Wrapper for cptsv.
zptsv(…)	Wrapper for zptsv.
sptsvx(d,e,b,[fact,df,ef])	Wrapper for sptsvx.
dptsvx(d,e,b,[fact,df,ef])	Wrapper for dptsvx.
cptsvx(d,e,b,[fact,df,ef])	Wrapper for cptsvx.
zptsvx(d,e,b,[fact,df,ef])	Wrapper for zptsvx.
spttrf(d,e,[overwrite_d,overwrite_e])	Wrapper for spttrf.
dpttrf(d,e,[overwrite_d,overwrite_e])	Wrapper for dpttrf.
cpttrf(d,e,[overwrite_d,overwrite_e])	Wrapper for cpttrf.
zpttrf(d,e,[overwrite_d,overwrite_e])	Wrapper for zpttrf.
spttrs(d,e,b,[overwrite_b])	Wrapper for spttrs.
dpttrs(d,e,b,[overwrite_b])	Wrapper for dpttrs.
cpttrs(d,e,b,[lower,overwrite_b])	Wrapper for cpttrs.
zpttrs(d,e,b,[lower,overwrite_b])	Wrapper for zpttrs.
spteqr(…)	Wrapper for spteqr.
dpteqr(…)	Wrapper for dpteqr.
cpteqr(…)	Wrapper for cpteqr.
zpteqr(…)	Wrapper for zpteqr.
crot(…)	Wrapper for crot.
zrot(…)	Wrapper for zrot.
ssbev(ab,[compute_v,lower,ldab,overwrite_ab])	Wrapper for ssbev.
dsbev(ab,[compute_v,lower,ldab,overwrite_ab])	Wrapper for dsbev.
ssbevd(…)	Wrapper for ssbevd.
dsbevd(…)	Wrapper for dsbevd.
ssbevx(…)	Wrapper for ssbevx.
dsbevx(…)	Wrapper for dsbevx.
ssfrk(…)	Wrapper for ssfrk.
dsfrk(…)	Wrapper for dsfrk.
sstebz(d,e,range,vl,vu,il,iu,tol,order)	Wrapper for sstebz.
dstebz(d,e,range,vl,vu,il,iu,tol,order)	Wrapper for dstebz.
sstein(d,e,w,iblock,isplit)	Wrapper for sstein.
dstein(d,e,w,iblock,isplit)	Wrapper for dstein.
sstemr(…)	Wrapper for sstemr.
dstemr(…)	Wrapper for dstemr.
sstemr_lwork(…)	Wrapper for sstemr_lwork.
dstemr_lwork(…)	Wrapper for dstemr_lwork.
ssterf(d,e,[overwrite_d,overwrite_e])	Wrapper for ssterf.
dsterf(d,e,[overwrite_d,overwrite_e])	Wrapper for dsterf.
sstev(d,e,[compute_v,overwrite_d,overwrite_e])	Wrapper for sstev.
dstev(d,e,[compute_v,overwrite_d,overwrite_e])	Wrapper for dstev.

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Table 105 – continued from previous page

ssycon(a,ipiv,anorm,[lower])	Wrapper for ssycon.
dsycon(a,ipiv,anorm,[lower])	Wrapper for dsycon.
csycon(a,ipiv,anorm,[lower])	Wrapper for csycon.
zsycon(a,ipiv,anorm,[lower])	Wrapper for zsycon.
ssyconv(a,ipiv,[lower,way,overwrite_a])	Wrapper for ssyconv.
dsyconv(a,ipiv,[lower,way,overwrite_a])	Wrapper for dsyconv.
csyconv(a,ipiv,[lower,way,overwrite_a])	Wrapper for csyconv.
zsyconv(a,ipiv,[lower,way,overwrite_a])	Wrapper for zsyconv.
ssyequb(a,[lower])	Wrapper for ssyequb.
dsyequb(a,[lower])	Wrapper for dsyequb.
csyequb(a,[lower])	Wrapper for csyequb.
zsyequb(a,[lower])	Wrapper for zsyequb.
ssyev(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for ssyev.
dsyev(a,[compute_v,lower,lwork,overwrite_a])	Wrapper for dsyev.
ssyev_lwork(n,[lower])	Wrapper for ssyev_lwork.
dsyev_lwork(n,[lower])	Wrapper for dsyev_lwork.
ssyevd(…)	Wrapper for ssyevd.
dsyevd(…)	Wrapper for dsyevd.
ssyevd_lwork(n,[compute_v,lower])	Wrapper for ssyevd_lwork.
dsyevd_lwork(n,[compute_v,lower])	Wrapper for dsyevd_lwork.
ssyevr(…)	Wrapper for ssyevr.
dsyevr(…)	Wrapper for dsyevr.
ssyevr_lwork(n,[lower])	Wrapper for ssyevr_lwork.
dsyevr_lwork(n,[lower])	Wrapper for dsyevr_lwork.
ssyevx(…)	Wrapper for ssyevx.
dsyevx(…)	Wrapper for dsyevx.
ssyevx_lwork(n,[lower])	Wrapper for ssyevx_lwork.
dsyevx_lwork(n,[lower])	Wrapper for dsyevx_lwork.
ssygst(a,b,[itype,lower,overwrite_a])	Wrapper for ssygst.
dsygst(a,b,[itype,lower,overwrite_a])	Wrapper for dsygst.
ssygv(…)	Wrapper for ssygv.
dsygv(…)	Wrapper for dsygv.
ssygv_lwork(n,[uplo])	Wrapper for ssygv_lwork.
dsygv_lwork(n,[uplo])	Wrapper for dsygv_lwork.
ssygvd(…)	Wrapper for ssygvd.
dsygvd(…)	Wrapper for dsygvd.
ssygvx(…)	Wrapper for ssygvx.
dsygvx(…)	Wrapper for dsygvx.
ssygvx_lwork(n,[uplo])	Wrapper for ssygvx_lwork.
dsygvx_lwork(n,[uplo])	Wrapper for dsygvx_lwork.
ssysv(a,b,[lwork,lower,overwrite_a,overwrite_b])	Wrapper for ssysv.
dsysv(a,b,[lwork,lower,overwrite_a,overwrite_b])	Wrapper for dsysv.
csysv(a,b,[lwork,lower,overwrite_a,overwrite_b])	Wrapper for csysv.
zsysv(a,b,[lwork,lower,overwrite_a,overwrite_b])	Wrapper for zsysv.
ssysv_lwork(n,[lower])	Wrapper for ssysv_lwork.
dsysv_lwork(n,[lower])	Wrapper for dsysv_lwork.
csysv_lwork(n,[lower])	Wrapper for csysv_lwork.
zsysv_lwork(n,[lower])	Wrapper for zsysv_lwork.
ssysvx(…)	Wrapper for ssysvx.
dsysvx(…)	Wrapper for dsysvx.

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csysvx(…)	Wrapper for csysvx.
zsysvx(…)	Wrapper for zsysvx.
ssysvx_lwork(n,[lower])	Wrapper for ssysvx_lwork.
dsysvx_lwork(n,[lower])	Wrapper for dsysvx_lwork.
csysvx_lwork(n,[lower])	Wrapper for csysvx_lwork.
zsysvx_lwork(n,[lower])	Wrapper for zsysvx_lwork.
ssytf2(a,[lower,overwrite_a])	Wrapper for ssytf2.
dsytf2(a,[lower,overwrite_a])	Wrapper for dsytf2.
csytf2(a,[lower,overwrite_a])	Wrapper for csytf2.
zsytf2(a,[lower,overwrite_a])	Wrapper for zsytf2.
ssytrd(a,[lower,lwork,overwrite_a])	Wrapper for ssytrd.
dsytrd(a,[lower,lwork,overwrite_a])	Wrapper for dsytrd.
ssytrd_lwork(n,[lower])	Wrapper for ssytrd_lwork.
dsytrd_lwork(n,[lower])	Wrapper for dsytrd_lwork.
ssytrf(a,[lower,lwork,overwrite_a])	Wrapper for ssytrf.
dsytrf(a,[lower,lwork,overwrite_a])	Wrapper for dsytrf.
csytrf(a,[lower,lwork,overwrite_a])	Wrapper for csytrf.
zsytrf(a,[lower,lwork,overwrite_a])	Wrapper for zsytrf.
ssytrf_lwork(n,[lower])	Wrapper for ssytrf_lwork.
dsytrf_lwork(n,[lower])	Wrapper for dsytrf_lwork.
csytrf_lwork(n,[lower])	Wrapper for csytrf_lwork.
zsytrf_lwork(n,[lower])	Wrapper for zsytrf_lwork.
stbtrs(ab,b,[uplo,trans,diag,overwrite_b])	Wrapper for stbtrs.
dtbtrs(ab,b,[uplo,trans,diag,overwrite_b])	Wrapper for dtbtrs.
ctbtrs(ab,b,[uplo,trans,diag,overwrite_b])	Wrapper for ctbtrs.
ztbtrs(ab,b,[uplo,trans,diag,overwrite_b])	Wrapper for ztbtrs.
stfsm(…)	Wrapper for stfsm.
dtfsm(…)	Wrapper for dtfsm.
ctfsm(…)	Wrapper for ctfsm.
ztfsm(…)	Wrapper for ztfsm.
stfttp(n,arf,[transr,uplo])	Wrapper for stfttp.
dtfttp(n,arf,[transr,uplo])	Wrapper for dtfttp.
ctfttp(n,arf,[transr,uplo])	Wrapper for ctfttp.
ztfttp(n,arf,[transr,uplo])	Wrapper for ztfttp.
stfttr(n,arf,[transr,uplo])	Wrapper for stfttr.
dtfttr(n,arf,[transr,uplo])	Wrapper for dtfttr.
ctfttr(n,arf,[transr,uplo])	Wrapper for ctfttr.
ztfttr(n,arf,[transr,uplo])	Wrapper for ztfttr.
stgexc(…)	Wrapper for stgexc.
dtgexc(…)	Wrapper for dtgexc.
ctgexc(…)	Wrapper for ctgexc.
ztgexc(…)	Wrapper for ztgexc.
stgsen(…)	Wrapper for stgsen.
dtgsen(…)	Wrapper for dtgsen.
ctgsen(…)	Wrapper for ctgsen.
ztgsen(…)	Wrapper for ztgsen.
stgsen_lwork(select,a,[ijob])	Wrapper for stgsen_lwork.
dtgsen_lwork(select,a,[ijob])	Wrapper for dtgsen_lwork.
ctgsen_lwork(select,a,b,[ijob])	Wrapper for ctgsen_lwork.
ztgsen_lwork(select,a,b,[ijob])	Wrapper for ztgsen_lwork.

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stpttf(n,ap,[transr,uplo])	Wrapper for stpttf.
dtpttf(n,ap,[transr,uplo])	Wrapper for dtpttf.
ctpttf(n,ap,[transr,uplo])	Wrapper for ctpttf.
ztpttf(n,ap,[transr,uplo])	Wrapper for ztpttf.
stpttr(n,ap,[uplo])	Wrapper for stpttr.
dtpttr(n,ap,[uplo])	Wrapper for dtpttr.
ctpttr(n,ap,[uplo])	Wrapper for ctpttr.
ztpttr(n,ap,[uplo])	Wrapper for ztpttr.
strsyl(a,b,c,[trana,tranb,isgn,overwrite_c])	Wrapper for strsyl.
dtrsyl(a,b,c,[trana,tranb,isgn,overwrite_c])	Wrapper for dtrsyl.
ctrsyl(a,b,c,[trana,tranb,isgn,overwrite_c])	Wrapper for ctrsyl.
ztrsyl(a,b,c,[trana,tranb,isgn,overwrite_c])	Wrapper for ztrsyl.
strtri(c,[lower,unitdiag,overwrite_c])	Wrapper for strtri.
dtrtri(c,[lower,unitdiag,overwrite_c])	Wrapper for dtrtri.
ctrtri(c,[lower,unitdiag,overwrite_c])	Wrapper for ctrtri.
ztrtri(c,[lower,unitdiag,overwrite_c])	Wrapper for ztrtri.
strtrs(…)	Wrapper for strtrs.
dtrtrs(…)	Wrapper for dtrtrs.
ctrtrs(…)	Wrapper for ctrtrs.
ztrtrs(…)	Wrapper for ztrtrs.
strttf(a,[transr,uplo])	Wrapper for strttf.
dtrttf(a,[transr,uplo])	Wrapper for dtrttf.
ctrttf(a,[transr,uplo])	Wrapper for ctrttf.
ztrttf(a,[transr,uplo])	Wrapper for ztrttf.
strttp(a,[uplo])	Wrapper for strttp.
dtrttp(a,[uplo])	Wrapper for dtrttp.
ctrttp(a,[uplo])	Wrapper for ctrttp.
ztrttp(a,[uplo])	Wrapper for ztrttp.
stzrzf(a,[lwork,overwrite_a])	Wrapper for stzrzf.
dtzrzf(a,[lwork,overwrite_a])	Wrapper for dtzrzf.
ctzrzf(a,[lwork,overwrite_a])	Wrapper for ctzrzf.
ztzrzf(a,[lwork,overwrite_a])	Wrapper for ztzrzf.
stzrzf_lwork(m,n)	Wrapper for stzrzf_lwork.
dtzrzf_lwork(m,n)	Wrapper for dtzrzf_lwork.
ctzrzf_lwork(m,n)	Wrapper for ctzrzf_lwork.
ztzrzf_lwork(m,n)	Wrapper for ztzrzf_lwork.
cunghr(a,tau,[lo,hi,lwork,overwrite_a])	Wrapper for cunghr.
zunghr(a,tau,[lo,hi,lwork,overwrite_a])	Wrapper for zunghr.
cunghr_lwork(n,[lo,hi])	Wrapper for cunghr_lwork.
zunghr_lwork(n,[lo,hi])	Wrapper for zunghr_lwork.
cungqr(a,tau,[lwork,overwrite_a])	Wrapper for cungqr.
zungqr(a,tau,[lwork,overwrite_a])	Wrapper for zungqr.
cungrq(a,tau,[lwork,overwrite_a])	Wrapper for cungrq.
zungrq(a,tau,[lwork,overwrite_a])	Wrapper for zungrq.
cunmqr(side,trans,a,tau,c,lwork,[overwrite_c])	Wrapper for cunmqr.
zunmqr(side,trans,a,tau,c,lwork,[overwrite_c])	Wrapper for zunmqr.
sgeqrt(nb,a,[overwrite_a])	Wrapper for sgeqrt.
dgeqrt(nb,a,[overwrite_a])	Wrapper for dgeqrt.
cgeqrt(nb,a,[overwrite_a])	Wrapper for cgeqrt.
zgeqrt(nb,a,[overwrite_a])	Wrapper for zgeqrt.

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sgemqrt(v,t,c,[side,trans,overwrite_c])	Wrapper for sgemqrt.
dgemqrt(v,t,c,[side,trans,overwrite_c])	Wrapper for dgemqrt.
cgemqrt(v,t,c,[side,trans,overwrite_c])	Wrapper for cgemqrt.
zgemqrt(v,t,c,[side,trans,overwrite_c])	Wrapper for zgemqrt.
sgttrf(…)	Wrapper for sgttrf.
dgttrf(…)	Wrapper for dgttrf.
cgttrf(…)	Wrapper for cgttrf.
zgttrf(…)	Wrapper for zgttrf.
sgttrs(dl,d,du,du2,ipiv,b,[trans,overwrite_b])	Wrapper for sgttrs.
dgttrs(dl,d,du,du2,ipiv,b,[trans,overwrite_b])	Wrapper for dgttrs.
cgttrs(dl,d,du,du2,ipiv,b,[trans,overwrite_b])	Wrapper for cgttrs.
zgttrs(dl,d,du,du2,ipiv,b,[trans,overwrite_b])	Wrapper for zgttrs.
stpqrt(l,nb,a,b,[overwrite_a,overwrite_b])	Wrapper for stpqrt.
dtpqrt(l,nb,a,b,[overwrite_a,overwrite_b])	Wrapper for dtpqrt.
ctpqrt(l,nb,a,b,[overwrite_a,overwrite_b])	Wrapper for ctpqrt.
ztpqrt(l,nb,a,b,[overwrite_a,overwrite_b])	Wrapper for ztpqrt.
stpmqrt(…)	Wrapper for stpmqrt.
dtpmqrt(…)	Wrapper for dtpmqrt.
ctpmqrt(…)	Wrapper for ctpmqrt.
ztpmqrt(…)	Wrapper for ztpmqrt.
cuncsd(…)	Wrapper for cuncsd.
zuncsd(…)	Wrapper for zuncsd.
cuncsd_lwork(m,p,q)	Wrapper for cuncsd_lwork.
zuncsd_lwork(m,p,q)	Wrapper for zuncsd_lwork.
cunmrz(a,tau,c,[side,trans,lwork,overwrite_c])	Wrapper for cunmrz.
zunmrz(a,tau,c,[side,trans,lwork,overwrite_c])	Wrapper for zunmrz.
cunmrz_lwork(m,n,[side,trans])	Wrapper for cunmrz_lwork.
zunmrz_lwork(m,n,[side,trans])	Wrapper for zunmrz_lwork.
ilaver()	Wrapper for ilaver.

scipy.linalg.lapack.sgbsv

scipy.linalg.lapack.**sgbsv**(*kl*, *ku*, *ab*, *b*[, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgbsv.

Parameters

kl [input int]
ku [input int]
ab [input rank-2 array('f') with bounds (2*kl+ku+1,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

lub [rank-2 array('f') with bounds (2*kl+ku+1,n) and ab storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dgbsv

scipy.linalg.lapack.**dgbsv**(*kl*, *ku*, *ab*, *b*[, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for dgbsv.

Parameters

kl [input int]
ku [input int]
ab [input rank-2 array('d') with bounds (2*kl+ku+1,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

lub [rank-2 array('d') with bounds (2*kl+ku+1,n) and ab storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cgbsv

scipy.linalg.lapack.**cgbsv**(*kl*, *ku*, *ab*, *b*[, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for cgbsv.

Parameters

kl [input int]
ku [input int]
ab [input rank-2 array('F') with bounds (2*kl+ku+1,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

lub [rank-2 array('F') with bounds (2*kl+ku+1,n) and ab storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zgbsv

scipy.linalg.lapack.**zgbsv**(*kl*, *ku*, *ab*, *b*[, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for zgbsv.

Parameters

kl [input int]
ku [input int]
ab [input rank-2 array('D') with bounds (2*kl+ku+1,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

lub [rank-2 array('D') with bounds (2*kl+ku+1,n) and ab storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.sgbtrf

scipy.linalg.lapack.**sgbtrf**(*ab*, *kl*, *ku*[, *m*, *n*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for sgbtrf.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]
kl [input int]
ku [input int]

Returns

lu [rank-2 array('f') with bounds (ldab,n) and ab storage]
ipiv [rank-1 array('i') with bounds (MIN(m,n))]
info [int]

Other Parameters

m [input int, optional] Default: shape(ab,1)
n [input int, optional] Default: shape(ab,1)
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: max(shape(ab,0),1)

scipy.linalg.lapack.dgbtrf

scipy.linalg.lapack.**dgbtrf**(*ab*, *kl*, *ku*[, *m*, *n*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for dgbtrf.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]
kl [input int]
ku [input int]

Returns

lu [rank-2 array('d') with bounds (ldab,n) and ab storage]
ipiv [rank-1 array('i') with bounds (MIN(m,n))]
info [int]

Other Parameters

m [input int, optional] Default: shape(ab,1)
n [input int, optional] Default: shape(ab,1)
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: max(shape(ab,0),1)

scipy.linalg.lapack.cgbtrf

scipy.linalg.lapack.**cgbtrf**(*ab*, *kl*, *ku*[, *m*, *n*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for cgbtrf.

Parameters

ab [input rank-2 array('F') with bounds (ldab,n)]
kl [input int]
ku [input int]

Returns

lu [rank-2 array('F') with bounds (ldab,n) and ab storage]
ipiv [rank-1 array('i') with bounds (MIN(m,n))]
info [int]

Other Parameters

m [input int, optional] Default: shape(ab,1)
n [input int, optional] Default: shape(ab,1)
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: max(shape(ab,0),1)

scipy.linalg.lapack.zgbtrf

scipy.linalg.lapack.**zgbtrf**(*ab*, *kl*, *ku*[, *m*, *n*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for zgbtrf.

Parameters

ab [input rank-2 array('D') with bounds (ldab,n)]
kl [input int]
ku [input int]

Returns

lu [rank-2 array('D') with bounds (ldab,n) and ab storage]
ipiv [rank-1 array('i') with bounds (MIN(m,n))]
info [int]

Other Parameters

m [input int, optional] Default: shape(ab,1)
n [input int, optional] Default: shape(ab,1)
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: max(shape(ab,0),1)

scipy.linalg.lapack.sgbtrs

scipy.linalg.lapack.**sgbtrs**(*ab*, *kl*, *ku*, *b*, *ipiv*[, *trans*, *n*, *ldab*, *ldb*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgbtrs.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]
kl [input int]
ku [input int]
b [input rank-2 array('f') with bounds (ldb,nrhs)]
ipiv [input rank-1 array('i') with bounds (n)]

Returns

x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
trans [input int, optional] Default: 0
n [input int, optional] Default: shape(ab,1)
ldab [input int, optional] Default: shape(ab,0)
ldb [input int, optional] Default: shape(b,0)

scipy.linalg.lapack.dgbtrs

scipy.linalg.lapack.**dgbtrs**(*ab*, *kl*, *ku*, *b*, *ipiv*[, *trans*, *n*, *ldab*, *ldb*, *overwrite_b*]) **= <fortran object>**

Wrapper for dgbtrs.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]
kl [input int]
ku [input int]
b [input rank-2 array('d') with bounds (ldb,nrhs)]
ipiv [input rank-1 array('i') with bounds (n)]

Returns

x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
trans [input int, optional] Default: 0
n [input int, optional] Default: shape(ab,1)
ldab [input int, optional] Default: shape(ab,0)
ldb [input int, optional] Default: shape(b,0)

scipy.linalg.lapack.cgbtrs

scipy.linalg.lapack.**cgbtrs**(*ab*, *kl*, *ku*, *b*, *ipiv*[, *trans*, *n*, *ldab*, *ldb*, *overwrite_b*]) **= <fortran object>**

Wrapper for cgbtrs.

Parameters

ab [input rank-2 array('F') with bounds (ldab,n)]
kl [input int]
ku [input int]
b [input rank-2 array('F') with bounds (ldb,nrhs)]
ipiv [input rank-1 array('i') with bounds (n)]

Returns

x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
trans [input int, optional] Default: 0
n [input int, optional] Default: shape(ab,1)
ldab [input int, optional] Default: shape(ab,0)
ldb [input int, optional] Default: shape(b,0)

scipy.linalg.lapack.zgbtrs

scipy.linalg.lapack.**zgbtrs**(*ab*, *kl*, *ku*, *b*, *ipiv*[, *trans*, *n*, *ldab*, *ldb*, *overwrite_b*]) **= <fortran object>**

Wrapper for zgbtrs.

Parameters

ab [input rank-2 array('D') with bounds (ldab,n)]
kl [input int]
ku [input int]
b [input rank-2 array('D') with bounds (ldb,nrhs)]
ipiv [input rank-1 array('i') with bounds (n)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
trans [input int, optional] Default: 0
n [input int, optional] Default: shape(ab,1)
ldab [input int, optional] Default: shape(ab,0)

ldb [input int, optional] Default: shape(b,0)

scipy.linalg.lapack.sgebal

`scipy.linalg.lapack.`**`sgebal`**(*a*[, *scale*, *permute*, *overwrite_a*]) **= <fortran object>**

Wrapper for `sgebal`.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

ba [rank-2 array('f') with bounds (m,n) and a storage]
lo [int]
hi [int]
pivscale [rank-1 array('f') with bounds (n)]
info [int]

Other Parameters

scale [input int, optional] Default: 0
permute [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.dgebal

`scipy.linalg.lapack.`**`dgebal`**(*a*[, *scale*, *permute*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dgebal`.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

ba [rank-2 array('d') with bounds (m,n) and a storage]
lo [int]
hi [int]
pivscale [rank-1 array('d') with bounds (n)]
info [int]

Other Parameters

scale [input int, optional] Default: 0
permute [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.cgebal

`scipy.linalg.lapack.`**`cgebal`**(*a*[, *scale*, *permute*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cgebal`.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

ba [rank-2 array('F') with bounds (m,n) and a storage]
lo [int]

hi [int]
pivscale [rank-1 array('f') with bounds (n)]
info [int]

Other Parameters

scale [input int, optional] Default: 0
permute [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.zgebal

scipy.linalg.lapack.**zgebal**(*a*[, *scale*, *permute*, *overwrite_a*]) **= <fortran object>**

Wrapper for zgebal.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

ba [rank-2 array('D') with bounds (m,n) and a storage]
lo [int]
hi [int]
pivscale [rank-1 array('d') with bounds (n)]
info [int]

Other Parameters

scale [input int, optional] Default: 0
permute [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.sgecon

scipy.linalg.lapack.**sgecon**(*a*, *anorm*[, *norm*]) **= <fortran object>**

Wrapper for sgecon.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

norm [input string(len=1), optional] Default: '1'

scipy.linalg.lapack.dgecon

scipy.linalg.lapack.**dgecon**(*a*, *anorm*[, *norm*]) **= <fortran object>**

Wrapper for dgecon.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

norm [input string(len=1), optional] Default: '1'

scipy.linalg.lapack.cgecon

scipy.linalg.lapack.**cgecon**(*a*, *anorm*[, *norm*]) **= <fortran object>**

Wrapper for cgecon.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

norm [input string(len=1), optional] Default: '1'

scipy.linalg.lapack.zgecon

scipy.linalg.lapack.**zgecon**(*a*, *anorm*[, *norm*]) **= <fortran object>**

Wrapper for zgecon.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

norm [input string(len=1), optional] Default: '1'

scipy.linalg.lapack.sgeequ

scipy.linalg.lapack.**sgeequ**(*a*) **= <fortran object>**

Wrapper for sgeequ.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

r [rank-1 array('f') with bounds (m)]
c [rank-1 array('f') with bounds (n)]
rowcnd [float]
colcnd [float]
amax [float]
info [int]

scipy.linalg.lapack.dgeequ

scipy.linalg.lapack.**dgeequ**(*a*) **= <fortran object>**

Wrapper for dgeequ.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

r [rank-1 array('d') with bounds (m)]
c [rank-1 array('d') with bounds (n)]
rowcnd [float]
colcnd [float]
amax [float]
info [int]

scipy.linalg.lapack.cgeequ

scipy.linalg.lapack.**cgeequ**(*a*) **= <fortran object>**

Wrapper for cgeequ.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

r [rank-1 array('f') with bounds (m)]
c [rank-1 array('f') with bounds (n)]
rowcnd [float]
colcnd [float]
amax [float]
info [int]

scipy.linalg.lapack.zgeequ

scipy.linalg.lapack.**zgeequ**(*a*) **= <fortran object>**
Wrapper for zgeequ.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

r [rank-1 array('d') with bounds (m)]
c [rank-1 array('d') with bounds (n)]
rowcnd [float]
colcnd [float]
amax [float]
info [int]

scipy.linalg.lapack.sgeequb

scipy.linalg.lapack.**sgeequb**(*a*) **= <fortran object>**
Wrapper for sgeequb.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

r [rank-1 array('f') with bounds (m)]
c [rank-1 array('f') with bounds (n)]
rowcnd [float]
colcnd [float]
amax [float]
info [int]

scipy.linalg.lapack.dgeequb

scipy.linalg.lapack.**dgeequb**(*a*) **= <fortran object>**
Wrapper for dgeequb.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

r [rank-1 array('d') with bounds (m)]
c [rank-1 array('d') with bounds (n)]
rowcnd [float]
colcnd [float]
amax [float]
info [int]

scipy.linalg.lapack.cgeequb

scipy.linalg.lapack.**cgeequb**(*a*) **= <fortran object>**

Wrapper for cgeequb.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

r [rank-1 array('f') with bounds (m)]
c [rank-1 array('f') with bounds (n)]
rowcnd [float]
colcnd [float]
amax [float]
info [int]

scipy.linalg.lapack.zgeequb

scipy.linalg.lapack.**zgeequb**(*a*) **= <fortran object>**

Wrapper for zgeequb.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

r [rank-1 array('d') with bounds (m)]
c [rank-1 array('d') with bounds (n)]
rowcnd [float]
colcnd [float]
amax [float]
info [int]

scipy.linalg.lapack.sgees

scipy.linalg.lapack.**sgees**(*sselect*, *a*[, *compute_v*, *sort_t*, *lwork*, *sselect_extra_args*, *overwrite_a*]) **= <fortran object>**

Wrapper for sgees.

Parameters

sselect [call-back function]
a [input rank-2 array('f') with bounds (n,n)]

Returns

t [rank-2 array('f') with bounds (n,n) and a storage]
sdim [int]
wr [rank-1 array('f') with bounds (n)]
wi [rank-1 array('f') with bounds (n)]
vs [rank-2 array('f') with bounds (ldvs,n)]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
sort_t [input int, optional] Default: 0

sselect_extra_args
[input tuple, optional] Default: ()
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

Notes

Call-back functions:

```
def sselect(arg1,arg2): return sselect
Required arguments:
  arg1 : input float
  arg2 : input float
Return objects:
  sselect : int
```

scipy.linalg.lapack.dgees

scipy.linalg.lapack.**dgees**(*dselect*, *a*[, *compute_v*, *sort_t*, *lwork*, *dselect_extra_args*, *overwrite_a*]) = **<fortran object>**

Wrapper for dgees.

Parameters

dselect [call-back function]
a [input rank-2 array('d') with bounds (n,n)]

Returns

t [rank-2 array('d') with bounds (n,n) and a storage]
sdim [int]
wr [rank-1 array('d') with bounds (n)]
wi [rank-1 array('d') with bounds (n)]
vs [rank-2 array('d') with bounds (ldvs,n)]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
sort_t [input int, optional] Default: 0
dselect_extra_args
[input tuple, optional] Default: ()
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

Notes

Call-back functions:

```
def dselect(arg1,arg2): return dselect
Required arguments:
  arg1 : input float
  arg2 : input float
Return objects:
  dselect : int
```

scipy.linalg.lapack.cgees

scipy.linalg.lapack.**cgees**(*cselect*, *a*[, *compute_v*, *sort_t*, *lwork*, *cselect_extra_args*, *overwrite_a*]) = **<fortran object>**

Wrapper for cgees.

Parameters

cselect [call-back function]
a [input rank-2 array('F') with bounds (n,n)]

Returns

t [rank-2 array('F') with bounds (n,n) and a storage]
sdim [int]
w [rank-1 array('F') with bounds (n)]
vs [rank-2 array('F') with bounds (ldvs,n)]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
sort_t [input int, optional] Default: 0
cselect_extra_args
[input tuple, optional] Default: ()
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

Notes

Call-back functions:

```
def cselect(arg): return cselect
Required arguments:
  arg : input complex
Return objects:
  cselect : int
```

scipy.linalg.lapack.zgees

scipy.linalg.lapack.**zgees**(*zselect*, *a*[, *compute_v*, *sort_t*, *lwork*, *zselect_extra_args*, *overwrite_a*]) = **<fortran object>**

Wrapper for zgees.

Parameters

zselect [call-back function]
a [input rank-2 array('D') with bounds (n,n)]

Returns

t [rank-2 array('D') with bounds (n,n) and a storage]
sdim [int]
w [rank-1 array('D') with bounds (n)]
vs [rank-2 array('D') with bounds (ldvs,n)]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
sort_t [input int, optional] Default: 0
zselect_extra_args
[input tuple, optional] Default: ()
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

Notes

Call-back functions:

```
def zselect(arg): return zselect
Required arguments:
  arg : input complex
Return objects:
  zselect : int
```

scipy.linalg.lapack.sgeev

scipy.linalg.lapack.**sgeev**(*a*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for sgeev.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

wr [rank-1 array('f') with bounds (n)]
wi [rank-1 array('f') with bounds (n)]
vl [rank-2 array('f') with bounds (ldvl,n)]
vr [rank-2 array('f') with bounds (ldvr,n)]
info [int]

Other Parameters

compute_vl
: [input int, optional] Default: 1

compute_vr
: [input int, optional] Default: 1

overwrite_a
: [input int, optional] Default: 0

lwork
: [input int, optional] Default: max(4*n,1)

scipy.linalg.lapack.dgeev

scipy.linalg.lapack.**dgeev**(*a*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dgeev.

Parameters

a
: [input rank-2 array('d') with bounds (n,n)]

Returns

wr
: [rank-1 array('d') with bounds (n)]

wi
: [rank-1 array('d') with bounds (n)]

vl
: [rank-2 array('d') with bounds (ldvl,n)]

vr
: [rank-2 array('d') with bounds (ldvr,n)]

info
: [int]

Other Parameters

compute_vl
: [input int, optional] Default: 1

compute_vr
: [input int, optional] Default: 1

overwrite_a
: [input int, optional] Default: 0

lwork
: [input int, optional] Default: max(4*n,1)

scipy.linalg.lapack.cgeev

scipy.linalg.lapack.**cgeev**(*a*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cgeev.

Parameters

a
: [input rank-2 array('F') with bounds (n,n)]

Returns

w
: [rank-1 array('F') with bounds (n)]

vl
: [rank-2 array('F') with bounds (ldvl,n)]

vr
: [rank-2 array('F') with bounds (ldvr,n)]

info
: [int]

Other Parameters

compute_vl
: [input int, optional] Default: 1

compute_vr
: [input int, optional] Default: 1

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.zgeev

scipy.linalg.lapack.**zgeev**(*a*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zgeev.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

w [rank-1 array('D') with bounds (n)]
vl [rank-2 array('D') with bounds (ldvl,n)]
vr [rank-2 array('D') with bounds (ldvr,n)]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.sgeev_lwork

scipy.linalg.lapack.**sgeev_lwork**(*n*[, *compute_vl*, *compute_vr*]) **= <fortran object>**

Wrapper for sgeev_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1

scipy.linalg.lapack.dgeev_lwork

scipy.linalg.lapack.**dgeev_lwork**(*n*[, *compute_vl*, *compute_vr*]) **= <fortran object>**

Wrapper for dgeev_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1

scipy.linalg.lapack.cgeev_lwork

scipy.linalg.lapack.**cgeev_lwork**(*n*[, *compute_vl*, *compute_vr*]) **= <fortran object>**

Wrapper for cgeev_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1

scipy.linalg.lapack.zgeev_lwork

scipy.linalg.lapack.**zgeev_lwork**(*n*[, *compute_vl*, *compute_vr*]) **= <fortran object>**

Wrapper for zgeev_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1

scipy.linalg.lapack.sgegv

scipy.linalg.lapack.**sgegv**(**args*, ***kwds*)

sgegv is deprecated! The **gegv* family of routines has been deprecated in LAPACK 3.6.0 in favor of the **ggev* family of routines. The corresponding wrappers will be removed from SciPy in a future release.

alphar,alphai,beta,vl,vr,info = sgegv(a,b,[compute_vl,compute_vr,lwork,overwrite_a,overwrite_b])

Wrapper for `sgegv`.

Parameters

a	[input rank-2 array('f') with bounds (n,n)]
b	[input rank-2 array('f') with bounds (n,n)]

Returns

alphar	[rank-1 array('f') with bounds (n)]
alphai	[rank-1 array('f') with bounds (n)]
beta	[rank-1 array('f') with bounds (n)]
vl	[rank-2 array('f') with bounds (ldvl,n)]
vr	[rank-2 array('f') with bounds (ldvr,n)]
info	[int]

Other Parameters

compute_vl
: [input int, optional] Default: 1

compute_vr
: [input int, optional] Default: 1

overwrite_a
: [input int, optional] Default: 0

overwrite_b
: [input int, optional] Default: 0

lwork
: [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.dgegv

scipy.linalg.lapack.**dgegv**(**args*, ***kwds*)

dgegv is deprecated! The **gegv* family of routines has been deprecated in LAPACK 3.6.0 in favor of the **ggev* family of routines. The corresponding wrappers will be removed from SciPy in a future release.

alphar,alphai,beta,vl,vr,info = dgegv(a,b,[compute_vl,compute_vr,lwork,overwrite_a,overwrite_b])

Wrapper for `dgegv`.

Parameters

a	[input rank-2 array('d') with bounds (n,n)]
b	[input rank-2 array('d') with bounds (n,n)]

Returns

alphar	[rank-1 array('d') with bounds (n)]
alphai	[rank-1 array('d') with bounds (n)]
beta	[rank-1 array('d') with bounds (n)]
vl	[rank-2 array('d') with bounds (ldvl,n)]
vr	[rank-2 array('d') with bounds (ldvr,n)]
info	[int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.cgegv

scipy.linalg.lapack.**cgegv**(**args*, ***kwds*)

cgegv is deprecated! The **gegv* family of routines has been deprecated in LAPACK 3.6.0 in favor of the **ggev* family of routines. The corresponding wrappers will be removed from SciPy in a future release.

alpha,beta,vl,vr,info = cgegv(a,b,[compute_vl,compute_vr,lwork,overwrite_a,overwrite_b])

Wrapper for `cgegv`.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,n)]

Returns

alpha [rank-1 array('F') with bounds (n)]
beta [rank-1 array('F') with bounds (n)]
vl [rank-2 array('F') with bounds (ldvl,n)]
vr [rank-2 array('F') with bounds (ldvr,n)]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.zgegv

scipy.linalg.lapack.**zgegv**(**args*, ***kwds*)

zgegv is deprecated! The **gegv* family of routines has been deprecated in LAPACK 3.6.0 in favor of the **ggev* family of routines. The corresponding wrappers will be removed from SciPy in a future release.

alpha,beta,vl,vr,info = zgegv(a,b,[compute_vl,compute_vr,lwork,overwrite_a,overwrite_b])

Wrapper for `zgegv`.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,n)]

Returns

alpha [rank-1 array('D') with bounds (n)]
beta [rank-1 array('D') with bounds (n)]
vl [rank-2 array('D') with bounds (ldvl,n)]
vr [rank-2 array('D') with bounds (ldvr,n)]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.sgehrd

scipy.linalg.lapack.**sgehrd**(*a*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for sgehrd.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

ht [rank-2 array('f') with bounds (n,n) and a storage]
tau [rank-1 array('f') with bounds (n - 1)]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.dgehrd

scipy.linalg.lapack.**dgehrd**(*a*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for dgehrd.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

ht [rank-2 array('d') with bounds (n,n) and a storage]
tau [rank-1 array('d') with bounds (n - 1)]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a
[input int, optional] Default: 0

lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.cgehrd

scipy.linalg.lapack.**cgehrd**(*a*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cgehrd.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

ht [rank-2 array('F') with bounds (n,n) and a storage]
tau [rank-1 array('F') with bounds (n - 1)]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.zgehrd

scipy.linalg.lapack.**zgehrd**(*a*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zgehrd.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

ht [rank-2 array('D') with bounds (n,n) and a storage]
tau [rank-1 array('D') with bounds (n - 1)]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.sgehrd_lwork

scipy.linalg.lapack.**sgehrd_lwork**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for sgehrd_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.dgehrd_lwork

scipy.linalg.lapack.**dgehrd_lwork**(*n*[, *lo*, *hi*]) **= <fortran object>**
Wrapper for dgehrd_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.cgehrd_lwork

scipy.linalg.lapack.**cgehrd_lwork**(*n*[, *lo*, *hi*]) **= <fortran object>**
Wrapper for cgehrd_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.zgehrd_lwork

scipy.linalg.lapack.**zgehrd_lwork**(*n*[, *lo*, *hi*]) **= <fortran object>**
Wrapper for zgehrd_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.sgejsv

scipy.linalg.lapack.**sgejsv**(*a*[, *joba*, *jobu*, *jobv*, *jobr*, *jobt*, *jobp*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for sgejsv.

Parameters

a [input rank-2 array('f') with bounds (lda,n)]

Returns

sva [rank-1 array('f') with bounds (n)]
u [rank-2 array('f') with bounds (((jobt == 0)&&(jobu == 3)?0:m),((jobt == 0)&&(jobu == 3)?0:(jobu == 1?m:n)))]
v [rank-2 array('f') with bounds (((jobt == 0)&&(jobv == 3)?0:ldv),((jobt == 0)&&(jobv == 3)?0:n))]
workout [rank-1 array('f') with bounds (7)]
iworkout [rank-1 array('i') with bounds (3)]
info [int]

Other Parameters

joba [input int, optional] Default: 4
jobu [input int, optional] Default: 0
jobv [input int, optional] Default: 0
jobr [input int, optional] Default: 1
jobt [input int, optional] Default: 0
jobp [input int, optional] Default: 1
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(6*n+2*n*n, max(2*m+n, max(4*n+n*n, max(2*n+n*n+6, 7))))

scipy.linalg.lapack.dgejsv

scipy.linalg.lapack.**dgejsv**(*a*[, *joba*, *jobu*, *jobv*, *jobr*, *jobt*, *jobp*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for dgejsv.

Parameters

a [input rank-2 array('d') with bounds (lda,n)]

Returns

sva [rank-1 array('d') with bounds (n)]
u [rank-2 array('d') with bounds (((jobt == 0)&&(jobu == 3)?0:m),((jobt == 0)&&(jobu == 3)?0:(jobu == 1?m:n)))]
v [rank-2 array('d') with bounds (((jobt == 0)&&(jobv == 3)?0:ldv),((jobt == 0)&&(jobv == 3)?0:n))]
workout [rank-1 array('d') with bounds (7)]
iworkout [rank-1 array('i') with bounds (3)]
info [int]

Other Parameters

joba [input int, optional] Default: 4
jobu [input int, optional] Default: 0
jobv [input int, optional] Default: 0
jobr [input int, optional] Default: 1

jobt [input int, optional] Default: 0
jobp [input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(6*n+2*n*n, max(2*m+n, max(4*n+n*n, max(2*n+n*n+6, 7))))

scipy.linalg.lapack.sgels

scipy.linalg.lapack.**sgels**(*a*, *b*[, *trans*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgels.

Parameters

a [input rank-2 array('f') with bounds (m,n)]
b [input rank-2 array('f') with bounds (MAX(m,n),nrhs)]

Returns

lqr [rank-2 array('f') with bounds (m,n) and a storage]
x [rank-2 array('f') with bounds (MAX(m,n),nrhs) and b storage]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(MIN(m,n)+MAX(MIN(m,n),nrhs),1)

scipy.linalg.lapack.dgels

scipy.linalg.lapack.**dgels**(*a*, *b*[, *trans*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dgels.

Parameters

a [input rank-2 array('d') with bounds (m,n)]
b [input rank-2 array('d') with bounds (MAX(m,n),nrhs)]

Returns

lqr [rank-2 array('d') with bounds (m,n) and a storage]
x [rank-2 array('d') with bounds (MAX(m,n),nrhs) and b storage]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(MIN(m,n)+MAX(MIN(m,n),nrhs),1)

scipy.linalg.lapack.cgels

scipy.linalg.lapack.**cgels**(*a*, *b*[, *trans*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for cgels.

Parameters

a [input rank-2 array('F') with bounds (m,n)]
b [input rank-2 array('F') with bounds (MAX(m,n),nrhs)]

Returns

lqr [rank-2 array('F') with bounds (m,n) and a storage]
x [rank-2 array('F') with bounds (MAX(m,n),nrhs) and b storage]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(MIN(m,n)+MAX(MIN(m,n),nrhs),1)

scipy.linalg.lapack.zgels

scipy.linalg.lapack.**zgels**(*a*, *b*[, *trans*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zgels.

Parameters

a [input rank-2 array('D') with bounds (m,n)]
b [input rank-2 array('D') with bounds (MAX(m,n),nrhs)]

Returns

lqr [rank-2 array('D') with bounds (m,n) and a storage]
x [rank-2 array('D') with bounds (MAX(m,n),nrhs) and b storage]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(MIN(m,n)+MAX(MIN(m,n),nrhs),1)

scipy.linalg.lapack.sgels_lwork

scipy.linalg.lapack.**sgels_lwork**(*m*, *n*, *nrhs*[, *trans*]) **= <fortran object>**

Wrapper for sgels_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [float]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'

scipy.linalg.lapack.dgels_lwork

scipy.linalg.lapack.**dgels_lwork**(*m*, *n*, *nrhs*[, *trans*]) **= <fortran object>**

Wrapper for dgels_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [float]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'

scipy.linalg.lapack.cgels_lwork

scipy.linalg.lapack.**cgels_lwork**(*m*, *n*, *nrhs*[, *trans*]) **= <fortran object>**

Wrapper for cgels_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [complex]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'

scipy.linalg.lapack.zgels_lwork

scipy.linalg.lapack.**zgels_lwork**(*m*, *n*, *nrhs*[, *trans*]) **= <fortran object>**

Wrapper for zgels_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [complex]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'

scipy.linalg.lapack.sgelsd

scipy.linalg.lapack.**sgelsd**(*a*, *b*, *lwork*, *size_iwork*[, *cond*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgelsd.

Parameters

a [input rank-2 array('f') with bounds (m,n)]
b [input rank-2 array('f') with bounds (maxmn,nrhs)]
lwork [input int]
size_iwork [input int]

Returns

x [rank-2 array('f') with bounds (maxmn,nrhs) and b storage]
s [rank-1 array('f') with bounds (minmn)]
rank [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
cond [input float, optional] Default: -1.0

scipy.linalg.lapack.dgelsd

scipy.linalg.lapack.**dgelsd**(*a*, *b*, *lwork*, *size_iwork*[, *cond*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dgelsd.

Parameters

a [input rank-2 array('d') with bounds (m,n)]
b [input rank-2 array('d') with bounds (maxmn,nrhs)]
lwork [input int]
size_iwork [input int]

Returns

x [rank-2 array('d') with bounds (maxmn,nrhs) and b storage]
s [rank-1 array('d') with bounds (minmn)]
rank [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
cond [input float, optional] Default: -1.0

scipy.linalg.lapack.cgelsd

scipy.linalg.lapack.**cgelsd**(*a*, *b*, *lwork*, *size_rwork*, *size_iwork*[, *cond*, *overwrite_a*, *overwrite_b*])
= <fortran object>

Wrapper for cgelsd.

Parameters

a [input rank-2 array('F') with bounds (m,n)]
b [input rank-2 array('F') with bounds (maxmn,nrhs)]
lwork [input int]
size_rwork
[input int]
size_iwork [input int]

Returns

x [rank-2 array('F') with bounds (maxmn,nrhs) and b storage]
s [rank-1 array('f') with bounds (minmn)]
rank [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
cond [input float, optional] Default: -1.0

scipy.linalg.lapack.zgelsd

scipy.linalg.lapack.**zgelsd**(*a*, *b*, *lwork*, *size_rwork*, *size_iwork*[, *cond*, *overwrite_a*, *overwrite_b*])
= <fortran object>

Wrapper for zgelsd.

Parameters

a [input rank-2 array('D') with bounds (m,n)]
b [input rank-2 array('D') with bounds (maxmn,nrhs)]
lwork [input int]
size_rwork
[input int]
size_iwork [input int]

Returns

x [rank-2 array('D') with bounds (maxmn,nrhs) and b storage]

s [rank-1 array('d') with bounds (minmn)]
rank [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
cond [input float, optional] Default: -1.0

scipy.linalg.lapack.sgelsd_lwork

scipy.linalg.lapack.**sgelsd_lwork**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**
Wrapper for sgelsd_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: -1

scipy.linalg.lapack.dgelsd_lwork

scipy.linalg.lapack.**dgelsd_lwork**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**
Wrapper for dgelsd_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: -1

scipy.linalg.lapack.cgelsd_lwork

scipy.linalg.lapack.**cgelsd_lwork**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for cgelsd_lwork.

Parameters

m	[input int]
n	[input int]
nrhs	[input int]

Returns

work	[complex]
rwork	[float]
iwork	[int]
info	[int]

Other Parameters

cond	[input float, optional] Default: -1.0
lwork	[input int, optional] Default: -1

scipy.linalg.lapack.zgelsd_lwork

scipy.linalg.lapack.**zgelsd_lwork**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for zgelsd_lwork.

Parameters

m	[input int]
n	[input int]
nrhs	[input int]

Returns

work	[complex]
rwork	[float]
iwork	[int]
info	[int]

Other Parameters

cond	[input float, optional] Default: -1.0
lwork	[input int, optional] Default: -1

scipy.linalg.lapack.sgelss

scipy.linalg.lapack.**sgelss**(*a*, *b*[, *cond*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgelss.

Parameters

a	[input rank-2 array('f') with bounds (m,n)]
b	[input rank-2 array('f') with bounds (maxmn,nrhs)]

Returns

v	[rank-2 array('f') with bounds (m,n) and a storage]
x	[rank-2 array('f') with bounds (maxmn,nrhs) and b storage]
s	[rank-1 array('f') with bounds (minmn)]
rank	[int]

work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: max(3*minmn+MAX(2*minmn,MAX(maxmn,nrhs)),1)

scipy.linalg.lapack.dgelss

scipy.linalg.lapack.**dgelss**(*a*, *b*[, *cond*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dgelss.

Parameters

a [input rank-2 array('d') with bounds (m,n)]
b [input rank-2 array('d') with bounds (maxmn,nrhs)]

Returns

v [rank-2 array('d') with bounds (m,n) and a storage]
x [rank-2 array('d') with bounds (maxmn,nrhs) and b storage]
s [rank-1 array('d') with bounds (minmn)]
rank [int]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: max(3*minmn+MAX(2*minmn,MAX(maxmn,nrhs)),1)

scipy.linalg.lapack.cgelss

scipy.linalg.lapack.**cgelss**(*a*, *b*[, *cond*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for cgelss.

Parameters

a [input rank-2 array('F') with bounds (m,n)]
b [input rank-2 array('F') with bounds (maxmn,nrhs)]

Returns

v [rank-2 array('F') with bounds (m,n) and a storage]
x [rank-2 array('F') with bounds (maxmn,nrhs) and b storage]
s [rank-1 array('f') with bounds (minmn)]
rank [int]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

overwrite_b
: [input int, optional] Default: 0

cond
: [input float, optional] Default: -1.0

lwork
: [input int, optional] Default: max(2*minmn+MAX(maxmn,nrhs),1)

scipy.linalg.lapack.zgelss

`scipy.linalg.lapack.`**`zgelss`**(*a*, *b*[, *cond*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for `zgelss`.

Parameters

a
: [input rank-2 array('D') with bounds (m,n)]

b
: [input rank-2 array('D') with bounds (maxmn,nrhs)]

Returns

v
: [rank-2 array('D') with bounds (m,n) and a storage]

x
: [rank-2 array('D') with bounds (maxmn,nrhs) and b storage]

s
: [rank-1 array('d') with bounds (minmn)]

rank
: [int]

work
: [rank-1 array('D') with bounds (MAX(lwork,1))]

info
: [int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

overwrite_b
: [input int, optional] Default: 0

cond
: [input float, optional] Default: -1.0

lwork
: [input int, optional] Default: max(2*minmn+MAX(maxmn,nrhs),1)

scipy.linalg.lapack.sgelss_lwork

`scipy.linalg.lapack.`**`sgelss_lwork`**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for `sgelss_lwork`.

Parameters

m
: [input int]

n
: [input int]

nrhs
: [input int]

Returns

work
: [float]

info
: [int]

Other Parameters

cond
: [input float, optional] Default: -1.0

lwork
: [input int, optional] Default: -1

scipy.linalg.lapack.dgelss_lwork

scipy.linalg.lapack.**dgelss_lwork**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for dgelss_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [float]
info [int]

Other Parameters

cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: -1

scipy.linalg.lapack.cgelss_lwork

scipy.linalg.lapack.**cgelss_lwork**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for cgelss_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [complex]
info [int]

Other Parameters

cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: -1

scipy.linalg.lapack.zgelss_lwork

scipy.linalg.lapack.**zgelss_lwork**(*m*, *n*, *nrhs*[, *cond*, *lwork*]) **= <fortran object>**

Wrapper for zgelss_lwork.

Parameters

m [input int]
n [input int]
nrhs [input int]

Returns

work [complex]
info [int]

Other Parameters

cond [input float, optional] Default: -1.0
lwork [input int, optional] Default: -1

scipy.linalg.lapack.sgelsy

scipy.linalg.lapack.**sgelsy**(*a*, *b*, *jptv*, *cond*, *lwork*[, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for sgelsy.

Parameters

a [input rank-2 array('f') with bounds (m,n)]
b [input rank-2 array('f') with bounds (maxmn,nrhs)]
jptv [input rank-1 array('i') with bounds (n)]
cond [input float]
lwork [input int]

Returns

v [rank-2 array('f') with bounds (m,n) and a storage]
x [rank-2 array('f') with bounds (maxmn,nrhs) and b storage]
j [rank-1 array('i') with bounds (n) and jptv storage]
rank [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dgelsy

scipy.linalg.lapack.**dgelsy**(*a*, *b*, *jptv*, *cond*, *lwork*[, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for dgelsy.

Parameters

a [input rank-2 array('d') with bounds (m,n)]
b [input rank-2 array('d') with bounds (maxmn,nrhs)]
jptv [input rank-1 array('i') with bounds (n)]
cond [input float]
lwork [input int]

Returns

v [rank-2 array('d') with bounds (m,n) and a storage]
x [rank-2 array('d') with bounds (maxmn,nrhs) and b storage]
j [rank-1 array('i') with bounds (n) and jptv storage]
rank [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cgelsy

scipy.linalg.lapack.**cgelsy**(*a*, *b*, *jptv*, *cond*, *lwork*[, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for cgelsy.

Parameters

a	[input rank-2 array('F') with bounds (m,n)]
b	[input rank-2 array('F') with bounds (maxmn,nrhs)]
jptv	[input rank-1 array('i') with bounds (n)]
cond	[input float]
lwork	[input int]

Returns

v	[rank-2 array('F') with bounds (m,n) and a storage]
x	[rank-2 array('F') with bounds (maxmn,nrhs) and b storage]
j	[rank-1 array('i') with bounds (n) and jptv storage]
rank	[int]
info	[int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

overwrite_b
: [input int, optional] Default: 0

scipy.linalg.lapack.zgelsy

scipy.linalg.lapack.**zgelsy**(*a*, *b*, *jptv*, *cond*, *lwork*[, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for zgelsy.

Parameters

a	[input rank-2 array('D') with bounds (m,n)]
b	[input rank-2 array('D') with bounds (maxmn,nrhs)]
jptv	[input rank-1 array('i') with bounds (n)]
cond	[input float]
lwork	[input int]

Returns

v	[rank-2 array('D') with bounds (m,n) and a storage]
x	[rank-2 array('D') with bounds (maxmn,nrhs) and b storage]
j	[rank-1 array('i') with bounds (n) and jptv storage]
rank	[int]
info	[int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

overwrite_b
: [input int, optional] Default: 0

scipy.linalg.lapack.sgelsy_lwork

scipy.linalg.lapack.**sgelsy_lwork**(*m*, *n*, *nrhs*, *cond*[, *lwork*]) **= <fortran object>**

Wrapper for sgelsy_lwork.

Parameters

m	[input int]
n	[input int]
nrhs	[input int]
cond	[input float]

Returns

work	[float]
info	[int]

Other Parameters

lwork	[input int, optional] Default: -1

scipy.linalg.lapack.dgelsy_lwork

scipy.linalg.lapack.**dgelsy_lwork**(*m*, *n*, *nrhs*, *cond*[, *lwork*]) **= <fortran object>**

Wrapper for dgelsy_lwork.

Parameters

m	[input int]
n	[input int]
nrhs	[input int]
cond	[input float]

Returns

work	[float]
info	[int]

Other Parameters

lwork	[input int, optional] Default: -1

scipy.linalg.lapack.cgelsy_lwork

scipy.linalg.lapack.**cgelsy_lwork**(*m*, *n*, *nrhs*, *cond*[, *lwork*]) **= <fortran object>**

Wrapper for cgelsy_lwork.

Parameters

m	[input int]
n	[input int]
nrhs	[input int]
cond	[input float]

Returns

work	[complex]
info	[int]

Other Parameters

lwork	[input int, optional] Default: -1

scipy.linalg.lapack.zgelsy_lwork

scipy.linalg.lapack.**zgelsy_lwork**(*m*, *n*, *nrhs*, *cond*[, *lwork*]) **= <fortran object>**

Wrapper for zgelsy_lwork.

Parameters

m	[input int]
n	[input int]
nrhs	[input int]
cond	[input float]

Returns

work	[complex]
info	[int]

Other Parameters

lwork	[input int, optional] Default: -1

scipy.linalg.lapack.sgeqp3

scipy.linalg.lapack.**sgeqp3**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for sgeqp3.

Parameters

a	[input rank-2 array('f') with bounds (m,n)]

Returns

qr	[rank-2 array('f') with bounds (m,n) and a storage]
jpvt	[rank-1 array('i') with bounds (n)]
tau	[rank-1 array('f') with bounds (MIN(m,n))]
work	[rank-1 array('f') with bounds (MAX(lwork,1))]
info	[int]

Other Parameters

overwrite_a	[input int, optional] Default: 0
lwork	[input int, optional] Default: max(3*(n+1),1)

scipy.linalg.lapack.dgeqp3

scipy.linalg.lapack.**dgeqp3**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dgeqp3.

Parameters

a	[input rank-2 array('d') with bounds (m,n)]

Returns

qr	[rank-2 array('d') with bounds (m,n) and a storage]
jpvt	[rank-1 array('i') with bounds (n)]
tau	[rank-1 array('d') with bounds (MIN(m,n))]
work	[rank-1 array('d') with bounds (MAX(lwork,1))]
info	[int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*(n+1),1)

scipy.linalg.lapack.cgeqp3

scipy.linalg.lapack.**cgeqp3**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for cgeqp3.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

qr [rank-2 array('F') with bounds (m,n) and a storage]
jpvt [rank-1 array('i') with bounds (n)]
tau [rank-1 array('F') with bounds (MIN(m,n))]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*(n+1),1)

scipy.linalg.lapack.zgeqp3

scipy.linalg.lapack.**zgeqp3**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for zgeqp3.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

qr [rank-2 array('D') with bounds (m,n) and a storage]
jpvt [rank-1 array('i') with bounds (n)]
tau [rank-1 array('D') with bounds (MIN(m,n))]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*(n+1),1)

scipy.linalg.lapack.sgeqrf

scipy.linalg.lapack.**sgeqrf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for sgeqrf.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

qr [rank-2 array('f') with bounds (m,n) and a storage]
tau [rank-1 array('f') with bounds (MIN(m,n))]

work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.dgeqrf

`scipy.linalg.lapack.`**`dgeqrf`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for `dgeqrf`.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

qr [rank-2 array('d') with bounds (m,n) and a storage]
tau [rank-1 array('d') with bounds (MIN(m,n))]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.cgeqrf

`scipy.linalg.lapack.`**`cgeqrf`**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for `cgeqrf`.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

qr [rank-2 array('F') with bounds (m,n) and a storage]
tau [rank-1 array('F') with bounds (MIN(m,n))]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.zgeqrf

scipy.linalg.lapack.**zgeqrf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zgeqrf.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

qr [rank-2 array('D') with bounds (m,n) and a storage]
tau [rank-1 array('D') with bounds (MIN(m,n))]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.sgeqrf_lwork

scipy.linalg.lapack.**sgeqrf_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for sgeqrf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.dgeqrf_lwork

scipy.linalg.lapack.**dgeqrf_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for dgeqrf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.cgeqrf_lwork

scipy.linalg.lapack.**cgeqrf_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for cgeqrf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]

info [int]

scipy.linalg.lapack.zgeqrf_lwork

scipy.linalg.lapack.**zgeqrf_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for zgeqrf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.sgeqrfp

scipy.linalg.lapack.**sgeqrfp**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for sgeqrfp.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

qr [rank-2 array('f') with bounds (m,n) and a storage]
tau [rank-1 array('f') with bounds (MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(1, n)

scipy.linalg.lapack.dgeqrfp

scipy.linalg.lapack.**dgeqrfp**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dgeqrfp.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

qr [rank-2 array('d') with bounds (m,n) and a storage]
tau [rank-1 array('d') with bounds (MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(1, n)

scipy.linalg.lapack.cgeqrfp

scipy.linalg.lapack.**cgeqrfp**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cgeqrfp.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

qr [rank-2 array('F') with bounds (m,n) and a storage]
tau [rank-1 array('F') with bounds (MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(1, n)

scipy.linalg.lapack.zgeqrfp

scipy.linalg.lapack.**zgeqrfp**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zgeqrfp.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

qr [rank-2 array('D') with bounds (m,n) and a storage]
tau [rank-1 array('D') with bounds (MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(1, n)

scipy.linalg.lapack.sgeqrfp_lwork

scipy.linalg.lapack.**sgeqrfp_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for sgeqrfp_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.dgeqrfp_lwork

scipy.linalg.lapack.**dgeqrfp_lwork**(*m*, *n*) **= <fortran object>**
Wrapper for dgeqrfp_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.cgeqrfp_lwork

scipy.linalg.lapack.**cgeqrfp_lwork**(*m*, *n*) **= <fortran object>**
Wrapper for cgeqrfp_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.zgeqrfp_lwork

scipy.linalg.lapack.**zgeqrfp_lwork**(*m*, *n*) **= <fortran object>**
Wrapper for zgeqrfp_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.sgerqf

scipy.linalg.lapack.**sgerqf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for sgerqf.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

qr [rank-2 array('f') with bounds (m,n) and a storage]
tau [rank-1 array('f') with bounds (MIN(m,n))]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.dgerqf

scipy.linalg.lapack.**dgerqf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dgerqf.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

qr [rank-2 array('d') with bounds (m,n) and a storage]
tau [rank-1 array('d') with bounds (MIN(m,n))]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.cgerqf

scipy.linalg.lapack.**cgerqf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cgerqf.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

qr [rank-2 array('F') with bounds (m,n) and a storage]
tau [rank-1 array('F') with bounds (MIN(m,n))]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.zgerqf

scipy.linalg.lapack.**zgerqf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zgerqf.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

qr [rank-2 array('D') with bounds (m,n) and a storage]
tau [rank-1 array('D') with bounds (MIN(m,n))]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.sgesdd

scipy.linalg.lapack.**sgesdd**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for sgesdd.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

u [rank-2 array('f') with bounds (u0,u1)]
s [rank-1 array('f') with bounds (minmn)]
vt [rank-2 array('f') with bounds (vt0,vt1)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork [input int, optional] Default: max((compute_uv?4*minmn*minmn+MAX(m,n)+9*minmn:MAX(14*minmn+

scipy.linalg.lapack.dgesdd

scipy.linalg.lapack.**dgesdd**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for dgesdd.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

u [rank-2 array('d') with bounds (u0,u1)]
s [rank-1 array('d') with bounds (minmn)]
vt [rank-2 array('d') with bounds (vt0,vt1)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork [input int, optional] Default: max((compute_uv?4*minmn*minmn+MAX(m,n)+9*minmn:MAX(14*minmn+

scipy.linalg.lapack.cgesdd

scipy.linalg.lapack.**cgesdd**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for cgesdd.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

u [rank-2 array('F') with bounds (u0,u1)]
s [rank-1 array('f') with bounds (minmn)]
vt [rank-2 array('F') with bounds (vt0,vt1)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork [input int, optional] Default: max((compute_uv?2*minmn*minmn+MAX(m,n)+2*minmn:2*minmn+MAX(n

scipy.linalg.lapack.zgesdd

scipy.linalg.lapack.**zgesdd**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for zgesdd.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

u [rank-2 array('D') with bounds (u0,u1)]
s [rank-1 array('d') with bounds (minmn)]
vt [rank-2 array('D') with bounds (vt0,vt1)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork [input int, optional] Default: max((compute_uv?2*minmn*minmn+MAX(m,n)+2*minmn:2*minmn+MAX(n

scipy.linalg.lapack.sgesdd_lwork

scipy.linalg.lapack.**sgesdd_lwork**(*m*, *n*[, *compute_uv*, *full_matrices*]) = **<fortran object>**

Wrapper for sgesdd_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

Other Parameters

compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.dgesdd_lwork

scipy.linalg.lapack.**dgesdd_lwork**(*m*, *n*[, *compute_uv*, *full_matrices*]) = **<fortran object>**

Wrapper for dgesdd_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

Other Parameters

compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.cgesdd_lwork

scipy.linalg.lapack.**cgesdd_lwork**(*m*, *n*[, *compute_uv*, *full_matrices*]) = **<fortran object>**

Wrapper for cgesdd_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

Other Parameters

compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.zgesdd_lwork

scipy.linalg.lapack.**zgesdd_lwork**(*m*, *n*[, *compute_uv*, *full_matrices*]) **= <fortran object>**

Wrapper for zgesdd_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

Other Parameters

compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.sgesv

scipy.linalg.lapack.**sgesv**(*a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgesv.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

lu [rank-2 array('f') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dgesv

scipy.linalg.lapack.**dgesv**(*a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dgesv.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

lu [rank-2 array('d') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cgesv

scipy.linalg.lapack.**cgesv**(*a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for cgesv.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

lu [rank-2 array('F') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zgesv

scipy.linalg.lapack.**zgesv**(*a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zgesv.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

lu [rank-2 array('D') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]

info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.sgesvd

scipy.linalg.lapack.**sgesvd**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for sgesvd.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

u [rank-2 array('f') with bounds (u0,u1)]
s [rank-1 array('f') with bounds (minmn)]
vt [rank-2 array('f') with bounds (vt0,vt1)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork [input int, optional] Default: max(MAX(3*minmn+MAX(m,n),5*minmn),1)

scipy.linalg.lapack.dgesvd

scipy.linalg.lapack.**dgesvd**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for dgesvd.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

u [rank-2 array('d') with bounds (u0,u1)]
s [rank-1 array('d') with bounds (minmn)]
vt [rank-2 array('d') with bounds (vt0,vt1)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork [input int, optional] Default: max(MAX(3*minmn+MAX(m,n),5*minmn),1)

scipy.linalg.lapack.cgesvd

scipy.linalg.lapack.**cgesvd**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for `cgesvd`.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

u [rank-2 array('F') with bounds (u0,u1)]
s [rank-1 array('f') with bounds (minmn)]
vt [rank-2 array('F') with bounds (vt0,vt1)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork [input int, optional] Default: MAX(2*minmn+MAX(m,n),1)

scipy.linalg.lapack.zgesvd

scipy.linalg.lapack.**zgesvd**(*a*[, *compute_uv*, *full_matrices*, *lwork*, *overwrite_a*]) = **<fortran object>**

Wrapper for `zgesvd`.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

u [rank-2 array('D') with bounds (u0,u1)]
s [rank-1 array('d') with bounds (minmn)]
vt [rank-2 array('D') with bounds (vt0,vt1)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1
lwork [input int, optional] Default: MAX(2*minmn+MAX(m,n),1)

scipy.linalg.lapack.sgesvd_lwork

scipy.linalg.lapack.**sgesvd_lwork**(*m*, *n*[, *compute_uv*, *full_matrices*]) = **<fortran object>**

Wrapper for sgesvd_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

Other Parameters

compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.dgesvd_lwork

scipy.linalg.lapack.**dgesvd_lwork**(*m*, *n*[, *compute_uv*, *full_matrices*]) = **<fortran object>**

Wrapper for dgesvd_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

Other Parameters

compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.cgesvd_lwork

scipy.linalg.lapack.**cgesvd_lwork**(*m*, *n*[, *compute_uv*, *full_matrices*]) = **<fortran object>**

Wrapper for cgesvd_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

Other Parameters

compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.zgesvd_lwork

scipy.linalg.lapack.**zgesvd_lwork**(*m*, *n*[, *compute_uv*, *full_matrices*]) = **<fortran object>**

Wrapper for zgesvd_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

Other Parameters

compute_uv
[input int, optional] Default: 1
full_matrices
[input int, optional] Default: 1

scipy.linalg.lapack.sgesvx

scipy.linalg.lapack.**sgesvx**(*a*, *b*[, *fact*, *trans*, *af*, *ipiv*, *equed*, *r*, *c*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for sgesvx.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

as [rank-2 array('f') with bounds (n,n) and a storage]
lu [rank-2 array('f') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
equed [string(len=1)]
rs [rank-1 array('f') with bounds (n) and r storage]
cs [rank-1 array('f') with bounds (n) and c storage]
bs [rank-2 array('f') with bounds (n,nrhs) and b storage]
x [rank-2 array('f') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'E'
trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('f') with bounds (n,n)]

ipiv [input rank-1 array('i') with bounds (n)]
equed [input string(len=1), optional] Default: 'B'
r [input rank-1 array('f') with bounds (n)]
c [input rank-1 array('f') with bounds (n)]
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dgesvx

scipy.linalg.lapack.**dgesvx**(*a*, *b*[, *fact*, *trans*, *af*, *ipiv*, *equed*, *r*, *c*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for dgesvx.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

as [rank-2 array('d') with bounds (n,n) and a storage]
lu [rank-2 array('d') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
equed [string(len=1)]
rs [rank-1 array('d') with bounds (n) and r storage]
cs [rank-1 array('d') with bounds (n) and c storage]
bs [rank-2 array('d') with bounds (n,nrhs) and b storage]
x [rank-2 array('d') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'E'
trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('d') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
equed [input string(len=1), optional] Default: 'B'
r [input rank-1 array('d') with bounds (n)]
c [input rank-1 array('d') with bounds (n)]
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cgesvx

scipy.linalg.lapack.**cgesvx**(*a*, *b*[, *fact*, *trans*, *af*, *ipiv*, *equed*, *r*, *c*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for cgesvx.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

as [rank-2 array('F') with bounds (n,n) and a storage]
lu [rank-2 array('F') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
equed [string(len=1)]
rs [rank-1 array('f') with bounds (n) and r storage]
cs [rank-1 array('f') with bounds (n) and c storage]
bs [rank-2 array('F') with bounds (n,nrhs) and b storage]
x [rank-2 array('F') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'E'
trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('F') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
equed [input string(len=1), optional] Default: 'B'
r [input rank-1 array('f') with bounds (n)]
c [input rank-1 array('f') with bounds (n)]
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zgesvx

scipy.linalg.lapack.**zgesvx**(*a*, *b*[, *fact*, *trans*, *af*, *ipiv*, *equed*, *r*, *c*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for zgesvx.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

as [rank-2 array('D') with bounds (n,n) and a storage]
lu [rank-2 array('D') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
equed [string(len=1)]
rs [rank-1 array('d') with bounds (n) and r storage]
cs [rank-1 array('d') with bounds (n) and c storage]
bs [rank-2 array('D') with bounds (n,nrhs) and b storage]
x [rank-2 array('D') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'E'
trans [input string(len=1), optional] Default: 'N'

overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('D') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
equed [input string(len=1), optional] Default: 'B'
r [input rank-1 array('d') with bounds (n)]
c [input rank-1 array('d') with bounds (n)]
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.sgetrf

`scipy.linalg.lapack.`**`sgetrf`**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for `sgetrf`.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

lu [rank-2 array('f') with bounds (m,n) and a storage]
piv [rank-1 array('i') with bounds (MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.dgetrf

`scipy.linalg.lapack.`**`dgetrf`**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for `dgetrf`.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

lu [rank-2 array('d') with bounds (m,n) and a storage]
piv [rank-1 array('i') with bounds (MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.cgetrf

`scipy.linalg.lapack.`**`cgetrf`**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for `cgetrf`.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

lu [rank-2 array('F') with bounds (m,n) and a storage]
piv [rank-1 array('i') with bounds (MIN(m,n))]

info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.zgetrf

scipy.linalg.lapack.**zgetrf**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for zgetrf.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

lu [rank-2 array('D') with bounds (m,n) and a storage]
piv [rank-1 array('i') with bounds (MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.sgetc2

scipy.linalg.lapack.**sgetc2**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for sgetc2.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

lu [rank-2 array('f') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
jpiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.dgetc2

scipy.linalg.lapack.**dgetc2**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for dgetc2.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

lu [rank-2 array('d') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
jpiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.cgetc2

scipy.linalg.lapack.**cgetc2**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for cgetc2.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

lu [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
jpiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.zgetc2

scipy.linalg.lapack.**zgetc2**(*a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for zgetc2.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

lu [rank-2 array('D') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
jpiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.sgetri

scipy.linalg.lapack.**sgetri**(*lu*, *piv*[, *lwork*, *overwrite_lu*]) **= <fortran object>**
Wrapper for sgetri.

Parameters

lu [input rank-2 array('f') with bounds (n,n)]
piv [input rank-1 array('i') with bounds (n)]

Returns

inv_a [rank-2 array('f') with bounds (n,n) and lu storage]
info [int]

Other Parameters

overwrite_lu
[input int, optional] Default: 0

lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.dgetri

scipy.linalg.lapack.**dgetri**(*lu*, *piv*[, *lwork*, *overwrite_lu*]) **= <fortran object>**

Wrapper for dgetri.

Parameters

lu [input rank-2 array('d') with bounds (n,n)]
piv [input rank-1 array('i') with bounds (n)]

Returns

inv_a [rank-2 array('d') with bounds (n,n) and lu storage]
info [int]

Other Parameters

overwrite_lu
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.cgetri

scipy.linalg.lapack.**cgetri**(*lu*, *piv*[, *lwork*, *overwrite_lu*]) **= <fortran object>**

Wrapper for cgetri.

Parameters

lu [input rank-2 array('F') with bounds (n,n)]
piv [input rank-1 array('i') with bounds (n)]

Returns

inv_a [rank-2 array('F') with bounds (n,n) and lu storage]
info [int]

Other Parameters

overwrite_lu
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.zgetri

scipy.linalg.lapack.**zgetri**(*lu*, *piv*[, *lwork*, *overwrite_lu*]) **= <fortran object>**

Wrapper for zgetri.

Parameters

lu [input rank-2 array('D') with bounds (n,n)]
piv [input rank-1 array('i') with bounds (n)]

Returns

inv_a [rank-2 array('D') with bounds (n,n) and lu storage]
info [int]

Other Parameters

overwrite_lu
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.sgetri_lwork

scipy.linalg.lapack.**sgetri_lwork**(*n*) **= <fortran object>**
Wrapper for sgetri_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.dgetri_lwork

scipy.linalg.lapack.**dgetri_lwork**(*n*) **= <fortran object>**
Wrapper for dgetri_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.cgetri_lwork

scipy.linalg.lapack.**cgetri_lwork**(*n*) **= <fortran object>**
Wrapper for cgetri_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.zgetri_lwork

scipy.linalg.lapack.**zgetri_lwork**(*n*) **= <fortran object>**
Wrapper for zgetri_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.sgetrs

scipy.linalg.lapack.**sgetrs**(*lu*, *piv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgetrs.

Parameters

lu [input rank-2 array('f') with bounds (n,n)]
piv [input rank-1 array('i') with bounds (n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
trans [input int, optional] Default: 0

scipy.linalg.lapack.dgetrs

scipy.linalg.lapack.**dgetrs**(*lu*, *piv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for dgetrs.

Parameters

lu [input rank-2 array('d') with bounds (n,n)]
piv [input rank-1 array('i') with bounds (n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
trans [input int, optional] Default: 0

scipy.linalg.lapack.cgetrs

scipy.linalg.lapack.**cgetrs**(*lu*, *piv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for cgetrs.

Parameters

lu [input rank-2 array('F') with bounds (n,n)]
piv [input rank-1 array('i') with bounds (n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0

trans [input int, optional] Default: 0

scipy.linalg.lapack.zgetrs

scipy.linalg.lapack.**zgetrs**(*lu*, *piv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for zgetrs.

Parameters

lu [input rank-2 array('D') with bounds (n,n)]
piv [input rank-1 array('i') with bounds (n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
trans [input int, optional] Default: 0

scipy.linalg.lapack.sgesc2

scipy.linalg.lapack.**sgesc2**(*lu*, *rhs*, *ipiv*, *jpiv*[, *overwrite_rhs*]) **= <fortran object>**

Wrapper for sgesc2.

Parameters

lu [input rank-2 array('f') with bounds (n,n)]
rhs [input rank-1 array('f') with bounds (n)]
ipiv [input rank-1 array('i') with bounds (n)]
jpiv [input rank-1 array('i') with bounds (n)]

Returns

x [rank-1 array('f') with bounds (n) and rhs storage]
scale [float]

Other Parameters

overwrite_rhs
[input int, optional] Default: 0

scipy.linalg.lapack.dgesc2

scipy.linalg.lapack.**dgesc2**(*lu*, *rhs*, *ipiv*, *jpiv*[, *overwrite_rhs*]) **= <fortran object>**

Wrapper for dgesc2.

Parameters

lu [input rank-2 array('d') with bounds (n,n)]
rhs [input rank-1 array('d') with bounds (n)]
ipiv [input rank-1 array('i') with bounds (n)]
jpiv [input rank-1 array('i') with bounds (n)]

Returns

x [rank-1 array('d') with bounds (n) and rhs storage]
scale [float]

Other Parameters

overwrite_rhs
[input int, optional] Default: 0

scipy.linalg.lapack.cgesc2

scipy.linalg.lapack.**cgesc2**(*lu*, *rhs*, *ipiv*, *jpiv*[, *overwrite_rhs*]) **= <fortran object>**

Wrapper for cgesc2.

Parameters

lu [input rank-2 array('F') with bounds (n,n)]
rhs [input rank-1 array('F') with bounds (n)]
ipiv [input rank-1 array('i') with bounds (n)]
jpiv [input rank-1 array('i') with bounds (n)]

Returns

x [rank-1 array('F') with bounds (n) and rhs storage]
scale [float]

Other Parameters

overwrite_rhs
[input int, optional] Default: 0

scipy.linalg.lapack.zgesc2

scipy.linalg.lapack.**zgesc2**(*lu*, *rhs*, *ipiv*, *jpiv*[, *overwrite_rhs*]) **= <fortran object>**

Wrapper for zgesc2.

Parameters

lu [input rank-2 array('D') with bounds (n,n)]
rhs [input rank-1 array('D') with bounds (n)]
ipiv [input rank-1 array('i') with bounds (n)]
jpiv [input rank-1 array('i') with bounds (n)]

Returns

x [rank-1 array('D') with bounds (n) and rhs storage]
scale [float]

Other Parameters

overwrite_rhs
[input int, optional] Default: 0

scipy.linalg.lapack.sgges

scipy.linalg.lapack.**sgges**(*sselect*, *a*, *b*[, *jobvsl*, *jobvsr*, *sort_t*, *ldvsl*, *ldvsr*, *lwork*, *sselect_extra_args*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgges.

Parameters

sselect [call-back function]
a [input rank-2 array('f') with bounds (lda,n)]
b [input rank-2 array('f') with bounds (ldb,n)]

Returns

a [rank-2 array('f') with bounds (lda,n)]
b [rank-2 array('f') with bounds (ldb,n)]

sdim [int]
alphar [rank-1 array('f') with bounds (n)]
alphai [rank-1 array('f') with bounds (n)]
beta [rank-1 array('f') with bounds (n)]
vsl [rank-2 array('f') with bounds (ldvsl,n)]
vsr [rank-2 array('f') with bounds (ldvsr,n)]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

jobvsl [input int, optional] Default: 1
jobvsr [input int, optional] Default: 1
sort_t [input int, optional] Default: 0
sselect_extra_args
[input tuple, optional] Default: ()
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
ldvsl [input int, optional] Default: ((jobvsl==1)?n:1)
ldvsr [input int, optional] Default: ((jobvsr==1)?n:1)
lwork [input int, optional] Default: max(8*n+16,1)

Notes

Call-back functions:

```
def sselect(alphar,alphai,beta): return sselect
Required arguments:
  alphar : input float
  alphai : input float
  beta : input float
Return objects:
  sselect : int
```

scipy.linalg.lapack.dgges

scipy.linalg.lapack.**dgges**(*dselect*, *a*, *b*[, *jobvsl*, *jobvsr*, *sort_t*, *ldvsl*, *ldvsr*, *lwork*, *dselect_extra_args*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dgges.

Parameters

dselect [call-back function]
a [input rank-2 array('d') with bounds (lda,n)]
b [input rank-2 array('d') with bounds (ldb,n)]

Returns

a [rank-2 array('d') with bounds (lda,n)]
b [rank-2 array('d') with bounds (ldb,n)]
sdim [int]
alphar [rank-1 array('d') with bounds (n)]
alphai [rank-1 array('d') with bounds (n)]
beta [rank-1 array('d') with bounds (n)]

vsl [rank-2 array('d') with bounds (ldvsl,n)]
vsr [rank-2 array('d') with bounds (ldvsr,n)]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

jobvsl [input int, optional] Default: 1
jobvsr [input int, optional] Default: 1
sort_t [input int, optional] Default: 0
dselect_extra_args
[input tuple, optional] Default: ()
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
ldvsl [input int, optional] Default: ((jobvsl==1)?n:1)
ldvsr [input int, optional] Default: ((jobvsr==1)?n:1)
lwork [input int, optional] Default: max(8*n+16,1)

Notes

Call-back functions:

```
def dselect(alphar,alphai,beta): return dselect
Required arguments:
  alphar : input float
  alphai : input float
  beta : input float
Return objects:
  dselect : int
```

scipy.linalg.lapack.cgges

scipy.linalg.lapack.**cgges**(*cselect*, *a*, *b*[, *jobvsl*, *jobvsr*, *sort_t*, *ldvsl*, *ldvsr*, *lwork*, *cselect_extra_args*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for cgges.

Parameters

cselect [call-back function]
a [input rank-2 array('F') with bounds (lda,n)]
b [input rank-2 array('F') with bounds (ldb,n)]

Returns

a [rank-2 array('F') with bounds (lda,n)]
b [rank-2 array('F') with bounds (ldb,n)]
sdim [int]
alpha [rank-1 array('F') with bounds (n)]
beta [rank-1 array('F') with bounds (n)]
vsl [rank-2 array('F') with bounds (ldvsl,n)]
vsr [rank-2 array('F') with bounds (ldvsr,n)]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

jobvsl [input int, optional] Default: 1
jobvsr [input int, optional] Default: 1
sort_t [input int, optional] Default: 0
cselect_extra_args
[input tuple, optional] Default: ()
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
ldvsl [input int, optional] Default: ((jobvsl==1)?n:1)
ldvsr [input int, optional] Default: ((jobvsr==1)?n:1)
lwork [input int, optional] Default: max(2*n,1)

Notes

Call-back functions:

```
def cselect(alpha,beta): return cselect
Required arguments:
  alpha : input complex
  beta : input complex
Return objects:
  cselect : int
```

scipy.linalg.lapack.zgges

scipy.linalg.lapack.**zgges**(*zselect*, *a*, *b*[, *jobvsl*, *jobvsr*, *sort_t*, *ldvsl*, *ldvsr*, *lwork*, *zselect_extra_args*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zgges.

Parameters

zselect [call-back function]
a [input rank-2 array('D') with bounds (lda,n)]
b [input rank-2 array('D') with bounds (ldb,n)]

Returns

a [rank-2 array('D') with bounds (lda,n)]
b [rank-2 array('D') with bounds (ldb,n)]
sdim [int]
alpha [rank-1 array('D') with bounds (n)]
beta [rank-1 array('D') with bounds (n)]
vsl [rank-2 array('D') with bounds (ldvsl,n)]
vsr [rank-2 array('D') with bounds (ldvsr,n)]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

jobvsl [input int, optional] Default: 1
jobvsr [input int, optional] Default: 1
sort_t [input int, optional] Default: 0
zselect_extra_args
[input tuple, optional] Default: ()

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
ldvsl [input int, optional] Default: ((jobvsl==1)?n:1)
ldvsr [input int, optional] Default: ((jobvsr==1)?n:1)
lwork [input int, optional] Default: max(2*n,1)

Notes

Call-back functions:

```
def zselect(alpha,beta): return zselect
Required arguments:
  alpha : input complex
  beta : input complex
Return objects:
  zselect : int
```

scipy.linalg.lapack.sggev

scipy.linalg.lapack.**sggev**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for sggev.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,n)]

Returns

alphar [rank-1 array('f') with bounds (n)]
alphai [rank-1 array('f') with bounds (n)]
beta [rank-1 array('f') with bounds (n)]
vl [rank-2 array('f') with bounds (ldvl,n)]
vr [rank-2 array('f') with bounds (ldvr,n)]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.dggev

scipy.linalg.lapack.**dggev**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for dggev.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,n)]

Returns

alphar [rank-1 array('d') with bounds (n)]
alphai [rank-1 array('d') with bounds (n)]
beta [rank-1 array('d') with bounds (n)]
vl [rank-2 array('d') with bounds (ldvl,n)]
vr [rank-2 array('d') with bounds (ldvr,n)]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.cggev

scipy.linalg.lapack.**cggev**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for cggev.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,n)]

Returns

alpha [rank-1 array('F') with bounds (n)]
beta [rank-1 array('F') with bounds (n)]
vl [rank-2 array('F') with bounds (ldvl,n)]
vr [rank-2 array('F') with bounds (ldvr,n)]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0

overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.zggev

scipy.linalg.lapack.**zggev**(*a*, *b*[, *compute_vl*, *compute_vr*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for zggev.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,n)]

Returns

alpha [rank-1 array('D') with bounds (n)]
beta [rank-1 array('D') with bounds (n)]
vl [rank-2 array('D') with bounds (ldvl,n)]
vr [rank-2 array('D') with bounds (ldvr,n)]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

compute_vl
[input int, optional] Default: 1
compute_vr
[input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.sgglse

scipy.linalg.lapack.**sgglse**(*a*, *b*, *c*, *d*[, *lwork*, *overwrite_a*, *overwrite_b*, *overwrite_c*, *overwrite_d*]) = **<fortran object>**

Wrapper for sgglse.

Parameters

a [input rank-2 array('f') with bounds (m,n)]
b [input rank-2 array('f') with bounds (p,n)]
c [input rank-1 array('f') with bounds (m)]
d [input rank-1 array('f') with bounds (p)]

Returns

t [rank-2 array('f') with bounds (m,n) and a storage]
r [rank-2 array('f') with bounds (p,n) and b storage]
res [rank-1 array('f') with bounds (m) and c storage]
x [rank-1 array('f') with bounds (n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

overwrite_b
[input int, optional] Default: 0
overwrite_c
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
lwork [input int, optional] Default: max(m+n+p,1)

scipy.linalg.lapack.dgglse

`scipy.linalg.lapack.`**`dgglse`**(*a*, *b*, *c*, *d*[, *lwork*, *overwrite_a*, *overwrite_b*, *overwrite_c*, *overwrite_d*])
= <fortran object>

Wrapper for `dgglse`.

Parameters

a [input rank-2 array('d') with bounds (m,n)]
b [input rank-2 array('d') with bounds (p,n)]
c [input rank-1 array('d') with bounds (m)]
d [input rank-1 array('d') with bounds (p)]

Returns

t [rank-2 array('d') with bounds (m,n) and a storage]
r [rank-2 array('d') with bounds (p,n) and b storage]
res [rank-1 array('d') with bounds (m) and c storage]
x [rank-1 array('d') with bounds (n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_c
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
lwork [input int, optional] Default: max(m+n+p,1)

scipy.linalg.lapack.cgglse

`scipy.linalg.lapack.`**`cgglse`**(*a*, *b*, *c*, *d*[, *lwork*, *overwrite_a*, *overwrite_b*, *overwrite_c*, *overwrite_d*])
= <fortran object>

Wrapper for `cgglse`.

Parameters

a [input rank-2 array('F') with bounds (m,n)]
b [input rank-2 array('F') with bounds (p,n)]
c [input rank-1 array('F') with bounds (m)]
d [input rank-1 array('F') with bounds (p)]

Returns

t [rank-2 array('F') with bounds (m,n) and a storage]
r [rank-2 array('F') with bounds (p,n) and b storage]
res [rank-1 array('F') with bounds (m) and c storage]
x [rank-1 array('F') with bounds (n)]

info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_c
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
lwork [input int, optional] Default: max(m+n+p,1)

scipy.linalg.lapack.zgglse

scipy.linalg.lapack.**zgglse**(*a*, *b*, *c*, *d*[, *lwork*, *overwrite_a*, *overwrite_b*, *overwrite_c*, *overwrite_d*])
= <fortran object>

Wrapper for zgglse.

Parameters

a [input rank-2 array('D') with bounds (m,n)]
b [input rank-2 array('D') with bounds (p,n)]
c [input rank-1 array('D') with bounds (m)]
d [input rank-1 array('D') with bounds (p)]

Returns

t [rank-2 array('D') with bounds (m,n) and a storage]
r [rank-2 array('D') with bounds (p,n) and b storage]
res [rank-1 array('D') with bounds (m) and c storage]
x [rank-1 array('D') with bounds (n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_c
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
lwork [input int, optional] Default: max(m+n+p,1)

scipy.linalg.lapack.sgglse_lwork

scipy.linalg.lapack.**sgglse_lwork**(*m*, *n*, *p*) **= <fortran object>**

Wrapper for sgglse_lwork.

Parameters

m [input int]
n [input int]
p [input int]

Returns

work [float]

info [int]

scipy.linalg.lapack.dgglse_lwork

scipy.linalg.lapack.**dgglse_lwork**(*m*, *n*, *p*) **= <fortran object>**

Wrapper for dgglse_lwork.

Parameters

m [input int]
n [input int]
p [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.cgglse_lwork

scipy.linalg.lapack.**cgglse_lwork**(*m*, *n*, *p*) **= <fortran object>**

Wrapper for cgglse_lwork.

Parameters

m [input int]
n [input int]
p [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.zgglse_lwork

scipy.linalg.lapack.**zgglse_lwork**(*m*, *n*, *p*) **= <fortran object>**

Wrapper for zgglse_lwork.

Parameters

m [input int]
n [input int]
p [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.sgtsv

scipy.linalg.lapack.**sgtsv**(*dl*, *d*, *du*, *b*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*, *overwrite_b*]) **= <fortran object>**

Wrapper for sgtsv.

Parameters

dl [input rank-1 array('f') with bounds (n - 1)]
d [input rank-1 array('f') with bounds (n)]
du [input rank-1 array('f') with bounds (n - 1)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

du2 [rank-1 array('f') with bounds (n - 1) and dl storage]
d [rank-1 array('f') with bounds (n)]
du [rank-1 array('f') with bounds (n - 1)]
x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_dl
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_du
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dgtsv

scipy.linalg.lapack.**dgtsv**(*dl*, *d*, *du*, *b*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*, *overwrite_b*]) **=**
<fortran object>

Wrapper for dgtsv.

Parameters

dl [input rank-1 array('d') with bounds (n - 1)]
d [input rank-1 array('d') with bounds (n)]
du [input rank-1 array('d') with bounds (n - 1)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

du2 [rank-1 array('d') with bounds (n - 1) and dl storage]
d [rank-1 array('d') with bounds (n)]
du [rank-1 array('d') with bounds (n - 1)]
x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_dl
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_du
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cgtsv

scipy.linalg.lapack.**cgtsv**(*dl*, *d*, *du*, *b*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*, *overwrite_b*]) = **<fortran object>**

Wrapper for cgtsv.

Parameters

dl [input rank-1 array('F') with bounds (n - 1)]
d [input rank-1 array('F') with bounds (n)]
du [input rank-1 array('F') with bounds (n - 1)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

du2 [rank-1 array('F') with bounds (n - 1) and dl storage]
d [rank-1 array('F') with bounds (n)]
du [rank-1 array('F') with bounds (n - 1)]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_dl
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_du
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zgtsv

scipy.linalg.lapack.**zgtsv**(*dl*, *d*, *du*, *b*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*, *overwrite_b*]) = **<fortran object>**

Wrapper for zgtsv.

Parameters

dl [input rank-1 array('D') with bounds (n - 1)]
d [input rank-1 array('D') with bounds (n)]
du [input rank-1 array('D') with bounds (n - 1)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

du2 [rank-1 array('D') with bounds (n - 1) and dl storage]
d [rank-1 array('D') with bounds (n)]
du [rank-1 array('D') with bounds (n - 1)]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_dl
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_du
[input int, optional] Default: 0

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.sgtsvx

scipy.linalg.lapack.**sgtsvx**(*dl*, *d*, *du*, *b*[, *fact*, *trans*, *dlf*, *df*, *duf*, *du2*, *ipiv*]) **= <fortran object>**

Wrapper for sgtsvx.

Parameters

dl [input rank-1 array('f') with bounds (MAX(0, n-1))]
d [input rank-1 array('f') with bounds (n)]
du [input rank-1 array('f') with bounds (MAX(0, n-1))]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

dlf [rank-1 array('f') with bounds (MAX(0,n-1))]
df [rank-1 array('f') with bounds (n)]
duf [rank-1 array('f') with bounds (MAX(0,n-1))]
du2 [rank-1 array('f') with bounds (MAX(0,n-2))]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('f') with bounds (ldx,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'N'
trans [input string(len=1), optional] Default: 'N'
dlf [input rank-1 array('f') with bounds (MAX(0,n-1))]
df [input rank-1 array('f') with bounds (n)]
duf [input rank-1 array('f') with bounds (MAX(0,n-1))]
du2 [input rank-1 array('f') with bounds (MAX(0,n-2))]
ipiv [input rank-1 array('i') with bounds (n)]

scipy.linalg.lapack.dgtsvx

scipy.linalg.lapack.**dgtsvx**(*dl*, *d*, *du*, *b*[, *fact*, *trans*, *dlf*, *df*, *duf*, *du2*, *ipiv*]) **= <fortran object>**

Wrapper for dgtsvx.

Parameters

dl [input rank-1 array('d') with bounds (MAX(0, n-1))]
d [input rank-1 array('d') with bounds (n)]
du [input rank-1 array('d') with bounds (MAX(0, n-1))]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

dlf [rank-1 array('d') with bounds (MAX(0,n-1))]
df [rank-1 array('d') with bounds (n)]
duf [rank-1 array('d') with bounds (MAX(0,n-1))]
du2 [rank-1 array('d') with bounds (MAX(0,n-2))]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('d') with bounds (ldx,nrhs)]

rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'N'
trans [input string(len=1), optional] Default: 'N'
dlf [input rank-1 array('d') with bounds (MAX(0,n-1))]
df [input rank-1 array('d') with bounds (n)]
duf [input rank-1 array('d') with bounds (MAX(0,n-1))]
du2 [input rank-1 array('d') with bounds (MAX(0,n-2))]
ipiv [input rank-1 array('i') with bounds (n)]

scipy.linalg.lapack.cgtsvx

scipy.linalg.lapack.**cgtsvx**(*dl*, *d*, *du*, *b*[, *fact*, *trans*, *dlf*, *df*, *duf*, *du2*, *ipiv*]) **= <fortran object>**

Wrapper for cgtsvx.

Parameters

dl [input rank-1 array('F') with bounds (MAX(0, n-1))]
d [input rank-1 array('F') with bounds (n)]
du [input rank-1 array('F') with bounds (MAX(0, n-1))]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

dlf [rank-1 array('F') with bounds (MAX(0,n-1))]
df [rank-1 array('F') with bounds (n)]
duf [rank-1 array('F') with bounds (MAX(0,n-1))]
du2 [rank-1 array('F') with bounds (MAX(0,n-2))]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('F') with bounds (ldx,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'N'
trans [input string(len=1), optional] Default: 'N'
dlf [input rank-1 array('F') with bounds (MAX(0,n-1))]
df [input rank-1 array('F') with bounds (n)]
duf [input rank-1 array('F') with bounds (MAX(0,n-1))]
du2 [input rank-1 array('F') with bounds (MAX(0,n-2))]
ipiv [input rank-1 array('i') with bounds (n)]

scipy.linalg.lapack.zgtsvx

scipy.linalg.lapack.**zgtsvx**(*dl*, *d*, *du*, *b*[, *fact*, *trans*, *dlf*, *df*, *duf*, *du2*, *ipiv*]) **= <fortran object>**

Wrapper for zgtsvx.

Parameters

dl	[input rank-1 array('D') with bounds (MAX(0, n-1))]
d	[input rank-1 array('D') with bounds (n)]
du	[input rank-1 array('D') with bounds (MAX(0, n-1))]
b	[input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

dlf	[rank-1 array('D') with bounds (MAX(0,n-1))]
df	[rank-1 array('D') with bounds (n)]
duf	[rank-1 array('D') with bounds (MAX(0,n-1))]
du2	[rank-1 array('D') with bounds (MAX(0,n-2))]
ipiv	[rank-1 array('i') with bounds (n)]
x	[rank-2 array('D') with bounds (ldx,nrhs)]
rcond	[float]
ferr	[rank-1 array('d') with bounds (nrhs)]
berr	[rank-1 array('d') with bounds (nrhs)]
info	[int]

Other Parameters

fact	[input string(len=1), optional] Default: 'N'
trans	[input string(len=1), optional] Default: 'N'
dlf	[input rank-1 array('D') with bounds (MAX(0,n-1))]
df	[input rank-1 array('D') with bounds (n)]
duf	[input rank-1 array('D') with bounds (MAX(0,n-1))]
du2	[input rank-1 array('D') with bounds (MAX(0,n-2))]
ipiv	[input rank-1 array('i') with bounds (n)]

scipy.linalg.lapack.chbevd

scipy.linalg.lapack.**chbevd**(*ab*[, *compute_v*, *lower*, *ldab*, *lrwork*, *liwork*, *overwrite_ab*]) **= <fortran object>**

Wrapper for chbevd.

Parameters

ab	[input rank-2 array('F') with bounds (ldab,n)]

Returns

w	[rank-1 array('f') with bounds (n)]
z	[rank-2 array('F') with bounds (ldz,ldz)]
info	[int]

Other Parameters

overwrite_ab	[input int, optional] Default: 1
compute_v	[input int, optional] Default: 1
lower	[input int, optional] Default: 0
ldab	[input int, optional] Default: shape(ab,0)
lrwork	[input int, optional] Default: (compute_v?1+5*n+2*n*n:n)

liwork [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.zhbevd

scipy.linalg.lapack.**zhbevd**(*ab*[, *compute_v*, *lower*, *ldab*, *lrwork*, *liwork*, *overwrite_ab*]) = **<fortran object>**

Wrapper for zhbevd.

Parameters

ab [input rank-2 array('D') with bounds (ldab,n)]

Returns

w [rank-1 array('d') with bounds (n)]
z [rank-2 array('D') with bounds (ldz,ldz)]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
lrwork [input int, optional] Default: (compute_v?1+5*n+2*n*n:n)
liwork [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.chbevx

scipy.linalg.lapack.**chbevx**(*ab*, *vl*, *vu*, *il*, *iu*[, *ldab*, *compute_v*, *range*, *lower*, *abstol*, *mmax*, *overwrite_ab*]) = **<fortran object>**

Wrapper for chbevx.

Parameters

ab [input rank-2 array('F') with bounds (ldab,n)]
vl [input float]
vu [input float]
il [input int]
iu [input int]

Returns

w [rank-1 array('f') with bounds (n)]
z [rank-2 array('F') with bounds (ldz,mmax)]
m [int]
ifail [rank-1 array('i') with bounds ((compute_v?n:1))]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
ldab [input int, optional] Default: shape(ab,0)
compute_v
[input int, optional] Default: 1
range [input int, optional] Default: 0
lower [input int, optional] Default: 0
abstol [input float, optional] Default: 0.0

mmax [input int, optional] Default: (compute_v?(range==2?(iu-il+1):n):1)

scipy.linalg.lapack.zhbevx

scipy.linalg.lapack.**zhbevx**(*ab*, *vl*, *vu*, *il*, *iu*[, *ldab*, *compute_v*, *range*, *lower*, *abstol*, *mmax*, *overwrite_ab*]) **= <fortran object>**

Wrapper for zhbevx.

Parameters

ab [input rank-2 array('D') with bounds (ldab,n)]
vl [input float]
vu [input float]
il [input int]
iu [input int]

Returns

w [rank-1 array('d') with bounds (n)]
z [rank-2 array('D') with bounds (ldz,mmax)]
m [int]
ifail [rank-1 array('i') with bounds ((compute_v?n:1))]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
ldab [input int, optional] Default: shape(ab,0)
compute_v
[input int, optional] Default: 1
range [input int, optional] Default: 0
lower [input int, optional] Default: 0
abstol [input float, optional] Default: 0.0
mmax [input int, optional] Default: (compute_v?(range==2?(iu-il+1):n):1)

scipy.linalg.lapack.checon

scipy.linalg.lapack.**checon**(*a*, *ipiv*, *anorm*[, *lower*]) **= <fortran object>**

Wrapper for checon.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zhecon

scipy.linalg.lapack.**zhecon**(*a*, *ipiv*, *anorm*[, *lower*]) **= <fortran object>**

Wrapper for zhecon.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.cheequb

scipy.linalg.lapack.**cheequb**(*a*[, *lower*]) **= <fortran object>**

Wrapper for cheequb.

Parameters

a [input rank-2 array('F') with bounds (lda,n)]

Returns

s [rank-1 array('f') with bounds (n)]
scond [float]
amax [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zheequb

scipy.linalg.lapack.**zheequb**(*a*[, *lower*]) **= <fortran object>**

Wrapper for zheequb.

Parameters

a [input rank-2 array('D') with bounds (lda,n)]

Returns

s [rank-1 array('d') with bounds (n)]
scond [float]
amax [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.cheev

scipy.linalg.lapack.**cheev**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cheev.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
v [rank-2 array('F') with bounds (n,n) and a storage]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n-1,1)

scipy.linalg.lapack.zheev

scipy.linalg.lapack.**zheev**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zheev.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
v [rank-2 array('D') with bounds (n,n) and a storage]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n-1,1)

scipy.linalg.lapack.cheev_lwork

scipy.linalg.lapack.**cheev_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for cheev_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zheev_lwork

scipy.linalg.lapack.**zheev_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for zheev_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.cheevd

scipy.linalg.lapack.**cheevd**(*a*[, *compute_v*, *lower*, *lwork*, *liwork*, *lrwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cheevd.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
v [rank-2 array('F') with bounds (n,n) and a storage]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max((compute_v?2*n+n*n:n+1),1)
liwork [input int, optional] Default: (compute_v?3+5*n:1)
lrwork [input int, optional] Default: (compute_v?1+5*n+2*n*n:n)

scipy.linalg.lapack.zheevd

scipy.linalg.lapack.**zheevd**(*a*[, *compute_v*, *lower*, *lwork*, *liwork*, *lrwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zheevd.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
v [rank-2 array('D') with bounds (n,n) and a storage]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max((compute_v?2*n+n*n:n+1),1)
liwork [input int, optional] Default: (compute_v?3+5*n:1)
lrwork [input int, optional] Default: (compute_v?1+5*n+2*n*n:n)

scipy.linalg.lapack.cheevd_lwork

`scipy.linalg.lapack.`**`cheevd_lwork`**(*n*[, *compute_v*, *lower*]) **= <fortran object>**

Wrapper for `cheevd_lwork`.

Parameters

n [input int]

Returns

work [complex]
iwork [int]
rwork [float]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.zheevd_lwork

`scipy.linalg.lapack.`**`zheevd_lwork`**(*n*[, *compute_v*, *lower*]) **= <fortran object>**

Wrapper for `zheevd_lwork`.

Parameters

n [input int]

Returns

work [complex]
iwork [int]
rwork [float]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.cheevr

scipy.linalg.lapack.**cheevr**(*a*[, *compute_v*, *range*, *lower*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *lrwork*, *liwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `cheevr`.

Parameters

a [input rank-2 array('F') with bounds `(n,n)`]

Returns

w [rank-1 array('f') with bounds `(n)`]
z [rank-2 array('F') with bounds `((compute_v?MAX(0,n):0),(compute_v?(*range=='I'?iu-il+1:MAX(1,n)):0))`]
m [int]
isuppz [rank-1 array('i') with bounds `(2*max(1,n))`]
info [int]

Other Parameters

compute_v
[input int, optional] Default `1`
range [input string(len=1), optional] Default `'A'`
lower [input int, optional] Default `0`
overwrite_a
[input int, optional] Default `0`
vl [input float, optional] Default `0.0`
vu [input float, optional] Default `1.0`
il [input int, optional] Default `1`
iu [input int, optional] Default `n`
abstol [input float, optional] Default `0.0`
lwork [input int, optional] Default `max(2*n,1)`
lrwork [input int, optional] Default `max(24*n,1)`
liwork [input int, optional] Default `max(1,10*n)`

scipy.linalg.lapack.zheevr

scipy.linalg.lapack.**zheevr**(*a*[, *compute_v*, *range*, *lower*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *lrwork*, *liwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `zheevr`.

Parameters

a [input rank-2 array('D') with bounds `(n,n)`]

Returns

w [rank-1 array('d') with bounds `(n)`]
z [rank-2 array('D') with bounds `((compute_v?MAX(0,n):0),(compute_v?(*range=='I'?iu-il+1:MAX(1,n)):0))`]
m [int]
isuppz [rank-1 array('i') with bounds `(2*max(1,n))`]
info [int]

Other Parameters

compute_v
[input int, optional] Default `1`
range [input string(len=1), optional] Default `'A'`
lower [input int, optional] Default `0`

overwrite_a
: [input int, optional] Default `0`

vl [input float, optional] Default `0.0`

vu [input float, optional] Default `1.0`

il [input int, optional] Default `1`

iu [input int, optional] Default `n`

abstol [input float, optional] Default `0.0`

lwork [input int, optional] Default `max(2*n,1)`

lrwork [input int, optional] Default `max(24*n,1)`

liwork [input int, optional] Default `max(1,10*n)`

scipy.linalg.lapack.cheevr_lwork

`scipy.linalg.lapack.`**`cheevr_lwork`**`(`*n*[, *lower*]`)` **`= <fortran object>`**

Wrapper for `cheevr_lwork`.

Parameters

n [input int]

Returns

work [complex]

rwork [float]

iwork [int]

info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zheevr_lwork

`scipy.linalg.lapack.`**`zheevr_lwork`**`(`*n*[, *lower*]`)` **`= <fortran object>`**

Wrapper for `zheevr_lwork`.

Parameters

n [input int]

Returns

work [complex]

rwork [float]

iwork [int]

info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.cheevx

scipy.linalg.lapack.**cheevx**(*a*[, *compute_v*, *range*, *lower*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *overwrite_a*])
= <fortran object>

Wrapper for `cheevx`.

Parameters

a [input rank-2 array('F') with bounds `(n,n)`]

Returns

w [rank-1 array('f') with bounds `(n)`]
z [rank-2 array('F') with bounds `((compute_v*n),(compute_v?(*range=='I'?iu-il+1:MAX(1,n)):0))`]
m [int]
ifail [rank-1 array('i') with bounds `(compute_v*n)`]
info [int]

Other Parameters

compute_v
[input int, optional] Default `1`
range [input string(len=1), optional] Default `'A'`
lower [input int, optional] Default `0`
overwrite_a
[input int, optional] Default `0`
vl [input float, optional] Default `0.0`
vu [input float, optional] Default `1.0`
il [input int, optional] Default `1`
iu [input int, optional] Default `n`
abstol [input float, optional] Default `0.0`
lwork [input int, optional] Default `max(2*n,1)`

scipy.linalg.lapack.zheevx

scipy.linalg.lapack.**zheevx**(*a*[, *compute_v*, *range*, *lower*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *overwrite_a*])
= <fortran object>

Wrapper for `zheevx`.

Parameters

a [input rank-2 array('D') with bounds `(n,n)`]

Returns

w [rank-1 array('d') with bounds `(n)`]
z [rank-2 array('D') with bounds `((compute_v*n),(compute_v?(*range=='I'?iu-il+1:MAX(1,n)):0))`]
m [int]
ifail [rank-1 array('i') with bounds `(compute_v*n)`]
info [int]

Other Parameters

compute_v
[input int, optional] Default `1`
range [input string(len=1), optional] Default `'A'`
lower [input int, optional] Default `0`
overwrite_a
[input int, optional] Default `0`

vl [input float, optional] Default `0.0`
vu [input float, optional] Default `1.0`
il [input int, optional] Default `1`
iu [input int, optional] Default `n`
abstol [input float, optional] Default `0.0`
lwork [input int, optional] Default `max(2*n,1)`

scipy.linalg.lapack.cheevx_lwork

`scipy.linalg.lapack.`**`cheevx_lwork`**(*n*[, *lower*]) **`= <fortran object>`**
Wrapper for `cheevx_lwork`.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zheevx_lwork

`scipy.linalg.lapack.`**`zheevx_lwork`**(*n*[, *lower*]) **`= <fortran object>`**
Wrapper for `zheevx_lwork`.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.chegst

`scipy.linalg.lapack.`**`chegst`**(*a*, *b*[, *itype*, *lower*, *overwrite_a*]) **`= <fortran object>`**
Wrapper for `chegst`.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,n)]

Returns

c [rank-2 array('F') with bounds (n,n) and a storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
itype [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.zhegst

scipy.linalg.lapack.**zhegst**(*a*, *b*[, *itype*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for zhegst.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,n)]

Returns

c [rank-2 array('D') with bounds (n,n) and a storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
itype [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.chegv

scipy.linalg.lapack.**chegv**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for chegv.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
v [rank-2 array('F') with bounds (n,n) and a storage]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n-1,1)

scipy.linalg.lapack.zhegv

scipy.linalg.lapack.**zhegv**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zhegv.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
v [rank-2 array('D') with bounds (n,n) and a storage]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n-1,1)

scipy.linalg.lapack.chegv_lwork

`scipy.linalg.lapack.`**`chegv_lwork`**`(`*n*[, *uplo*]`) = <fortran object>`

Wrapper for `chegv_lwork`.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'L'

scipy.linalg.lapack.zhegv_lwork

`scipy.linalg.lapack.`**`zhegv_lwork`**`(`*n*[, *uplo*]`) = <fortran object>`

Wrapper for `zhegv_lwork`.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'L'

scipy.linalg.lapack.chegvd

`scipy.linalg.lapack.`**`chegvd`**`(`*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *lrwork*, *liwork*, *overwrite_a*, *overwrite_b*]`) = <fortran object>`

Wrapper for `chegvd`.

Parameters

a [input rank-2 array('F') with bounds `(n,n)`]
b [input rank-2 array('F') with bounds `(n,n)`]

Returns

w [rank-1 array('f') with bounds (n)]
v [rank-2 array('F') with bounds (n,n) with a storage]
info [int]

Other Parameters

itype [input int, optional] Default 1
jobz [input string(len=1), optional] Default 'V'
uplo [input string(len=1), optional] Default 'L'
overwrite_a
[input int, optional] Default 0
overwrite_b
[input int, optional] Default 0
lwork [input int, optional] Default (*jobz=='N'?n+1:n*(n+2))
lrwork [input int, optional] Default max((*jobz=='N'?n:2*n*n+5*n+1),1)
liwork [input int, optional] Default (*jobz=='N'?1:5*n+3)

scipy.linalg.lapack.zhegvd

scipy.linalg.lapack.**zhegvd**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *lrwork*, *liwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zhegvd.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
v [rank-2 array('D') with bounds (n,n) with a storage]
info [int]

Other Parameters

itype [input int, optional] Default 1
jobz [input string(len=1), optional] Default 'V'
uplo [input string(len=1), optional] Default 'L'
overwrite_a
[input int, optional] Default 0
overwrite_b
[input int, optional] Default 0
lwork [input int, optional] Default (*jobz=='N'?n+1:n*(n+2))
lrwork [input int, optional] Default max((*jobz=='N'?n:2*n*n+5*n+1),1)
liwork [input int, optional] Default (*jobz=='N'?1:5*n+3)

scipy.linalg.lapack.chegvx

scipy.linalg.lapack.**chegvx**(*a*, *b*[, *itype*, *jobz*, *range*, *uplo*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for chegvx.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]

z [rank-2 array('F') with bounds ((jobz[0]=='V'?MAX(0,n):0),(jobz[0]=='V'?(range[0]=='I'?iu-il+1:MAX(1,n)):0))]
m [int]
ifail [rank-1 array('i') with bounds ((jobz[0]=='N'?0:n))]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
range [input string(len=1), optional] Default: 'A'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
vl [input float, optional] Default: 0.0
vu [input float, optional] Default: 1.0
il [input int, optional] Default: 1
iu [input int, optional] Default: n
abstol [input float, optional] Default: 0.0
lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.zhegvx

scipy.linalg.lapack.**zhegvx**(*a*, *b*[, *itype*, *jobz*, *range*, *uplo*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zhegvx.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
z [rank-2 array('D') with bounds ((jobz[0]=='V'?MAX(0,n):0),(jobz[0]=='V'?(range[0]=='I'?iu-il+1:MAX(1,n)):0))]
m [int]
ifail [rank-1 array('i') with bounds ((jobz[0]=='N'?0:n))]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
range [input string(len=1), optional] Default: 'A'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a [input int, optional] Default: 0
overwrite_b [input int, optional] Default: 0
vl [input float, optional] Default: 0.0
vu [input float, optional] Default: 1.0
il [input int, optional] Default: 1
iu [input int, optional] Default: n
abstol [input float, optional] Default: 0.0

lwork [input int, optional] Default: max(2*n,1)

scipy.linalg.lapack.chegvx_lwork

scipy.linalg.lapack.**chegvx_lwork**(*n*[, *uplo*]) **= <fortran object>**

Wrapper for chegvx_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'L'

scipy.linalg.lapack.zhegvx_lwork

scipy.linalg.lapack.**zhegvx_lwork**(*n*[, *uplo*]) **= <fortran object>**

Wrapper for zhegvx_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'L'

scipy.linalg.lapack.chesv

scipy.linalg.lapack.**chesv**(*a*, *b*[, *lwork*, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for chesv.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

uduh [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.zhesv

scipy.linalg.lapack.**zhesv**(*a*, *b*[, *lwork*, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zhesv.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

uduh [rank-2 array('D') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.chesv_lwork

scipy.linalg.lapack.**chesv_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for chesv_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zhesv_lwork

scipy.linalg.lapack.**zhesv_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for zhesv_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.chesvx

scipy.linalg.lapack.**chesvx**(*a*, *b*[, *af*, *ipiv*, *lwork*, *factored*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `chesvx`.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

uduh [rank-2 array('F') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('F') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('F') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)
factored [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.zhesvx

scipy.linalg.lapack.**zhesvx**(*a*, *b*[, *af*, *ipiv*, *lwork*, *factored*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `zhesvx`.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

uduh [rank-2 array('D') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('D') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('D') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]

overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(2*n,1)
factored [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.chesvx_lwork

scipy.linalg.lapack.**chesvx_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for chesvx_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zhesvx_lwork

scipy.linalg.lapack.**zhesvx_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for zhesvx_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.chetrd

scipy.linalg.lapack.**chetrd**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for chetrd.

Parameters

a [input rank-2 array('F') with bounds (lda,n)]

Returns

c [rank-2 array('F') with bounds (lda,n) and a storage]
d [rank-1 array('f') with bounds (n)]
e [rank-1 array('f') with bounds (n - 1)]
tau [rank-1 array('F') with bounds (n - 1)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0

lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.zhetrd

scipy.linalg.lapack.**zhetrd**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zhetrd.

Parameters

a [input rank-2 array('D') with bounds (lda,n)]

Returns

c [rank-2 array('D') with bounds (lda,n) and a storage]
d [rank-1 array('d') with bounds (n)]
e [rank-1 array('d') with bounds (n - 1)]
tau [rank-1 array('D') with bounds (n - 1)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.chetrd_lwork

scipy.linalg.lapack.**chetrd_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for chetrd_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zhetrd_lwork

scipy.linalg.lapack.**zhetrd_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for zhetrd_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.chetrf

scipy.linalg.lapack.**chetrf**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for chetrf.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

ldu [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)

scipy.linalg.lapack.zhetrf

scipy.linalg.lapack.**zhetrf**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zhetrf.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

ldu [rank-2 array('D') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)

scipy.linalg.lapack.chetrf_lwork

scipy.linalg.lapack.**chetrf_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for chetrf_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zhetrf_lwork

scipy.linalg.lapack.**zhetrf_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for zhetrf_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.chfrk

scipy.linalg.lapack.**chfrk**(*n*, *k*, *alpha*, *a*, *beta*, *c*[, *transr*, *uplo*, *trans*, *overwrite_c*]) **= <fortran object>**

Wrapper for chfrk.

Parameters

n [input int]
k [input int]
alpha [input float]
a [input rank-2 array('F') with bounds (lda,ka)]
beta [input float]
c [input rank-1 array('F') with bounds (nt)]

Returns

cout [rank-1 array('F') with bounds (nt) and c storage]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
overwrite_c [input int, optional] Default: 0

scipy.linalg.lapack.zhfrk

scipy.linalg.lapack.**zhfrk**(*n*, *k*, *alpha*, *a*, *beta*, *c*[, *transr*, *uplo*, *trans*, *overwrite_c*]) **= <fortran object>**

Wrapper for zhfrk.

Parameters

n [input int]
k [input int]
alpha [input float]
a [input rank-2 array('D') with bounds (lda,ka)]
beta [input float]
c [input rank-1 array('D') with bounds (nt)]

Returns

cout [rank-1 array('D') with bounds (nt) and c storage]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.slamch

`scipy.linalg.lapack.`**`slamch`**(*cmach*) **`= <fortran slamch>`**
Wrapper for `slamch`.

Parameters

cmach [input string(len=1)]

Returns

slamch [float]

scipy.linalg.lapack.dlamch

`scipy.linalg.lapack.`**`dlamch`**(*cmach*) **`= <fortran dlamch>`**
Wrapper for `dlamch`.

Parameters

cmach [input string(len=1)]

Returns

dlamch [float]

scipy.linalg.lapack.slange

`scipy.linalg.lapack.`**`slange`**(*norm*, *a*) **`= <fortran slange>`**
Wrapper for `slange`.

Parameters

norm [input string(len=1)]
a [input rank-2 array('f') with bounds (m,n)]

Returns

n2 [float]

scipy.linalg.lapack.dlange

`scipy.linalg.lapack.`**`dlange`**(*norm*, *a*) **`= <fortran dlange>`**
Wrapper for `dlange`.

Parameters

norm [input string(len=1)]
a [input rank-2 array('d') with bounds (m,n)]

Returns

n2 [float]

scipy.linalg.lapack.clange

scipy.linalg.lapack.**clange**(*norm*, *a*) **= <fortran clange>**

Wrapper for clange.

Parameters

norm [input string(len=1)]
a [input rank-2 array('F') with bounds (m,n)]

Returns

n2 [float]

scipy.linalg.lapack.zlange

scipy.linalg.lapack.**zlange**(*norm*, *a*) **= <fortran zlange>**

Wrapper for zlange.

Parameters

norm [input string(len=1)]
a [input rank-2 array('D') with bounds (m,n)]

Returns

n2 [float]

scipy.linalg.lapack.slarf

scipy.linalg.lapack.**slarf**(*v*, *tau*, *c*, *work*[, *side*, *incv*, *overwrite_c*]) **= <fortran object>**

Wrapper for slarf.

Parameters

v [input rank-1 array('f') with bounds ((side[0]=='L'?(1 + (m-1)*abs(incv)):(1 + (n-1)*abs(incv))))]
tau [input float]
c [input rank-2 array('f') with bounds (m,n)]
work [input rank-1 array('f') with bounds (lwork)]

Returns

c [rank-2 array('f') with bounds (m,n)]

Other Parameters

side [input string(len=1), optional] Default: 'L'
incv [input int, optional] Default: 1
overwrite_c [input int, optional] Default: 0

scipy.linalg.lapack.dlarf

scipy.linalg.lapack.**dlarf**(*v*, *tau*, *c*, *work*[, *side*, *incv*, *overwrite_c*]) **= <fortran object>**

Wrapper for dlarf.

Parameters

v [input rank-1 array('d') with bounds ((side[0]=='L'?(1 + (m-1)*abs(incv)):(1 + (n-1)*abs(incv))))]
tau [input float]
c [input rank-2 array('d') with bounds (m,n)]
work [input rank-1 array('d') with bounds (lwork)]

Returns

c [rank-2 array('d') with bounds (m,n)]

Other Parameters

side [input string(len=1), optional] Default: 'L'
incv [input int, optional] Default: 1
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.clarf

scipy.linalg.lapack.**clarf**(*v*, *tau*, *c*, *work*[, *side*, *incv*, *overwrite_c*]) **= <fortran object>**
Wrapper for clarf.

Parameters

v [input rank-1 array('F') with bounds ((side[0]=='L'?(1 + (m-1)*abs(incv)):(1 + (n-1)*abs(incv))))]
tau [input complex]
c [input rank-2 array('F') with bounds (m,n)]
work [input rank-1 array('F') with bounds (lwork)]

Returns

c [rank-2 array('F') with bounds (m,n)]

Other Parameters

side [input string(len=1), optional] Default: 'L'
incv [input int, optional] Default: 1
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.zlarf

scipy.linalg.lapack.**zlarf**(*v*, *tau*, *c*, *work*[, *side*, *incv*, *overwrite_c*]) **= <fortran object>**
Wrapper for zlarf.

Parameters

v [input rank-1 array('D') with bounds ((side[0]=='L'?(1 + (m-1)*abs(incv)):(1 + (n-1)*abs(incv))))]
tau [input complex]
c [input rank-2 array('D') with bounds (m,n)]
work [input rank-1 array('D') with bounds (lwork)]

Returns

c [rank-2 array('D') with bounds (m,n)]

Other Parameters

side [input string(len=1), optional] Default: 'L'
incv [input int, optional] Default: 1
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.slarfg

scipy.linalg.lapack.**slarfg**(*n*, *alpha*, *x*[, *incx*, *overwrite_x*]) **= <fortran object>**

Wrapper for slarfg.

Parameters

n [input int]
alpha [input float]
x [input rank-1 array('f') with bounds (lx)]

Returns

alpha [float]
x [rank-1 array('f') with bounds (lx)]
tau [float]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.lapack.dlarfg

scipy.linalg.lapack.**dlarfg**(*n*, *alpha*, *x*[, *incx*, *overwrite_x*]) **= <fortran object>**

Wrapper for dlarfg.

Parameters

n [input int]
alpha [input float]
x [input rank-1 array('d') with bounds (lx)]

Returns

alpha [float]
x [rank-1 array('d') with bounds (lx)]
tau [float]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.lapack.clarfg

scipy.linalg.lapack.**clarfg**(*n*, *alpha*, *x*[, *incx*, *overwrite_x*]) **= <fortran object>**

Wrapper for clarfg.

Parameters

n [input int]
alpha [input complex]
x [input rank-1 array('F') with bounds (lx)]

Returns

alpha [complex]
x [rank-1 array('F') with bounds (lx)]
tau [complex]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.lapack.zlarfg

scipy.linalg.lapack.**zlarfg**(*n*, *alpha*, *x*[, *incx*, *overwrite_x*]) **= <fortran object>**
Wrapper for zlarfg.

Parameters

n [input int]
alpha [input complex]
x [input rank-1 array('D') with bounds (lx)]

Returns

alpha [complex]
x [rank-1 array('D') with bounds (lx)]
tau [complex]

Other Parameters

overwrite_x
[input int, optional] Default: 0
incx [input int, optional] Default: 1

scipy.linalg.lapack.slartg

scipy.linalg.lapack.**slartg**(*f*, *g*) **= <fortran object>**
Wrapper for slartg.

Parameters

f [input float]
g [input float]

Returns

cs [float]
sn [float]
r [float]

scipy.linalg.lapack.dlartg

scipy.linalg.lapack.**dlartg**(*f*, *g*) **= <fortran object>**
Wrapper for dlartg.

Parameters

f [input float]
g [input float]

Returns

cs [float]
sn [float]
r [float]

scipy.linalg.lapack.clartg

scipy.linalg.lapack.**clartg**(*f*, *g*) **= <fortran object>**

Wrapper for clartg.

Parameters

f	[input complex]
g	[input complex]

Returns

cs	[float]
sn	[complex]
r	[complex]

scipy.linalg.lapack.zlartg

scipy.linalg.lapack.**zlartg**(*f*, *g*) **= <fortran object>**

Wrapper for zlartg.

Parameters

f	[input complex]
g	[input complex]

Returns

cs	[float]
sn	[complex]
r	[complex]

scipy.linalg.lapack.slasd4

scipy.linalg.lapack.**slasd4**(*i*, *d*, *z*[, *rho*]) **= <fortran object>**

Wrapper for slasd4.

Parameters

i	[input int]
d	[input rank-1 array('f') with bounds (n)]
z	[input rank-1 array('f') with bounds (n)]

Returns

delta	[rank-1 array('f') with bounds (n)]
sigma	[float]
work	[rank-1 array('f') with bounds (n)]
info	[int]

Other Parameters

rho	[input float, optional] Default: 1.0

scipy.linalg.lapack.dlasd4

scipy.linalg.lapack.**dlasd4**(*i*, *d*, *z*[, *rho*]) **= <fortran object>**

Wrapper for dlasd4.

Parameters

i [input int]
d [input rank-1 array('d') with bounds (n)]
z [input rank-1 array('d') with bounds (n)]

Returns

delta [rank-1 array('d') with bounds (n)]
sigma [float]
work [rank-1 array('d') with bounds (n)]
info [int]

Other Parameters

rho [input float, optional] Default: 1.0

scipy.linalg.lapack.slaswp

scipy.linalg.lapack.**slaswp**(*a*, *piv*[, *k1*, *k2*, *off*, *inc*, *overwrite_a*]) **= <fortran object>**

Wrapper for slaswp.

Parameters

a [input rank-2 array('f') with bounds (nrows,n)]
piv [input rank-1 array('i') with bounds (npiv)]

Returns

a [rank-2 array('f') with bounds (nrows,n)]

Other Parameters

overwrite_a
[input int, optional] Default: 0
k1 [input int, optional] Default: 0
k2 [input int, optional] Default: npiv-1
off [input int, optional] Default: 0
inc [input int, optional] Default: 1

scipy.linalg.lapack.dlaswp

scipy.linalg.lapack.**dlaswp**(*a*, *piv*[, *k1*, *k2*, *off*, *inc*, *overwrite_a*]) **= <fortran object>**

Wrapper for dlaswp.

Parameters

a [input rank-2 array('d') with bounds (nrows,n)]
piv [input rank-1 array('i') with bounds (npiv)]

Returns

a [rank-2 array('d') with bounds (nrows,n)]

Other Parameters

overwrite_a
[input int, optional] Default: 0
k1 [input int, optional] Default: 0

k2 [input int, optional] Default: npiv-1
off [input int, optional] Default: 0
inc [input int, optional] Default: 1

scipy.linalg.lapack.claswp

scipy.linalg.lapack.**claswp**(*a*, *piv*[, *k1*, *k2*, *off*, *inc*, *overwrite_a*]) **= <fortran object>**

Wrapper for claswp.

Parameters

a [input rank-2 array('F') with bounds (nrows,n)]
piv [input rank-1 array('i') with bounds (npiv)]

Returns

a [rank-2 array('F') with bounds (nrows,n)]

Other Parameters

overwrite_a
[input int, optional] Default: 0
k1 [input int, optional] Default: 0
k2 [input int, optional] Default: npiv-1
off [input int, optional] Default: 0
inc [input int, optional] Default: 1

scipy.linalg.lapack.zlaswp

scipy.linalg.lapack.**zlaswp**(*a*, *piv*[, *k1*, *k2*, *off*, *inc*, *overwrite_a*]) **= <fortran object>**

Wrapper for zlaswp.

Parameters

a [input rank-2 array('D') with bounds (nrows,n)]
piv [input rank-1 array('i') with bounds (npiv)]

Returns

a [rank-2 array('D') with bounds (nrows,n)]

Other Parameters

overwrite_a
[input int, optional] Default: 0
k1 [input int, optional] Default: 0
k2 [input int, optional] Default: npiv-1
off [input int, optional] Default: 0
inc [input int, optional] Default: 1

scipy.linalg.lapack.slauum

scipy.linalg.lapack.**slauum**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for slauum.

Parameters

c [input rank-2 array('f') with bounds (n,n)]

Returns

a [rank-2 array('f') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

scipy.linalg.lapack.dlauum

scipy.linalg.lapack.**dlauum**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for dlauum.

Parameters

c
: [input rank-2 array('d') with bounds (n,n)]

Returns

a
: [rank-2 array('d') with bounds (n,n) and c storage]

info
: [int]

Other Parameters

overwrite_c
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

scipy.linalg.lapack.clauum

scipy.linalg.lapack.**clauum**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for clauum.

Parameters

c
: [input rank-2 array('F') with bounds (n,n)]

Returns

a
: [rank-2 array('F') with bounds (n,n) and c storage]

info
: [int]

Other Parameters

overwrite_c
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

scipy.linalg.lapack.zlauum

scipy.linalg.lapack.**zlauum**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for zlauum.

Parameters

c
: [input rank-2 array('D') with bounds (n,n)]

Returns

a
: [rank-2 array('D') with bounds (n,n) and c storage]

info
: [int]

Other Parameters

overwrite_c
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

scipy.linalg.lapack.sorcsd

scipy.linalg.lapack.**sorcsd**(*x11*, *x12*, *x21*, *x22*[, *compute_u1*, *compute_u2*, *compute_v1t*, *compute_v2t*, *trans*, *signs*, *lwork*, *overwrite_x11*, *overwrite_x12*, *overwrite_x21*, *overwrite_x22*]) **= <fortran object>**

Wrapper for sorcsd.

Parameters

x11 [input rank-2 array('f') with bounds (p,q)]
x12 [input rank-2 array('f') with bounds (p,mmq)]
x21 [input rank-2 array('f') with bounds (mmp,q)]
x22 [input rank-2 array('f') with bounds (mmp,mmq)]

Returns

cs11 [rank-2 array('f') with bounds (p,q) and x11 storage]
cs12 [rank-2 array('f') with bounds (p,mmq) and x12 storage]
cs21 [rank-2 array('f') with bounds (mmp,q) and x21 storage]
cs22 [rank-2 array('f') with bounds (mmp,mmq) and x22 storage]
theta [rank-1 array('f') with bounds (min(min(p,mmp),min(q,mmq)))]
u1 [rank-2 array('f') with bounds ((compute_u1?p:0),(compute_u1?p:0))]
u2 [rank-2 array('f') with bounds ((compute_u2?mmp:0),(compute_u2?mmp:0))]
v1t [rank-2 array('f') with bounds ((compute_v1t?q:0),(compute_v1t?q:0))]
v2t [rank-2 array('f') with bounds ((compute_v2t?mmq:0),(compute_v2t?mmq:0))]
info [int]

Other Parameters

compute_u1
[input int, optional] Default: 1
compute_u2
[input int, optional] Default: 1
compute_v1t
[input int, optional] Default: 1
compute_v2t
[input int, optional] Default: 1
trans [input int, optional] Default: 0
signs [input int, optional] Default: 0
overwrite_x11
[input int, optional] Default: 0
overwrite_x12
[input int, optional] Default: 0
overwrite_x21
[input int, optional] Default: 0
overwrite_x22
[input int, optional] Default: 0
lwork [input int, optional] Default: 2+2*m+5*MAX(1,q-1)+4*MAX(1,q)+8*q

scipy.linalg.lapack.dorcsd

scipy.linalg.lapack.**dorcsd**(*x11*, *x12*, *x21*, *x22*[, *compute_u1*, *compute_u2*, *compute_v1t*, *compute_v2t*, *trans*, *signs*, *lwork*, *overwrite_x11*, *overwrite_x12*, *overwrite_x21*, *overwrite_x22*]) **= <fortran object>**

Wrapper for dorcsd.

Parameters

x11 [input rank-2 array('d') with bounds (p,q)]
x12 [input rank-2 array('d') with bounds (p,mmq)]
x21 [input rank-2 array('d') with bounds (mmp,q)]
x22 [input rank-2 array('d') with bounds (mmp,mmq)]

Returns

cs11 [rank-2 array('d') with bounds (p,q) and x11 storage]
cs12 [rank-2 array('d') with bounds (p,mmq) and x12 storage]
cs21 [rank-2 array('d') with bounds (mmp,q) and x21 storage]
cs22 [rank-2 array('d') with bounds (mmp,mmq) and x22 storage]
theta [rank-1 array('d') with bounds (min(min(p,mmp),min(q,mmq)))]
u1 [rank-2 array('d') with bounds ((compute_u1?p:0),(compute_u1?p:0))]
u2 [rank-2 array('d') with bounds ((compute_u2?mmp:0),(compute_u2?mmp:0))]
v1t [rank-2 array('d') with bounds ((compute_v1t?q:0),(compute_v1t?q:0))]
v2t [rank-2 array('d') with bounds ((compute_v2t?mmq:0),(compute_v2t?mmq:0))]
info [int]

Other Parameters

compute_u1
[input int, optional] Default: 1
compute_u2
[input int, optional] Default: 1
compute_v1t
[input int, optional] Default: 1
compute_v2t
[input int, optional] Default: 1
trans [input int, optional] Default: 0
signs [input int, optional] Default: 0
overwrite_x11
[input int, optional] Default: 0
overwrite_x12
[input int, optional] Default: 0
overwrite_x21
[input int, optional] Default: 0
overwrite_x22
[input int, optional] Default: 0
lwork [input int, optional] Default: 2+2*m+5*MAX(1,q-1)+4*MAX(1,q)+8*q

scipy.linalg.lapack.sorcsd_lwork

scipy.linalg.lapack.**sorcsd_lwork**(*m*, *p*, *q*) **= <fortran object>**

Wrapper for sorcsd_lwork.

Parameters

m [input int]
p [input int]
q [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.dorcsd_lwork

scipy.linalg.lapack.**dorcsd_lwork**(*m*, *p*, *q*) **= <fortran object>**

Wrapper for dorcsd_lwork.

Parameters

m [input int]
p [input int]
q [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.sorghr

scipy.linalg.lapack.**sorghr**(*a*, *tau*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for sorghr.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
tau [input rank-1 array('f') with bounds (n - 1)]

Returns

ht [rank-2 array('f') with bounds (n,n) and a storage]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(hi-lo,1)

scipy.linalg.lapack.dorghr

scipy.linalg.lapack.**dorghr**(*a*, *tau*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dorghr.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
tau [input rank-1 array('d') with bounds (n - 1)]

Returns

ht [rank-2 array('d') with bounds (n,n) and a storage]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(hi-lo,1)

scipy.linalg.lapack.sorghr_lwork

scipy.linalg.lapack.**sorghr_lwork**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for sorghr_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.dorghr_lwork

scipy.linalg.lapack.**dorghr_lwork**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for dorghr_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.sorgqr

scipy.linalg.lapack.**sorgqr**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for sorgqr.

Parameters

a [input rank-2 array('f') with bounds (m,n)]
tau [input rank-1 array('f') with bounds (k)]

Returns

q [rank-2 array('f') with bounds (m,n) and a storage]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.dorgqr

scipy.linalg.lapack.**dorgqr**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dorgqr.

Parameters

a [input rank-2 array('d') with bounds (m,n)]
tau [input rank-1 array('d') with bounds (k)]

Returns

q [rank-2 array('d') with bounds (m,n) and a storage]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.sorgrq

scipy.linalg.lapack.**sorgrq**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for sorgrq.

Parameters

a [input rank-2 array('f') with bounds (m,n)]
tau [input rank-1 array('f') with bounds (k)]

Returns

q [rank-2 array('f') with bounds (m,n) and a storage]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.dorgrq

scipy.linalg.lapack.**dorgrq**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dorgrq.

Parameters

a [input rank-2 array('d') with bounds (m,n)]
tau [input rank-1 array('d') with bounds (k)]

Returns

q [rank-2 array('d') with bounds (m,n) and a storage]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.sormqr

scipy.linalg.lapack.**sormqr**(*side*, *trans*, *a*, *tau*, *c*, *lwork*[, *overwrite_c*]) **= <fortran object>**

Wrapper for sormqr.

Parameters

side [input string(len=1)]
trans [input string(len=1)]
a [input rank-2 array('f') with bounds (lda,k)]
tau [input rank-1 array('f') with bounds (k)]
c [input rank-2 array('f') with bounds (ldc,n)]
lwork [input int]

Returns

cq [rank-2 array('f') with bounds (ldc,n) and c storage]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.dormqr

scipy.linalg.lapack.**dormqr**(*side*, *trans*, *a*, *tau*, *c*, *lwork*[, *overwrite_c*]) **= <fortran object>**

Wrapper for dormqr.

Parameters

side [input string(len=1)]
trans [input string(len=1)]
a [input rank-2 array('d') with bounds (lda,k)]
tau [input rank-1 array('d') with bounds (k)]
c [input rank-2 array('d') with bounds (ldc,n)]
lwork [input int]

Returns

cq [rank-2 array('d') with bounds (ldc,n) and c storage]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.sormrz

scipy.linalg.lapack.**sormrz**(*a*, *tau*, *c*[, *side*, *trans*, *lwork*, *overwrite_c*]) **= <fortran object>**
Wrapper for sormrz.

Parameters

a [input rank-2 array('f') with bounds (k,nt)]
tau [input rank-1 array('f') with bounds (k)]
c [input rank-2 array('f') with bounds (m,n)]

Returns

cq [rank-2 array('f') with bounds (m,n) and c storage]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX((side[0]=='L'?n:m),1)

scipy.linalg.lapack.dormrz

scipy.linalg.lapack.**dormrz**(*a*, *tau*, *c*[, *side*, *trans*, *lwork*, *overwrite_c*]) **= <fortran object>**
Wrapper for dormrz.

Parameters

a [input rank-2 array('d') with bounds (k,nt)]
tau [input rank-1 array('d') with bounds (k)]
c [input rank-2 array('d') with bounds (m,n)]

Returns

cq [rank-2 array('d') with bounds (m,n) and c storage]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX((side[0]=='L'?n:m),1)

scipy.linalg.lapack.sormrz_lwork

scipy.linalg.lapack.**sormrz_lwork**(*m*, *n*[, *side*, *trans*]) **= <fortran object>**

Wrapper for sormrz_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'

scipy.linalg.lapack.dormrz_lwork

scipy.linalg.lapack.**dormrz_lwork**(*m*, *n*[, *side*, *trans*]) **= <fortran object>**

Wrapper for dormrz_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'

scipy.linalg.lapack.spbsv

scipy.linalg.lapack.**spbsv**(*ab*, *b*[, *lower*, *ldab*, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for spbsv.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

c [rank-2 array('f') with bounds (ldab,n) and ab storage]
x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dpbsv

scipy.linalg.lapack.**dpbsv**(*ab*, *b*[, *lower*, *ldab*, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for dpbsv.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

c [rank-2 array('d') with bounds (ldab,n) and ab storage]
x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cpbsv

scipy.linalg.lapack.**cpbsv**(*ab*, *b*[, *lower*, *ldab*, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for cpbsv.

Parameters

ab [input rank-2 array('F') with bounds (ldab,n)]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

c [rank-2 array('F') with bounds (ldab,n) and ab storage]
x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zpbsv

scipy.linalg.lapack.**zpbsv**(*ab*, *b*[, *lower*, *ldab*, *overwrite_ab*, *overwrite_b*]) **= <fortran object>**

Wrapper for zpbsv.

Parameters

ab [input rank-2 array('D') with bounds (ldab,n)]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

c [rank-2 array('D') with bounds (ldab,n) and ab storage]
x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.spbtrf

scipy.linalg.lapack.**spbtrf**(*ab*[, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for spbtrf.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]

Returns

c [rank-2 array('f') with bounds (ldab,n) and ab storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.dpbtrf

scipy.linalg.lapack.**dpbtrf**(*ab*[, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for dpbtrf.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]

Returns

c [rank-2 array('d') with bounds (ldab,n) and ab storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0

overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.cpbtrf

scipy.linalg.lapack.**cpbtrf**(*ab*[, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**
Wrapper for cpbtrf.

Parameters

ab [input rank-2 array('F') with bounds (ldab,n)]

Returns

c [rank-2 array('F') with bounds (ldab,n) and ab storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.zpbtrf

scipy.linalg.lapack.**zpbtrf**(*ab*[, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**
Wrapper for zpbtrf.

Parameters

ab [input rank-2 array('D') with bounds (ldab,n)]

Returns

c [rank-2 array('D') with bounds (ldab,n) and ab storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ab
[input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.spbtrs

scipy.linalg.lapack.**spbtrs**(*ab*, *b*[, *lower*, *ldab*, *overwrite_b*]) **= <fortran object>**
Wrapper for spbtrs.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0

ldab [input int, optional] Default: shape(ab,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dpbtrs

scipy.linalg.lapack.**dpbtrs**(*ab*, *b*[, *lower*, *ldab*, *overwrite_b*]) **= <fortran object>**
Wrapper for dpbtrs.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cpbtrs

scipy.linalg.lapack.**cpbtrs**(*ab*, *b*[, *lower*, *ldab*, *overwrite_b*]) **= <fortran object>**
Wrapper for cpbtrs.

Parameters

ab [input rank-2 array('F') with bounds (ldab,n)]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zpbtrs

scipy.linalg.lapack.**zpbtrs**(*ab*, *b*[, *lower*, *ldab*, *overwrite_b*]) **= <fortran object>**
Wrapper for zpbtrs.

Parameters

ab [input rank-2 array('D') with bounds (ldab,n)]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.spftrf

scipy.linalg.lapack.**spftrf**(*n*, *a*[, *transr*, *uplo*, *overwrite_a*]) **= <fortran object>**
Wrapper for spftrf.

Parameters

n [input int]
a [input rank-1 array('f') with bounds (nt)]

Returns

achol [rank-1 array('f') with bounds (nt) and a storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.dpftrf

scipy.linalg.lapack.**dpftrf**(*n*, *a*[, *transr*, *uplo*, *overwrite_a*]) **= <fortran object>**
Wrapper for dpftrf.

Parameters

n [input int]
a [input rank-1 array('d') with bounds (nt)]

Returns

achol [rank-1 array('d') with bounds (nt) and a storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.cpftrf

scipy.linalg.lapack.**cpftrf**(*n*, *a*[, *transr*, *uplo*, *overwrite_a*]) **= <fortran object>**
Wrapper for cpftrf.

Parameters

n [input int]
a [input rank-1 array('F') with bounds (nt)]

Returns

achol [rank-1 array('F') with bounds (nt) and a storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.zpftrf

scipy.linalg.lapack.**zpftrf**(*n*, *a*[, *transr*, *uplo*, *overwrite_a*]) **= <fortran object>**
Wrapper for zpftrf.

Parameters

n [input int]
a [input rank-1 array('D') with bounds (nt)]

Returns

achol [rank-1 array('D') with bounds (nt) and a storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.spftri

scipy.linalg.lapack.**spftri**(*n*, *a*[, *transr*, *uplo*, *overwrite_a*]) **= <fortran object>**
Wrapper for spftri.

Parameters

n [input int]
a [input rank-1 array('f') with bounds (nt)]

Returns

ainv [rank-1 array('f') with bounds (nt) and a storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.dpftri

scipy.linalg.lapack.**dpftri**(*n*, *a*[, *transr*, *uplo*, *overwrite_a*]) **= <fortran object>**
Wrapper for dpftri.

Parameters

n [input int]
a [input rank-1 array('d') with bounds (nt)]

Returns

ainv [rank-1 array('d') with bounds (nt) and a storage]

info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.cpftri

`scipy.linalg.lapack.`**`cpftri`**(*n*, *a*[, *transr*, *uplo*, *overwrite_a*]) **`= <fortran object>`**
Wrapper for `cpftri`.

Parameters

n [input int]
a [input rank-1 array('F') with bounds (nt)]

Returns

ainv [rank-1 array('F') with bounds (nt) and a storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.zpftri

`scipy.linalg.lapack.`**`zpftri`**(*n*, *a*[, *transr*, *uplo*, *overwrite_a*]) **`= <fortran object>`**
Wrapper for `zpftri`.

Parameters

n [input int]
a [input rank-1 array('D') with bounds (nt)]

Returns

ainv [rank-1 array('D') with bounds (nt) and a storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.spftrs

scipy.linalg.lapack.**spftrs**(*n*, *a*, *b*[, *transr*, *uplo*, *overwrite_b*]) **= <fortran object>**

Wrapper for spftrs.

Parameters

n [input int]
a [input rank-1 array('f') with bounds (nt)]
b [input rank-2 array('f') with bounds (ldb,nhrs)]

Returns

x [rank-2 array('f') with bounds (ldb,nhrs) and b storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.dpftrs

scipy.linalg.lapack.**dpftrs**(*n*, *a*, *b*[, *transr*, *uplo*, *overwrite_b*]) **= <fortran object>**

Wrapper for dpftrs.

Parameters

n [input int]
a [input rank-1 array('d') with bounds (nt)]
b [input rank-2 array('d') with bounds (ldb,nhrs)]

Returns

x [rank-2 array('d') with bounds (ldb,nhrs) and b storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.cpftrs

scipy.linalg.lapack.**cpftrs**(*n*, *a*, *b*[, *transr*, *uplo*, *overwrite_b*]) **= <fortran object>**

Wrapper for cpftrs.

Parameters

n [input int]
a [input rank-1 array('F') with bounds (nt)]
b [input rank-2 array('F') with bounds (ldb,nhrs)]

Returns

x [rank-2 array('F') with bounds (ldb,nhrs) and b storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zpftrs

scipy.linalg.lapack.**zpftrs**(*n*, *a*, *b*[, *transr*, *uplo*, *overwrite_b*]) **= <fortran object>**
Wrapper for zpftrs.

Parameters

n [input int]
a [input rank-1 array('D') with bounds (nt)]
b [input rank-2 array('D') with bounds (ldb,nhrs)]

Returns

x [rank-2 array('D') with bounds (ldb,nhrs) and b storage]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.spocon

scipy.linalg.lapack.**spocon**(*a*, *anorm*[, *uplo*]) **= <fortran object>**
Wrapper for spocon.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.dpocon

scipy.linalg.lapack.**dpocon**(*a*, *anorm*[, *uplo*]) **= <fortran object>**
Wrapper for dpocon.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.cpocon

scipy.linalg.lapack.**cpocon**(*a*, *anorm*[, *uplo*]) **= <fortran object>**

Wrapper for cpocon.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.zpocon

scipy.linalg.lapack.**zpocon**(*a*, *anorm*[, *uplo*]) **= <fortran object>**

Wrapper for zpocon.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.spstrf

scipy.linalg.lapack.**spstrf**(*a*[, *tol*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for spstrf.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

c [rank-2 array('f') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
rank_c [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
tol [input float, optional] Default: -1.0
lower [input int, optional] Default: 0

scipy.linalg.lapack.dpstrf

scipy.linalg.lapack.**dpstrf**(*a*[, *tol*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for dpstrf.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

c [rank-2 array('d') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
rank_c [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
tol [input float, optional] Default: -1.0
lower [input int, optional] Default: 0

scipy.linalg.lapack.cpstrf

scipy.linalg.lapack.**cpstrf**(*a*[, *tol*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for cpstrf.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

c [rank-2 array('F') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
rank_c [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
tol [input float, optional] Default: -1.0
lower [input int, optional] Default: 0

scipy.linalg.lapack.zpstrf

scipy.linalg.lapack.**zpstrf**(*a*[, *tol*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for zpstrf.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

c [rank-2 array('D') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
rank_c [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
tol [input float, optional] Default: -1.0
lower [input int, optional] Default: 0

scipy.linalg.lapack.spstf2

scipy.linalg.lapack.**spstf2**(*a*[, *tol*, *lower*, *overwrite_a*]) **= <fortran object>**
Wrapper for spstf2.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

c [rank-2 array('f') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
rank_c [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
tol [input float, optional] Default: -1.0
lower [input int, optional] Default: 0

scipy.linalg.lapack.dpstf2

scipy.linalg.lapack.**dpstf2**(*a*[, *tol*, *lower*, *overwrite_a*]) **= <fortran object>**
Wrapper for dpstf2.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

c [rank-2 array('d') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
rank_c [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
tol [input float, optional] Default: -1.0
lower [input int, optional] Default: 0

scipy.linalg.lapack.cpstf2

scipy.linalg.lapack.**cpstf2**(*a*[, *tol*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for cpstf2.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

c [rank-2 array('F') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
rank_c [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
tol [input float, optional] Default: -1.0
lower [input int, optional] Default: 0

scipy.linalg.lapack.zpstf2

scipy.linalg.lapack.**zpstf2**(*a*[, *tol*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for zpstf2.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

c [rank-2 array('D') with bounds (n,n) and a storage]
piv [rank-1 array('i') with bounds (n)]
rank_c [int]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
tol [input float, optional] Default: -1.0
lower [input int, optional] Default: 0

scipy.linalg.lapack.sposv

scipy.linalg.lapack.**sposv**(*a*, *b*[, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for sposv.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

c [rank-2 array('f') with bounds (n,n) and a storage]
x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.dposv

scipy.linalg.lapack.**dposv**(*a*, *b*[, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**
Wrapper for dposv.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

c [rank-2 array('d') with bounds (n,n) and a storage]
x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.cposv

scipy.linalg.lapack.**cposv**(*a*, *b*[, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**
Wrapper for cposv.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

c [rank-2 array('F') with bounds (n,n) and a storage]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.zposv

scipy.linalg.lapack.**zposv**(*a*, *b*[, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zposv.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

c [rank-2 array('D') with bounds (n,n) and a storage]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.sposvx

scipy.linalg.lapack.**sposvx**(*a*, *b*[, *fact*, *af*, *equed*, *s*, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for sposvx.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

a_s [rank-2 array('f') with bounds (n,n) and a storage]
lu [rank-2 array('f') with bounds (n,n) and af storage]
equed [string(len=1)]
s [rank-1 array('f') with bounds (n)]
b_s [rank-2 array('f') with bounds (n,nrhs) and b storage]
x [rank-2 array('f') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'E'
overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('f') with bounds (n,n)]
equed [input string(len=1), optional] Default: 'Y'
s [input rank-1 array('f') with bounds (n)]
overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.dposvx

scipy.linalg.lapack.**dposvx**(*a*, *b*[, *fact*, *af*, *equed*, *s*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for dposvx.

Parameters

a	[input rank-2 array('d') with bounds (n,n)]
b	[input rank-2 array('d') with bounds (n,nrhs)]

Returns

a_s	[rank-2 array('d') with bounds (n,n) and a storage]
lu	[rank-2 array('d') with bounds (n,n) and af storage]
equed	[string(len=1)]
s	[rank-1 array('d') with bounds (n)]
b_s	[rank-2 array('d') with bounds (n,nrhs) and b storage]
x	[rank-2 array('d') with bounds (n,nrhs)]
rcond	[float]
ferr	[rank-1 array('d') with bounds (nrhs)]
berr	[rank-1 array('d') with bounds (nrhs)]
info	[int]

Other Parameters

fact	[input string(len=1), optional] Default: 'E'
overwrite_a	[input int, optional] Default: 0
af	[input rank-2 array('d') with bounds (n,n)]
equed	[input string(len=1), optional] Default: 'Y'
s	[input rank-1 array('d') with bounds (n)]
overwrite_b	[input int, optional] Default: 0
lower	[input int, optional] Default: 0

scipy.linalg.lapack.cposvx

scipy.linalg.lapack.**cposvx**(*a*, *b*[, *fact*, *af*, *equed*, *s*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for cposvx.

Parameters

a	[input rank-2 array('F') with bounds (n,n)]
b	[input rank-2 array('F') with bounds (n,nrhs)]

Returns

a_s	[rank-2 array('F') with bounds (n,n) and a storage]
lu	[rank-2 array('F') with bounds (n,n) and af storage]
equed	[string(len=1)]
s	[rank-1 array('f') with bounds (n)]
b_s	[rank-2 array('F') with bounds (n,nrhs) and b storage]
x	[rank-2 array('F') with bounds (n,nrhs)]
rcond	[float]
ferr	[rank-1 array('f') with bounds (nrhs)]
berr	[rank-1 array('f') with bounds (nrhs)]
info	[int]

Other Parameters

fact [input string(len=1), optional] Default: 'E'
overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('F') with bounds (n,n)]
equed [input string(len=1), optional] Default: 'Y'
s [input rank-1 array('f') with bounds (n)]
overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.zposvx

scipy.linalg.lapack.**zposvx**(*a*, *b*[, *fact*, *af*, *equed*, *s*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for zposvx.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

a_s [rank-2 array('D') with bounds (n,n) and a storage]
lu [rank-2 array('D') with bounds (n,n) and af storage]
equed [string(len=1)]
s [rank-1 array('d') with bounds (n)]
b_s [rank-2 array('D') with bounds (n,nrhs) and b storage]
x [rank-2 array('D') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'E'
overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('D') with bounds (n,n)]
equed [input string(len=1), optional] Default: 'Y'
s [input rank-1 array('d') with bounds (n)]
overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.spotrf

scipy.linalg.lapack.**spotrf**(*a*[, *lower*, *clean*, *overwrite_a*]) = **<fortran object>**

Wrapper for spotrf.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

c [rank-2 array('f') with bounds (n,n) and a storage]
info [int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

clean
: [input int, optional] Default: 1

scipy.linalg.lapack.dpotrf

scipy.linalg.lapack.**dpotrf**(*a*[, *lower*, *clean*, *overwrite_a*]) **= <fortran object>**

Wrapper for dpotrf.

Parameters

a
: [input rank-2 array('d') with bounds (n,n)]

Returns

c
: [rank-2 array('d') with bounds (n,n) and a storage]

info
: [int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

clean
: [input int, optional] Default: 1

scipy.linalg.lapack.cpotrf

scipy.linalg.lapack.**cpotrf**(*a*[, *lower*, *clean*, *overwrite_a*]) **= <fortran object>**

Wrapper for cpotrf.

Parameters

a
: [input rank-2 array('F') with bounds (n,n)]

Returns

c
: [rank-2 array('F') with bounds (n,n) and a storage]

info
: [int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

clean
: [input int, optional] Default: 1

scipy.linalg.lapack.zpotrf

scipy.linalg.lapack.**zpotrf**(*a*[, *lower*, *clean*, *overwrite_a*]) **= <fortran object>**

Wrapper for zpotrf.

Parameters

a
: [input rank-2 array('D') with bounds (n,n)]

Returns

c
: [rank-2 array('D') with bounds (n,n) and a storage]

info
: [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lower [input int, optional] Default: 0
clean [input int, optional] Default: 1

scipy.linalg.lapack.spotri

scipy.linalg.lapack.**spotri**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for spotri.

Parameters

c [input rank-2 array('f') with bounds (n,n)]

Returns

inv_a [rank-2 array('f') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.dpotri

scipy.linalg.lapack.**dpotri**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for dpotri.

Parameters

c [input rank-2 array('d') with bounds (n,n)]

Returns

inv_a [rank-2 array('d') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.cpotri

scipy.linalg.lapack.**cpotri**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**
Wrapper for cpotri.

Parameters

c [input rank-2 array('F') with bounds (n,n)]

Returns

inv_a [rank-2 array('F') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.zpotri

scipy.linalg.lapack.**zpotri**(*c*[, *lower*, *overwrite_c*]) **= <fortran object>**

Wrapper for zpotri.

Parameters

c [input rank-2 array('D') with bounds (n,n)]

Returns

inv_a [rank-2 array('D') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.spotrs

scipy.linalg.lapack.**spotrs**(*c*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for spotrs.

Parameters

c [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.dpotrs

scipy.linalg.lapack.**dpotrs**(*c*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for dpotrs.

Parameters

c [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.cpotrs

scipy.linalg.lapack.**cpotrs**(*c*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for cpotrs.

Parameters

c [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.zpotrs

scipy.linalg.lapack.**zpotrs**(*c*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for zpotrs.

Parameters

c [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.sppcon

scipy.linalg.lapack.**sppcon**(*n*, *ap*, *anorm*[, *lower*]) **= <fortran object>**

Wrapper for sppcon.

Parameters

n [input int]
ap [input rank-1 array('f') with bounds (L)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dppcon

scipy.linalg.lapack.**dppcon**(*n*, *ap*, *anorm*[, *lower*]) **= <fortran object>**

Wrapper for dppcon.

Parameters

n [input int]
ap [input rank-1 array('d') with bounds (L)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.cppcon

scipy.linalg.lapack.**cppcon**(*n*, *ap*, *anorm*[, *lower*]) **= <fortran object>**

Wrapper for cppcon.

Parameters

n [input int]
ap [input rank-1 array('F') with bounds (L)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zppcon

scipy.linalg.lapack.**zppcon**(*n*, *ap*, *anorm*[, *lower*]) **= <fortran object>**

Wrapper for zppcon.

Parameters

n [input int]
ap [input rank-1 array('D') with bounds (L)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.sppsv

scipy.linalg.lapack.**sppsv**(*n*, *ap*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for sppsv.

Parameters

n [input int]
ap [input rank-1 array('f') with bounds (L)]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dppsv

scipy.linalg.lapack.**dppsv**(*n*, *ap*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for dppsv.

Parameters

n [input int]
ap [input rank-1 array('d') with bounds (L)]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cppsv

scipy.linalg.lapack.**cppsv**(*n*, *ap*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for cppsv.

Parameters

n [input int]
ap [input rank-1 array('F') with bounds (L)]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zppsv

scipy.linalg.lapack.**zppsv**(*n*, *ap*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**
Wrapper for zppsv.

Parameters

n [input int]
ap [input rank-1 array('D') with bounds (L)]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.spptrf

scipy.linalg.lapack.**spptrf**(*n*, *ap*[, *lower*, *overwrite_ap*]) **= <fortran object>**
Wrapper for spptrf.

Parameters

n [input int]
ap [input rank-1 array('f') with bounds (L)]

Returns

ul [rank-1 array('f') with bounds (L) and ap storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ap
[input int, optional] Default: 0

scipy.linalg.lapack.dpptrf

scipy.linalg.lapack.**dpptrf**(*n*, *ap*[, *lower*, *overwrite_ap*]) **= <fortran object>**
Wrapper for dpptrf.

Parameters

n [input int]
ap [input rank-1 array('d') with bounds (L)]

Returns

ul [rank-1 array('d') with bounds (L) and ap storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0

overwrite_ap
[input int, optional] Default: 0

scipy.linalg.lapack.cpptrf

scipy.linalg.lapack.**cpptrf**(*n*, *ap*[, *lower*, *overwrite_ap*]) **= <fortran object>**
Wrapper for cpptrf.

Parameters

n [input int]
ap [input rank-1 array('F') with bounds (L)]

Returns

ul [rank-1 array('F') with bounds (L) and ap storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ap
[input int, optional] Default: 0

scipy.linalg.lapack.zpptrf

scipy.linalg.lapack.**zpptrf**(*n*, *ap*[, *lower*, *overwrite_ap*]) **= <fortran object>**
Wrapper for zpptrf.

Parameters

n [input int]
ap [input rank-1 array('D') with bounds (L)]

Returns

ul [rank-1 array('D') with bounds (L) and ap storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ap
[input int, optional] Default: 0

scipy.linalg.lapack.spptri

scipy.linalg.lapack.**spptri**(*n*, *ap*[, *lower*, *overwrite_ap*]) **= <fortran object>**
Wrapper for spptri.

Parameters

n [input int]
ap [input rank-1 array('f') with bounds (L)]

Returns

uli [rank-1 array('f') with bounds (L) and ap storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0

overwrite_ap
[input int, optional] Default: 0

scipy.linalg.lapack.dpptri

scipy.linalg.lapack.**dpptri**(*n*, *ap*[, *lower*, *overwrite_ap*]) **= <fortran object>**
Wrapper for dpptri.

Parameters

n [input int]
ap [input rank-1 array('d') with bounds (L)]

Returns

uli [rank-1 array('d') with bounds (L) and ap storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ap
[input int, optional] Default: 0

scipy.linalg.lapack.cpptri

scipy.linalg.lapack.**cpptri**(*n*, *ap*[, *lower*, *overwrite_ap*]) **= <fortran object>**
Wrapper for cpptri.

Parameters

n [input int]
ap [input rank-1 array('F') with bounds (L)]

Returns

uli [rank-1 array('F') with bounds (L) and ap storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_ap
[input int, optional] Default: 0

scipy.linalg.lapack.zpptri

scipy.linalg.lapack.**zpptri**(*n*, *ap*[, *lower*, *overwrite_ap*]) **= <fortran object>**
Wrapper for zpptri.

Parameters

n [input int]
ap [input rank-1 array('D') with bounds (L)]

Returns

uli [rank-1 array('D') with bounds (L) and ap storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0

overwrite_ap
[input int, optional] Default: 0

scipy.linalg.lapack.spptrs

scipy.linalg.lapack.**spptrs**(*n*, *ap*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**
Wrapper for spptrs.

Parameters

n [input int]
ap [input rank-1 array('f') with bounds (L)]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dpptrs

scipy.linalg.lapack.**dpptrs**(*n*, *ap*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**
Wrapper for dpptrs.

Parameters

n [input int]
ap [input rank-1 array('d') with bounds (L)]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cpptrs

scipy.linalg.lapack.**cpptrs**(*n*, *ap*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**
Wrapper for cpptrs.

Parameters

n [input int]
ap [input rank-1 array('F') with bounds (L)]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zpptrs

scipy.linalg.lapack.**zpptrs**(*n*, *ap*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**
Wrapper for zpptrs.

Parameters

n [input int]
ap [input rank-1 array('D') with bounds (L)]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.sptsv

scipy.linalg.lapack.**sptsv**(*d*, *e*, *b*[, *overwrite_d*, *overwrite_e*, *overwrite_b*]) **= <fortran object>**
Wrapper for sptsv.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (n - 1)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

d [rank-1 array('f') with bounds (n)]
du [rank-1 array('f') with bounds (n - 1) and e storage]
x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dptsv

scipy.linalg.lapack.**dptsv**(*d*, *e*, *b*[, *overwrite_d*, *overwrite_e*, *overwrite_b*]) **= <fortran object>**

Wrapper for dptsv.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds (n - 1)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

d [rank-1 array('d') with bounds (n)]
du [rank-1 array('d') with bounds (n - 1) and e storage]
x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cptsv

scipy.linalg.lapack.**cptsv**(*d*, *e*, *b*[, *overwrite_d*, *overwrite_e*, *overwrite_b*]) **= <fortran object>**

Wrapper for cptsv.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('F') with bounds (n - 1)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

d [rank-1 array('f') with bounds (n)]
du [rank-1 array('F') with bounds (n - 1) and e storage]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zptsv

scipy.linalg.lapack.**zptsv**(*d*, *e*, *b*[, *overwrite_d*, *overwrite_e*, *overwrite_b*]) **= <fortran object>**

Wrapper for zptsv.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('D') with bounds (n - 1)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

d [rank-1 array('d') with bounds (n)]
du [rank-1 array('D') with bounds (n - 1) and e storage]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.sptsvx

scipy.linalg.lapack.**sptsvx**(*d*, *e*, *b*[, *fact*, *df*, *ef*]) **= <fortran object>**

Wrapper for sptsvx.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (max(0, n-1))]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

df [rank-1 array('f') with bounds (n)]
ef [rank-1 array('f') with bounds (max(0, n-1))]
x [rank-2 array('f') with bounds (ldx,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'N'
df [input rank-1 array('f') with bounds (n)]
ef [input rank-1 array('f') with bounds (max(0, n-1))]

scipy.linalg.lapack.dptsvx

scipy.linalg.lapack.**dptsvx**(*d*, *e*, *b*[, *fact*, *df*, *ef*]) **= <fortran object>**

Wrapper for dptsvx.

Parameters

d	[input rank-1 array('d') with bounds (n)]
e	[input rank-1 array('d') with bounds (max(0, n-1))]
b	[input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

df	[rank-1 array('d') with bounds (n)]
ef	[rank-1 array('d') with bounds (max(0, n-1))]
x	[rank-2 array('d') with bounds (ldx,nrhs)]
rcond	[float]
ferr	[rank-1 array('d') with bounds (nrhs)]
berr	[rank-1 array('d') with bounds (nrhs)]
info	[int]

Other Parameters

fact	[input string(len=1), optional] Default: 'N'
df	[input rank-1 array('d') with bounds (n)]
ef	[input rank-1 array('d') with bounds (max(0, n-1))]

scipy.linalg.lapack.cptsvx

scipy.linalg.lapack.**cptsvx**(*d*, *e*, *b*[, *fact*, *df*, *ef*]) **= <fortran object>**

Wrapper for cptsvx.

Parameters

d	[input rank-1 array('f') with bounds (n)]
e	[input rank-1 array('F') with bounds (max(0, n-1))]
b	[input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

df	[rank-1 array('f') with bounds (n)]
ef	[rank-1 array('F') with bounds (max(0, n-1))]
x	[rank-2 array('F') with bounds (ldx,nrhs)]
rcond	[float]
ferr	[rank-1 array('f') with bounds (nrhs)]
berr	[rank-1 array('f') with bounds (nrhs)]
info	[int]

Other Parameters

fact	[input string(len=1), optional] Default: 'N'
df	[input rank-1 array('f') with bounds (n)]
ef	[input rank-1 array('F') with bounds (max(0, n-1))]

scipy.linalg.lapack.zptsvx

scipy.linalg.lapack.**zptsvx**(*d*, *e*, *b*[, *fact*, *df*, *ef*]) **= <fortran object>**

Wrapper for zptsvx.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('D') with bounds (max(0, n-1))]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

df [rank-1 array('d') with bounds (n)]
ef [rank-1 array('D') with bounds (max(0, n-1))]
x [rank-2 array('D') with bounds (ldx,nrhs)]
rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

fact [input string(len=1), optional] Default: 'N'
df [input rank-1 array('d') with bounds (n)]
ef [input rank-1 array('D') with bounds (max(0, n-1))]

scipy.linalg.lapack.spttrf

scipy.linalg.lapack.**spttrf**(*d*, *e*[, *overwrite_d*, *overwrite_e*]) **= <fortran object>**

Wrapper for spttrf.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds ((n>0?n-1:0))]

Returns

d [rank-1 array('f') with bounds (n)]
e [rank-1 array('f') with bounds ((n>0?n-1:0))]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0

scipy.linalg.lapack.dpttrf

scipy.linalg.lapack.**dpttrf**(*d*, *e*[, *overwrite_d*, *overwrite_e*]) **= <fortran object>**

Wrapper for dpttrf.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds ((n>0?n-1:0))]

Returns

d [rank-1 array('d') with bounds (n)]

e [rank-1 array('d') with bounds ((n>0?n-1:0))]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0

scipy.linalg.lapack.cpttrf

scipy.linalg.lapack.**cpttrf**(*d*, *e*[, *overwrite_d*, *overwrite_e*]) **= <fortran object>**
Wrapper for cpttrf.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('F') with bounds ((n>0?n-1:0))]

Returns

d [rank-1 array('f') with bounds (n)]
e [rank-1 array('F') with bounds ((n>0?n-1:0))]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0

scipy.linalg.lapack.zpttrf

scipy.linalg.lapack.**zpttrf**(*d*, *e*[, *overwrite_d*, *overwrite_e*]) **= <fortran object>**
Wrapper for zpttrf.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('D') with bounds ((n>0?n-1:0))]

Returns

d [rank-1 array('d') with bounds (n)]
e [rank-1 array('D') with bounds ((n>0?n-1:0))]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0

scipy.linalg.lapack.spttrs

scipy.linalg.lapack.**spttrs**(*d*, *e*, *b*[, *overwrite_b*]) **= <fortran object>**

Wrapper for spttrs.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds ((n>0?n-1:0))]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dpttrs

scipy.linalg.lapack.**dpttrs**(*d*, *e*, *b*[, *overwrite_b*]) **= <fortran object>**

Wrapper for dpttrs.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds ((n>0?n-1:0))]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cpttrs

scipy.linalg.lapack.**cpttrs**(*d*, *e*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for cpttrs.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('F') with bounds ((n>0?n-1:0))]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.zpttrs

scipy.linalg.lapack.**zpttrs**(*d*, *e*, *b*[, *lower*, *overwrite_b*]) **= <fortran object>**

Wrapper for zpttrs.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('D') with bounds ((n>0?n-1:0))]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.spteqr

scipy.linalg.lapack.**spteqr**(*d*, *e*, *z*[, *compute_z*, *overwrite_d*, *overwrite_e*, *overwrite_z*]) **= <fortran object>**

Wrapper for spteqr.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds ((n>0?n-1:0))]
z [input rank-2 array('f') with bounds ((compute_z==0?shape(z, 0):max(1,n)),(compute_z==0?shape(z, 1):n))]

Returns

d [rank-1 array('f') with bounds (n)]
e [rank-1 array('f') with bounds ((n>0?n-1:0))]
z [rank-2 array('f') with bounds ((compute_z==0?shape(z, 0):max(1,n)),(compute_z==0?shape(z, 1):n))]
info [int]

Other Parameters

compute_z
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0

scipy.linalg.lapack.dpteqr

scipy.linalg.lapack.**dpteqr**(*d*, *e*, *z*[, *compute_z*, *overwrite_d*, *overwrite_e*, *overwrite_z*]) = **<fortran object>**

Wrapper for dpteqr.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds ((n>0?n-1:0))]
z [input rank-2 array('d') with bounds ((compute_z==0?shape(z, 0):max(1,n)),(compute_z==0?shape(z, 1):n))]

Returns

d [rank-1 array('d') with bounds (n)]
e [rank-1 array('d') with bounds ((n>0?n-1:0))]
z [rank-2 array('d') with bounds ((compute_z==0?shape(z, 0):max(1,n)),(compute_z==0?shape(z, 1):n))]
info [int]

Other Parameters

compute_z
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0

scipy.linalg.lapack.cpteqr

scipy.linalg.lapack.**cpteqr**(*d*, *e*, *z*[, *compute_z*, *overwrite_d*, *overwrite_e*, *overwrite_z*]) = **<fortran object>**

Wrapper for cpteqr.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds ((n>0?n-1:0))]
z [input rank-2 array('F') with bounds ((compute_z==0?shape(z, 0):max(1,n)),(compute_z==0?shape(z, 1):n))]

Returns

d [rank-1 array('f') with bounds (n)]
e [rank-1 array('f') with bounds ((n>0?n-1:0))]
z [rank-2 array('F') with bounds ((compute_z==0?shape(z, 0):max(1,n)),(compute_z==0?shape(z, 1):n))]
info [int]

Other Parameters

compute_z
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0

overwrite_z
[input int, optional] Default: 0

scipy.linalg.lapack.zpteqr

scipy.linalg.lapack.**zpteqr**(*d*, *e*, *z*[, *compute_z*, *overwrite_d*, *overwrite_e*, *overwrite_z*]) = **<fortran object>**

Wrapper for zpteqr.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds ((n>0?n-1:0))]
z [input rank-2 array('D') with bounds ((compute_z==0?shape(z, 0):max(1,n)),(compute_z==0?shape(z, 1):n))]

Returns

d [rank-1 array('d') with bounds (n)]
e [rank-1 array('d') with bounds ((n>0?n-1:0))]
z [rank-2 array('D') with bounds ((compute_z==0?shape(z, 0):max(1,n)),(compute_z==0?shape(z, 1):n))]
info [int]

Other Parameters

compute_z
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0

scipy.linalg.lapack.crot

scipy.linalg.lapack.**crot**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) = **<fortran object>**

Wrapper for crot.

Parameters

x [input rank-1 array('F') with bounds (lx)]
y [input rank-1 array('F') with bounds (ly)]
c [input float]
s [input complex]

Returns

x [rank-1 array('F') with bounds (lx)]
y [rank-1 array('F') with bounds (ly)]

Other Parameters

n [input int, optional] Default: (lx-1-offx)/abs(incx)+1
overwrite_x
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1

overwrite_y
[input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.lapack.zrot

scipy.linalg.lapack.**zrot**(*x*, *y*, *c*, *s*[, *n*, *offx*, *incx*, *offy*, *incy*, *overwrite_x*, *overwrite_y*]) = **<fortran object>**

Wrapper for `zrot`.

Parameters

x [input rank-1 array('D') with bounds (lx)]
y [input rank-1 array('D') with bounds (ly)]
c [input float]
s [input complex]

Returns

x [rank-1 array('D') with bounds (lx)]
y [rank-1 array('D') with bounds (ly)]

Other Parameters

n [input int, optional] Default: (lx-1-offx)/abs(incx)+1
overwrite_x
[input int, optional] Default: 0
offx [input int, optional] Default: 0
incx [input int, optional] Default: 1
overwrite_y
[input int, optional] Default: 0
offy [input int, optional] Default: 0
incy [input int, optional] Default: 1

scipy.linalg.lapack.ssbev

scipy.linalg.lapack.**ssbev**(*ab*[, *compute_v*, *lower*, *ldab*, *overwrite_ab*]) = **<fortran object>**

Wrapper for `ssbev`.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]

Returns

w [rank-1 array('f') with bounds (n)]
z [rank-2 array('f') with bounds (ldz,ldz)]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.dsbev

scipy.linalg.lapack.**dsbev**(*ab*[, *compute_v*, *lower*, *ldab*, *overwrite_ab*]) **= <fortran object>**

Wrapper for dsbev.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]

Returns

w [rank-1 array('d') with bounds (n)]
z [rank-2 array('d') with bounds (ldz,ldz)]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)

scipy.linalg.lapack.ssbevd

scipy.linalg.lapack.**ssbevd**(*ab*[, *compute_v*, *lower*, *ldab*, *liwork*, *overwrite_ab*]) **= <fortran object>**

Wrapper for ssbevd.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]

Returns

w [rank-1 array('f') with bounds (n)]
z [rank-2 array('f') with bounds (ldz,ldz)]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
liwork [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.dsbevd

scipy.linalg.lapack.**dsbevd**(*ab*[, *compute_v*, *lower*, *ldab*, *liwork*, *overwrite_ab*]) **= <fortran object>**

Wrapper for dsbevd.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]

Returns

w [rank-1 array('d') with bounds (n)]

z [rank-2 array('d') with bounds (ldz,ldz)]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
ldab [input int, optional] Default: shape(ab,0)
liwork [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.ssbevx

scipy.linalg.lapack.**ssbevx**(*ab*, *vl*, *vu*, *il*, *iu*[, *ldab*, *compute_v*, *range*, *lower*, *abstol*, *mmax*, *overwrite_ab*]) **= <fortran object>**

Wrapper for ssbevx.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]
vl [input float]
vu [input float]
il [input int]
iu [input int]

Returns

w [rank-1 array('f') with bounds (n)]
z [rank-2 array('f') with bounds (ldz,mmax)]
m [int]
ifail [rank-1 array('i') with bounds ((compute_v?n:1))]
info [int]

Other Parameters

overwrite_ab
[input int, optional] Default: 1
ldab [input int, optional] Default: shape(ab,0)
compute_v
[input int, optional] Default: 1
range [input int, optional] Default: 0
lower [input int, optional] Default: 0
abstol [input float, optional] Default: 0.0
mmax [input int, optional] Default: (compute_v?(range==2?(iu-il+1):n):1)

scipy.linalg.lapack.dsbevx

scipy.linalg.lapack.**dsbevx**(*ab*, *vl*, *vu*, *il*, *iu*[, *ldab*, *compute_v*, *range*, *lower*, *abstol*, *mmax*, *overwrite_ab*]) **= <fortran object>**

Wrapper for dsbevx.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]
vl [input float]
vu [input float]
il [input int]
iu [input int]

Returns

w	[rank-1 array('d') with bounds (n)]
z	[rank-2 array('d') with bounds (ldz,mmax)]
m	[int]
ifail	[rank-1 array('i') with bounds ((compute_v?n:1))]
info	[int]

Other Parameters

overwrite_ab	[input int, optional] Default: 1
ldab	[input int, optional] Default: shape(ab,0)
compute_v	[input int, optional] Default: 1
range	[input int, optional] Default: 0
lower	[input int, optional] Default: 0
abstol	[input float, optional] Default: 0.0
mmax	[input int, optional] Default: (compute_v?(range==2?(iu-il+1):n):1)

scipy.linalg.lapack.ssfrk

scipy.linalg.lapack.**ssfrk**(*n*, *k*, *alpha*, *a*, *beta*, *c*[, *transr*, *uplo*, *trans*, *overwrite_c*]) **= <fortran object>**

Wrapper for `ssfrk`.

Parameters

n	[input int]
k	[input int]
alpha	[input float]
a	[input rank-2 array('f') with bounds (lda,ka)]
beta	[input float]
c	[input rank-1 array('f') with bounds (nt)]

Returns

cout	[rank-1 array('f') with bounds (nt) and c storage]

Other Parameters

transr	[input string(len=1), optional] Default: 'N'
uplo	[input string(len=1), optional] Default: 'U'
trans	[input string(len=1), optional] Default: 'N'
overwrite_c	[input int, optional] Default: 0

scipy.linalg.lapack.dsfrk

scipy.linalg.lapack.**dsfrk**(*n*, *k*, *alpha*, *a*, *beta*, *c*[, *transr*, *uplo*, *trans*, *overwrite_c*]) **= <fortran object>**

Wrapper for `dsfrk`.

Parameters

n	[input int]
k	[input int]
alpha	[input float]
a	[input rank-2 array('d') with bounds (lda,ka)]
beta	[input float]
c	[input rank-1 array('d') with bounds (nt)]

Returns

cout [rank-1 array('d') with bounds (nt) and c storage]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.sstebz

scipy.linalg.lapack.**sstebz**(*d*, *e*, *range*, *vl*, *vu*, *il*, *iu*, *tol*, *order*) **= <fortran object>**
Wrapper for sstebz.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (n - 1)]
range [input int]
vl [input float]
vu [input float]
il [input int]
iu [input int]
tol [input float]
order [input string(len=1)]

Returns

m [int]
w [rank-1 array('f') with bounds (n)]
iblock [rank-1 array('i') with bounds (n)]
isplit [rank-1 array('i') with bounds (n)]
info [int]

scipy.linalg.lapack.dstebz

scipy.linalg.lapack.**dstebz**(*d*, *e*, *range*, *vl*, *vu*, *il*, *iu*, *tol*, *order*) **= <fortran object>**
Wrapper for dstebz.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds (n - 1)]
range [input int]
vl [input float]
vu [input float]
il [input int]
iu [input int]
tol [input float]
order [input string(len=1)]

Returns

m [int]
w [rank-1 array('d') with bounds (n)]
iblock [rank-1 array('i') with bounds (n)]
isplit [rank-1 array('i') with bounds (n)]
info [int]

scipy.linalg.lapack.sstein

scipy.linalg.lapack.**sstein**(*d*, *e*, *w*, *iblock*, *isplit*) **= <fortran object>**

Wrapper for sstein.

Parameters

d	[input rank-1 array('f') with bounds (n)]
e	[input rank-1 array('f') with bounds (n - 1)]
w	[input rank-1 array('f') with bounds (m)]
iblock	[input rank-1 array('i') with bounds (n)]
isplit	[input rank-1 array('i') with bounds (n)]

Returns

z	[rank-2 array('f') with bounds (ldz,m)]
info	[int]

scipy.linalg.lapack.dstein

scipy.linalg.lapack.**dstein**(*d*, *e*, *w*, *iblock*, *isplit*) **= <fortran object>**

Wrapper for dstein.

Parameters

d	[input rank-1 array('d') with bounds (n)]
e	[input rank-1 array('d') with bounds (n - 1)]
w	[input rank-1 array('d') with bounds (m)]
iblock	[input rank-1 array('i') with bounds (n)]
isplit	[input rank-1 array('i') with bounds (n)]

Returns

z	[rank-2 array('d') with bounds (ldz,m)]
info	[int]

scipy.linalg.lapack.sstemr

scipy.linalg.lapack.**sstemr**(*d*, *e*, *range*, *vl*, *vu*, *il*, *iu*[, *compute_v*, *lwork*, *liwork*, *overwrite_d*]) **= <fortran object>**

Wrapper for sstemr.

Parameters

d	[input rank-1 array('f') with bounds (n)]
e	[input rank-1 array('f') with bounds (n)]
range	[input int]
vl	[input float]
vu	[input float]
il	[input int]
iu	[input int]

Returns

m	[int]
w	[rank-1 array('f') with bounds (n)]
z	[rank-2 array('f') with bounds (n,n)]
info	[int]

Other Parameters

overwrite_d
: [input int, optional] Default: 0

compute_v
[input int, optional] Default: 1
lwork [input int, optional] Default: max((compute_v?18*n:12*n),1)
liwork [input int, optional] Default: (compute_v?10*n:8*n)

scipy.linalg.lapack.dstemr

scipy.linalg.lapack.**dstemr**(*d*, *e*, *range*, *vl*, *vu*, *il*, *iu*[, *compute_v*, *lwork*, *liwork*, *overwrite_d*]) = **<fortran object>**

Wrapper for dstemr.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds (n)]
range [input int]
vl [input float]
vu [input float]
il [input int]
iu [input int]

Returns

m [int]
w [rank-1 array('d') with bounds (n)]
z [rank-2 array('d') with bounds (n,n)]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
compute_v
[input int, optional] Default: 1
lwork [input int, optional] Default: max((compute_v?18*n:12*n),1)
liwork [input int, optional] Default: (compute_v?10*n:8*n)

scipy.linalg.lapack.sstemr_lwork

scipy.linalg.lapack.**sstemr_lwork**(*d*, *e*, *range*, *vl*, *vu*, *il*, *iu*[, *compute_v*, *overwrite_d*, *overwrite_e*]) = **<fortran object>**

Wrapper for sstemr_lwork.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (n)]
range [input int]
vl [input float]
vu [input float]
il [input int]
iu [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
compute_v
[input int, optional] Default: 1

scipy.linalg.lapack.dstemr_lwork

scipy.linalg.lapack.**dstemr_lwork**(*d*, *e*, *range*, *vl*, *vu*, *il*, *iu*[, *compute_v*, *overwrite_d*, *overwrite_e*]) **= <fortran object>**

Wrapper for dstemr_lwork.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds (n)]
range [input int]
vl [input float]
vu [input float]
il [input int]
iu [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
compute_v
[input int, optional] Default: 1

scipy.linalg.lapack.ssterf

scipy.linalg.lapack.**ssterf**(*d*, *e*[, *overwrite_d*, *overwrite_e*]) **= <fortran object>**

Wrapper for ssterf.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (n - 1)]

Returns

vals [rank-1 array('f') with bounds (n) and d storage]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0

scipy.linalg.lapack.dsterf

scipy.linalg.lapack.**dsterf**(*d*, *e*[, *overwrite_d*, *overwrite_e*]) **= <fortran object>**

Wrapper for dsterf.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds (n - 1)]

Returns

vals [rank-1 array('d') with bounds (n) and d storage]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0

scipy.linalg.lapack.sstev

scipy.linalg.lapack.**sstev**(*d*, *e*[, *compute_v*, *overwrite_d*, *overwrite_e*]) **= <fortran object>**

Wrapper for sstev.

Parameters

d [input rank-1 array('f') with bounds (n)]
e [input rank-1 array('f') with bounds (MAX(n-1,1))]

Returns

vals [rank-1 array('f') with bounds (n) and d storage]
z [rank-2 array('f') with bounds (ldz,(compute_v?n:1))]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
compute_v
[input int, optional] Default: 1

scipy.linalg.lapack.dstev

scipy.linalg.lapack.**dstev**(*d*, *e*[, *compute_v*, *overwrite_d*, *overwrite_e*]) **= <fortran object>**

Wrapper for dstev.

Parameters

d [input rank-1 array('d') with bounds (n)]
e [input rank-1 array('d') with bounds (MAX(n-1,1))]

Returns

vals [rank-1 array('d') with bounds (n) and d storage]
z [rank-2 array('d') with bounds (ldz,(compute_v?n:1))]
info [int]

Other Parameters

overwrite_d
[input int, optional] Default: 0
overwrite_e
[input int, optional] Default: 0
compute_v
[input int, optional] Default: 1

scipy.linalg.lapack.ssycon

scipy.linalg.lapack.**ssycon**(*a*, *ipiv*, *anorm*[, *lower*]) **= <fortran object>**
Wrapper for ssycon.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsycon

scipy.linalg.lapack.**dsycon**(*a*, *ipiv*, *anorm*[, *lower*]) **= <fortran object>**
Wrapper for dsycon.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.csycon

scipy.linalg.lapack.**csycon**(*a*, *ipiv*, *anorm*[, *lower*]) **= <fortran object>**
Wrapper for csycon.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zsycon

scipy.linalg.lapack.**zsycon**(*a*, *ipiv*, *anorm*[, *lower*]) **= <fortran object>**

Wrapper for zsycon.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
anorm [input float]

Returns

rcond [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.ssyconv

scipy.linalg.lapack.**ssyconv**(*a*, *ipiv*[, *lower*, *way*, *overwrite_a*]) **= <fortran object>**

Wrapper for ssyconv.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]

Returns

a [rank-2 array('f') with bounds (n,n)]
e [rank-1 array('f') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
way [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.dsyconv

scipy.linalg.lapack.**dsyconv**(*a*, *ipiv*[, *lower*, *way*, *overwrite_a*]) **= <fortran object>**

Wrapper for dsyconv.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]

Returns

a [rank-2 array('d') with bounds (n,n)]
e [rank-1 array('d') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0

way [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.csyconv

scipy.linalg.lapack.**csyconv**(*a*, *ipiv*[, *lower*, *way*, *overwrite_a*]) **= <fortran object>**
Wrapper for csyconv.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]

Returns

a [rank-2 array('F') with bounds (n,n)]
e [rank-1 array('F') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
way [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.zsyconv

scipy.linalg.lapack.**zsyconv**(*a*, *ipiv*[, *lower*, *way*, *overwrite_a*]) **= <fortran object>**
Wrapper for zsyconv.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]

Returns

a [rank-2 array('D') with bounds (n,n)]
e [rank-1 array('D') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
way [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.ssyequb

scipy.linalg.lapack.**ssyequb**(*a*[, *lower*]) **= <fortran object>**
Wrapper for ssyequb.

Parameters

a [input rank-2 array('f') with bounds (lda,n)]

Returns

s [rank-1 array('f') with bounds (n)]
scond [float]

amax [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsyequb

scipy.linalg.lapack.**dsyequb**(*a*[, *lower*]) **= <fortran object>**
Wrapper for dsyequb.

Parameters

a [input rank-2 array('d') with bounds (lda,n)]

Returns

s [rank-1 array('d') with bounds (n)]
scond [float]
amax [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.csyequb

scipy.linalg.lapack.**csyequb**(*a*[, *lower*]) **= <fortran object>**
Wrapper for csyequb.

Parameters

a [input rank-2 array('F') with bounds (lda,n)]

Returns

s [rank-1 array('f') with bounds (n)]
scond [float]
amax [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zsyequb

scipy.linalg.lapack.**zsyequb**(*a*[, *lower*]) **= <fortran object>**
Wrapper for zsyequb.

Parameters

a [input rank-2 array('D') with bounds (lda,n)]

Returns

s [rank-1 array('d') with bounds (n)]
scond [float]
amax [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.ssyev

scipy.linalg.lapack.**ssyev**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for ssyev.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
v [rank-2 array('f') with bounds (n,n) and a storage]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n-1,1)

scipy.linalg.lapack.dsyev

scipy.linalg.lapack.**dsyev**(*a*[, *compute_v*, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dsyev.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
v [rank-2 array('d') with bounds (n,n) and a storage]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n-1,1)

scipy.linalg.lapack.ssyev_lwork

scipy.linalg.lapack.**ssyev_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for ssyev_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsyev_lwork

scipy.linalg.lapack.**dsyev_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for dsyev_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.ssyevd

scipy.linalg.lapack.**ssyevd**(*a*[, *compute_v*, *lower*, *lwork*, *liwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for ssyevd.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
v [rank-2 array('f') with bounds (n,n) and a storage]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max((compute_v?1+6*n+2*n*n:2*n+1),1)
liwork [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.dsyevd

scipy.linalg.lapack.**dsyevd**(*a*[, *compute_v*, *lower*, *lwork*, *liwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dsyevd.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
v [rank-2 array('d') with bounds (n,n) and a storage]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max((compute_v?1+6*n+2*n*n:2*n+1),1)
liwork [input int, optional] Default: (compute_v?3+5*n:1)

scipy.linalg.lapack.ssyevd_lwork

scipy.linalg.lapack.**ssyevd_lwork**(*n*[, *compute_v*, *lower*]) **= <fortran object>**
Wrapper for ssyevd_lwork.

Parameters

n [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.dsyevd_lwork

scipy.linalg.lapack.**dsyevd_lwork**(*n*[, *compute_v*, *lower*]) **= <fortran object>**
Wrapper for dsyevd_lwork.

Parameters

n [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

compute_v
[input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.ssyevr

scipy.linalg.lapack.**ssyevr**(*a*[, *compute_v*, *range*, *lower*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *liwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for ssyevr.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]

z [rank-2 array('f') with bounds `((compute_v?MAX(0,n):0),(compute_v?(*range=='I'?iu-il+1:MAX(1,n)):0))`]
m [int]
isuppz [rank-1 array('i') with bounds `((compute_v?(2*(*range=='A'||(*range=='I' && iu-il+1==n)?n:0)):0))`]
info [int]

Other Parameters

compute_v
[input int, optional] Default `1`
range [input string(len=1), optional] Default `'A'`
lower [input int, optional] Default `0`
overwrite_a
[input int, optional] Default `0`
vl [input float, optional] Default `0.0`
vu [input float, optional] Default `1.0`
il [input int, optional] Default `1`
iu [input int, optional] Default `n`
abstol [input float, optional] Default `0.0`
lwork [input int, optional] Default `max(26*n,1)`
liwork [input int, optional] Default `max(1,10*n)`

scipy.linalg.lapack.dsyevr

`scipy.linalg.lapack.`**`dsyevr`**(*a*[, *compute_v*, *range*, *lower*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *liwork*, *overwrite_a*]) **`= <fortran object>`**

Wrapper for `dsyevr`.

Parameters

a [input rank-2 array('d') with bounds `(n,n)`]

Returns

w [rank-1 array('d') with bounds `(n)`]
z [rank-2 array('d') with bounds `((compute_v?MAX(0,n):0),(compute_v?(*range=='I'?iu-il+1:MAX(1,n)):0))`]
m [int]
isuppz [rank-1 array('i') with bounds `((compute_v?(2*(*range=='A'||(*range=='I' && iu-il+1==n)?n:0)):0))`]
info [int]

Other Parameters

compute_v
[input int, optional] Default `1`
range [input string(len=1), optional] Default `'A'`
lower [input int, optional] Default `0`
overwrite_a
[input int, optional] Default `0`
vl [input float, optional] Default `0.0`
vu [input float, optional] Default `1.0`
il [input int, optional] Default `1`
iu [input int, optional] Default `n`
abstol [input float, optional] Default `0.0`
lwork [input int, optional] Default `max(26*n,1)`
liwork [input int, optional] Default `max(1,10*n)`

scipy.linalg.lapack.ssyevr_lwork

scipy.linalg.lapack.**ssyevr_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for ssyevr_lwork.

Parameters

n [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsyevr_lwork

scipy.linalg.lapack.**dsyevr_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for dsyevr_lwork.

Parameters

n [input int]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.ssyevx

scipy.linalg.lapack.**ssyevx**(*a*[, *compute_v*, *range*, *lower*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for ssyevx.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
z [rank-2 array('f') with bounds ((compute_v?MAX(0,n):0),(compute_v?(*range=='I'?iu-il+1:MAX(1,n)):0))]
m [int]
ifail [rank-1 array('i') with bounds ((compute_v?n:0))]
info [int]

Other Parameters

compute_v
[input int, optional] Default 1
range [input string(len=1), optional] Default 'A'
lower [input int, optional] Default 0

overwrite_a
[input int, optional] Default `0`
vl [input float, optional] Default `0.0`
vu [input float, optional] Default `1.0`
il [input int, optional] Default `1`
iu [input int, optional] Default `n`
abstol [input float, optional] Default `0.0`
lwork [input int, optional] Default `max(8*n,1)`

scipy.linalg.lapack.dsyevx

`scipy.linalg.lapack.`**`dsyevx`**(*a*[, *compute_v*, *range*, *lower*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *overwrite_a*])
`= <fortran object>`

Wrapper for `dsyevx`.

Parameters

a [input rank-2 array('d') with bounds `(n,n)`]

Returns

w [rank-1 array('d') with bounds `(n)`]
z [rank-2 array('d') with bounds `((compute_v?MAX(0,n):0),(compute_v?(*range=='I'?iu-il+1:MAX(1,n)):0))`]
m [int]
ifail [rank-1 array('i') with bounds `((compute_v?n:0))`]
info [int]

Other Parameters

compute_v
[input int, optional] Default `1`
range [input string(len=1), optional] Default `'A'`
lower [input int, optional] Default `0`
overwrite_a
[input int, optional] Default `0`
vl [input float, optional] Default `0.0`
vu [input float, optional] Default `1.0`
il [input int, optional] Default `1`
iu [input int, optional] Default `n`
abstol [input float, optional] Default `0.0`
lwork [input int, optional] Default `max(8*n,1)`

scipy.linalg.lapack.ssyevx_lwork

`scipy.linalg.lapack.`**`ssyevx_lwork`**(*n*[, *lower*]) **`= <fortran object>`**

Wrapper for `ssyevx_lwork`.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsyevx_lwork

scipy.linalg.lapack.**dsyevx_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for dsyevx_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.ssygst

scipy.linalg.lapack.**ssygst**(*a*, *b*[, *itype*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for ssygst.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,n)]

Returns

c [rank-2 array('f') with bounds (n,n) and a storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
itype [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.dsygst

scipy.linalg.lapack.**dsygst**(*a*, *b*[, *itype*, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for dsygst.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,n)]

Returns

c [rank-2 array('d') with bounds (n,n) and a storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
itype [input int, optional] Default: 1
lower [input int, optional] Default: 0

scipy.linalg.lapack.ssygv

scipy.linalg.lapack.**ssygv**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for ssygv.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
v [rank-2 array('f') with bounds (n,n) and a storage]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n-1,1)

scipy.linalg.lapack.dsygv

scipy.linalg.lapack.**dsygv**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dsygv.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
v [rank-2 array('d') with bounds (n,n) and a storage]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n-1,1)

scipy.linalg.lapack.ssygv_lwork

scipy.linalg.lapack.**ssygv_lwork**(*n*[, *uplo*]) **= <fortran object>**

Wrapper for ssygv_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'L'

scipy.linalg.lapack.dsygv_lwork

scipy.linalg.lapack.**dsygv_lwork**(*n*[, *uplo*]) **= <fortran object>**

Wrapper for dsygv_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'L'

scipy.linalg.lapack.ssygvd

scipy.linalg.lapack.**ssygvd**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *liwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for ssygvd.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
v [rank-2 array('f') with bounds (n,n) with a storage]
info [int]

Other Parameters

itype [input int, optional] Default 1
jobz [input string(len=1), optional] Default 'V'
uplo [input string(len=1), optional] Default 'L'
overwrite_a
[input int, optional] Default 0
overwrite_b
[input int, optional] Default 0
lwork [input int, optional] Default (*jobz=='N'?2*n+1:1+6*n+2*n*n)
liwork [input int, optional] Default (*jobz=='N'?1:5*n+3)

scipy.linalg.lapack.dsygvd

scipy.linalg.lapack.**dsygvd**(*a*, *b*[, *itype*, *jobz*, *uplo*, *lwork*, *liwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for dsygvd.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
v [rank-2 array('d') with bounds (n,n) with a storage]
info [int]

Other Parameters

itype [input int, optional] Default 1
jobz [input string(len=1), optional] Default 'V'
uplo [input string(len=1), optional] Default 'L'
overwrite_a
[input int, optional] Default 0
overwrite_b
[input int, optional] Default 0
lwork [input int, optional] Default (*jobz=='N'?2*n+1:1+6*n+2*n*n)
liwork [input int, optional] Default (*jobz=='N'?1:5*n+3)

scipy.linalg.lapack.ssygvx

scipy.linalg.lapack.**ssygvx**(*a*, *b*[, *itype*, *jobz*, *range*, *uplo*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for ssygvx.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,n)]

Returns

w [rank-1 array('f') with bounds (n)]
z [rank-2 array('f') with bounds ((jobz[0]=='V'?MAX(0,n):0),(jobz[0]=='V'?(range[0]=='I'?iu-il+1:MAX(1,n)):0))]
m [int]
ifail [rank-1 array('i') with bounds ((jobz[0]=='N'?0:n))]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
range [input string(len=1), optional] Default: 'A'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
vl [input float, optional] Default: 0.0
vu [input float, optional] Default: 1.0

il [input int, optional] Default: 1
iu [input int, optional] Default: n
abstol [input float, optional] Default: 0.0
lwork [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.dsygvx

scipy.linalg.lapack.**dsygvx**(*a*, *b*[, *itype*, *jobz*, *range*, *uplo*, *vl*, *vu*, *il*, *iu*, *abstol*, *lwork*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dsygvx.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,n)]

Returns

w [rank-1 array('d') with bounds (n)]
z [rank-2 array('d') with bounds ((jobz[0]=='V'?MAX(0,n):0),(jobz[0]=='V'?(range[0]=='I'?iu-il+1:MAX(1,n)):0))]
m [int]
ifail [rank-1 array('i') with bounds ((jobz[0]=='N'?0:n))]
info [int]

Other Parameters

itype [input int, optional] Default: 1
jobz [input string(len=1), optional] Default: 'V'
range [input string(len=1), optional] Default: 'A'
uplo [input string(len=1), optional] Default: 'L'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
vl [input float, optional] Default: 0.0
vu [input float, optional] Default: 1.0
il [input int, optional] Default: 1
iu [input int, optional] Default: n
abstol [input float, optional] Default: 0.0
lwork [input int, optional] Default: max(8*n,1)

scipy.linalg.lapack.ssygvx_lwork

scipy.linalg.lapack.**ssygvx_lwork**(*n*[, *uplo*]) **= <fortran object>**

Wrapper for ssygvx_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'L'

scipy.linalg.lapack.dsygvx_lwork

scipy.linalg.lapack.**dsygvx_lwork**(*n*[, *uplo*]) **= <fortran object>**

Wrapper for dsygvx_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'L'

scipy.linalg.lapack.ssysv

scipy.linalg.lapack.**ssysv**(*a*, *b*[, *lwork*, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for ssysv.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

udut [rank-2 array('f') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('f') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.dsysv

scipy.linalg.lapack.**dsysv**(*a*, *b*[, *lwork*, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dsysv.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

udut [rank-2 array('d') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('d') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.csysv

scipy.linalg.lapack.**csysv**(*a*, *b*[, *lwork*, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for csysv.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,nrhs)]

Returns

udut [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('F') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.zsysv

scipy.linalg.lapack.**zsysv**(*a*, *b*[, *lwork*, *lower*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for zsysv.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,nrhs)]

Returns

udut [rank-2 array('D') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
x [rank-2 array('D') with bounds (n,nrhs) and b storage]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)
lower [input int, optional] Default: 0

scipy.linalg.lapack.ssysv_lwork

scipy.linalg.lapack.**ssysv_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for ssysv_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsysv_lwork

scipy.linalg.lapack.**dsysv_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for dsysv_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.csysv_lwork

scipy.linalg.lapack.**csysv_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for csysv_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zsysv_lwork

scipy.linalg.lapack.**zsysv_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for zsysv_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.ssysvx

scipy.linalg.lapack.**ssysvx**(*a*, *b*[, *af*, *ipiv*, *lwork*, *factored*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for ssysvx.

Parameters

a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (n,nrhs)]

Returns

a_s [rank-2 array('f') with bounds (n,n) and a storage]
udut [rank-2 array('f') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
b_s [rank-2 array('f') with bounds (n,nrhs) and b storage]
x [rank-2 array('f') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('f') with bounds (nrhs)]
berr [rank-1 array('f') with bounds (nrhs)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('f') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)
factored [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.dsysvx

scipy.linalg.lapack.**dsysvx**(*a*, *b*[, *af*, *ipiv*, *lwork*, *factored*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for dsysvx.

Parameters

a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (n,nrhs)]

Returns

a_s [rank-2 array('d') with bounds (n,n) and a storage]
udut [rank-2 array('d') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
b_s [rank-2 array('d') with bounds (n,nrhs) and b storage]
x [rank-2 array('d') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

af
: [input rank-2 array('d') with bounds (n,n)]

ipiv
: [input rank-1 array('i') with bounds (n)]

overwrite_b
: [input int, optional] Default: 0

lwork
: [input int, optional] Default: max(3*n,1)

factored
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

scipy.linalg.lapack.csysvx

scipy.linalg.lapack.**csysvx**(*a*, *b*[, *af*, *ipiv*, *lwork*, *factored*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `csysvx`.

Parameters

a
: [input rank-2 array('F') with bounds (n,n)]

b
: [input rank-2 array('F') with bounds (n,nrhs)]

Returns

a_s
: [rank-2 array('F') with bounds (n,n) and a storage]

udut
: [rank-2 array('F') with bounds (n,n) and af storage]

ipiv
: [rank-1 array('i') with bounds (n)]

b_s
: [rank-2 array('F') with bounds (n,nrhs) and b storage]

x
: [rank-2 array('F') with bounds (n,nrhs)]

rcond
: [float]

ferr
: [rank-1 array('f') with bounds (nrhs)]

berr
: [rank-1 array('f') with bounds (nrhs)]

info
: [int]

Other Parameters

overwrite_a
: [input int, optional] Default: 0

af
: [input rank-2 array('F') with bounds (n,n)]

ipiv
: [input rank-1 array('i') with bounds (n)]

overwrite_b
: [input int, optional] Default: 0

lwork
: [input int, optional] Default: max(3*n,1)

factored
: [input int, optional] Default: 0

lower
: [input int, optional] Default: 0

scipy.linalg.lapack.zsysvx

scipy.linalg.lapack.**zsysvx**(*a*, *b*[, *af*, *ipiv*, *lwork*, *factored*, *lower*, *overwrite_a*, *overwrite_b*]) = **<fortran object>**

Wrapper for `zsysvx`.

Parameters

a
: [input rank-2 array('D') with bounds (n,n)]

b
: [input rank-2 array('D') with bounds (n,nrhs)]

Returns

a_s
: [rank-2 array('D') with bounds (n,n) and a storage]

udut [rank-2 array('D') with bounds (n,n) and af storage]
ipiv [rank-1 array('i') with bounds (n)]
b_s [rank-2 array('D') with bounds (n,nrhs) and b storage]
x [rank-2 array('D') with bounds (n,nrhs)]
rcond [float]
ferr [rank-1 array('d') with bounds (nrhs)]
berr [rank-1 array('d') with bounds (nrhs)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
af [input rank-2 array('D') with bounds (n,n)]
ipiv [input rank-1 array('i') with bounds (n)]
overwrite_b
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)
factored [input int, optional] Default: 0
lower [input int, optional] Default: 0

scipy.linalg.lapack.ssysvx_lwork

scipy.linalg.lapack.**ssysvx_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for ssysvx_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsysvx_lwork

scipy.linalg.lapack.**dsysvx_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for dsysvx_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.csysvx_lwork

scipy.linalg.lapack.**csysvx_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for csysvx_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zsysvx_lwork

scipy.linalg.lapack.**zsysvx_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for zsysvx_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.ssytf2

scipy.linalg.lapack.**ssytf2**(*a*[, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for ssytf2.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

ldu [rank-2 array('f') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.dsytf2

scipy.linalg.lapack.**dsytf2**(*a*[, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for dsytf2.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

ldu [rank-2 array('d') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.csytf2

scipy.linalg.lapack.**csytf2**(*a*[, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for csytf2.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

ldu [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.zsytf2

scipy.linalg.lapack.**zsytf2**(*a*[, *lower*, *overwrite_a*]) **= <fortran object>**

Wrapper for zsytf2.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

ldu [rank-2 array('D') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0

scipy.linalg.lapack.ssytrd

scipy.linalg.lapack.**ssytrd**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for ssytrd.

Parameters

a [input rank-2 array('f') with bounds (lda,n)]

Returns

c [rank-2 array('f') with bounds (lda,n) and a storage]
d [rank-1 array('f') with bounds (n)]
e [rank-1 array('f') with bounds (n - 1)]
tau [rank-1 array('f') with bounds (n - 1)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.dsytrd

scipy.linalg.lapack.**dsytrd**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for dsytrd.

Parameters

a [input rank-2 array('d') with bounds (lda,n)]

Returns

c [rank-2 array('d') with bounds (lda,n) and a storage]
d [rank-1 array('d') with bounds (n)]
e [rank-1 array('d') with bounds (n - 1)]
tau [rank-1 array('d') with bounds (n - 1)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(n,1)

scipy.linalg.lapack.ssytrd_lwork

scipy.linalg.lapack.**ssytrd_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for ssytrd_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsytrd_lwork

scipy.linalg.lapack.**dsytrd_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for dsytrd_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.ssytrf

scipy.linalg.lapack.**ssytrf**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for ssytrf.

Parameters

a [input rank-2 array('f') with bounds (n,n)]

Returns

ldu [rank-2 array('f') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)

scipy.linalg.lapack.dsytrf

scipy.linalg.lapack.**dsytrf**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**
Wrapper for dsytrf.

Parameters

a [input rank-2 array('d') with bounds (n,n)]

Returns

ldu [rank-2 array('d') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)

scipy.linalg.lapack.csytrf

scipy.linalg.lapack.**csytrf**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for csytrf.

Parameters

a [input rank-2 array('F') with bounds (n,n)]

Returns

ldu [rank-2 array('F') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)

scipy.linalg.lapack.zsytrf

scipy.linalg.lapack.**zsytrf**(*a*[, *lower*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zsytrf.

Parameters

a [input rank-2 array('D') with bounds (n,n)]

Returns

ldu [rank-2 array('D') with bounds (n,n) and a storage]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

lower [input int, optional] Default: 0
overwrite_a [input int, optional] Default: 0
lwork [input int, optional] Default: max(n,1)

scipy.linalg.lapack.ssytrf_lwork

scipy.linalg.lapack.**ssytrf_lwork**(*n*[, *lower*]) **= <fortran object>**

Wrapper for ssytrf_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.dsytrf_lwork

scipy.linalg.lapack.**dsytrf_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for dsytrf_lwork.

Parameters

n [input int]

Returns

work [float]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.csytrf_lwork

scipy.linalg.lapack.**csytrf_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for csytrf_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.zsytrf_lwork

scipy.linalg.lapack.**zsytrf_lwork**(*n*[, *lower*]) **= <fortran object>**
Wrapper for zsytrf_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lower [input int, optional] Default: 0

scipy.linalg.lapack.stbtrs

scipy.linalg.lapack.**stbtrs**(*ab*, *b*[, *uplo*, *trans*, *diag*, *overwrite_b*]) **= <fortran object>**
Wrapper for stbtrs.

Parameters

ab [input rank-2 array('f') with bounds (ldab,n)]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]

info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
diag [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dtbtrs

scipy.linalg.lapack.**dtbtrs**(*ab*, *b*[, *uplo*, *trans*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for dtbtrs.

Parameters

ab [input rank-2 array('d') with bounds (ldab,n)]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
diag [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ctbtrs

scipy.linalg.lapack.**ctbtrs**(*ab*, *b*[, *uplo*, *trans*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for ctbtrs.

Parameters

ab [input rank-2 array('F') with bounds (ldab,n)]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
diag [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ztbtrs

scipy.linalg.lapack.**ztbtrs**(*ab*, *b*[, *uplo*, *trans*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for ztbtrs.

Parameters

ab [input rank-2 array('D') with bounds (ldab,n)]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
diag [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.stfsm

scipy.linalg.lapack.**stfsm**(*alpha*, *a*, *b*[, *transr*, *side*, *uplo*, *trans*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for stfsm.

Parameters

alpha [input float]
a [input rank-1 array('f') with bounds (nt)]
b [input rank-2 array('f') with bounds (m,n)]

Returns

x [rank-2 array('f') with bounds (m,n) and b storage]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
side [input string(len=1), optional] Default: 'L'
uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
diag [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dtfsm

scipy.linalg.lapack.**dtfsm**(*alpha*, *a*, *b*[, *transr*, *side*, *uplo*, *trans*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for dtfsm.

Parameters

alpha [input float]
a [input rank-1 array('d') with bounds (nt)]
b [input rank-2 array('d') with bounds (m,n)]

Returns

x [rank-2 array('d') with bounds (m,n) and b storage]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
side [input string(len=1), optional] Default: 'L'
uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
diag [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ctfsm

scipy.linalg.lapack.**ctfsm**(*alpha*, *a*, *b*[, *transr*, *side*, *uplo*, *trans*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for `ctfsm`.

Parameters

alpha [input complex]
a [input rank-1 array('F') with bounds (nt)]
b [input rank-2 array('F') with bounds (m,n)]

Returns

x [rank-2 array('F') with bounds (m,n) and b storage]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
side [input string(len=1), optional] Default: 'L'
uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
diag [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ztfsm

scipy.linalg.lapack.**ztfsm**(*alpha*, *a*, *b*[, *transr*, *side*, *uplo*, *trans*, *diag*, *overwrite_b*]) **= <fortran object>**

Wrapper for `ztfsm`.

Parameters

alpha [input complex]
a [input rank-1 array('D') with bounds (nt)]
b [input rank-2 array('D') with bounds (m,n)]

Returns

x [rank-2 array('D') with bounds (m,n) and b storage]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
side [input string(len=1), optional] Default: 'L'
uplo [input string(len=1), optional] Default: 'U'
trans [input string(len=1), optional] Default: 'N'
diag [input string(len=1), optional] Default: 'N'

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.stfttp

`scipy.linalg.lapack.`**`stfttp`**(*n*, *arf*[, *transr*, *uplo*]) **= <fortran object>**
Wrapper for `stfttp`.

Parameters

n [input int]
arf [input rank-1 array('f') with bounds (nt)]

Returns

ap [rank-1 array('f') with bounds (nt)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.dtfttp

`scipy.linalg.lapack.`**`dtfttp`**(*n*, *arf*[, *transr*, *uplo*]) **= <fortran object>**
Wrapper for `dtfttp`.

Parameters

n [input int]
arf [input rank-1 array('d') with bounds (nt)]

Returns

ap [rank-1 array('d') with bounds (nt)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ctfttp

`scipy.linalg.lapack.`**`ctfttp`**(*n*, *arf*[, *transr*, *uplo*]) **= <fortran object>**
Wrapper for `ctfttp`.

Parameters

n [input int]
arf [input rank-1 array('F') with bounds (nt)]

Returns

ap [rank-1 array('F') with bounds (nt)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ztfttp

scipy.linalg.lapack.**ztfttp**(*n*, *arf*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for ztfttp.

Parameters

n [input int]
arf [input rank-1 array('D') with bounds (nt)]

Returns

ap [rank-1 array('D') with bounds (nt)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.stfttr

scipy.linalg.lapack.**stfttr**(*n*, *arf*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for stfttr.

Parameters

n [input int]
arf [input rank-1 array('f') with bounds (nt)]

Returns

a [rank-2 array('f') with bounds (lda,n)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.dtfttr

scipy.linalg.lapack.**dtfttr**(*n*, *arf*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for dtfttr.

Parameters

n [input int]
arf [input rank-1 array('d') with bounds (nt)]

Returns

a [rank-2 array('d') with bounds (lda,n)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ctfttr

scipy.linalg.lapack.**ctfttr**(*n*, *arf*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for ctfttr.

Parameters

n [input int]
arf [input rank-1 array('F') with bounds (nt)]

Returns

a [rank-2 array('F') with bounds (lda,n)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ztfttr

scipy.linalg.lapack.**ztfttr**(*n*, *arf*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for ztfttr.

Parameters

n [input int]
arf [input rank-1 array('D') with bounds (nt)]

Returns

a [rank-2 array('D') with bounds (lda,n)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.stgexc

scipy.linalg.lapack.**stgexc**(*a*, *b*, *q*, *z*, *ifst*, *ilst*[, *lwork*, *overwrite_a*, *overwrite_b*, *overwrite_q*, *overwrite_z*]) **= <fortran object>**

Wrapper for stgexc.

Parameters

a [input rank-2 array('f') with bounds (lda,n)]
b [input rank-2 array('f') with bounds (ldb,n)]
q [input rank-2 array('f') with bounds (ldq,n)]
z [input rank-2 array('f') with bounds (ldz,n)]
ifst [input int]
ilst [input int]

Returns

a [rank-2 array('f') with bounds (lda,n)]
b [rank-2 array('f') with bounds (ldb,n)]
q [rank-2 array('f') with bounds (ldq,n)]
z [rank-2 array('f') with bounds (ldz,n)]
work [rank-1 array('f') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_q
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0
lwork [input int, optional] Default: max(4*n+16,1)

scipy.linalg.lapack.dtgexc

scipy.linalg.lapack.**dtgexc**(*a*, *b*, *q*, *z*, *ifst*, *ilst*[, *lwork*, *overwrite_a*, *overwrite_b*, *overwrite_q*, *overwrite_z*]) **= <fortran object>**

Wrapper for dtgexc.

Parameters

a [input rank-2 array('d') with bounds (lda,n)]
b [input rank-2 array('d') with bounds (ldb,n)]
q [input rank-2 array('d') with bounds (ldq,n)]
z [input rank-2 array('d') with bounds (ldz,n)]
ifst [input int]
ilst [input int]

Returns

a [rank-2 array('d') with bounds (lda,n)]
b [rank-2 array('d') with bounds (ldb,n)]
q [rank-2 array('d') with bounds (ldq,n)]
z [rank-2 array('d') with bounds (ldz,n)]
work [rank-1 array('d') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_q
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0
lwork [input int, optional] Default: max(4*n+16,1)

scipy.linalg.lapack.ctgexc

scipy.linalg.lapack.**ctgexc**(*a*, *b*, *q*, *z*, *ifst*, *ilst*[, *overwrite_a*, *overwrite_b*, *overwrite_q*, *overwrite_z*]) **= <fortran object>**

Wrapper for ctgexc.

Parameters

a [input rank-2 array('F') with bounds (lda,n)]
b [input rank-2 array('F') with bounds (ldb,n)]
q [input rank-2 array('F') with bounds (ldq,n)]
z [input rank-2 array('F') with bounds (ldz,n)]

ifst [input int]
ilst [input int]

Returns

a [rank-2 array('F') with bounds (lda,n)]
b [rank-2 array('F') with bounds (ldb,n)]
q [rank-2 array('F') with bounds (ldq,n)]
z [rank-2 array('F') with bounds (ldz,n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_q
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0

scipy.linalg.lapack.ztgexc

scipy.linalg.lapack.**ztgexc**(*a*, *b*, *q*, *z*, *ifst*, *ilst*[, *overwrite_a*, *overwrite_b*, *overwrite_q*, *overwrite_z*])
= <fortran object>

Wrapper for ztgexc.

Parameters

a [input rank-2 array('D') with bounds (lda,n)]
b [input rank-2 array('D') with bounds (ldb,n)]
q [input rank-2 array('D') with bounds (ldq,n)]
z [input rank-2 array('D') with bounds (ldz,n)]
ifst [input int]
ilst [input int]

Returns

a [rank-2 array('D') with bounds (lda,n)]
b [rank-2 array('D') with bounds (ldb,n)]
q [rank-2 array('D') with bounds (ldq,n)]
z [rank-2 array('D') with bounds (ldz,n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_q
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0

scipy.linalg.lapack.stgsen

scipy.linalg.lapack.**stgsen**(*select*, *a*, *b*, *q*, *z*[, *ijob*, *wantq*, *wantz*, *lwork*, *liwork*, *overwrite_a*, *overwrite_b*, *overwrite_q*, *overwrite_z*]) **= <fortran object>**

Wrapper for stgsen.

Parameters

select	[input rank-1 array('i') with bounds (n)]
a	[input rank-2 array('f') with bounds (n,n)]
b	[input rank-2 array('f') with bounds (n,n)]
q	[input rank-2 array('f') with bounds (n,n)]
z	[input rank-2 array('f') with bounds (n,n)]

Returns

as	[rank-2 array('f') with bounds (n,n) and a storage]
bs	[rank-2 array('f') with bounds (n,n) and b storage]
alphar	[rank-1 array('f') with bounds (n)]
alphai	[rank-1 array('f') with bounds (n)]
beta	[rank-1 array('f') with bounds (n)]
qs	[rank-2 array('f') with bounds (n,n) and q storage]
zs	[rank-2 array('f') with bounds (n,n) and z storage]
m	[int]
pl	[float]
pr	[float]
dif	[rank-1 array('f') with bounds (2)]
info	[int]

Other Parameters

ijob	[input int, optional] Default: 4
wantq	[input int, optional] Default: 1
wantz	[input int, optional] Default: 1
overwrite_a	[input int, optional] Default: 0
overwrite_b	[input int, optional] Default: 0
overwrite_q	[input int, optional] Default: 0
overwrite_z	[input int, optional] Default: 0
lwork	[input int, optional] Default: 4*n+16
liwork	[input int, optional] Default: n+6

scipy.linalg.lapack.dtgsen

scipy.linalg.lapack.**dtgsen**(*select*, *a*, *b*, *q*, *z*[, *ijob*, *wantq*, *wantz*, *lwork*, *liwork*, *overwrite_a*, *overwrite_b*, *overwrite_q*, *overwrite_z*]) **= <fortran object>**

Wrapper for dtgsen.

Parameters

select	[input rank-1 array('i') with bounds (n)]
a	[input rank-2 array('d') with bounds (n,n)]
b	[input rank-2 array('d') with bounds (n,n)]
q	[input rank-2 array('d') with bounds (n,n)]
z	[input rank-2 array('d') with bounds (n,n)]

Returns

as	[rank-2 array('d') with bounds (n,n) and a storage]
bs	[rank-2 array('d') with bounds (n,n) and b storage]
alphar	[rank-1 array('d') with bounds (n)]
alphai	[rank-1 array('d') with bounds (n)]
beta	[rank-1 array('d') with bounds (n)]
qs	[rank-2 array('d') with bounds (n,n) and q storage]
zs	[rank-2 array('d') with bounds (n,n) and z storage]
m	[int]
pl	[float]
pr	[float]
dif	[rank-1 array('d') with bounds (2)]
info	[int]

Other Parameters

ijob	[input int, optional] Default: 4
wantq	[input int, optional] Default: 1
wantz	[input int, optional] Default: 1
overwrite_a	[input int, optional] Default: 0
overwrite_b	[input int, optional] Default: 0
overwrite_q	[input int, optional] Default: 0
overwrite_z	[input int, optional] Default: 0
lwork	[input int, optional] Default: 4*n+16
liwork	[input int, optional] Default: n+6

scipy.linalg.lapack.ctgsen

scipy.linalg.lapack.**ctgsen**(*select*, *a*, *b*, *q*, *z*[, *ijob*, *wantq*, *wantz*, *lwork*, *liwork*, *overwrite_a*, *overwrite_b*, *overwrite_q*, *overwrite_z*]) **= <fortran object>**

Wrapper for ctgsen.

Parameters

select	[input rank-1 array('i') with bounds (n)]
a	[input rank-2 array('F') with bounds (n,n)]
b	[input rank-2 array('F') with bounds (n,n)]
q	[input rank-2 array('F') with bounds (n,n)]
z	[input rank-2 array('F') with bounds (n,n)]

Returns

as	[rank-2 array('F') with bounds (n,n) and a storage]
bs	[rank-2 array('F') with bounds (n,n) and b storage]
alpha	[rank-1 array('F') with bounds (n)]
beta	[rank-1 array('F') with bounds (n)]
qs	[rank-2 array('F') with bounds (n,n) and q storage]
zs	[rank-2 array('F') with bounds (n,n) and z storage]
m	[int]
pl	[float]
pr	[float]
dif	[rank-1 array('f') with bounds (2)]
info	[int]

Other Parameters

ijob [input int, optional] Default: 4
wantq [input int, optional] Default: 1
wantz [input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_q
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0
lwork [input int, optional] Default: (ijob==0?1:n+2)
liwork [input int, optional] Default: (ijob==0?1:n+2)

scipy.linalg.lapack.ztgsen

scipy.linalg.lapack.**ztgsen**(*select*, *a*, *b*, *q*, *z*[, *ijob*, *wantq*, *wantz*, *lwork*, *liwork*, *overwrite_a*, *overwrite_b*, *overwrite_q*, *overwrite_z*]) **= <fortran object>**

Wrapper for ztgsen.

Parameters

select [input rank-1 array('i') with bounds (n)]
a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (n,n)]
q [input rank-2 array('D') with bounds (n,n)]
z [input rank-2 array('D') with bounds (n,n)]

Returns

as [rank-2 array('D') with bounds (n,n) and a storage]
bs [rank-2 array('D') with bounds (n,n) and b storage]
alpha [rank-1 array('D') with bounds (n)]
beta [rank-1 array('D') with bounds (n)]
qs [rank-2 array('D') with bounds (n,n) and q storage]
zs [rank-2 array('D') with bounds (n,n) and z storage]
m [int]
pl [float]
pr [float]
dif [rank-1 array('d') with bounds (2)]
info [int]

Other Parameters

ijob [input int, optional] Default: 4
wantq [input int, optional] Default: 1
wantz [input int, optional] Default: 1
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0
overwrite_q
[input int, optional] Default: 0
overwrite_z
[input int, optional] Default: 0
lwork [input int, optional] Default: (ijob==0?1:n+2)

liwork [input int, optional] Default: (ijob==0?1:n+2)

scipy.linalg.lapack.stgsen_lwork

scipy.linalg.lapack.**stgsen_lwork**(*select*, *a*[, *ijob*]) **= <fortran object>**
Wrapper for stgsen_lwork.

Parameters

select [input rank-1 array('i') with bounds (n)]
a [input rank-2 array('f') with bounds (n,n)]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

ijob [input int, optional] Default: 4

scipy.linalg.lapack.dtgsen_lwork

scipy.linalg.lapack.**dtgsen_lwork**(*select*, *a*[, *ijob*]) **= <fortran object>**
Wrapper for dtgsen_lwork.

Parameters

select [input rank-1 array('i') with bounds (n)]
a [input rank-2 array('d') with bounds (n,n)]

Returns

work [float]
iwork [int]
info [int]

Other Parameters

ijob [input int, optional] Default: 4

scipy.linalg.lapack.ctgsen_lwork

scipy.linalg.lapack.**ctgsen_lwork**(*select*, *a*, *b*[, *ijob*]) **= <fortran object>**
Wrapper for ctgsen_lwork.

Parameters

select [input rank-1 array('i') with bounds (n)]
a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (n,n)]

Returns

work [complex]
iwork [int]
info [int]

Other Parameters

ijob [input int, optional] Default: 4

scipy.linalg.lapack.ztgsen_lwork

scipy.linalg.lapack.**ztgsen_lwork**(*select*, *a*, *b*[, *ijob*]) **= <fortran object>**

Wrapper for ztgsen_lwork.

Parameters

select	[input rank-1 array('i') with bounds (n)]
a	[input rank-2 array('D') with bounds (n,n)]
b	[input rank-2 array('D') with bounds (n,n)]

Returns

work	[complex]
iwork	[int]
info	[int]

Other Parameters

ijob	[input int, optional] Default: 4

scipy.linalg.lapack.stpttf

scipy.linalg.lapack.**stpttf**(*n*, *ap*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for stpttf.

Parameters

n	[input int]
ap	[input rank-1 array('f') with bounds (nt)]

Returns

arf	[rank-1 array('f') with bounds (nt)]
info	[int]

Other Parameters

transr	[input string(len=1), optional] Default: 'N'
uplo	[input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.dtpttf

scipy.linalg.lapack.**dtpttf**(*n*, *ap*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for dtpttf.

Parameters

n	[input int]
ap	[input rank-1 array('d') with bounds (nt)]

Returns

arf	[rank-1 array('d') with bounds (nt)]
info	[int]

Other Parameters

transr	[input string(len=1), optional] Default: 'N'
uplo	[input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ctpttf

scipy.linalg.lapack.**ctpttf**(*n*, *ap*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for ctpttf.

Parameters

n [input int]
ap [input rank-1 array('F') with bounds (nt)]

Returns

arf [rank-1 array('F') with bounds (nt)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ztpttf

scipy.linalg.lapack.**ztpttf**(*n*, *ap*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for ztpttf.

Parameters

n [input int]
ap [input rank-1 array('D') with bounds (nt)]

Returns

arf [rank-1 array('D') with bounds (nt)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.stpttr

scipy.linalg.lapack.**stpttr**(*n*, *ap*[, *uplo*]) **= <fortran object>**

Wrapper for stpttr.

Parameters

n [input int]
ap [input rank-1 array('f') with bounds (nt)]

Returns

a [rank-2 array('f') with bounds (n,n)]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.dtpttr

scipy.linalg.lapack.**dtpttr**(*n*, *ap*[, *uplo*]) **= <fortran object>**

Wrapper for dtpttr.

Parameters

n [input int]
ap [input rank-1 array('d') with bounds (nt)]

Returns

a [rank-2 array('d') with bounds (n,n)]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ctpttr

scipy.linalg.lapack.**ctpttr**(*n*, *ap*[, *uplo*]) **= <fortran object>**

Wrapper for ctpttr.

Parameters

n [input int]
ap [input rank-1 array('F') with bounds (nt)]

Returns

a [rank-2 array('F') with bounds (n,n)]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ztpttr

scipy.linalg.lapack.**ztpttr**(*n*, *ap*[, *uplo*]) **= <fortran object>**

Wrapper for ztpttr.

Parameters

n [input int]
ap [input rank-1 array('D') with bounds (nt)]

Returns

a [rank-2 array('D') with bounds (n,n)]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.strsyl

scipy.linalg.lapack.**strsyl**(*a*, *b*, *c*[, *trana*, *tranb*, *isgn*, *overwrite_c*]) **= <fortran object>**

Wrapper for strsyl.

Parameters

a [input rank-2 array('f') with bounds (m,m)]
b [input rank-2 array('f') with bounds (n,n)]
c [input rank-2 array('f') with bounds (m,n)]

Returns

x [rank-2 array('f') with bounds (m,n) and c storage]
scale [float]
info [int]

Other Parameters

trana [input string(len=1), optional] Default: 'N'
tranb [input string(len=1), optional] Default: 'N'
isgn [input int, optional] Default: 1
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.dtrsyl

scipy.linalg.lapack.**dtrsyl**(*a*, *b*, *c*[, *trana*, *tranb*, *isgn*, *overwrite_c*]) **= <fortran object>**

Wrapper for dtrsyl.

Parameters

a [input rank-2 array('d') with bounds (m,m)]
b [input rank-2 array('d') with bounds (n,n)]
c [input rank-2 array('d') with bounds (m,n)]

Returns

x [rank-2 array('d') with bounds (m,n) and c storage]
scale [float]
info [int]

Other Parameters

trana [input string(len=1), optional] Default: 'N'
tranb [input string(len=1), optional] Default: 'N'
isgn [input int, optional] Default: 1
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.ctrsyl

scipy.linalg.lapack.**ctrsyl**(*a*, *b*, *c*[, *trana*, *tranb*, *isgn*, *overwrite_c*]) **= <fortran object>**

Wrapper for ctrsyl.

Parameters

a [input rank-2 array('F') with bounds (m,m)]
b [input rank-2 array('F') with bounds (n,n)]
c [input rank-2 array('F') with bounds (m,n)]

Returns

x [rank-2 array('F') with bounds (m,n) and c storage]
scale [float]
info [int]

Other Parameters

trana [input string(len=1), optional] Default: 'N'
tranb [input string(len=1), optional] Default: 'N'
isgn [input int, optional] Default: 1
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.ztrsyl

scipy.linalg.lapack.**ztrsyl**(*a*, *b*, *c*[, *trana*, *tranb*, *isgn*, *overwrite_c*]) **= <fortran object>**
Wrapper for ztrsyl.

Parameters

a [input rank-2 array('D') with bounds (m,m)]
b [input rank-2 array('D') with bounds (n,n)]
c [input rank-2 array('D') with bounds (m,n)]

Returns

x [rank-2 array('D') with bounds (m,n) and c storage]
scale [float]
info [int]

Other Parameters

trana [input string(len=1), optional] Default: 'N'
tranb [input string(len=1), optional] Default: 'N'
isgn [input int, optional] Default: 1
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.strtri

scipy.linalg.lapack.**strtri**(*c*[, *lower*, *unitdiag*, *overwrite_c*]) **= <fortran object>**
Wrapper for strtri.

Parameters

c [input rank-2 array('f') with bounds (n,n)]

Returns

inv_c [rank-2 array('f') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0
lower [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0

scipy.linalg.lapack.dtrtri

scipy.linalg.lapack.**dtrtri**(*c*[, *lower*, *unitdiag*, *overwrite_c*]) **= <fortran object>**

Wrapper for dtrtri.

Parameters

c [input rank-2 array('d') with bounds (n,n)]

Returns

inv_c [rank-2 array('d') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0
lower [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0

scipy.linalg.lapack.ctrtri

scipy.linalg.lapack.**ctrtri**(*c*[, *lower*, *unitdiag*, *overwrite_c*]) **= <fortran object>**

Wrapper for ctrtri.

Parameters

c [input rank-2 array('F') with bounds (n,n)]

Returns

inv_c [rank-2 array('F') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0
lower [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0

scipy.linalg.lapack.ztrtri

scipy.linalg.lapack.**ztrtri**(*c*[, *lower*, *unitdiag*, *overwrite_c*]) **= <fortran object>**

Wrapper for ztrtri.

Parameters

c [input rank-2 array('D') with bounds (n,n)]

Returns

inv_c [rank-2 array('D') with bounds (n,n) and c storage]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0
lower [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0

scipy.linalg.lapack.strtrs

scipy.linalg.lapack.**strtrs**(*a*, *b*[, *lower*, *trans*, *unitdiag*, *lda*, *overwrite_b*]) **= <fortran object>**

Wrapper for strtrs.

Parameters

a [input rank-2 array('f') with bounds (lda,n)]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0
lda [input int, optional] Default: shape(a,0)
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.dtrtrs

scipy.linalg.lapack.**dtrtrs**(*a*, *b*[, *lower*, *trans*, *unitdiag*, *lda*, *overwrite_b*]) **= <fortran object>**

Wrapper for dtrtrs.

Parameters

a [input rank-2 array('d') with bounds (lda,n)]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0
lda [input int, optional] Default: shape(a,0)
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.ctrtrs

scipy.linalg.lapack.**ctrtrs**(*a*, *b*[, *lower*, *trans*, *unitdiag*, *lda*, *overwrite_b*]) **= <fortran object>**

Wrapper for ctrtrs.

Parameters

a [input rank-2 array('F') with bounds (lda,n)]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]

info [int]

Other Parameters

lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0
lda [input int, optional] Default: shape(a,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ztrtrs

scipy.linalg.lapack.**ztrtrs**(*a*, *b*[, *lower*, *trans*, *unitdiag*, *lda*, *overwrite_b*]) **= <fortran object>**

Wrapper for ztrtrs.

Parameters

a [input rank-2 array('D') with bounds (lda,n)]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

lower [input int, optional] Default: 0
trans [input int, optional] Default: 0
unitdiag [input int, optional] Default: 0
lda [input int, optional] Default: shape(a,0)
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.strttf

scipy.linalg.lapack.**strttf**(*a*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for strttf.

Parameters

a [input rank-2 array('f') with bounds (lda,n)]

Returns

arf [rank-1 array('f') with bounds (n*(n+1)/2)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.dtrttf

scipy.linalg.lapack.**dtrttf**(*a*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for dtrttf.

Parameters

a [input rank-2 array('d') with bounds (lda,n)]

Returns

arf [rank-1 array('d') with bounds (n*(n+1)/2)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ctrttf

scipy.linalg.lapack.**ctrttf**(*a*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for ctrttf.

Parameters

a [input rank-2 array('F') with bounds (lda,n)]

Returns

arf [rank-1 array('F') with bounds (n*(n+1)/2)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ztrttf

scipy.linalg.lapack.**ztrttf**(*a*[, *transr*, *uplo*]) **= <fortran object>**

Wrapper for ztrttf.

Parameters

a [input rank-2 array('D') with bounds (lda,n)]

Returns

arf [rank-1 array('D') with bounds (n*(n+1)/2)]
info [int]

Other Parameters

transr [input string(len=1), optional] Default: 'N'
uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.strttp

scipy.linalg.lapack.**strttp**(*a*[, *uplo*]) **= <fortran object>**

Wrapper for strttp.

Parameters

a [input rank-2 array('f') with bounds (lda,n)]

Returns

ap [rank-1 array('f') with bounds (n*(n+1)/2)]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.dtrttp

scipy.linalg.lapack.**dtrttp**(*a*[, *uplo*]) **= <fortran object>**

Wrapper for dtrttp.

Parameters

a [input rank-2 array('d') with bounds (lda,n)]

Returns

ap [rank-1 array('d') with bounds (n*(n+1)/2)]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ctrttp

scipy.linalg.lapack.**ctrttp**(*a*[, *uplo*]) **= <fortran object>**

Wrapper for ctrttp.

Parameters

a [input rank-2 array('F') with bounds (lda,n)]

Returns

ap [rank-1 array('F') with bounds (n*(n+1)/2)]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.ztrttp

scipy.linalg.lapack.**ztrttp**(*a*[, *uplo*]) **= <fortran object>**

Wrapper for ztrttp.

Parameters

a [input rank-2 array('D') with bounds (lda,n)]

Returns

ap [rank-1 array('D') with bounds (n*(n+1)/2)]
info [int]

Other Parameters

uplo [input string(len=1), optional] Default: 'U'

scipy.linalg.lapack.stzrzf

scipy.linalg.lapack.**stzrzf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `stzrzf`.

Parameters

a [input rank-2 array('f') with bounds (m,n)]

Returns

rz [rank-2 array('f') with bounds (m,n) and a storage]
tau [rank-1 array('f') with bounds (m)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(m,1)

scipy.linalg.lapack.dtzrzf

scipy.linalg.lapack.**dtzrzf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `dtzrzf`.

Parameters

a [input rank-2 array('d') with bounds (m,n)]

Returns

rz [rank-2 array('d') with bounds (m,n) and a storage]
tau [rank-1 array('d') with bounds (m)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(m,1)

scipy.linalg.lapack.ctzrzf

scipy.linalg.lapack.**ctzrzf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for `ctzrzf`.

Parameters

a [input rank-2 array('F') with bounds (m,n)]

Returns

rz [rank-2 array('F') with bounds (m,n) and a storage]
tau [rank-1 array('F') with bounds (m)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

lwork [input int, optional] Default: MAX(m,1)

scipy.linalg.lapack.ztzrzf

scipy.linalg.lapack.**ztzrzf**(*a*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for ztzrzf.

Parameters

a [input rank-2 array('D') with bounds (m,n)]

Returns

rz [rank-2 array('D') with bounds (m,n) and a storage]
tau [rank-1 array('D') with bounds (m)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX(m,1)

scipy.linalg.lapack.stzrzf_lwork

scipy.linalg.lapack.**stzrzf_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for stzrzf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.dtzrzf_lwork

scipy.linalg.lapack.**dtzrzf_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for dtzrzf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [float]
info [int]

scipy.linalg.lapack.ctzrzf_lwork

scipy.linalg.lapack.**ctzrzf_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for ctzrzf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.ztzrzf_lwork

scipy.linalg.lapack.**ztzrzf_lwork**(*m*, *n*) **= <fortran object>**

Wrapper for ztzrzf_lwork.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

scipy.linalg.lapack.cunghr

scipy.linalg.lapack.**cunghr**(*a*, *tau*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cunghr.

Parameters

a [input rank-2 array('F') with bounds (n,n)]
tau [input rank-1 array('F') with bounds (n - 1)]

Returns

ht [rank-2 array('F') with bounds (n,n) and a storage]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(hi-lo,1)

scipy.linalg.lapack.zunghr

scipy.linalg.lapack.**zunghr**(*a*, *tau*[, *lo*, *hi*, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zunghr.

Parameters

a [input rank-2 array('D') with bounds (n,n)]
tau [input rank-1 array('D') with bounds (n - 1)]

Returns

ht [rank-2 array('D') with bounds (n,n) and a storage]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1
overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(hi-lo,1)

scipy.linalg.lapack.cunghr_lwork

scipy.linalg.lapack.**cunghr_lwork**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for cunghr_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.zunghr_lwork

scipy.linalg.lapack.**zunghr_lwork**(*n*[, *lo*, *hi*]) **= <fortran object>**

Wrapper for zunghr_lwork.

Parameters

n [input int]

Returns

work [complex]
info [int]

Other Parameters

lo [input int, optional] Default: 0
hi [input int, optional] Default: n-1

scipy.linalg.lapack.cungqr

scipy.linalg.lapack.**cungqr**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cungqr.

Parameters

a [input rank-2 array('F') with bounds (m,n)]
tau [input rank-1 array('F') with bounds (k)]

Returns

q [rank-2 array('F') with bounds (m,n) and a storage]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.zungqr

scipy.linalg.lapack.**zungqr**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zungqr.

Parameters

a [input rank-2 array('D') with bounds (m,n)]
tau [input rank-1 array('D') with bounds (k)]

Returns

q [rank-2 array('D') with bounds (m,n) and a storage]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*n,1)

scipy.linalg.lapack.cungrq

scipy.linalg.lapack.**cungrq**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for cungrq.

Parameters

a [input rank-2 array('F') with bounds (m,n)]
tau [input rank-1 array('F') with bounds (k)]

Returns

q [rank-2 array('F') with bounds (m,n) and a storage]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.zungrq

scipy.linalg.lapack.**zungrq**(*a*, *tau*[, *lwork*, *overwrite_a*]) **= <fortran object>**

Wrapper for zungrq.

Parameters

a [input rank-2 array('D') with bounds (m,n)]
tau [input rank-1 array('D') with bounds (k)]

Returns

q [rank-2 array('D') with bounds (m,n) and a storage]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
lwork [input int, optional] Default: max(3*m,1)

scipy.linalg.lapack.cunmqr

scipy.linalg.lapack.**cunmqr**(*side*, *trans*, *a*, *tau*, *c*, *lwork*[, *overwrite_c*]) **= <fortran object>**

Wrapper for cunmqr.

Parameters

side [input string(len=1)]
trans [input string(len=1)]
a [input rank-2 array('F') with bounds (lda,k)]
tau [input rank-1 array('F') with bounds (k)]
c [input rank-2 array('F') with bounds (ldc,n)]
lwork [input int]

Returns

cq [rank-2 array('F') with bounds (ldc,n) and c storage]
work [rank-1 array('F') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.zunmqr

scipy.linalg.lapack.**zunmqr**(*side*, *trans*, *a*, *tau*, *c*, *lwork*[, *overwrite_c*]) **= <fortran object>**

Wrapper for zunmqr.

Parameters

side [input string(len=1)]
trans [input string(len=1)]
a [input rank-2 array('D') with bounds (lda,k)]
tau [input rank-1 array('D') with bounds (k)]
c [input rank-2 array('D') with bounds (ldc,n)]
lwork [input int]

Returns

cq [rank-2 array('D') with bounds (ldc,n) and c storage]
work [rank-1 array('D') with bounds (MAX(lwork,1))]
info [int]

Other Parameters

overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.sgeqrt

scipy.linalg.lapack.**sgeqrt**(*nb*, *a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for sgeqrt.

Parameters

nb [input int]
a [input rank-2 array('f') with bounds (m,n)]

Returns

a [rank-2 array('f') with bounds (m,n)]
t [rank-2 array('f') with bounds (nb,MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.dgeqrt

scipy.linalg.lapack.**dgeqrt**(*nb*, *a*[, *overwrite_a*]) **= <fortran object>**
Wrapper for dgeqrt.

Parameters

nb [input int]
a [input rank-2 array('d') with bounds (m,n)]

Returns

a [rank-2 array('d') with bounds (m,n)]
t [rank-2 array('d') with bounds (nb,MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.cgeqrt

scipy.linalg.lapack.**cgeqrt**(*nb*, *a*[, *overwrite_a*]) **= <fortran object>**

Wrapper for cgeqrt.

Parameters

nb [input int]
a [input rank-2 array('F') with bounds (m,n)]

Returns

a [rank-2 array('F') with bounds (m,n)]
t [rank-2 array('F') with bounds (nb,MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.zgeqrt

scipy.linalg.lapack.**zgeqrt**(*nb*, *a*[, *overwrite_a*]) **= <fortran object>**

Wrapper for zgeqrt.

Parameters

nb [input int]
a [input rank-2 array('D') with bounds (m,n)]

Returns

a [rank-2 array('D') with bounds (m,n)]
t [rank-2 array('D') with bounds (nb,MIN(m,n))]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

scipy.linalg.lapack.sgemqrt

scipy.linalg.lapack.**sgemqrt**(*v*, *t*, *c*[, *side*, *trans*, *overwrite_c*]) **= <fortran object>**

Wrapper for sgemqrt.

Parameters

v [input rank-2 array('f') with bounds ((side[0]=='L'?m:n),k)]
t [input rank-2 array('f') with bounds (nb,k)]
c [input rank-2 array('f') with bounds (m,n)]

Returns

c [rank-2 array('f') with bounds (m,n)]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.dgemqrt

scipy.linalg.lapack.**dgemqrt**(*v*, *t*, *c*[, *side*, *trans*, *overwrite_c*]) **= <fortran object>**

Wrapper for dgemqrt.

Parameters

v [input rank-2 array('d') with bounds ((side[0]=='L'?m:n),k)]
t [input rank-2 array('d') with bounds (nb,k)]
c [input rank-2 array('d') with bounds (m,n)]

Returns

c [rank-2 array('d') with bounds (m,n)]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.cgemqrt

scipy.linalg.lapack.**cgemqrt**(*v*, *t*, *c*[, *side*, *trans*, *overwrite_c*]) **= <fortran object>**

Wrapper for cgemqrt.

Parameters

v [input rank-2 array('F') with bounds ((side[0]=='L'?m:n),k)]
t [input rank-2 array('F') with bounds (nb,k)]
c [input rank-2 array('F') with bounds (m,n)]

Returns

c [rank-2 array('F') with bounds (m,n)]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.zgemqrt

scipy.linalg.lapack.**zgemqrt**(*v*, *t*, *c*[, *side*, *trans*, *overwrite_c*]) **= <fortran object>**

Wrapper for zgemqrt.

Parameters

v [input rank-2 array('D') with bounds ((side[0]=='L'?m:n),k)]
t [input rank-2 array('D') with bounds (nb,k)]
c [input rank-2 array('D') with bounds (m,n)]

Returns

c [rank-2 array('D') with bounds (m,n)]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0

scipy.linalg.lapack.sgttrf

scipy.linalg.lapack.**sgttrf**(*dl*, *d*, *du*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*]) = **<fortran object>**

Wrapper for sgttrf.

Parameters

dl [input rank-1 array('f') with bounds (n - 1)]
d [input rank-1 array('f') with bounds (n)]
du [input rank-1 array('f') with bounds (n - 1)]

Returns

dl [rank-1 array('f') with bounds (n - 1)]
d [rank-1 array('f') with bounds (n)]
du [rank-1 array('f') with bounds (n - 1)]
du2 [rank-1 array('f') with bounds (n - 2)]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

overwrite_dl
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_du
[input int, optional] Default: 0

scipy.linalg.lapack.dgttrf

scipy.linalg.lapack.**dgttrf**(*dl*, *d*, *du*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*]) = **<fortran object>**

Wrapper for dgttrf.

Parameters

dl [input rank-1 array('d') with bounds (n - 1)]
d [input rank-1 array('d') with bounds (n)]
du [input rank-1 array('d') with bounds (n - 1)]

Returns

dl [rank-1 array('d') with bounds (n - 1)]
d [rank-1 array('d') with bounds (n)]
du [rank-1 array('d') with bounds (n - 1)]
du2 [rank-1 array('d') with bounds (n - 2)]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

overwrite_dl
[input int, optional] Default: 0

overwrite_d
[input int, optional] Default: 0
overwrite_du
[input int, optional] Default: 0

scipy.linalg.lapack.cgttrf

scipy.linalg.lapack.**cgttrf**(*dl*, *d*, *du*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*]) = **<fortran object>**

Wrapper for cgttrf.

Parameters

dl [input rank-1 array('F') with bounds (n - 1)]
d [input rank-1 array('F') with bounds (n)]
du [input rank-1 array('F') with bounds (n - 1)]

Returns

dl [rank-1 array('F') with bounds (n - 1)]
d [rank-1 array('F') with bounds (n)]
du [rank-1 array('F') with bounds (n - 1)]
du2 [rank-1 array('F') with bounds (n - 2)]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

overwrite_dl
[input int, optional] Default: 0
overwrite_d
[input int, optional] Default: 0
overwrite_du
[input int, optional] Default: 0

scipy.linalg.lapack.zgttrf

scipy.linalg.lapack.**zgttrf**(*dl*, *d*, *du*[, *overwrite_dl*, *overwrite_d*, *overwrite_du*]) = **<fortran object>**

Wrapper for zgttrf.

Parameters

dl [input rank-1 array('D') with bounds (n - 1)]
d [input rank-1 array('D') with bounds (n)]
du [input rank-1 array('D') with bounds (n - 1)]

Returns

dl [rank-1 array('D') with bounds (n - 1)]
d [rank-1 array('D') with bounds (n)]
du [rank-1 array('D') with bounds (n - 1)]
du2 [rank-1 array('D') with bounds (n - 2)]
ipiv [rank-1 array('i') with bounds (n)]
info [int]

Other Parameters

overwrite_dl
[input int, optional] Default: 0

overwrite_d
[input int, optional] Default: 0
overwrite_du
[input int, optional] Default: 0

scipy.linalg.lapack.sgttrs

scipy.linalg.lapack.**sgttrs**(*dl*, *d*, *du*, *du2*, *ipiv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**
Wrapper for sgttrs.

Parameters

dl [input rank-1 array('f') with bounds (n - 1)]
d [input rank-1 array('f') with bounds (n)]
du [input rank-1 array('f') with bounds (n - 1)]
du2 [input rank-1 array('f') with bounds (n - 2)]
ipiv [input rank-1 array('i') with bounds (n)]
b [input rank-2 array('f') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('f') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dgttrs

scipy.linalg.lapack.**dgttrs**(*dl*, *d*, *du*, *du2*, *ipiv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**
Wrapper for dgttrs.

Parameters

dl [input rank-1 array('d') with bounds (n - 1)]
d [input rank-1 array('d') with bounds (n)]
du [input rank-1 array('d') with bounds (n - 1)]
du2 [input rank-1 array('d') with bounds (n - 2)]
ipiv [input rank-1 array('i') with bounds (n)]
b [input rank-2 array('d') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('d') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.cgttrs

scipy.linalg.lapack.**cgttrs**(*dl*, *d*, *du*, *du2*, *ipiv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for cgttrs.

Parameters

dl [input rank-1 array('F') with bounds (n - 1)]
d [input rank-1 array('F') with bounds (n)]
du [input rank-1 array('F') with bounds (n - 1)]
du2 [input rank-1 array('F') with bounds (n - 2)]
ipiv [input rank-1 array('i') with bounds (n)]
b [input rank-2 array('F') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('F') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.zgttrs

scipy.linalg.lapack.**zgttrs**(*dl*, *d*, *du*, *du2*, *ipiv*, *b*[, *trans*, *overwrite_b*]) **= <fortran object>**

Wrapper for zgttrs.

Parameters

dl [input rank-1 array('D') with bounds (n - 1)]
d [input rank-1 array('D') with bounds (n)]
du [input rank-1 array('D') with bounds (n - 1)]
du2 [input rank-1 array('D') with bounds (n - 2)]
ipiv [input rank-1 array('i') with bounds (n)]
b [input rank-2 array('D') with bounds (ldb,nrhs)]

Returns

x [rank-2 array('D') with bounds (ldb,nrhs) and b storage]
info [int]

Other Parameters

trans [input string(len=1), optional] Default: 'N'
overwrite_b [input int, optional] Default: 0

scipy.linalg.lapack.stpqrt

scipy.linalg.lapack.**stpqrt**(*l*, *nb*, *a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for stpqrt.

Parameters

l [input int]
nb [input int]
a [input rank-2 array('f') with bounds (n,n)]
b [input rank-2 array('f') with bounds (m,n)]

Returns

a [rank-2 array('f') with bounds (n,n)]
b [rank-2 array('f') with bounds (m,n)]
t [rank-2 array('f') with bounds (nb,n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dtpqrt

`scipy.linalg.lapack.`**`dtpqrt`**(*l*, *nb*, *a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**
Wrapper for `dtpqrt`.

Parameters

l [input int]
nb [input int]
a [input rank-2 array('d') with bounds (n,n)]
b [input rank-2 array('d') with bounds (m,n)]

Returns

a [rank-2 array('d') with bounds (n,n)]
b [rank-2 array('d') with bounds (m,n)]
t [rank-2 array('d') with bounds (nb,n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ctpqrt

`scipy.linalg.lapack.`**`ctpqrt`**(*l*, *nb*, *a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**
Wrapper for `ctpqrt`.

Parameters

l [input int]
nb [input int]
a [input rank-2 array('F') with bounds (n,n)]
b [input rank-2 array('F') with bounds (m,n)]

Returns

a [rank-2 array('F') with bounds (n,n)]
b [rank-2 array('F') with bounds (m,n)]
t [rank-2 array('F') with bounds (nb,n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0

overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ztpqrt

scipy.linalg.lapack.**ztpqrt**(*l*, *nb*, *a*, *b*[, *overwrite_a*, *overwrite_b*]) **= <fortran object>**
Wrapper for ztpqrt.

Parameters

l [input int]
nb [input int]
a [input rank-2 array('D') with bounds (n,n)]
b [input rank-2 array('D') with bounds (m,n)]

Returns

a [rank-2 array('D') with bounds (n,n)]
b [rank-2 array('D') with bounds (m,n)]
t [rank-2 array('D') with bounds (nb,n)]
info [int]

Other Parameters

overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.stpmqrt

scipy.linalg.lapack.**stpmqrt**(*l*, *v*, *t*, *a*, *b*[, *side*, *trans*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**
Wrapper for stpmqrt.

Parameters

l [input int]
v [input rank-2 array('f') with bounds ((side[0]=='L'?m:n),k)]
t [input rank-2 array('f') with bounds (nb,k)]
a [input rank-2 array('f') with bounds ((side[0]=='L'?k:m),(side[0]=='L'?n:k))]
b [input rank-2 array('f') with bounds (m,n)]

Returns

a [rank-2 array('f') with bounds ((side[0]=='L'?k:m),(side[0]=='L'?n:k))]
b [rank-2 array('f') with bounds (m,n)]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.dtpmqrt

scipy.linalg.lapack.**dtpmqrt**(*l*, *v*, *t*, *a*, *b*[, *side*, *trans*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for dtpmqrt.

Parameters

l [input int]
v [input rank-2 array('d') with bounds ((side[0]=='L'?m:n),k)]
t [input rank-2 array('d') with bounds (nb,k)]
a [input rank-2 array('d') with bounds ((side[0]=='L'?k:m),(side[0]=='L'?n:k))]
b [input rank-2 array('d') with bounds (m,n)]

Returns

a [rank-2 array('d') with bounds ((side[0]=='L'?k:m),(side[0]=='L'?n:k))]
b [rank-2 array('d') with bounds (m,n)]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ctpmqrt

scipy.linalg.lapack.**ctpmqrt**(*l*, *v*, *t*, *a*, *b*[, *side*, *trans*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for ctpmqrt.

Parameters

l [input int]
v [input rank-2 array('F') with bounds ((side[0]=='L'?m:n),k)]
t [input rank-2 array('F') with bounds (nb,k)]
a [input rank-2 array('F') with bounds ((side[0]=='L'?k:m),(side[0]=='L'?n:k))]
b [input rank-2 array('F') with bounds (m,n)]

Returns

a [rank-2 array('F') with bounds ((side[0]=='L'?k:m),(side[0]=='L'?n:k))]
b [rank-2 array('F') with bounds (m,n)]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_a
[input int, optional] Default: 0
overwrite_b
[input int, optional] Default: 0

scipy.linalg.lapack.ztpmqrt

scipy.linalg.lapack.**ztpmqrt**(*l*, *v*, *t*, *a*, *b*[, *side*, *trans*, *overwrite_a*, *overwrite_b*]) **= <fortran object>**

Wrapper for ztpmqrt.

Parameters

l	[input int]
v	[input rank-2 array('D') with bounds ((side[0]=='L'?m:n),k)]
t	[input rank-2 array('D') with bounds (nb,k)]
a	[input rank-2 array('D') with bounds ((side[0]=='L'?k:m),(side[0]=='L'?n:k))]
b	[input rank-2 array('D') with bounds (m,n)]

Returns

a	[rank-2 array('D') with bounds ((side[0]=='L'?k:m),(side[0]=='L'?n:k))]
b	[rank-2 array('D') with bounds (m,n)]
info	[int]

Other Parameters

side	[input string(len=1), optional] Default: 'L'
trans	[input string(len=1), optional] Default: 'N'
overwrite_a	[input int, optional] Default: 0
overwrite_b	[input int, optional] Default: 0

scipy.linalg.lapack.cuncsd

scipy.linalg.lapack.**cuncsd**(*x11*, *x12*, *x21*, *x22*[, *compute_u1*, *compute_u2*, *compute_v1t*, *compute_v2t*, *trans*, *signs*, *lwork*, *lrwork*, *overwrite_x11*, *overwrite_x12*, *overwrite_x21*, *overwrite_x22*]) **= <fortran object>**

Wrapper for cuncsd.

Parameters

x11	[input rank-2 array('F') with bounds (p,q)]
x12	[input rank-2 array('F') with bounds (p,mmq)]
x21	[input rank-2 array('F') with bounds (mmp,q)]
x22	[input rank-2 array('F') with bounds (mmp,mmq)]

Returns

cs11	[rank-2 array('F') with bounds (p,q) and x11 storage]
cs12	[rank-2 array('F') with bounds (p,mmq) and x12 storage]
cs21	[rank-2 array('F') with bounds (mmp,q) and x21 storage]
cs22	[rank-2 array('F') with bounds (mmp,mmq) and x22 storage]
theta	[rank-1 array('f') with bounds (min(min(p,mmp),min(q,mmq)))]
u1	[rank-2 array('F') with bounds ((compute_u1?p:0),(compute_u1?p:0))]
u2	[rank-2 array('F') with bounds ((compute_u2?mmp:0),(compute_u2?mmp:0))]
v1t	[rank-2 array('F') with bounds ((compute_v1t?q:0),(compute_v1t?q:0))]
v2t	[rank-2 array('F') with bounds ((compute_v2t?mmq:0),(compute_v2t?mmq:0))]
info	[int]

Other Parameters

compute_u1	[input int, optional] Default: 1

compute_u2
[input int, optional] Default: 1
compute_v1t
[input int, optional] Default: 1
compute_v2t
[input int, optional] Default: 1
trans [input int, optional] Default: 0
signs [input int, optional] Default: 0
overwrite_x11
[input int, optional] Default: 0
overwrite_x12
[input int, optional] Default: 0
overwrite_x21
[input int, optional] Default: 0
overwrite_x22
[input int, optional] Default: 0
lwork [input int, optional] Default: 2*m+MAX(1,MAX(mmp,mmq))+1
lrwork [input int, optional] Default: 5*MAX(1,q-1)+4*MAX(1,q)+8*q+1

scipy.linalg.lapack.zuncsd

scipy.linalg.lapack.**zuncsd**(*x11*, *x12*, *x21*, *x22*[, *compute_u1*, *compute_u2*, *compute_v1t*, *compute_v2t*, *trans*, *signs*, *lwork*, *lrwork*, *overwrite_x11*, *overwrite_x12*, *overwrite_x21*, *overwrite_x22*]) **= <fortran object>**

Wrapper for zuncsd.

Parameters

x11 [input rank-2 array('D') with bounds (p,q)]
x12 [input rank-2 array('D') with bounds (p,mmq)]
x21 [input rank-2 array('D') with bounds (mmp,q)]
x22 [input rank-2 array('D') with bounds (mmp,mmq)]

Returns

cs11 [rank-2 array('D') with bounds (p,q) and x11 storage]
cs12 [rank-2 array('D') with bounds (p,mmq) and x12 storage]
cs21 [rank-2 array('D') with bounds (mmp,q) and x21 storage]
cs22 [rank-2 array('D') with bounds (mmp,mmq) and x22 storage]
theta [rank-1 array('d') with bounds (min(min(p,mmp),min(q,mmq)))]
u1 [rank-2 array('D') with bounds ((compute_u1?p:0),(compute_u1?p:0))]
u2 [rank-2 array('D') with bounds ((compute_u2?mmp:0),(compute_u2?mmp:0))]
v1t [rank-2 array('D') with bounds ((compute_v1t?q:0),(compute_v1t?q:0))]
v2t [rank-2 array('D') with bounds ((compute_v2t?mmq:0),(compute_v2t?mmq:0))]
info [int]

Other Parameters

compute_u1
[input int, optional] Default: 1
compute_u2
[input int, optional] Default: 1
compute_v1t
[input int, optional] Default: 1
compute_v2t
[input int, optional] Default: 1
trans [input int, optional] Default: 0

signs [input int, optional] Default: 0
overwrite_x11
[input int, optional] Default: 0
overwrite_x12
[input int, optional] Default: 0
overwrite_x21
[input int, optional] Default: 0
overwrite_x22
[input int, optional] Default: 0
lwork [input int, optional] Default: 2*m+MAX(1,MAX(mmp,mmq))+1
lrwork [input int, optional] Default: 5*MAX(1,q-1)+4*MAX(1,q)+8*q+1

scipy.linalg.lapack.cuncsd_lwork

scipy.linalg.lapack.**cuncsd_lwork**(*m*, *p*, *q*) **= <fortran object>**
Wrapper for cuncsd_lwork.

Parameters

m [input int]
p [input int]
q [input int]

Returns

work [complex]
rwork [float]
info [int]

scipy.linalg.lapack.zuncsd_lwork

scipy.linalg.lapack.**zuncsd_lwork**(*m*, *p*, *q*) **= <fortran object>**
Wrapper for zuncsd_lwork.

Parameters

m [input int]
p [input int]
q [input int]

Returns

work [complex]
rwork [float]
info [int]

scipy.linalg.lapack.cunmrz

scipy.linalg.lapack.**cunmrz**(*a*, *tau*, *c*[, *side*, *trans*, *lwork*, *overwrite_c*]) **= <fortran object>**
Wrapper for cunmrz.

Parameters

a [input rank-2 array('F') with bounds (k,nt)]
tau [input rank-1 array('F') with bounds (k)]
c [input rank-2 array('F') with bounds (m,n)]

Returns

cq [rank-2 array('F') with bounds (m,n) and c storage]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX((side[0]=='L'?n:m),1)

scipy.linalg.lapack.zunmrz

`scipy.linalg.lapack.`**`zunmrz`**(*a*, *tau*, *c*[, *side*, *trans*, *lwork*, *overwrite_c*]) **`= <fortran object>`**
Wrapper for `zunmrz`.

Parameters

a [input rank-2 array('D') with bounds (k,nt)]
tau [input rank-1 array('D') with bounds (k)]
c [input rank-2 array('D') with bounds (m,n)]

Returns

cq [rank-2 array('D') with bounds (m,n) and c storage]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'
overwrite_c
[input int, optional] Default: 0
lwork [input int, optional] Default: MAX((side[0]=='L'?n:m),1)

scipy.linalg.lapack.cunmrz_lwork

`scipy.linalg.lapack.`**`cunmrz_lwork`**(*m*, *n*[, *side*, *trans*]) **`= <fortran object>`**
Wrapper for `cunmrz_lwork`.

Parameters

m [input int]
n [input int]

Returns

work [complex]
info [int]

Other Parameters

side [input string(len=1), optional] Default: 'L'
trans [input string(len=1), optional] Default: 'N'

scipy.linalg.lapack.zunmrz_lwork

scipy.linalg.lapack.**zunmrz_lwork**(*m*, *n*[, *side*, *trans*]) **= <fortran object>**

Wrapper for zunmrz_lwork.

Parameters

m	[input int]
n	[input int]

Returns

work	[complex]
info	[int]

Other Parameters

side	[input string(len=1), optional] Default: 'L'
trans	[input string(len=1), optional] Default: 'N'

scipy.linalg.lapack.ilaver

scipy.linalg.lapack.**ilaver = <fortran object>**

Wrapper for ilaver.

Returns

major	[int]
minor	[int]
patch	[int]

3.3.13 BLAS Functions for Cython

Usable from Cython via:

```
cimport scipy.linalg.cython_blas
```

These wrappers do not check for alignment of arrays. Alignment should be checked before these wrappers are used.

Raw function pointers (Fortran-style pointer arguments):

- caxpy
- ccopy
- cdotc
- cdotu
- cgbmv
- cgemm
- cgemv
- cgerc
- cgeru
- chbmv
- chemm
- chemv

- cher
- cher2
- cher2k
- cherk
- chpmv
- chpr
- chpr2
- crotg
- cscal
- csrot
- csscal
- cswap
- csymm
- csyr2k
- csyrk
- ctbmv
- ctbsv
- ctpmv
- ctpsv
- ctrmm
- ctrmv
- ctrsm
- ctrsv
- dasum
- daxpy
- dcabs1
- dcopy
- ddot
- dgbmv
- dgemm
- dgemv
- dger
- dnrm2
- drot
- drotg
- drotm

- drotmg
- dsbmv
- dscal
- dsdot
- dspmv
- dspr
- dspr2
- dswap
- dsymm
- dsymv
- dsyr
- dsyr2
- dsyr2k
- dsyrk
- dtbmv
- dtbsv
- dtpmv
- dtpsv
- dtrmm
- dtrmv
- dtrsm
- dtrsv
- dzasum
- dznrm2
- icamax
- idamax
- isamax
- izamax
- lsame
- sasum
- saxpy
- scasum
- scnrm2
- scopy
- sdot
- sdsdot

- sgbmv
- sgemm
- sgemv
- sger
- snrm2
- srot
- srotg
- srotm
- srotmg
- ssbmv
- sscal
- sspmv
- sspr
- sspr2
- sswap
- ssymm
- ssymv
- ssyr
- ssyr2
- ssyr2k
- ssyrk
- stbmv
- stbsv
- stpmv
- stpsv
- strmm
- strmv
- strsm
- strsv
- zaxpy
- zcopy
- zdotc
- zdotu
- zdrot
- zdscal
- zgbmv

- zgemm
- zgemv
- zgerc
- zgeru
- zhbmv
- zhemm
- zhemv
- zher
- zher2
- zher2k
- zherk
- zhpmv
- zhpr
- zhpr2
- zrotg
- zscal
- zswap
- zsymm
- zsyr2k
- zsyrk
- ztbmv
- ztbsv
- ztpmv
- ztpsv
- ztrmm
- ztrmv
- ztrsm
- ztrsv

3.3.14 LAPACK functions for Cython

Usable from Cython via:

```
cimport scipy.linalg.cython_lapack
```

This module provides Cython-level wrappers for all primary routines included in LAPACK 3.4.0 except for `zcgesv` since its interface is not consistent from LAPACK 3.4.0 to 3.6.0. It also provides some of the fixed-api auxiliary routines.

These wrappers do not check for alignment of arrays. Alignment should be checked before these wrappers are used.

Raw function pointers (Fortran-style pointer arguments):

- cbbcsd
- cbdsqr
- cgbbrd
- cgbcon
- cgbequ
- cgbequb
- cgbrfs
- cgbsv
- cgbsvx
- cgbtf2
- cgbtrf
- cgbtrs
- cgebak
- cgebal
- cgebd2
- cgebrd
- cgecon
- cgeequ
- cgeequb
- cgees
- cgeesx
- cgeev
- cgeevx
- cgehd2
- cgehrd
- cgelq2
- cgelqf
- cgels
- cgelsd
- cgelss
- cgelsy
- cgemqrt
- cgeql2
- cgeqlf
- cgeqp3
- cgeqr2

- cgeqr2p
- cgeqrf
- cgeqrfp
- cgeqrt
- cgeqrt2
- cgeqrt3
- cgerfs
- cgerq2
- cgerqf
- cgesc2
- cgesdd
- cgesv
- cgesvd
- cgesvx
- cgetc2
- cgetf2
- cgetrf
- cgetri
- cgetrs
- cggbak
- cggbal
- cgges
- cggesx
- cggev
- cggevx
- cgggl m
- cgghrd
- cgglse
- cggqrf
- cggrqf
- cgtcon
- cgtrfs
- cgtsv
- cgtsvx
- cgttrf
- cgttrs

- cgtts2
- chbev
- chbevd
- chbevx
- chbgst
- chbgv
- chbgvd
- chbgvx
- chbtrd
- checon
- cheequb
- cheev
- cheevd
- cheevr
- cheevx
- chegs2
- chegst
- chegv
- chegvd
- chegvx
- cherfs
- chesv
- chesvx
- cheswapr
- chetd2
- chetf2
- chetrd
- chetrf
- chetri
- chetri2
- chetri2x
- chetrs
- chetrs2
- chfrk
- chgeqz
- chla_transtype

- chpcon
- chpev
- chpevd
- chpevx
- chpgst
- chpgv
- chpgvd
- chpgvx
- chprfs
- chpsv
- chpsvx
- chptrd
- chptrf
- chptri
- chptrs
- chsein
- chseqr
- clabrd
- clacgv
- clacn2
- clacon
- clacp2
- clacpy
- clacrm
- clacrt
- cladiv
- claed0
- claed7
- claed8
- claein
- claesy
- claev2
- clag2z
- clags2
- clagtm
- clahef

- clahqr
- clahr2
- claic1
- clals0
- clalsa
- clalsd
- clangb
- clange
- clangt
- clanhb
- clanhe
- clanhf
- clanhp
- clanhs
- clanht
- clansb
- clansp
- clansy
- clantb
- clantp
- clantr
- clapll
- clapmr
- clapmt
- claqgb
- claqge
- claqhb
- claqhe
- claqhp
- claqp2
- claqps
- claqr0
- claqr1
- claqr2
- claqr3
- claqr4

- claqr5
- claqsb
- claqsp
- claqsy
- clar1v
- clar2v
- clarcm
- clarf
- clarfb
- clarfg
- clarfgp
- clarft
- clarfx
- clargv
- clarnv
- clarrv
- clartg
- clartv
- clarz
- clarzb
- clarzt
- clascl
- claset
- clasr
- classq
- claswp
- clasyf
- clatbs
- clatdf
- clatps
- clatrd
- clatrs
- clatrz
- clauu2
- clauum
- cpbcon

- cpbequ
- cpbrfs
- cpbstf
- cpbsv
- cpbsvx
- cpbtf2
- cpbtrf
- cpbtrs
- cpftrf
- cpftri
- cpftrs
- cpocon
- cpoequ
- cpoequb
- cporfs
- cposv
- cposvx
- cpotf2
- cpotrf
- cpotri
- cpotrs
- cppcon
- cppequ
- cpprfs
- cppsv
- cppsvx
- cpptrf
- cpptri
- cpptrs
- cpstf2
- cpstrf
- cptcon
- cpteqr
- cptrfs
- cptsv
- cptsvx

- cpttrf
- cpttrs
- cptts2
- crot
- cspcon
- cspmv
- cspr
- csprfs
- cspsv
- cspsvx
- csptrf
- csptri
- csptrs
- csrscl
- cstedc
- cstegr
- cstein
- cstemr
- csteqr
- csycon
- csyconv
- csyequb
- csymv
- csyr
- csyrfs
- csysv
- csysvx
- csyswapr
- csytf2
- csytrf
- csytri
- csytri2
- csytri2x
- csytrs
- csytrs2
- ctbcon

- ctbrfs
- ctbtrs
- ctfsm
- ctftri
- ctfttp
- ctfttr
- ctgevc
- ctgex2
- ctgexc
- ctgsen
- ctgsja
- ctgsna
- ctgsy2
- ctgsyl
- ctpcon
- ctpmqrt
- ctpqrt
- ctpqrt2
- ctprfb
- ctprfs
- ctptri
- ctptrs
- ctpttf
- ctpttr
- ctrcon
- ctrevc
- ctrexc
- ctrrfs
- ctrsen
- ctrsna
- ctrsyl
- ctrti2
- ctrtri
- ctrtrs
- ctrttf
- ctrttp

- ctzrzf
- cunbdb
- cuncsd
- cung2l
- cung2r
- cungbr
- cunghr
- cungl2
- cunglq
- cungql
- cungqr
- cungr2
- cungrq
- cungtr
- cunm2l
- cunm2r
- cunmbr
- cunmhr
- cunml2
- cunmlq
- cunmql
- cunmqr
- cunmr2
- cunmr3
- cunmrq
- cunmrz
- cunmtr
- cupgtr
- cupmtr
- dbbcsd
- dbdsdc
- dbdsqr
- ddisna
- dgbbrd
- dgbcon
- dgbequ

- dgbequb
- dgbrfs
- dgbsv
- dgbsvx
- dgbtf2
- dgbtrf
- dgbtrs
- dgebak
- dgebal
- dgebd2
- dgebrd
- dgecon
- dgeequ
- dgeequb
- dgees
- dgeesx
- dgeev
- dgeevx
- dgehd2
- dgehrd
- dgejsv
- dgelq2
- dgelqf
- dgels
- dgelsd
- dgelss
- dgelsy
- dgemqrt
- dgeql2
- dgeqlf
- dgeqp3
- dgeqr2
- dgeqr2p
- dgeqrf
- dgeqrfp
- dgeqrt

- dgeqrt2
- dgeqrt3
- dgerfs
- dgerq2
- dgerqf
- dgesc2
- dgesdd
- dgesv
- dgesvd
- dgesvj
- dgesvx
- dgetc2
- dgetf2
- dgetrf
- dgetri
- dgetrs
- dggbak
- dggbal
- dgges
- dggesx
- dggev
- dggevx
- dggglm
- dgghrd
- dgglse
- dggqrf
- dggrqf
- dgsvj0
- dgsvj1
- dgtcon
- dgtrfs
- dgtsv
- dgtsvx
- dgttrf
- dgttrs
- dgtts2

- dhgeqz
- dhsein
- dhseqr
- disnan
- dlabad
- dlabrd
- dlacn2
- dlacon
- dlacpy
- dladiv
- dlae2
- dlaebz
- dlaed0
- dlaed1
- dlaed2
- dlaed3
- dlaed4
- dlaed5
- dlaed6
- dlaed7
- dlaed8
- dlaed9
- dlaeda
- dlaein
- dlaev2
- dlaexc
- dlag2
- dlag2s
- dlags2
- dlagtf
- dlagtm
- dlagts
- dlagv2
- dlahqr
- dlahr2
- dlaic1

- dlaln2
- dlals0
- dlalsa
- dlalsd
- dlamch
- dlamrg
- dlaneg
- dlangb
- dlange
- dlangt
- dlanhs
- dlansb
- dlansf
- dlansp
- dlanst
- dlansy
- dlantb
- dlantp
- dlantr
- dlanv2
- dlapll
- dlapmr
- dlapmt
- dlapy2
- dlapy3
- dlaqgb
- dlaqge
- dlaqp2
- dlaqps
- dlaqr0
- dlaqr1
- dlaqr2
- dlaqr3
- dlaqr4
- dlaqr5
- dlaqsb

- dlaqsp
- dlaqsy
- dlaqtr
- dlar1v
- dlar2v
- dlarf
- dlarfb
- dlarfg
- dlarfgp
- dlarft
- dlarfx
- dlargv
- dlarnv
- dlarra
- dlarrb
- dlarrc
- dlarrd
- dlarre
- dlarrf
- dlarrj
- dlarrk
- dlarrr
- dlarrv
- dlartg
- dlartgp
- dlartgs
- dlartv
- dlaruv
- dlarz
- dlarzb
- dlarzt
- dlas2
- dlascl
- dlasd0
- dlasd1
- dlasd2

- dlasd3
- dlasd4
- dlasd5
- dlasd6
- dlasd7
- dlasd8
- dlasda
- dlasdq
- dlasdt
- dlaset
- dlasq1
- dlasq2
- dlasq3
- dlasq4
- dlasq6
- dlasr
- dlasrt
- dlassq
- dlasv2
- dlaswp
- dlasy2
- dlasyf
- dlat2s
- dlatbs
- dlatdf
- dlatps
- dlatrd
- dlatrs
- dlatrz
- dlauu2
- dlauum
- dopgtr
- dopmtr
- dorbdb
- dorcsd
- dorg2l

- dorg2r
- dorgbr
- dorghr
- dorgl2
- dorglq
- dorgql
- dorgqr
- dorgr2
- dorgrq
- dorgtr
- dorm2l
- dorm2r
- dormbr
- dormhr
- dorml2
- dormlq
- dormql
- dormqr
- dormr2
- dormr3
- dormrq
- dormrz
- dormtr
- dpbcon
- dpbequ
- dpbrfs
- dpbstf
- dpbsv
- dpbsvx
- dpbtf2
- dpbtrf
- dpbtrs
- dpftrf
- dpftri
- dpftrs
- dpocon

- dpoequ
- dpoequb
- dporfs
- dposv
- dposvx
- dpotf2
- dpotrf
- dpotri
- dpotrs
- dppcon
- dppequ
- dpprfs
- dppsv
- dppsvx
- dpptrf
- dpptri
- dpptrs
- dpstf2
- dpstrf
- dptcon
- dpteqr
- dptrfs
- dptsv
- dptsvx
- dpttrf
- dpttrs
- dptts2
- drscl
- dsbev
- dsbevd
- dsbevx
- dsbgst
- dsbgv
- dsbgvd
- dsbgvx
- dsbtrd

- dsfrk
- dsgesv
- dspcon
- dspev
- dspevd
- dspevx
- dspgst
- dspgv
- dspgvd
- dspgvx
- dsposv
- dsprfs
- dspsv
- dspsvx
- dsptrd
- dsptrf
- dsptri
- dsptrs
- dstebz
- dstedc
- dstegr
- dstein
- dstemr
- dsteqr
- dsterf
- dstev
- dstevd
- dstevr
- dstevx
- dsycon
- dsyconv
- dsyequb
- dsyev
- dsyevd
- dsyevr
- dsyevx

- dsygs2
- dsygst
- dsygv
- dsygvd
- dsygvx
- dsyrfs
- dsysv
- dsysvx
- dsyswapr
- dsytd2
- dsytf2
- dsytrd
- dsytrf
- dsytri
- dsytri2
- dsytri2x
- dsytrs
- dsytrs2
- dtbcon
- dtbrfs
- dtbtrs
- dtfsm
- dtftri
- dtfttp
- dtfttr
- dtgevc
- dtgex2
- dtgexc
- dtgsen
- dtgsja
- dtgsna
- dtgsy2
- dtgsyl
- dtpcon
- dtpmqrt
- dtpqrt

- dtpqrt2
- dtprfb
- dtprfs
- dtptri
- dtptrs
- dtpttf
- dtpttr
- dtrcon
- dtrevc
- dtrexc
- dtrrfs
- dtrsen
- dtrsna
- dtrsyl
- dtrti2
- dtrtri
- dtrtrs
- dtrttf
- dtrttp
- dtzrzf
- dzsum1
- icmax1
- ieeeck
- ilaclc
- ilaclr
- iladiag
- iladlc
- iladlr
- ilaprec
- ilaslc
- ilaslr
- ilatrans
- ilauplo
- ilaver
- ilazlc
- ilazlr

- izmax1
- sbbcsd
- sbdsdc
- sbdsqr
- scsum1
- sdisna
- sgbbrd
- sgbcon
- sgbequ
- sgbequb
- sgbrfs
- sgbsv
- sgbsvx
- sgbtf2
- sgbtrf
- sgbtrs
- sgebak
- sgebal
- sgebd2
- sgebrd
- sgecon
- sgeequ
- sgeequb
- sgees
- sgeesx
- sgeev
- sgeevx
- sgehd2
- sgehrd
- sgejsv
- sgelq2
- sgelqf
- sgels
- sgelsd
- sgelss
- sgelsy

- sgemqrt
- sgeql2
- sgeqlf
- sgeqp3
- sgeqr2
- sgeqr2p
- sgeqrf
- sgeqrfp
- sgeqrt
- sgeqrt2
- sgeqrt3
- sgerfs
- sgerq2
- sgerqf
- sgesc2
- sgesdd
- sgesv
- sgesvd
- sgesvj
- sgesvx
- sgetc2
- sgetf2
- sgetrf
- sgetri
- sgetrs
- sggbak
- sggbal
- sgges
- sggesx
- sggev
- sggevx
- sggglm
- sgghrd
- sgglse
- sggqrf
- sggrqf

- sgsvj0
- sgsvj1
- sgtcon
- sgtrfs
- sgtsv
- sgtsvx
- sgttrf
- sgttrs
- sgtts2
- shgeqz
- shsein
- shseqr
- slabad
- slabrd
- slacn2
- slacon
- slacpy
- sladiv
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- slaebz
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- slaed3
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- slaed5
- slaed6
- slaed7
- slaed8
- slaed9
- slaeda
- slaein
- slaev2
- slaexc
- slag2
- slag2d

- slags2
- slagtf
- slagtm
- slagts
- slagv2
- slahqr
- slahr2
- slaic1
- slaln2
- slals0
- slalsa
- slalsd
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- slamrg
- slangb
- slange
- slangt
- slanhs
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- slapmr
- slapmt
- slapy2
- slapy3
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- slaqr4
- slaqr5
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- slaqsp
- slaqsy
- slaqtr
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- slar2v
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- slarfb
- slarfg
- slarfgp
- slarft
- slarfx
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- slarnv
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- slarzt
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- slasd0
- slasd1
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- slasd4
- slasd5
- slasd6
- slasd7
- slasd8
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- slasdq
- slasdt
- slaset
- slasq1
- slasq2
- slasq3
- slasq4
- slasq6
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- slasrt
- slassq
- slasv2
- slaswp
- slasy2
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- slauu2

- slauum
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- sopmtr
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- sorcsd
- sorg2l
- sorg2r
- sorgbr
- sorghr
- sorgl2
- sorglq
- sorgql
- sorgqr
- sorgr2
- sorgrq
- sorgtr
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- sorm2r
- sormbr
- sormhr
- sorml2
- sormlq
- sormql
- sormqr
- sormr2
- sormr3
- sormrq
- sormrz
- sormtr
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- spbequ
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- spbstf
- spbsv
- spbsvx
- spbtf2

- spbtrf
- spbtrs
- spftrf
- spftri
- spftrs
- spocon
- spoequ
- spoequb
- sporfs
- sposv
- sposvx
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- spotrf
- spotri
- spotrs
- sppcon
- sppequ
- spprfs
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- sppsvx
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- spptri
- spptrs
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- spteqr
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- sptts2
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- ssbevd

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- ssbgv
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- ssbgvx
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- ssfrk
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- sspevd
- sspevx
- sspgst
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- sspgvd
- sspgvx
- ssprfs
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- sspsvx
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- ssygv
- ssygvd
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- ssyrfs
- ssysv
- ssysvx
- ssyswapr
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- ssytrf
- ssytri
- ssytri2
- ssytri2x
- ssytrs
- ssytrs2
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- stbrfs
- stbtrs
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- stftri
- stfttp
- stfttr
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- stgexc
- stgsen
- stgsja
- stgsna
- stgsy2

- stgsyl
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- stpqrt
- stpqrt2
- stprfb
- stprfs
- stptri
- stptrs
- stpttf
- stpttr
- strcon
- strevc
- strexc
- strrfs
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- strsna
- strsyl
- strti2
- strtri
- strtrs
- strttf
- strttp
- stzrzf
- xerbla_array
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- zcposv
- zdrscl
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- zgbcon
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- zgbequb
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- zgbsvx
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- zgbtrs
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- zgebal
- zgebd2
- zgebrd
- zgecon
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- zgeequb
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- zgeesx
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- zgeevx
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- zgelqf
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- zgelsd
- zgelss
- zgelsy
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- zgeqrf
- zgeqrfp
- zgeqrt
- zgeqrt2
- zgeqrt3
- zgerfs
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- zgerqf
- zgesc2
- zgesdd
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- zggesx
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- zgglse
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- zggrqf
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- zlaqhp
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- zpttrf
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- zptts2
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- zspmv
- zspr
- zsprfs

- zspsv
- zspsvx
- zsptrf
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- zsptrs
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- zstegr
- zstein
- zstemr
- zsteqr
- zsycon
- zsyconv
- zsyequb
- zsymv
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- zsyrfs
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- zsysvx
- zsyswapr
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- zsytrf
- zsytri
- zsytri2
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- zsytrs2
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- ztbrfs
- ztbtrs
- ztfsm
- ztftri
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- ztfttr
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- ztgex2
- ztgexc

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- ztgsna
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- ztpttf
- ztpttr
- ztrcon
- ztrevc
- ztrexc
- ztrrfs
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- ztrsyl
- ztrti2
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- ztrtrs
- ztrttf
- ztrttp
- ztzrzf
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- zuncsd
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- zung2r
- zungbr
- zunghr
- zungl2
- zunglq

- zungql
- zungqr
- zungr2
- zungrq
- zungtr
- zunm2l
- zunm2r
- zunmbr
- zunmhr
- zunml2
- zunmlq
- zunmql
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- zunmr2
- zunmr3
- zunmrq
- zunmrz
- zunmtr
- zupgtr
- zupmtr

3.3.15 Interpolative matrix decomposition (`scipy.linalg.interpolative`)

New in version 0.13.

An interpolative decomposition (ID) of a matrix $A \in \mathbb{C}^{m \times n}$ of rank $k \leq \min\{m, n\}$ is a factorization

$$A\Pi = \begin{bmatrix} A\Pi_1 & A\Pi_2 \end{bmatrix} = A\Pi_1 \begin{bmatrix} I & T \end{bmatrix},$$

where $\Pi = [\Pi_1, \Pi_2]$ is a permutation matrix with $\Pi_1 \in \{0, 1\}^{n \times k}$, i.e., $A\Pi_2 = A\Pi_1 T$. This can equivalently be written as $A = BP$, where $B = A\Pi_1$ and $P = [I, T]\Pi^{\mathsf{T}}$ are the *skeleton* and *interpolation matrices*, respectively.

If A does not have exact rank k, then there exists an approximation in the form of an ID such that $A = BP + E$, where $\|E\| \sim \sigma_{k+1}$ is on the order of the $(k+1)$-th largest singular value of A. Note that σ_{k+1} is the best possible error for a rank-k approximation and, in fact, is achieved by the singular value decomposition (SVD) $A \approx USV^*$, where $U \in \mathbb{C}^{m \times k}$ and $V \in \mathbb{C}^{n \times k}$ have orthonormal columns and $S = \mathrm{diag}(\sigma_i) \in \mathbb{C}^{k \times k}$ is diagonal with nonnegative entries. The principal advantages of using an ID over an SVD are that:

- it is cheaper to construct;
- it preserves the structure of A; and
- it is more efficient to compute with in light of the identity submatrix of P.

Routines

Main functionality:

interp_decomp(A, eps_or_k[, rand])	Compute ID of a matrix.
reconstruct_matrix_from_id(B, idx, proj)	Reconstruct matrix from its ID.
reconstruct_interp_matrix(idx, proj)	Reconstruct interpolation matrix from ID.
reconstruct_skel_matrix(A, k, idx)	Reconstruct skeleton matrix from ID.
id_to_svd(B, idx, proj)	Convert ID to SVD.
svd(A, eps_or_k[, rand])	Compute SVD of a matrix via an ID.
estimate_spectral_norm(A[, its])	Estimate spectral norm of a matrix by the randomized power method.
estimate_spectral_norm_diff(A, B[, its])	Estimate spectral norm of the difference of two matrices by the randomized power method.
estimate_rank(A, eps)	Estimate matrix rank to a specified relative precision using randomized methods.

scipy.linalg.interpolative.interp_decomp

scipy.linalg.interpolative.**interp_decomp**(*A*, *eps_or_k*, *rand=True*)

Compute ID of a matrix.

An ID of a matrix *A* is a factorization defined by a rank *k*, a column index array *idx*, and interpolation coefficients *proj* such that:

```
numpy.dot(A[:,idx[:k]], proj) = A[:,idx[k:]]
```

The original matrix can then be reconstructed as:

```
numpy.hstack([A[:,idx[:k]],
                              numpy.dot(A[:,idx[:k]], proj)]
                           )[:,numpy.argsort(idx)]
```

or via the routine *reconstruct_matrix_from_id*. This can equivalently be written as:

```
numpy.dot(A[:,idx[:k]],
                      numpy.hstack([numpy.eye(k), proj])
                    )[:,np.argsort(idx)]
```

in terms of the skeleton and interpolation matrices:

```
B = A[:,idx[:k]]
```

and:

```
P = numpy.hstack([numpy.eye(k), proj])[:,np.argsort(idx)]
```

respectively. See also *reconstruct_interp_matrix* and *reconstruct_skel_matrix*.

The ID can be computed to any relative precision or rank (depending on the value of *eps_or_k*). If a precision is specified (*eps_or_k < 1*), then this function has the output signature:

```
k, idx, proj = interp_decomp(A, eps_or_k)
```

Otherwise, if a rank is specified (*eps_or_k >= 1*), then the output signature is:

```
idx, proj = interp_decomp(A, eps_or_k)
```

Parameters

A [numpy.ndarray or *scipy.sparse.linalg.LinearOperator* with *rmatvec*] Matrix to be factored

eps_or_k [float or int] Relative error (if *eps_or_k* < *1*) or rank (if *eps_or_k* >= *1*) of approximation.

rand [bool, optional] Whether to use random sampling if *A* is of type numpy.ndarray (randomized algorithms are always used if *A* is of type *scipy.sparse.linalg.LinearOperator*).

Returns

k [int] Rank required to achieve specified relative precision if *eps_or_k* < *1*.

idx [numpy.ndarray] Column index array.

proj [numpy.ndarray] Interpolation coefficients.

scipy.linalg.interpolative.reconstruct_matrix_from_id

scipy.linalg.interpolative.**reconstruct_matrix_from_id**(*B*, *idx*, *proj*)

Reconstruct matrix from its ID.

A matrix *A* with skeleton matrix *B* and ID indices and coefficients *idx* and *proj*, respectively, can be reconstructed as:

```
numpy.hstack([B, numpy.dot(B, proj)])[:,numpy.argsort(idx)]
```

See also *reconstruct_interp_matrix* and *reconstruct_skel_matrix*.

Parameters

B [numpy.ndarray] Skeleton matrix.

idx [numpy.ndarray] Column index array.

proj [numpy.ndarray] Interpolation coefficients.

Returns

numpy.ndarray

Reconstructed matrix.

scipy.linalg.interpolative.reconstruct_interp_matrix

scipy.linalg.interpolative.**reconstruct_interp_matrix**(*idx*, *proj*)

Reconstruct interpolation matrix from ID.

The interpolation matrix can be reconstructed from the ID indices and coefficients *idx* and *proj*, respectively, as:

```
P = numpy.hstack([numpy.eye(proj.shape[0]), proj])[:,numpy.argsort(idx)]
```

The original matrix can then be reconstructed from its skeleton matrix *B* via:

```
numpy.dot(B, P)
```

See also *reconstruct_matrix_from_id* and *reconstruct_skel_matrix*.

Parameters

idx [numpy.ndarray] Column index array.

proj [numpy.ndarray] Interpolation coefficients.

Returns

numpy.ndarray
Interpolation matrix.

scipy.linalg.interpolative.reconstruct_skel_matrix

scipy.linalg.interpolative.**reconstruct_skel_matrix**(*A*, *k*, *idx*)
Reconstruct skeleton matrix from ID.

The skeleton matrix can be reconstructed from the original matrix *A* and its ID rank and indices *k* and *idx*, respectively, as:

```
B = A[:,idx[:k]]
```

The original matrix can then be reconstructed via:

```
numpy.hstack([B, numpy.dot(B, proj)])[:,numpy.argsort(idx)]
```

See also *reconstruct_matrix_from_id* and *reconstruct_interp_matrix*.

Parameters

A [numpy.ndarray] Original matrix.
k [int] Rank of ID.
idx [numpy.ndarray] Column index array.

Returns

numpy.ndarray
Skeleton matrix.

scipy.linalg.interpolative.id_to_svd

scipy.linalg.interpolative.**id_to_svd**(*B*, *idx*, *proj*)
Convert ID to SVD.

The SVD reconstruction of a matrix with skeleton matrix *B* and ID indices and coefficients *idx* and *proj*, respectively, is:

```
U, S, V = id_to_svd(B, idx, proj)
A = numpy.dot(U, numpy.dot(numpy.diag(S), V.conj().T))
```

See also *svd*.

Parameters

B [numpy.ndarray] Skeleton matrix.
idx [numpy.ndarray] Column index array.
proj [numpy.ndarray] Interpolation coefficients.

Returns

U [numpy.ndarray] Left singular vectors.
S [numpy.ndarray] Singular values.
V [numpy.ndarray] Right singular vectors.

scipy.linalg.interpolative.svd

scipy.linalg.interpolative.**svd**(*A*, *eps_or_k*, *rand=True*)

Compute SVD of a matrix via an ID.

An SVD of a matrix *A* is a factorization:

```
A = numpy.dot(U, numpy.dot(numpy.diag(S), V.conj().T))
```

where *U* and *V* have orthonormal columns and *S* is nonnegative.

The SVD can be computed to any relative precision or rank (depending on the value of *eps_or_k*).

See also *interp_decomp* and *id_to_svd*.

Parameters

A [numpy.ndarray or *scipy.sparse.linalg.LinearOperator*] Matrix to be factored, given as either a numpy.ndarray or a *scipy.sparse.linalg.LinearOperator* with the *matvec* and *rmatvec* methods (to apply the matrix and its adjoint).

eps_or_k [float or int] Relative error (if *eps_or_k* < *1*) or rank (if *eps_or_k* >= *1*) of approximation.

rand [bool, optional] Whether to use random sampling if *A* is of type numpy.ndarray (randomized algorithms are always used if *A* is of type *scipy.sparse.linalg.LinearOperator*).

Returns

U [numpy.ndarray] Left singular vectors.

S [numpy.ndarray] Singular values.

V [numpy.ndarray] Right singular vectors.

scipy.linalg.interpolative.estimate_spectral_norm

scipy.linalg.interpolative.**estimate_spectral_norm**(*A*, *its=20*)

Estimate spectral norm of a matrix by the randomized power method.

Parameters

A [*scipy.sparse.linalg.LinearOperator*] Matrix given as a *scipy.sparse.linalg.LinearOperator* with the *matvec* and *rmatvec* methods (to apply the matrix and its adjoint).

its [int, optional] Number of power method iterations.

Returns

float Spectral norm estimate.

scipy.linalg.interpolative.estimate_spectral_norm_diff

scipy.linalg.interpolative.**estimate_spectral_norm_diff**(*A*, *B*, *its=20*)

Estimate spectral norm of the difference of two matrices by the randomized power method.

Parameters

A [*scipy.sparse.linalg.LinearOperator*] First matrix given as a *scipy.sparse.linalg.LinearOperator* with the *matvec* and *rmatvec* methods (to apply the matrix and its adjoint).

B [*scipy.sparse.linalg.LinearOperator*] Second matrix given as a *scipy.sparse.linalg.LinearOperator* with the *matvec* and *rmatvec* methods (to apply the matrix and its adjoint).

its [int, optional] Number of power method iterations.

Returns

float Spectral norm estimate of matrix difference.

scipy.linalg.interpolative.estimate_rank

scipy.linalg.interpolative.**estimate_rank**(*A*, *eps*)

Estimate matrix rank to a specified relative precision using randomized methods.

The matrix *A* can be given as either a `numpy.ndarray` or a *`scipy.sparse.linalg.LinearOperator`*, with different algorithms used for each case. If *A* is of type `numpy.ndarray`, then the output rank is typically about 8 higher than the actual numerical rank.

Parameters

A [`numpy.ndarray` or *`scipy.sparse.linalg.LinearOperator`*] Matrix whose rank is to be estimated, given as either a `numpy.ndarray` or a *`scipy.sparse.linalg.LinearOperator`* with the *rmatvec* method (to apply the matrix adjoint).

eps [float] Relative error for numerical rank definition.

Returns

int Estimated matrix rank.

Support functions:

`seed`([seed])	Seed the internal random number generator used in this ID package.
`rand`(*shape)	Generate standard uniform pseudorandom numbers via a very efficient lagged Fibonacci method.

scipy.linalg.interpolative.seed

scipy.linalg.interpolative.**seed**(*seed=None*)

Seed the internal random number generator used in this ID package.

The generator is a lagged Fibonacci method with 55-element internal state.

Parameters

seed [int, sequence, 'default', optional] If 'default', the random seed is reset to a default value.
If *`seed`* is a sequence containing 55 floating-point numbers in range [0,1], these are used to set the internal state of the generator.
If the value is an integer, the internal state is obtained from `numpy.random.RandomState` (MT19937) with the integer used as the initial seed.
If *`seed`* is omitted (None), `numpy.random.rand` is used to initialize the generator.

scipy.linalg.interpolative.rand

scipy.linalg.interpolative.**rand**(**shape*)

Generate standard uniform pseudorandom numbers via a very efficient lagged Fibonacci method.

This routine is used for all random number generation in this package and can affect ID and SVD results.

Parameters

shape Shape of output array

References

This module uses the ID software package [R5a82238cdab4-1] by Martinsson, Rokhlin, Shkolnisky, and Tygert, which is a Fortran library for computing IDs using various algorithms, including the rank-revealing QR approach of [R5a82238cdab4-2] and the more recent randomized methods described in [R5a82238cdab4-3], [R5a82238cdab4-4], and [R5a82238cdab4-5]. This module exposes its functionality in a way convenient for Python users. Note that this module does not add any functionality beyond that of organizing a simpler and more consistent interface.

We advise the user to consult also the documentation for the ID package.

Tutorial

Initializing

The first step is to import *scipy.linalg.interpolative* by issuing the command:

```
>>> import scipy.linalg.interpolative as sli
```

Now let's build a matrix. For this, we consider a Hilbert matrix, which is well know to have low rank:

```
>>> from scipy.linalg import hilbert
>>> n = 1000
>>> A = hilbert(n)
```

We can also do this explicitly via:

```
>>> import numpy as np
>>> n = 1000
>>> A = np.empty((n, n), order='F')
>>> for j in range(n):
>>>     for i in range(m):
>>>         A[i,j] = 1. / (i + j + 1)
```

Note the use of the flag `order='F'` in `numpy.empty`. This instantiates the matrix in Fortran-contiguous order and is important for avoiding data copying when passing to the backend.

We then define multiplication routines for the matrix by regarding it as a *scipy.sparse.linalg.LinearOperator*:

```
>>> from scipy.sparse.linalg import aslinearoperator
>>> L = aslinearoperator(A)
```

This automatically sets up methods describing the action of the matrix and its adjoint on a vector.

Computing an ID

We have several choices of algorithm to compute an ID. These fall largely according to two dichotomies:

1. how the matrix is represented, i.e., via its entries or via its action on a vector; and
2. whether to approximate it to a fixed relative precision or to a fixed rank.

We step through each choice in turn below.

In all cases, the ID is represented by three parameters:

1. a rank `k`;
2. an index array `idx`; and

3. interpolation coefficients `proj`.

The ID is specified by the relation `np.dot(A[:,idx[:k]], proj) == A[:,idx[k:]]`.

From matrix entries

We first consider a matrix given in terms of its entries.

To compute an ID to a fixed precision, type:

```
>>> k, idx, proj = sli.interp_decomp(A, eps)
```

where `eps < 1` is the desired precision.

To compute an ID to a fixed rank, use:

```
>>> idx, proj = sli.interp_decomp(A, k)
```

where `k >= 1` is the desired rank.

Both algorithms use random sampling and are usually faster than the corresponding older, deterministic algorithms, which can be accessed via the commands:

```
>>> k, idx, proj = sli.interp_decomp(A, eps, rand=False)
```

and:

```
>>> idx, proj = sli.interp_decomp(A, k, rand=False)
```

respectively.

From matrix action

Now consider a matrix given in terms of its action on a vector as a *scipy.sparse.linalg.LinearOperator*.

To compute an ID to a fixed precision, type:

```
>>> k, idx, proj = sli.interp_decomp(L, eps)
```

To compute an ID to a fixed rank, use:

```
>>> idx, proj = sli.interp_decomp(L, k)
```

These algorithms are randomized.

Reconstructing an ID

The ID routines above do not output the skeleton and interpolation matrices explicitly but instead return the relevant information in a more compact (and sometimes more useful) form. To build these matrices, write:

```
>>> B = sli.reconstruct_skel_matrix(A, k, idx)
```

for the skeleton matrix and:

```
>>> P = sli.reconstruct_interp_matrix(idx, proj)
```

for the interpolation matrix. The ID approximation can then be computed as:

```
>>> C = np.dot(B, P)
```

This can also be constructed directly using:

```
>>> C = sli.reconstruct_matrix_from_id(B, idx, proj)
```

without having to first compute `P`.

Alternatively, this can be done explicitly as well using:

```
>>> B = A[:,idx[:k]]
>>> P = np.hstack([np.eye(k), proj])[:,np.argsort(idx)]
>>> C = np.dot(B, P)
```

Computing an SVD

An ID can be converted to an SVD via the command:

```
>>> U, S, V = sli.id_to_svd(B, idx, proj)
```

The SVD approximation is then:

```
>>> C = np.dot(U, np.dot(np.diag(S), np.dot(V.conj().T)))
```

The SVD can also be computed "fresh" by combining both the ID and conversion steps into one command. Following the various ID algorithms above, there are correspondingly various SVD algorithms that one can employ.

From matrix entries

We consider first SVD algorithms for a matrix given in terms of its entries.

To compute an SVD to a fixed precision, type:

```
>>> U, S, V = sli.svd(A, eps)
```

To compute an SVD to a fixed rank, use:

```
>>> U, S, V = sli.svd(A, k)
```

Both algorithms use random sampling; for the determinstic versions, issue the keyword `rand=False` as above.

From matrix action

Now consider a matrix given in terms of its action on a vector.

To compute an SVD to a fixed precision, type:

```
>>> U, S, V = sli.svd(L, eps)
```

To compute an SVD to a fixed rank, use:

```
>>> U, S, V = sli.svd(L, k)
```

Utility routines

Several utility routines are also available.

To estimate the spectral norm of a matrix, use:

```
>>> snorm = sli.estimate_spectral_norm(A)
```

This algorithm is based on the randomized power method and thus requires only matrix-vector products. The number of iterations to take can be set using the keyword `its` (default: `its=20`). The matrix is interpreted as a *scipy.sparse.linalg.LinearOperator*, but it is also valid to supply it as a `numpy.ndarray`, in which case it is trivially converted using *scipy.sparse.linalg.aslinearoperator*.

The same algorithm can also estimate the spectral norm of the difference of two matrices `A1` and `A2` as follows:

```
>>> diff = sli.estimate_spectral_norm_diff(A1, A2)
```

This is often useful for checking the accuracy of a matrix approximation.

Some routines in *scipy.linalg.interpolative* require estimating the rank of a matrix as well. This can be done with either:

```
>>> k = sli.estimate_rank(A, eps)
```

or:

```
>>> k = sli.estimate_rank(L, eps)
```

depending on the representation. The parameter `eps` controls the definition of the numerical rank.

Finally, the random number generation required for all randomized routines can be controlled via *scipy.linalg.interpolative.seed*. To reset the seed values to their original values, use:

```
>>> sli.seed('default')
```

To specify the seed values, use:

```
>>> sli.seed(s)
```

where `s` must be an integer or array of 55 floats. If an integer, the array of floats is obtained by using `numpy.random.rand` with the given integer seed.

To simply generate some random numbers, type:

```
>>> sli.rand(n)
```

where `n` is the number of random numbers to generate.

Remarks

The above functions all automatically detect the appropriate interface and work with both real and complex data types, passing input arguments to the proper backend routine.

3.3.16 Miscellaneous routines (scipy.misc)

Various utilities that don't have another home.

ascent()	Get an 8-bit grayscale bit-depth, 512 x 512 derived image for easy use in demos
central_diff_weights(Np[, ndiv])	Return weights for an Np-point central derivative.
derivative(func, x0[, dx, n, args, order])	Find the nth derivative of a function at a point.
face([gray])	Get a 1024 x 768, color image of a raccoon face.
electrocardiogram()	Load an electrocardiogram as an example for a 1-D signal.

scipy.misc.ascent

scipy.misc.**ascent**()

Get an 8-bit grayscale bit-depth, 512 x 512 derived image for easy use in demos

The image is derived from accent-to-the-top.jpg at http://www.public-domain-image.com/people-public-domain-images-pictures/

Parameters

None

Returns

ascent [ndarray] convenient image to use for testing and demonstration

Examples

```
>>> import scipy.misc
>>> ascent = scipy.misc.ascent()
>>> ascent.shape
(512, 512)
>>> ascent.max()
255
```

```
>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.imshow(ascent)
>>> plt.show()
```

scipy.misc.central_diff_weights

scipy.misc.**central_diff_weights**(*Np*, *ndiv=1*)

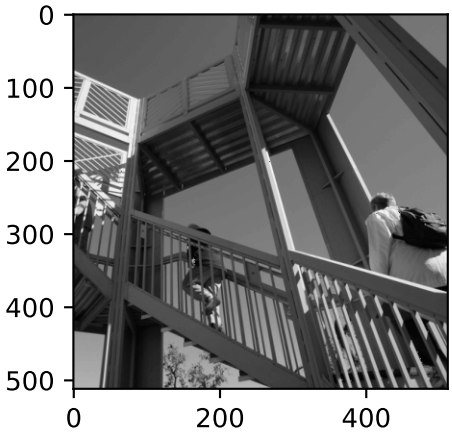
Return weights for an Np-point central derivative.

Assumes equally-spaced function points.

If weights are in the vector w, then derivative is w[0] * f(x-ho*dx) + … + w[-1] * f(x+h0*dx)

Parameters

Np [int] Number of points for the central derivative.
ndiv [int, optional] Number of divisions. Default is 1.



Returns

w [ndarray] Weights for an Np-point central derivative. Its size is *Np*.

Notes

Can be inaccurate for a large number of points.

References

[1]

Examples

We can calculate a derivative value of a function.

```
>>> from scipy.misc import central_diff_weights
>>> def f(x):
...     return 2 * x**2 + 3
>>> x = 3.0 # derivative point
>>> h = 0.1 # differential step
>>> Np = 3 # point number for central derivative
>>> weights = central_diff_weights(Np) # weights for first derivative
>>> vals = [f(x + (i - Np/2) * h) for i in range(Np)]
>>> sum(w * v for (w, v) in zip(weights, vals))/h
11.79999999999998
```

This value is close to the analytical solution: f'(x) = 4x, so f'(3) = 12

scipy.misc.derivative

scipy.misc.**derivative**(*func*, *x0*, *dx=1.0*, *n=1*, *args=()*, *order=3*)

Find the nth derivative of a function at a point.

Given a function, use a central difference formula with spacing *dx* to compute the nth derivative at *x0*.

Parameters

func	[function] Input function.
x0	[float] The point at which the nth derivative is found.
dx	[float, optional] Spacing.
n	[int, optional] Order of the derivative. Default is 1.
args	[tuple, optional] Arguments
order	[int, optional] Number of points to use, must be odd.

Notes

Decreasing the step size too small can result in round-off error.

Examples

```
>>> from scipy.misc import derivative
>>> def f(x):
...     return x**3 + x**2
>>> derivative(f, 1.0, dx=1e-6)
4.9999999999217337
```

scipy.misc.face

scipy.misc.**face**(*gray=False*)

Get a 1024 x 768, color image of a raccoon face.

raccoon-procyon-lotor.jpg at http://www.public-domain-image.com

Parameters

gray	[bool, optional] If True return 8-bit grey-scale image, otherwise return a color image

Returns

face	[ndarray] image of a racoon face

Examples

```
>>> import scipy.misc
>>> face = scipy.misc.face()
>>> face.shape
(768, 1024, 3)
>>> face.max()
255
>>> face.dtype
dtype('uint8')
```

```
>>> import matplotlib.pyplot as plt
>>> plt.gray()
>>> plt.imshow(face)
>>> plt.show()
```

scipy.misc.electrocardiogram

scipy.misc.**electrocardiogram**()

Load an electrocardiogram as an example for a 1-D signal.

The returned signal is a 5 minute long electrocardiogram (ECG), a medical recording of the heart's electrical activity, sampled at 360 Hz.

Returns

ecg [ndarray] The electrocardiogram in millivolt (mV) sampled at 360 Hz.

Notes

The provided signal is an excerpt (19:35 to 24:35) from the record 208 (lead MLII) provided by the MIT-BIH Arrhythmia Database [1] on PhysioNet [2]. The excerpt includes noise induced artifacts, typical heartbeats as well as pathological changes.

New in version 1.1.0.

References

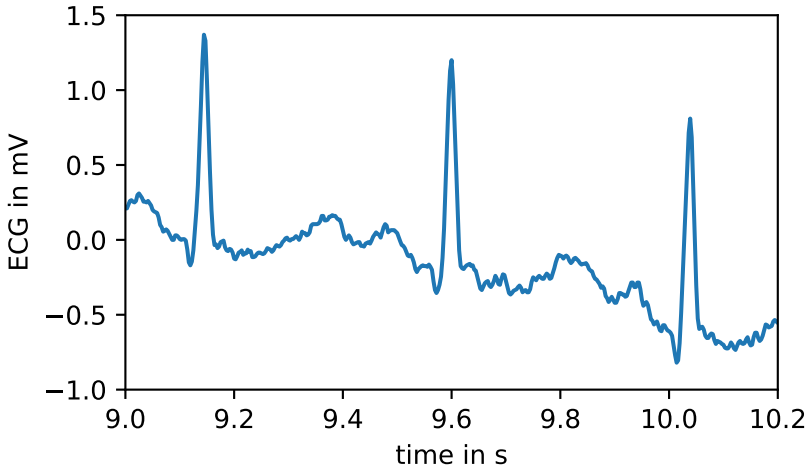
[1], [2]

Examples

```
>>> from scipy.misc import electrocardiogram
>>> ecg = electrocardiogram()
>>> ecg
array([-0.245, -0.215, -0.185, ..., -0.405, -0.395, -0.385])
>>> ecg.shape, ecg.mean(), ecg.std()
((108000,), -0.16510875, 0.5992473991177294)
```

As stated the signal features several areas with a different morphology. E.g., the first few seconds show the electrical activity of a heart in normal sinus rhythm as seen below.

```
>>> import matplotlib.pyplot as plt
>>> fs = 360
>>> time = np.arange(ecg.size) / fs
>>> plt.plot(time, ecg)
>>> plt.xlabel("time in s")
>>> plt.ylabel("ECG in mV")
>>> plt.xlim(9, 10.2)
>>> plt.ylim(-1, 1.5)
>>> plt.show()
```



After second 16, however, the first premature ventricular contractions, also called extrasystoles, appear. These have a different morphology compared to typical heartbeats. The difference can easily be observed in the following plot.

```
>>> plt.plot(time, ecg)
>>> plt.xlabel("time in s")
>>> plt.ylabel("ECG in mV")
>>> plt.xlim(46.5, 50)
```

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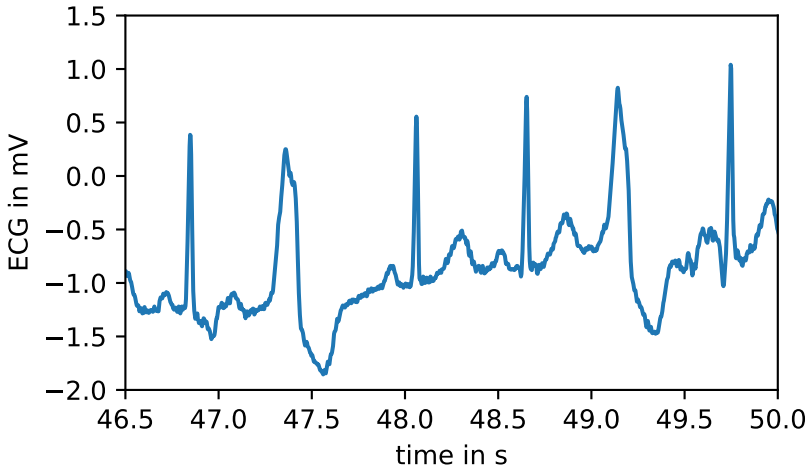
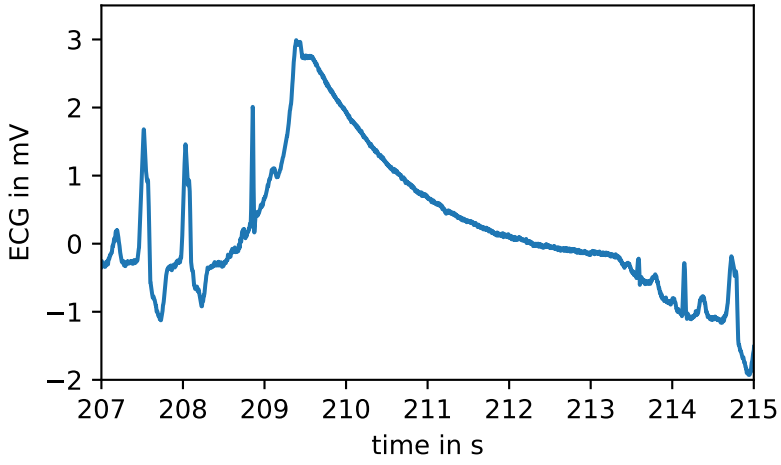
```
>>> plt.ylim(-2, 1.5)
>>> plt.show()
```



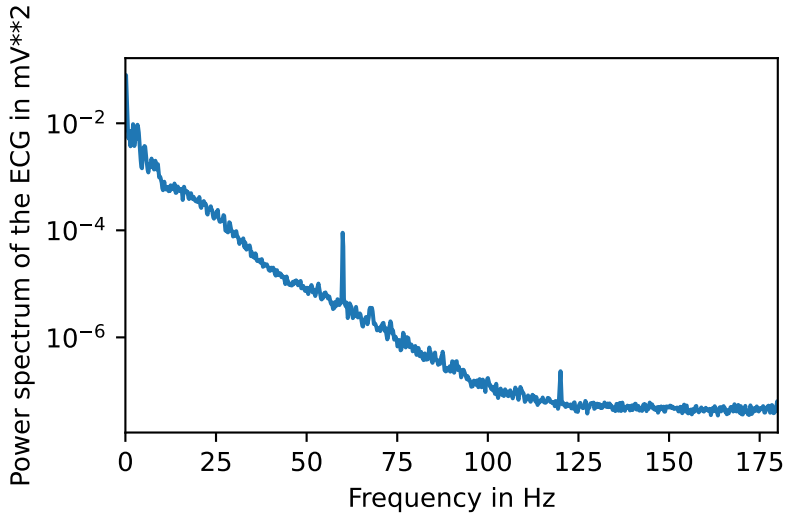
At several points large artifacts disturb the recording, e.g.:

```
>>> plt.plot(time, ecg)
>>> plt.xlabel("time in s")
>>> plt.ylabel("ECG in mV")
>>> plt.xlim(207, 215)
>>> plt.ylim(-2, 3.5)
>>> plt.show()
```



Finally, examining the power spectrum reveals that most of the biosignal is made up of lower frequencies. At 60 Hz the noise induced by the mains electricity can be clearly observed.

```
>>> from scipy.signal import welch
>>> f, Pxx = welch(ecg, fs=fs, nperseg=2048, scaling="spectrum")
>>> plt.semilogy(f, Pxx)
>>> plt.xlabel("Frequency in Hz")
>>> plt.ylabel("Power spectrum of the ECG in mV**2")
>>> plt.xlim(f[[0, -1]])
>>> plt.show()
```



3.3.17 Multidimensional image processing (`scipy.ndimage`)

This package contains various functions for multidimensional image processing.

Filters

convolve(input, weights[, output, mode, …])	Multidimensional convolution.
convolve1d(input, weights[, axis, output, …])	Calculate a 1-D convolution along the given axis.
correlate(input, weights[, output, mode, …])	Multidimensional correlation.
correlate1d(input, weights[, axis, output, …])	Calculate a 1-D correlation along the given axis.
gaussian_filter(input, sigma[, order, …])	Multidimensional Gaussian filter.
gaussian_filter1d(input, sigma[, axis, …])	1-D Gaussian filter.
gaussian_gradient_magnitude(input, sigma[, …])	Multidimensional gradient magnitude using Gaussian derivatives.
gaussian_laplace(input, sigma[, output, …])	Multidimensional Laplace filter using Gaussian second derivatives.
generic_filter(input, function[, size, …])	Calculate a multidimensional filter using the given function.
generic_filter1d(input, function, filter_size)	Calculate a 1-D filter along the given axis.
generic_gradient_magnitude(input, derivative)	Gradient magnitude using a provided gradient function.

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generic_laplace(input, derivative2[, …])	N-D Laplace filter using a provided second derivative function.
laplace(input[, output, mode, cval])	N-D Laplace filter based on approximate second derivatives.
maximum_filter(input[, size, footprint, …])	Calculate a multidimensional maximum filter.
maximum_filter1d(input, size[, axis, …])	Calculate a 1-D maximum filter along the given axis.
median_filter(input[, size, footprint, …])	Calculate a multidimensional median filter.
minimum_filter(input[, size, footprint, …])	Calculate a multidimensional minimum filter.
minimum_filter1d(input, size[, axis, …])	Calculate a 1-D minimum filter along the given axis.
percentile_filter(input, percentile[, size, …])	Calculate a multidimensional percentile filter.
prewitt(input[, axis, output, mode, cval])	Calculate a Prewitt filter.
rank_filter(input, rank[, size, footprint, …])	Calculate a multidimensional rank filter.
sobel(input[, axis, output, mode, cval])	Calculate a Sobel filter.
uniform_filter(input[, size, output, mode, …])	Multidimensional uniform filter.
uniform_filter1d(input, size[, axis, …])	Calculate a 1-D uniform filter along the given axis.

scipy.ndimage.convolve

scipy.ndimage.**convolve**(*input*, *weights*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional convolution.

The array is convolved with the given kernel.

Parameters

input [array_like] The input array.

weights [array_like] Array of weights, same number of dimensions as input

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.

'grid-constant'
This is a synonym for 'constant'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0

origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

result [ndarray] The result of convolution of *input* with *weights*.

See also:

`correlate`

Correlate an image with a kernel.

Notes

Each value in result is $C_i = \sum_j I_{i+k-j} W_j$, where W is the *weights* kernel, j is the N-D spatial index over W, I is the *input* and k is the coordinate of the center of W, specified by *origin* in the input parameters.

Examples

Perhaps the simplest case to understand is `mode='constant', cval=0.0`, because in this case borders (i.e., where the *weights* kernel, centered on any one value, extends beyond an edge of *input*) are treated as zeros.

```
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> k = np.array([[1,1,1],[1,1,0],[1,0,0]])
>>> from scipy import ndimage
>>> ndimage.convolve(a, k, mode='constant', cval=0.0)
array([[11, 10,  7,  4],
       [10,  3, 11, 11],
       [15, 12, 14,  7],
       [12,  3,  7,  0]])
```

Setting `cval=1.0` is equivalent to padding the outer edge of *input* with 1.0's (and then extracting only the original region of the result).

```
>>> ndimage.convolve(a, k, mode='constant', cval=1.0)
array([[13, 11,  8,  7],
       [11,  3, 11, 14],
       [16, 12, 14, 10],
       [15,  6, 10,  5]])
```

With `mode='reflect'` (the default), outer values are reflected at the edge of *input* to fill in missing values.

```
>>> b = np.array([[2, 0, 0],
...               [1, 0, 0],
...               [0, 0, 0]])
>>> k = np.array([[0,1,0], [0,1,0], [0,1,0]])
>>> ndimage.convolve(b, k, mode='reflect')
```

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```
array([[5, 0, 0],
       [3, 0, 0],
       [1, 0, 0]])
```

This includes diagonally at the corners.

```
>>> k = np.array([[1,0,0],[0,1,0],[0,0,1]])
>>> ndimage.convolve(b, k)
array([[4, 2, 0],
       [3, 2, 0],
       [1, 1, 0]])
```

With `mode='nearest'`, the single nearest value in to an edge in *input* is repeated as many times as needed to match the overlapping *weights*.

```
>>> c = np.array([[2, 0, 1],
...               [1, 0, 0],
...               [0, 0, 0]])
>>> k = np.array([[0, 1, 0],
...               [0, 1, 0],
...               [0, 1, 0],
...               [0, 1, 0],
...               [0, 1, 0]])
>>> ndimage.convolve(c, k, mode='nearest')
array([[7, 0, 3],
       [5, 0, 2],
       [3, 0, 1]])
```

scipy.ndimage.convolve1d

scipy.ndimage.**convolve1d**(*input*, *weights*, *axis=- 1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a 1-D convolution along the given axis.

The lines of the array along the given axis are convolved with the given weights.

Parameters

input [array_like] The input array.

weights [ndarray] 1-D sequence of numbers.

axis [int, optional] The axis of *input* along which to calculate. Default is -1.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)

The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.

'grid-constant'
This is a synonym for 'constant'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

Returns

convolve1d
[ndarray] Convolved array with same shape as input

Examples

```
>>> from scipy.ndimage import convolve1d
>>> convolve1d([2, 8, 0, 4, 1, 9, 9, 0], weights=[1, 3])
array([14, 24,  4, 13, 12, 36, 27,  0])
```

scipy.ndimage.correlate

scipy.ndimage.**correlate**(*input*, *weights*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional correlation.

The array is correlated with the given kernel.

Parameters

input [array_like] The input array.

weights [ndarray] array of weights, same number of dimensions as input

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.
For consistency with the interpolation functions, the following mode names can also be used:
'grid-mirror'
This is a synonym for 'reflect'.
'grid-constant'
This is a synonym for 'constant'.
'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

result [ndarray] The result of correlation of *input* with *weights*.

See also:

`convolve`

Convolve an image with a kernel.

Examples

Correlation is the process of moving a filter mask often referred to as kernel over the image and computing the sum of products at each location.

```
>>> from scipy.ndimage import correlate
>>> input_img = np.arange(25).reshape(5,5)
>>> print(input_img)
[[ 0  1  2  3  4]
[ 5  6  7  8  9]
[10 11 12 13 14]
[15 16 17 18 19]
[20 21 22 23 24]]
```

Define a kernel (weights) for correlation. In this example, it is for sum of center and up, down, left and right next elements.

```
>>> weights = [[0, 1, 0],
...            [1, 1, 1],
...            [0, 1, 0]]
```

We can calculate a correlation result: For example, element `[2,2]` is `7 + 11 + 12 + 13 + 17 = 60`.

```
>>> correlate(input_img, weights)
array([[  6,  10,  15,  20,  24],
    [ 26,  30,  35,  40,  44],
    [ 51,  55,  60,  65,  69],
    [ 76,  80,  85,  90,  94],
    [ 96, 100, 105, 110, 114]])
```

scipy.ndimage.correlate1d

scipy.ndimage.**correlate1d**(*input*, *weights*, *axis=- 1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a 1-D correlation along the given axis.

The lines of the array along the given axis are correlated with the given weights.

Parameters

input [array_like] The input array.

weights [array] 1-D sequence of numbers.

axis [int, optional] The axis of *input* along which to calculate. Default is -1.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.

'grid-constant'
This is a synonym for 'constant'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

Examples

```
>>> from scipy.ndimage import correlate1d
>>> correlate1d([2, 8, 0, 4, 1, 9, 9, 0], weights=[1, 3])
array([ 8, 26,  8, 12,  7, 28, 36,  9])
```

scipy.ndimage.gaussian_filter

scipy.ndimage.**gaussian_filter**(*input*, *sigma*, *order=0*, *output=None*, *mode='reflect'*, *cval=0.0*, *truncate=4.0*)

Multidimensional Gaussian filter.

Parameters

input [array_like] The input array.

sigma [scalar or sequence of scalars] Standard deviation for Gaussian kernel. The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes.

order [int or sequence of ints, optional] The order of the filter along each axis is given as a sequence of integers, or as a single number. An order of 0 corresponds to convolution with a Gaussian kernel. A positive order corresponds to convolution with that derivative of a Gaussian.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-constant'
This is a synonym for 'constant'.

'grid-mirror'
This is a synonym for 'reflect'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

truncate [float] Truncate the filter at this many standard deviations. Default is 4.0.

Returns

gaussian_filter
[ndarray] Returned array of same shape as *input*.

Notes

The multidimensional filter is implemented as a sequence of 1-D convolution filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.

Examples

```
>>> from scipy.ndimage import gaussian_filter
>>> a = np.arange(50, step=2).reshape((5,5))
>>> a
array([[ 0,  2,  4,  6,  8],
       [10, 12, 14, 16, 18],
       [20, 22, 24, 26, 28],
       [30, 32, 34, 36, 38],
       [40, 42, 44, 46, 48]])
>>> gaussian_filter(a, sigma=1)
array([[ 4,  6,  8,  9, 11],
       [10, 12, 14, 15, 17],
       [20, 22, 24, 25, 27],
       [29, 31, 33, 34, 36],
       [35, 37, 39, 40, 42]])
```

```
>>> from scipy import misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = gaussian_filter(ascent, sigma=5)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

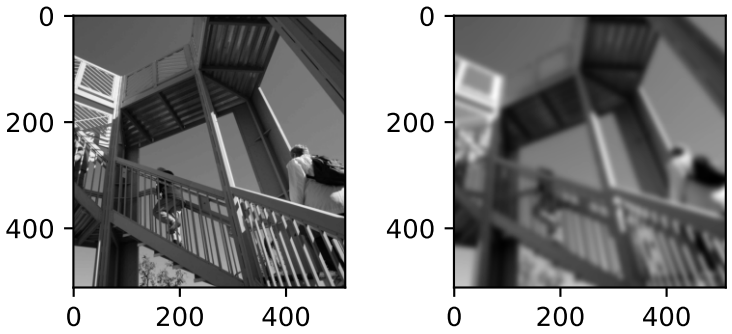
scipy.ndimage.gaussian_filter1d

scipy.ndimage.**gaussian_filter1d**(*input*, *sigma*, *axis=- 1*, *order=0*, *output=None*, *mode='reflect'*, *cval=0.0*, *truncate=4.0*)

1-D Gaussian filter.

Parameters

input	[array_like] The input array.
sigma	[scalar] standard deviation for Gaussian kernel
axis	[int, optional] The axis of *input* along which to calculate. Default is -1.
order	[int, optional] An order of 0 corresponds to convolution with a Gaussian kernel. A positive order corresponds to convolution with that derivative of a Gaussian.
output	[array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.
mode	[{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:



'reflect' (*d c b a | a b c d | d c b a*)
: The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
: The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
: The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
: The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
: The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
: This is a synonym for 'reflect'.

'grid-constant'
: This is a synonym for 'constant'.

'grid-wrap'
: This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

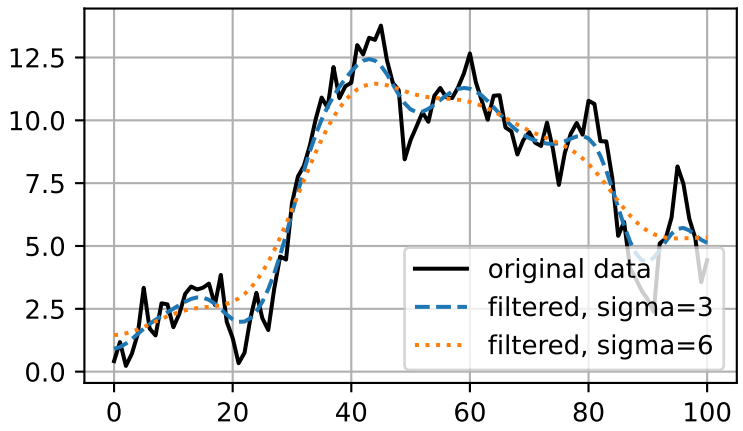
truncate [float, optional] Truncate the filter at this many standard deviations. Default is 4.0.

Returns

gaussian_filter1d
: [ndarray]

Examples

```
>>> from scipy.ndimage import gaussian_filter1d
>>> gaussian_filter1d([1.0, 2.0, 3.0, 4.0, 5.0], 1)
array([ 1.42704095,  2.06782203,  3.        ,  3.93217797,  4.57295905])
>>> gaussian_filter1d([1.0, 2.0, 3.0, 4.0, 5.0], 4)
array([ 2.91948343,  2.95023502,  3.        ,  3.04976498,  3.08051657])
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> x = rng.standard_normal(101).cumsum()
>>> y3 = gaussian_filter1d(x, 3)
>>> y6 = gaussian_filter1d(x, 6)
>>> plt.plot(x, 'k', label='original data')
>>> plt.plot(y3, '--', label='filtered, sigma=3')
>>> plt.plot(y6, ':', label='filtered, sigma=6')
>>> plt.legend()
>>> plt.grid()
>>> plt.show()
```



scipy.ndimage.gaussian_gradient_magnitude

scipy.ndimage.**gaussian_gradient_magnitude**(*input*, *sigma*, *output=None*, *mode='reflect'*, *cval=0.0*, ***kwargs*)

Multidimensional gradient magnitude using Gaussian derivatives.

Parameters

input [array_like] The input array.

sigma [scalar or sequence of scalars] The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.
'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.
'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.
'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.
'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.
For consistency with the interpolation functions, the following mode names can also be used:
'grid-constant'
This is a synonym for 'constant'.
'grid-mirror'
This is a synonym for 'reflect'.
'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.
Extra keyword arguments will be passed to gaussian_filter().

Returns

gaussian_gradient_magnitude
[ndarray] Filtered array. Has the same shape as *input*.

Examples

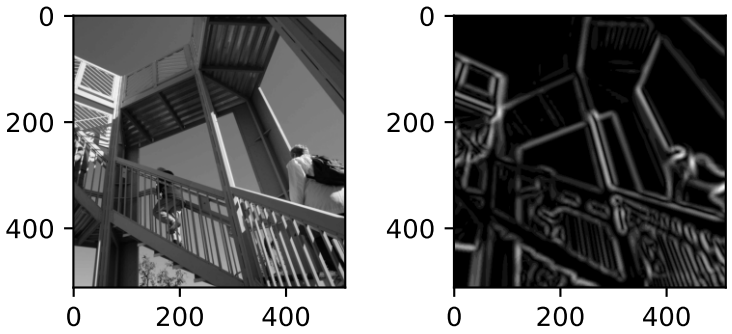
```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.gaussian_gradient_magnitude(ascent, sigma=5)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

scipy.ndimage.gaussian_laplace

scipy.ndimage.**gaussian_laplace**(*input*, *sigma*, *output=None*, *mode='reflect'*, *cval=0.0*, ***kwargs*)
Multidimensional Laplace filter using Gaussian second derivatives.

Parameters

input [array_like] The input array.
sigma [scalar or sequence of scalars] The standard deviations of the Gaussian filter are given for each axis as a sequence, or as a single number, in which case it is equal for all axes.
output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.



mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-constant'
This is a synonym for 'constant'.

'grid-mirror'
This is a synonym for 'reflect'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

Extra keyword arguments will be passed to gaussian_filter().

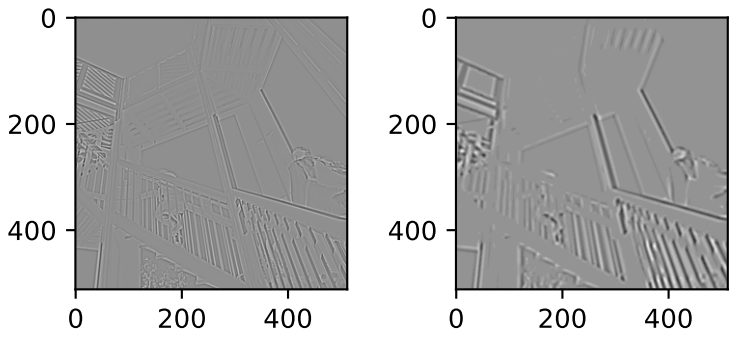
Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> ascent = misc.ascent()
```

```
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
```

```
>>> result = ndimage.gaussian_laplace(ascent, sigma=1)
>>> ax1.imshow(result)
```

```
>>> result = ndimage.gaussian_laplace(ascent, sigma=3)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.generic_filter

scipy.ndimage.**generic_filter**(*input*, *function*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*, *extra_arguments=()*, *extra_keywords=None*)

Calculate a multidimensional filter using the given function.

At each element the provided function is called. The input values within the filter footprint at that element are passed to the function as a 1-D array of double values.

Parameters

input [array_like] The input array.

function [{callable, scipy.LowLevelCallable}] Function to apply at each element.

size [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.

footprint [array, optional] Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function.

footprint is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2). When *footprint* is given, *size* is ignored.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.

'grid-constant'
This is a synonym for 'constant'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

extra_arguments
[sequence, optional] Sequence of extra positional arguments to pass to passed function.

extra_keywords
[dict, optional] dict of extra keyword arguments to pass to passed function.

Notes

This function also accepts low-level callback functions with one of the following signatures and wrapped in *scipy.LowLevelCallable*:

```
int callback(double *buffer, npy_intp filter_size,
             double *return_value, void *user_data)
int callback(double *buffer, intptr_t filter_size,
             double *return_value, void *user_data)
```

The calling function iterates over the elements of the input and output arrays, calling the callback function at each element. The elements within the footprint of the filter at the current element are passed through the `buffer`

parameter, and the number of elements within the footprint through `filter_size`. The calculated value is returned in `return_value`. `user_data` is the data pointer provided to *scipy.LowLevelCallable* as-is.

The callback function must return an integer error status that is zero if something went wrong and one otherwise. If an error occurs, you should normally set the python error status with an informative message before returning, otherwise a default error message is set by the calling function.

In addition, some other low-level function pointer specifications are accepted, but these are for backward compatibility only and should not be used in new code.

scipy.ndimage.generic_filter1d

scipy.ndimage.**generic_filter1d**(*input*, *function*, *filter_size*, *axis=- 1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*, *extra_arguments=()*, *extra_keywords=None*)

Calculate a 1-D filter along the given axis.

generic_filter1d iterates over the lines of the array, calling the given function at each line. The arguments of the line are the input line, and the output line. The input and output lines are 1-D double arrays. The input line is extended appropriately according to the filter size and origin. The output line must be modified in-place with the result.

Parameters

input [array_like] The input array.

function [{callable, scipy.LowLevelCallable}] Function to apply along given axis.

filter_size [scalar] Length of the filter.

axis [int, optional] The axis of *input* along which to calculate. Default is -1.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.

'grid-constant'
This is a synonym for 'constant'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

extra_arguments
[sequence, optional] Sequence of extra positional arguments to pass to passed function.

extra_keywords
[dict, optional] dict of extra keyword arguments to pass to passed function.

Notes

This function also accepts low-level callback functions with one of the following signatures and wrapped in *scipy.LowLevelCallable*:

```
int function(double *input_line, npy_intp input_length,
             double *output_line, npy_intp output_length,
             void *user_data)
int function(double *input_line, intptr_t input_length,
             double *output_line, intptr_t output_length,
             void *user_data)
```

The calling function iterates over the lines of the input and output arrays, calling the callback function at each line. The current line is extended according to the border conditions set by the calling function, and the result is copied into the array that is passed through `input_line`. The length of the input line (after extension) is passed through `input_length`. The callback function should apply the filter and store the result in the array passed through `output_line`. The length of the output line is passed through `output_length`. `user_data` is the data pointer provided to *scipy.LowLevelCallable* as-is.

The callback function must return an integer error status that is zero if something went wrong and one otherwise. If an error occurs, you should normally set the python error status with an informative message before returning, otherwise a default error message is set by the calling function.

In addition, some other low-level function pointer specifications are accepted, but these are for backward compatibility only and should not be used in new code.

scipy.ndimage.generic_gradient_magnitude

scipy.ndimage.**generic_gradient_magnitude**(*input*, *derivative*, *output=None*, *mode='reflect'*, *cval=0.0*, *extra_arguments=()*, *extra_keywords=None*)

Gradient magnitude using a provided gradient function.

Parameters

input [array_like] The input array.

derivative [callable] Callable with the following signature:

```
derivative(input, axis, output, mode, cval,
           *extra_arguments, **extra_keywords)
```

See *extra_arguments*, *extra_keywords* below. *derivative* can assume that *input* and *output* are ndarrays. Note that the output from *derivative* is modified inplace; be careful to copy important inputs before returning them.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.
'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.
'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.
'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.
'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.
For consistency with the interpolation functions, the following mode names can also be used:
'grid-constant'
This is a synonym for 'constant'.
'grid-mirror'
This is a synonym for 'reflect'.
'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

extra_keywords
[dict, optional] dict of extra keyword arguments to pass to passed function.

extra_arguments
[sequence, optional] Sequence of extra positional arguments to pass to passed function.

scipy.ndimage.generic_laplace

scipy.ndimage.**generic_laplace**(*input*, *derivative2*, *output=None*, *mode='reflect'*, *cval=0.0*, *extra_arguments=()*, *extra_keywords=None*)

N-D Laplace filter using a provided second derivative function.

Parameters

input [array_like] The input array.

derivative2
[callable] Callable with the following signature:

```
derivative2(input, axis, output, mode, cval,
            *extra_arguments, **extra_keywords)
```

See *extra_arguments*, *extra_keywords* below.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:
'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.
'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.
'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.
'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.
For consistency with the interpolation functions, the following mode names can also be used:
'grid-constant'
This is a synonym for 'constant'.
'grid-mirror'
This is a synonym for 'reflect'.
'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

extra_keywords
[dict, optional] dict of extra keyword arguments to pass to passed function.

extra_arguments
[sequence, optional] Sequence of extra positional arguments to pass to passed function.

scipy.ndimage.laplace

`scipy.ndimage.`**`laplace`**(*input*, *output=None*, *mode='reflect'*, *cval=0.0*)

N-D Laplace filter based on approximate second derivatives.

Parameters

input [array_like] The input array.

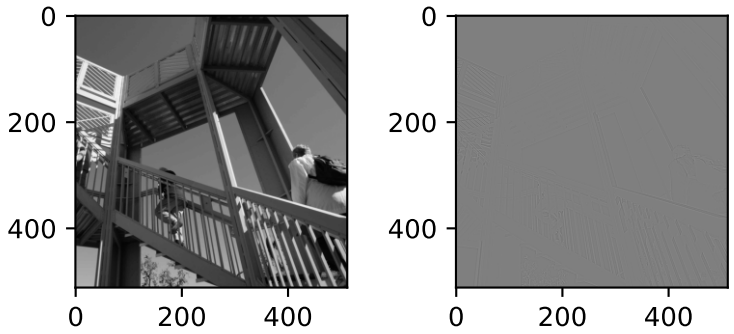
output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:
'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.
'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.
'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.
'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.
'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.
For consistency with the interpolation functions, the following mode names can also be used:
'grid-constant'
This is a synonym for 'constant'.
'grid-mirror'
This is a synonym for 'reflect'.
'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.laplace(ascent)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.maximum_filter

scipy.ndimage.**maximum_filter**(*input*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a multidimensional maximum filter.

Parameters

input [array_like] The input array.

size [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.

footprint [array, optional] Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2). When *footprint* is given, *size* is ignored.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the

number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-constant'
This is a synonym for 'constant'.

'grid-mirror'
This is a synonym for 'reflect'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

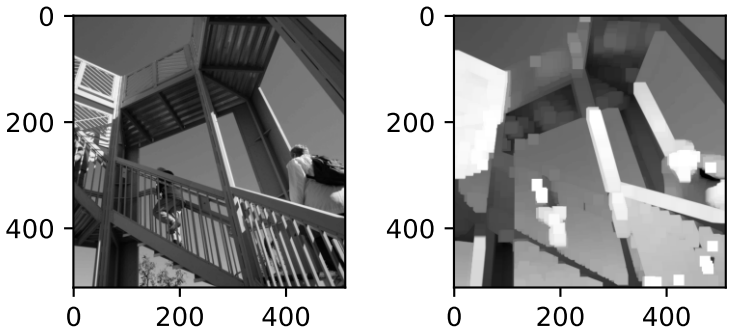
maximum_filter
[ndarray] Filtered array. Has the same shape as *input*.

Notes

A sequence of modes (one per axis) is only supported when the footprint is separable. Otherwise, a single mode string must be provided.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.maximum_filter(ascent, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.maximum_filter1d

scipy.ndimage.**maximum_filter1d**(*input*, *size*, *axis=- 1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a 1-D maximum filter along the given axis.

The lines of the array along the given axis are filtered with a maximum filter of given size.

Parameters

input [array_like] The input array.

size [int] Length along which to calculate the 1-D maximum.

axis [int, optional] The axis of *input* along which to calculate. Default is -1.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.

'grid-constant'
This is a synonym for 'constant'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

Returns

maximum1d
[ndarray, None] Maximum-filtered array with same shape as input. None if *output* is not None

Notes

This function implements the MAXLIST algorithm [1], as described by Richard Harter [2], and has a guaranteed O(n) performance, *n* being the *input* length, regardless of filter size.

References

[1], [2]

Examples

```
>>> from scipy.ndimage import maximum_filter1d
>>> maximum_filter1d([2, 8, 0, 4, 1, 9, 9, 0], size=3)
array([8, 8, 8, 4, 9, 9, 9, 9])
```

scipy.ndimage.median_filter

scipy.ndimage.**median_filter**(*input*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a multidimensional median filter.

Parameters

input [array_like] The input array.

size [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.

footprint [array, optional] Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2). When *footprint* is given, *size* is ignored.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
: The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
: The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
: The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
: The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
: This is a synonym for 'reflect'.

'grid-constant'
: This is a synonym for 'constant'.

'grid-wrap'
: This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

median_filter
: [ndarray] Filtered array. Has the same shape as *input*.

See also:

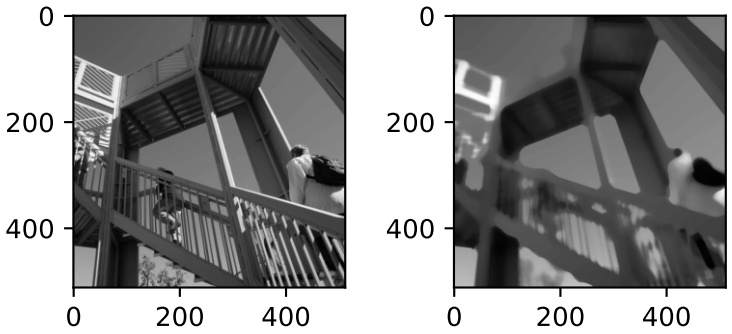
`scipy.signal.medfilt2d`

Notes

For 2-dimensional images with `uint8`, `float32` or `float64` dtypes the specialised function *scipy.signal.medfilt2d* may be faster. It is however limited to constant mode with `cval=0`.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.median_filter(ascent, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.minimum_filter

scipy.ndimage.**minimum_filter**(*input*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a multidimensional minimum filter.

Parameters

input [array_like] The input array.

size [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.

footprint [array, optional] Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2). When *footprint* is given, *size* is ignored.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-constant'
: This is a synonym for 'constant'.

'grid-mirror'
: This is a synonym for 'reflect'.

'grid-wrap'
: This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

minimum_filter
: [ndarray] Filtered array. Has the same shape as *input*.

Notes

A sequence of modes (one per axis) is only supported when the footprint is separable. Otherwise, a single mode string must be provided.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.minimum_filter(ascent, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```

scipy.ndimage.minimum_filter1d

scipy.ndimage.**minimum_filter1d**(*input*, *size*, *axis=- 1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a 1-D minimum filter along the given axis.

The lines of the array along the given axis are filtered with a minimum filter of given size.

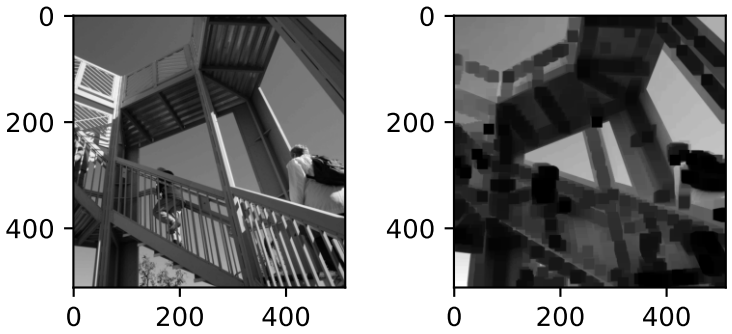
Parameters

input [array_like] The input array.

size [int] length along which to calculate 1D minimum

axis [int, optional] The axis of *input* along which to calculate. Default is -1.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.



mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.

'grid-constant'
This is a synonym for 'constant'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

Notes

This function implements the MINLIST algorithm [1], as described by Richard Harter [2], and has a guaranteed O(n) performance, *n* being the *input* length, regardless of filter size.

References

[1], [2]

Examples

```
>>> from scipy.ndimage import minimum_filter1d
>>> minimum_filter1d([2, 8, 0, 4, 1, 9, 9, 0], size=3)
array([2, 0, 0, 0, 1, 1, 0, 0])
```

scipy.ndimage.percentile_filter

scipy.ndimage.**percentile_filter**(*input*, *percentile*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a multidimensional percentile filter.

Parameters

input [array_like] The input array.

percentile [scalar] The percentile parameter may be less then zero, i.e., percentile = -20 equals percentile = 80

size [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.

footprint [array, optional] Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2). When *footprint* is given, *size* is ignored.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.
'grid-constant'
This is a synonym for 'constant'.
'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

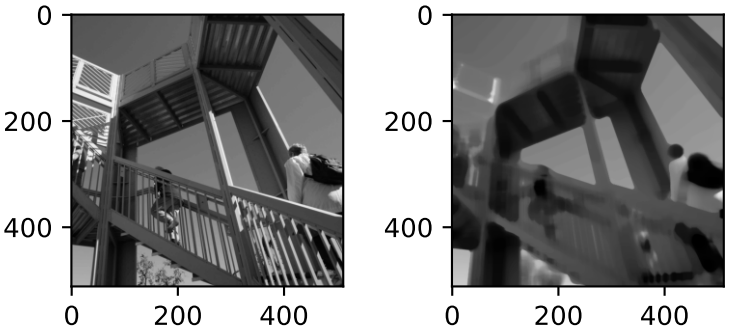
origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

percentile_filter
[ndarray] Filtered array. Has the same shape as *input*.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.percentile_filter(ascent, percentile=20, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.prewitt

scipy.ndimage.**prewitt**(*input*, *axis=- 1*, *output=None*, *mode='reflect'*, *cval=0.0*)

Calculate a Prewitt filter.

Parameters

input [array_like] The input array.

axis [int, optional] The axis of *input* along which to calculate. Default is -1.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-constant'
This is a synonym for 'constant'.

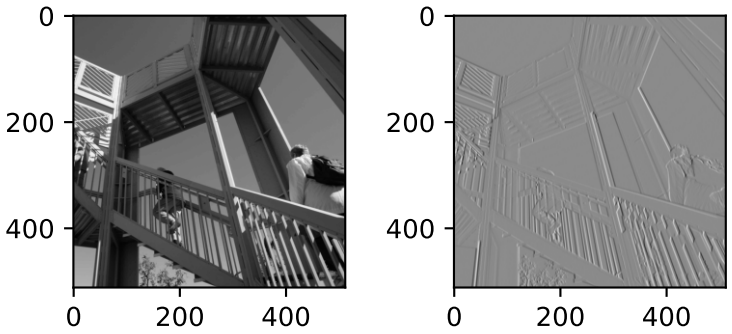
'grid-mirror'
This is a synonym for 'reflect'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.prewitt(ascent)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.rank_filter

scipy.ndimage.**rank_filter**(*input*, *rank*, *size=None*, *footprint=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a multidimensional rank filter.

Parameters

input [array_like] The input array.

rank [int] The rank parameter may be less then zero, i.e., rank = -1 indicates the largest element.

size [scalar or tuple, optional] See footprint, below. Ignored if footprint is given.

footprint [array, optional] Either *size* or *footprint* must be defined. *size* gives the shape that is taken from the input array, at every element position, to define the input to the filter function. *footprint* is a boolean array that specifies (implicitly) a shape, but also which of the elements within this shape will get passed to the filter function. Thus `size=(n,m)` is equivalent to `footprint=np.ones((n,m))`. We adjust *size* to the number of dimensions of the input array, so that, if the input array is shape (10,10,10), and *size* is 2, then the actual size used is (2,2,2). When *footprint* is given, *size* is ignored.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
: This is a synonym for 'reflect'.

'grid-constant'
: This is a synonym for 'constant'.

'grid-wrap'
: This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

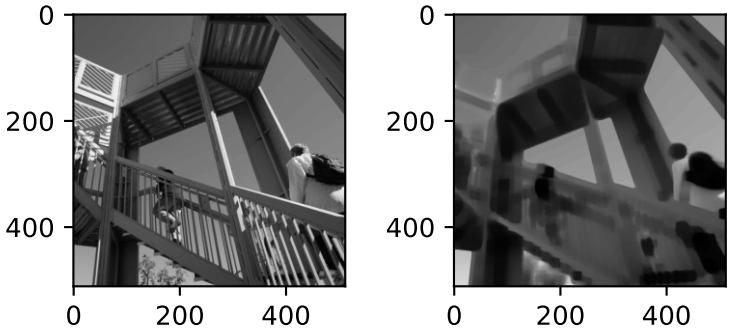
origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

rank_filter
: [ndarray] Filtered array. Has the same shape as *input*.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.rank_filter(ascent, rank=42, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.sobel

scipy.ndimage.**sobel**(*input*, *axis=- 1*, *output=None*, *mode='reflect'*, *cval=0.0*)

Calculate a Sobel filter.

Parameters

input [array_like] The input array.

axis [int, optional] The axis of *input* along which to calculate. Default is -1.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-constant'
This is a synonym for 'constant'.

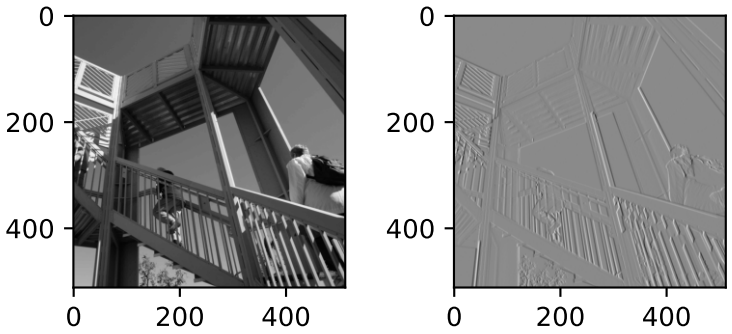
'grid-mirror'
This is a synonym for 'reflect'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.sobel(ascent)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.uniform_filter

scipy.ndimage.**uniform_filter**(*input*, *size=3*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional uniform filter.

Parameters

input [array_like] The input array.

size [int or sequence of ints, optional] The sizes of the uniform filter are given for each axis as a sequence, or as a single number, in which case the size is equal for all axes.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [str or sequence, optional] The *mode* parameter determines how the input array is extended when the filter overlaps a border. By passing a sequence of modes with length equal to the number of dimensions of the input array, different modes can be specified along each axis. Default value is 'reflect'. The valid values and their behavior is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-constant'
This is a synonym for 'constant'.

'grid-mirror'
This is a synonym for 'reflect'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int or sequence, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right. By passing a sequence of origins with length equal to the number of dimensions of the input array, different shifts can be specified along each axis.

Returns

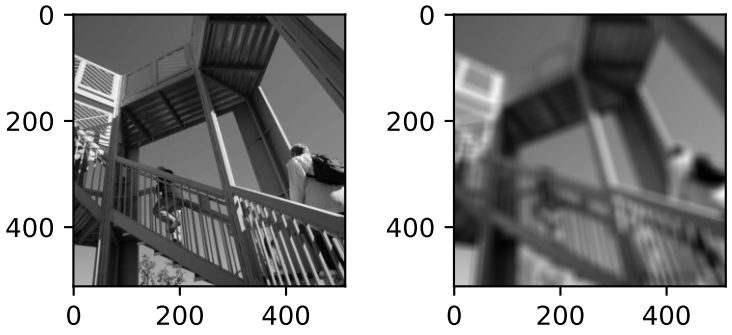
uniform_filter
[ndarray] Filtered array. Has the same shape as *input*.

Notes

The multidimensional filter is implemented as a sequence of 1-D uniform filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> plt.gray()  # show the filtered result in grayscale
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.uniform_filter(ascent, size=20)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result)
>>> plt.show()
```



scipy.ndimage.uniform_filter1d

scipy.ndimage.**uniform_filter1d**(*input*, *size*, *axis=- 1*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a 1-D uniform filter along the given axis.

The lines of the array along the given axis are filtered with a uniform filter of given size.

Parameters

input [array_like] The input array.

size [int] length of uniform filter

axis [int, optional] The axis of *input* along which to calculate. Default is -1.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'reflect'. Behavior for each valid value is as follows:

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

For consistency with the interpolation functions, the following mode names can also be used:

'grid-mirror'
This is a synonym for 'reflect'.

'grid-constant'
This is a synonym for 'constant'.

'grid-wrap'
This is a synonym for 'wrap'.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [int, optional] Controls the placement of the filter on the input array's pixels. A value of 0 (the default) centers the filter over the pixel, with positive values shifting the filter to the left, and negative ones to the right.

Examples

```
>>> from scipy.ndimage import uniform_filter1d
>>> uniform_filter1d([2, 8, 0, 4, 1, 9, 9, 0], size=3)
array([4, 3, 4, 1, 4, 6, 6, 3])
```

Fourier filters

fourier_ellipsoid(input, size[, n, axis, output])	Multidimensional ellipsoid Fourier filter.
fourier_gaussian(input, sigma[, n, axis, output])	Multidimensional Gaussian fourier filter.
fourier_shift(input, shift[, n, axis, output])	Multidimensional Fourier shift filter.
fourier_uniform(input, size[, n, axis, output])	Multidimensional uniform fourier filter.

scipy.ndimage.fourier_ellipsoid

scipy.ndimage.**fourier_ellipsoid**(*input*, *size*, *n=- 1*, *axis=- 1*, *output=None*)

Multidimensional ellipsoid Fourier filter.

The array is multiplied with the fourier transform of a ellipsoid of given sizes.

Parameters

input [array_like] The input array.

size [float or sequence] The size of the box used for filtering. If a float, *size* is the same for all axes. If a sequence, *size* has to contain one value for each axis.

n [int, optional] If *n* is negative (default), then the input is assumed to be the result of a complex fft. If *n* is larger than or equal to zero, the input is assumed to be the result of a real fft, and *n* gives the length of the array before transformation along the real transform direction.

axis [int, optional] The axis of the real transform.

output [ndarray, optional] If given, the result of filtering the input is placed in this array. None is returned in this case.

Returns

fourier_ellipsoid

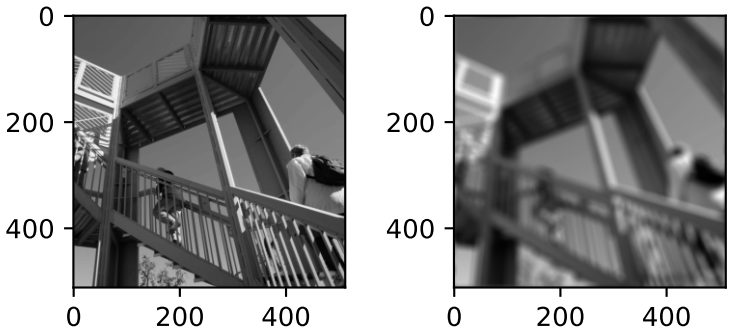
[ndarray] The filtered input.

Notes

This function is implemented for arrays of rank 1, 2, or 3.

Examples

```
>>> from scipy import ndimage, misc
>>> import numpy.fft
>>> import matplotlib.pyplot as plt
>>> fig, (ax1, ax2) = plt.subplots(1, 2)
>>> plt.gray()  # show the filtered result in grayscale
>>> ascent = misc.ascent()
>>> input_ = numpy.fft.fft2(ascent)
>>> result = ndimage.fourier_ellipsoid(input_, size=20)
>>> result = numpy.fft.ifft2(result)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result.real)  # the imaginary part is an artifact
>>> plt.show()
```



scipy.ndimage.fourier_gaussian

scipy.ndimage.**fourier_gaussian**(*input*, *sigma*, *n=- 1*, *axis=- 1*, *output=None*)

Multidimensional Gaussian fourier filter.

The array is multiplied with the fourier transform of a Gaussian kernel.

Parameters

input [array_like] The input array.

sigma [float or sequence] The sigma of the Gaussian kernel. If a float, *sigma* is the same for all axes. If a sequence, *sigma* has to contain one value for each axis.

n [int, optional] If *n* is negative (default), then the input is assumed to be the result of a complex fft. If *n* is larger than or equal to zero, the input is assumed to be the result of a real fft, and *n* gives the length of the array before transformation along the real transform direction.

axis [int, optional] The axis of the real transform.

output [ndarray, optional] If given, the result of filtering the input is placed in this array. None is returned in this case.

Returns

fourier_gaussian

[ndarray] The filtered input.

Examples

```
>>> from scipy import ndimage, misc
>>> import numpy.fft
>>> import matplotlib.pyplot as plt
>>> fig, (ax1, ax2) = plt.subplots(1, 2)
>>> plt.gray()  # show the filtered result in grayscale
>>> ascent = misc.ascent()
>>> input_ = numpy.fft.fft2(ascent)
>>> result = ndimage.fourier_gaussian(input_, sigma=4)
>>> result = numpy.fft.ifft2(result)
```

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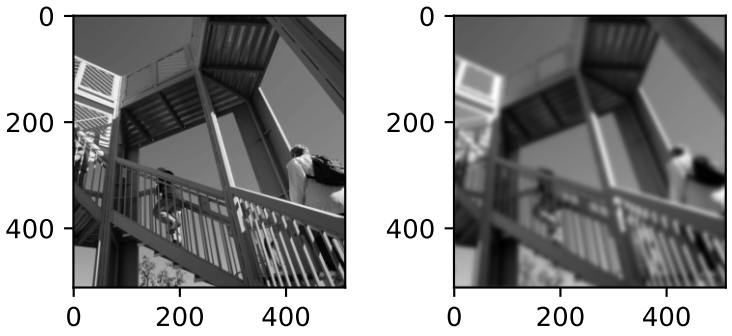
```
>>> ax1.imshow(ascent)
>>> ax2.imshow(result.real)  # the imaginary part is an artifact
>>> plt.show()
```



scipy.ndimage.fourier_shift

scipy.ndimage.**fourier_shift**(*input*, *shift*, *n=- 1*, *axis=- 1*, *output=None*)

Multidimensional Fourier shift filter.

The array is multiplied with the Fourier transform of a shift operation.

Parameters

input [array_like] The input array.

shift [float or sequence] The size of the box used for filtering. If a float, `shift` is the same for all axes. If a sequence, `shift` has to contain one value for each axis.

n [int, optional] If *n* is negative (default), then the input is assumed to be the result of a complex fft. If *n* is larger than or equal to zero, the input is assumed to be the result of a real fft, and *n* gives the length of the array before transformation along the real transform direction.

axis [int, optional] The axis of the real transform.

output [ndarray, optional] If given, the result of shifting the input is placed in this array. None is returned in this case.

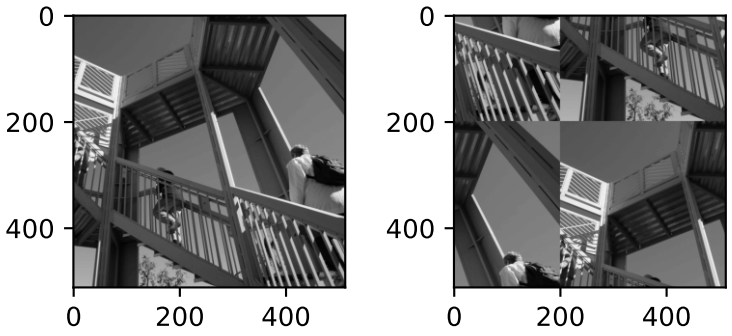
Returns

fourier_shift

[ndarray] The shifted input.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> import numpy.fft
>>> fig, (ax1, ax2) = plt.subplots(1, 2)
>>> plt.gray()  # show the filtered result in grayscale
>>> ascent = misc.ascent()
>>> input_ = numpy.fft.fft2(ascent)
>>> result = ndimage.fourier_shift(input_, shift=200)
>>> result = numpy.fft.ifft2(result)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result.real)  # the imaginary part is an artifact
>>> plt.show()
```



scipy.ndimage.fourier_uniform

scipy.ndimage.**fourier_uniform**(*input*, *size*, *n=- 1*, *axis=- 1*, *output=None*)

Multidimensional uniform fourier filter.

The array is multiplied with the Fourier transform of a box of given size.

Parameters

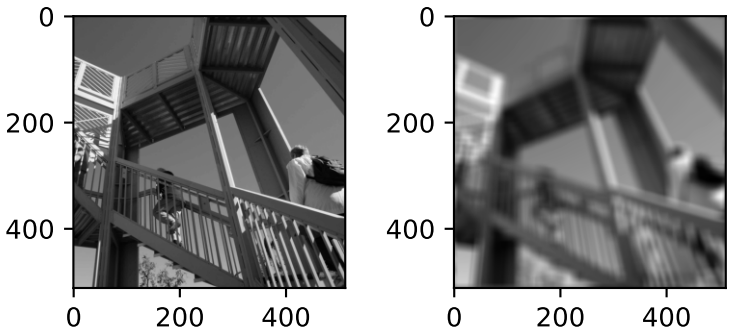
input	[array_like] The input array.
size	[float or sequence] The size of the box used for filtering. If a float, *size* is the same for all axes. If a sequence, *size* has to contain one value for each axis.
n	[int, optional] If *n* is negative (default), then the input is assumed to be the result of a complex fft. If *n* is larger than or equal to zero, the input is assumed to be the result of a real fft, and *n* gives the length of the array before transformation along the real transform direction.
axis	[int, optional] The axis of the real transform.
output	[ndarray, optional] If given, the result of filtering the input is placed in this array. None is returned in this case.

Returns

fourier_uniform
[ndarray] The filtered input.

Examples

```
>>> from scipy import ndimage, misc
>>> import numpy.fft
>>> import matplotlib.pyplot as plt
>>> fig, (ax1, ax2) = plt.subplots(1, 2)
>>> plt.gray()  # show the filtered result in grayscale
>>> ascent = misc.ascent()
>>> input_ = numpy.fft.fft2(ascent)
>>> result = ndimage.fourier_uniform(input_, size=20)
>>> result = numpy.fft.ifft2(result)
>>> ax1.imshow(ascent)
>>> ax2.imshow(result.real)  # the imaginary part is an artifact
>>> plt.show()
```



Interpolation

affine_transform(input, matrix[, offset, …])	Apply an affine transformation.
geometric_transform(input, mapping[, …])	Apply an arbitrary geometric transform.
map_coordinates(input, coordinates[, …])	Map the input array to new coordinates by interpolation.
rotate(input, angle[, axes, reshape, …])	Rotate an array.
shift(input, shift[, output, order, mode, …])	Shift an array.
spline_filter(input[, order, output, mode])	Multidimensional spline filter.
spline_filter1d(input[, order, axis, …])	Calculate a 1-D spline filter along the given axis.
zoom(input, zoom[, output, order, mode, …])	Zoom an array.

scipy.ndimage.affine_transform

scipy.ndimage.**affine_transform**(*input*, *matrix*, *offset=0.0*, *output_shape=None*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Apply an affine transformation.

Given an output image pixel index vector `o`, the pixel value is determined from the input image at position `np.dot(matrix, o) + offset`.

This does 'pull' (or 'backward') resampling, transforming the output space to the input to locate data. Affine transformations are often described in the 'push' (or 'forward') direction, transforming input to output. If you have a matrix for the 'push' transformation, use its inverse (`numpy.linalg.inv`) in this function.

Parameters

input [array_like] The input array.

matrix [ndarray] The inverse coordinate transformation matrix, mapping output coordinates to input coordinates. If `ndim` is the number of dimensions of `input`, the given matrix must have one of the following shapes:

- `(ndim, ndim)`: the linear transformation matrix for each output coordinate.
- `(ndim,)`: assume that the 2-D transformation matrix is diagonal, with the diagonal specified by the given value. A more efficient algorithm is then used that exploits the separability of the problem.
- `(ndim + 1, ndim + 1)`: assume that the transformation is specified using homogeneous coordinates [1]. In this case, any value passed to `offset` is ignored.
- `(ndim, ndim + 1)`: as above, but the bottom row of a homogeneous transformation matrix is always `[0, 0, ..., 1]`, and may be omitted.

offset [float or sequence, optional] The offset into the array where the transform is applied. If a float, *offset* is the same for each axis. If a sequence, *offset* should contain one value for each axis.

output_shape [tuple of ints, optional] Shape tuple.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

order [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode [{'reflect', 'grid-mirror', 'constant', 'grid-constant', 'nearest', 'mirror', 'grid-wrap', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows (see additional plots and details on *boundary modes*):

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'grid-mirror'
This is a synonym for 'reflect'.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. No interpolation is performed beyond the edges of the input.

'grid-constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. Interpolation occurs for samples outside the input's extent as well.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.
'grid-wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.
'wrap' (*d b c d | a b c d | b c a b*)
The input is extended by wrapping around to the opposite edge, but in a way such that the last point and initial point exactly overlap. In this case it is not well defined which sample will be chosen at the point of overlap.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

prefilter [bool, optional] Determines if the input array is prefiltered with `spline_filter` before interpolation. The default is True, which will create a temporary *float64* array of filtered values if *order* > *1*. If setting this to False, the output will be slightly blurred if *order* > *1*, unless the input is prefiltered, i.e. it is the result of calling `spline_filter` on the original input.

Returns

affine_transform
[ndarray] The transformed input.

Notes

The given matrix and offset are used to find for each point in the output the corresponding coordinates in the input by an affine transformation. The value of the input at those coordinates is determined by spline interpolation of the requested order. Points outside the boundaries of the input are filled according to the given mode.

Changed in version 0.18.0: Previously, the exact interpretation of the affine transformation depended on whether the matrix was supplied as a 1-D or a 2-D array. If a 1-D array was supplied to the matrix parameter, the output pixel value at index `o` was determined from the input image at position `matrix * (o + offset)`.

For complex-valued *input*, this function transforms the real and imaginary components independently.

New in version 1.6.0: Complex-valued support added.

References

[1]

scipy.ndimage.geometric_transform

`scipy.ndimage.`**`geometric_transform`**(*input*, *mapping*, *output_shape=None*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*, *extra_arguments=()*, *extra_keywords={}*)

Apply an arbitrary geometric transform.

The given mapping function is used to find, for each point in the output, the corresponding coordinates in the input. The value of the input at those coordinates is determined by spline interpolation of the requested order.

Parameters

input [array_like] The input array.

mapping [{callable, scipy.LowLevelCallable}] A callable object that accepts a tuple of length equal to the output array rank, and returns the corresponding input coordinates as a tuple of length equal to the input array rank.

output_shape
[tuple of ints, optional] Shape tuple.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

order [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode [{'reflect', 'grid-mirror', 'constant', 'grid-constant', 'nearest', 'mirror', 'grid-wrap', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows (see additional plots and details on *boundary modes*):

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'grid-mirror'
This is a synonym for 'reflect'.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. No interpolation is performed beyond the edges of the input.

'grid-constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. Interpolation occurs for samples outside the input's extent as well.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'grid-wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

'wrap' (*d b c d | a b c d | b c a b*)
The input is extended by wrapping around to the opposite edge, but in a way such that the last point and initial point exactly overlap. In this case it is not well defined which sample will be chosen at the point of overlap.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

prefilter [bool, optional] Determines if the input array is prefiltered with `spline_filter` before interpolation. The default is True, which will create a temporary *float64* array of filtered values if *order > 1*. If setting this to False, the output will be slightly blurred if *order > 1*, unless the input is prefiltered, i.e. it is the result of calling `spline_filter` on the original input.

extra_arguments
[tuple, optional] Extra arguments passed to *mapping*.

extra_keywords
[dict, optional] Extra keywords passed to *mapping*.

Returns

output [ndarray] The filtered input.

See also:

`map_coordinates`, `affine_transform`, `spline_filter1d`

Notes

This function also accepts low-level callback functions with one the following signatures and wrapped in *scipy.LowLevelCallable*:

```
int mapping(npy_intp *output_coordinates, double *input_coordinates,
            int output_rank, int input_rank, void *user_data)
int mapping(intptr_t *output_coordinates, double *input_coordinates,
            int output_rank, int input_rank, void *user_data)
```

The calling function iterates over the elements of the output array, calling the callback function at each element. The coordinates of the current output element are passed through `output_coordinates`. The callback function must return the coordinates at which the input must be interpolated in `input_coordinates`. The rank of the input and output arrays are given by `input_rank` and `output_rank` respectively. `user_data` is the data pointer provided to *scipy.LowLevelCallable* as-is.

The callback function must return an integer error status that is zero if something went wrong and one otherwise. If an error occurs, you should normally set the Python error status with an informative message before returning, otherwise a default error message is set by the calling function.

In addition, some other low-level function pointer specifications are accepted, but these are for backward compatibility only and should not be used in new code.

For complex-valued *input*, this function transforms the real and imaginary components independently.

New in version 1.6.0: Complex-valued support added.

Examples

```
>>> import numpy as np
>>> from scipy.ndimage import geometric_transform
>>> a = np.arange(12.).reshape((4, 3))
>>> def shift_func(output_coords):
...     return (output_coords[0] - 0.5, output_coords[1] - 0.5)
...
>>> geometric_transform(a, shift_func)
array([[ 0.   ,  0.   ,  0.   ],
       [ 0.   ,  1.362,  2.738],
       [ 0.   ,  4.812,  6.187],
       [ 0.   ,  8.263,  9.637]])
```

```
>>> b = [1, 2, 3, 4, 5]
>>> def shift_func(output_coords):
...     return (output_coords[0] - 3,)
...
>>> geometric_transform(b, shift_func, mode='constant')
array([0, 0, 0, 1, 2])
>>> geometric_transform(b, shift_func, mode='nearest')
array([1, 1, 1, 1, 2])
>>> geometric_transform(b, shift_func, mode='reflect')
array([3, 2, 1, 1, 2])
>>> geometric_transform(b, shift_func, mode='wrap')
array([2, 3, 4, 1, 2])
```

scipy.ndimage.map_coordinates

scipy.ndimage.**map_coordinates**(*input*, *coordinates*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Map the input array to new coordinates by interpolation.

The array of coordinates is used to find, for each point in the output, the corresponding coordinates in the input. The value of the input at those coordinates is determined by spline interpolation of the requested order.

The shape of the output is derived from that of the coordinate array by dropping the first axis. The values of the array along the first axis are the coordinates in the input array at which the output value is found.

Parameters

input [array_like] The input array.

coordinates [array_like] The coordinates at which *input* is evaluated.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

order [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode [{'reflect', 'grid-mirror', 'constant', 'grid-constant', 'nearest', 'mirror', 'grid-wrap', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows (see additional plots and details on *boundary modes*):

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'grid-mirror'
This is a synonym for 'reflect'.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. No interpolation is performed beyond the edges of the input.

'grid-constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. Interpolation occurs for samples outside the input's extent as well.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'grid-wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

'wrap' (*d b c d | a b c d | b c a b*)
The input is extended by wrapping around to the opposite edge, but in a way such that the last point and initial point exactly overlap. In this case it is not well defined which sample will be chosen at the point of overlap.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

prefilter [bool, optional] Determines if the input array is prefiltered with `spline_filter` before interpolation. The default is True, which will create a temporary *float64* array of filtered values if *order* > *1*. If setting this to False, the output will be slightly blurred if *order* > *1*, unless the input is prefiltered, i.e. it is the result of calling `spline_filter` on the original input.

Returns

map_coordinates
[ndarray] The result of transforming the input. The shape of the output is derived from that of *coordinates* by dropping the first axis.

See also:

spline_filter, **geometric_transform**, **scipy.interpolate**

Notes

For complex-valued *input*, this function maps the real and imaginary components independently.

New in version 1.6.0: Complex-valued support added.

Examples

```
>>> from scipy import ndimage
>>> a = np.arange(12.).reshape((4, 3))
>>> a
array([[  0.,   1.,   2.],
       [  3.,   4.,   5.],
       [  6.,   7.,   8.],
       [  9.,  10.,  11.]])
>>> ndimage.map_coordinates(a, [[0.5, 2], [0.5, 1]], order=1)
array([ 2.,  7.])
```

Above, the interpolated value of a[0.5, 0.5] gives output[0], while a[2, 1] is output[1].

```
>>> inds = np.array([[0.5, 2], [0.5, 4]])
>>> ndimage.map_coordinates(a, inds, order=1, cval=-33.3)
array([  2. , -33.3])
>>> ndimage.map_coordinates(a, inds, order=1, mode='nearest')
array([ 2.,  8.])
>>> ndimage.map_coordinates(a, inds, order=1, cval=0, output=bool)
array([ True, False], dtype=bool)
```

scipy.ndimage.rotate

scipy.ndimage.**rotate**(*input*, *angle*, *axes=(1, 0)*, *reshape=True*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Rotate an array.

The array is rotated in the plane defined by the two axes given by the *axes* parameter using spline interpolation of the requested order.

Parameters

input [array_like] The input array.
angle [float] The rotation angle in degrees.
axes [tuple of 2 ints, optional] The two axes that define the plane of rotation. Default is the first two axes.
reshape [bool, optional] If *reshape* is true, the output shape is adapted so that the input array is contained completely in the output. Default is True.
output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

order [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode [{'reflect', 'grid-mirror', 'constant', 'grid-constant', 'nearest', 'mirror', 'grid-wrap', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows (see additional plots and details on *boundary modes*):

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'grid-mirror'
This is a synonym for 'reflect'.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. No interpolation is performed beyond the edges of the input.

'grid-constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. Interpolation occurs for samples outside the input's extent as well.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'grid-wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

'wrap' (*d b c d | a b c d | b c a b*)
The input is extended by wrapping around to the opposite edge, but in a way such that the last point and initial point exactly overlap. In this case it is not well defined which sample will be chosen at the point of overlap.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

prefilter [bool, optional] Determines if the input array is prefiltered with `spline_filter` before interpolation. The default is True, which will create a temporary *float64* array of filtered values if *order* > *1*. If setting this to False, the output will be slightly blurred if *order* > *1*, unless the input is prefiltered, i.e. it is the result of calling `spline_filter` on the original input.

Returns

rotate [ndarray] The rotated input.

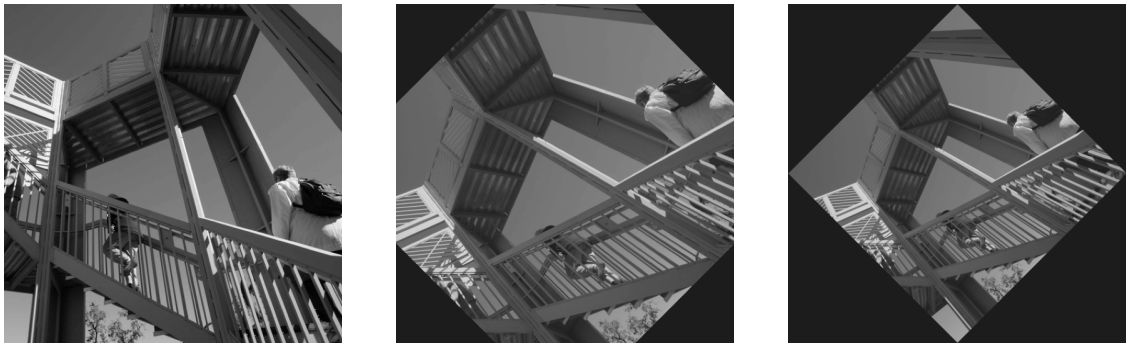
Notes

For complex-valued *input*, this function rotates the real and imaginary components independently.

New in version 1.6.0: Complex-valued support added.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure(figsize=(10, 3))
>>> ax1, ax2, ax3 = fig.subplots(1, 3)
>>> img = misc.ascent()
>>> img_45 = ndimage.rotate(img, 45, reshape=False)
>>> full_img_45 = ndimage.rotate(img, 45, reshape=True)
>>> ax1.imshow(img, cmap='gray')
>>> ax1.set_axis_off()
>>> ax2.imshow(img_45, cmap='gray')
>>> ax2.set_axis_off()
>>> ax3.imshow(full_img_45, cmap='gray')
>>> ax3.set_axis_off()
>>> fig.set_tight_layout(True)
>>> plt.show()
```



```
>>> print(img.shape)
(512, 512)
>>> print(img_45.shape)
(512, 512)
>>> print(full_img_45.shape)
(724, 724)
```

scipy.ndimage.shift

scipy.ndimage.**shift**(*input*, *shift*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*)

Shift an array.

The array is shifted using spline interpolation of the requested order. Points outside the boundaries of the input are filled according to the given mode.

Parameters

input [array_like] The input array.

shift [float or sequence] The shift along the axes. If a float, *shift* is the same for each axis. If a sequence, *shift* should contain one value for each axis.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

order [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode [{'reflect', 'grid-mirror', 'constant', 'grid-constant', 'nearest', 'mirror', 'grid-wrap', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows (see additional plots and details on *boundary modes*):

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'grid-mirror'
This is a synonym for 'reflect'.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. No interpolation is performed beyond the edges of the input.

'grid-constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. Interpolation occurs for samples outside the input's extent as well.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'grid-wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

'wrap' (*d b c d | a b c d | b c a b*)
The input is extended by wrapping around to the opposite edge, but in a way such that the last point and initial point exactly overlap. In this case it is not well defined which sample will be chosen at the point of overlap.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

prefilter [bool, optional] Determines if the input array is prefiltered with `spline_filter` before interpolation. The default is True, which will create a temporary *float64* array of filtered values if *order > 1*. If setting this to False, the output will be slightly blurred if *order > 1*, unless the input is prefiltered, i.e. it is the result of calling `spline_filter` on the original input.

Returns

shift [ndarray] The shifted input.

Notes

For complex-valued *input*, this function shifts the real and imaginary components independently.

New in version 1.6.0: Complex-valued support added.

scipy.ndimage.spline_filter

scipy.ndimage.**spline_filter**(*input*, *order=3*, *output=<class 'numpy.float64'>*, *mode='mirror'*)

Multidimensional spline filter.

For more details, see *spline_filter1d*.

See also:

spline_filter1d

Calculate a 1-D spline filter along the given axis.

Notes

The multidimensional filter is implemented as a sequence of 1-D spline filters. The intermediate arrays are stored in the same data type as the output. Therefore, for output types with a limited precision, the results may be imprecise because intermediate results may be stored with insufficient precision.

For complex-valued *input*, this function processes the real and imaginary components independently.

New in version 1.6.0: Complex-valued support added.

Examples

We can filter an image using multidimentional splines:

```
>>> from scipy.ndimage import spline_filter
>>> import matplotlib.pyplot as plt
>>> orig_img = np.eye(20)  # create an image
>>> orig_img[10, :] = 1.0
>>> sp_filter = spline_filter(orig_img, order=3)
>>> f, ax = plt.subplots(1, 2, sharex=True)
>>> for ind, data in enumerate([[orig_img, "original image"],
...                             [sp_filter, "spline filter"]]):
...     ax[ind].imshow(data[0], cmap='gray_r')
...     ax[ind].set_title(data[1])
>>> plt.tight_layout()
>>> plt.show()
```

scipy.ndimage.spline_filter1d

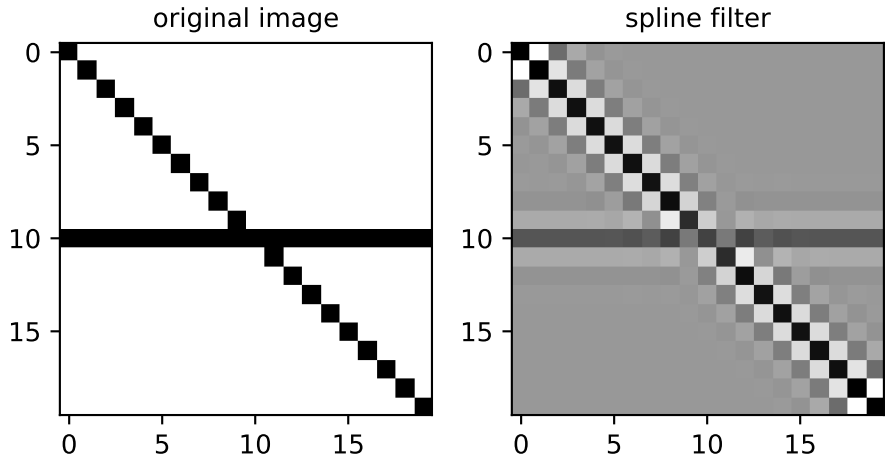
scipy.ndimage.**spline_filter1d**(*input*, *order=3*, *axis=-1*, *output=<class 'numpy.float64'>*, *mode='mirror'*)

Calculate a 1-D spline filter along the given axis.

The lines of the array along the given axis are filtered by a spline filter. The order of the spline must be >= 2 and <= 5.

Parameters

input	[array_like] The input array.
order	[int, optional] The order of the spline, default is 3.
axis	[int, optional] The axis along which the spline filter is applied. Default is the last axis.
output	[ndarray or dtype, optional] The array in which to place the output, or the dtype of the returned array. Default is `numpy.float64`.



mode [{'reflect', 'grid-mirror', 'constant', 'grid-constant', 'nearest', 'mirror', 'grid-wrap', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'mirror'. Behavior for each valid value is as follows (see additional plots and details on *boundary modes*):

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'grid-mirror'
This is a synonym for 'reflect'.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. No interpolation is performed beyond the edges of the input.

'grid-constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. Interpolation occurs for samples outside the input's extent as well.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'grid-wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

'wrap' (*d b c d | a b c d | b c a b*)
The input is extended by wrapping around to the opposite edge, but in a way such that the last point and initial point exactly overlap. In this case it is not well defined which sample will be chosen at the point of overlap.

Returns

spline_filter1d
[ndarray] The filtered input.

See also:

spline_filter

Multidimensional spline filter.

Notes

All functions in *ndimage.interpolation* do spline interpolation of the input image. If using B-splines of *order* > *1*, the input image values have to be converted to B-spline coefficients first, which is done by applying this 1-D filter sequentially along all axes of the input. All functions that require B-spline coefficients will automatically filter their inputs, a behavior controllable with the *prefilter* keyword argument. For functions that accept a *mode* parameter, the result will only be correct if it matches the *mode* used when filtering.

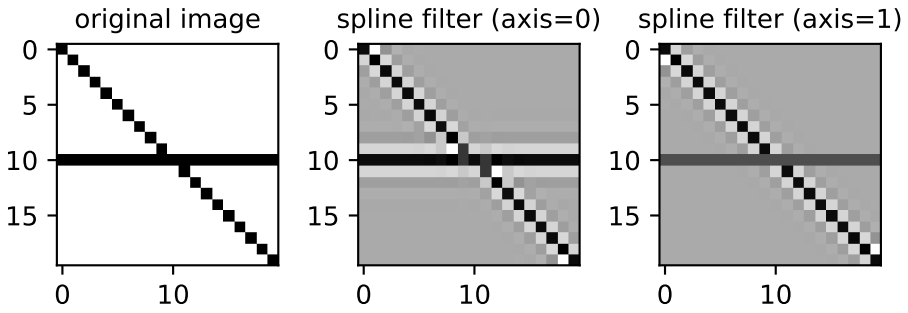
For complex-valued *input*, this function processes the real and imaginary components independently.

New in version 1.6.0: Complex-valued support added.

Examples

We can filter an image using 1-D spline along the given axis:

```
>>> from scipy.ndimage import spline_filter1d
>>> import matplotlib.pyplot as plt
>>> orig_img = np.eye(20)  # create an image
>>> orig_img[10, :] = 1.0
>>> sp_filter_axis_0 = spline_filter1d(orig_img, axis=0)
>>> sp_filter_axis_1 = spline_filter1d(orig_img, axis=1)
>>> f, ax = plt.subplots(1, 3, sharex=True)
>>> for ind, data in enumerate([[orig_img, "original image"],
...                             [sp_filter_axis_0, "spline filter (axis=0)"],
...                             [sp_filter_axis_1, "spline filter (axis=1)"]]):
...     ax[ind].imshow(data[0], cmap='gray_r')
...     ax[ind].set_title(data[1])
>>> plt.tight_layout()
>>> plt.show()
```



scipy.ndimage.zoom

scipy.ndimage.**zoom**(*input*, *zoom*, *output=None*, *order=3*, *mode='constant'*, *cval=0.0*, *prefilter=True*, ***, *grid_mode=False*)

Zoom an array.

The array is zoomed using spline interpolation of the requested order.

Parameters

input [array_like] The input array.

zoom [float or sequence] The zoom factor along the axes. If a float, *zoom* is the same for each axis. If a sequence, *zoom* should contain one value for each axis.

output [array or dtype, optional] The array in which to place the output, or the dtype of the returned array. By default an array of the same dtype as input will be created.

order [int, optional] The order of the spline interpolation, default is 3. The order has to be in the range 0-5.

mode [{'reflect', 'grid-mirror', 'constant', 'grid-constant', 'nearest', 'mirror', 'grid-wrap', 'wrap'}, optional] The *mode* parameter determines how the input array is extended beyond its boundaries. Default is 'constant'. Behavior for each valid value is as follows (see additional plots and details on *boundary modes*):

'reflect' (*d c b a | a b c d | d c b a*)
The input is extended by reflecting about the edge of the last pixel. This mode is also sometimes referred to as half-sample symmetric.

'grid-mirror'
This is a synonym for 'reflect'.

'constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. No interpolation is performed beyond the edges of the input.

'grid-constant' (*k k k k | a b c d | k k k k*)
The input is extended by filling all values beyond the edge with the same constant value, defined by the *cval* parameter. Interpolation occurs for samples outside the input's extent as well.

'nearest' (*a a a a | a b c d | d d d d*)
The input is extended by replicating the last pixel.

'mirror' (*d c b | a b c d | c b a*)
The input is extended by reflecting about the center of the last pixel. This mode is also sometimes referred to as whole-sample symmetric.

'grid-wrap' (*a b c d | a b c d | a b c d*)
The input is extended by wrapping around to the opposite edge.

'wrap' (*d b c d | a b c d | b c a b*)
The input is extended by wrapping around to the opposite edge, but in a way such that the last point and initial point exactly overlap. In this case it is not well defined which sample will be chosen at the point of overlap.

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

prefilter [bool, optional] Determines if the input array is prefiltered with *spline_filter* before interpolation. The default is True, which will create a temporary *float64* array of filtered values if *order > 1*. If setting this to False, the output will be slightly blurred if *order > 1*, unless the input is prefiltered, i.e. it is the result of calling *spline_filter* on the original input.

grid_mode
[bool, optional] If False, the distance from the pixel centers is zoomed. Otherwise, the distance including the full pixel extent is used. For example, a 1d signal of length 5 is considered to have length 4 when *grid_mode* is False, but length 5 when *grid_mode* is True. See the following visual illustration:

```
| pixel 1 | pixel 2 | pixel 3 | pixel 4 | pixel 5 |
     |<-------------------------------------->|
                          vs.
|<----------------------------------------------->|
```

The starting point of the arrow in the diagram above corresponds to coordinate location 0 in each mode.

Returns

zoom [ndarray] The zoomed input.

Notes

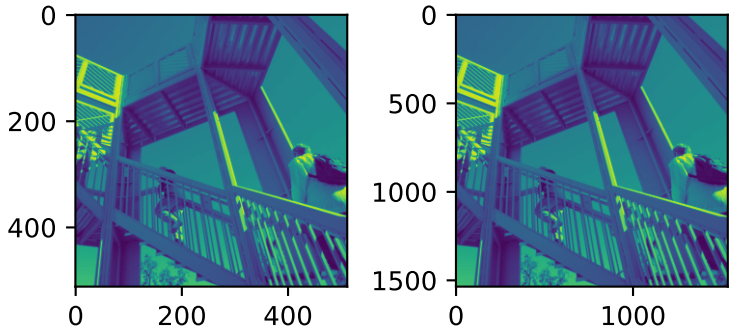
For complex-valued *input*, this function zooms the real and imaginary components independently.

New in version 1.6.0: Complex-valued support added.

Examples

```
>>> from scipy import ndimage, misc
>>> import matplotlib.pyplot as plt
```

```
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(121)  # left side
>>> ax2 = fig.add_subplot(122)  # right side
>>> ascent = misc.ascent()
>>> result = ndimage.zoom(ascent, 3.0)
>>> ax1.imshow(ascent, vmin=0, vmax=255)
>>> ax2.imshow(result, vmin=0, vmax=255)
>>> plt.show()
```



```
>>> print(ascent.shape)
(512, 512)
```

```
>>> print(result.shape)
(1536, 1536)
```

Measurements

center_of_mass(input[, labels, index])	Calculate the center of mass of the values of an array at labels.
extrema(input[, labels, index])	Calculate the minimums and maximums of the values of an array at labels, along with their positions.
find_objects(input[, max_label])	Find objects in a labeled array.
histogram(input, min, max, bins[, labels, index])	Calculate the histogram of the values of an array, optionally at labels.
label(input[, structure, output])	Label features in an array.
labeled_comprehension(input, labels, index, …)	Roughly equivalent to [func(input[labels == i]) for i in index].
maximum(input[, labels, index])	Calculate the maximum of the values of an array over labeled regions.
maximum_position(input[, labels, index])	Find the positions of the maximums of the values of an array at labels.
mean(input[, labels, index])	Calculate the mean of the values of an array at labels.
median(input[, labels, index])	Calculate the median of the values of an array over labeled regions.
minimum(input[, labels, index])	Calculate the minimum of the values of an array over labeled regions.
minimum_position(input[, labels, index])	Find the positions of the minimums of the values of an array at labels.
standard_deviation(input[, labels, index])	Calculate the standard deviation of the values of an N-D image array, optionally at specified sub-regions.
sum_labels(input[, labels, index])	Calculate the sum of the values of the array.
variance(input[, labels, index])	Calculate the variance of the values of an N-D image array, optionally at specified sub-regions.
watershed_ift(input, markers[, structure, …])	Apply watershed from markers using image foresting transform algorithm.

scipy.ndimage.center_of_mass

scipy.ndimage.**center_of_mass**(*input*, *labels=None*, *index=None*)

Calculate the center of mass of the values of an array at labels.

Parameters

input [ndarray] Data from which to calculate center-of-mass. The masses can either be positive or negative.

labels [ndarray, optional] Labels for objects in *input*, as generated by *ndimage.label*. Only used with *index*. Dimensions must be the same as *input*.

index [int or sequence of ints, optional] Labels for which to calculate centers-of-mass. If not specified, all labels greater than zero are used. Only used with *labels*.

Returns

center_of_mass
[tuple, or list of tuples] Coordinates of centers-of-mass.

Examples

```
>>> a = np.array(([0,0,0,0],
...               [0,1,1,0],
...               [0,1,1,0],
...               [0,1,1,0]))
>>> from scipy import ndimage
>>> ndimage.measurements.center_of_mass(a)
(2.0, 1.5)
```

Calculation of multiple objects in an image

```
>>> b = np.array(([0,1,1,0],
...               [0,1,0,0],
...               [0,0,0,0],
...               [0,0,1,1],
...               [0,0,1,1]))
>>> lbl = ndimage.label(b)[0]
>>> ndimage.measurements.center_of_mass(b, lbl, [1,2])
[(0.33333333333333331, 1.3333333333333333), (3.5, 2.5)]
```

Negative masses are also accepted, which can occur for example when bias is removed from measured data due to random noise.

```
>>> c = np.array(([-1,0,0,0],
...               [0,-1,-1,0],
...               [0,1,-1,0],
...               [0,1,1,0]))
>>> ndimage.measurements.center_of_mass(c)
(-4.0, 1.0)
```

If there are division by zero issues, the function does not raise an error but rather issues a RuntimeWarning before returning inf and/or NaN.

```
>>> d = np.array([-1, 1])
>>> ndimage.measurements.center_of_mass(d)
(inf,)
```

scipy.ndimage.extrema

scipy.ndimage.**extrema**(*input*, *labels=None*, *index=None*)
Calculate the minimums and maximums of the values of an array at labels, along with their positions.

Parameters

input [ndarray] N-D image data to process.
labels [ndarray, optional] Labels of features in input. If not None, must be same shape as *input*.
index [int or sequence of ints, optional] Labels to include in output. If None (default), all values where non-zero *labels* are used.

Returns

minimums, maximums
: [int or ndarray] Values of minimums and maximums in each feature.

min_positions, max_positions
: [tuple or list of tuples] Each tuple gives the N-D coordinates of the corresponding minimum or maximum.

See also:

`maximum`, `minimum`, `maximum_position`, `minimum_position`, `center_of_mass`

Examples

```
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> ndimage.extrema(a)
(0, 9, (0, 2), (3, 0))
```

Features to process can be specified using *labels* and *index*:

```
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.extrema(a, lbl, index=np.arange(1, nlbl+1))
(array([1, 4, 3]),
 array([5, 7, 9]),
 [(0, 0), (1, 3), (3, 1)],
 [(1, 0), (2, 3), (3, 0)])
```

If no index is given, non-zero *labels* are processed:

```
>>> ndimage.extrema(a, lbl)
(1, 9, (0, 0), (3, 0))
```

scipy.ndimage.find_objects

scipy.ndimage.**find_objects**(*input*, *max_label=0*)
Find objects in a labeled array.

Parameters

input
: [ndarray of ints] Array containing objects defined by different labels. Labels with value 0 are ignored.

max_label
: [int, optional] Maximum label to be searched for in *input*. If max_label is not given, the positions of all objects are returned.

Returns

object_slices
: [list of tuples] A list of tuples, with each tuple containing N slices (with N the dimension of the input array). Slices correspond to the minimal parallelepiped that contains the object. If a number is missing, None is returned instead of a slice.

See also:

`label`, `center_of_mass`

Notes

This function is very useful for isolating a volume of interest inside a 3-D array, that cannot be "seen through".

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((6,6), dtype=int)
>>> a[2:4, 2:4] = 1
>>> a[4, 4] = 1
>>> a[:2, :3] = 2
>>> a[0, 5] = 3
>>> a
array([[2, 2, 2, 0, 0, 3],
       [2, 2, 2, 0, 0, 0],
       [0, 0, 1, 1, 0, 0],
       [0, 0, 1, 1, 0, 0],
       [0, 0, 0, 0, 1, 0],
       [0, 0, 0, 0, 0, 0]])
>>> ndimage.find_objects(a)
[(slice(2, 5, None), slice(2, 5, None)), (slice(0, 2, None), slice(0, 3,␣
↪None)), (slice(0, 1, None), slice(5, 6, None))]
>>> ndimage.find_objects(a, max_label=2)
[(slice(2, 5, None), slice(2, 5, None)), (slice(0, 2, None), slice(0, 3,␣
↪None))]
>>> ndimage.find_objects(a == 1, max_label=2)
[(slice(2, 5, None), slice(2, 5, None)), None]
```

```
>>> loc = ndimage.find_objects(a)[0]
>>> a[loc]
array([[1, 1, 0],
       [1, 1, 0],
       [0, 0, 1]])
```

scipy.ndimage.histogram

scipy.ndimage.**histogram**(*input*, *min*, *max*, *bins*, *labels=None*, *index=None*)

Calculate the histogram of the values of an array, optionally at labels.

Histogram calculates the frequency of values in an array within bins determined by *min*, *max*, and *bins*. The *labels* and *index* keywords can limit the scope of the histogram to specified sub-regions within the array.

Parameters

input	[array_like] Data for which to calculate histogram.
min, max	[int] Minimum and maximum values of range of histogram bins.
bins	[int] Number of bins.
labels	[array_like, optional] Labels for objects in *input*. If not None, must be same shape as *input*.
index	[int or sequence of ints, optional] Label or labels for which to calculate histogram. If None, all values where label is greater than zero are used

Returns

hist	[ndarray] Histogram counts.

Examples

```
>>> a = np.array([[ 0.    ,  0.2146,  0.5962,  0.    ],
...               [ 0.    ,  0.7778,  0.    ,  0.    ],
...               [ 0.    ,  0.    ,  0.    ,  0.    ],
...               [ 0.    ,  0.    ,  0.7181,  0.2787],
...               [ 0.    ,  0.    ,  0.6573,  0.3094]])
>>> from scipy import ndimage
>>> ndimage.measurements.histogram(a, 0, 1, 10)
array([13,  0,  2,  1,  0,  1,  1,  2,  0,  0])
```

With labels and no indices, non-zero elements are counted:

```
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.measurements.histogram(a, 0, 1, 10, lbl)
array([0, 0, 2, 1, 0, 1, 1, 2, 0, 0])
```

Indices can be used to count only certain objects:

```
>>> ndimage.measurements.histogram(a, 0, 1, 10, lbl, 2)
array([0, 0, 1, 1, 0, 0, 1, 1, 0, 0])
```

scipy.ndimage.label

scipy.ndimage.**label**(*input*, *structure=None*, *output=None*)

Label features in an array.

Parameters

input [array_like] An array-like object to be labeled. Any non-zero values in *input* are counted as features and zero values are considered the background.

structure [array_like, optional] A structuring element that defines feature connections. *structure* must be centrosymmetric (see Notes). If no structuring element is provided, one is automatically generated with a squared connectivity equal to one. That is, for a 2-D *input* array, the default structuring element is:

```
[[0,1,0],
 [1,1,1],
 [0,1,0]]
```

output [(None, data-type, array_like), optional] If *output* is a data type, it specifies the type of the resulting labeled feature array. If *output* is an array-like object, then *output* will be updated with the labeled features from this function. This function can operate in-place, by passing output=input. Note that the output must be able to store the largest label, or this function will raise an Exception.

Returns

label [ndarray or int] An integer ndarray where each unique feature in *input* has a unique label in the returned array.

num_features

[int] How many objects were found.

If *output* is None, this function returns a tuple of (*labeled_array*, *num_features*).

If *output* is a ndarray, then it will be updated with values in *labeled_array* and only *num_features* will be returned by this function.

See also:

find_objects

generate a list of slices for the labeled features (or objects); useful for finding features' position or dimensions

Notes

A centrosymmetric matrix is a matrix that is symmetric about the center. See [1] for more information.

The *structure* matrix must be centrosymmetric to ensure two-way connections. For instance, if the *structure* matrix is not centrosymmetric and is defined as:

```
[[0,1,0],
 [1,1,0],
 [0,0,0]]
```

and the *input* is:

```
[[1,2],
 [0,3]]
```

then the structure matrix would indicate the entry 2 in the input is connected to 1, but 1 is not connected to 2.

References

[1]

Examples

Create an image with some features, then label it using the default (cross-shaped) structuring element:

```
>>> from scipy.ndimage import label, generate_binary_structure
>>> a = np.array([[0,0,1,1,0,0],
...               [0,0,0,1,0,0],
...               [1,1,0,0,1,0],
...               [0,0,0,1,0,0]])
>>> labeled_array, num_features = label(a)
```

Each of the 4 features are labeled with a different integer:

```
>>> num_features
4
>>> labeled_array
array([[0, 0, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [2, 2, 0, 0, 3, 0],
       [0, 0, 0, 4, 0, 0]])
```

Generate a structuring element that will consider features connected even if they touch diagonally:

```
>>> s = generate_binary_structure(2,2)
```

or,

```
>>> s = [[1,1,1],
...      [1,1,1],
...      [1,1,1]]
```

Label the image using the new structuring element:

```
>>> labeled_array, num_features = label(a, structure=s)
```

Show the 2 labeled features (note that features 1, 3, and 4 from above are now considered a single feature):

```
>>> num_features
2
>>> labeled_array
array([[0, 0, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [2, 2, 0, 0, 1, 0],
       [0, 0, 0, 1, 0, 0]])
```

scipy.ndimage.labeled_comprehension

scipy.ndimage.**labeled_comprehension**(*input*, *labels*, *index*, *func*, *out_dtype*, *default*, *pass_positions=False*)

Roughly equivalent to [func(input[labels == i]) for i in index].

Sequentially applies an arbitrary function (that works on array_like input) to subsets of an N-D image array specified by *labels* and *index*. The option exists to provide the function with positional parameters as the second argument.

Parameters

input [array_like] Data from which to select *labels* to process.

labels [array_like or None] Labels to objects in *input*. If not None, array must be same shape as *input*. If None, *func* is applied to raveled *input*.

index [int, sequence of ints or None] Subset of *labels* to which to apply *func*. If a scalar, a single value is returned. If None, *func* is applied to all non-zero values of *labels*.

func [callable] Python function to apply to *labels* from *input*.

out_dtype [dtype] Dtype to use for *result*.

default [int, float or None] Default return value when a element of *index* does not exist in *labels*.

pass_positions [bool, optional] If True, pass linear indices to *func* as a second argument. Default is False.

Returns

result [ndarray] Result of applying *func* to each of *labels* to *input* in *index*.

Examples

```
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> lbl, nlbl = ndimage.label(a)
>>> lbls = np.arange(1, nlbl+1)
>>> ndimage.labeled_comprehension(a, lbl, lbls, np.mean, float, 0)
array([ 2.75,  5.5 ,  6.  ])
```

Falling back to *default*:

```
>>> lbls = np.arange(1, nlbl+2)
>>> ndimage.labeled_comprehension(a, lbl, lbls, np.mean, float, -1)
array([ 2.75,  5.5 ,  6.  , -1.  ])
```

Passing positions:

```
>>> def fn(val, pos):
...     print("fn says: %s : %s" % (val, pos))
...     return (val.sum()) if (pos.sum() % 2 == 0) else (-val.sum())
...
>>> ndimage.labeled_comprehension(a, lbl, lbls, fn, float, 0, True)
fn says: [1 2 5 3] : [0 1 4 5]
fn says: [4 7] : [ 7 11]
fn says: [9 3] : [12 13]
array([ 11.,  11., -12.,   0.])
```

scipy.ndimage.maximum

scipy.ndimage.**maximum**(*input*, *labels=None*, *index=None*)

Calculate the maximum of the values of an array over labeled regions.

Parameters

input [array_like] Array_like of values. For each region specified by *labels*, the maximal values of *input* over the region is computed.

labels [array_like, optional] An array of integers marking different regions over which the maximum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the maximum over the whole array is returned.

index [array_like, optional] A list of region labels that are taken into account for computing the maxima. If index is None, the maximum over all elements where *labels* is non-zero is returned.

Returns

output [float or list of floats] List of maxima of *input* over the regions determined by *labels* and whose index is in *index*. If *index* or *labels* are not specified, a float is returned: the maximal value of *input* if *labels* is None, and the maximal value of elements where *labels* is greater than zero if *index* is None.

See also:

label, **minimum**, **median**, **maximum_position**, **extrema**, ***sum***, **mean**, **variance**

standard_deviation

Notes

The function returns a Python list and not a NumPy array, use *np.array* to convert the list to an array.

Examples

```
>>> a = np.arange(16).reshape((4,4))
>>> a
array([[ 0,  1,  2,  3],
       [ 4,  5,  6,  7],
       [ 8,  9, 10, 11],
       [12, 13, 14, 15]])
>>> labels = np.zeros_like(a)
>>> labels[:2,:2] = 1
>>> labels[2:, 1:3] = 2
>>> labels
array([[1, 1, 0, 0],
       [1, 1, 0, 0],
       [0, 2, 2, 0],
       [0, 2, 2, 0]])
>>> from scipy import ndimage
>>> ndimage.maximum(a)
15.0
>>> ndimage.maximum(a, labels=labels, index=[1,2])
[5.0, 14.0]
>>> ndimage.maximum(a, labels=labels)
14.0
```

```
>>> b = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> labels, labels_nb = ndimage.label(b)
>>> labels
array([[1, 1, 0, 0],
       [1, 1, 0, 2],
       [0, 0, 0, 2],
       [3, 3, 0, 0]])
>>> ndimage.maximum(b, labels=labels, index=np.arange(1, labels_nb + 1))
[5.0, 7.0, 9.0]
```

scipy.ndimage.maximum_position

scipy.ndimage.**maximum_position**(*input*, *labels=None*, *index=None*)

Find the positions of the maximums of the values of an array at labels.

For each region specified by *labels*, the position of the maximum value of *input* within the region is returned.

Parameters

input [array_like] Array_like of values.

labels [array_like, optional] An array of integers marking different regions over which the position of the maximum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the location of the first maximum over the whole array is returned.

The *labels* argument only works when *index* is specified.

index [array_like, optional] A list of region labels that are taken into account for finding the location of the maxima. If *index* is None, the first maximum over all elements where *labels* is non-zero is returned.
The *index* argument only works when *labels* is specified.

Returns

output [list of tuples of ints] List of tuples of ints that specify the location of maxima of *input* over the regions determined by *labels* and whose index is in *index*.
If *index* or *labels* are not specified, a tuple of ints is returned specifying the location of the `first` maximal value of *input*.

See also:

label, **minimum**, **median**, **maximum_position**, **extrema**, ***sum***, **mean**, **variance**

standard_deviation

Examples

```
>>> from scipy import ndimage
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> ndimage.maximum_position(a)
(3, 0)
```

Features to process can be specified using *labels* and *index*:

```
>>> lbl = np.array([[0, 1, 2, 3],
...                 [0, 1, 2, 3],
...                 [0, 1, 2, 3],
...                 [0, 1, 2, 3]])
>>> ndimage.maximum_position(a, lbl, 1)
(1, 1)
```

If no index is given, non-zero *labels* are processed:

```
>>> ndimage.maximum_position(a, lbl)
(2, 3)
```

If there are no maxima, the position of the first element is returned:

```
>>> ndimage.maximum_position(a, lbl, 2)
(0, 2)
```

scipy.ndimage.mean

scipy.ndimage.**mean**(*input*, *labels=None*, *index=None*)

Calculate the mean of the values of an array at labels.

Parameters

input [array_like] Array on which to compute the mean of elements over distinct regions.

labels [array_like, optional] Array of labels of same shape, or broadcastable to the same shape as *input*. All elements sharing the same label form one region over which the mean of the elements is computed.

index [int or sequence of ints, optional] Labels of the objects over which the mean is to be computed. Default is None, in which case the mean for all values where label is greater than 0 is calculated.

Returns

out [list] Sequence of same length as *index*, with the mean of the different regions labeled by the labels in *index*.

See also:

variance, **standard_deviation**, **minimum**, **maximum**, ***sum***, **label**

Examples

```
>>> from scipy import ndimage
>>> a = np.arange(25).reshape((5,5))
>>> labels = np.zeros_like(a)
>>> labels[3:5,3:5] = 1
>>> index = np.unique(labels)
>>> labels
array([[0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 1, 1],
       [0, 0, 0, 1, 1]])
>>> index
array([0, 1])
>>> ndimage.mean(a, labels=labels, index=index)
[10.285714285714286, 21.0]
```

scipy.ndimage.median

scipy.ndimage.**median**(*input*, *labels=None*, *index=None*)

Calculate the median of the values of an array over labeled regions.

Parameters

input [array_like] Array_like of values. For each region specified by *labels*, the median value of *input* over the region is computed.

labels [array_like, optional] An array_like of integers marking different regions over which the median value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the median over the whole array is returned.

index [array_like, optional] A list of region labels that are taken into account for computing the medians. If index is None, the median over all elements where *labels* is non-zero is returned.

Returns

median [float or list of floats] List of medians of *input* over the regions determined by *labels* and whose index is in *index*. If *index* or *labels* are not specified, a float is returned: the median value of *input* if *labels* is None, and the median value of elements where *labels* is greater than zero if *index* is None.

See also:

`label`, `minimum`, `maximum`, `extrema`, `sum`, `mean`, `variance`, `standard_deviation`

Notes

The function returns a Python list and not a NumPy array, use *np.array* to convert the list to an array.

Examples

```
>>> from scipy import ndimage
>>> a = np.array([[1, 2, 0, 1],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> labels, labels_nb = ndimage.label(a)
>>> labels
array([[1, 1, 0, 2],
       [1, 1, 0, 2],
       [0, 0, 0, 2],
       [3, 3, 0, 0]])
>>> ndimage.median(a, labels=labels, index=np.arange(1, labels_nb + 1))
[2.5, 4.0, 6.0]
>>> ndimage.median(a)
1.0
>>> ndimage.median(a, labels=labels)
3.0
```

scipy.ndimage.minimum

scipy.ndimage.**minimum**(*input*, *labels=None*, *index=None*)

Calculate the minimum of the values of an array over labeled regions.

Parameters

input [array_like] Array_like of values. For each region specified by *labels*, the minimal values of *input* over the region is computed.

labels [array_like, optional] An array_like of integers marking different regions over which the minimum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the minimum over the whole array is returned.

index [array_like, optional] A list of region labels that are taken into account for computing the minima. If index is None, the minimum over all elements where *labels* is non-zero is returned.

Returns

minimum [float or list of floats] List of minima of *input* over the regions determined by *labels* and whose index is in *index*. If *index* or *labels* are not specified, a float is returned: the minimal

value of *input* if *labels* is None, and the minimal value of elements where *labels* is greater than zero if *index* is None.

See also:

label, **maximum**, **median**, **minimum_position**, **extrema**, ***sum***, **mean**, **variance**

standard_deviation

Notes

The function returns a Python list and not a NumPy array, use *np.array* to convert the list to an array.

Examples

```
>>> from scipy import ndimage
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> labels, labels_nb = ndimage.label(a)
>>> labels
array([[1, 1, 0, 0],
       [1, 1, 0, 2],
       [0, 0, 0, 2],
       [3, 3, 0, 0]])
>>> ndimage.minimum(a, labels=labels, index=np.arange(1, labels_nb + 1))
[1.0, 4.0, 3.0]
>>> ndimage.minimum(a)
0.0
>>> ndimage.minimum(a, labels=labels)
1.0
```

scipy.ndimage.minimum_position

scipy.ndimage.**minimum_position**(*input*, *labels=None*, *index=None*)

Find the positions of the minimums of the values of an array at labels.

Parameters

input [array_like] Array_like of values.

labels [array_like, optional] An array of integers marking different regions over which the position of the minimum value of *input* is to be computed. *labels* must have the same shape as *input*. If *labels* is not specified, the location of the first minimum over the whole array is returned. The *labels* argument only works when *index* is specified.

index [array_like, optional] A list of region labels that are taken into account for finding the location of the minima. If *index* is None, the `first` minimum over all elements where *labels* is non-zero is returned.
The *index* argument only works when *labels* is specified.

Returns

output [list of tuples of ints] Tuple of ints or list of tuples of ints that specify the location of minima of *input* over the regions determined by *labels* and whose index is in *index*.

If *index* or *labels* are not specified, a tuple of ints is returned specifying the location of the first minimal value of *input*.

See also:

label, **minimum**, **median**, **maximum_position**, **extrema**, ***sum***, **mean**, **variance**

standard_deviation

Examples

```
>>> a = np.array([[10, 20, 30],
...               [40, 80, 100],
...               [1, 100, 200]])
>>> b = np.array([[1, 2, 0, 1],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
```

```
>>> from scipy import ndimage
```

```
>>> ndimage.minimum_position(a)
(2, 0)
>>> ndimage.minimum_position(b)
(0, 2)
```

Features to process can be specified using *labels* and *index*:

```
>>> label, pos = ndimage.label(a)
>>> ndimage.minimum_position(a, label, index=np.arange(1, pos+1))
[(2, 0)]
```

```
>>> label, pos = ndimage.label(b)
>>> ndimage.minimum_position(b, label, index=np.arange(1, pos+1))
[(0, 0), (0, 3), (3, 1)]
```

scipy.ndimage.standard_deviation

scipy.ndimage.**standard_deviation**(*input*, *labels=None*, *index=None*)

Calculate the standard deviation of the values of an N-D image array, optionally at specified sub-regions.

Parameters

input [array_like] N-D image data to process.

labels [array_like, optional] Labels to identify sub-regions in *input*. If not None, must be same shape as *input*.

index [int or sequence of ints, optional] *labels* to include in output. If None (default), all values where *labels* is non-zero are used.

Returns

standard_deviation
[float or ndarray] Values of standard deviation, for each sub-region if *labels* and *index* are specified.

See also:

label, **variance**, **maximum**, **minimum**, **extrema**

Examples

```
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> ndimage.standard_deviation(a)
2.7585095613392387
```

Features to process can be specified using *labels* and *index*:

```
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.standard_deviation(a, lbl, index=np.arange(1, nlbl+1))
array([ 1.479,  1.5  ,  3.   ])
```

If no index is given, non-zero *labels* are processed:

```
>>> ndimage.standard_deviation(a, lbl)
2.4874685927665499
```

scipy.ndimage.sum_labels

scipy.ndimage.**sum_labels**(*input*, *labels=None*, *index=None*)

Calculate the sum of the values of the array.

Parameters

input [array_like] Values of *input* inside the regions defined by *labels* are summed together.

labels [array_like of ints, optional] Assign labels to the values of the array. Has to have the same shape as *input*.

index [array_like, optional] A single label number or a sequence of label numbers of the objects to be measured.

Returns

sum [ndarray or scalar] An array of the sums of values of *input* inside the regions defined by *labels* with the same shape as *index*. If 'index' is None or scalar, a scalar is returned.

See also:

mean, **median**

Examples

```
>>> from scipy import ndimage
>>> input =  [0,1,2,3]
>>> labels = [1,1,2,2]
>>> ndimage.sum(input, labels, index=[1,2])
[1.0, 5.0]
>>> ndimage.sum(input, labels, index=1)
1
```

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```
>>> ndimage.sum(input, labels)
6
```

scipy.ndimage.variance

scipy.ndimage.**variance**(*input*, *labels=None*, *index=None*)

Calculate the variance of the values of an N-D image array, optionally at specified sub-regions.

Parameters

input [array_like] Nd-image data to process.

labels [array_like, optional] Labels defining sub-regions in *input*. If not None, must be same shape as *input*.

index [int or sequence of ints, optional] *labels* to include in output. If None (default), all values where *labels* is non-zero are used.

Returns

variance [float or ndarray] Values of variance, for each sub-region if *labels* and *index* are specified.

See also:

label, **standard_deviation**, **maximum**, **minimum**, **extrema**

Examples

```
>>> a = np.array([[1, 2, 0, 0],
...               [5, 3, 0, 4],
...               [0, 0, 0, 7],
...               [9, 3, 0, 0]])
>>> from scipy import ndimage
>>> ndimage.variance(a)
7.609375
```

Features to process can be specified using *labels* and *index*:

```
>>> lbl, nlbl = ndimage.label(a)
>>> ndimage.variance(a, lbl, index=np.arange(1, nlbl+1))
array([ 2.1875,  2.25  ,  9.    ])
```

If no index is given, all non-zero *labels* are processed:

```
>>> ndimage.variance(a, lbl)
6.1875
```

scipy.ndimage.watershed_ift

scipy.ndimage.**watershed_ift**(*input*, *markers*, *structure=None*, *output=None*)

Apply watershed from markers using image foresting transform algorithm.

Parameters

input [array_like] Input.

markers [array_like] Markers are points within each watershed that form the beginning of the process. Negative markers are considered background markers which are processed after the other markers.

structure [structure element, optional] A structuring element defining the connectivity of the object can be provided. If None, an element is generated with a squared connectivity equal to one.

output [ndarray, optional] An output array can optionally be provided. The same shape as input.

Returns

watershed_ift

[ndarray] Output. Same shape as *input*.

References

[1]

Morphology

binary_closing(input[, structure, …])	Multidimensional binary closing with the given structuring element.
binary_dilation(input[, structure, …])	Multidimensional binary dilation with the given structuring element.
binary_erosion(input[, structure, …])	Multidimensional binary erosion with a given structuring element.
binary_fill_holes(input[, structure, …])	Fill the holes in binary objects.
binary_hit_or_miss(input[, structure1, …])	Multidimensional binary hit-or-miss transform.
binary_opening(input[, structure, …])	Multidimensional binary opening with the given structuring element.
binary_propagation(input[, structure, mask, …])	Multidimensional binary propagation with the given structuring element.
black_tophat(input[, size, footprint, …])	Multidimensional black tophat filter.
distance_transform_bf(input[, metric, …])	Distance transform function by a brute force algorithm.
distance_transform_cdt(input[, metric, …])	Distance transform for chamfer type of transforms.
distance_transform_edt(input[, sampling, …])	Exact Euclidean distance transform.
generate_binary_structure(rank, connectivity)	Generate a binary structure for binary morphological operations.
grey_closing(input[, size, footprint, …])	Multidimensional grayscale closing.
grey_dilation(input[, size, footprint, …])	Calculate a greyscale dilation, using either a structuring element, or a footprint corresponding to a flat structuring element.
grey_erosion(input[, size, footprint, …])	Calculate a greyscale erosion, using either a structuring element, or a footprint corresponding to a flat structuring element.
grey_opening(input[, size, footprint, …])	Multidimensional grayscale opening.
iterate_structure(structure, iterations[, …])	Iterate a structure by dilating it with itself.

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morphological_gradient(input[, size, …])	Multidimensional morphological gradient.
morphological_laplace(input[, size, …])	Multidimensional morphological laplace.
white_tophat(input[, size, footprint, …])	Multidimensional white tophat filter.

scipy.ndimage.binary_closing

scipy.ndimage.**binary_closing**(*input*, *structure=None*, *iterations=1*, *output=None*, *origin=0*, *mask=None*, *border_value=0*, *brute_force=False*)

Multidimensional binary closing with the given structuring element.

The *closing* of an input image by a structuring element is the *erosion* of the *dilation* of the image by the structuring element.

Parameters

input [array_like] Binary array_like to be closed. Non-zero (True) elements form the subset to be closed.

structure [array_like, optional] Structuring element used for the closing. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square connectivity equal to one (i.e., only nearest neighbors are connected to the center, diagonally-connected elements are not considered neighbors).

iterations [int, optional] The dilation step of the closing, then the erosion step are each repeated *iterations* times (one, by default). If iterations is less than 1, each operations is repeated until the result does not change anymore. Only an integer of iterations is accepted.

output [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin [int or tuple of ints, optional] Placement of the filter, by default 0.

mask [array_like, optional] If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration.
New in version 1.1.0.

border_value
[int (cast to 0 or 1), optional] Value at the border in the output array.
New in version 1.1.0.

brute_force
[boolean, optional] Memory condition: if False, only the pixels whose value was changed in the last iteration are tracked as candidates to be updated in the current iteration; if true al pixels are considered as candidates for update, regardless of what happened in the previous iteration. False by default.
New in version 1.1.0.

Returns

binary_closing
[ndarray of bools] Closing of the input by the structuring element.

See also:

grey_closing, **binary_opening**, **binary_dilation**, **binary_erosion**

generate_binary_structure

Notes

Closing [1] is a mathematical morphology operation [2] that consists in the succession of a dilation and an erosion of the input with the same structuring element. Closing therefore fills holes smaller than the structuring element.

Together with *opening* (`binary_opening`), closing can be used for noise removal.

References

[1], [2]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((5,5), dtype=int)
>>> a[1:-1, 1:-1] = 1; a[2,2] = 0
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Closing removes small holes
>>> ndimage.binary_closing(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Closing is the erosion of the dilation of the input
>>> ndimage.binary_dilation(a).astype(int)
array([[0, 1, 1, 1, 0],
       [1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1],
       [1, 1, 1, 1, 1],
       [0, 1, 1, 1, 0]])
>>> ndimage.binary_erosion(ndimage.binary_dilation(a)).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
```

```
>>> a = np.zeros((7,7), dtype=int)
>>> a[1:6, 2:5] = 1; a[1:3,3] = 0
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
```

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```
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> # In addition to removing holes, closing can also
>>> # coarsen boundaries with fine hollows.
>>> ndimage.binary_closing(a).astype(int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.binary_closing(a, structure=np.ones((2,2))).astype(int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

scipy.ndimage.binary_dilation

scipy.ndimage.**binary_dilation**(*input*, *structure=None*, *iterations=1*, *mask=None*, *output=None*, *border_value=0*, *origin=0*, *brute_force=False*)

Multidimensional binary dilation with the given structuring element.

Parameters

input [array_like] Binary array_like to be dilated. Non-zero (True) elements form the subset to be dilated.

structure [array_like, optional] Structuring element used for the dilation. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square connectivity equal to one.

iterations [int, optional] The dilation is repeated *iterations* times (one, by default). If iterations is less than 1, the dilation is repeated until the result does not change anymore. Only an integer of iterations is accepted.

mask [array_like, optional] If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration.

output [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.

border_value [int (cast to 0 or 1), optional] Value at the border in the output array.

origin [int or tuple of ints, optional] Placement of the filter, by default 0.

brute_force [boolean, optional] Memory condition: if False, only the pixels whose value was changed in the last iteration are tracked as candidates to be updated (dilated) in the current iteration; if True all pixels are considered as candidates for dilation, regardless of what happened in the previous iteration. False by default.

Returns

binary_dilation [ndarray of bools] Dilation of the input by the structuring element.

See also:

grey_dilation, **binary_erosion**, **binary_closing**, **binary_opening**

generate_binary_structure

Notes

Dilation [1] is a mathematical morphology operation [2] that uses a structuring element for expanding the shapes in an image. The binary dilation of an image by a structuring element is the locus of the points covered by the structuring element, when its center lies within the non-zero points of the image.

References

[1], [2]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((5, 5))
>>> a[2, 2] = 1
>>> a
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(a)
array([[False, False, False, False, False],
       [False, False,  True, False, False],
       [False,  True,  True,  True, False],
       [False, False,  True, False, False],
       [False, False, False, False, False]], dtype=bool)
>>> ndimage.binary_dilation(a).astype(a.dtype)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> # 3x3 structuring element with connectivity 1, used by default
>>> struct1 = ndimage.generate_binary_structure(2, 1)
>>> struct1
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> # 3x3 structuring element with connectivity 2
>>> struct2 = ndimage.generate_binary_structure(2, 2)
>>> struct2
array([[ True,  True,  True],
       [ True,  True,  True],
       [ True,  True,  True]], dtype=bool)
```

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```
>>> ndimage.binary_dilation(a, structure=struct1).astype(a.dtype)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(a, structure=struct2).astype(a.dtype)
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(a, structure=struct1,\
... iterations=2).astype(a.dtype)
array([[ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 1.,  1.,  1.,  1.,  1.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.]])
```

scipy.ndimage.binary_erosion

scipy.ndimage.**binary_erosion**(*input*, *structure=None*, *iterations=1*, *mask=None*, *output=None*, *border_value=0*, *origin=0*, *brute_force=False*)

Multidimensional binary erosion with a given structuring element.

Binary erosion is a mathematical morphology operation used for image processing.

Parameters

input [array_like] Binary image to be eroded. Non-zero (True) elements form the subset to be eroded.

structure [array_like, optional] Structuring element used for the erosion. Non-zero elements are considered True. If no structuring element is provided, an element is generated with a square connectivity equal to one.

iterations [int, optional] The erosion is repeated *iterations* times (one, by default). If iterations is less than 1, the erosion is repeated until the result does not change anymore.

mask [array_like, optional] If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration.

output [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.

border_value [int (cast to 0 or 1), optional] Value at the border in the output array.

origin [int or tuple of ints, optional] Placement of the filter, by default 0.

brute_force [boolean, optional] Memory condition: if False, only the pixels whose value was changed in the last iteration are tracked as candidates to be updated (eroded) in the current iteration; if True all pixels are considered as candidates for erosion, regardless of what happened in the previous iteration. False by default.

Returns

binary_erosion [ndarray of bools] Erosion of the input by the structuring element.

See also:

grey_erosion, **binary_dilation**, **binary_closing**, **binary_opening**

generate_binary_structure

Notes

Erosion [1] is a mathematical morphology operation [2] that uses a structuring element for shrinking the shapes in an image. The binary erosion of an image by a structuring element is the locus of the points where a superimposition of the structuring element centered on the point is entirely contained in the set of non-zero elements of the image.

References

[1], [2]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[1:6, 2:5] = 1
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.binary_erosion(a).astype(a.dtype)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> #Erosion removes objects smaller than the structure
>>> ndimage.binary_erosion(a, structure=np.ones((5,5))).astype(a.dtype)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

scipy.ndimage.binary_fill_holes

scipy.ndimage.**binary_fill_holes**(*input*, *structure=None*, *output=None*, *origin=0*)

Fill the holes in binary objects.

Parameters

input	[array_like] N-D binary array with holes to be filled
structure	[array_like, optional] Structuring element used in the computation; large-size elements make computations faster but may miss holes separated from the background by thin regions. The default element (with a square connectivity equal to one) yields the intuitive result where all holes in the input have been filled.
output	[ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.
origin	[int, tuple of ints, optional] Position of the structuring element.

Returns

out	[ndarray] Transformation of the initial image *input* where holes have been filled.

See also:

binary_dilation, **binary_propagation**, **label**

Notes

The algorithm used in this function consists in invading the complementary of the shapes in *input* from the outer boundary of the image, using binary dilations. Holes are not connected to the boundary and are therefore not invaded. The result is the complementary subset of the invaded region.

References

[1]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((5, 5), dtype=int)
>>> a[1:4, 1:4] = 1
>>> a[2,2] = 0
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> ndimage.binary_fill_holes(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Too big structuring element
```

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```
>>> ndimage.binary_fill_holes(a, structure=np.ones((5,5))).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 0, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
```

scipy.ndimage.binary_hit_or_miss

scipy.ndimage.**binary_hit_or_miss**(*input*, *structure1=None*, *structure2=None*, *output=None*, *origin1=0*, *origin2=None*)

Multidimensional binary hit-or-miss transform.

The hit-or-miss transform finds the locations of a given pattern inside the input image.

Parameters

input [array_like (cast to booleans)] Binary image where a pattern is to be detected.

structure1 [array_like (cast to booleans), optional] Part of the structuring element to be fitted to the foreground (non-zero elements) of *input*. If no value is provided, a structure of square connectivity 1 is chosen.

structure2 [array_like (cast to booleans), optional] Second part of the structuring element that has to miss completely the foreground. If no value is provided, the complementary of *structure1* is taken.

output [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin1 [int or tuple of ints, optional] Placement of the first part of the structuring element *structure1*, by default 0 for a centered structure.

origin2 [int or tuple of ints, optional] Placement of the second part of the structuring element *structure2*, by default 0 for a centered structure. If a value is provided for *origin1* and not for *origin2*, then *origin2* is set to *origin1*.

Returns

binary_hit_or_miss

[ndarray] Hit-or-miss transform of *input* with the given structuring element (*structure1*, *structure2*).

See also:

binary_erosion

References

[1]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[1, 1] = 1; a[2:4, 2:4] = 1; a[4:6, 4:6] = 1
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 0, 0, 0],
       [0, 0, 1, 1, 0, 0, 0],
       [0, 0, 0, 0, 1, 1, 0],
       [0, 0, 0, 0, 1, 1, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> structure1 = np.array([[1, 0, 0], [0, 1, 1], [0, 1, 1]])
>>> structure1
array([[1, 0, 0],
       [0, 1, 1],
       [0, 1, 1]])
>>> # Find the matches of structure1 in the array a
>>> ndimage.binary_hit_or_miss(a, structure1=structure1).astype(int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> # Change the origin of the filter
>>> # origin1=1 is equivalent to origin1=(1,1) here
>>> ndimage.binary_hit_or_miss(a, structure1=structure1,\
... origin1=1).astype(int)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 1, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

scipy.ndimage.binary_opening

scipy.ndimage.**binary_opening**(*input*, *structure=None*, *iterations=1*, *output=None*, *origin=0*, *mask=None*, *border_value=0*, *brute_force=False*)

Multidimensional binary opening with the given structuring element.

The *opening* of an input image by a structuring element is the *dilation* of the *erosion* of the image by the structuring element.

Parameters

input [array_like] Binary array_like to be opened. Non-zero (True) elements form the subset to be opened.

structure [array_like, optional] Structuring element used for the opening. Non-zero elements are considered True. If no structuring element is provided an element is generated with a square

connectivity equal to one (i.e., only nearest neighbors are connected to the center, diagonally-connected elements are not considered neighbors).

iterations [int, optional] The erosion step of the opening, then the dilation step are each repeated *iterations* times (one, by default). If *iterations* is less than 1, each operation is repeated until the result does not change anymore. Only an integer of iterations is accepted.

output [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.

origin [int or tuple of ints, optional] Placement of the filter, by default 0.

mask [array_like, optional] If a mask is given, only those elements with a True value at the corresponding mask element are modified at each iteration.
New in version 1.1.0.

border_value
[int (cast to 0 or 1), optional] Value at the border in the output array.
New in version 1.1.0.

brute_force
[boolean, optional] Memory condition: if False, only the pixels whose value was changed in the last iteration are tracked as candidates to be updated in the current iteration; if true all pixels are considered as candidates for update, regardless of what happened in the previous iteration. False by default.
New in version 1.1.0.

Returns

binary_opening
[ndarray of bools] Opening of the input by the structuring element.

See also:

grey_opening, **binary_closing**, **binary_erosion**, **binary_dilation**

generate_binary_structure

Notes

Opening [1] is a mathematical morphology operation [2] that consists in the succession of an erosion and a dilation of the input with the same structuring element. Opening, therefore, removes objects smaller than the structuring element.

Together with *closing* (*binary_closing*), opening can be used for noise removal.

References

[1], [2]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((5,5), dtype=int)
>>> a[1:4, 1:4] = 1; a[4, 4] = 1
>>> a
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
```

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```
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 1]])
>>> # Opening removes small objects
>>> ndimage.binary_opening(a, structure=np.ones((3,3))).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0]])
>>> # Opening can also smooth corners
>>> ndimage.binary_opening(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0]])
>>> # Opening is the dilation of the erosion of the input
>>> ndimage.binary_erosion(a).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0]])
>>> ndimage.binary_dilation(ndimage.binary_erosion(a)).astype(int)
array([[0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0]])
```

scipy.ndimage.binary_propagation

scipy.ndimage.**binary_propagation**(*input*, *structure=None*, *mask=None*, *output=None*, *border_value=0*, *origin=0*)

Multidimensional binary propagation with the given structuring element.

Parameters

input [array_like] Binary image to be propagated inside *mask*.

structure [array_like, optional] Structuring element used in the successive dilations. The output may depend on the structuring element, especially if *mask* has several connex components. If no structuring element is provided, an element is generated with a squared connectivity equal to one.

mask [array_like, optional] Binary mask defining the region into which *input* is allowed to propagate.

output [ndarray, optional] Array of the same shape as input, into which the output is placed. By default, a new array is created.

border_value [int (cast to 0 or 1), optional] Value at the border in the output array.

origin [int or tuple of ints, optional] Placement of the filter, by default 0.

Returns

binary_propagation [ndarray] Binary propagation of *input* inside *mask*.

Notes

This function is functionally equivalent to calling binary_dilation with the number of iterations less than one: iterative dilation until the result does not change anymore.

The succession of an erosion and propagation inside the original image can be used instead of an *opening* for deleting small objects while keeping the contours of larger objects untouched.

References

[1], [2]

Examples

```
>>> from scipy import ndimage
>>> input = np.zeros((8, 8), dtype=int)
>>> input[2, 2] = 1
>>> mask = np.zeros((8, 8), dtype=int)
>>> mask[1:4, 1:4] = mask[4, 4]  = mask[6:8, 6:8] = 1
>>> input
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
>>> mask
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 1, 1],
       [0, 0, 0, 0, 0, 0, 1, 1]])
>>> ndimage.binary_propagation(input, mask=mask).astype(int)
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.binary_propagation(input, mask=mask,\
... structure=np.ones((3,3))).astype(int)
array([[0, 0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
       [0, 1, 1, 1, 0, 0, 0, 0],
```

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```
       [0, 0, 0, 0, 1, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0, 0]])
```

```
>>> # Comparison between opening and erosion+propagation
>>> a = np.zeros((6,6), dtype=int)
>>> a[2:5, 2:5] = 1; a[0, 0] = 1; a[5, 5] = 1
>>> a
array([[1, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 1]])
>>> ndimage.binary_opening(a).astype(int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0, 0]])
>>> b = ndimage.binary_erosion(a)
>>> b.astype(int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0]])
>>> ndimage.binary_propagation(b, mask=a).astype(int)
array([[0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 0]])
```

scipy.ndimage.black_tophat

scipy.ndimage.**black_tophat**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional black tophat filter.

Parameters

input	[array_like] Input.
size	[tuple of ints, optional] Shape of a flat and full structuring element used for the filter. Optional if *footprint* or *structure* is provided.
footprint	[array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the black tophat filter.
structure	[array of ints, optional] Structuring element used for the filter. *structure* may be a non-flat structuring element.
output	[array, optional] An array used for storing the output of the filter may be provided.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [scalar, optional] The *origin* parameter controls the placement of the filter. Default 0

Returns

black_tophat
[ndarray] Result of the filter of *input* with *structure*.

See also:

white_tophat, **grey_opening**, **grey_closing**

Examples

Change dark peak to bright peak and subtract background.

```
>>> from scipy.ndimage import generate_binary_structure, black_tophat
>>> square = generate_binary_structure(rank=2, connectivity=3)
>>> dark_on_gray = np.array([[7, 6, 6, 6, 7],
...                          [6, 5, 4, 5, 6],
...                          [6, 4, 0, 4, 6],
...                          [6, 5, 4, 5, 6],
...                          [7, 6, 6, 6, 7]])
>>> black_tophat(input=dark_on_gray, structure=square)
array([[0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 1, 5, 1, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0]])
```

scipy.ndimage.distance_transform_bf

scipy.ndimage.**distance_transform_bf**(*input*, *metric='euclidean'*, *sampling=None*, *return_distances=True*, *return_indices=False*, *distances=None*, *indices=None*)

Distance transform function by a brute force algorithm.

This function calculates the distance transform of the *input*, by replacing each foreground (non-zero) element, with its shortest distance to the background (any zero-valued element).

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element to each foreground element is returned in a separate array.

Parameters

input [array_like] Input

metric [{'euclidean', 'taxicab', 'chessboard'}, optional] 'cityblock' and 'manhattan' are also valid, and map to 'taxicab'. The default is 'euclidean'.

sampling [float, or sequence of float, optional] This parameter is only used when *metric* is 'euclidean'. Spacing of elements along each dimension. If a sequence, must be of length equal to the input rank; if a single number, this is used for all axes. If not specified, a grid spacing of unity is implied.

return_distances
[bool, optional] Whether to calculate the distance transform. Default is True.

return_indices
: [bool, optional] Whether to calculate the feature transform. Default is False.

distances
: [ndarray, optional] An output array to store the calculated distance transform, instead of returning it. *return_distances* must be True. It must be the same shape as *input*, and of type float64 if *metric* is 'euclidean', uint32 otherwise.

indices
: [int32 ndarray, optional] An output array to store the calculated feature transform, instead of returning it. *return_indicies* must be True. Its shape must be *(input.ndim,) + input.shape*.

Returns

distances
: [ndarray, optional] The calculated distance transform. Returned only when *return_distances* is True and *distances* is not supplied. It will have the same shape as the input array.

indices
: [int32 ndarray, optional] The calculated feature transform. It has an input-shaped array for each dimension of the input. See distance_transform_edt documentation for an example. Returned only when *return_indices* is True and *indices* is not supplied.

Notes

This function employs a slow brute force algorithm, see also the function distance_transform_cdt for more efficient taxicab and chessboard algorithms.

scipy.ndimage.distance_transform_cdt

scipy.ndimage.**distance_transform_cdt**(*input*, *metric='chessboard'*, *return_distances=True*, *return_indices=False*, *distances=None*, *indices=None*)

Distance transform for chamfer type of transforms.

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element to each foreground element is returned in a separate array.

Parameters

input
: [array_like] Input

metric
: [{'chessboard', 'taxicab'} or array_like, optional] The *metric* determines the type of chamfering that is done. If the *metric* is equal to 'taxicab' a structure is generated using generate_binary_structure with a squared distance equal to 1. If the *metric* is equal to 'chessboard', a *metric* is generated using generate_binary_structure with a squared distance equal to the dimensionality of the array. These choices correspond to the common interpretations of the 'taxicab' and the 'chessboard' distance metrics in two dimensions. A custom metric may be provided, in the form of a matrix where each dimension has a length of three. 'cityblock' and 'manhattan' are also valid, and map to 'taxicab'. The default is 'chessboard'.

return_distances
: [bool, optional] Whether to calculate the distance transform. Default is True.

return_indices
: [bool, optional] Whether to calculate the feature transform. Default is False.

distances
: [int32 ndarray, optional] An output array to store the calculated distance transform, instead of returning it. *return_distances* must be True. It must be the same shape as *input*.

indices
: [int32 ndarray, optional] An output array to store the calculated feature transform, instead of returning it. *return_indicies* must be True. Its shape must be *(input.ndim,) + input.shape*.

Returns

distances
: [int32 ndarray, optional] The calculated distance transform. Returned only when *return_distances* is True, and *distances* is not supplied. It will have the same shape as the input array.

indices [int32 ndarray, optional] The calculated feature transform. It has an input-shaped array for each dimension of the input. See distance_transform_edt documentation for an example. Returned only when *return_indices* is True, and *indices* is not supplied.

scipy.ndimage.distance_transform_edt

scipy.ndimage.**distance_transform_edt**(*input*, *sampling=None*, *return_distances=True*, *return_indices=False*, *distances=None*, *indices=None*)

Exact Euclidean distance transform.

In addition to the distance transform, the feature transform can be calculated. In this case the index of the closest background element to each foreground element is returned in a separate array.

Parameters

input [array_like] Input data to transform. Can be any type but will be converted into binary: 1 wherever input equates to True, 0 elsewhere.

sampling [float, or sequence of float, optional] Spacing of elements along each dimension. If a sequence, must be of length equal to the input rank; if a single number, this is used for all axes. If not specified, a grid spacing of unity is implied.

return_distances [bool, optional] Whether to calculate the distance transform. Default is True.

return_indices [bool, optional] Whether to calculate the feature transform. Default is False.

distances [float64 ndarray, optional] An output array to store the calculated distance transform, instead of returning it. *return_distances* must be True. It must be the same shape as *input*.

indices [int32 ndarray, optional] An output array to store the calculated feature transform, instead of returning it. *return_indicies* must be True. Its shape must be *(input.ndim,) + input.shape*.

Returns

distances [float64 ndarray, optional] The calculated distance transform. Returned only when *return_distances* is True and *distances* is not supplied. It will have the same shape as the input array.

indices [int32 ndarray, optional] The calculated feature transform. It has an input-shaped array for each dimension of the input. See example below. Returned only when *return_indices* is True and *indices* is not supplied.

Notes

The Euclidean distance transform gives values of the Euclidean distance:

```
                n
y_i = sqrt(sum (x[i]-b[i])**2)
                i
```

where b[i] is the background point (value 0) with the smallest Euclidean distance to input points x[i], and n is the number of dimensions.

Examples

```
>>> from scipy import ndimage
>>> a = np.array(([0,1,1,1,1],
...               [0,0,1,1,1],
...               [0,1,1,1,1],
...               [0,1,1,1,0],
...               [0,1,1,0,0]))
>>> ndimage.distance_transform_edt(a)
array([[ 0.    ,  1.    ,  1.4142,  2.2361,  3.    ],
       [ 0.    ,  0.    ,  1.    ,  2.    ,  2.    ],
       [ 0.    ,  1.    ,  1.4142,  1.4142,  1.    ],
       [ 0.    ,  1.    ,  1.4142,  1.    ,  0.    ],
       [ 0.    ,  1.    ,  1.    ,  0.    ,  0.    ]])
```

With a sampling of 2 units along x, 1 along y:

```
>>> ndimage.distance_transform_edt(a, sampling=[2,1])
array([[ 0.    ,  1.    ,  2.    ,  2.8284,  3.6056],
       [ 0.    ,  0.    ,  1.    ,  2.    ,  3.    ],
       [ 0.    ,  1.    ,  2.    ,  2.2361,  2.    ],
       [ 0.    ,  1.    ,  2.    ,  1.    ,  0.    ],
       [ 0.    ,  1.    ,  1.    ,  0.    ,  0.    ]])
```

Asking for indices as well:

```
>>> edt, inds = ndimage.distance_transform_edt(a, return_indices=True)
>>> inds
array([[[0, 0, 1, 1, 3],
        [1, 1, 1, 1, 3],
        [2, 2, 1, 3, 3],
        [3, 3, 4, 4, 3],
        [4, 4, 4, 4, 4]],
       [[0, 0, 1, 1, 4],
        [0, 1, 1, 1, 4],
        [0, 0, 1, 4, 4],
        [0, 0, 3, 3, 4],
        [0, 0, 3, 3, 4]]])
```

With arrays provided for inplace outputs:

```
>>> indices = np.zeros(((np.ndim(a),) + a.shape), dtype=np.int32)
>>> ndimage.distance_transform_edt(a, return_indices=True,␣
↪indices=indices)
array([[ 0.    ,  1.    ,  1.4142,  2.2361,  3.    ],
       [ 0.    ,  0.    ,  1.    ,  2.    ,  2.    ],
       [ 0.    ,  1.    ,  1.4142,  1.4142,  1.    ],
       [ 0.    ,  1.    ,  1.4142,  1.    ,  0.    ],
       [ 0.    ,  1.    ,  1.    ,  0.    ,  0.    ]])
>>> indices
array([[[0, 0, 1, 1, 3],
        [1, 1, 1, 1, 3],
        [2, 2, 1, 3, 3],
```

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```
         [3, 3, 4, 4, 3],
         [4, 4, 4, 4, 4]],
        [[0, 0, 1, 1, 4],
         [0, 1, 1, 1, 4],
         [0, 0, 1, 4, 4],
         [0, 0, 3, 3, 4],
         [0, 0, 3, 3, 4]]])
```

scipy.ndimage.generate_binary_structure

scipy.ndimage.**generate_binary_structure**(*rank*, *connectivity*)

Generate a binary structure for binary morphological operations.

Parameters

rank [int] Number of dimensions of the array to which the structuring element will be applied, as returned by *np.ndim*.

connectivity [int] *connectivity* determines which elements of the output array belong to the structure, i.e., are considered as neighbors of the central element. Elements up to a squared distance of *connectivity* from the center are considered neighbors. *connectivity* may range from 1 (no diagonal elements are neighbors) to *rank* (all elements are neighbors).

Returns

output [ndarray of bools] Structuring element which may be used for binary morphological operations, with *rank* dimensions and all dimensions equal to 3.

See also:

iterate_structure, **binary_dilation**, **binary_erosion**

Notes

generate_binary_structure can only create structuring elements with dimensions equal to 3, i.e., minimal dimensions. For larger structuring elements, that are useful e.g., for eroding large objects, one may either use *iterate_structure*, or create directly custom arrays with numpy functions such as numpy.ones.

Examples

```
>>> from scipy import ndimage
>>> struct = ndimage.generate_binary_structure(2, 1)
>>> struct
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> a = np.zeros((5,5))
>>> a[2, 2] = 1
>>> a
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.],
```

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```
       [ 0.,  0.,  0.,  0.,  0.]])
>>> b = ndimage.binary_dilation(a, structure=struct).astype(a.dtype)
>>> b
array([[ 0.,  0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  0.,  0.,  0.,  0.]])
>>> ndimage.binary_dilation(b, structure=struct).astype(a.dtype)
array([[ 0.,  0.,  1.,  0.,  0.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 1.,  1.,  1.,  1.,  1.],
       [ 0.,  1.,  1.,  1.,  0.],
       [ 0.,  0.,  1.,  0.,  0.]])
>>> struct = ndimage.generate_binary_structure(2, 2)
>>> struct
array([[ True,  True,  True],
       [ True,  True,  True],
       [ True,  True,  True]], dtype=bool)
>>> struct = ndimage.generate_binary_structure(3, 1)
>>> struct # no diagonal elements
array([[[False, False, False],
        [False,  True, False],
        [False, False, False]],
       [[False,  True, False],
        [ True,  True,  True],
        [False,  True, False]],
       [[False, False, False],
        [False,  True, False],
        [False, False, False]]], dtype=bool)
```

scipy.ndimage.grey_closing

scipy.ndimage.**grey_closing**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional grayscale closing.

A grayscale closing consists in the succession of a grayscale dilation, and a grayscale erosion.

Parameters

input	[array_like] Array over which the grayscale closing is to be computed.
size	[tuple of ints] Shape of a flat and full structuring element used for the grayscale closing. Optional if *footprint* or *structure* is provided.
footprint	[array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the grayscale closing.
structure	[array of ints, optional] Structuring element used for the grayscale closing. *structure* may be a non-flat structuring element.
output	[array, optional] An array used for storing the output of the closing may be provided.
mode	[{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'
cval	[scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.
origin	[scalar, optional] The *origin* parameter controls the placement of the filter. Default 0

Returns

grey_closing
[ndarray] Result of the grayscale closing of *input* with *structure*.

See also:

binary_closing, **grey_dilation**, **grey_erosion**, **grey_opening**

generate_binary_structure

Notes

The action of a grayscale closing with a flat structuring element amounts to smoothen deep local minima, whereas binary closing fills small holes.

References

[1]

Examples

```
>>> from scipy import ndimage
>>> a = np.arange(36).reshape((6,6))
>>> a[3,3] = 0
>>> a
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20,  0, 22, 23],
       [24, 25, 26, 27, 28, 29],
       [30, 31, 32, 33, 34, 35]])
>>> ndimage.grey_closing(a, size=(3,3))
array([[ 7,  7,  8,  9, 10, 11],
       [ 7,  7,  8,  9, 10, 11],
       [13, 13, 14, 15, 16, 17],
       [19, 19, 20, 20, 22, 23],
       [25, 25, 26, 27, 28, 29],
       [31, 31, 32, 33, 34, 35]])
>>> # Note that the local minimum a[3,3] has disappeared
```

scipy.ndimage.grey_dilation

scipy.ndimage.**grey_dilation**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a greyscale dilation, using either a structuring element, or a footprint corresponding to a flat structuring element.

Grayscale dilation is a mathematical morphology operation. For the simple case of a full and flat structuring element, it can be viewed as a maximum filter over a sliding window.

Parameters

input [array_like] Array over which the grayscale dilation is to be computed.

size [tuple of ints] Shape of a flat and full structuring element used for the grayscale dilation. Optional if *footprint* or *structure* is provided.

footprint [array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the grayscale dilation. Non-zero values give the set of neighbors of the center over which the maximum is chosen.

structure [array of ints, optional] Structuring element used for the grayscale dilation. *structure* may be a non-flat structuring element.

output [array, optional] An array used for storing the output of the dilation may be provided.

mode [{'reflect','constant','nearest','mirror', 'wrap'}, optional] The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [scalar, optional] The *origin* parameter controls the placement of the filter. Default 0

Returns

grey_dilation
[ndarray] Grayscale dilation of *input*.

See also:

binary_dilation, **grey_erosion**, **grey_closing**, **grey_opening**

generate_binary_structure, **maximum_filter**

Notes

The grayscale dilation of an image input by a structuring element s defined over a domain E is given by:

(input+s)(x) = max {input(y) + s(x-y), for y in E}

In particular, for structuring elements defined as s(y) = 0 for y in E, the grayscale dilation computes the maximum of the input image inside a sliding window defined by E.

Grayscale dilation [1] is a *mathematical morphology* operation [2].

References

[1], [2]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[2:5, 2:5] = 1
>>> a[4,4] = 2; a[2,3] = 3
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 3, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

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```
>>> ndimage.grey_dilation(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_dilation(a, footprint=np.ones((3,3)))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> s = ndimage.generate_binary_structure(2,1)
>>> s
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> ndimage.grey_dilation(a, footprint=s)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 3, 1, 0, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 1, 3, 2, 1, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 1, 1, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_dilation(a, size=(3,3), structure=np.ones((3,3)))
array([[1, 1, 1, 1, 1, 1, 1],
       [1, 2, 4, 4, 4, 2, 1],
       [1, 2, 4, 4, 4, 2, 1],
       [1, 2, 4, 4, 4, 3, 1],
       [1, 2, 2, 3, 3, 3, 1],
       [1, 2, 2, 3, 3, 3, 1],
       [1, 1, 1, 1, 1, 1, 1]])
```

scipy.ndimage.grey_erosion

scipy.ndimage.**grey_erosion**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Calculate a greyscale erosion, using either a structuring element, or a footprint corresponding to a flat structuring element.

Grayscale erosion is a mathematical morphology operation. For the simple case of a full and flat structuring element, it can be viewed as a minimum filter over a sliding window.

Parameters

input [array_like] Array over which the grayscale erosion is to be computed.

size [tuple of ints] Shape of a flat and full structuring element used for the grayscale erosion. Optional if *footprint* or *structure* is provided.

footprint [array of ints, optional] Positions of non-infinite elements of a flat structuring element used

for the grayscale erosion. Non-zero values give the set of neighbors of the center over which the minimum is chosen.

structure [array of ints, optional] Structuring element used for the grayscale erosion. *structure* may be a non-flat structuring element.

output [array, optional] An array used for storing the output of the erosion may be provided.

mode [{'reflect','constant','nearest','mirror', 'wrap'}, optional] The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [scalar, optional] The *origin* parameter controls the placement of the filter. Default 0

Returns

output [ndarray] Grayscale erosion of *input*.

See also:

binary_erosion, **grey_dilation**, **grey_opening**, **grey_closing**

generate_binary_structure, **minimum_filter**

Notes

The grayscale erosion of an image input by a structuring element s defined over a domain E is given by:

(input+s)(x) = min {input(y) - s(x-y), for y in E}

In particular, for structuring elements defined as s(y) = 0 for y in E, the grayscale erosion computes the minimum of the input image inside a sliding window defined by E.

Grayscale erosion [1] is a *mathematical morphology* operation [2].

References

[1], [2]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[1:6, 1:6] = 3
>>> a[4,4] = 2; a[2,3] = 1
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 3, 3, 1, 3, 3, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 3, 3, 3, 2, 3, 0],
       [0, 3, 3, 3, 3, 3, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.grey_erosion(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
```

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```
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 3, 2, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> footprint = ndimage.generate_binary_structure(2, 1)
>>> footprint
array([[False,  True, False],
       [ True,  True,  True],
       [False,  True, False]], dtype=bool)
>>> # Diagonally-connected elements are not considered neighbors
>>> ndimage.grey_erosion(a, size=(3,3), footprint=footprint)
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 3, 1, 2, 0, 0],
       [0, 0, 3, 2, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

scipy.ndimage.grey_opening

scipy.ndimage.**grey_opening**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional grayscale opening.

A grayscale opening consists in the succession of a grayscale erosion, and a grayscale dilation.

Parameters

input [array_like] Array over which the grayscale opening is to be computed.

size [tuple of ints] Shape of a flat and full structuring element used for the grayscale opening. Optional if *footprint* or *structure* is provided.

footprint [array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the grayscale opening.

structure [array of ints, optional] Structuring element used for the grayscale opening. *structure* may be a non-flat structuring element.

output [array, optional] An array used for storing the output of the opening may be provided.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [scalar, optional] The *origin* parameter controls the placement of the filter. Default 0

Returns

grey_opening
[ndarray] Result of the grayscale opening of *input* with *structure*.

See also:

binary_opening, **grey_dilation**, **grey_erosion**, **grey_closing**

generate_binary_structure

Notes

The action of a grayscale opening with a flat structuring element amounts to smoothen high local maxima, whereas binary opening erases small objects.

References

[1]

Examples

```
>>> from scipy import ndimage
>>> a = np.arange(36).reshape((6,6))
>>> a[3, 3] = 50
>>> a
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20, 50, 22, 23],
       [24, 25, 26, 27, 28, 29],
       [30, 31, 32, 33, 34, 35]])
>>> ndimage.grey_opening(a, size=(3,3))
array([[ 0,  1,  2,  3,  4,  4],
       [ 6,  7,  8,  9, 10, 10],
       [12, 13, 14, 15, 16, 16],
       [18, 19, 20, 22, 22, 22],
       [24, 25, 26, 27, 28, 28],
       [24, 25, 26, 27, 28, 28]])
>>> # Note that the local maximum a[3,3] has disappeared
```

scipy.ndimage.iterate_structure

scipy.ndimage.**iterate_structure**(*structure*, *iterations*, *origin=None*)

Iterate a structure by dilating it with itself.

Parameters

structure [array_like] Structuring element (an array of bools, for example), to be dilated with itself.

iterations [int] number of dilations performed on the structure with itself

origin [optional] If origin is None, only the iterated structure is returned. If not, a tuple of the iterated structure and the modified origin is returned.

Returns

iterate_structure

[ndarray of bools] A new structuring element obtained by dilating *structure* (*iterations* - 1) times with itself.

See also:

generate_binary_structure

Examples

```
>>> from scipy import ndimage
>>> struct = ndimage.generate_binary_structure(2, 1)
>>> struct.astype(int)
array([[0, 1, 0],
       [1, 1, 1],
       [0, 1, 0]])
>>> ndimage.iterate_structure(struct, 2).astype(int)
array([[0, 0, 1, 0, 0],
       [0, 1, 1, 1, 0],
       [1, 1, 1, 1, 1],
       [0, 1, 1, 1, 0],
       [0, 0, 1, 0, 0]])
>>> ndimage.iterate_structure(struct, 3).astype(int)
array([[0, 0, 0, 1, 0, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [1, 1, 1, 1, 1, 1, 1],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 0, 1, 0, 0, 0]])
```

scipy.ndimage.morphological_gradient

scipy.ndimage.**morphological_gradient**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional morphological gradient.

The morphological gradient is calculated as the difference between a dilation and an erosion of the input with a given structuring element.

Parameters

input [array_like] Array over which to compute the morphlogical gradient.

size [tuple of ints] Shape of a flat and full structuring element used for the mathematical morphology operations. Optional if *footprint* or *structure* is provided. A larger *size* yields a more blurred gradient.

footprint [array of ints, optional] Positions of non-infinite elements of a flat structuring element used for the morphology operations. Larger footprints give a more blurred morphological gradient.

structure [array of ints, optional] Structuring element used for the morphology operations. *structure* may be a non-flat structuring element.

output [array, optional] An array used for storing the output of the morphological gradient may be provided.

mode [{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'

cval [scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.

origin [scalar, optional] The *origin* parameter controls the placement of the filter. Default 0

Returns

morphological_gradient
[ndarray] Morphological gradient of *input*.

See also:

grey_dilation, **grey_erosion**, **gaussian_gradient_magnitude**

Notes

For a flat structuring element, the morphological gradient computed at a given point corresponds to the maximal difference between elements of the input among the elements covered by the structuring element centered on the point.

References

[1]

Examples

```
>>> from scipy import ndimage
>>> a = np.zeros((7,7), dtype=int)
>>> a[2:5, 2:5] = 1
>>> ndimage.morphological_gradient(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 0, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> # The morphological gradient is computed as the difference
>>> # between a dilation and an erosion
>>> ndimage.grey_dilation(a, size=(3,3)) -\
...  ndimage.grey_erosion(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 0, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 1, 1, 1, 1, 1, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> a = np.zeros((7,7), dtype=int)
>>> a[2:5, 2:5] = 1
>>> a[4,4] = 2; a[2,3] = 3
>>> a
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 1, 3, 1, 0, 0],
       [0, 0, 1, 1, 1, 0, 0],
       [0, 0, 1, 1, 2, 0, 0],
       [0, 0, 0, 0, 0, 0, 0],
       [0, 0, 0, 0, 0, 0, 0]])
>>> ndimage.morphological_gradient(a, size=(3,3))
array([[0, 0, 0, 0, 0, 0, 0],
       [0, 1, 3, 3, 3, 1, 0],
       [0, 1, 3, 3, 3, 1, 0],
```

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```
       [0, 1, 3, 2, 3, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 1, 1, 2, 2, 2, 0],
       [0, 0, 0, 0, 0, 0, 0]])
```

scipy.ndimage.morphological_laplace

scipy.ndimage.**morphological_laplace**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional morphological laplace.

Parameters

input	[array_like] Input.
size	[int or sequence of ints, optional] See *structure*.
footprint	[bool or ndarray, optional] See *structure*.
structure	[structure, optional] Either *size*, *footprint*, or the *structure* must be provided.
output	[ndarray, optional] An output array can optionally be provided.
mode	[{'reflect','constant','nearest','mirror', 'wrap'}, optional] The mode parameter determines how the array borders are handled. For 'constant' mode, values beyond borders are set to be *cval*. Default is 'reflect'.
cval	[scalar, optional] Value to fill past edges of input if mode is 'constant'. Default is 0.0
origin	[origin, optional] The origin parameter controls the placement of the filter.

Returns

morphological_laplace
: [ndarray] Output

scipy.ndimage.white_tophat

scipy.ndimage.**white_tophat**(*input*, *size=None*, *footprint=None*, *structure=None*, *output=None*, *mode='reflect'*, *cval=0.0*, *origin=0*)

Multidimensional white tophat filter.

Parameters

input	[array_like] Input.
size	[tuple of ints] Shape of a flat and full structuring element used for the filter. Optional if *footprint* or *structure* is provided.
footprint	[array of ints, optional] Positions of elements of a flat structuring element used for the white tophat filter.
structure	[array of ints, optional] Structuring element used for the filter. *structure* may be a non-flat structuring element.
output	[array, optional] An array used for storing the output of the filter may be provided.
mode	[{'reflect', 'constant', 'nearest', 'mirror', 'wrap'}, optional] The *mode* parameter determines how the array borders are handled, where *cval* is the value when mode is equal to 'constant'. Default is 'reflect'
cval	[scalar, optional] Value to fill past edges of input if *mode* is 'constant'. Default is 0.0.
origin	[scalar, optional] The *origin* parameter controls the placement of the filter. Default is 0.

Returns

output	[ndarray] Result of the filter of *input* with *structure*.

See also:

black_tophat

Examples

Subtract gray background from a bright peak.

```
>>> from scipy.ndimage import generate_binary_structure, white_tophat
>>> square = generate_binary_structure(rank=2, connectivity=3)
>>> bright_on_gray = np.array([[2, 3, 3, 3, 2],
...                            [3, 4, 5, 4, 3],
...                            [3, 5, 9, 5, 3],
...                            [3, 4, 5, 4, 3],
...                            [2, 3, 3, 3, 2]])
>>> white_tophat(input=bright_on_gray, structure=square)
array([[0, 0, 0, 0, 0],
       [0, 0, 1, 0, 0],
       [0, 1, 5, 1, 0],
       [0, 0, 1, 0, 0],
       [0, 0, 0, 0, 0]])
```

3.3.18 Orthogonal distance regression (`scipy.odr`)

Package Content

Data(x[, y, we, wd, fix, meta])	The data to fit.
RealData(x[, y, sx, sy, covx, covy, fix, meta])	The data, with weightings as actual standard deviations and/or covariances.
Model(fcn[, fjacb, fjacd, extra_args, …])	The Model class stores information about the function you wish to fit.
ODR(data, model[, beta0, delta0, ifixb, …])	The ODR class gathers all information and coordinates the running of the main fitting routine.
Output(output)	The Output class stores the output of an ODR run.
odr(fcn, beta0, y, x[, we, wd, fjacb, …])	Low-level function for ODR.
OdrWarning	Warning indicating that the data passed into ODR will cause problems when passed into 'odr' that the user should be aware of.
OdrError	Exception indicating an error in fitting.
OdrStop	Exception stopping fitting.
polynomial(order)	Factory function for a general polynomial model.
exponential	Exponential model
multilinear	Arbitrary-dimensional linear model
unilinear	Univariate linear model
quadratic	Quadratic model

scipy.odr.Data

class scipy.odr.**Data**(*x*, *y=None*, *we=None*, *wd=None*, *fix=None*, *meta={}*)

The data to fit.

Parameters

x [array_like] Observed data for the independent variable of the regression

y [array_like, optional] If array-like, observed data for the dependent variable of the regression. A scalar input implies that the model to be used on the data is implicit.

we [array_like, optional] If *we* is a scalar, then that value is used for all data points (and all dimensions of the response variable). If *we* is a rank-1 array of length q (the dimensionality of the response variable), then this vector is the diagonal of the covariant weighting matrix for all data points. If *we* is a rank-1 array of length n (the number of data points), then the i'th element is the weight for the i'th response variable observation (single-dimensional only). If *we* is a rank-2 array of shape (q, q), then this is the full covariant weighting matrix broadcast to each observation. If *we* is a rank-2 array of shape (q, n), then *we[:,i]* is the diagonal of the covariant weighting matrix for the i'th observation. If *we* is a rank-3 array of shape (q, q, n), then *we[:,:,i]* is the full specification of the covariant weighting matrix for each observation. If the fit is implicit, then only a positive scalar value is used.

wd [array_like, optional] If *wd* is a scalar, then that value is used for all data points (and all dimensions of the input variable). If *wd* = 0, then the covariant weighting matrix for each observation is set to the identity matrix (so each dimension of each observation has the same weight). If *wd* is a rank-1 array of length m (the dimensionality of the input variable), then this vector is the diagonal of the covariant weighting matrix for all data points. If *wd* is a rank-1 array of length n (the number of data points), then the i'th element is the weight for the ith input variable observation (single-dimensional only). If *wd* is a rank-2 array of shape (m, m), then this is the full covariant weighting matrix broadcast to each observation. If *wd* is a rank-2 array of shape (m, n), then *wd[:,i]* is the diagonal of the covariant weighting matrix for the ith observation. If *wd* is a rank-3 array of shape (m, m, n), then *wd[:,:,i]* is the full specification of the covariant weighting matrix for each observation.

fix [array_like of ints, optional] The *fix* argument is the same as ifixx in the class ODR. It is an array of integers with the same shape as data.x that determines which input observations are treated as fixed. One can use a sequence of length m (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value > 0 makes it free.

meta [dict, optional] Free-form dictionary for metadata.

Notes

Each argument is attached to the member of the instance of the same name. The structures of *x* and *y* are described in the Model class docstring. If *y* is an integer, then the Data instance can only be used to fit with implicit models where the dimensionality of the response is equal to the specified value of *y*.

The *we* argument weights the effect a deviation in the response variable has on the fit. The *wd* argument weights the effect a deviation in the input variable has on the fit. To handle multidimensional inputs and responses easily, the structure of these arguments has the n'th dimensional axis first. These arguments heavily use the structured arguments feature of ODRPACK to conveniently and flexibly support all options. See the ODRPACK User's Guide for a full explanation of how these weights are used in the algorithm. Basically, a higher value of the weight for a particular data point makes a deviation at that point more detrimental to the fit.

Methods

set_meta(**kwds)	Update the metadata dictionary with the keywords and data provided by keywords.

scipy.odr.Data.set_meta

Data.**set_meta**(***kwds*)

Update the metadata dictionary with the keywords and data provided by keywords.

Examples

```
data.set_meta(lab="Ph 7; Lab 26", title="Ag110 + Ag108 Decay")
```

scipy.odr.RealData

class scipy.odr.**RealData**(*x*, *y=None*, *sx=None*, *sy=None*, *covx=None*, *covy=None*, *fix=None*, *meta={}*)

The data, with weightings as actual standard deviations and/or covariances.

Parameters

x	[array_like] Observed data for the independent variable of the regression
y	[array_like, optional] If array-like, observed data for the dependent variable of the regression. A scalar input implies that the model to be used on the data is implicit.
sx	[array_like, optional] Standard deviations of *x*. *sx* are standard deviations of *x* and are converted to weights by dividing 1.0 by their squares.
sy	[array_like, optional] Standard deviations of *y*. *sy* are standard deviations of *y* and are converted to weights by dividing 1.0 by their squares.
covx	[array_like, optional] Covariance of *x* *covx* is an array of covariance matrices of *x* and are converted to weights by performing a matrix inversion on each observation's covariance matrix.
covy	[array_like, optional] Covariance of *y* *covy* is an array of covariance matrices and are converted to weights by performing a matrix inversion on each observation's covariance matrix.
fix	[array_like, optional] The argument and member fix is the same as Data.fix and ODR.ifixx: It is an array of integers with the same shape as *x* that determines which input observations are treated as fixed. One can use a sequence of length m (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value > 0 makes it free.
meta	[dict, optional] Free-form dictionary for metadata.

Notes

The weights *wd* and *we* are computed from provided values as follows:

sx and *sy* are converted to weights by dividing 1.0 by their squares. For example, `wd = 1./numpy.power(`sx`, 2)`.

covx and *covy* are arrays of covariance matrices and are converted to weights by performing a matrix inversion on each observation's covariance matrix. For example, `we[i] = numpy.linalg.inv(covy[i])`.

These arguments follow the same structured argument conventions as wd and we only restricted by their natures: *sx* and *sy* can't be rank-3, but *covx* and *covy* can be.

Only set *either sx* or *covx* (not both). Setting both will raise an exception. Same with *sy* and *covy*.

Methods

set_meta(**kwds)	Update the metadata dictionary with the keywords and data provided by keywords.

scipy.odr.RealData.set_meta

RealData.**set_meta**(**kwds)
Update the metadata dictionary with the keywords and data provided by keywords.

Examples

```
data.set_meta(lab="Ph 7; Lab 26", title="Ag110 + Ag108 Decay")
```

scipy.odr.Model

class scipy.odr.**Model**(*fcn*, *fjacb=None*, *fjacd=None*, *extra_args=None*, *estimate=None*, *implicit=0*, *meta=None*)
The Model class stores information about the function you wish to fit.

It stores the function itself, at the least, and optionally stores functions which compute the Jacobians used during fitting. Also, one can provide a function that will provide reasonable starting values for the fit parameters possibly given the set of data.

Parameters

fcn	[function] fcn(beta, x) –> y
fjacb	[function] Jacobian of fcn wrt the fit parameters beta. fjacb(beta, x) –> @f_i(x,B)/@B_j
fjacd	[function] Jacobian of fcn wrt the (possibly multidimensional) input variable. fjacd(beta, x) –> @f_i(x,B)/@x_j
extra_args	[tuple, optional] If specified, *extra_args* should be a tuple of extra arguments to pass to *fcn*, *fjacb*, and *fjacd*. Each will be called by *apply(fcn, (beta, x) + extra_args)*
estimate	[array_like of rank-1] Provides estimates of the fit parameters from the data estimate(data) –> estbeta
implicit	[boolean] If TRUE, specifies that the model is implicit; i.e *fcn(beta, x)* ~= 0 and there is no y data to fit against
meta	[dict, optional] freeform dictionary of metadata for the model

Notes

Note that the *fcn*, *fjacb*, and *fjacd* operate on NumPy arrays and return a NumPy array. The *estimate* object takes an instance of the Data class.

Here are the rules for the shapes of the argument and return arrays of the callback functions:

x if the input data is single-dimensional, then *x* is rank-1 array; i.e., `x = array([1, 2, 3, ...]); x.shape = (n,)` If the input data is multi-dimensional, then *x* is a rank-2 array; i.e., `x = array([[1, 2, ...], [2, 4, ...]]); x.shape = (m, n)`. In all cases, it has the same shape as the input data array passed to *odr*. *m* is the dimensionality of the input data, *n* is the number of observations.

y if the response variable is single-dimensional, then *y* is a rank-1 array, i.e., `y = array([2, 4, ...]); y.shape = (n,)`. If the response variable is multi-dimensional, then *y* is a rank-2 array, i.e., `y = array([[2, 4, ...], [3, 6, ...]]); y.shape = (q, n)` where *q* is the dimensionality of the response variable.

beta

rank-1 array of length *p* where *p* is the number of parameters; i.e. `beta = array([B_1, B_2, ..., B_p])`

fjacb

if the response variable is multi-dimensional, then the return array's shape is *(q, p, n)* such that `fjacb(x, beta)[l,k,i] = d f_l(X,B)/d B_k` evaluated at the ith data point. If *q == 1*, then the return array is only rank-2 and with shape *(p, n)*.

fjacd

as with fjacb, only the return array's shape is *(q, m, n)* such that `fjacd(x,beta)[l,j,i] = d f_l(X, B)/d X_j` at the ith data point. If *q == 1*, then the return array's shape is *(m, n)*. If *m == 1*, the shape is (q, n). If *m == q == 1*, the shape is *(n,)*.

Methods

set_meta(**kwds)	Update the metadata dictionary with the keywords and data provided here.

scipy.odr.Model.set_meta

Model.**set_meta**(***kwds*)

Update the metadata dictionary with the keywords and data provided here.

Examples

set_meta(name="Exponential", equation="y = a exp(b x) + c")

scipy.odr.ODR

class scipy.odr.**ODR**(*data*, *model*, *beta0=None*, *delta0=None*, *ifixb=None*, *ifixx=None*, *job=None*, *iprint=None*, *errfile=None*, *rptfile=None*, *ndigit=None*, *taufac=None*, *sstol=None*, *partol=None*, *maxit=None*, *stpb=None*, *stpd=None*, *sclb=None*, *scld=None*, *work=None*, *iwork=None*, *overwrite=False*)

The ODR class gathers all information and coordinates the running of the main fitting routine.

Members of instances of the ODR class have the same names as the arguments to the initialization routine.

Parameters

data [Data class instance] instance of the Data class

model [Model class instance] instance of the Model class

Other Parameters

beta0 [array_like of rank-1] a rank-1 sequence of initial parameter values. Optional if model provides an "estimate" function to estimate these values.

delta0 [array_like of floats of rank-1, optional] a (double-precision) float array to hold the initial values of the errors in the input variables. Must be same shape as data.x

ifixb [array_like of ints of rank-1, optional] sequence of integers with the same length as beta0 that determines which parameters are held fixed. A value of 0 fixes the parameter, a value > 0 makes the parameter free.

ifixx [array_like of ints with same shape as data.x, optional] an array of integers with the same shape as data.x that determines which input observations are treated as fixed. One can use a sequence of length m (the dimensionality of the input observations) to fix some dimensions for all observations. A value of 0 fixes the observation, a value > 0 makes it free.

job [int, optional] an integer telling ODRPACK what tasks to perform. See p. 31 of the ODRPACK User's Guide if you absolutely must set the value here. Use the method set_job post-initialization for a more readable interface.

iprint [int, optional] an integer telling ODRPACK what to print. See pp. 33-34 of the ODRPACK User's Guide if you absolutely must set the value here. Use the method set_iprint post-initialization for a more readable interface.

errfile [str, optional] string with the filename to print ODRPACK errors to. If the file already exists, an error will be thrown. The *overwrite* argument can be used to prevent this. *Do Not Open This File Yourself!*

rptfile [str, optional] string with the filename to print ODRPACK summaries to. If the file already exists, an error will be thrown. The *overwrite* argument can be used to prevent this. *Do Not Open This File Yourself!*

ndigit [int, optional] integer specifying the number of reliable digits in the computation of the function.

taufac [float, optional] float specifying the initial trust region. The default value is 1. The initial trust region is equal to taufac times the length of the first computed Gauss-Newton step. taufac must be less than 1.

sstol [float, optional] float specifying the tolerance for convergence based on the relative change in the sum-of-squares. The default value is eps**(1/2) where eps is the smallest value such that 1 + eps > 1 for double precision computation on the machine. sstol must be less than 1.

partol [float, optional] float specifying the tolerance for convergence based on the relative change in the estimated parameters. The default value is eps**(2/3) for explicit models and `eps**(1/3)` for implicit models. partol must be less than 1.

maxit [int, optional] integer specifying the maximum number of iterations to perform. For first runs, maxit is the total number of iterations performed and defaults to 50. For restarts, maxit is the number of additional iterations to perform and defaults to 10.

stpb [array_like, optional] sequence (`len(stpb) == len(beta0)`) of relative step sizes to compute finite difference derivatives wrt the parameters.

stpd [optional] array (`stpd.shape == data.x.shape` or `stpd.shape == (m,)`) of relative step sizes to compute finite difference derivatives wrt the input variable errors. If stpd is a rank-1 array with length m (the dimensionality of the input variable), then the values are broadcast to all observations.

sclb [array_like, optional] sequence (`len(stpb) == len(beta0)`) of scaling factors for the parameters. The purpose of these scaling factors are to scale all of the parameters to around unity. Normally appropriate scaling factors are computed if this argument is not specified. Specify them yourself if the automatic procedure goes awry.

scld [array_like, optional] array (scld.shape == data.x.shape or scld.shape == (m,)) of scaling factors for the *errors* in the input variables. Again, these factors are automatically computed if you do not provide them. If scld.shape == (m,), then the scaling factors are broadcast to all observations.

work [ndarray, optional] array to hold the double-valued working data for ODRPACK. When restarting, takes the value of self.output.work.

iwork [ndarray, optional] array to hold the integer-valued working data for ODRPACK. When restarting, takes the value of self.output.iwork.

overwrite [bool, optional] If it is True, output files defined by *errfile* and *rptfile* are overwritten. The default is False.

Attributes

data [Data] The data for this fit
model [Model] The model used in fit
output [Output] An instance if the Output class containing all of the returned data from an invocation of ODR.run() or ODR.restart()

Methods

restart([iter])	Restarts the run with iter more iterations.
run()	Run the fitting routine with all of the information given and with `full_output=1`.
set_iprint([init, so_init, iter, so_iter, …])	Set the iprint parameter for the printing of computation reports.
set_job([fit_type, deriv, var_calc, …])	Sets the "job" parameter is a hopefully comprehensible way.

scipy.odr.ODR.restart

ODR.**restart**(*iter=None*)
Restarts the run with iter more iterations.

Parameters

iter [int, optional] ODRPACK's default for the number of new iterations is 10.

Returns

output [Output instance] This object is also assigned to the attribute .output .

scipy.odr.ODR.run

ODR.**run**()
Run the fitting routine with all of the information given and with `full_output=1`.

Returns

output [Output instance] This object is also assigned to the attribute .output .

scipy.odr.ODR.set_iprint

ODR.**set_iprint**(*init=None*, *so_init=None*, *iter=None*, *so_iter=None*, *iter_step=None*, *final=None*, *so_final=None*)
Set the iprint parameter for the printing of computation reports.

If any of the arguments are specified here, then they are set in the iprint member. If iprint is not set manually or with this method, then ODRPACK defaults to no printing. If no filename is specified with the member rptfile, then ODRPACK prints to stdout. One can tell ODRPACK to print to stdout in addition to the specified filename by setting the so_* arguments to this function, but one cannot specify to print to stdout but not a file since one can do that by not specifying a rptfile filename.

There are three reports: initialization, iteration, and final reports. They are represented by the arguments init, iter, and final respectively. The permissible values are 0, 1, and 2 representing “no report”, “short report”, and “long report” respectively.

The argument iter_step (0 <= iter_step <= 9) specifies how often to make the iteration report; the report will be made for every iter_step’th iteration starting with iteration one. If iter_step == 0, then no iteration report is made, regardless of the other arguments.

If the rptfile is None, then any so_* arguments supplied will raise an exception.

scipy.odr.ODR.set_job

ODR.**set_job**(*fit_type=None*, *deriv=None*, *var_calc=None*, *del_init=None*, *restart=None*)

Sets the “job” parameter is a hopefully comprehensible way.

If an argument is not specified, then the value is left as is. The default value from class initialization is for all of these options set to 0.

Parameters

fit_type [{0, 1, 2} int] 0 -> explicit ODR
1 -> implicit ODR
2 -> ordinary least-squares

deriv [{0, 1, 2, 3} int] 0 -> forward finite differences
1 -> central finite differences
2 -> user-supplied derivatives (Jacobians) with results checked by ODRPACK
3 -> user-supplied derivatives, no checking

var_calc [{0, 1, 2} int]
0 -> calculate asymptotic covariance matrix and fit parameter uncertainties (V_B, s_B) using derivatives recomputed at the final solution
1 -> calculate V_B and s_B using derivatives from last iteration
2 -> do not calculate V_B and s_B

del_init [{0, 1} int] 0 -> initial input variable offsets set to 0
1 -> initial offsets provided by user in variable “work”

restart [{0, 1} int] 0 -> fit is not a restart
1 -> fit is a restart

Notes

The permissible values are different from those given on pg. 31 of the ODRPACK User’s Guide only in that one cannot specify numbers greater than the last value for each variable.

If one does not supply functions to compute the Jacobians, the fitting procedure will change deriv to 0, finite differences, as a default. To initialize the input variable offsets by yourself, set del_init to 1 and put the offsets into the “work” variable correctly.

scipy.odr.Output

class scipy.odr.**Output**(*output*)

The Output class stores the output of an ODR run.

Notes

Takes one argument for initialization, the return value from the function *odr*. The attributes listed as "optional" above are only present if *odr* was run with `full_output=1`.

Attributes

beta [ndarray] Estimated parameter values, of shape (q,).
sd_beta [ndarray] Standard deviations of the estimated parameters, of shape (p,).
cov_beta [ndarray] Covariance matrix of the estimated parameters, of shape (p,p).
delta [ndarray, optional] Array of estimated errors in input variables, of same shape as *x*.
eps [ndarray, optional] Array of estimated errors in response variables, of same shape as *y*.
xplus [ndarray, optional] Array of `x + delta`.
y [ndarray, optional] Array `y = fcn(x + delta)`.
res_var [float, optional] Residual variance.
sum_square [float, optional] Sum of squares error.
sum_square_delta [float, optional] Sum of squares of delta error.
sum_square_eps [float, optional] Sum of squares of eps error.
inv_condnum [float, optional] Inverse condition number (cf. ODRPACK UG p. 77).
rel_error [float, optional] Relative error in function values computed within fcn.
work [ndarray, optional] Final work array.
work_ind [dict, optional] Indices into work for drawing out values (cf. ODRPACK UG p. 83).
info [int, optional] Reason for returning, as output by ODRPACK (cf. ODRPACK UG p. 38).
stopreason [list of str, optional] *info* interpreted into English.

Methods

pprint()	Pretty-print important results.

scipy.odr.Output.pprint

Output.**pprint**()

Pretty-print important results.

scipy.odr.odr

scipy.odr.**odr**(*fcn*, *beta0*, *y*, *x*, *we=None*, *wd=None*, *fjacb=None*, *fjacd=None*, *extra_args=None*, *ifixx=None*, *ifixb=None*, *job=0*, *iprint=0*, *errfile=None*, *rptfile=None*, *ndigit=0*, *taufac=0.0*, *sstol=- 1.0*, *partol=- 1.0*, *maxit=- 1*, *stpb=None*, *stpd=None*, *sclb=None*, *scld=None*, *work=None*, *iwork=None*, *full_output=0*)

Low-level function for ODR.

See also:

ODR

The ODR class gathers all information and coordinates the running of the main fitting routine.

Model

The Model class stores information about the function you wish to fit.

Data

The data to fit.

RealData

Data with weights as actual std. dev.s and/or covariances.

Notes

This is a function performing the same operation as the *ODR*, *Model*, and *Data* classes together. The parameters of this function are explained in the class documentation.

scipy.odr.OdrWarning

exception scipy.odr.**OdrWarning**

Warning indicating that the data passed into ODR will cause problems when passed into 'odr' that the user should be aware of.

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.odr.OdrError

exception scipy.odr.**OdrError**

Exception indicating an error in fitting.

This is raised by *odr* if an error occurs during fitting.

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.odr.OdrStop

exception scipy.odr.**OdrStop**

Exception stopping fitting.

You can raise this exception in your objective function to tell *odr* to stop fitting.

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.odr.polynomial

scipy.odr.**polynomial**(*order*)

Factory function for a general polynomial model.

Parameters

order [int or sequence] If an integer, it becomes the order of the polynomial to fit. If a sequence of numbers, then these are the explicit powers in the polynomial. A constant term (power 0) is always included, so don't include 0. Thus, polynomial(n) is equivalent to polynomial(range(1, n+1)).

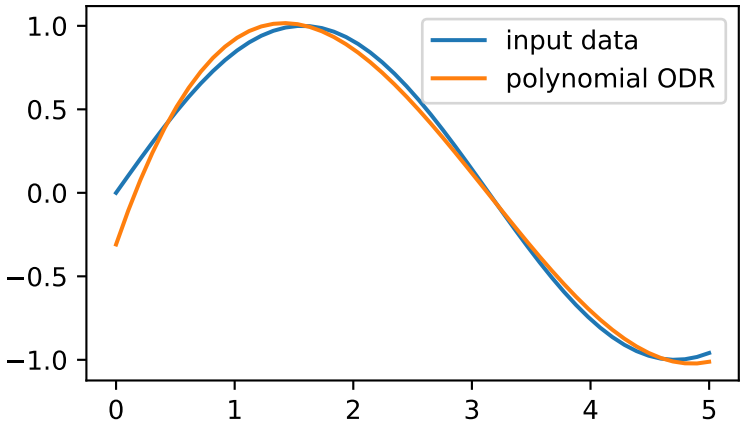
Returns

polynomial
[Model instance] Model instance.

Examples

We can fit an input data using orthogonal distance regression (ODR) with a polynomial model:

```
>>> import matplotlib.pyplot as plt
>>> from scipy import odr
>>> x = np.linspace(0.0, 5.0)
>>> y = np.sin(x)
>>> poly_model = odr.polynomial(3)  # using third order polynomial model
>>> data = odr.Data(x, y)
>>> odr_obj = odr.ODR(data, poly_model)
>>> output = odr_obj.run()  # running ODR fitting
>>> poly = np.poly1d(output.beta[::-1])
>>> poly_y = poly(x)
>>> plt.plot(x, y, label="input data")
>>> plt.plot(x, poly_y, label="polynomial ODR")
>>> plt.legend()
>>> plt.show()
```



scipy.odr.exponential

scipy.odr.**exponential = <scipy.odr.models._ExponentialModel object>**

Exponential model

This model is defined by $y = \beta_0 + e^{\beta_1 x}$

Examples

We can calculate orthogonal distance regression with an exponential model:

```
>>> from scipy import odr
>>> x = np.linspace(0.0, 5.0)
>>> y = -10.0 + np.exp(0.5*x)
>>> data = odr.Data(x, y)
>>> odr_obj = odr.ODR(data, odr.exponential)
>>> output = odr_obj.run()
>>> print(output.beta)
[-10.    0.5]
```

scipy.odr.multilinear

scipy.odr.**multilinear = <scipy.odr.models._MultilinearModel object>**

Arbitrary-dimensional linear model

This model is defined by $y = \beta_0 + \sum_{i=1}^{m} \beta_i x_i$

Examples

We can calculate orthogonal distance regression with an arbitrary dimensional linear model:

```
>>> from scipy import odr
>>> x = np.linspace(0.0, 5.0)
>>> y = 10.0 + 5.0 * x
>>> data = odr.Data(x, y)
>>> odr_obj = odr.ODR(data, odr.multilinear)
>>> output = odr_obj.run()
>>> print(output.beta)
[10.  5.]
```

scipy.odr.unilinear

scipy.odr.**unilinear = <scipy.odr.models._UnilinearModel object>**

Univariate linear model

This model is defined by $y = \beta_0 x + \beta_1$

Examples

We can calculate orthogonal distance regression with an unilinear model:

```
>>> from scipy import odr
>>> x = np.linspace(0.0, 5.0)
>>> y = 1.0 * x + 2.0
>>> data = odr.Data(x, y)
>>> odr_obj = odr.ODR(data, odr.unilinear)
>>> output = odr_obj.run()
>>> print(output.beta)
[1. 2.]
```

scipy.odr.quadratic

scipy.odr.**quadratic = <scipy.odr.models._QuadraticModel object>**

Quadratic model

This model is defined by $y = \beta_0 x^2 + \beta_1 x + \beta_2$

Examples

We can calculate orthogonal distance regression with a quadratic model:

```
>>> from scipy import odr
>>> x = np.linspace(0.0, 5.0)
>>> y = 1.0 * x ** 2 + 2.0 * x + 3.0
>>> data = odr.Data(x, y)
>>> odr_obj = odr.ODR(data, odr.quadratic)
>>> output = odr_obj.run()
>>> print(output.beta)
[1. 2. 3.]
```

Usage information

Introduction

Why Orthogonal Distance Regression (ODR)? Sometimes one has measurement errors in the explanatory (a.k.a., "independent") variable(s), not just the response (a.k.a., "dependent") variable(s). Ordinary Least Squares (OLS) fitting procedures treat the data for explanatory variables as fixed, i.e., not subject to error of any kind. Furthermore, OLS procedures require that the response variables be an explicit function of the explanatory variables; sometimes making the equation explicit is impractical and/or introduces errors. ODR can handle both of these cases with ease, and can even reduce to the OLS case if that is sufficient for the problem.

ODRPACK is a FORTRAN-77 library for performing ODR with possibly non-linear fitting functions. It uses a modified trust-region Levenberg-Marquardt-type algorithm [1] to estimate the function parameters. The fitting functions are provided by Python functions operating on NumPy arrays. The required derivatives may be provided by Python functions as well, or may be estimated numerically. ODRPACK can do explicit or implicit ODR fits, or it can do OLS. Input and output variables may be multidimensional. Weights can be provided to account for different variances of the observations, and even covariances between dimensions of the variables.

The *scipy.odr* package offers an object-oriented interface to ODRPACK, in addition to the low-level *odr* function.

Additional background information about ODRPACK can be found in the ODRPACK User's Guide, reading which is recommended.

Basic usage

1. Define the function you want to fit against.:

```
def f(B, x):
    '''Linear function y = m*x + b'''
    # B is a vector of the parameters.
    # x is an array of the current x values.
    # x is in the same format as the x passed to Data or RealData.
    #
    # Return an array in the same format as y passed to Data or RealData.
    return B[0]*x + B[1]
```

2. Create a Model.:

```
linear = Model(f)
```

3. Create a Data or RealData instance.:

```
mydata = Data(x, y, wd=1./power(sx,2), we=1./power(sy,2))
```

   or, when the actual covariances are known:

```
mydata = RealData(x, y, sx=sx, sy=sy)
```

4. Instantiate ODR with your data, model and initial parameter estimate.:

```
myodr = ODR(mydata, linear, beta0=[1., 2.])
```

5. Run the fit.:

```
myoutput = myodr.run()
```

6. Examine output.:

```
myoutput.pprint()
```

References

3.3.19 Optimization and root finding (`scipy.optimize`)

SciPy `optimize` provides functions for minimizing (or maximizing) objective functions, possibly subject to constraints. It includes solvers for nonlinear problems (with support for both local and global optimization algorithms), linear programing, constrained and nonlinear least-squares, root finding, and curve fitting.

Common functions and objects, shared across different solvers, are:

show_options([solver, method, disp])	Show documentation for additional options of optimization solvers.
OptimizeResult	Represents the optimization result.
OptimizeWarning	

scipy.optimize.show_options

scipy.optimize.**show_options**(*solver=None*, *method=None*, *disp=True*)

Show documentation for additional options of optimization solvers.

These are method-specific options that can be supplied through the `options` dict.

Parameters

solver	[str] Type of optimization solver. One of 'minimize', 'minimize_scalar', 'root', 'root_scalar', 'linprog', or 'quadratic_assignment'.
method	[str, optional] If not given, shows all methods of the specified solver. Otherwise, show only the options for the specified method. Valid values corresponds to methods' names of respective solver (e.g., 'BFGS' for 'minimize').
disp	[bool, optional] Whether to print the result rather than returning it.

Returns

text	Either None (for disp=True) or the text string (disp=False)

Notes

The solver-specific methods are:

`scipy.optimize.minimize`

- *Nelder-Mead*
- *Powell*
- *CG*
- *BFGS*
- *Newton-CG*
- *L-BFGS-B*
- *TNC*
- *COBYLA*
- *SLSQP*
- *dogleg*
- *trust-ncg*

`scipy.optimize.root`

- *hybr*
- *lm*
- *broyden1*
- *broyden2*
- *anderson*
- *linearmixing*
- *diagbroyden*
- *excitingmixing*
- *krylov*

- *df-sane*

scipy.optimize.minimize_scalar

- *brent*
- *golden*
- *bounded*

scipy.optimize.root_scalar

- *bisect*
- *brentq*
- *brenth*
- *ridder*
- *toms748*
- *newton*
- *secant*
- *halley*

scipy.optimize.linprog

- *simplex*
- *interior-point*
- *revised simplex*
- *highs*
- *highs-ds*
- *highs-ipm*

scipy.optimize.quadratic_assignment

- *faq*
- *2opt*

Examples

We can print documentations of a solver in stdout:

```
>>> from scipy.optimize import show_options
>>> show_options(solver="minimize")
...
```

Specifying a method is possible:

```
>>> show_options(solver="minimize", method="Nelder-Mead")
...
```

We can also get the documentations as a string:

```
>>> show_options(solver="minimize", method="Nelder-Mead", disp=False)
Minimization of scalar function of one or more variables using the ...
```

scipy.optimize.OptimizeResult

class scipy.optimize.**OptimizeResult**
Represents the optimization result.

Notes

There may be additional attributes not listed above depending of the specific solver. Since this class is essentially a subclass of dict with attribute accessors, one can see which attributes are available using the *keys()* method.

Attributes

x [ndarray] The solution of the optimization.
success [bool] Whether or not the optimizer exited successfully.
status [int] Termination status of the optimizer. Its value depends on the underlying solver. Refer to *message* for details.
message [str] Description of the cause of the termination.
fun, jac, hess: ndarray
Values of objective function, its Jacobian and its Hessian (if available). The Hessians may be approximations, see the documentation of the function in question.
hess_inv [object] Inverse of the objective function's Hessian; may be an approximation. Not available for all solvers. The type of this attribute may be either np.ndarray or scipy.sparse.linalg.LinearOperator.
nfev, njev, nhev
[int] Number of evaluations of the objective functions and of its Jacobian and Hessian.
nit [int] Number of iterations performed by the optimizer.
maxcv [float] The maximum constraint violation.

Methods

__getitem__	x.__getitem__(y) <==> x[y]
__len__(/)	Return len(self).
clear()	
copy()	
fromkeys(iterable[, value])	Create a new dictionary with keys from iterable and values set to value.
get(key[, default])	Return the value for key if key is in the dictionary, else default.
items()	
keys()	
pop(k[,d])	If key is not found, d is returned if given, otherwise KeyError is raised
popitem(/)	Remove and return a (key, value) pair as a 2-tuple.
setdefault(key[, default])	Insert key with a value of default if key is not in the dictionary.

continues on next page

Table 121 – continued from previous page

update([E,]**F)	If E is present and has a .keys() method, then does: for k in E: D[k] = E[k] If E is present and lacks a .keys() method, then does: for k, v in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]
values()	

scipy.optimize.OptimizeResult.__getitem__

OptimizeResult.**__getitem__**()
x.__getitem__(y) <==> x[y]

scipy.optimize.OptimizeResult.__len__

OptimizeResult.**__len__**(/)
Return len(self).

scipy.optimize.OptimizeResult.clear

OptimizeResult.**clear**() → None. Remove all items from D.

scipy.optimize.OptimizeResult.copy

OptimizeResult.**copy**() → a shallow copy of D

scipy.optimize.OptimizeResult.fromkeys

OptimizeResult.**fromkeys**(*iterable*, *value=None*, /)
Create a new dictionary with keys from iterable and values set to value.

scipy.optimize.OptimizeResult.get

OptimizeResult.**get**(*key*, *default=None*, /)
Return the value for key if key is in the dictionary, else default.

scipy.optimize.OptimizeResult.items

OptimizeResult.**items**() → a set-like object providing a view on D's items

scipy.optimize.OptimizeResult.keys

OptimizeResult.**keys**() → a set-like object providing a view on D's keys

scipy.optimize.OptimizeResult.pop

OptimizeResult.**pop**(*k*[, *d*]) → v, remove specified key and return the corresponding value.
If key is not found, d is returned if given, otherwise KeyError is raised

scipy.optimize.OptimizeResult.popitem

OptimizeResult.**popitem**(/)
Remove and return a (key, value) pair as a 2-tuple.

Pairs are returned in LIFO (last-in, first-out) order. Raises KeyError if the dict is empty.

scipy.optimize.OptimizeResult.setdefault

OptimizeResult.**setdefault**(*key*, *default=None*, */*)
Insert key with a value of default if key is not in the dictionary.

Return the value for key if key is in the dictionary, else default.

scipy.optimize.OptimizeResult.update

OptimizeResult.**update**([*E*], ***F*) → None. Update D from dict/iterable E and F.
If E is present and has a .keys() method, then does: for k in E: D[k] = E[k] If E is present and lacks a .keys() method, then does: for k, v in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]

scipy.optimize.OptimizeResult.values

OptimizeResult.**values**() → an object providing a view on D's values

scipy.optimize.OptimizeWarning

exception scipy.optimize.**OptimizeWarning**

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

Optimization

Scalar functions optimization

minimize_scalar(fun[, bracket, bounds, …])	Minimization of scalar function of one variable.

scipy.optimize.minimize_scalar

scipy.optimize.**minimize_scalar**(*fun*, *bracket=None*, *bounds=None*, *args=()*, *method='brent'*, *tol=None*, *options=None*)
Minimization of scalar function of one variable.

Parameters

fun [callable] Objective function. Scalar function, must return a scalar.

bracket [sequence, optional] For methods 'brent' and 'golden', *bracket* defines the bracketing interval and can either have three items `(a, b, c)` so that `a < b < c` and `fun(b) < fun(a), fun(c)` or two items `a` and `c` which are assumed to be a starting interval for a downhill bracket search (see *bracket*); it doesn't always mean that the obtained solution will satisfy `a <= x <= c`.

bounds [sequence, optional] For method 'bounded', *bounds* is mandatory and must have two items corresponding to the optimization bounds.

args [tuple, optional] Extra arguments passed to the objective function.

method [str or callable, optional] Type of solver. Should be one of:

- 'Brent' *(see here)*
- 'Bounded' *(see here)*
- 'Golden' *(see here)*
- custom - a callable object (added in version 0.14.0), see below

tol [float, optional] Tolerance for termination. For detailed control, use solver-specific options.

options [dict, optional] A dictionary of solver options.
maxiter [int] Maximum number of iterations to perform.
disp [bool] Set to True to print convergence messages.
See *show_options* for solver-specific options.

Returns

res [OptimizeResult] The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the optimizer exited successfully and `message` which describes the cause of the termination. See *OptimizeResult* for a description of other attributes.

See also:

minimize

Interface to minimization algorithms for scalar multivariate functions

show_options

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *Brent*.

Method *Brent* uses Brent's algorithm to find a local minimum. The algorithm uses inverse parabolic interpolation when possible to speed up convergence of the golden section method.

Method *Golden* uses the golden section search technique. It uses analog of the bisection method to decrease the bracketed interval. It is usually preferable to use the *Brent* method.

Method *Bounded* can perform bounded minimization. It uses the Brent method to find a local minimum in the interval x1 < xopt < x2.

Custom minimizers

It may be useful to pass a custom minimization method, for example when using some library frontend to minimize_scalar. You can simply pass a callable as the `method` parameter.

The callable is called as `method(fun, args, **kwargs, **options)` where `kwargs` corresponds to any other parameters passed to *minimize* (such as *bracket*, *tol*, etc.), except the *options* dict, which has its contents also passed as *method* parameters pair by pair. The method shall return an *OptimizeResult* object.

The provided *method* callable must be able to accept (and possibly ignore) arbitrary parameters; the set of parameters accepted by *minimize* may expand in future versions and then these parameters will be passed to the method. You can find an example in the scipy.optimize tutorial.

New in version 0.11.0.

Examples

Consider the problem of minimizing the following function.

```
>>> def f(x):
...     return (x - 2) * x * (x + 2)**2
```

Using the *Brent* method, we find the local minimum as:

```
>>> from scipy.optimize import minimize_scalar
>>> res = minimize_scalar(f)
>>> res.x
1.28077640403
```

Using the *Bounded* method, we find a local minimum with specified bounds as:

```
>>> res = minimize_scalar(f, bounds=(-3, -1), method='bounded')
>>> res.x
-2.0000002026
```

The *minimize_scalar* function supports the following methods:

minimize_scalar(method='brent')

scipy.optimize.**minimize_scalar**(*fun*, *args=()*, *method='brent'*, *tol=None*, *options={'func': None, 'brack': None, 'xtol': 1.48e-08, 'maxiter': 500}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize_scalar*

Options

maxiter [int] Maximum number of iterations to perform.
xtol [float] Relative error in solution *xopt* acceptable for convergence.

Notes

Uses inverse parabolic interpolation when possible to speed up convergence of golden section method.

minimize_scalar(method='bounded')

scipy.optimize.**minimize_scalar**(*fun*, *bounds=None*, *args=()*, *method='bounded'*, *tol=None*, *options={'func': None, 'xatol': 1e-05, 'maxiter': 500, 'disp': 0}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize_scalar*

Options

maxiter [int] Maximum number of iterations to perform.
disp: int, optional

If non-zero, print messages.
0 : no message printing. 1 : non-convergence notification messages only. 2 : print a message on convergence too. 3 : print iteration results.

xatol [float] Absolute error in solution *xopt* acceptable for convergence.

minimize_scalar(method='golden')

scipy.optimize.**minimize_scalar**(*fun*, *args=()*, *method='golden'*, *tol=None*, *options={'func': None, 'brack': None, 'xtol': 1.4901161193847656e-08, 'maxiter': 5000}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize_scalar*

Options

maxiter [int] Maximum number of iterations to perform.
xtol [float] Relative error in solution *xopt* acceptable for convergence.

Local (multivariate) optimization

minimize(fun, x0[, args, method, jac, hess, …])	Minimization of scalar function of one or more variables.

scipy.optimize.minimize

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method=None*, *jac=None*, *hess=None*, *hessp=None*, *bounds=None*, *constraints=()*, *tol=None*, *callback=None*, *options=None*)

Minimization of scalar function of one or more variables.

Parameters

fun [callable] The objective function to be minimized.

```
fun(x, *args) -> float
```

where `x` is an 1-D array with shape (n,) and `args` is a tuple of the fixed parameters needed to completely specify the function.

x0 [ndarray, shape (n,)] Initial guess. Array of real elements of size (n,), where 'n' is the number of independent variables.

args [tuple, optional] Extra arguments passed to the objective function and its derivatives (*fun*, *jac* and *hess* functions).

method [str or callable, optional] Type of solver. Should be one of

- 'Nelder-Mead' *(see here)*
- 'Powell' *(see here)*
- 'CG' *(see here)*
- 'BFGS' *(see here)*
- 'Newton-CG' *(see here)*
- 'L-BFGS-B' *(see here)*
- 'TNC' *(see here)*
- 'COBYLA' *(see here)*
- 'SLSQP' *(see here)*
- 'trust-constr'*(see here)*
- 'dogleg' *(see here)*
- 'trust-ncg' *(see here)*
- 'trust-exact' *(see here)*

- 'trust-krylov' *(see here)*
- custom - a callable object (added in version 0.14.0), see below for description.

If not given, chosen to be one of `BFGS`, `L-BFGS-B`, `SLSQP`, depending if the problem has constraints or bounds.

jac [{callable, '2-point', '3-point', 'cs', bool}, optional] Method for computing the gradient vector. Only for CG, BFGS, Newton-CG, L-BFGS-B, TNC, SLSQP, dogleg, trust-ncg, trust-krylov, trust-exact and trust-constr. If it is a callable, it should be a function that returns the gradient vector:

```
jac(x, *args) -> array_like, shape (n,)
```

where `x` is an array with shape (n,) and `args` is a tuple with the fixed parameters. If *jac* is a Boolean and is True, *fun* is assumed to return a tuple `(f, g)` containing the objective function and the gradient. Methods 'Newton-CG', 'trust-ncg', 'dogleg', 'trust-exact', and 'trust-krylov' require that either a callable be supplied, or that *fun* return the objective and gradient. If None or False, the gradient will be estimated using 2-point finite difference estimation with an absolute step size. Alternatively, the keywords {'2-point', '3-point', 'cs'} can be used to select a finite difference scheme for numerical estimation of the gradient with a relative step size. These finite difference schemes obey any specified *bounds*.

hess [{callable, '2-point', '3-point', 'cs', HessianUpdateStrategy}, optional] Method for computing the Hessian matrix. Only for Newton-CG, dogleg, trust-ncg, trust-krylov, trust-exact and trust-constr. If it is callable, it should return the Hessian matrix:

```
hess(x, *args) -> {LinearOperator, spmatrix, array}, (n, n)
```

where x is a (n,) ndarray and *args* is a tuple with the fixed parameters. LinearOperator and sparse matrix returns are only allowed for 'trust-constr' method. Alternatively, the keywords {'2-point', '3-point', 'cs'} select a finite difference scheme for numerical estimation. Or, objects implementing the *HessianUpdateStrategy* interface can be used to approximate the Hessian. Available quasi-Newton methods implementing this interface are:

- *BFGS*;
- *SR1*.

Whenever the gradient is estimated via finite-differences, the Hessian cannot be estimated with options {'2-point', '3-point', 'cs'} and needs to be estimated using one of the quasi-Newton strategies. 'trust-exact' cannot use a finite-difference scheme, and must be used with a callable returning an (n, n) array.

hessp [callable, optional] Hessian of objective function times an arbitrary vector p. Only for Newton-CG, trust-ncg, trust-krylov, trust-constr. Only one of *hessp* or *hess* needs to be given. If *hess* is provided, then *hessp* will be ignored. *hessp* must compute the Hessian times an arbitrary vector:

```
hessp(x, p, *args) -> ndarray shape (n,)
```

where x is a (n,) ndarray, p is an arbitrary vector with dimension (n,) and *args* is a tuple with the fixed parameters.

bounds [sequence or *Bounds*, optional] Bounds on variables for Nelder-Mead, L-BFGS-B, TNC, SLSQP, Powell, and trust-constr methods. There are two ways to specify the bounds:

1. Instance of *Bounds* class.
2. Sequence of `(min, max)` pairs for each element in *x*. None is used to specify no bound.

constraints

[{Constraint, dict} or List of {Constraint, dict}, optional] Constraints definition (only for COBYLA, SLSQP and trust-constr).

Constraints for 'trust-constr' are defined as a single object or a list of objects specifying constraints to the optimization problem. Available constraints are:

- *LinearConstraint*
- *NonlinearConstraint*

Constraints for COBYLA, SLSQP are defined as a list of dictionaries. Each dictionary with fields:

type [str] Constraint type: 'eq' for equality, 'ineq' for inequality.

fun [callable] The function defining the constraint.

jac [callable, optional] The Jacobian of *fun* (only for SLSQP).
args [sequence, optional] Extra arguments to be passed to the function and Jacobian.

Equality constraint means that the constraint function result is to be zero whereas inequality means that it is to be non-negative. Note that COBYLA only supports inequality constraints.

tol [float, optional] Tolerance for termination. When *tol* is specified, the selected minimization algorithm sets some relevant solver-specific tolerance(s) equal to *tol*. For detailed control, use solver-specific options.

options [dict, optional] A dictionary of solver options. All methods accept the following generic options:

maxiter [int] Maximum number of iterations to perform. Depending on the method each iteration may use several function evaluations.
disp [bool] Set to True to print convergence messages.

For method-specific options, see `show_options`.

callback [callable, optional] Called after each iteration. For 'trust-constr' it is a callable with the signature:

```
callback(xk, OptimizeResult state) -> bool
```

where `xk` is the current parameter vector. and `state` is an `OptimizeResult` object, with the same fields as the ones from the return. If callback returns True the algorithm execution is terminated. For all the other methods, the signature is:

```
callback(xk)
```

where `xk` is the current parameter vector.

Returns

res [OptimizeResult] The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the optimizer exited successfully and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes.

See also:

minimize_scalar

Interface to minimization algorithms for scalar univariate functions

show_options

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *BFGS*.

Unconstrained minimization

Method *CG* uses a nonlinear conjugate gradient algorithm by Polak and Ribiere, a variant of the Fletcher-Reeves method described in [5] pp.120-122. Only the first derivatives are used.

Method *BFGS* uses the quasi-Newton method of Broyden, Fletcher, Goldfarb, and Shanno (BFGS) [5] pp. 136. It uses the first derivatives only. BFGS has proven good performance even for non-smooth optimizations. This method also returns an approximation of the Hessian inverse, stored as *hess_inv* in the OptimizeResult object.

Method *Newton-CG* uses a Newton-CG algorithm [5] pp. 168 (also known as the truncated Newton method). It uses a CG method to the compute the search direction. See also *TNC* method for a box-constrained minimization with a similar algorithm. Suitable for large-scale problems.

Method *dogleg* uses the dog-leg trust-region algorithm [5] for unconstrained minimization. This algorithm requires the gradient and Hessian; furthermore the Hessian is required to be positive definite.

Method *trust-ncg* uses the Newton conjugate gradient trust-region algorithm [5] for unconstrained minimization. This algorithm requires the gradient and either the Hessian or a function that computes the product of the Hessian with a given vector. Suitable for large-scale problems.

Method *trust-krylov* uses the Newton GLTR trust-region algorithm [14], [15] for unconstrained minimization. This algorithm requires the gradient and either the Hessian or a function that computes the product of the Hessian with a given vector. Suitable for large-scale problems. On indefinite problems it requires usually less iterations than the *trust-ncg* method and is recommended for medium and large-scale problems.

Method *trust-exact* is a trust-region method for unconstrained minimization in which quadratic subproblems are solved almost exactly [13]. This algorithm requires the gradient and the Hessian (which is *not* required to be positive definite). It is, in many situations, the Newton method to converge in fewer iteraction and the most recommended for small and medium-size problems.

Bound-Constrained minimization

Method *Nelder-Mead* uses the Simplex algorithm [1], [2]. This algorithm is robust in many applications. However, if numerical computation of derivative can be trusted, other algorithms using the first and/or second derivatives information might be preferred for their better performance in general.

Method *L-BFGS-B* uses the L-BFGS-B algorithm [6], [7] for bound constrained minimization.

Method *Powell* is a modification of Powell's method [3], [4] which is a conjugate direction method. It performs sequential one-dimensional minimizations along each vector of the directions set (*direc* field in *options* and *info*), which is updated at each iteration of the main minimization loop. The function need not be differentiable, and no derivatives are taken. If bounds are not provided, then an unbounded line search will be used. If bounds are provided and the initial guess is within the bounds, then every function evaluation throughout the minimization procedure will be within the bounds. If bounds are provided, the initial guess is outside the bounds, and *direc* is full rank (default has full rank), then some function evaluations during the first iteration may be outside the bounds, but every function evaluation after the first iteration will be within the bounds. If *direc* is not full rank, then some parameters may not be optimized and the solution is not guaranteed to be within the bounds.

Method *TNC* uses a truncated Newton algorithm [5], [8] to minimize a function with variables subject to bounds. This algorithm uses gradient information; it is also called Newton Conjugate-Gradient. It differs from the *Newton-CG* method described above as it wraps a C implementation and allows each variable to be given upper and lower bounds.

Constrained Minimization

Method *COBYLA* uses the Constrained Optimization BY Linear Approximation (COBYLA) method [9], [10], [11]. The algorithm is based on linear approximations to the objective function and each constraint. The method wraps a FORTRAN implementation of the algorithm. The constraints functions 'fun' may return either a single number or an array or list of numbers.

Method *SLSQP* uses Sequential Least SQuares Programming to minimize a function of several variables with any combination of bounds, equality and inequality constraints. The method wraps the SLSQP Optimization subroutine originally implemented by Dieter Kraft [12]. Note that the wrapper handles infinite values in bounds by converting them into large floating values.

Method *trust-constr* is a trust-region algorithm for constrained optimization. It swiches between two implementations depending on the problem definition. It is the most versatile constrained minimization algorithm implemented in SciPy and the most appropriate for large-scale problems. For equality constrained problems it is an implementation of Byrd-Omojokun Trust-Region SQP method described in [17] and in [5], p. 549. When inequality constraints are imposed as well, it swiches to the trust-region interior point method described in [16]. This interior point algorithm, in turn, solves inequality constraints by introducing slack variables and solving a sequence of equality-constrained barrier problems for progressively smaller values of the barrier parameter. The previously

described equality constrained SQP method is used to solve the subproblems with increasing levels of accuracy as the iterate gets closer to a solution.

Finite-Difference Options

For Method *trust-constr* the gradient and the Hessian may be approximated using three finite-difference schemes: {'2-point', '3-point', 'cs'}. The scheme 'cs' is, potentially, the most accurate but it requires the function to correctly handles complex inputs and to be differentiable in the complex plane. The scheme '3-point' is more accurate than '2-point' but requires twice as many operations.

Custom minimizers

It may be useful to pass a custom minimization method, for example when using a frontend to this method such as *scipy.optimize.basinhopping* or a different library. You can simply pass a callable as the `method` parameter.

The callable is called as `method(fun, x0, args, **kwargs, **options)` where `kwargs` corresponds to any other parameters passed to *minimize* (such as *callback*, *hess*, etc.), except the *options* dict, which has its contents also passed as *method* parameters pair by pair. Also, if *jac* has been passed as a bool type, *jac* and *fun* are mangled so that *fun* returns just the function values and *jac* is converted to a function returning the Jacobian. The method shall return an *OptimizeResult* object.

The provided *method* callable must be able to accept (and possibly ignore) arbitrary parameters; the set of parameters accepted by *minimize* may expand in future versions and then these parameters will be passed to the method. You can find an example in the scipy.optimize tutorial.

New in version 0.11.0.

References

[1], [2], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14], [15], [16], [17]

Examples

Let us consider the problem of minimizing the Rosenbrock function. This function (and its respective derivatives) is implemented in *rosen* (resp. *rosen_der*, *rosen_hess*) in the *scipy.optimize*.

```
>>> from scipy.optimize import minimize, rosen, rosen_der
```

A simple application of the *Nelder-Mead* method is:

```
>>> x0 = [1.3, 0.7, 0.8, 1.9, 1.2]
>>> res = minimize(rosen, x0, method='Nelder-Mead', tol=1e-6)
>>> res.x
array([ 1.,  1.,  1.,  1.,  1.])
```

Now using the *BFGS* algorithm, using the first derivative and a few options:

```
>>> res = minimize(rosen, x0, method='BFGS', jac=rosen_der,
...                options={'gtol': 1e-6, 'disp': True})
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 26
         Function evaluations: 31
         Gradient evaluations: 31
>>> res.x
```

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```
array([ 1.,  1.,  1.,  1.,  1.])
>>> print(res.message)
Optimization terminated successfully.
>>> res.hess_inv
array([[ 0.00749589,  0.01255155,  0.02396251,  0.04750988,  0.09495377],␣
 ↪ # may vary
       [ 0.01255155,  0.02510441,  0.04794055,  0.09502834,  0.18996269],
       [ 0.02396251,  0.04794055,  0.09631614,  0.19092151,  0.38165151],
       [ 0.04750988,  0.09502834,  0.19092151,  0.38341252,  0.7664427 ],
       [ 0.09495377,  0.18996269,  0.38165151,  0.7664427,   1.53713523]])
```

Next, consider a minimization problem with several constraints (namely Example 16.4 from [5]). The objective function is:

```
>>> fun = lambda x: (x[0] - 1)**2 + (x[1] - 2.5)**2
```

There are three constraints defined as:

```
>>> cons = ({'type': 'ineq', 'fun': lambda x:  x[0] - 2 * x[1] + 2},
...         {'type': 'ineq', 'fun': lambda x: -x[0] - 2 * x[1] + 6},
...         {'type': 'ineq', 'fun': lambda x: -x[0] + 2 * x[1] + 2})
```

And variables must be positive, hence the following bounds:

```
>>> bnds = ((0, None), (0, None))
```

The optimization problem is solved using the SLSQP method as:

```
>>> res = minimize(fun, (2, 0), method='SLSQP', bounds=bnds,
...                constraints=cons)
```

It should converge to the theoretical solution (1.4 ,1.7).

The *minimize* function supports the following methods:

minimize(method='Nelder-Mead')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='Nelder-Mead'*, *bounds=None*, *tol=None*, *callback=None*, *options={'func': None, 'maxiter': None, 'maxfev': None, 'disp': False, 'return_all': False, 'initial_simplex': None, 'xatol': 0.0001, 'fatol': 0.0001, 'adaptive': False}*)

Minimization of scalar function of one or more variables using the Nelder-Mead algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

disp [bool] Set to True to print convergence messages.

maxiter, maxfev
[int] Maximum allowed number of iterations and function evaluations. Will default to `N*200`, where `N` is the number of variables, if neither *maxiter* or *maxfev* is set. If both *maxiter* and *maxfev* are set, minimization will stop at the first reached.

return_all [bool, optional] Set to True to return a list of the best solution at each of the iterations.

initial_simplex
: [array_like of shape (N + 1, N)] Initial simplex. If given, overrides *x0*. `initial_simplex[j,:]` should contain the coordinates of the jth vertex of the `N+1` vertices in the simplex, where `N` is the dimension.

xatol
: [float, optional] Absolute error in xopt between iterations that is acceptable for convergence.

fatol
: [number, optional] Absolute error in func(xopt) between iterations that is acceptable for convergence.

adaptive
: [bool, optional] Adapt algorithm parameters to dimensionality of problem. Useful for high-dimensional minimization [1].

bounds
: [sequence or *Bounds*, optional] Bounds on variables. There are two ways to specify the bounds:
  1. Instance of *Bounds* class.
  2. Sequence of `(min, max)` pairs for each element in *x*. None is used to specify no bound.

  Note that this just clips all vertices in simplex based on the bounds.

References

[1]

minimize(method='Powell')

`scipy.optimize.`**`minimize`**(*fun*, *x0*, *args=()*, *method='Powell'*, *bounds=None*, *tol=None*, *callback=None*, *options={'func': None, 'xtol': 0.0001, 'ftol': 0.0001, 'maxiter': None, 'maxfev': None, 'disp': False, 'direc': None, 'return_all': False}*)

Minimization of scalar function of one or more variables using the modified Powell algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

disp
: [bool] Set to True to print convergence messages.

xtol
: [float] Relative error in solution *xopt* acceptable for convergence.

ftol
: [float] Relative error in `fun(xopt)` acceptable for convergence.

maxiter, maxfev
: [int] Maximum allowed number of iterations and function evaluations. Will default to `N*1000`, where `N` is the number of variables, if neither *maxiter* or *maxfev* is set. If both *maxiter* and *maxfev* are set, minimization will stop at the first reached.

direc
: [ndarray] Initial set of direction vectors for the Powell method.

return_all
: [bool, optional] Set to True to return a list of the best solution at each of the iterations.

bounds
: [*Bounds*] If bounds are not provided, then an unbounded line search will be used. If bounds are provided and the initial guess is within the bounds, then every function evaluation throughout the minimization procedure will be within the bounds. If bounds are provided, the initial guess is outside the bounds, and *direc* is full rank (or left to default), then some function evaluations during the first iteration may be outside the bounds, but every function evaluation after the first iteration will be within the bounds. If *direc* is not full rank, then some parameters may not be optimized and the solution is not guaranteed to be within the bounds.

return_all
: [bool, optional] Set to True to return a list of the best solution at each of the iterations.

minimize(method='CG')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='CG'*, *jac=None*, *tol=None*, *callback=None*, *options={'gtol': 1e-05, 'norm': inf, 'eps': 1.4901161193847656e-08, 'maxiter': None, 'disp': False, 'return_all': False, 'finite_diff_rel_step': None}*)

Minimization of scalar function of one or more variables using the conjugate gradient algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

disp [bool] Set to True to print convergence messages.
maxiter [int] Maximum number of iterations to perform.
gtol [float] Gradient norm must be less than *gtol* before successful termination.
norm [float] Order of norm (Inf is max, -Inf is min).
eps [float or ndarray] If *jac is None* the absolute step size used for numerical approximation of the jacobian via forward differences.
return_all [bool, optional] Set to True to return a list of the best solution at each of the iterations.
finite_diff_rel_step [None or array_like, optional] If *jac in ['2-point', '3-point', 'cs']* the relative step size to use for numerical approximation of the jacobian. The absolute step size is computed as `h = rel_step * sign(x0) * max(1, abs(x0))`, possibly adjusted to fit into the bounds. For `method='3-point'` the sign of *h* is ignored. If None (default) then step is selected automatically.

minimize(method='BFGS')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='BFGS'*, *jac=None*, *tol=None*, *callback=None*, *options={'gtol': 1e-05, 'norm': inf, 'eps': 1.4901161193847656e-08, 'maxiter': None, 'disp': False, 'return_all': False, 'finite_diff_rel_step': None}*)

Minimization of scalar function of one or more variables using the BFGS algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

disp [bool] Set to True to print convergence messages.
maxiter [int] Maximum number of iterations to perform.
gtol [float] Gradient norm must be less than *gtol* before successful termination.
norm [float] Order of norm (Inf is max, -Inf is min).
eps [float or ndarray] If *jac is None* the absolute step size used for numerical approximation of the jacobian via forward differences.
return_all [bool, optional] Set to True to return a list of the best solution at each of the iterations.
finite_diff_rel_step [None or array_like, optional] If *jac in ['2-point', '3-point', 'cs']* the relative step size to use for numerical approximation of the jacobian. The absolute step size is computed as `h = rel_step * sign(x0) * max(1, abs(x0))`, possibly adjusted to fit into the bounds. For `method='3-point'` the sign of *h* is ignored. If None (default) then step is selected automatically.

minimize(method='Newton-CG')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='Newton-CG'*, *jac=None*, *hess=None*, *hessp=None*, *tol=None*, *callback=None*, *options={'xtol': 1e-05, 'eps': 1.4901161193847656e-08, 'maxiter': None, 'disp': False, 'return_all': False}*)

Minimization of scalar function of one or more variables using the Newton-CG algorithm.

Note that the *jac* parameter (Jacobian) is required.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

disp	[bool] Set to True to print convergence messages.
xtol	[float] Average relative error in solution *xopt* acceptable for convergence.
maxiter	[int] Maximum number of iterations to perform.
eps	[float or ndarray] If *hessp* is approximated, use this value for the step size.
return_all	[bool, optional] Set to True to return a list of the best solution at each of the iterations.

minimize(method='L-BFGS-B')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='L-BFGS-B'*, *jac=None*, *bounds=None*, *tol=None*, *callback=None*, *options={'disp': None, 'maxcor': 10, 'ftol': 2.220446049250313e-09, 'gtol': 1e-05, 'eps': 1e-08, 'maxfun': 15000, 'maxiter': 15000, 'iprint': - 1, 'maxls': 20, 'finite_diff_rel_step': None}*)

Minimize a scalar function of one or more variables using the L-BFGS-B algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

disp	[None or int] If *disp is None* (the default), then the supplied version of *iprint* is used. If *disp is not None*, then it overrides the supplied version of *iprint* with the behaviour you outlined.
maxcor	[int] The maximum number of variable metric corrections used to define the limited memory matrix. (The limited memory BFGS method does not store the full hessian but uses this many terms in an approximation to it.)
ftol	[float] The iteration stops when `(f^k - f^{k+1})/max{|f^k|,|f^{k+1}|,1} <= ftol`.
gtol	[float] The iteration will stop when `max{|proj g_i | i = 1, ..., n} <= gtol` where `pg_i` is the i-th component of the projected gradient.
eps	[float or ndarray] If *jac is None* the absolute step size used for numerical approximation of the jacobian via forward differences.
maxfun	[int] Maximum number of function evaluations.
maxiter	[int] Maximum number of iterations.
iprint	[int, optional] Controls the frequency of output. `iprint < 0` means no output; `iprint = 0` print only one line at the last iteration; `0 < iprint < 99` print also f and `|proj g|` every iprint iterations; `iprint = 99` print details of every iteration except n-vectors; `iprint = 100` print also the changes of active set and final x; `iprint > 100` print details of every iteration including x and g.
callback	[callable, optional] Called after each iteration, as `callback(xk)`, where `xk` is the current parameter vector.

maxls [int, optional] Maximum number of line search steps (per iteration). Default is 20.

finite_diff_rel_step
[None or array_like, optional] If *jac in ['2-point', '3-point', 'cs']* the relative step size to use for numerical approximation of the jacobian. The absolute step size is computed as `h = rel_step * sign(x0) * max(1, abs(x0))`, possibly adjusted to fit into the bounds. For `method='3-point'` the sign of *h* is ignored. If None (default) then step is selected automatically.

Notes

The option *ftol* is exposed via the *scipy.optimize.minimize* interface, but calling *scipy.optimize.fmin_l_bfgs_b* directly exposes *factr*. The relationship between the two is `ftol = factr * numpy.finfo(float).eps`. I.e., *factr* multiplies the default machine floating-point precision to arrive at *ftol*.

minimize(method='TNC')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='TNC'*, *jac=None*, *bounds=None*, *tol=None*, *callback=None*, *options={'eps': 1e-08, 'scale': None, 'offset': None, 'mesg_num': None, 'maxCGit': - 1, 'maxiter': None, 'eta': - 1, 'stepmx': 0, 'accuracy': 0, 'minfev': 0, 'ftol': - 1, 'xtol': - 1, 'gtol': - 1, 'rescale': - 1, 'disp': False, 'finite_diff_rel_step': None, 'maxfun': None}*)

Minimize a scalar function of one or more variables using a truncated Newton (TNC) algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

eps [float or ndarray] If *jac is None* the absolute step size used for numerical approximation of the jacobian via forward differences.

scale [list of floats] Scaling factors to apply to each variable. If None, the factors are up-low for interval bounded variables and 1+|x] fo the others. Defaults to None.

offset [float] Value to subtract from each variable. If None, the offsets are (up+low)/2 for interval bounded variables and x for the others.

disp [bool] Set to True to print convergence messages.

maxCGit [int] Maximum number of hessian*vector evaluations per main iteration. If maxCGit == 0, the direction chosen is -gradient if maxCGit < 0, maxCGit is set to max(1,min(50,n/2)). Defaults to -1.

maxiter [int, optional] Maximum number of function evaluations. This keyword is deprecated in favor of *maxfun*. Only if *maxfun* is None is this keyword used.

eta [float] Severity of the line search. If < 0 or > 1, set to 0.25. Defaults to -1.

stepmx [float] Maximum step for the line search. May be increased during call. If too small, it will be set to 10.0. Defaults to 0.

accuracy [float] Relative precision for finite difference calculations. If <= machine_precision, set to sqrt(machine_precision). Defaults to 0.

minfev [float] Minimum function value estimate. Defaults to 0.

ftol [float] Precision goal for the value of f in the stopping criterion. If ftol < 0.0, ftol is set to 0.0 defaults to -1.

xtol [float] Precision goal for the value of x in the stopping criterion (after applying x scaling factors). If xtol < 0.0, xtol is set to sqrt(machine_precision). Defaults to -1.

gtol [float] Precision goal for the value of the projected gradient in the stopping criterion (after applying x scaling factors). If gtol < 0.0, gtol is set to 1e-2 * sqrt(accuracy). Setting it to 0.0 is not recommended. Defaults to -1.

rescale [float] Scaling factor (in log10) used to trigger f value rescaling. If 0, rescale at each iteration. If a large value, never rescale. If < 0, rescale is set to 1.3.

finite_diff_rel_step
[None or array_like, optional] If *jac in ['2-point', '3-point', 'cs']* the relative step size to use for numerical approximation of the jacobian. The absolute step size is computed as `h = rel_step * sign(x0) * max(1, abs(x0))`, possibly adjusted to fit into the bounds. For `method='3-point'` the sign of *h* is ignored. If None (default) then step is selected automatically.

maxfun [int] Maximum number of function evaluations. If None, *maxfun* is set to max(100, 10*len(x0)). Defaults to None.

minimize(method='COBYLA')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='COBYLA'*, *constraints=()*, *tol=None*, *callback=None*, *options={'rhobeg': 1.0, 'maxiter': 1000, 'disp': False, 'catol': 0.0002}*)

Minimize a scalar function of one or more variables using the Constrained Optimization BY Linear Approximation (COBYLA) algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

rhobeg [float] Reasonable initial changes to the variables.

tol [float] Final accuracy in the optimization (not precisely guaranteed). This is a lower bound on the size of the trust region.

disp [bool] Set to True to print convergence messages. If False, *verbosity* is ignored as set to 0.

maxiter [int] Maximum number of function evaluations.

catol [float] Tolerance (absolute) for constraint violations

minimize(method='SLSQP')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='SLSQP'*, *jac=None*, *bounds=None*, *constraints=()*, *tol=None*, *callback=None*, *options={'func': None, 'maxiter': 100, 'ftol': 1e-06, 'iprint': 1, 'disp': False, 'eps': 1.4901161193847656e-08, 'finite_diff_rel_step': None}*)

Minimize a scalar function of one or more variables using Sequential Least Squares Programming (SLSQP).

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

ftol [float] Precision goal for the value of f in the stopping criterion.

eps [float] Step size used for numerical approximation of the Jacobian.

disp [bool] Set to True to print convergence messages. If False, *verbosity* is ignored and set to 0.

maxiter [int] Maximum number of iterations.

finite_diff_rel_step
[None or array_like, optional] If *jac in ['2-point', '3-point', 'cs']* the relative step size to use for numerical approximation of *jac*. The absolute step size is computed as `h = rel_step * sign(x0) * max(1, abs(x0))`, possibly adjusted to fit into the bounds. For

`method='3-point'` the sign of *h* is ignored. If None (default) then step is selected automatically.

minimize(method='trust-constr')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='trust-constr'*, *hess=None*, *hessp=None*, *bounds=None*, *constraints=()*, *tol=None*, *callback=None*, *options={'grad': None, 'xtol': 1e-08, 'gtol': 1e-08, 'barrier_tol': 1e-08, 'sparse_jacobian': None, 'maxiter': 1000, 'verbose': 0, 'finite_diff_rel_step': None, 'initial_constr_penalty': 1.0, 'initial_tr_radius': 1.0, 'initial_barrier_parameter': 0.1, 'initial_barrier_tolerance': 0.1, 'factorization_method': None, 'disp': False}*)

Minimize a scalar function subject to constraints.

Parameters

gtol [float, optional] Tolerance for termination by the norm of the Lagrangian gradient. The algorithm will terminate when both the infinity norm (i.e., max abs value) of the Lagrangian gradient and the constraint violation are smaller than `gtol`. Default is 1e-8.

xtol [float, optional] Tolerance for termination by the change of the independent variable. The algorithm will terminate when `tr_radius < xtol`, where `tr_radius` is the radius of the trust region used in the algorithm. Default is 1e-8.

barrier_tol
[float, optional] Threshold on the barrier parameter for the algorithm termination. When inequality constraints are present, the algorithm will terminate only when the barrier parameter is less than *barrier_tol*. Default is 1e-8.

sparse_jacobian
[{bool, None}, optional] Determines how to represent Jacobians of the constraints. If bool, then Jacobians of all the constraints will be converted to the corresponding format. If None (default), then Jacobians won't be converted, but the algorithm can proceed only if they all have the same format.

initial_tr_radius: float, optional
Initial trust radius. The trust radius gives the maximum distance between solution points in consecutive iterations. It reflects the trust the algorithm puts in the local approximation of the optimization problem. For an accurate local approximation the trust-region should be large and for an approximation valid only close to the current point it should be a small one. The trust radius is automatically updated throughout the optimization process, with `initial_tr_radius` being its initial value. Default is 1 (recommended in [1], p. 19).

initial_constr_penalty
[float, optional] Initial constraints penalty parameter. The penalty parameter is used for balancing the requirements of decreasing the objective function and satisfying the constraints. It is used for defining the merit function: `merit_function(x) = fun(x) + constr_penalty * constr_norm_l2(x)`, where `constr_norm_l2(x)` is the l2 norm of a vector containing all the constraints. The merit function is used for accepting or rejecting trial points and `constr_penalty` weights the two conflicting goals of reducing objective function and constraints. The penalty is automatically updated throughout the optimization process, with `initial_constr_penalty` being its initial value. Default is 1 (recommended in [1], p 19).

initial_barrier_parameter, initial_barrier_tolerance: float, optional
Initial barrier parameter and initial tolerance for the barrier subproblem. Both are used only when inequality constraints are present. For dealing with optimization problems `min_x f(x)` subject to inequality constraints `c(x) <= 0` the algorithm introduces slack variables, solving the problem `min_(x,s) f(x) + barrier_parameter*sum(ln(s))`

subject to the equality constraints `c(x) + s = 0` instead of the original problem. This subproblem is solved for decreasing values of `barrier_parameter` and with decreasing tolerances for the termination, starting with `initial_barrier_parameter` for the barrier parameter and `initial_barrier_tolerance` for the barrier tolerance. Default is 0.1 for both values (recommended in [1] p. 19). Also note that `barrier_parameter` and `barrier_tolerance` are updated with the same prefactor.

factorization_method
: [string or None, optional] Method to factorize the Jacobian of the constraints. Use None (default) for the auto selection or one of:
- 'NormalEquation' (requires scikit-sparse)
- 'AugmentedSystem'
- 'QRFactorization'
- 'SVDFactorization'

The methods 'NormalEquation' and 'AugmentedSystem' can be used only with sparse constraints. The projections required by the algorithm will be computed using, respectively, the the normal equation and the augmented system approaches explained in [1]. 'NormalEquation' computes the Cholesky factorization of `A A.T` and 'AugmentedSystem' performs the LU factorization of an augmented system. They usually provide similar results. 'AugmentedSystem' is used by default for sparse matrices.
The methods 'QRFactorization' and 'SVDFactorization' can be used only with dense constraints. They compute the required projections using, respectively, QR and SVD factorizations. The 'SVDFactorization' method can cope with Jacobian matrices with deficient row rank and will be used whenever other factorization methods fail (which may imply the conversion of sparse matrices to a dense format when required). By default, 'QRFactorization' is used for dense matrices.

finite_diff_rel_step
: [None or array_like, optional] Relative step size for the finite difference approximation.

maxiter
: [int, optional] Maximum number of algorithm iterations. Default is 1000.

verbose
: [{0, 1, 2}, optional] Level of algorithm's verbosity:
- 0 (default) : work silently.
- 1 : display a termination report.
- 2 : display progress during iterations.
- 3 : display progress during iterations (more complete report).

disp
: [bool, optional] If True (default), then *verbose* will be set to 1 if it was 0.

Returns

`OptimizeResult` with the fields documented below. Note the following:

1. All values corresponding to the constraints are ordered as they were passed to the solver. And values corresponding to *bounds* constraints are put *after* other constraints.
2. All numbers of function, Jacobian or Hessian evaluations correspond to numbers of actual Python function calls. It means, for example, that if a Jacobian is estimated by finite differences, then the number of Jacobian evaluations will be zero and the number of function evaluations will be incremented by all calls during the finite difference estimation.

x
: [ndarray, shape (n,)] Solution found.

optimality
: [float] Infinity norm of the Lagrangian gradient at the solution.

constr_violation
: [float] Maximum constraint violation at the solution.

fun
: [float] Objective function at the solution.

grad
: [ndarray, shape (n,)] Gradient of the objective function at the solution.

lagrangian_grad
: [ndarray, shape (n,)] Gradient of the Lagrangian function at the solution.

nit
: [int] Total number of iterations.

nfev
: [integer] Number of the objective function evaluations.

njev [integer] Number of the objective function gradient evaluations.
nhev [integer] Number of the objective function Hessian evaluations.
cg_niter [int] Total number of the conjugate gradient method iterations.
method [{'equality_constrained_sqp', 'tr_interior_point'}] Optimization method used.
constr [list of ndarray] List of constraint values at the solution.
jac [list of {ndarray, sparse matrix}] List of the Jacobian matrices of the constraints at the solution.
v [list of ndarray] List of the Lagrange multipliers for the constraints at the solution. For an inequality constraint a positive multiplier means that the upper bound is active, a negative multiplier means that the lower bound is active and if a multiplier is zero it means the constraint is not active.
constr_nfev
[list of int] Number of constraint evaluations for each of the constraints.
constr_njev
[list of int] Number of Jacobian matrix evaluations for each of the constraints.
constr_nhev
[list of int] Number of Hessian evaluations for each of the constraints.
tr_radius [float] Radius of the trust region at the last iteration.
constr_penalty
[float] Penalty parameter at the last iteration, see *initial_constr_penalty*.
barrier_tolerance
[float] Tolerance for the barrier subproblem at the last iteration. Only for problems with inequality constraints.
barrier_parameter
[float] Barrier parameter at the last iteration. Only for problems with inequality constraints.
execution_time
[float] Total execution time.
message [str] Termination message.
status [{0, 1, 2, 3}] Termination status:
- 0 : The maximum number of function evaluations is exceeded.
- 1 : *gtol* termination condition is satisfied.
- 2 : *xtol* termination condition is satisfied.
- 3 : *callback* function requested termination.

cg_stop_cond
[int] Reason for CG subproblem termination at the last iteration:
- 0 : CG subproblem not evaluated.
- 1 : Iteration limit was reached.
- 2 : Reached the trust-region boundary.
- 3 : Negative curvature detected.
- 4 : Tolerance was satisfied.

References

[1]

minimize(method='dogleg')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='dogleg'*, *jac=None*, *hess=None*, *tol=None*, *callback=None*, *options={}*)

Minimization of scalar function of one or more variables using the dog-leg trust-region algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

initial_trust_radius
: [float] Initial trust-region radius.

max_trust_radius
: [float] Maximum value of the trust-region radius. No steps that are longer than this value will be proposed.

eta
: [float] Trust region related acceptance stringency for proposed steps.

gtol
: [float] Gradient norm must be less than *gtol* before successful termination.

minimize(method='trust-ncg')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='trust-ncg'*, *jac=None*, *hess=None*, *hessp=None*, *tol=None*, *callback=None*, *options={}*)

Minimization of scalar function of one or more variables using the Newton conjugate gradient trust-region algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

initial_trust_radius
: [float] Initial trust-region radius.

max_trust_radius
: [float] Maximum value of the trust-region radius. No steps that are longer than this value will be proposed.

eta
: [float] Trust region related acceptance stringency for proposed steps.

gtol
: [float] Gradient norm must be less than *gtol* before successful termination.

minimize(method='trust-krylov')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='trust-krylov'*, *jac=None*, *hess=None*, *hessp=None*, *tol=None*, *callback=None*, *options={'inexact': True}*)

Minimization of a scalar function of one or more variables using a nearly exact trust-region algorithm that only requires matrix vector products with the hessian matrix.

New in version 1.0.0.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

inexact [bool, optional] Accuracy to solve subproblems. If True requires less nonlinear iterations, but more vector products.

minimize(method='trust-exact')

scipy.optimize.**minimize**(*fun*, *x0*, *args=()*, *method='trust-exact'*, *jac=None*, *hess=None*, *tol=None*, *callback=None*, *options={}*)

Minimization of scalar function of one or more variables using a nearly exact trust-region algorithm.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.minimize*

Options

initial_tr_radius
[float] Initial trust-region radius.

max_tr_radius
[float] Maximum value of the trust-region radius. No steps that are longer than this value will be proposed.

eta [float] Trust region related acceptance stringency for proposed steps.

gtol [float] Gradient norm must be less than `gtol` before successful termination.

Constraints are passed to *minimize* function as a single object or as a list of objects from the following classes:

NonlinearConstraint(fun, lb, ub[, jac, …])	Nonlinear constraint on the variables.
LinearConstraint(A, lb, ub[, keep_feasible])	Linear constraint on the variables.

scipy.optimize.NonlinearConstraint

class scipy.optimize.**NonlinearConstraint**(*fun*, *lb*, *ub*, *jac='2-point'*, *hess=<scipy.optimize._hessian_update_strategy.BFGS object>*, *keep_feasible=False*, *finite_diff_rel_step=None*, *finite_diff_jac_sparsity=None*)

Nonlinear constraint on the variables.

The constraint has the general inequality form:

```
lb <= fun(x) <= ub
```

Here the vector of independent variables x is passed as ndarray of shape (n,) and `fun` returns a vector with m components.

It is possible to use equal bounds to represent an equality constraint or infinite bounds to represent a one-sided constraint.

Parameters

fun [callable] The function defining the constraint. The signature is `fun(x) -> array_like, shape (m,)`.

lb, ub [array_like] Lower and upper bounds on the constraint. Each array must have the shape (m,) or be a scalar, in the latter case a bound will be the same for all components of the constraint. Use `np.inf` with an appropriate sign to specify a one-sided constraint. Set components of *lb* and *ub* equal to represent an equality constraint. Note that you can mix constraints of

different types: interval, one-sided or equality, by setting different components of *lb* and *ub* as necessary.

jac [{callable, '2-point', '3-point', 'cs'}, optional] Method of computing the Jacobian matrix (an m-by-n matrix, where element (i, j) is the partial derivative of f[i] with respect to x[j]). The keywords {'2-point', '3-point', 'cs'} select a finite difference scheme for the numerical estimation. A callable must have the following signature: `jac(x) -> {ndarray, sparse matrix}, shape (m, n)`. Default is '2-point'.

hess [{callable, '2-point', '3-point', 'cs', HessianUpdateStrategy, None}, optional] Method for computing the Hessian matrix. The keywords {'2-point', '3-point', 'cs'} select a finite difference scheme for numerical estimation. Alternatively, objects implementing *HessianUpdateStrategy* interface can be used to approximate the Hessian. Currently available implementations are:

- *BFGS* (default option)
- *SR1*

A callable must return the Hessian matrix of `dot(fun, v)` and must have the following signature: `hess(x, v) -> {LinearOperator, sparse matrix, array_like}, shape (n, n)`. Here `v` is ndarray with shape (m,) containing Lagrange multipliers.

keep_feasible

[array_like of bool, optional] Whether to keep the constraint components feasible throughout iterations. A single value set this property for all components. Default is False. Has no effect for equality constraints.

finite_diff_rel_step: None or array_like, optional

Relative step size for the finite difference approximation. Default is None, which will select a reasonable value automatically depending on a finite difference scheme.

finite_diff_jac_sparsity: {None, array_like, sparse matrix}, optional

Defines the sparsity structure of the Jacobian matrix for finite difference estimation, its shape must be (m, n). If the Jacobian has only few non-zero elements in *each* row, providing the sparsity structure will greatly speed up the computations. A zero entry means that a corresponding element in the Jacobian is identically zero. If provided, forces the use of 'lsmr' trust-region solver. If None (default) then dense differencing will be used.

Notes

Finite difference schemes {'2-point', '3-point', 'cs'} may be used for approximating either the Jacobian or the Hessian. We, however, do not allow its use for approximating both simultaneously. Hence whenever the Jacobian is estimated via finite-differences, we require the Hessian to be estimated using one of the quasi-Newton strategies.

The scheme 'cs' is potentially the most accurate, but requires the function to correctly handles complex inputs and be analytically continuable to the complex plane. The scheme '3-point' is more accurate than '2-point' but requires twice as many operations.

Examples

Constrain `x[0] < sin(x[1]) + 1.9`

```
>>> from scipy.optimize import NonlinearConstraint
>>> con = lambda x: x[0] - np.sin(x[1])
>>> nlc = NonlinearConstraint(con, -np.inf, 1.9)
```

scipy.optimize.LinearConstraint

class scipy.optimize.**LinearConstraint**(*A*, *lb*, *ub*, *keep_feasible=False*)

Linear constraint on the variables.

The constraint has the general inequality form:

```
lb <= A.dot(x) <= ub
```

Here the vector of independent variables x is passed as ndarray of shape (n,) and the matrix A has shape (m, n).

It is possible to use equal bounds to represent an equality constraint or infinite bounds to represent a one-sided constraint.

Parameters

A [{array_like, sparse matrix}, shape (m, n)] Matrix defining the constraint.

lb, ub [array_like] Lower and upper bounds on the constraint. Each array must have the shape (m,) or be a scalar, in the latter case a bound will be the same for all components of the constraint. Use `np.inf` with an appropriate sign to specify a one-sided constraint. Set components of *lb* and *ub* equal to represent an equality constraint. Note that you can mix constraints of different types: interval, one-sided or equality, by setting different components of *lb* and *ub* as necessary.

keep_feasible [array_like of bool, optional] Whether to keep the constraint components feasible throughout iterations. A single value set this property for all components. Default is False. Has no effect for equality constraints.

Simple bound constraints are handled separately and there is a special class for them:

Bounds(lb, ub[, keep_feasible])	Bounds constraint on the variables.

scipy.optimize.Bounds

class scipy.optimize.**Bounds**(*lb*, *ub*, *keep_feasible=False*)

Bounds constraint on the variables.

The constraint has the general inequality form:

```
lb <= x <= ub
```

It is possible to use equal bounds to represent an equality constraint or infinite bounds to represent a one-sided constraint.

Parameters

lb, ub [array_like] Lower and upper bounds on independent variables. Each array must have the same size as x or be a scalar, in which case a bound will be the same for all the variables. Set components of *lb* and *ub* equal to fix a variable. Use `np.inf` with an appropriate sign to disable bounds on all or some variables. Note that you can mix constraints of different types: interval, one-sided or equality, by setting different components of *lb* and *ub* as necessary.

keep_feasible [array_like of bool, optional] Whether to keep the constraint components feasible throughout iterations. A single value set this property for all components. Default is False. Has no effect for equality constraints.

Quasi-Newton strategies implementing `HessianUpdateStrategy` interface can be used to approximate the Hessian in `minimize` function (available only for the 'trust-constr' method). Available quasi-Newton methods implementing this interface are:

`BFGS`([exception_strategy, min_curvature, …])	Broyden-Fletcher-Goldfarb-Shanno (BFGS) Hessian update strategy.
`SR1`([min_denominator, init_scale])	Symmetric-rank-1 Hessian update strategy.

scipy.optimize.BFGS

class scipy.optimize.**BFGS**(*exception_strategy='skip_update'*, *min_curvature=None*, *init_scale='auto'*)

Broyden-Fletcher-Goldfarb-Shanno (BFGS) Hessian update strategy.

Parameters

exception_strategy
: [{'skip_update', 'damp_update'}, optional] Define how to proceed when the curvature condition is violated. Set it to 'skip_update' to just skip the update. Or, alternatively, set it to 'damp_update' to interpolate between the actual BFGS result and the unmodified matrix. Both exceptions strategies are explained in [1], p.536-537.

min_curvature
: [float] This number, scaled by a normalization factor, defines the minimum curvature `dot(delta_grad, delta_x)` allowed to go unaffected by the exception strategy. By default is equal to 1e-8 when `exception_strategy = 'skip_update'` and equal to 0.2 when `exception_strategy = 'damp_update'`.

init_scale
: [{float, 'auto'}] Matrix scale at first iteration. At the first iteration the Hessian matrix or its inverse will be initialized with `init_scale*np.eye(n)`, where `n` is the problem dimension. Set it to 'auto' in order to use an automatic heuristic for choosing the initial scale. The heuristic is described in [1], p.143. By default uses 'auto'.

Notes

The update is based on the description in [1], p.140.

References

[1]

Methods

`dot`(p)	Compute the product of the internal matrix with the given vector.
`get_matrix`()	Return the current internal matrix.
`initialize`(n, approx_type)	Initialize internal matrix.
`update`(delta_x, delta_grad)	Update internal matrix.

scipy.optimize.BFGS.dot

BFGS.**dot**(*p*)

Compute the product of the internal matrix with the given vector.

Parameters

p [array_like] 1-D array representing a vector.

Returns

Hp [array] 1-D represents the result of multiplying the approximation matrix by vector p.

scipy.optimize.BFGS.get_matrix

BFGS.**get_matrix**()

Return the current internal matrix.

Returns

M [ndarray, shape (n, n)] Dense matrix containing either the Hessian or its inverse (depending on how *approx_type* was defined).

scipy.optimize.BFGS.initialize

BFGS.**initialize**(*n*, *approx_type*)

Initialize internal matrix.

Allocate internal memory for storing and updating the Hessian or its inverse.

Parameters

n [int] Problem dimension.

approx_type

[{'hess', 'inv_hess'}] Selects either the Hessian or the inverse Hessian. When set to 'hess' the Hessian will be stored and updated. When set to 'inv_hess' its inverse will be used instead.

scipy.optimize.BFGS.update

BFGS.**update**(*delta_x*, *delta_grad*)

Update internal matrix.

Update Hessian matrix or its inverse (depending on how 'approx_type' is defined) using information about the last evaluated points.

Parameters

delta_x [ndarray] The difference between two points the gradient function have been evaluated at: `delta_x = x2 - x1`.

delta_grad

[ndarray] The difference between the gradients: `delta_grad = grad(x2) - grad(x1)`.

scipy.optimize.SR1

class scipy.optimize.**SR1**(*min_denominator=1e-08*, *init_scale='auto'*)

Symmetric-rank-1 Hessian update strategy.

Parameters

min_denominator
: [float] This number, scaled by a normalization factor, defines the minimum denominator magnitude allowed in the update. When the condition is violated we skip the update. By default uses `1e-8`.

init_scale
: [{float, 'auto'}, optional] Matrix scale at first iteration. At the first iteration the Hessian matrix or its inverse will be initialized with `init_scale*np.eye(n)`, where `n` is the problem dimension. Set it to 'auto' in order to use an automatic heuristic for choosing the initial scale. The heuristic is described in [1], p.143. By default uses 'auto'.

Notes

The update is based on the description in [1], p.144-146.

References

[1]

Methods

dot(p)	Compute the product of the internal matrix with the given vector.
get_matrix()	Return the current internal matrix.
initialize(n, approx_type)	Initialize internal matrix.
update(delta_x, delta_grad)	Update internal matrix.

scipy.optimize.SR1.dot

SR1.**dot**(*p*)

Compute the product of the internal matrix with the given vector.

Parameters

p [array_like] 1-D array representing a vector.

Returns

Hp [array] 1-D represents the result of multiplying the approximation matrix by vector p.

scipy.optimize.SR1.get_matrix

SR1.**get_matrix**()
Return the current internal matrix.

Returns

M [ndarray, shape (n, n)] Dense matrix containing either the Hessian or its inverse (depending on how *approx_type* was defined).

scipy.optimize.SR1.initialize

SR1.**initialize**(*n*, *approx_type*)
Initialize internal matrix.

Allocate internal memory for storing and updating the Hessian or its inverse.

Parameters

n [int] Problem dimension.

approx_type
[{'hess', 'inv_hess'}] Selects either the Hessian or the inverse Hessian. When set to 'hess' the Hessian will be stored and updated. When set to 'inv_hess' its inverse will be used instead.

scipy.optimize.SR1.update

SR1.**update**(*delta_x*, *delta_grad*)
Update internal matrix.

Update Hessian matrix or its inverse (depending on how 'approx_type' is defined) using information about the last evaluated points.

Parameters

delta_x [ndarray] The difference between two points the gradient function have been evaluated at: `delta_x = x2 - x1`.

delta_grad
[ndarray] The difference between the gradients: `delta_grad = grad(x2) - grad(x1)`.

Global optimization

basinhopping(func, x0[, niter, T, stepsize, …])	Find the global minimum of a function using the basin-hopping algorithm.
brute(func, ranges[, args, Ns, full_output, …])	Minimize a function over a given range by brute force.
differential_evolution(func, bounds[, args, …])	Finds the global minimum of a multivariate function.
shgo(func, bounds[, args, constraints, n, …])	Finds the global minimum of a function using SHG optimization.
dual_annealing(func, bounds[, args, …])	Find the global minimum of a function using Dual Annealing.

scipy.optimize.basinhopping

scipy.optimize.**basinhopping**(*func*, *x0*, *niter=100*, *T=1.0*, *stepsize=0.5*, *minimizer_kwargs=None*, *take_step=None*, *accept_test=None*, *callback=None*, *interval=50*, *disp=False*, *niter_success=None*, *seed=None*)

Find the global minimum of a function using the basin-hopping algorithm.

Basin-hopping is a two-phase method that combines a global stepping algorithm with local minimization at each step. Designed to mimic the natural process of energy minimization of clusters of atoms, it works well for similar problems with "funnel-like, but rugged" energy landscapes [5].

As the step-taking, step acceptance, and minimization methods are all customizable, this function can also be used to implement other two-phase methods.

Parameters

func [callable `f(x, *args)`] Function to be optimized. `args` can be passed as an optional item in the dict `minimizer_kwargs`

x0 [array_like] Initial guess.

niter [integer, optional] The number of basin-hopping iterations. There will be a total of `niter + 1` runs of the local minimizer.

T [float, optional] The "temperature" parameter for the accept or reject criterion. Higher "temperatures" mean that larger jumps in function value will be accepted. For best results `T` should be comparable to the separation (in function value) between local minima.

stepsize [float, optional] Maximum step size for use in the random displacement.

minimizer_kwargs [dict, optional] Extra keyword arguments to be passed to the local minimizer `scipy.optimize.minimize()` Some important options could be:

- **method** [str] The minimization method (e.g. `"L-BFGS-B"`)
- **args** [tuple] Extra arguments passed to the objective function (`func`) and its derivatives (Jacobian, Hessian).

take_step [callable `take_step(x)`, optional] Replace the default step-taking routine with this routine. The default step-taking routine is a random displacement of the coordinates, but other step-taking algorithms may be better for some systems. `take_step` can optionally have the attribute `take_step.stepsize`. If this attribute exists, then `basinhopping` will adjust `take_step.stepsize` in order to try to optimize the global minimum search.

accept_test [callable, `accept_test(f_new=f_new, x_new=x_new, f_old=fold, x_old=x_old)`, optional] Define a test which will be used to judge whether or not to accept the step. This will be used in addition to the Metropolis test based on "temperature" `T`. The acceptable return values are True, False, or `"force accept"`. If any of the tests return False then the step is rejected. If the latter, then this will override any other tests in order to accept the step. This can be used, for example, to forcefully escape from a local minimum that `basinhopping` is trapped in.

callback [callable, `callback(x, f, accept)`, optional] A callback function which will be called for all minima found. `x` and `f` are the coordinates and function value of the trial minimum, and `accept` is whether or not that minimum was accepted. This can be used, for example, to save the lowest N minima found. Also, `callback` can be used to specify a user defined stop criterion by optionally returning True to stop the `basinhopping` routine.

interval [integer, optional] interval for how often to update the `stepsize`

disp [bool, optional] Set to True to print status messages

niter_success [integer, optional] Stop the run if the global minimum candidate remains the same for this number of iterations.

seed [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional

If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used. Specify *seed* for repeatable minimizations. The random numbers generated with this seed only affect the default Metropolis *accept_test* and the default *take_step*. If you supply your own *take_step* and *accept_test*, and these functions use random number generation, then those functions are responsible for the state of their random number generator.

Returns

res [OptimizeResult] The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `fun` the value of the function at the solution, and `message` which describes the cause of the termination. The `OptimizeResult` object returned by the selected minimizer at the lowest minimum is also contained within this object and can be accessed through the `lowest_optimization_result` attribute. See *`OptimizeResult`* for a description of other attributes.

See also:

`minimize`

The local minimization function called once for each basinhopping step. `minimizer_kwargs` is passed to this routine.

Notes

Basin-hopping is a stochastic algorithm which attempts to find the global minimum of a smooth scalar function of one or more variables [1] [2] [3] [4]. The algorithm in its current form was described by David Wales and Jonathan Doye [2] http://www-wales.ch.cam.ac.uk/.

The algorithm is iterative with each cycle composed of the following features

1) random perturbation of the coordinates

2) local minimization

3) accept or reject the new coordinates based on the minimized function value

The acceptance test used here is the Metropolis criterion of standard Monte Carlo algorithms, although there are many other possibilities [3].

This global minimization method has been shown to be extremely efficient for a wide variety of problems in physics and chemistry. It is particularly useful when the function has many minima separated by large barriers. See the Cambridge Cluster Database http://www-wales.ch.cam.ac.uk/CCD.html for databases of molecular systems that have been optimized primarily using basin-hopping. This database includes minimization problems exceeding 300 degrees of freedom.

See the free software program GMIN (http://www-wales.ch.cam.ac.uk/GMIN) for a Fortran implementation of basin-hopping. This implementation has many different variations of the procedure described above, including more advanced step taking algorithms and alternate acceptance criterion.

For stochastic global optimization there is no way to determine if the true global minimum has actually been found. Instead, as a consistency check, the algorithm can be run from a number of different random starting points to ensure the lowest minimum found in each example has converged to the global minimum. For this reason, `basinhopping` will by default simply run for the number of iterations `niter` and return the lowest minimum found. It is left to the user to ensure that this is in fact the global minimum.

Choosing `stepsize`: This is a crucial parameter in `basinhopping` and depends on the problem being solved. The step is chosen uniformly in the region from x0-stepsize to x0+stepsize, in each dimension. Ideally, it should be comparable to the typical separation (in argument values) between local minima of the function being optimized.

`basinhopping` will, by default, adjust `stepsize` to find an optimal value, but this may take many iterations. You will get quicker results if you set a sensible initial value for `stepsize`.

Choosing `T`: The parameter `T` is the "temperature" used in the Metropolis criterion. Basinhopping steps are always accepted if `func(xnew) < func(xold)`. Otherwise, they are accepted with probability:

```
exp( -(func(xnew) - func(xold)) / T )
```

So, for best results, `T` should to be comparable to the typical difference (in function values) between local minima. (The height of "walls" between local minima is irrelevant.)

If `T` is 0, the algorithm becomes Monotonic Basin-Hopping, in which all steps that increase energy are rejected.

New in version 0.12.0.

References

[1], [2], [3], [4], [5]

Examples

The following example is a 1-D minimization problem, with many local minima superimposed on a parabola.

```
>>> from scipy.optimize import basinhopping
>>> func = lambda x: np.cos(14.5 * x - 0.3) + (x + 0.2) * x
>>> x0=[1.]
```

Basinhopping, internally, uses a local minimization algorithm. We will use the parameter `minimizer_kwargs` to tell basinhopping which algorithm to use and how to set up that minimizer. This parameter will be passed to `scipy.optimize.minimize()`.

```
>>> minimizer_kwargs = {"method": "BFGS"}
>>> ret = basinhopping(func, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=200)
>>> print("global minimum: x = %.4f, f(x0) = %.4f" % (ret.x, ret.fun))
global minimum: x = -0.1951, f(x0) = -1.0009
```

Next consider a 2-D minimization problem. Also, this time, we will use gradient information to significantly speed up the search.

```
>>> def func2d(x):
...     f = np.cos(14.5 * x[0] - 0.3) + (x[1] + 0.2) * x[1] + (x[0] +
...                                                             0.2) * x[0]
...     df = np.zeros(2)
...     df[0] = -14.5 * np.sin(14.5 * x[0] - 0.3) + 2. * x[0] + 0.2
...     df[1] = 2. * x[1] + 0.2
...     return f, df
```

We'll also use a different local minimization algorithm. Also, we must tell the minimizer that our function returns both energy and gradient (Jacobian).

```
>>> minimizer_kwargs = {"method":"L-BFGS-B", "jac":True}
>>> x0 = [1.0, 1.0]
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
```

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```
...                       niter=200)
>>> print("global minimum: x = [%.4f, %.4f], f(x0) = %.4f" % (ret.x[0],
...                                                          ret.x[1],
...                                                          ret.fun))
global minimum: x = [-0.1951, -0.1000], f(x0) = -1.0109
```

Here is an example using a custom step-taking routine. Imagine you want the first coordinate to take larger steps than the rest of the coordinates. This can be implemented like so:

```
>>> class MyTakeStep:
...     def __init__(self, stepsize=0.5):
...         self.stepsize = stepsize
...         self.rng = np.random.default_rng()
...     def __call__(self, x):
...         s = self.stepsize
...         x[0] += self.rng.uniform(-2.*s, 2.*s)
...         x[1:] += self.rng.uniform(-s, s, x[1:].shape)
...         return x
```

Since `MyTakeStep.stepsize` exists basinhopping will adjust the magnitude of `stepsize` to optimize the search. We'll use the same 2-D function as before

```
>>> mytakestep = MyTakeStep()
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=200, take_step=mytakestep)
>>> print("global minimum: x = [%.4f, %.4f], f(x0) = %.4f" % (ret.x[0],
...                                                          ret.x[1],
...                                                          ret.fun))
global minimum: x = [-0.1951, -0.1000], f(x0) = -1.0109
```

Now, let's do an example using a custom callback function which prints the value of every minimum found

```
>>> def print_fun(x, f, accepted):
...         print("at minimum %.4f accepted %d" % (f, int(accepted)))
```

We'll run it for only 10 basinhopping steps this time.

```
>>> rng = np.random.default_rng()
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=10, callback=print_fun, seed=rng)
at minimum 0.4159 accepted 1
at minimum -0.4317 accepted 1
at minimum -1.0109 accepted 1
at minimum -0.9073 accepted 1
at minimum -0.4317 accepted 0
at minimum -0.1021 accepted 1
at minimum -0.7425 accepted 1
at minimum -0.9073 accepted 1
at minimum -0.4317 accepted 0
at minimum -0.7425 accepted 1
at minimum -0.9073 accepted 1
```

The minimum at -1.0109 is actually the global minimum, found already on the 8th iteration.

Now let's implement bounds on the problem using a custom `accept_test`:

```
>>> class MyBounds:
...     def __init__(self, xmax=[1.1,1.1], xmin=[-1.1,-1.1] ):
...         self.xmax = np.array(xmax)
...         self.xmin = np.array(xmin)
...     def __call__(self, **kwargs):
...         x = kwargs["x_new"]
...         tmax = bool(np.all(x <= self.xmax))
...         tmin = bool(np.all(x >= self.xmin))
...         return tmax and tmin
```

```
>>> mybounds = MyBounds()
>>> ret = basinhopping(func2d, x0, minimizer_kwargs=minimizer_kwargs,
...                    niter=10, accept_test=mybounds)
```

scipy.optimize.brute

scipy.optimize.**brute**(*func*, *ranges*, *args=()*, *Ns=20*, *full_output=0*, *finish=<function fmin>*, *disp=False*, *workers=1*)

Minimize a function over a given range by brute force.

Uses the "brute force" method, i.e., computes the function's value at each point of a multidimensional grid of points, to find the global minimum of the function.

The function is evaluated everywhere in the range with the datatype of the first call to the function, as enforced by the `vectorize` NumPy function. The value and type of the function evaluation returned when `full_output=True` are affected in addition by the `finish` argument (see Notes).

The brute force approach is inefficient because the number of grid points increases exponentially - the number of grid points to evaluate is `Ns ** len(x)`. Consequently, even with coarse grid spacing, even moderately sized problems can take a long time to run, and/or run into memory limitations.

Parameters

func [callable] The objective function to be minimized. Must be in the form `f(x, *args)`, where `x` is the argument in the form of a 1-D array and `args` is a tuple of any additional fixed parameters needed to completely specify the function.

ranges [tuple] Each component of the *ranges* tuple must be either a "slice object" or a range tuple of the form `(low, high)`. The program uses these to create the grid of points on which the objective function will be computed. See *Note 2* for more detail.

args [tuple, optional] Any additional fixed parameters needed to completely specify the function.

Ns [int, optional] Number of grid points along the axes, if not otherwise specified. See *Note2*.

full_output [bool, optional] If True, return the evaluation grid and the objective function's values on it.

finish [callable, optional] An optimization function that is called with the result of brute force minimization as initial guess. *finish* should take *func* and the initial guess as positional arguments, and take *args* as keyword arguments. It may additionally take *full_output* and/or *disp* as keyword arguments. Use None if no "polishing" function is to be used. See Notes for more details.

disp [bool, optional] Set to True to print convergence messages from the *finish* callable.

workers [int or map-like callable, optional] If *workers* is an int the grid is subdivided into *workers* sections and evaluated in parallel (uses `multiprocessing.Pool`). Supply *-1* to use

all cores available to the Process. Alternatively supply a map-like callable, such as *multiprocessing.Pool.map* for evaluating the grid in parallel. This evaluation is carried out as `workers(func, iterable)`. Requires that *func* be pickleable.
New in version 1.3.0.

Returns

x0 [ndarray] A 1-D array containing the coordinates of a point at which the objective function had its minimum value. (See *Note 1* for which point is returned.)

fval [float] Function value at the point *x0*. (Returned when *full_output* is True.)

grid [tuple] Representation of the evaluation grid. It has the same length as *x0*. (Returned when *full_output* is True.)

Jout [ndarray] Function values at each point of the evaluation grid, i.e., `Jout = func(*grid)`. (Returned when *full_output* is True.)

See also:

basinhopping, **differential_evolution**

Notes

Note 1: The program finds the gridpoint at which the lowest value of the objective function occurs. If *finish* is None, that is the point returned. When the global minimum occurs within (or not very far outside) the grid's boundaries, and the grid is fine enough, that point will be in the neighborhood of the global minimum.

However, users often employ some other optimization program to "polish" the gridpoint values, i.e., to seek a more precise (local) minimum near *brute's* best gridpoint. The *brute* function's *finish* option provides a convenient way to do that. Any polishing program used must take *brute's* output as its initial guess as a positional argument, and take *brute's* input values for *args* as keyword arguments, otherwise an error will be raised. It may additionally take *full_output* and/or *disp* as keyword arguments.

brute assumes that the *finish* function returns either an *OptimizeResult* object or a tuple in the form: `(xmin, Jmin, ... , statuscode)`, where `xmin` is the minimizing value of the argument, `Jmin` is the minimum value of the objective function, "..." may be some other returned values (which are not used by *brute*), and `statuscode` is the status code of the *finish* program.

Note that when *finish* is not None, the values returned are those of the *finish* program, *not* the gridpoint ones. Consequently, while *brute* confines its search to the input grid points, the *finish* program's results usually will not coincide with any gridpoint, and may fall outside the grid's boundary. Thus, if a minimum only needs to be found over the provided grid points, make sure to pass in *finish=None*.

Note 2: The grid of points is a `numpy.mgrid` object. For *brute* the *ranges* and *Ns* inputs have the following effect. Each component of the *ranges* tuple can be either a slice object or a two-tuple giving a range of values, such as (0, 5). If the component is a slice object, *brute* uses it directly. If the component is a two-tuple range, *brute* internally converts it to a slice object that interpolates *Ns* points from its low-value to its high-value, inclusive.

Examples

We illustrate the use of *brute* to seek the global minimum of a function of two variables that is given as the sum of a positive-definite quadratic and two deep "Gaussian-shaped" craters. Specifically, define the objective function *f* as the sum of three other functions, `f = f1 + f2 + f3`. We suppose each of these has a signature `(z, *params)`, where `z = (x, y)`, and `params` and the functions are as defined below.

```
>>> params = (2, 3, 7, 8, 9, 10, 44, -1, 2, 26, 1, -2, 0.5)
>>> def f1(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (a * x**2 + b * x * y + c * y**2 + d*x + e*y + f)
```

```
>>> def f2(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (-g*np.exp(-((x-h)**2 + (y-i)**2) / scale))
```

```
>>> def f3(z, *params):
...     x, y = z
...     a, b, c, d, e, f, g, h, i, j, k, l, scale = params
...     return (-j*np.exp(-((x-k)**2 + (y-l)**2) / scale))
```

```
>>> def f(z, *params):
...     return f1(z, *params) + f2(z, *params) + f3(z, *params)
```

Thus, the objective function may have local minima near the minimum of each of the three functions of which it is composed. To use *fmin* to polish its gridpoint result, we may then continue as follows:

```
>>> rranges = (slice(-4, 4, 0.25), slice(-4, 4, 0.25))
>>> from scipy import optimize
>>> resbrute = optimize.brute(f, rranges, args=params, full_output=True,
...                           finish=optimize.fmin)
>>> resbrute[0]  # global minimum
array([-1.05665192,  1.80834843])
>>> resbrute[1]  # function value at global minimum
-3.4085818767
```

Note that if *finish* had been set to None, we would have gotten the gridpoint [-1.0 1.75] where the rounded function value is -2.892.

scipy.optimize.differential_evolution

scipy.optimize.**differential_evolution**(*func*, *bounds*, *args=()*, *strategy='best1bin'*, *maxiter=1000*, *popsize=15*, *tol=0.01*, *mutation=(0.5, 1)*, *recombination=0.7*, *seed=None*, *callback=None*, *disp=False*, *polish=True*, *init='latinhypercube'*, *atol=0*, *updating='immediate'*, *workers=1*, *constraints=()*, *x0=None*)

Finds the global minimum of a multivariate function.

Differential Evolution is stochastic in nature (does not use gradient methods) to find the minimum, and can search

large areas of candidate space, but often requires larger numbers of function evaluations than conventional gradient-based techniques.

The algorithm is due to Storn and Price [1].

Parameters

func [callable] The objective function to be minimized. Must be in the form `f(x, *args)`, where `x` is the argument in the form of a 1-D array and `args` is a tuple of any additional fixed parameters needed to completely specify the function.

bounds [sequence or *Bounds*] Bounds for variables. There are two ways to specify the bounds: 1. Instance of *Bounds* class. 2. `(min, max)` pairs for each element in `x`, defining the finite lower and upper bounds for the optimizing argument of *func*. It is required to have `len(bounds) == len(x)`. `len(bounds)` is used to determine the number of parameters in `x`.

args [tuple, optional] Any additional fixed parameters needed to completely specify the objective function.

strategy [str, optional] The differential evolution strategy to use. Should be one of:

- 'best1bin'
- 'best1exp'
- 'rand1exp'
- 'randtobest1exp'
- 'currenttobest1exp'
- 'best2exp'
- 'rand2exp'
- 'randtobest1bin'
- 'currenttobest1bin'
- 'best2bin'
- 'rand2bin'
- 'rand1bin'

The default is 'best1bin'.

maxiter [int, optional] The maximum number of generations over which the entire population is evolved. The maximum number of function evaluations (with no polishing) is: `(maxiter + 1) * popsize * len(x)`

popsize [int, optional] A multiplier for setting the total population size. The population has `popsize * len(x)` individuals. This keyword is overridden if an initial population is supplied via the *init* keyword. When using `init='sobol'` the population size is calculated as the next power of 2 after `popsize * len(x)`.

tol [float, optional] Relative tolerance for convergence, the solving stops when `np.std(pop) <= atol + tol * np.abs(np.mean(population_energies))`, where and *atol* and *tol* are the absolute and relative tolerance respectively.

mutation [float or tuple(float, float), optional] The mutation constant. In the literature this is also known as differential weight, being denoted by F. If specified as a float it should be in the range [0, 2]. If specified as a tuple `(min, max)` dithering is employed. Dithering randomly changes the mutation constant on a generation by generation basis. The mutation constant for that generation is taken from `U[min, max)`. Dithering can help speed convergence significantly. Increasing the mutation constant increases the search radius, but will slow down convergence.

recombination [float, optional] The recombination constant, should be in the range [0, 1]. In the literature this is also known as the crossover probability, being denoted by CR. Increasing this value allows a larger number of mutants to progress into the next generation, but at the risk of population stability.

seed [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional

If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used. Specify *seed* for repeatable minimizations.

disp [bool, optional] Prints the evaluated *func* at every iteration.

callback [callable, *callback(xk, convergence=val)*, optional] A function to follow the progress of the minimization. `xk` is the current value of `x0`. `val` represents the fractional value of the population convergence. When `val` is greater than one the function halts. If callback returns *True*, then the minimization is halted (any polishing is still carried out).

polish [bool, optional] If True (default), then *scipy.optimize.minimize* with the *L-BFGS-B* method is used to polish the best population member at the end, which can improve the minimization slightly. If a constrained problem is being studied then the *trust-constr* method is used instead.

init [str or array-like, optional] Specify which type of population initialization is performed. Should be one of:

- 'latinhypercube'
- 'sobol'
- 'halton'
- 'random'
- array specifying the initial population. The array should have shape `(M, len(x))`, where M is the total population size and len(x) is the number of parameters. *init* is clipped to *bounds* before use.

The default is 'latinhypercube'. Latin Hypercube sampling tries to maximize coverage of the available parameter space.

'sobol' and 'halton' are superior alternatives and maximize even more the parameter space. 'sobol' will enforce an initial population size which is calculated as the next power of 2 after `popsize * len(x)`. 'halton' has no requirements but is a bit less efficient. See *scipy.stats.qmc* for more details.

'random' initializes the population randomly - this has the drawback that clustering can occur, preventing the whole of parameter space being covered. Use of an array to specify a population could be used, for example, to create a tight bunch of initial guesses in an location where the solution is known to exist, thereby reducing time for convergence.

atol [float, optional] Absolute tolerance for convergence, the solving stops when `np.std(pop) <= atol + tol * np.abs(np.mean(population_energies))`, where and *atol* and *tol* are the absolute and relative tolerance respectively.

updating [{'immediate', 'deferred'}, optional] If `'immediate'`, the best solution vector is continuously updated within a single generation [4]. This can lead to faster convergence as trial vectors can take advantage of continuous improvements in the best solution. With `'deferred'`, the best solution vector is updated once per generation. Only `'deferred'` is compatible with parallelization, and the *workers* keyword can over-ride this option.

New in version 1.2.0.

workers [int or map-like callable, optional] If *workers* is an int the population is subdivided into *workers* sections and evaluated in parallel (uses `multiprocessing.Pool`). Supply -1 to use all available CPU cores. Alternatively supply a map-like callable, such as *multiprocessing.Pool.map* for evaluating the population in parallel. This evaluation is carried out as `workers(func, iterable)`. This option will override the *updating* keyword to `updating='deferred'` if `workers != 1`. Requires that *func* be pickleable.

New in version 1.2.0.

constraints [{NonLinearConstraint, LinearConstraint, Bounds}] Constraints on the solver, over and above those applied by the *bounds* kwd. Uses the approach by Lampinen [5].

New in version 1.4.0.

x0 [None or array-like, optional] Provides an initial guess to the minimization. Once the population has been initialized this vector replaces the first (best) member. This replacement is

done even if *init* is given an initial population.
New in version 1.7.0.

Returns

res [OptimizeResult] The optimization result represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the optimizer exited successfully and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes. If *polish* was employed, and a lower minimum was obtained by the polishing, then OptimizeResult also contains the `jac` attribute. If the eventual solution does not satisfy the applied constraints `success` will be *False*.

Notes

Differential evolution is a stochastic population based method that is useful for global optimization problems. At each pass through the population the algorithm mutates each candidate solution by mixing with other candidate solutions to create a trial candidate. There are several strategies [2] for creating trial candidates, which suit some problems more than others. The 'best1bin' strategy is a good starting point for many systems. In this strategy two members of the population are randomly chosen. Their difference is used to mutate the best member (the 'best' in 'best1bin'), b_0, so far:

$$b' = b_0 + mutation * (population[rand0] - population[rand1])$$

A trial vector is then constructed. Starting with a randomly chosen ith parameter the trial is sequentially filled (in modulo) with parameters from `b'` or the original candidate. The choice of whether to use `b'` or the original candidate is made with a binomial distribution (the 'bin' in 'best1bin') - a random number in [0, 1) is generated. If this number is less than the *recombination* constant then the parameter is loaded from `b'`, otherwise it is loaded from the original candidate. The final parameter is always loaded from `b'`. Once the trial candidate is built its fitness is assessed. If the trial is better than the original candidate then it takes its place. If it is also better than the best overall candidate it also replaces that. To improve your chances of finding a global minimum use higher *popsize* values, with higher *mutation* and (dithering), but lower *recombination* values. This has the effect of widening the search radius, but slowing convergence. By default the best solution vector is updated continuously within a single iteration (`updating='immediate'`). This is a modification [4] of the original differential evolution algorithm which can lead to faster convergence as trial vectors can immediately benefit from improved solutions. To use the original Storn and Price behaviour, updating the best solution once per iteration, set `updating='deferred'`.

New in version 0.15.0.

References

[1], [2], [3], [4], [5]

Examples

Let us consider the problem of minimizing the Rosenbrock function. This function is implemented in `rosen` in `scipy.optimize`.

```
>>> from scipy.optimize import rosen, differential_evolution
>>> bounds = [(0,2), (0, 2), (0, 2), (0, 2), (0, 2)]
>>> result = differential_evolution(rosen, bounds)
>>> result.x, result.fun
(array([1., 1., 1., 1., 1.]), 1.9216496320061384e-19)
```

Now repeat, but with parallelization.

```
>>> bounds = [(0,2), (0, 2), (0, 2), (0, 2), (0, 2)]
>>> result = differential_evolution(rosen, bounds, updating='deferred',
...                                 workers=2)
>>> result.x, result.fun
(array([1., 1., 1., 1., 1.]), 1.9216496320061384e-19)
```

Let's try and do a constrained minimization

```
>>> from scipy.optimize import NonlinearConstraint, Bounds
>>> def constr_f(x):
...     return np.array(x[0] + x[1])
>>>
>>> # the sum of x[0] and x[1] must be less than 1.9
>>> nlc = NonlinearConstraint(constr_f, -np.inf, 1.9)
>>> # specify limits using a `Bounds` object.
>>> bounds = Bounds([0., 0.], [2., 2.])
>>> result = differential_evolution(rosen, bounds, constraints=(nlc),
...                                 seed=1)
>>> result.x, result.fun
(array([0.96633867, 0.93363577]), 0.0011361355854792312)
```

Next find the minimum of the Ackley function (https://en.wikipedia.org/wiki/Test_functions_for_optimization).

```
>>> from scipy.optimize import differential_evolution
>>> import numpy as np
>>> def ackley(x):
...     arg1 = -0.2 * np.sqrt(0.5 * (x[0] ** 2 + x[1] ** 2))
...     arg2 = 0.5 * (np.cos(2. * np.pi * x[0]) + np.cos(2. * np.pi *␣
↪x[1]))
...     return -20. * np.exp(arg1) - np.exp(arg2) + 20. + np.e
>>> bounds = [(-5, 5), (-5, 5)]
>>> result = differential_evolution(ackley, bounds)
>>> result.x, result.fun
(array([ 0.,  0.]), 4.440892098500626e-16)
```

scipy.optimize.shgo

scipy.optimize.**shgo**(*func*, *bounds*, *args=()*, *constraints=None*, *n=None*, *iters=1*, *callback=None*, *minimizer_kwargs=None*, *options=None*, *sampling_method='simplicial'*)

Finds the global minimum of a function using SHG optimization.

SHGO stands for "simplicial homology global optimization".

Parameters

func [callable] The objective function to be minimized. Must be in the form `f(x, *args)`, where `x` is the argument in the form of a 1-D array and `args` is a tuple of any additional fixed parameters needed to completely specify the function.

bounds [sequence] Bounds for variables. `(min, max)` pairs for each element in `x`, defining the lower and upper bounds for the optimizing argument of *func*. It is required to have `len(bounds) == len(x)`. `len(bounds)` is used to determine the number of parameters in `x`. Use `None` for one of min or max when there is no bound in that direction. By default bounds are `(None, None)`.

args [tuple, optional] Any additional fixed parameters needed to completely specify the objective function.

constraints

[dict or sequence of dict, optional] Constraints definition. Function(s) `R**n` in the form:

```
g(x) >= 0 applied as g : R^n -> R^m
h(x) == 0 applied as h : R^n -> R^p
```

Each constraint is defined in a dictionary with fields:

- **type** [str] Constraint type: 'eq' for equality, 'ineq' for inequality.
- **fun** [callable] The function defining the constraint.
- **jac** [callable, optional] The Jacobian of *fun* (only for SLSQP).
- **args** [sequence, optional] Extra arguments to be passed to the function and Jacobian.

Equality constraint means that the constraint function result is to be zero whereas inequality means that it is to be non-negative. Note that COBYLA only supports inequality constraints.

Note: Only the COBYLA and SLSQP local minimize methods currently support constraint arguments. If the `constraints` sequence used in the local optimization problem is not defined in `minimizer_kwargs` and a constrained method is used then the global `constraints` will be used. (Defining a `constraints` sequence in `minimizer_kwargs` means that `constraints` will not be added so if equality constraints and so forth need to be added then the inequality functions in `constraints` need to be added to `minimizer_kwargs` too).

---

n [int, optional] Number of sampling points used in the construction of the simplicial complex. Note that this argument is only used for `sobol` and other arbitrary *sampling_methods*. In case of `sobol`, it must be a power of 2: `n=2**m`, and the argument will automatically be converted to the next higher power of 2. Default is 100 for `sampling_method='simplicial'` and 128 for `sampling_method='sobol'`.

iters [int, optional] Number of iterations used in the construction of the simplicial complex. Default is 1.

callback [callable, optional] Called after each iteration, as `callback(xk)`, where `xk` is the current parameter vector.

minimizer_kwargs

[dict, optional] Extra keyword arguments to be passed to the minimizer `scipy.optimize.minimize` Some important options could be:

- **method** [str] The minimization method, the default is `SLSQP`.
- **args** [tuple] Extra arguments passed to the objective function (`func`) and its derivatives (Jacobian, Hessian).
- **options** [dict, optional] Note that by default the tolerance is specified as `{ftol: 1e-12}`

options [dict, optional] A dictionary of solver options. Many of the options specified for the global routine are also passed to the scipy.optimize.minimize routine. The options that are also passed to the local routine are marked with "(L)".

Stopping criteria, the algorithm will terminate if any of the specified criteria are met. However, the default algorithm does not require any to be specified:

- **maxfev** [int (L)] Maximum number of function evaluations in the feasible domain. (Note only methods that support this option will terminate the routine at precisely exact specified value. Otherwise the criterion will only terminate during a global iteration)
- **f_min** Specify the minimum objective function value, if it is known.
- **f_tol** [float] Precision goal for the value of f in the stopping criterion. Note that the global routine will also terminate if a sampling point in the global routine is within this tolerance.

- **maxiter** [int] Maximum number of iterations to perform.
- **maxev** [int] Maximum number of sampling evaluations to perform (includes searching in infeasible points).
- **maxtime** [float] Maximum processing runtime allowed
- **minhgrd** [int] Minimum homology group rank differential. The homology group of the objective function is calculated (approximately) during every iteration. The rank of this group has a one-to-one correspondence with the number of locally convex subdomains in the objective function (after adequate sampling points each of these subdomains contain a unique global minimum). If the difference in the hgr is 0 between iterations for `maxhgrd` specified iterations the algorithm will terminate.

Objective function knowledge:

- **symmetry** [bool] Specify True if the objective function contains symmetric variables. The search space (and therefore performance) is decreased by O(n!).
- **jac** [bool or callable, optional] Jacobian (gradient) of objective function. Only for CG, BFGS, Newton-CG, L-BFGS-B, TNC, SLSQP, dogleg, trust-ncg. If `jac` is a boolean and is True, `fun` is assumed to return the gradient along with the objective function. If False, the gradient will be estimated numerically. `jac` can also be a callable returning the gradient of the objective. In this case, it must accept the same arguments as `fun`. (Passed to *scipy.optimize.minmize* automatically)
- **hess, hessp** [callable, optional] Hessian (matrix of second-order derivatives) of objective function or Hessian of objective function times an arbitrary vector p. Only for Newton-CG, dogleg, trust-ncg. Only one of `hessp` or `hess` needs to be given. If `hess` is provided, then `hessp` will be ignored. If neither `hess` nor `hessp` is provided, then the Hessian product will be approximated using finite differences on `jac`. `hessp` must compute the Hessian times an arbitrary vector. (Passed to *scipy.optimize.minmize* automatically)

Algorithm settings:

- **minimize_every_iter** [bool] If True then promising global sampling points will be passed to a local minimization routine every iteration. If False then only the final minimizer pool will be run. Defaults to False.
- **local_iter** [int] Only evaluate a few of the best minimizer pool candidates every iteration. If False all potential points are passed to the local minimization routine.
- **infty_constraints: bool** If True then any sampling points generated which are outside will the feasible domain will be saved and given an objective function value of `inf`. If False then these points will be discarded. Using this functionality could lead to higher performance with respect to function evaluations before the global minimum is found, specifying False will use less memory at the cost of a slight decrease in performance. Defaults to True.

Feedback:

- **disp** [bool (L)] Set to True to print convergence messages.

sampling_method

[str or function, optional] Current built in sampling method options are `halton`, `sobol` and `simplicial`. The default `simplicial` provides the theoretical guarantee of convergence to the global minimum in finite time. `halton` and `sobol` method are faster in terms of sampling point generation at the cost of the loss of guaranteed convergence. It is more appropriate for most "easier" problems where the convergence is relatively fast. User defined sampling functions must accept two arguments of `n` sampling points of dimension `dim` per call and output an array of sampling points with shape *n x dim*.

Returns

res [OptimizeResult] The optimization result represented as a *OptimizeResult* object. Important attributes are: `x` the solution array corresponding to the global minimum, `fun` the function output at the global solution, `xl` an ordered list of local minima solutions, `funl` the function output at the corresponding local solutions, `success` a Boolean flag indicating if the optimizer exited successfully, `message` which describes the cause of the termination, `nfev` the total number of objective function evaluations including the sampling calls, `nlfev` the total number of objective function evaluations culminating from all local search optimizations, `nit` number of iterations performed by the global routine.

Notes

Global optimization using simplicial homology global optimization [1]. Appropriate for solving general purpose NLP and blackbox optimization problems to global optimality (low-dimensional problems).

In general, the optimization problems are of the form:

```
minimize f(x) subject to

g_i(x) >= 0,  i = 1,...,m
h_j(x)  = 0,  j = 1,...,p
```

where x is a vector of one or more variables. `f(x)` is the objective function `R^n -> R`, `g_i(x)` are the inequality constraints, and `h_j(x)` are the equality constraints.

Optionally, the lower and upper bounds for each element in x can also be specified using the *bounds* argument.

While most of the theoretical advantages of SHGO are only proven for when `f(x)` is a Lipschitz smooth function, the algorithm is also proven to converge to the global optimum for the more general case where `f(x)` is non-continuous, non-convex and non-smooth, if the default sampling method is used [1].

The local search method may be specified using the `minimizer_kwargs` parameter which is passed on to `scipy.optimize.minimize`. By default, the `SLSQP` method is used. In general, it is recommended to use the `SLSQP` or `COBYLA` local minimization if inequality constraints are defined for the problem since the other methods do not use constraints.

The `halton` and `sobol` method points are generated using *scipy.stats.qmc*. Any other QMC method could be used.

References

[1], [2], [3], [4]

Examples

First consider the problem of minimizing the Rosenbrock function, *rosen*:

```
>>> from scipy.optimize import rosen, shgo
>>> bounds = [(0,2), (0, 2), (0, 2), (0, 2), (0, 2)]
>>> result = shgo(rosen, bounds)
>>> result.x, result.fun
(array([1., 1., 1., 1., 1.]), 2.920392374190081e-18)
```

Note that bounds determine the dimensionality of the objective function and is therefore a required input, however you can specify empty bounds using `None` or objects like `np.inf` which will be converted to large float numbers.

```
>>> bounds = [(None, None), ]*4
>>> result = shgo(rosen, bounds)
>>> result.x
array([0.99999851, 0.99999704, 0.99999411, 0.9999882 ])
```

Next, we consider the Eggholder function, a problem with several local minima and one global minimum. We will demonstrate the use of arguments and the capabilities of *shgo*. (https://en.wikipedia.org/wiki/Test_functions_for_optimization)

```
>>> def eggholder(x):
...     return (-(x[1] + 47.0)
...             * np.sin(np.sqrt(abs(x[0]/2.0 + (x[1] + 47.0))))
...             - x[0] * np.sin(np.sqrt(abs(x[0] - (x[1] + 47.0))))
...             )
...
>>> bounds = [(-512, 512), (-512, 512)]
```

shgo has built-in low discrepancy sampling sequences. First, we will input 64 initial sampling points of the *Sobol'* sequence:

```
>>> result = shgo(eggholder, bounds, n=64, sampling_method='sobol')
>>> result.x, result.fun
(array([512.        , 404.23180824]), -959.6406627208397)
```

shgo also has a return for any other local minima that was found, these can be called using:

```
>>> result.xl
array([[ 512.        ,  404.23180824],
       [ 283.0759062 , -487.12565635],
       [-294.66820039, -462.01964031],
       [-105.87688911,  423.15323845],
       [-242.97926   ,  274.38030925],
       [-506.25823477,    6.3131022 ],
       [-408.71980731, -156.10116949],
       [ 150.23207937,  301.31376595],
       [  91.00920901, -391.283763  ],
       [ 202.89662724, -269.38043241],
       [ 361.66623976, -106.96493868],
       [-219.40612786, -244.06020508]])
```

```
>>> result.funl
array([-959.64066272, -718.16745962, -704.80659592, -565.99778097,
       -559.78685655, -557.36868733, -507.87385942, -493.9605115 ,
       -426.48799655, -421.15571437, -419.31194957, -410.98477763])
```

These results are useful in applications where there are many global minima and the values of other global minima are desired or where the local minima can provide insight into the system (for example morphologies in physical chemistry [4]).

If we want to find a larger number of local minima, we can increase the number of sampling points or the number of iterations. We'll increase the number of sampling points to 64 and the number of iterations from the default of 1 to 3. Using `simplicial` this would have given us 64 x 3 = 192 initial sampling points.

```
>>> result_2 = shgo(eggholder, bounds, n=64, iters=3, sampling_method=
↪'sobol')
>>> len(result.xl), len(result_2.xl)
(12, 20)
```

Note the difference between, e.g., `n=192, iters=1` and `n=64, iters=3`. In the first case the promising points contained in the minimiser pool are processed only once. In the latter case it is processed every 64 sampling points for a total of 3 times.

To demonstrate solving problems with non-linear constraints consider the following example from Hock and Schittkowski problem 73 (cattle-feed) [3]:

```
minimize: f = 24.55 * x_1 + 26.75 * x_2 + 39 * x_3 + 40.50 * x_4

subject to: 2.3 * x_1 + 5.6 * x_2 + 11.1 * x_3 + 1.3 * x_4 - 5     >= 0,

            12 * x_1 + 11.9 * x_2 + 41.8 * x_3 + 52.1 * x_4 - 21
                -1.645 * sqrt(0.28 * x_1**2 + 0.19 * x_2**2 +
                              20.5 * x_3**2 + 0.62 * x_4**2)        >= 0,

            x_1 + x_2 + x_3 + x_4 - 1                               == 0,

            1 >= x_i >= 0 for all i
```

The approximate answer given in [3] is:

```
f([0.6355216, -0.12e-11, 0.3127019, 0.05177655]) = 29.894378
```

```
>>> def f(x):  # (cattle-feed)
...     return 24.55*x[0] + 26.75*x[1] + 39*x[2] + 40.50*x[3]
...
>>> def g1(x):
...     return 2.3*x[0] + 5.6*x[1] + 11.1*x[2] + 1.3*x[3] - 5  # >=0
...
>>> def g2(x):
...     return (12*x[0] + 11.9*x[1] +41.8*x[2] + 52.1*x[3] - 21
...             - 1.645 * np.sqrt(0.28*x[0]**2 + 0.19*x[1]**2
...                               + 20.5*x[2]**2 + 0.62*x[3]**2)
...             ) # >=0
...
>>> def h1(x):
...     return x[0] + x[1] + x[2] + x[3] - 1  # == 0
...
>>> cons = ({'type': 'ineq', 'fun': g1},
...         {'type': 'ineq', 'fun': g2},
...         {'type': 'eq', 'fun': h1})
>>> bounds = [(0, 1.0),]*4
>>> res = shgo(f, bounds, iters=3, constraints=cons)
>>> res
     fun: 29.894378159142136
    funl: array([29.89437816])
 message: 'Optimization terminated successfully.'
    nfev: 114
```

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```
     nit: 3
    nlfev: 35
    nlhev: 0
    nljev: 5
 success: True
       x: array([6.35521569e-01, 1.13700270e-13, 3.12701881e-01, 5.
↪17765506e-02])
      xl: array([[6.35521569e-01, 1.13700270e-13, 3.12701881e-01, 5.
↪17765506e-02]])
```

```
>>> g1(res.x), g2(res.x), h1(res.x)
(-5.062616992290714e-14, -2.9594104944408173e-12, 0.0)
```

scipy.optimize.dual_annealing

scipy.optimize.**dual_annealing**(*func*, *bounds*, *args=()*, *maxiter=1000*, *local_search_options={}*, *initial_temp=5230.0*, *restart_temp_ratio=2e-05*, *visit=2.62*, *accept=-5.0*, *maxfun=10000000.0*, *seed=None*, *no_local_search=False*, *callback=None*, *x0=None*)

Find the global minimum of a function using Dual Annealing.

Parameters

func [callable] The objective function to be minimized. Must be in the form `f(x, *args)`, where `x` is the argument in the form of a 1-D array and `args` is a tuple of any additional fixed parameters needed to completely specify the function.

bounds [sequence, shape (n, 2)] Bounds for variables. `(min, max)` pairs for each element in `x`, defining bounds for the objective function parameter.

args [tuple, optional] Any additional fixed parameters needed to completely specify the objective function.

maxiter [int, optional] The maximum number of global search iterations. Default value is 1000.

local_search_options
[dict, optional] Extra keyword arguments to be passed to the local minimizer (*minimize*). Some important options could be: `method` for the minimizer method to use and `args` for objective function additional arguments.

initial_temp
[float, optional] The initial temperature, use higher values to facilitates a wider search of the energy landscape, allowing dual_annealing to escape local minima that it is trapped in. Default value is 5230. Range is (0.01, 5.e4].

restart_temp_ratio
[float, optional] During the annealing process, temperature is decreasing, when it reaches `initial_temp * restart_temp_ratio`, the reannealing process is triggered. Default value of the ratio is 2e-5. Range is (0, 1).

visit [float, optional] Parameter for visiting distribution. Default value is 2.62. Higher values give the visiting distribution a heavier tail, this makes the algorithm jump to a more distant region. The value range is (1, 3].

accept [float, optional] Parameter for acceptance distribution. It is used to control the probability of acceptance. The lower the acceptance parameter, the smaller the probability of acceptance. Default value is -5.0 with a range (-1e4, -5].

maxfun [int, optional] Soft limit for the number of objective function calls. If the algorithm is in the middle of a local search, this number will be exceeded, the algorithm will stop just after the local search is done. Default value is 1e7.

seed [{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used. Specify *seed* for repeatable minimizations. The random numbers generated with this seed only affect the visiting distribution function and new coordinates generation.

no_local_search
[bool, optional] If *no_local_search* is set to True, a traditional Generalized Simulated Annealing will be performed with no local search strategy applied.

callback [callable, optional] A callback function with signature `callback(x, f, context)`, which will be called for all minima found. `x` and `f` are the coordinates and function value of the latest minimum found, and `context` has value in [0, 1, 2], with the following meaning:
- 0: minimum detected in the annealing process.
- 1: detection occurred in the local search process.
- 2: detection done in the dual annealing process.

If the callback implementation returns True, the algorithm will stop.

x0 [ndarray, shape(n,), optional] Coordinates of a single N-D starting point.

Returns

res [OptimizeResult] The optimization result represented as a *`OptimizeResult`* object. Important attributes are: `x` the solution array, `fun` the value of the function at the solution, and `message` which describes the cause of the termination. See *`OptimizeResult`* for a description of other attributes.

Notes

This function implements the Dual Annealing optimization. This stochastic approach derived from [3] combines the generalization of CSA (Classical Simulated Annealing) and FSA (Fast Simulated Annealing) [1] [2] coupled to a strategy for applying a local search on accepted locations [4]. An alternative implementation of this same algorithm is described in [5] and benchmarks are presented in [6]. This approach introduces an advanced method to refine the solution found by the generalized annealing process. This algorithm uses a distorted Cauchy-Lorentz visiting distribution, with its shape controlled by the parameter q_v

$$g_{q_v}(\Delta x(t)) \propto \frac{[T_{q_v}(t)]^{-\frac{D}{3-q_v}}}{\left[1+(q_v-1)\frac{(\Delta x(t))^2}{[T_{q_v}(t)]^{\frac{2}{3-q_v}}}\right]^{\frac{1}{q_v-1}+\frac{D-1}{2}}}$$

Where t is the artificial time. This visiting distribution is used to generate a trial jump distance $\Delta x(t)$ of variable $x(t)$ under artificial temperature $T_{q_v}(t)$.

From the starting point, after calling the visiting distribution function, the acceptance probability is computed as follows:

$$p_{q_a} = \min\left\{1, \left[1-(1-q_a)\beta\Delta E\right]^{\frac{1}{1-q_a}}\right\}$$

Where q_a is a acceptance parameter. For $q_a < 1$, zero acceptance probability is assigned to the cases where

$$[1-(1-q_a)\beta\Delta E] < 0$$

The artificial temperature $T_{q_v}(t)$ is decreased according to

$$T_{q_v}(t) = T_{q_v}(1)\frac{2^{q_v-1}-1}{(1+t)^{q_v-1}-1}$$

Where q_v is the visiting parameter.

New in version 1.2.0.

References

[1], [2], [3], [4], [5], [6]

Examples

The following example is a 10-D problem, with many local minima. The function involved is called Rastrigin (https://en.wikipedia.org/wiki/Rastrigin_function)

```
>>> from scipy.optimize import dual_annealing
>>> func = lambda x: np.sum(x*x - 10*np.cos(2*np.pi*x)) + 10*np.size(x)
>>> lw = [-5.12] * 10
>>> up = [5.12] * 10
>>> ret = dual_annealing(func, bounds=list(zip(lw, up)))
>>> ret.x
array([-4.26437714e-09, -3.91699361e-09, -1.86149218e-09, -3.97165720e-09,
       -6.29151648e-09, -6.53145322e-09, -3.93616815e-09, -6.55623025e-09,
       -6.05775280e-09, -5.00668935e-09]) # random
>>> ret.fun
0.000000
```

Least-squares and curve fitting

Nonlinear least-squares

least_squares(fun, x0[, jac, bounds, …])	Solve a nonlinear least-squares problem with bounds on the variables.

scipy.optimize.least_squares

scipy.optimize.**least_squares**(*fun*, *x0*, *jac='2-point'*, *bounds=(- inf, inf)*, *method='trf'*, *ftol=1e-08*, *xtol=1e-08*, *gtol=1e-08*, *x_scale=1.0*, *loss='linear'*, *f_scale=1.0*, *diff_step=None*, *tr_solver=None*, *tr_options={}*, *jac_sparsity=None*, *max_nfev=None*, *verbose=0*, *args=()*, *kwargs={}*)

Solve a nonlinear least-squares problem with bounds on the variables.

Given the residuals f(x) (an m-D real function of n real variables) and the loss function rho(s) (a scalar function), *least_squares* finds a local minimum of the cost function F(x):

```
minimize F(x) = 0.5 * sum(rho(f_i(x)**2), i = 0, ..., m - 1)
subject to lb <= x <= ub
```

The purpose of the loss function rho(s) is to reduce the influence of outliers on the solution.

Parameters

fun [callable] Function which computes the vector of residuals, with the signature `fun(x, *args, **kwargs)`, i.e., the minimization proceeds with respect to its first argument.

The argument `x` passed to this function is an ndarray of shape (n,) (never a scalar, even for n=1). It must allocate and return a 1-D array_like of shape (m,) or a scalar. If the argument `x` is complex or the function `fun` returns complex residuals, it must be wrapped in a real function of real arguments, as shown at the end of the Examples section.

x0 [array_like with shape (n,) or float] Initial guess on independent variables. If float, it will be treated as a 1-D array with one element.

jac [{'2-point', '3-point', 'cs', callable}, optional] Method of computing the Jacobian matrix (an m-by-n matrix, where element (i, j) is the partial derivative of f[i] with respect to x[j]). The keywords select a finite difference scheme for numerical estimation. The scheme '3-point' is more accurate, but requires twice as many operations as '2-point' (default). The scheme 'cs' uses complex steps, and while potentially the most accurate, it is applicable only when *fun* correctly handles complex inputs and can be analytically continued to the complex plane. Method 'lm' always uses the '2-point' scheme. If callable, it is used as `jac(x, *args, **kwargs)` and should return a good approximation (or the exact value) for the Jacobian as an array_like (np.atleast_2d is applied), a sparse matrix (csr_matrix preferred for performance) or a *scipy.sparse.linalg.LinearOperator*.

bounds [2-tuple of array_like, optional] Lower and upper bounds on independent variables. Defaults to no bounds. Each array must match the size of *x0* or be a scalar, in the latter case a bound will be the same for all variables. Use `np.inf` with an appropriate sign to disable bounds on all or some variables.

method [{'trf', 'dogbox', 'lm'}, optional] Algorithm to perform minimization.

- 'trf' : Trust Region Reflective algorithm, particularly suitable for large sparse problems with bounds. Generally robust method.
- 'dogbox' : dogleg algorithm with rectangular trust regions, typical use case is small problems with bounds. Not recommended for problems with rank-deficient Jacobian.
- 'lm' : Levenberg-Marquardt algorithm as implemented in MINPACK. Doesn't handle bounds and sparse Jacobians. Usually the most efficient method for small unconstrained problems.

Default is 'trf'. See Notes for more information.

ftol [float or None, optional] Tolerance for termination by the change of the cost function. Default is 1e-8. The optimization process is stopped when `dF < ftol * F`, and there was an adequate agreement between a local quadratic model and the true model in the last step.
If None and 'method' is not 'lm', the termination by this condition is disabled. If 'method' is 'lm', this tolerance must be higher than machine epsilon.

xtol [float or None, optional] Tolerance for termination by the change of the independent variables. Default is 1e-8. The exact condition depends on the *method* used:

- For 'trf' and 'dogbox' : `norm(dx) < xtol * (xtol + norm(x))`.
- For 'lm' : `Delta < xtol * norm(xs)`, where `Delta` is a trust-region radius and `xs` is the value of `x` scaled according to *x_scale* parameter (see below).

If None and 'method' is not 'lm', the termination by this condition is disabled. If 'method' is 'lm', this tolerance must be higher than machine epsilon.

gtol [float or None, optional] Tolerance for termination by the norm of the gradient. Default is 1e-8. The exact condition depends on a *method* used:

- For 'trf' : `norm(g_scaled, ord=np.inf) < gtol`, where `g_scaled` is the value of the gradient scaled to account for the presence of the bounds [STIR].
- For 'dogbox' : `norm(g_free, ord=np.inf) < gtol`, where `g_free` is the gradient with respect to the variables which are not in the optimal state on the boundary.
- For 'lm' : the maximum absolute value of the cosine of angles between columns of the Jacobian and the residual vector is less than *gtol*, or the residual vector is zero.

If None and 'method' is not 'lm', the termination by this condition is disabled. If 'method' is 'lm', this tolerance must be higher than machine epsilon.

x_scale [array_like or 'jac', optional] Characteristic scale of each variable. Setting *x_scale* is equivalent to reformulating the problem in scaled variables `xs = x / x_scale`. An alternative view is that the size of a trust region along jth dimension is proportional to `x_scale[j]`.

Improved convergence may be achieved by setting *x_scale* such that a step of a given size along any of the scaled variables has a similar effect on the cost function. If set to 'jac', the scale is iteratively updated using the inverse norms of the columns of the Jacobian matrix (as described in [JJMore]).

loss [str or callable, optional] Determines the loss function. The following keyword values are allowed:

- 'linear' (default) : `rho(z) = z`. Gives a standard least-squares problem.
- 'soft_l1' : `rho(z) = 2 * ((1 + z)**0.5 - 1)`. The smooth approximation of l1 (absolute value) loss. Usually a good choice for robust least squares.
- 'huber' : `rho(z) = z if z <= 1 else 2*z**0.5 - 1`. Works similarly to 'soft_l1'.
- 'cauchy' : `rho(z) = ln(1 + z)`. Severely weakens outliers influence, but may cause difficulties in optimization process.
- 'arctan' : `rho(z) = arctan(z)`. Limits a maximum loss on a single residual, has properties similar to 'cauchy'.

If callable, it must take a 1-D ndarray `z=f**2` and return an array_like with shape (3, m) where row 0 contains function values, row 1 contains first derivatives and row 2 contains second derivatives. Method 'lm' supports only 'linear' loss.

f_scale [float, optional] Value of soft margin between inlier and outlier residuals, default is 1.0. The loss function is evaluated as follows `rho_(f**2) = C**2 * rho(f**2 / C**2)`, where `C` is *f_scale*, and `rho` is determined by *loss* parameter. This parameter has no effect with `loss='linear'`, but for other *loss* values it is of crucial importance.

max_nfev [None or int, optional] Maximum number of function evaluations before the termination. If None (default), the value is chosen automatically:

- For 'trf' and 'dogbox' : 100 * n.
- For 'lm' : 100 * n if *jac* is callable and 100 * n * (n + 1) otherwise (because 'lm' counts function calls in Jacobian estimation).

diff_step [None or array_like, optional] Determines the relative step size for the finite difference approximation of the Jacobian. The actual step is computed as `x * diff_step`. If None (default), then *diff_step* is taken to be a conventional "optimal" power of machine epsilon for the finite difference scheme used [NR].

tr_solver [{None, 'exact', 'lsmr'}, optional] Method for solving trust-region subproblems, relevant only for 'trf' and 'dogbox' methods.

- 'exact' is suitable for not very large problems with dense Jacobian matrices. The computational complexity per iteration is comparable to a singular value decomposition of the Jacobian matrix.
- 'lsmr' is suitable for problems with sparse and large Jacobian matrices. It uses the iterative procedure *scipy.sparse.linalg.lsmr* for finding a solution of a linear least-squares problem and only requires matrix-vector product evaluations.

If None (default), the solver is chosen based on the type of Jacobian returned on the first iteration.

tr_options [dict, optional] Keyword options passed to trust-region solver.

- `tr_solver='exact'`: *tr_options* are ignored.
- `tr_solver='lsmr'`: options for *scipy.sparse.linalg.lsmr*. Additionally, `method='trf'` supports 'regularize' option (bool, default is True), which adds a regularization term to the normal equation, which improves convergence if the Jacobian is rank-deficient [Byrd] (eq. 3.4).

jac_sparsity [{None, array_like, sparse matrix}, optional] Defines the sparsity structure of the Jacobian matrix for finite difference estimation, its shape must be (m, n). If the Jacobian has only few non-zero elements in *each* row, providing the sparsity structure will greatly speed up the computations [Curtis]. A zero entry means that a corresponding element in the Jacobian is identically zero. If provided, forces the use of 'lsmr' trust-region solver. If None (default), then dense differencing will be used. Has no effect for 'lm' method.

verbose [{0, 1, 2}, optional] Level of algorithm's verbosity:
- 0 (default) : work silently.
- 1 : display a termination report.
- 2 : display progress during iterations (not supported by 'lm' method).

args, kwargs
[tuple and dict, optional] Additional arguments passed to *fun* and *jac*. Both empty by default. The calling signature is `fun(x, *args, **kwargs)` and the same for *jac*.

Returns

result [OptimizeResult] `OptimizeResult` with the following fields defined:

x [ndarray, shape (n,)] Solution found.

cost [float] Value of the cost function at the solution.

fun [ndarray, shape (m,)] Vector of residuals at the solution.

jac [ndarray, sparse matrix or LinearOperator, shape (m, n)] Modified Jacobian matrix at the solution, in the sense that J^T J is a Gauss-Newton approximation of the Hessian of the cost function. The type is the same as the one used by the algorithm.

grad [ndarray, shape (m,)] Gradient of the cost function at the solution.

optimality [float] First-order optimality measure. In unconstrained problems, it is always the uniform norm of the gradient. In constrained problems, it is the quantity which was compared with *gtol* during iterations.

active_mask
[ndarray of int, shape (n,)] Each component shows whether a corresponding constraint is active (that is, whether a variable is at the bound):
- 0 : a constraint is not active.
- -1 : a lower bound is active.
- 1 : an upper bound is active.

Might be somewhat arbitrary for 'trf' method as it generates a sequence of strictly feasible iterates and *active_mask* is determined within a tolerance threshold.

nfev [int] Number of function evaluations done. Methods 'trf' and 'dogbox' do not count function calls for numerical Jacobian approximation, as opposed to 'lm' method.

njev [int or None] Number of Jacobian evaluations done. If numerical Jacobian approximation is used in 'lm' method, it is set to None.

status [int] The reason for algorithm termination:
- -1 : improper input parameters status returned from MINPACK.
- 0 : the maximum number of function evaluations is exceeded.
- 1 : *gtol* termination condition is satisfied.
- 2 : *ftol* termination condition is satisfied.
- 3 : *xtol* termination condition is satisfied.
- 4 : Both *ftol* and *xtol* termination conditions are satisfied.

message [str] Verbal description of the termination reason.

success [bool] True if one of the convergence criteria is satisfied (*status* > 0).

See also:

`leastsq`

A legacy wrapper for the MINPACK implementation of the Levenberg-Marquadt algorithm.

`curve_fit`

Least-squares minimization applied to a curve-fitting problem.

Notes

Method 'lm' (Levenberg-Marquardt) calls a wrapper over least-squares algorithms implemented in MINPACK (lmder, lmdif). It runs the Levenberg-Marquardt algorithm formulated as a trust-region type algorithm. The implementation is based on paper [JJMore], it is very robust and efficient with a lot of smart tricks. It should be your first choice for unconstrained problems. Note that it doesn't support bounds. Also, it doesn't work when m < n.

Method 'trf' (Trust Region Reflective) is motivated by the process of solving a system of equations, which constitute the first-order optimality condition for a bound-constrained minimization problem as formulated in [STIR]. The algorithm iteratively solves trust-region subproblems augmented by a special diagonal quadratic term and with trust-region shape determined by the distance from the bounds and the direction of the gradient. This enhancements help to avoid making steps directly into bounds and efficiently explore the whole space of variables. To further improve convergence, the algorithm considers search directions reflected from the bounds. To obey theoretical requirements, the algorithm keeps iterates strictly feasible. With dense Jacobians trust-region subproblems are solved by an exact method very similar to the one described in [JJMore] (and implemented in MINPACK). The difference from the MINPACK implementation is that a singular value decomposition of a Jacobian matrix is done once per iteration, instead of a QR decomposition and series of Givens rotation eliminations. For large sparse Jacobians a 2-D subspace approach of solving trust-region subproblems is used [STIR], [Byrd]. The subspace is spanned by a scaled gradient and an approximate Gauss-Newton solution delivered by *scipy.sparse.linalg.lsmr*. When no constraints are imposed the algorithm is very similar to MINPACK and has generally comparable performance. The algorithm works quite robust in unbounded and bounded problems, thus it is chosen as a default algorithm.

Method 'dogbox' operates in a trust-region framework, but considers rectangular trust regions as opposed to conventional ellipsoids [Voglis]. The intersection of a current trust region and initial bounds is again rectangular, so on each iteration a quadratic minimization problem subject to bound constraints is solved approximately by Powell's dogleg method [NumOpt]. The required Gauss-Newton step can be computed exactly for dense Jacobians or approximately by *scipy.sparse.linalg.lsmr* for large sparse Jacobians. The algorithm is likely to exhibit slow convergence when the rank of Jacobian is less than the number of variables. The algorithm often outperforms 'trf' in bounded problems with a small number of variables.

Robust loss functions are implemented as described in [BA]. The idea is to modify a residual vector and a Jacobian matrix on each iteration such that computed gradient and Gauss-Newton Hessian approximation match the true gradient and Hessian approximation of the cost function. Then the algorithm proceeds in a normal way, i.e., robust loss functions are implemented as a simple wrapper over standard least-squares algorithms.

New in version 0.17.0.

References

[STIR], [NR], [Byrd], [Curtis], [JJMore], [Voglis], [NumOpt], [BA]

Examples

In this example we find a minimum of the Rosenbrock function without bounds on independent variables.

```
>>> def fun_rosenbrock(x):
...     return np.array([10 * (x[1] - x[0]**2), (1 - x[0])])
```

Notice that we only provide the vector of the residuals. The algorithm constructs the cost function as a sum of squares of the residuals, which gives the Rosenbrock function. The exact minimum is at `x = [1.0, 1.0]`.

```
>>> from scipy.optimize import least_squares
>>> x0_rosenbrock = np.array([2, 2])
>>> res_1 = least_squares(fun_rosenbrock, x0_rosenbrock)
```

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```
>>> res_1.x
array([ 1.,  1.])
>>> res_1.cost
9.8669242910846867e-30
>>> res_1.optimality
8.8928864934219529e-14
```

We now constrain the variables, in such a way that the previous solution becomes infeasible. Specifically, we require that `x[1] >= 1.5`, and `x[0]` left unconstrained. To this end, we specify the *bounds* parameter to *`least_squares`* in the form `bounds=([-np.inf, 1.5], np.inf)`.

We also provide the analytic Jacobian:

```
>>> def jac_rosenbrock(x):
...     return np.array([
...         [-20 * x[0], 10],
...         [-1, 0]])
```

Putting this all together, we see that the new solution lies on the bound:

```
>>> res_2 = least_squares(fun_rosenbrock, x0_rosenbrock, jac_rosenbrock,
...                       bounds=([-np.inf, 1.5], np.inf))
>>> res_2.x
array([ 1.22437075,  1.5       ])
>>> res_2.cost
0.025213093946805685
>>> res_2.optimality
1.5885401433157753e-07
```

Now we solve a system of equations (i.e., the cost function should be zero at a minimum) for a Broyden tridiagonal vector-valued function of 100000 variables:

```
>>> def fun_broyden(x):
...     f = (3 - x) * x + 1
...     f[1:] -= x[:-1]
...     f[:-1] -= 2 * x[1:]
...     return f
```

The corresponding Jacobian matrix is sparse. We tell the algorithm to estimate it by finite differences and provide the sparsity structure of Jacobian to significantly speed up this process.

```
>>> from scipy.sparse import lil_matrix
>>> def sparsity_broyden(n):
...     sparsity = lil_matrix((n, n), dtype=int)
...     i = np.arange(n)
...     sparsity[i, i] = 1
...     i = np.arange(1, n)
...     sparsity[i, i - 1] = 1
...     i = np.arange(n - 1)
...     sparsity[i, i + 1] = 1
...     return sparsity
...
>>> n = 100000
```

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```
>>> x0_broyden = -np.ones(n)
...
>>> res_3 = least_squares(fun_broyden, x0_broyden,
...                       jac_sparsity=sparsity_broyden(n))
>>> res_3.cost
4.5687069299604613e-23
>>> res_3.optimality
1.1650454296851518e-11
```

Let's also solve a curve fitting problem using robust loss function to take care of outliers in the data. Define the model function as `y = a + b * exp(c * t)`, where t is a predictor variable, y is an observation and a, b, c are parameters to estimate.

First, define the function which generates the data with noise and outliers, define the model parameters, and generate data:

```
>>> from numpy.random import default_rng
>>> rng = default_rng()
>>> def gen_data(t, a, b, c, noise=0., n_outliers=0, seed=None):
...     rng = default_rng(seed)
...
...     y = a + b * np.exp(t * c)
...
...     error = noise * rng.standard_normal(t.size)
...     outliers = rng.integers(0, t.size, n_outliers)
...     error[outliers] *= 10
...
...     return y + error
...
>>> a = 0.5
>>> b = 2.0
>>> c = -1
>>> t_min = 0
>>> t_max = 10
>>> n_points = 15
...
>>> t_train = np.linspace(t_min, t_max, n_points)
>>> y_train = gen_data(t_train, a, b, c, noise=0.1, n_outliers=3)
```

Define function for computing residuals and initial estimate of parameters.

```
>>> def fun(x, t, y):
...     return x[0] + x[1] * np.exp(x[2] * t) - y
...
>>> x0 = np.array([1.0, 1.0, 0.0])
```

Compute a standard least-squares solution:

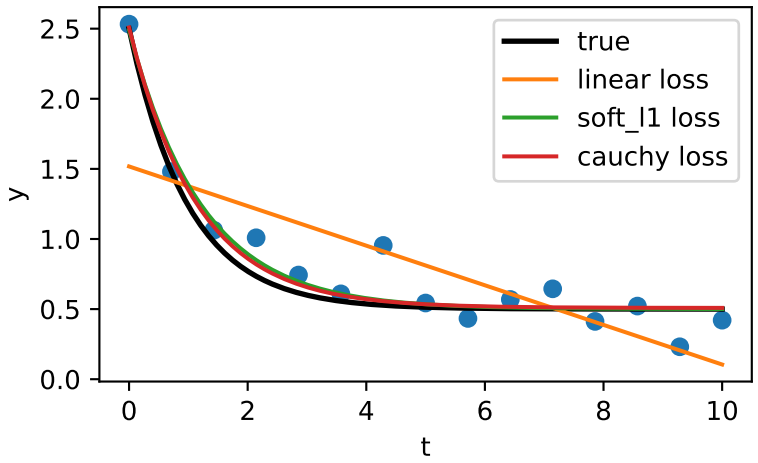
```
>>> res_lsq = least_squares(fun, x0, args=(t_train, y_train))
```

Now compute two solutions with two different robust loss functions. The parameter *f_scale* is set to 0.1, meaning that inlier residuals should not significantly exceed 0.1 (the noise level used).

```
>>> res_soft_l1 = least_squares(fun, x0, loss='soft_l1', f_scale=0.1,
...                             args=(t_train, y_train))
>>> res_log = least_squares(fun, x0, loss='cauchy', f_scale=0.1,
...                         args=(t_train, y_train))
```

And, finally, plot all the curves. We see that by selecting an appropriate *loss* we can get estimates close to optimal even in the presence of strong outliers. But keep in mind that generally it is recommended to try 'soft_l1' or 'huber' losses first (if at all necessary) as the other two options may cause difficulties in optimization process.

```
>>> t_test = np.linspace(t_min, t_max, n_points * 10)
>>> y_true = gen_data(t_test, a, b, c)
>>> y_lsq = gen_data(t_test, *res_lsq.x)
>>> y_soft_l1 = gen_data(t_test, *res_soft_l1.x)
>>> y_log = gen_data(t_test, *res_log.x)
...
>>> import matplotlib.pyplot as plt
>>> plt.plot(t_train, y_train, 'o')
>>> plt.plot(t_test, y_true, 'k', linewidth=2, label='true')
>>> plt.plot(t_test, y_lsq, label='linear loss')
>>> plt.plot(t_test, y_soft_l1, label='soft_l1 loss')
>>> plt.plot(t_test, y_log, label='cauchy loss')
>>> plt.xlabel("t")
>>> plt.ylabel("y")
>>> plt.legend()
>>> plt.show()
```



In the next example, we show how complex-valued residual functions of complex variables can be optimized with `least_squares()`. Consider the following function:

```
>>> def f(z):
...     return z - (0.5 + 0.5j)
```

We wrap it into a function of real variables that returns real residuals by simply handling the real and imaginary parts as independent variables:

```
>>> def f_wrap(x):
...     fx = f(x[0] + 1j*x[1])
...     return np.array([fx.real, fx.imag])
```

Thus, instead of the original m-D complex function of n complex variables we optimize a 2m-D real function of 2n real variables:

```
>>> from scipy.optimize import least_squares
>>> res_wrapped = least_squares(f_wrap, (0.1, 0.1), bounds=([0, 0], [1,␣
↪1]))
>>> z = res_wrapped.x[0] + res_wrapped.x[1]*1j
>>> z
(0.49999999999925893+0.49999999999925893j)
```

Linear least-squares

nnls(A, b[, maxiter])	Solve `argmin_x || Ax - b ||_2` for `x>=0`.
lsq_linear(A, b[, bounds, method, tol, …])	Solve a linear least-squares problem with bounds on the variables.

scipy.optimize.nnls

scipy.optimize.**nnls**(*A*, *b*, *maxiter=None*)

Solve `argmin_x || Ax - b ||_2` for `x>=0`. This is a wrapper for a FORTRAN non-negative least squares solver.

Parameters

A [ndarray] Matrix `A` as shown above.

b [ndarray] Right-hand side vector.

maxiter: int, optional

Maximum number of iterations, optional. Default is `3 * A.shape[1]`.

Returns

x [ndarray] Solution vector.

rnorm [float] The residual, `|| Ax-b ||_2`.

See also:

lsq_linear

Linear least squares with bounds on the variables

Notes

The FORTRAN code was published in the book below. The algorithm is an active set method. It solves the KKT (Karush-Kuhn-Tucker) conditions for the non-negative least squares problem.

References

Lawson C., Hanson R.J., (1987) Solving Least Squares Problems, SIAM

Examples

```
>>> from scipy.optimize import nnls
...
>>> A = np.array([[1, 0], [1, 0], [0, 1]])
>>> b = np.array([2, 1, 1])
>>> nnls(A, b)
(array([1.5, 1. ]), 0.7071067811865475)
```

```
>>> b = np.array([-1, -1, -1])
>>> nnls(A, b)
(array([0., 0.]), 1.7320508075688772)
```

scipy.optimize.lsq_linear

scipy.optimize.**lsq_linear**(*A*, *b*, *bounds=(- inf, inf)*, *method='trf'*, *tol=1e-10*, *lsq_solver=None*, *lsmr_tol=None*, *max_iter=None*, *verbose=0*)

Solve a linear least-squares problem with bounds on the variables.

Given a m-by-n design matrix A and a target vector b with m elements, *lsq_linear* solves the following optimization problem:

```
minimize 0.5 * ||A x - b||**2
subject to lb <= x <= ub
```

This optimization problem is convex, hence a found minimum (if iterations have converged) is guaranteed to be global.

Parameters

A [array_like, sparse matrix of LinearOperator, shape (m, n)] Design matrix. Can be *scipy.sparse.linalg.LinearOperator*.

b [array_like, shape (m,)] Target vector.

bounds [2-tuple of array_like, optional] Lower and upper bounds on independent variables. Defaults to no bounds. Each array must have shape (n,) or be a scalar, in the latter case a bound will be the same for all variables. Use `np.inf` with an appropriate sign to disable bounds on all or some variables.

method ['trf' or 'bvls', optional] Method to perform minimization.

- 'trf' : Trust Region Reflective algorithm adapted for a linear least-squares problem. This is an interior-point-like method and the required number of iterations is weakly correlated with the number of variables.

- 'bvls' : Bounded-variable least-squares algorithm. This is an active set method, which requires the number of iterations comparable to the number of variables. Can't be used when *A* is sparse or LinearOperator.

Default is 'trf'.

tol [float, optional] Tolerance parameter. The algorithm terminates if a relative change of the cost function is less than *tol* on the last iteration. Additionally, the first-order optimality measure is considered:

- `method='trf'` terminates if the uniform norm of the gradient, scaled to account for the presence of the bounds, is less than *tol*.
- `method='bvls'` terminates if Karush-Kuhn-Tucker conditions are satisfied within *tol* tolerance.

lsq_solver [{None, 'exact', 'lsmr'}, optional] Method of solving unbounded least-squares problems throughout iterations:

- 'exact' : Use dense QR or SVD decomposition approach. Can't be used when *A* is sparse or LinearOperator.
- 'lsmr' : Use *scipy.sparse.linalg.lsmr* iterative procedure which requires only matrix-vector product evaluations. Can't be used with `method='bvls'`.

If None (default), the solver is chosen based on type of *A*.

lsmr_tol [None, float or 'auto', optional] Tolerance parameters 'atol' and 'btol' for *scipy.sparse.linalg.lsmr* If None (default), it is set to `1e-2 * tol`. If 'auto', the tolerance will be adjusted based on the optimality of the current iterate, which can speed up the optimization process, but is not always reliable.

max_iter [None or int, optional] Maximum number of iterations before termination. If None (default), it is set to 100 for `method='trf'` or to the number of variables for `method='bvls'` (not counting iterations for 'bvls' initialization).

verbose [{0, 1, 2}, optional] Level of algorithm's verbosity:

- 0 : work silently (default).
- 1 : display a termination report.
- 2 : display progress during iterations.

Returns

OptimizeResult with the following fields defined:

x [ndarray, shape (n,)] Solution found.

cost [float] Value of the cost function at the solution.

fun [ndarray, shape (m,)] Vector of residuals at the solution.

optimality [float] First-order optimality measure. The exact meaning depends on *method*, refer to the description of *tol* parameter.

active_mask

[ndarray of int, shape (n,)] Each component shows whether a corresponding constraint is active (that is, whether a variable is at the bound):

- 0 : a constraint is not active.
- -1 : a lower bound is active.
- 1 : an upper bound is active.

Might be somewhat arbitrary for the *trf* method as it generates a sequence of strictly feasible iterates and active_mask is determined within a tolerance threshold.

nit [int] Number of iterations. Zero if the unconstrained solution is optimal.

status [int] Reason for algorithm termination:

- -1 : the algorithm was not able to make progress on the last iteration.
- 0 : the maximum number of iterations is exceeded.
- 1 : the first-order optimality measure is less than *tol*.
- 2 : the relative change of the cost function is less than *tol*.
- 3 : the unconstrained solution is optimal.

message [str] Verbal description of the termination reason.

success [bool] True if one of the convergence criteria is satisfied (*status* > 0).

See also:

`nnls`

Linear least squares with non-negativity constraint.

`least_squares`

Nonlinear least squares with bounds on the variables.

Notes

The algorithm first computes the unconstrained least-squares solution by `numpy.linalg.lstsq` or *`scipy.sparse.linalg.lsmr`* depending on *lsq_solver*. This solution is returned as optimal if it lies within the bounds.

Method 'trf' runs the adaptation of the algorithm described in [STIR] for a linear least-squares problem. The iterations are essentially the same as in the nonlinear least-squares algorithm, but as the quadratic function model is always accurate, we don't need to track or modify the radius of a trust region. The line search (backtracking) is used as a safety net when a selected step does not decrease the cost function. Read more detailed description of the algorithm in *`scipy.optimize.least_squares`*.

Method 'bvls' runs a Python implementation of the algorithm described in [BVLS]. The algorithm maintains active and free sets of variables, on each iteration chooses a new variable to move from the active set to the free set and then solves the unconstrained least-squares problem on free variables. This algorithm is guaranteed to give an accurate solution eventually, but may require up to n iterations for a problem with n variables. Additionally, an ad-hoc initialization procedure is implemented, that determines which variables to set free or active initially. It takes some number of iterations before actual BVLS starts, but can significantly reduce the number of further iterations.

References

[STIR], [BVLS]

Examples

In this example, a problem with a large sparse matrix and bounds on the variables is solved.

```
>>> from scipy.sparse import rand
>>> from scipy.optimize import lsq_linear
>>> rng = np.random.default_rng()
...
>>> m = 20000
>>> n = 10000
...
>>> A = rand(m, n, density=1e-4, random_state=rng)
>>> b = rng.standard_normal(m)
...
>>> lb = rng.standard_normal(n)
>>> ub = lb + 1
...
>>> res = lsq_linear(A, b, bounds=(lb, ub), lsmr_tol='auto', verbose=1)
# may vary
The relative change of the cost function is less than `tol`.
```

(continues on next page)

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```
Number of iterations 16, initial cost 1.5039e+04, final cost 1.1112e+04,
first-order optimality 4.66e-08.
```

Curve fitting

curve_fit(f, xdata, ydata[, p0, sigma, …])	Use non-linear least squares to fit a function, f, to data.

scipy.optimize.curve_fit

scipy.optimize.**curve_fit**(*f*, *xdata*, *ydata*, *p0=None*, *sigma=None*, *absolute_sigma=False*, *check_finite=True*, *bounds=(- inf, inf)*, *method=None*, *jac=None*, ***kwargs*)

Use non-linear least squares to fit a function, f, to data.

Assumes `ydata = f(xdata, *params) + eps`.

Parameters

f [callable] The model function, f(x, …). It must take the independent variable as the first argument and the parameters to fit as separate remaining arguments.

xdata [array_like or object] The independent variable where the data is measured. Should usually be an M-length sequence or an (k,M)-shaped array for functions with k predictors, but can actually be any object.

ydata [array_like] The dependent data, a length M array - nominally `f(xdata, ...)`.

p0 [array_like, optional] Initial guess for the parameters (length N). If None, then the initial values will all be 1 (if the number of parameters for the function can be determined using introspection, otherwise a ValueError is raised).

sigma [None or M-length sequence or MxM array, optional] Determines the uncertainty in *ydata*. If we define residuals as `r = ydata - f(xdata, *popt)`, then the interpretation of *sigma* depends on its number of dimensions:

- A 1-D *sigma* should contain values of standard deviations of errors in *ydata*. In this case, the optimized function is `chisq = sum((r / sigma) ** 2)`.
- A 2-D *sigma* should contain the covariance matrix of errors in *ydata*. In this case, the optimized function is `chisq = r.T @ inv(sigma) @ r`.
  New in version 0.19.

None (default) is equivalent of 1-D *sigma* filled with ones.

absolute_sigma [bool, optional] If True, *sigma* is used in an absolute sense and the estimated parameter covariance *pcov* reflects these absolute values.
If False (default), only the relative magnitudes of the *sigma* values matter. The returned parameter covariance matrix *pcov* is based on scaling *sigma* by a constant factor. This constant is set by demanding that the reduced *chisq* for the optimal parameters *popt* when using the *scaled sigma* equals unity. In other words, *sigma* is scaled to match the sample variance of the residuals after the fit. Default is False. Mathematically, `pcov(absolute_sigma=False) = pcov(absolute_sigma=True) * chisq(popt)/(M-N)`

check_finite [bool, optional] If True, check that the input arrays do not contain nans of infs, and raise a ValueError if they do. Setting this parameter to False may silently produce nonsensical results if the input arrays do contain nans. Default is True.

bounds [2-tuple of array_like, optional] Lower and upper bounds on parameters. Defaults to no bounds. Each element of the tuple must be either an array with the length equal to the

number of parameters, or a scalar (in which case the bound is taken to be the same for all parameters). Use `np.inf` with an appropriate sign to disable bounds on all or some parameters.
New in version 0.17.

method [{'lm', 'trf', 'dogbox'}, optional] Method to use for optimization. See *least_squares* for more details. Default is 'lm' for unconstrained problems and 'trf' if *bounds* are provided. The method 'lm' won't work when the number of observations is less than the number of variables, use 'trf' or 'dogbox' in this case.
New in version 0.17.

jac [callable, string or None, optional] Function with signature `jac(x, ...)` which computes the Jacobian matrix of the model function with respect to parameters as a dense array_like structure. It will be scaled according to provided *sigma*. If None (default), the Jacobian will be estimated numerically. String keywords for 'trf' and 'dogbox' methods can be used to select a finite difference scheme, see *least_squares*.
New in version 0.18.

kwargs Keyword arguments passed to *leastsq* for `method='lm'` or *least_squares* otherwise.

Returns

popt [array] Optimal values for the parameters so that the sum of the squared residuals of `f(xdata, *popt) - ydata` is minimized.

pcov [2-D array] The estimated covariance of popt. The diagonals provide the variance of the parameter estimate. To compute one standard deviation errors on the parameters use `perr = np.sqrt(np.diag(pcov))`.
How the *sigma* parameter affects the estimated covariance depends on *absolute_sigma* argument, as described above.
If the Jacobian matrix at the solution doesn't have a full rank, then 'lm' method returns a matrix filled with `np.inf`, on the other hand 'trf' and 'dogbox' methods use Moore-Penrose pseudoinverse to compute the covariance matrix.

Raises

ValueError
if either *ydata* or *xdata* contain NaNs, or if incompatible options are used.

RuntimeError
if the least-squares minimization fails.

OptimizeWarning
if covariance of the parameters can not be estimated.

See also:

least_squares

Minimize the sum of squares of nonlinear functions.

scipy.stats.linregress

Calculate a linear least squares regression for two sets of measurements.

Notes

With `method='lm'`, the algorithm uses the Levenberg-Marquardt algorithm through *leastsq*. Note that this algorithm can only deal with unconstrained problems.

Box constraints can be handled by methods 'trf' and 'dogbox'. Refer to the docstring of *least_squares* for more information.

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.optimize import curve_fit
```

```
>>> def func(x, a, b, c):
...     return a * np.exp(-b * x) + c
```

Define the data to be fit with some noise:

```
>>> xdata = np.linspace(0, 4, 50)
>>> y = func(xdata, 2.5, 1.3, 0.5)
>>> rng = np.random.default_rng()
>>> y_noise = 0.2 * rng.normal(size=xdata.size)
>>> ydata = y + y_noise
>>> plt.plot(xdata, ydata, 'b-', label='data')
```

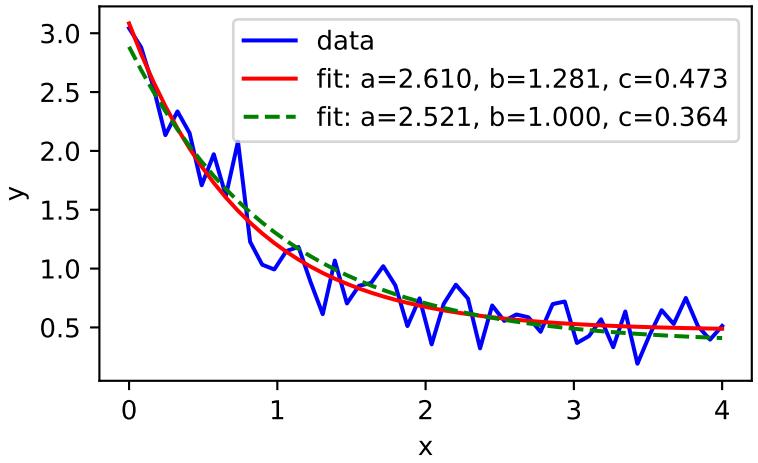
Fit for the parameters a, b, c of the function *func*:

```
>>> popt, pcov = curve_fit(func, xdata, ydata)
>>> popt
array([2.56274217, 1.37268521, 0.47427475])
>>> plt.plot(xdata, func(xdata, *popt), 'r-',
...          label='fit: a=%5.3f, b=%5.3f, c=%5.3f' % tuple(popt))
```

Constrain the optimization to the region of `0 <= a <= 3`, `0 <= b <= 1` and `0 <= c <= 0.5`:

```
>>> popt, pcov = curve_fit(func, xdata, ydata, bounds=(0, [3., 1., 0.5]))
>>> popt
array([2.43736712, 1.        , 0.34463856])
>>> plt.plot(xdata, func(xdata, *popt), 'g--',
...          label='fit: a=%5.3f, b=%5.3f, c=%5.3f' % tuple(popt))
```

```
>>> plt.xlabel('x')
>>> plt.ylabel('y')
>>> plt.legend()
>>> plt.show()
```



Root finding

Scalar functions

`root_scalar`(f[, args, method, bracket, …])	Find a root of a scalar function.
`brentq`(f, a, b[, args, xtol, rtol, maxiter, …])	Find a root of a function in a bracketing interval using Brent's method.
`brenth`(f, a, b[, args, xtol, rtol, maxiter, …])	Find a root of a function in a bracketing interval using Brent's method with hyperbolic extrapolation.
`ridder`(f, a, b[, args, xtol, rtol, maxiter, …])	Find a root of a function in an interval using Ridder's method.
`bisect`(f, a, b[, args, xtol, rtol, maxiter, …])	Find root of a function within an interval using bisection.
`newton`(func, x0[, fprime, args, tol, …])	Find a zero of a real or complex function using the Newton-Raphson (or secant or Halley's) method.
`toms748`(f, a, b[, args, k, xtol, rtol, …])	Find a zero using TOMS Algorithm 748 method.
`RootResults`(root, iterations, …)	Represents the root finding result.

scipy.optimize.root_scalar

scipy.optimize.**root_scalar**(*f*, *args=()*, *method=None*, *bracket=None*, *fprime=None*, *fprime2=None*, *x0=None*, *x1=None*, *xtol=None*, *rtol=None*, *maxiter=None*, *options=None*)

Find a root of a scalar function.

Parameters

f [callable] A function to find a root of.

args [tuple, optional] Extra arguments passed to the objective function and its derivative(s).

method [str, optional] Type of solver. Should be one of

- 'bisect' *(see here)*
- 'brentq' *(see here)*
- 'brenth' *(see here)*
- 'ridder' *(see here)*
- 'toms748' *(see here)*
- 'newton' *(see here)*
- 'secant' *(see here)*
- 'halley' *(see here)*

bracket: A sequence of 2 floats, optional

An interval bracketing a root. *f(x, *args)* must have different signs at the two endpoints.

x0 [float, optional] Initial guess.

sol [RootResults] The solution represented as a `RootResults` object. Important attributes are: `root` the solution , `converged` a boolean flag indicating if the algorithm exited successfully and `flag` which describes the cause of the termination. See *RootResults* for a description of other attributes.

See also:

show_options

Additional options accepted by the solvers

root

Find a root of a vector function.

Notes

This section describes the available solvers that can be selected by the 'method' parameter.

The default is to use the best method available for the situation presented. If a bracket is provided, it may use one of the bracketing methods. If a derivative and an initial value are specified, it may select one of the derivative-based methods. If no method is judged applicable, it will raise an Exception.

Examples

Find the root of a simple cubic

```
>>> from scipy import optimize
>>> def f(x):
...     return (x**3 - 1)  # only one real root at x = 1
```

```
>>> def fprime(x):
...     return 3*x**2
```

The *brentq* method takes as input a bracket

```
>>> sol = optimize.root_scalar(f, bracket=[0, 3], method='brentq')
>>> sol.root, sol.iterations, sol.function_calls
(1.0, 10, 11)
```

The *newton* method takes as input a single point and uses the derivative(s)

```
>>> sol = optimize.root_scalar(f, x0=0.2, fprime=fprime, method='newton')
>>> sol.root, sol.iterations, sol.function_calls
(1.0, 11, 22)
```

The function can provide the value and derivative(s) in a single call.

```
>>> def f_p_pp(x):
...     return (x**3 - 1), 3*x**2, 6*x
```

```
>>> sol = optimize.root_scalar(f_p_pp, x0=0.2, fprime=True, method='newton
↪')
>>> sol.root, sol.iterations, sol.function_calls
(1.0, 11, 11)
```

```
>>> sol = optimize.root_scalar(f_p_pp, x0=0.2, fprime=True, fprime2=True,␣
↪method='halley')
>>> sol.root, sol.iterations, sol.function_calls
(1.0, 7, 8)
```

scipy.optimize.brentq

scipy.optimize.**brentq**(*f*, *a*, *b*, *args=()*, *xtol=2e-12*, *rtol=8.881784197001252e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find a root of a function in a bracketing interval using Brent's method.

Uses the classic Brent's method to find a zero of the function f on the sign changing interval [a , b]. Generally considered the best of the rootfinding routines here. It is a safe version of the secant method that uses inverse quadratic extrapolation. Brent's method combines root bracketing, interval bisection, and inverse quadratic interpolation. It is sometimes known as the van Wijngaarden-Dekker-Brent method. Brent (1973) claims convergence is guaranteed for functions computable within [a,b].

[Brent1973] provides the classic description of the algorithm. Another description can be found in a recent edition of Numerical Recipes, including [PressEtal1992]. A third description is at http://mathworld.wolfram.com/BrentsMethod.html. It should be easy to understand the algorithm just by reading our code. Our code diverges a bit from standard presentations: we choose a different formula for the extrapolation step.

Parameters

f [function] Python function returning a number. The function f must be continuous, and $f(a)$ and $f(b)$ must have opposite signs.

a [scalar] One end of the bracketing interval $[a, b]$.

b [scalar] The other end of the bracketing interval $[a, b]$.

xtol [number, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter must be nonnegative. For nice functions, Brent's method will often satisfy the above condition with `xtol/2` and `rtol/2`. [Brent1973]

rtol [number, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter cannot be smaller than its default value of `4*np.finfo(float).eps`. For nice functions, Brent's method will often satisfy the above condition with `xtol/2` and `rtol/2`. [Brent1973]

maxiter [int, optional] If convergence is not achieved in *maxiter* iterations, an error is raised. Must be >= 0.

args [tuple, optional] Containing extra arguments for the function f. f is called by `apply(f, (x)+args)`.

full_output

[bool, optional] If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a *RootResults* object.

disp [bool, optional] If True, raise RuntimeError if the algorithm didn't converge. Otherwise, the convergence status is recorded in any *RootResults* return object.

Returns

x0 [float] Zero of f between *a* and *b*.

r [*RootResults* (present if `full_output = True`)] Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

Notes

f must be continuous. f(a) and f(b) must have opposite signs.

Related functions fall into several classes:

multivariate local optimizers

fmin, *fmin_powell*, *fmin_cg*, *fmin_bfgs*, *fmin_ncg*

nonlinear least squares minimizer

leastsq

constrained multivariate optimizers

fmin_l_bfgs_b, *fmin_tnc*, *fmin_cobyla*

global optimizers

basinhopping, *brute*, *differential_evolution*

local scalar minimizers

fminbound, *brent*, *golden*, *bracket*

N-D root-finding

fsolve

1-D root-finding

brenth, *ridder*, *bisect*, *newton*

scalar fixed-point finder

fixed_point

References

[Brent1973], [PressEtal1992]

Examples

```
>>> def f(x):
...     return (x**2 - 1)
```

```
>>> from scipy import optimize
```

```
>>> root = optimize.brentq(f, -2, 0)
>>> root
-1.0
```

```
>>> root = optimize.brentq(f, 0, 2)
>>> root
1.0
```

scipy.optimize.brenth

scipy.optimize.**brenth**(*f*, *a*, *b*, *args=()*, *xtol=2e-12*, *rtol=8.881784197001252e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find a root of a function in a bracketing interval using Brent's method with hyperbolic extrapolation.

A variation on the classic Brent routine to find a zero of the function f between the arguments a and b that uses hyperbolic extrapolation instead of inverse quadratic extrapolation. There was a paper back in the 1980's ... f(a) and f(b) cannot have the same signs. Generally, on a par with the brent routine, but not as heavily tested. It is a safe version of the secant method that uses hyperbolic extrapolation. The version here is by Chuck Harris.

Parameters

f [function] Python function returning a number. f must be continuous, and f(a) and f(b) must have opposite signs.

a [scalar] One end of the bracketing interval [a,b].

b [scalar] The other end of the bracketing interval [a,b].

xtol [number, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter must be nonnegative. As with *brentq*, for nice functions the method will often satisfy the above condition with `xtol/2` and `rtol/2`.

rtol [number, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter cannot be smaller than its default value of `4*np.finfo(float).eps`. As with *brentq*, for nice functions the method will often satisfy the above condition with `xtol/2` and `rtol/2`.

maxiter [int, optional] If convergence is not achieved in *maxiter* iterations, an error is raised. Must be >= 0.

args [tuple, optional] Containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output [bool, optional] If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a *RootResults* object.

disp [bool, optional] If True, raise RuntimeError if the algorithm didn't converge. Otherwise, the convergence status is recorded in any *RootResults* return object.

Returns

x0 [float] Zero of *f* between *a* and *b*.

r [*RootResults* (present if `full_output = True`)] Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

See also:

fmin, **fmin_powell**, **fmin_cg**

fmin_bfgs, **fmin_ncg**

multivariate local optimizers

leastsq

nonlinear least squares minimizer

fmin_l_bfgs_b, **fmin_tnc**, **fmin_cobyla**

constrained multivariate optimizers

basinhopping, **differential_evolution**, **brute**

global optimizers

fminbound, **brent**, **golden**, **bracket**

local scalar minimizers

fsolve

N-D root-finding

brentq, **brenth**, **ridder**, **bisect**, **newton**

1-D root-finding

fixed_point

scalar fixed-point finder

Examples

```
>>> def f(x):
...     return (x**2 - 1)
```

```
>>> from scipy import optimize
```

```
>>> root = optimize.brenth(f, -2, 0)
>>> root
-1.0
```

```
>>> root = optimize.brenth(f, 0, 2)
>>> root
1.0
```

scipy.optimize.ridder

scipy.optimize.**ridder**(*f*, *a*, *b*, *args=()*, *xtol=2e-12*, *rtol=8.881784197001252e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find a root of a function in an interval using Ridder's method.

Parameters

f	[function] Python function returning a number. f must be continuous, and f(a) and f(b) must have opposite signs.
a	[scalar] One end of the bracketing interval [a,b].
b	[scalar] The other end of the bracketing interval [a,b].
xtol	[number, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter must be non-negative.
rtol	[number, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter cannot be smaller than its default value of `4*np.finfo(float).eps`.
maxiter	[int, optional] If convergence is not achieved in *maxiter* iterations, an error is raised. Must be >= 0.
args	[tuple, optional] Containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output
: [bool, optional] If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a `RootResults` object.

disp
: [bool, optional] If True, raise RuntimeError if the algorithm didn't converge. Otherwise, the convergence status is recorded in any `RootResults` return object.

Returns

x0
: [float] Zero of *f* between *a* and *b*.

r
: [`RootResults` (present if `full_output = True`)] Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

See also:

brentq, **brenth**, **bisect**, **newton**

1-D root-finding

fixed_point

scalar fixed-point finder

Notes

Uses [Ridders1979] method to find a zero of the function *f* between the arguments *a* and *b*. Ridders' method is faster than bisection, but not generally as fast as the Brent routines. [Ridders1979] provides the classic description and source of the algorithm. A description can also be found in any recent edition of Numerical Recipes.

The routine used here diverges slightly from standard presentations in order to be a bit more careful of tolerance.

References

[Ridders1979]

Examples

```
>>> def f(x):
...     return (x**2 - 1)
```

```
>>> from scipy import optimize
```

```
>>> root = optimize.ridder(f, 0, 2)
>>> root
1.0
```

```
>>> root = optimize.ridder(f, -2, 0)
>>> root
-1.0
```

scipy.optimize.bisect

scipy.optimize.**bisect**(*f*, *a*, *b*, *args=()*, *xtol=2e-12*, *rtol=8.881784197001252e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find root of a function within an interval using bisection.

Basic bisection routine to find a zero of the function *f* between the arguments *a* and *b*. *f(a)* and *f(b)* cannot have the same signs. Slow but sure.

Parameters

f [function] Python function returning a number. *f* must be continuous, and f(a) and f(b) must have opposite signs.

a [scalar] One end of the bracketing interval [a,b].

b [scalar] The other end of the bracketing interval [a,b].

xtol [number, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter must be non-negative.

rtol [number, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter cannot be smaller than its default value of `4*np.finfo(float).eps`.

maxiter [int, optional] If convergence is not achieved in *maxiter* iterations, an error is raised. Must be >= 0.

args [tuple, optional] Containing extra arguments for the function *f*. *f* is called by `apply(f, (x)+args)`.

full_output

[bool, optional] If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where x is the root, and r is a *RootResults* object.

disp [bool, optional] If True, raise RuntimeError if the algorithm didn't converge. Otherwise, the convergence status is recorded in a *RootResults* return object.

Returns

x0 [float] Zero of *f* between *a* and *b*.

r [*RootResults* (present if `full_output = True`)] Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

See also:

brentq, **brenth**, **bisect**, **newton**

fixed_point

scalar fixed-point finder

fsolve

n-dimensional root-finding

Examples

```
>>> def f(x):
...     return (x**2 - 1)
```

```
>>> from scipy import optimize
```

```
>>> root = optimize.bisect(f, 0, 2)
>>> root
1.0
```

```
>>> root = optimize.bisect(f, -2, 0)
>>> root
-1.0
```

scipy.optimize.newton

scipy.optimize.**newton**(*func*, *x0*, *fprime=None*, *args=()*, *tol=1.48e-08*, *maxiter=50*, *fprime2=None*, *x1=None*, *rtol=0.0*, *full_output=False*, *disp=True*)

Find a zero of a real or complex function using the Newton-Raphson (or secant or Halley's) method.

Find a zero of the function *func* given a nearby starting point *x0*. The Newton-Raphson method is used if the derivative *fprime* of *func* is provided, otherwise the secant method is used. If the second order derivative *fprime2* of *func* is also provided, then Halley's method is used.

If *x0* is a sequence with more than one item, then *newton* returns an array, and *func* must be vectorized and return a sequence or array of the same shape as its first argument. If *fprime* or *fprime2* is given, then its return must also have the same shape.

Parameters

func [callable] The function whose zero is wanted. It must be a function of a single variable of the form `f(x,a,b,c...)`, where `a,b,c...` are extra arguments that can be passed in the *args* parameter.

x0 [float, sequence, or ndarray] An initial estimate of the zero that should be somewhere near the actual zero. If not scalar, then *func* must be vectorized and return a sequence or array of the same shape as its first argument.

fprime [callable, optional] The derivative of the function when available and convenient. If it is None (default), then the secant method is used.

args [tuple, optional] Extra arguments to be used in the function call.

tol [float, optional] The allowable error of the zero value. If *func* is complex-valued, a larger *tol* is recommended as both the real and imaginary parts of *x* contribute to `|x - x0|`.

maxiter [int, optional] Maximum number of iterations.

fprime2 [callable, optional] The second order derivative of the function when available and convenient. If it is None (default), then the normal Newton-Raphson or the secant method is used. If it is not None, then Halley's method is used.

x1 [float, optional] Another estimate of the zero that should be somewhere near the actual zero. Used if *fprime* is not provided.

rtol [float, optional] Tolerance (relative) for termination.

full_output [bool, optional] If *full_output* is False (default), the root is returned. If True and *x0* is scalar, the return value is `(x, r)`, where `x` is the root and `r` is a *RootResults* object. If True and *x0* is non-scalar, the return value is `(x, converged, zero_der)` (see Returns section for details).

disp [bool, optional] If True, raise a RuntimeError if the algorithm didn't converge, with the error message containing the number of iterations and current function value. Otherwise, the convergence status is recorded in a `RootResults` return object. Ignored if *x0* is not scalar. *Note: this has little to do with displaying, however, the `disp` keyword cannot be renamed for backwards compatibility.*

Returns

root [float, sequence, or ndarray] Estimated location where function is zero.

r [`RootResults`, optional] Present if `full_output=True` and *x0* is scalar. Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

converged [ndarray of bool, optional] Present if `full_output=True` and *x0* is non-scalar. For vector functions, indicates which elements converged successfully.

zero_der [ndarray of bool, optional] Present if `full_output=True` and *x0* is non-scalar. For vector functions, indicates which elements had a zero derivative.

See also:

brentq, **brenth**, **ridder**, **bisect**

fsolve

find zeros in N dimensions.

Notes

The convergence rate of the Newton-Raphson method is quadratic, the Halley method is cubic, and the secant method is sub-quadratic. This means that if the function is well-behaved the actual error in the estimated zero after the nth iteration is approximately the square (cube for Halley) of the error after the (n-1)th step. However, the stopping criterion used here is the step size and there is no guarantee that a zero has been found. Consequently, the result should be verified. Safer algorithms are brentq, brenth, ridder, and bisect, but they all require that the root first be bracketed in an interval where the function changes sign. The brentq algorithm is recommended for general use in one dimensional problems when such an interval has been found.

When `newton` is used with arrays, it is best suited for the following types of problems:

- The initial guesses, *x0*, are all relatively the same distance from the roots.
- Some or all of the extra arguments, *args*, are also arrays so that a class of similar problems can be solved together.
- The size of the initial guesses, *x0*, is larger than O(100) elements. Otherwise, a naive loop may perform as well or better than a vector.

Examples

```
>>> from scipy import optimize
>>> import matplotlib.pyplot as plt
```

```
>>> def f(x):
...     return (x**3 - 1)  # only one real root at x = 1
```

`fprime` is not provided, use the secant method:

```
>>> root = optimize.newton(f, 1.5)
>>> root
1.0000000000000016
>>> root = optimize.newton(f, 1.5, fprime2=lambda x: 6 * x)
>>> root
1.0000000000000016
```

Only `fprime` is provided, use the Newton-Raphson method:

```
>>> root = optimize.newton(f, 1.5, fprime=lambda x: 3 * x**2)
>>> root
1.0
```

Both `fprime2` and `fprime` are provided, use Halley's method:

```
>>> root = optimize.newton(f, 1.5, fprime=lambda x: 3 * x**2,
...                        fprime2=lambda x: 6 * x)
>>> root
1.0
```

When we want to find zeros for a set of related starting values and/or function parameters, we can provide both of those as an array of inputs:

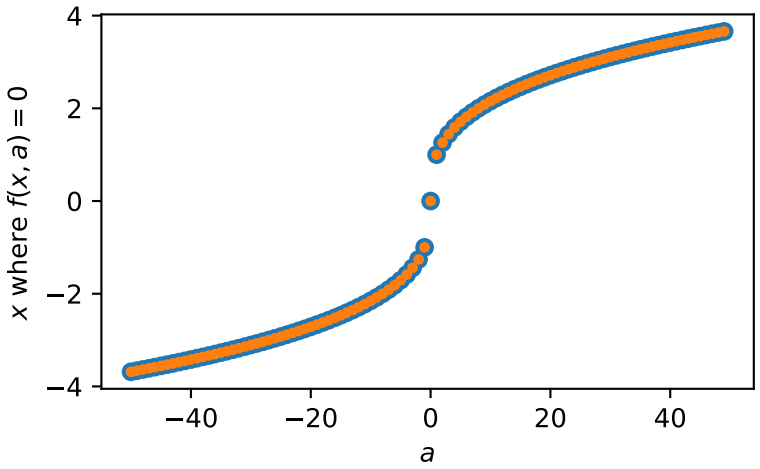
```
>>> f = lambda x, a: x**3 - a
>>> fder = lambda x, a: 3 * x**2
>>> rng = np.random.default_rng()
>>> x = rng.standard_normal(100)
>>> a = np.arange(-50, 50)
>>> vec_res = optimize.newton(f, x, fprime=fder, args=(a, ), maxiter=200)
```

The above is the equivalent of solving for each value in `(x, a)` separately in a for-loop, just faster:

```
>>> loop_res = [optimize.newton(f, x0, fprime=fder, args=(a0,))
...             for x0, a0 in zip(x, a)]
>>> np.allclose(vec_res, loop_res)
True
```

Plot the results found for all values of `a`:

```
>>> analytical_result = np.sign(a) * np.abs(a)**(1/3)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(a, analytical_result, 'o')
>>> ax.plot(a, vec_res, '.')
>>> ax.set_xlabel('$a$')
>>> ax.set_ylabel('$x$ where $f(x, a)=0$')
>>> plt.show()
```



scipy.optimize.toms748

`scipy.optimize.`**`toms748`**(*f*, *a*, *b*, *args=()*, *k=1*, *xtol=2e-12*, *rtol=8.881784197001252e-16*, *maxiter=100*, *full_output=False*, *disp=True*)

Find a zero using TOMS Algorithm 748 method.

Implements the Algorithm 748 method of Alefeld, Potro and Shi to find a zero of the function f on the interval *[a , b]*, where *f(a)* and *f(b)* must have opposite signs.

It uses a mixture of inverse cubic interpolation and "Newton-quadratic" steps. [APS1995].

Parameters

f [function] Python function returning a scalar. The function f must be continuous, and $f(a)$ and $f(b)$ have opposite signs.

a [scalar,] lower boundary of the search interval

b [scalar,] upper boundary of the search interval

args [tuple, optional] containing extra arguments for the function f. f is called by `f(x, *args)`.

k [int, optional] The number of Newton quadratic steps to perform each iteration. `k>=1`.

xtol [scalar, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root. The parameter must be non-negative.

rtol [scalar, optional] The computed root `x0` will satisfy `np.allclose(x, x0, atol=xtol, rtol=rtol)`, where `x` is the exact root.

maxiter [int, optional] If convergence is not achieved in *maxiter* iterations, an error is raised. Must be >= 0.

full_output

[bool, optional] If *full_output* is False, the root is returned. If *full_output* is True, the return value is `(x, r)`, where *x* is the root, and *r* is a *RootResults* object.

disp [bool, optional] If True, raise RuntimeError if the algorithm didn't converge. Otherwise, the convergence status is recorded in the *RootResults* return object.

Returns

x0 [float] Approximate Zero of f

r [*RootResults* (present if `full_output = True`)] Object containing information about the convergence. In particular, `r.converged` is True if the routine converged.

See also:

brentq, **brenth**, **ridder**, **bisect**, **newton**

fsolve

find zeroes in N dimensions.

Notes

f must be continuous. Algorithm 748 with `k=2` is asymptotically the most efficient algorithm known for finding roots of a four times continuously differentiable function. In contrast with Brent's algorithm, which may only decrease the length of the enclosing bracket on the last step, Algorithm 748 decreases it each iteration with the same asymptotic efficiency as it finds the root.

For easy statement of efficiency indices, assume that *f* has 4 continuouous deriviatives. For `k=1`, the convergence order is at least 2.7, and with about asymptotically 2 function evaluations per iteration, the efficiency index is approximately 1.65. For `k=2`, the order is about 4.6 with asymptotically 3 function evaluations per iteration, and the efficiency index 1.66. For higher values of *k*, the efficiency index approaches the kth root of `(3k-2)`, hence `k=1` or `k=2` are usually appropriate.

References

[APS1995]

Examples

```
>>> def f(x):
...     return (x**3 - 1)  # only one real root at x = 1
```

```
>>> from scipy import optimize
>>> root, results = optimize.toms748(f, 0, 2, full_output=True)
>>> root
1.0
>>> results
      converged: True
           flag: 'converged'
 function_calls: 11
     iterations: 5
           root: 1.0
```

scipy.optimize.RootResults

class scipy.optimize.**RootResults**(*root*, *iterations*, *function_calls*, *flag*)

Represents the root finding result.

Attributes

root [float] Estimated root location.
iterations [int] Number of iterations needed to find the root.
function_calls [int] Number of times the function was called.

converged [bool] True if the routine converged.
flag [str] Description of the cause of termination.

The *root_scalar* function supports the following methods:

root_scalar(method='brentq')

scipy.optimize.**root_scalar**(*args=()*, *method='brentq'*, *x0=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root_scalar*

Options

args [tuple, optional] Extra arguments passed to the objective function.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
options: dict, optional
Specifies any method-specific options not covered above

root_scalar(method='brenth')

scipy.optimize.**root_scalar**(*args=()*, *method='brenth'*, *x0=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root_scalar*

Options

args [tuple, optional] Extra arguments passed to the objective function.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
options: dict, optional
Specifies any method-specific options not covered above.

root_scalar(method='bisect')

scipy.optimize.**root_scalar**(*args=()*, *method='bisect'*, *x0=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root_scalar*

Options

args [tuple, optional] Extra arguments passed to the objective function.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.

options: dict, optional
Specifies any method-specific options not covered above.

root_scalar(method='ridder')

scipy.optimize.**root_scalar**(*args=()*, *method='ridder'*, *x0=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root_scalar*

Options

args [tuple, optional] Extra arguments passed to the objective function.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
options: dict, optional
Specifies any method-specific options not covered above.

root_scalar(method='newton')

scipy.optimize.**root_scalar**(*args=()*, *method='newton'*, *x0=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root_scalar*

Options

args [tuple, optional] Extra arguments passed to the objective function and its derivative.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
x0 [float, required] Initial guess.
fprime [bool or callable, optional] If *fprime* is a boolean and is True, f is assumed to return the value of derivative along with the objective function. *fprime* can also be a callable returning the derivative of f. In this case, it must accept the same arguments as f.
options: dict, optional
Specifies any method-specific options not covered above.

root_scalar(method='toms748')

scipy.optimize.**root_scalar**(*args=()*, *method='toms748'*, *x0=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root_scalar*

Options

args [tuple, optional] Extra arguments passed to the objective function.

xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
options: dict, optional
Specifies any method-specific options not covered above.

root_scalar(method='secant')

scipy.optimize.**root_scalar**(*args=()*, *method='secant'*, *x0=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root_scalar*

Options

args [tuple, optional] Extra arguments passed to the objective function.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
x0 [float, required] Initial guess.
x1 [float, required] A second guess.
options: dict, optional
Specifies any method-specific options not covered above.

root_scalar(method='halley')

scipy.optimize.**root_scalar**(*args=()*, *method='halley'*, *x0=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root_scalar*

Options

args [tuple, optional] Extra arguments passed to the objective function and its derivatives.
xtol [float, optional] Tolerance (absolute) for termination.
rtol [float, optional] Tolerance (relative) for termination.
maxiter [int, optional] Maximum number of iterations.
x0 [float, required] Initial guess.
fprime [bool or callable, required] If *fprime* is a boolean and is True, f is assumed to return the value of derivative along with the objective function. *fprime* can also be a callable returning the derivative of f. In this case, it must accept the same arguments as f.
fprime2 [bool or callable, required] If *fprime2* is a boolean and is True, f is assumed to return the value of 1st and 2nd derivatives along with the objective function. *fprime2* can also be a callable returning the 2nd derivative of f. In this case, it must accept the same arguments as f.
options: dict, optional
Specifies any method-specific options not covered above.

The table below lists situations and appropriate methods, along with *asymptotic* convergence rates per iteration (and per function evaluation) for successful convergence to a simple root(*). Bisection is the slowest of them all, adding one bit of accuracy for each function evaluation, but is guaranteed to converge. The other bracketing methods all (eventually) increase the number of accurate bits by about 50% for every function evaluation. The derivative-based methods, all built on `newton`, can converge quite quickly if the initial value is close to the root. They can also be applied to functions defined on (a subset of) the complex plane.

Domain of f	Bracket?	Derivatives?		Solvers	Convergence	
		fprime	*fprime2*		Guaranteed?	Rate(s)(*)
R	Yes	N/A	N/A	• bisection • brentq • brenth • ridder • toms748	• Yes • Yes • Yes • Yes • Yes	• 1 "Linear" • >=1, <= 1.62 • >=1, <= 1.62 • 2.0 (1.41) • 2.7 (1.65)
R or *C*	No	No	No	secant	No	1.62 (1.62)
R or *C*	No	Yes	No	newton	No	2.00 (1.41)
R or *C*	No	Yes	Yes	halley	No	3.00 (1.44)

See also:

`scipy.optimize.cython_optimize` – Typed Cython versions of zeros functions

Fixed point finding:

`fixed_point`(func, x0[, args, xtol, maxiter, …])	Find a fixed point of the function.

scipy.optimize.fixed_point

scipy.optimize.**fixed_point**(*func*, *x0*, *args=()*, *xtol=1e-08*, *maxiter=500*, *method='del2'*)

Find a fixed point of the function.

Given a function of one or more variables and a starting point, find a fixed point of the function: i.e., where `func(x0) == x0`.

Parameters

func [function] Function to evaluate.
x0 [array_like] Fixed point of function.
args [tuple, optional] Extra arguments to *func*.
xtol [float, optional] Convergence tolerance, defaults to 1e-08.
maxiter [int, optional] Maximum number of iterations, defaults to 500.
method [{"del2", "iteration"}, optional] Method of finding the fixed-point, defaults to "del2", which uses Steffensen's Method with Aitken's `Del^2` convergence acceleration [1]. The "iteration" method simply iterates the function until convergence is detected, without attempting

to accelerate the convergence.

References

[1]

Examples

```
>>> from scipy import optimize
>>> def func(x, c1, c2):
...     return np.sqrt(c1/(x+c2))
>>> c1 = np.array([10,12.])
>>> c2 = np.array([3, 5.])
>>> optimize.fixed_point(func, [1.2, 1.3], args=(c1,c2))
array([ 1.4920333 ,  1.37228132])
```

Multidimensional

root(fun, x0[, args, method, jac, tol, …])	Find a root of a vector function.

scipy.optimize.root

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='hybr'*, *jac=None*, *tol=None*, *callback=None*, *options=None*)

Find a root of a vector function.

Parameters

fun [callable] A vector function to find a root of.

x0 [ndarray] Initial guess.

args [tuple, optional] Extra arguments passed to the objective function and its Jacobian.

method [str, optional] Type of solver. Should be one of

- 'hybr' *(see here)*
- 'lm' *(see here)*
- 'broyden1' *(see here)*
- 'broyden2' *(see here)*
- 'anderson' *(see here)*
- 'linearmixing' *(see here)*
- 'diagbroyden' *(see here)*
- 'excitingmixing' *(see here)*
- 'krylov' *(see here)*
- 'df-sane' *(see here)*

jac [bool or callable, optional] If *jac* is a Boolean and is True, *fun* is assumed to return the value of Jacobian along with the objective function. If False, the Jacobian will be estimated numerically. *jac* can also be a callable returning the Jacobian of *fun*. In this case, it must accept the same arguments as *fun*.

tol [float, optional] Tolerance for termination. For detailed control, use solver-specific options.

callback [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual. For all methods but 'hybr' and 'lm'.

options [dict, optional] A dictionary of solver options. E.g., *xtol* or *maxiter*, see `show_options()` for details.

Returns

sol [OptimizeResult] The solution represented as a `OptimizeResult` object. Important attributes are: `x` the solution array, `success` a Boolean flag indicating if the algorithm exited successfully and `message` which describes the cause of the termination. See `OptimizeResult` for a description of other attributes.

See also:

`show_options`

Additional options accepted by the solvers

Notes

This section describes the available solvers that can be selected by the 'method' parameter. The default method is *hybr*.

Method *hybr* uses a modification of the Powell hybrid method as implemented in MINPACK [1].

Method *lm* solves the system of nonlinear equations in a least squares sense using a modification of the Levenberg-Marquardt algorithm as implemented in MINPACK [1].

Method *df-sane* is a derivative-free spectral method. [3]

Methods *broyden1*, *broyden2*, *anderson*, *linearmixing*, *diagbroyden*, *excitingmixing*, *krylov* are inexact Newton methods, with backtracking or full line searches [2]. Each method corresponds to a particular Jacobian approximations. See `nonlin` for details.

- Method *broyden1* uses Broyden's first Jacobian approximation, it is known as Broyden's good method.
- Method *broyden2* uses Broyden's second Jacobian approximation, it is known as Broyden's bad method.
- Method *anderson* uses (extended) Anderson mixing.
- Method *Krylov* uses Krylov approximation for inverse Jacobian. It is suitable for large-scale problem.
- Method *diagbroyden* uses diagonal Broyden Jacobian approximation.
- Method *linearmixing* uses a scalar Jacobian approximation.
- Method *excitingmixing* uses a tuned diagonal Jacobian approximation.

Warning: The algorithms implemented for methods *diagbroyden*, *linearmixing* and *excitingmixing* may be useful for specific problems, but whether they will work may depend strongly on the problem.

New in version 0.11.0.

References

[1], [2], [3]

Examples

The following functions define a system of nonlinear equations and its jacobian.

```
>>> def fun(x):
...     return [x[0]  + 0.5 * (x[0] - x[1])**3 - 1.0,
...             0.5 * (x[1] - x[0])**3 + x[1]]
```

```
>>> def jac(x):
...     return np.array([[1 + 1.5 * (x[0] - x[1])**2,
...                       -1.5 * (x[0] - x[1])**2],
...                      [-1.5 * (x[1] - x[0])**2,
...                       1 + 1.5 * (x[1] - x[0])**2]])
```

A solution can be obtained as follows.

```
>>> from scipy import optimize
>>> sol = optimize.root(fun, [0, 0], jac=jac, method='hybr')
>>> sol.x
array([ 0.8411639,  0.1588361])
```

The *root* function supports the following methods:

root(method='hybr')

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='hybr'*, *jac=None*, *tol=None*, *callback=None*, *options={'func': None, 'col_deriv': 0, 'xtol': 1.49012e-08, 'maxfev': 0, 'band': None, 'eps': None, 'factor': 100, 'diag': None}*)

Find the roots of a multivariate function using MINPACK's hybrd and hybrj routines (modified Powell method).

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

col_deriv [bool] Specify whether the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

xtol [float] The calculation will terminate if the relative error between two consecutive iterates is at most *xtol*.

maxfev [int] The maximum number of calls to the function. If zero, then `100*(N+1)` is the maximum where N is the number of elements in *x0*.

band [tuple] If set to a two-sequence containing the number of sub- and super-diagonals within the band of the Jacobi matrix, the Jacobi matrix is considered banded (only for `fprime=None`).

eps [float] A suitable step length for the forward-difference approximation of the Jacobian (for `fprime=None`). If *eps* is less than the machine precision, it is assumed that the relative errors in the functions are of the order of the machine precision.

factor [float] A parameter determining the initial step bound (`factor * || diag * x||`). Should be in the interval `(0.1, 100)`.

diag [sequence] N positive entries that serve as a scale factors for the variables.

root(method='lm')

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='lm'*, *jac=None*, *tol=None*, *callback=None*, *options={'col_deriv': 0, 'xtol': 1.49012e-08, 'ftol': 1.49012e-08, 'gtol': 0.0, 'maxiter': 0, 'eps': 0.0, 'factor': 100, 'diag': None}*)

Solve for least squares with Levenberg-Marquardt

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

col_deriv [bool] non-zero to specify that the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).
ftol [float] Relative error desired in the sum of squares.
xtol [float] Relative error desired in the approximate solution.
gtol [float] Orthogonality desired between the function vector and the columns of the Jacobian.
maxiter [int] The maximum number of calls to the function. If zero, then 100*(N+1) is the maximum where N is the number of elements in x0.
epsfcn [float] A suitable step length for the forward-difference approximation of the Jacobian (for Dfun=None). If epsfcn is less than the machine precision, it is assumed that the relative errors in the functions are of the order of the machine precision.
factor [float] A parameter determining the initial step bound (`factor * || diag * x||`). Should be in interval `(0.1, 100)`.
diag [sequence] N positive entries that serve as a scale factors for the variables.

root(method='broyden1')

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='broyden1'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

nit [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
disp [bool, optional] Print status to stdout on every iteration.
maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.
ftol [float, optional] Relative tolerance for the residual. If omitted, not used.
fatol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
xtol [float, optional] Relative minimum step size. If omitted, not used.
xatol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search
[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options
[dict, optional]
Options for the respective Jacobian approximation.

alpha [float, optional] Initial guess for the Jacobian is (-1/alpha).

reduction_method
[str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form `(method, param1, param2, ...)` that gives the name of the method and values for additional parameters.
Methods available:

- **restart** Drop all matrix columns. Has no extra parameters.
- **simple** Drop oldest matrix column. Has no extra parameters.
- **svd** Keep only the most significant SVD components.
  Extra parameters:
  – to_retain
  Number of SVD components to retain when rank reduction is done. Default is `max_rank - 2`.

max_rank [int, optional] Maximum rank for the Broyden matrix. Default is infinity (i.e., no rank reduction).

root(method='broyden2')

`scipy.optimize.`**`root`**(*fun*, *x0*, *args=()*, *method='broyden2'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

nit [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol [float, optional] Relative tolerance for the residual. If omitted, not used.

fatol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol [float, optional] Relative minimum step size. If omitted, not used.

xatol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search
[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options
[dict, optional] Options for the respective Jacobian approximation.
alpha [float, optional] Initial guess for the Jacobian is (-1/alpha).
reduction_method
[str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form `(method, param1, param2, ...)` that gives the name of the method and values for additional parameters.
Methods available:
- **restart** Drop all matrix columns. Has no extra parameters.
- **simple** Drop oldest matrix column. Has no extra parameters.
- **svd** Keep only the most significant SVD components.
  Extra parameters:
  - **to_retain**
    Number of SVD components to retain when rank reduction is done. Default is `max_rank - 2`.

max_rank [int, optional] Maximum rank for the Broyden matrix. Default is infinity (i.e., no rank reduction).

root(method='anderson')

`scipy.optimize.root` (*fun*, *x0*, *args=()*, *method='anderson'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

nit [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
disp [bool, optional] Print status to stdout on every iteration.
maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.
ftol [float, optional] Relative tolerance for the residual. If omitted, not used.
fatol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
xtol [float, optional] Relative minimum step size. If omitted, not used.
xatol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.
line_search
[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.
jac_options
[dict, optional] Options for the respective Jacobian approximation.
alpha [float, optional] Initial guess for the Jacobian is (-1/alpha).
M [float, optional] Number of previous vectors to retain. Defaults to 5.
w0 [float, optional] Regularization parameter for numerical stability. Compared to unity, good values of the order of 0.01.

root(method='linearmixing')

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='linearmixing'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

nit [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, `NoConvergence` is raised.

ftol [float, optional] Relative tolerance for the residual. If omitted, not used.

fatol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol [float, optional] Relative minimum step size. If omitted, not used.

xatol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search

[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options

[dict, optional] Options for the respective Jacobian approximation.

alpha [float, optional] initial guess for the jacobian is (-1/alpha).

root(method='diagbroyden')

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='diagbroyden'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

nit [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol [float, optional] Relative tolerance for the residual. If omitted, not used.

fatol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol [float, optional] Relative minimum step size. If omitted, not used.

xatol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search
[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options
[dict, optional] Options for the respective Jacobian approximation.

alpha [float, optional] initial guess for the jacobian is (-1/alpha).

root(method='excitingmixing')

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='excitingmixing'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

nit [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

disp [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

ftol [float, optional] Relative tolerance for the residual. If omitted, not used.

fatol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

xtol [float, optional] Relative minimum step size. If omitted, not used.

xatol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search
[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

jac_options
[dict, optional] Options for the respective Jacobian approximation.

alpha [float, optional] Initial Jacobian approximation is (-1/alpha).

alphamax [float, optional] The entries of the diagonal Jacobian are kept in the range `[alpha, alphamax]`.

root(method='krylov')

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='krylov'*, *tol=None*, *callback=None*, *options={}*)

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

nit [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
disp [bool, optional] Print status to stdout on every iteration.
maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.
ftol [float, optional] Relative tolerance for the residual. If omitted, not used.
fatol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
xtol [float, optional] Relative minimum step size. If omitted, not used.
xatol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.
line_search
[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.
jac_options
[dict, optional] Options for the respective Jacobian approximation.
rdiff [float, optional] Relative step size to use in numerical differentiation.
method [{'lgmres', 'gmres', 'bicgstab', 'cgs', 'minres'} or function] Krylov method to use to approximate the Jacobian. Can be a string, or a function implementing the same interface as the iterative solvers in *scipy.sparse.linalg*. The default is *scipy.sparse.linalg.lgmres*.
inner_M [LinearOperator or InverseJacobian] Preconditioner for the inner Krylov iteration. Note that you can use also inverse Jacobians as (adaptive) preconditioners. For example,

```
>>> jac = BroydenFirst()
>>> kjac = KrylovJacobian(inner_M=jac.inverse).
```

If the preconditioner has a method named 'update', it will be called as `update(x, f)` after each nonlinear step, with `x` giving the current point, and `f` the current function value.
inner_tol, inner_maxiter, …
Parameters to pass on to the "inner" Krylov solver. See *scipy.sparse.linalg.gmres* for details.
outer_k [int, optional] Size of the subspace kept across LGMRES nonlinear iterations. See *scipy.sparse.linalg.lgmres* for details.

root(method='df-sane')

scipy.optimize.**root**(*fun*, *x0*, *args=()*, *method='df-sane'*, *tol=None*, *callback=None*, *options={'func': None, 'ftol': 1e-08, 'fatol': 1e-300, 'maxfev': 1000, 'fnorm': None, 'disp': False, 'M': 10, 'eta_strategy': None, 'sigma_eps': 1e-10, 'sigma_0': 1.0, 'line_search': 'cruz'}*)

Solve nonlinear equation with the DF-SANE method

See also:

For documentation for the rest of the parameters, see *scipy.optimize.root*

Options

ftol [float, optional] Relative norm tolerance.

fatol [float, optional] Absolute norm tolerance. Algorithm terminates when `||func(x)|| < fatol + ftol ||func(x_0)||`.

fnorm [callable, optional] Norm to use in the convergence check. If None, 2-norm is used.

maxfev [int, optional] Maximum number of function evaluations.

disp [bool, optional] Whether to print convergence process to stdout.

eta_strategy [callable, optional] Choice of the `eta_k` parameter, which gives slack for growth of `||F||**2`. Called as `eta_k = eta_strategy(k, x, F)` with *k* the iteration number, *x* the current iterate and *F* the current residual. Should satisfy `eta_k > 0` and `sum(eta, k=0..inf) < inf`. Default: `||F||**2 / (1 + k)**2`.

sigma_eps [float, optional] The spectral coefficient is constrained to `sigma_eps < sigma < 1/sigma_eps`. Default: 1e-10

sigma_0 [float, optional] Initial spectral coefficient. Default: 1.0

M [int, optional] Number of iterates to include in the nonmonotonic line search. Default: 10

line_search [{'cruz', 'cheng'}] Type of line search to employ. 'cruz' is the original one defined in [Martinez & Raydan. Math. Comp. 75, 1429 (2006)], 'cheng' is a modified search defined in [Cheng & Li. IMA J. Numer. Anal. 29, 814 (2009)]. Default: 'cruz'

References

[1], [2], [3]

Linear programming

linprog(c[, A_ub, b_ub, A_eq, b_eq, bounds, …])	Linear programming: minimize a linear objective function subject to linear equality and inequality constraints.

scipy.optimize.linprog

scipy.optimize.**linprog**(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='interior-point'*, *callback=None*, *options=None*, *x0=None*)

Linear programming: minimize a linear objective function subject to linear equality and inequality constraints.

Linear programming solves problems of the following form:

$$\begin{aligned} \min_x \ & c^T x \\ \text{such that } & A_{ub} x \leq b_{ub}, \\ & A_{eq} x = b_{eq}, \\ & l \leq x \leq u, \end{aligned}$$

where x is a vector of decision variables; c, b_{ub}, b_{eq}, l, and u are vectors; and A_{ub} and A_{eq} are matrices.

Alternatively, that's:

minimize:

```
c @ x
```

such that:

```
A_ub @ x <= b_ub
A_eq @ x == b_eq
lb <= x <= ub
```

Note that by default `lb = 0` and `ub = None` unless specified with `bounds`.

Parameters

c [1-D array] The coefficients of the linear objective function to be minimized.

A_ub [2-D array, optional] The inequality constraint matrix. Each row of `A_ub` specifies the coefficients of a linear inequality constraint on `x`.

b_ub [1-D array, optional] The inequality constraint vector. Each element represents an upper bound on the corresponding value of `A_ub @ x`.

A_eq [2-D array, optional] The equality constraint matrix. Each row of `A_eq` specifies the coefficients of a linear equality constraint on `x`.

b_eq [1-D array, optional] The equality constraint vector. Each element of `A_eq @ x` must equal the corresponding element of `b_eq`.

bounds [sequence, optional] A sequence of `(min, max)` pairs for each element in `x`, defining the minimum and maximum values of that decision variable. Use `None` to indicate that there is no bound. By default, bounds are `(0, None)` (all decision variables are non-negative). If a single tuple `(min, max)` is provided, then `min` and `max` will serve as bounds for all decision variables.

method [str, optional] The algorithm used to solve the standard form problem. *'highs-ds'*, *'highs-ipm'*, *'highs'*, *'interior-point'* (default), *'revised simplex'*, and *'simplex'* (legacy) are supported.

callback [callable, optional] If a callback function is provided, it will be called at least once per iteration of the algorithm. The callback function must accept a single *scipy.optimize.OptimizeResult* consisting of the following fields:

- **x** [1-D array] The current solution vector.
- **fun** [float] The current value of the objective function `c @ x`.
- **success** [bool] `True` when the algorithm has completed successfully.
- **slack** [1-D array] The (nominally positive) values of the slack, `b_ub - A_ub @ x`.
- **con** [1-D array] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
- **phase** [int] The phase of the algorithm being executed.
- **status** [int] An integer representing the status of the algorithm.
  - `0` : Optimization proceeding nominally.
  - `1` : Iteration limit reached.
  - `2` : Problem appears to be infeasible.
  - `3` : Problem appears to be unbounded.
  - `4` : Numerical difficulties encountered.
- **nit** [int] The current iteration number.
- **message** [str] A string descriptor of the algorithm status.

Callback functions are not currently supported by the HiGHS methods.

options [dict, optional] A dictionary of solver options. All methods accept the following options:

- **maxiter** [int] Maximum number of iterations to perform. Default: see method-specific documentation.
- **disp** [bool] Set to `True` to print convergence messages. Default: `False`.
- **presolve** [bool] Set to `False` to disable automatic presolve. Default: `True`.

All methods except the HiGHS solvers also accept:

- **tol** [float] A tolerance which determines when a residual is "close enough" to zero to be considered exactly zero.

autoscale [bool] Set to `True` to automatically perform equilibration. Consider using this option if the numerical values in the constraints are separated by several orders of magnitude. Default: `False`.

rr [bool] Set to `False` to disable automatic redundancy removal. Default: `True`.

rr_method

[string] Method used to identify and remove redundant rows from the equality constraint matrix after presolve. For problems with dense input, the available methods for redundancy removal are:

"SVD": Repeatedly performs singular value decomposition on the matrix, detecting redundant rows based on nonzeros in the left singular vectors that correspond with zero singular values. May be fast when the matrix is nearly full rank.

"pivot": Uses the algorithm presented in [5] to identify redundant rows.

"ID": Uses a randomized interpolative decomposition. Identifies columns of the matrix transpose not used in a full-rank interpolative decomposition of the matrix.

None: Uses "svd" if the matrix is nearly full rank, that is, the difference between the matrix rank and the number of rows is less than five. If not, uses "pivot". The behavior of this default is subject to change without prior notice.

Default: None. For problems with sparse input, this option is ignored, and the pivot-based algorithm presented in [5] is used.

For method-specific options, see *show_options('linprog')*.

x0 [1-D array, optional] Guess values of the decision variables, which will be refined by the optimization algorithm. This argument is currently used only by the 'revised simplex' method, and can only be used if *x0* represents a basic feasible solution.

Returns

res [OptimizeResult] A *scipy.optimize.OptimizeResult* consisting of the fields:

x [1-D array] The values of the decision variables that minimizes the objective function while satisfying the constraints.

fun [float] The optimal value of the objective function `c @ x`.

slack [1-D array] The (nominally positive) values of the slack variables, `b_ub - A_ub @ x`.

con [1-D array] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.

success [bool] `True` when the algorithm succeeds in finding an optimal solution.

status [int] An integer representing the exit status of the algorithm.

`0` : Optimization terminated successfully.

`1` : Iteration limit reached.

`2` : Problem appears to be infeasible.

`3` : Problem appears to be unbounded.

`4` : Numerical difficulties encountered.

nit [int] The total number of iterations performed in all phases.

message [str] A string descriptor of the exit status of the algorithm.

See also:

show_options

Additional options accepted by the solvers.

Notes

This section describes the available solvers that can be selected by the 'method' parameter.

'highs-ds' and *'highs-ipm'* are interfaces to the HiGHS simplex and interior-point method solvers [13], respectively. *'highs'* chooses between the two automatically. These are the fastest linear programming solvers in SciPy, especially for large, sparse problems; which of these two is faster is problem-dependent. *'interior-point'* is the default as it was the fastest and most robust method before the recent addition of the HiGHS solvers. *'revised simplex'* is more accurate than interior-point for the problems it solves. *'simplex'* is the legacy method and is included for backwards compatibility and educational purposes.

Method *highs-ds* is a wrapper of the C++ high performance dual revised simplex implementation (HSOL) [13], [14]. Method *highs-ipm* is a wrapper of a C++ implementation of an **i**nterior-**p**oint **m**ethod [13]; it features a crossover routine, so it is as accurate as a simplex solver. Method *highs* chooses between the two automatically. For new code involving `linprog`, we recommend explicitly choosing one of these three method values.

New in version 1.6.0.

Method *interior-point* uses the primal-dual path following algorithm as outlined in [4]. This algorithm supports sparse constraint matrices and is typically faster than the simplex methods, especially for large, sparse problems. Note, however, that the solution returned may be slightly less accurate than those of the simplex methods and will not, in general, correspond with a vertex of the polytope defined by the constraints.

New in version 1.0.0.

Method *revised simplex* uses the revised simplex method as described in [9], except that a factorization [11] of the basis matrix, rather than its inverse, is efficiently maintained and used to solve the linear systems at each iteration of the algorithm.

New in version 1.3.0.

Method *simplex* uses a traditional, full-tableau implementation of Dantzig's simplex algorithm [1], [2] (*not* the Nelder-Mead simplex). This algorithm is included for backwards compatibility and educational purposes.

New in version 0.15.0.

Before applying *interior-point*, *revised simplex*, or *simplex*, a presolve procedure based on [8] attempts to identify trivial infeasibilities, trivial unboundedness, and potential problem simplifications. Specifically, it checks for:

- rows of zeros in `A_eq` or `A_ub`, representing trivial constraints;
- columns of zeros in `A_eq` *and* `A_ub`, representing unconstrained variables;
- column singletons in `A_eq`, representing fixed variables; and
- column singletons in `A_ub`, representing simple bounds.

If presolve reveals that the problem is unbounded (e.g. an unconstrained and unbounded variable has negative cost) or infeasible (e.g., a row of zeros in `A_eq` corresponds with a nonzero in `b_eq`), the solver terminates with the appropriate status code. Note that presolve terminates as soon as any sign of unboundedness is detected; consequently, a problem may be reported as unbounded when in reality the problem is infeasible (but infeasibility has not been detected yet). Therefore, if it is important to know whether the problem is actually infeasible, solve the problem again with option `presolve=False`.

If neither infeasibility nor unboundedness are detected in a single pass of the presolve, bounds are tightened where possible and fixed variables are removed from the problem. Then, linearly dependent rows of the `A_eq` matrix are removed, (unless they represent an infeasibility) to avoid numerical difficulties in the primary solve routine. Note that rows that are nearly linearly dependent (within a prescribed tolerance) may also be removed, which can change the optimal solution in rare cases. If this is a concern, eliminate redundancy from your problem formulation and run with option `rr=False` or `presolve=False`.

Several potential improvements can be made here: additional presolve checks outlined in [8] should be implemented, the presolve routine should be run multiple times (until no further simplifications can be made), and more of the efficiency improvements from [5] should be implemented in the redundancy removal routines.

After presolve, the problem is transformed to standard form by converting the (tightened) simple bounds to upper bound constraints, introducing non-negative slack variables for inequality constraints, and expressing unbounded variables as the difference between two non-negative variables. Optionally, the problem is automatically scaled via equilibration [12]. The selected algorithm solves the standard form problem, and a postprocessing routine converts the result to a solution to the original problem.

References

[1], [2], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14]

Examples

Consider the following problem:

$$\begin{aligned} \min_{x_0, x_1} \quad & -x_0 + 4x_1 \\ \text{such that} \quad & -3x_0 + x_1 \leq 6, \\ & -x_0 - 2x_1 \geq -4, \\ & x_1 \geq -3. \end{aligned}$$

The problem is not presented in the form accepted by *linprog*. This is easily remedied by converting the "greater than" inequality constraint to a "less than" inequality constraint by multiplying both sides by a factor of -1. Note also that the last constraint is really the simple bound $-3 \leq x_1 \leq \infty$. Finally, since there are no bounds on x_0, we must explicitly specify the bounds $-\infty \leq x_0 \leq \infty$, as the default is for variables to be non-negative. After collecting coeffecients into arrays and tuples, the input for this problem is:

```
>>> c = [-1, 4]
>>> A = [[-3, 1], [1, 2]]
>>> b = [6, 4]
>>> x0_bounds = (None, None)
>>> x1_bounds = (-3, None)
>>> from scipy.optimize import linprog
>>> res = linprog(c, A_ub=A, b_ub=b, bounds=[x0_bounds, x1_bounds])
```

Note that the default method for *linprog* is 'interior-point', which is approximate by nature.

```
>>> print(res)
     con: array([], dtype=float64)
     fun: -21.99999984082494 # may vary
 message: 'Optimization terminated successfully.'
     nit: 6 # may vary
   slack: array([3.89999997e+01, 8.46872439e-08] # may vary
  status: 0
 success: True
       x: array([ 9.99999989, -2.99999999]) # may vary
```

If you need greater accuracy, try 'revised simplex'.

```
>>> res = linprog(c, A_ub=A, b_ub=b, bounds=[x0_bounds, x1_bounds],␣
↪method='revised simplex')
>>> print(res)
     con: array([], dtype=float64)
     fun: -22.0 # may vary
 message: 'Optimization terminated successfully.'
     nit: 1 # may vary
   slack: array([39.,  0.]) # may vary
  status: 0
 success: True
       x: array([10., -3.]) # may vary
```

The *linprog* function supports the following methods:

linprog(method='simplex')

scipy.optimize.**linprog**(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='simplex'*, *callback=None*, *options={'maxiter': 5000, 'disp': False, 'presolve': True, 'tol': 1e-12, 'autoscale': False, 'rr': True, 'bland': False}*, *x0=None*)

Linear programming: minimize a linear objective function subject to linear equality and inequality constraints using the tableau-based simplex method.

Linear programming solves problems of the following form:

$$\begin{aligned} \min_x \ & c^T x \\ \text{such that } & A_{ub} x \leq b_{ub}, \\ & A_{eq} x = b_{eq}, \\ & l \leq x \leq u, \end{aligned}$$

where x is a vector of decision variables; c, b_{ub}, b_{eq}, l, and u are vectors; and A_{ub} and A_{eq} are matrices.

Alternatively, that's:

minimize:

```
c @ x
```

such that:

```
A_ub @ x <= b_ub
A_eq @ x == b_eq
lb <= x <= ub
```

Note that by default `lb = 0` and `ub = None` unless specified with `bounds`.

Parameters

c [1-D array] The coefficients of the linear objective function to be minimized.

A_ub [2-D array, optional] The inequality constraint matrix. Each row of `A_ub` specifies the coefficients of a linear inequality constraint on `x`.

b_ub [1-D array, optional] The inequality constraint vector. Each element represents an upper bound on the corresponding value of `A_ub @ x`.

A_eq [2-D array, optional] The equality constraint matrix. Each row of `A_eq` specifies the coefficients of a linear equality constraint on `x`.

b_eq [1-D array, optional] The equality constraint vector. Each element of `A_eq @ x` must equal the corresponding element of `b_eq`.

bounds [sequence, optional] A sequence of `(min, max)` pairs for each element in `x`, defining the minimum and maximum values of that decision variable. Use `None` to indicate that there is no bound. By default, bounds are `(0, None)` (all decision variables are non-negative). If a single tuple `(min, max)` is provided, then `min` and `max` will serve as bounds for all decision variables.

method [str] This is the method-specific documentation for 'simplex'. *'highs'*, *'highs-ds'*, *'highs-ipm'*, *'interior-point'* (default), and *'revised simplex'* are also available.

callback [callable, optional] Callback function to be executed once per iteration.

Returns

res [OptimizeResult] A *scipy.optimize.OptimizeResult* consisting of the fields:

- **x** [1-D array] The values of the decision variables that minimizes the objective function while satisfying the constraints.
- **fun** [float] The optimal value of the objective function `c @ x`.
- **slack** [1-D array] The (nominally positive) values of the slack variables, `b_ub - A_ub @ x`.
- **con** [1-D array] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
- **success** [bool] `True` when the algorithm succeeds in finding an optimal solution.
- **status** [int] An integer representing the exit status of the algorithm.
  `0` : Optimization terminated successfully.
  `1` : Iteration limit reached.
  `2` : Problem appears to be infeasible.
  `3` : Problem appears to be unbounded.
  `4` : Numerical difficulties encountered.
- **message** [str] A string descriptor of the exit status of the algorithm.
- **nit** [int] The total number of iterations performed in all phases.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.linprog*

Options

maxiter [int (default: 5000)] The maximum number of iterations to perform in either phase.

disp [bool (default: False)] Set to `True` if indicators of optimization status are to be printed to the console each iteration.

presolve [bool (default: True)] Presolve attempts to identify trivial infeasibilities, identify trivial unboundedness, and simplify the problem before sending it to the main solver. It is generally recommended to keep the default setting `True`; set to `False` if presolve is to be disabled.

tol [float (default: 1e-12)] The tolerance which determines when a solution is "close enough" to zero in Phase 1 to be considered a basic feasible solution or close enough to positive to serve as an optimal solution.

autoscale [bool (default: False)] Set to `True` to automatically perform equilibration. Consider using this option if the numerical values in the constraints are separated by several orders of magnitude.

rr [bool (default: True)] Set to `False` to disable automatic redundancy removal.

bland [bool] If True, use Bland's anti-cycling rule [3] to choose pivots to prevent cycling. If False, choose pivots which should lead to a converged solution more quickly. The latter method is subject to cycling (non-convergence) in rare instances.

unknown_options
[dict] Optional arguments not used by this particular solver. If *unknown_options* is non-empty a warning is issued listing all unused options.

References

[1], [2], [3]

linprog(method='interior-point')

scipy.optimize.**linprog**(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='interior-point'*, *callback=None*, *options={'maxiter': 1000, 'disp': False, 'presolve': True, 'tol': 1e-08, 'autoscale': False, 'rr': True, 'alpha0': 0.99995, 'beta': 0.1, 'sparse': False, 'lstsq': False, 'sym_pos': True, 'cholesky': True, 'pc': True, 'ip': False, 'permc_spec': 'MMD_AT_PLUS_A'}*, *x0=None*)

Linear programming: minimize a linear objective function subject to linear equality and inequality constraints using the interior-point method of [4].

Linear programming solves problems of the following form:

$$\min_x c^T x$$
$$\text{such that } A_{ub} x \leq b_{ub},$$
$$A_{eq} x = b_{eq},$$
$$l \leq x \leq u,$$

where x is a vector of decision variables; c, b_{ub}, b_{eq}, l, and u are vectors; and A_{ub} and A_{eq} are matrices.

Alternatively, that's:

minimize:

```
c @ x
```

such that:

```
A_ub @ x <= b_ub
A_eq @ x == b_eq
lb <= x <= ub
```

Note that by default `lb = 0` and `ub = None` unless specified with `bounds`.

Parameters

c [1-D array] The coefficients of the linear objective function to be minimized.

A_ub [2-D array, optional] The inequality constraint matrix. Each row of `A_ub` specifies the coefficients of a linear inequality constraint on `x`.

b_ub [1-D array, optional] The inequality constraint vector. Each element represents an upper bound on the corresponding value of `A_ub @ x`.

A_eq [2-D array, optional] The equality constraint matrix. Each row of `A_eq` specifies the coefficients of a linear equality constraint on `x`.

b_eq [1-D array, optional] The equality constraint vector. Each element of `A_eq @ x` must equal the corresponding element of `b_eq`.

bounds [sequence, optional] A sequence of `(min, max)` pairs for each element in `x`, defining the minimum and maximum values of that decision variable. Use `None` to indicate that there is no bound. By default, bounds are `(0, None)` (all decision variables are non-negative). If a single tuple `(min, max)` is provided, then `min` and `max` will serve as bounds for all decision variables.

method [str] This is the method-specific documentation for 'interior-point'. *'highs'*, *'highs-ds'*, *'highs-ipm'*, *'revised simplex'*, and *'simplex'* (legacy) are also available.

callback [callable, optional] Callback function to be executed once per iteration.

Returns

res [OptimizeResult] A *scipy.optimize.OptimizeResult* consisting of the fields:

- **x** [1-D array] The values of the decision variables that minimizes the objective function while satisfying the constraints.
- **fun** [float] The optimal value of the objective function `c @ x`.
- **slack** [1-D array] The (nominally positive) values of the slack variables, `b_ub - A_ub @ x`.
- **con** [1-D array] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
- **success** [bool] `True` when the algorithm succeeds in finding an optimal solution.
- **status** [int] An integer representing the exit status of the algorithm.
  `0` : Optimization terminated successfully.
  `1` : Iteration limit reached.
  `2` : Problem appears to be infeasible.
  `3` : Problem appears to be unbounded.
  `4` : Numerical difficulties encountered.
- **message** [str] A string descriptor of the exit status of the algorithm.
- **nit** [int] The total number of iterations performed in all phases.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.linprog*

Options

- **maxiter** [int (default: 1000)] The maximum number of iterations of the algorithm.
- **disp** [bool (default: False)] Set to `True` if indicators of optimization status are to be printed to the console each iteration.
- **presolve** [bool (default: True)] Presolve attempts to identify trivial infeasibilities, identify trivial unboundedness, and simplify the problem before sending it to the main solver. It is generally recommended to keep the default setting `True`; set to `False` if presolve is to be disabled.
- **tol** [float (default: 1e-8)] Termination tolerance to be used for all termination criteria; see [4] Section 4.5.
- **autoscale** [bool (default: False)] Set to `True` to automatically perform equilibration. Consider using this option if the numerical values in the constraints are separated by several orders of magnitude.
- **rr** [bool (default: True)] Set to `False` to disable automatic redundancy removal.
- **alpha0** [float (default: 0.99995)] The maximal step size for Mehrota's predictor-corrector search direction; see β_3 of [4] Table 8.1.
- **beta** [float (default: 0.1)] The desired reduction of the path parameter μ (see [6]) when Mehrota's predictor-corrector is not in use (uncommon).
- **sparse** [bool (default: False)] Set to `True` if the problem is to be treated as sparse after presolve. If either `A_eq` or `A_ub` is a sparse matrix, this option will automatically be set `True`, and the problem will be treated as sparse even during presolve. If your constraint matrices contain mostly zeros and the problem is not very small (less than about 100 constraints or variables), consider setting `True` or providing `A_eq` and `A_ub` as sparse matrices.
- **lstsq** [bool (default: `False`)] Set to `True` if the problem is expected to be very poorly conditioned. This should always be left `False` unless severe numerical difficulties are encountered. Leave this at the default unless you receive a warning message suggesting otherwise.
- **sym_pos** [bool (default: True)] Leave `True` if the problem is expected to yield a well conditioned symmetric positive definite normal equation matrix (almost always). Leave this at the default unless you receive a warning message suggesting otherwise.
- **cholesky** [bool (default: True)] Set to `True` if the normal equations are to be solved by explicit Cholesky decomposition followed by explicit forward/backward substitution. This is typically faster for problems that are numerically well-behaved.

pc [bool (default: True)] Leave `True` if the predictor-corrector method of Mehrota is to be used. This is almost always (if not always) beneficial.

ip [bool (default: False)] Set to `True` if the improved initial point suggestion due to [4] Section 4.3 is desired. Whether this is beneficial or not depends on the problem.

permc_spec
[str (default: 'MMD_AT_PLUS_A')] (Has effect only with `sparse = True`, `lstsq = False`, `sym_pos = True`, and no SuiteSparse.) A matrix is factorized in each iteration of the algorithm. This option specifies how to permute the columns of the matrix for sparsity preservation. Acceptable values are:
- `NATURAL`: natural ordering.
- `MMD_ATA`: minimum degree ordering on the structure of A^T A.
- `MMD_AT_PLUS_A`: minimum degree ordering on the structure of A^T+A.
- `COLAMD`: approximate minimum degree column ordering.

This option can impact the convergence of the interior point algorithm; test different values to determine which performs best for your problem. For more information, refer to `scipy.sparse.linalg.splu`.

unknown_options
[dict] Optional arguments not used by this particular solver. If *unknown_options* is non-empty a warning is issued listing all unused options.

Notes

This method implements the algorithm outlined in [4] with ideas from [8] and a structure inspired by the simpler methods of [6].

The primal-dual path following method begins with initial 'guesses' of the primal and dual variables of the standard form problem and iteratively attempts to solve the (nonlinear) Karush-Kuhn-Tucker conditions for the problem with a gradually reduced logarithmic barrier term added to the objective. This particular implementation uses a homogeneous self-dual formulation, which provides certificates of infeasibility or unboundedness where applicable.

The default initial point for the primal and dual variables is that defined in [4] Section 4.4 Equation 8.22. Optionally (by setting initial point option `ip=True`), an alternate (potentially improved) starting point can be calculated according to the additional recommendations of [4] Section 4.4.

A search direction is calculated using the predictor-corrector method (single correction) proposed by Mehrota and detailed in [4] Section 4.1. (A potential improvement would be to implement the method of multiple corrections described in [4] Section 4.2.) In practice, this is accomplished by solving the normal equations, [4] Section 5.1 Equations 8.31 and 8.32, derived from the Newton equations [4] Section 5 Equations 8.25 (compare to [4] Section 4 Equations 8.6-8.8). The advantage of solving the normal equations rather than 8.25 directly is that the matrices involved are symmetric positive definite, so Cholesky decomposition can be used rather than the more expensive LU factorization.

With default options, the solver used to perform the factorization depends on third-party software availability and the conditioning of the problem.

For dense problems, solvers are tried in the following order:

1. `scipy.linalg.cho_factor`
2. `scipy.linalg.solve` with option `sym_pos=True`
3. `scipy.linalg.solve` with option `sym_pos=False`
4. `scipy.linalg.lstsq`

For sparse problems:

1. `sksparse.cholmod.cholesky` (if scikit-sparse and SuiteSparse are installed)

2. `scipy.sparse.linalg.factorized` (if scikit-umfpack and SuiteSparse are installed)
3. `scipy.sparse.linalg.splu` (which uses SuperLU distributed with SciPy)
4. `scipy.sparse.linalg.lsqr`

If the solver fails for any reason, successively more robust (but slower) solvers are attempted in the order indicated. Attempting, failing, and re-starting factorization can be time consuming, so if the problem is numerically challenging, options can be set to bypass solvers that are failing. Setting `cholesky=False` skips to solver 2, `sym_pos=False` skips to solver 3, and `lstsq=True` skips to solver 4 for both sparse and dense problems.

Potential improvements for combatting issues associated with dense columns in otherwise sparse problems are outlined in [4] Section 5.3 and [10] Section 4.1-4.2; the latter also discusses the alleviation of accuracy issues associated with the substitution approach to free variables.

After calculating the search direction, the maximum possible step size that does not activate the non-negativity constraints is calculated, and the smaller of this step size and unity is applied (as in [4] Section 4.1.) [4] Section 4.3 suggests improvements for choosing the step size.

The new point is tested according to the termination conditions of [4] Section 4.5. The same tolerance, which can be set using the `tol` option, is used for all checks. (A potential improvement would be to expose the different tolerances to be set independently.) If optimality, unboundedness, or infeasibility is detected, the solve procedure terminates; otherwise it repeats.

Whereas the top level `linprog` module expects a problem of form:

Minimize:

```
c @ x
```

Subject to:

```
A_ub @ x <= b_ub
A_eq @ x == b_eq
 lb <= x <= ub
```

where `lb = 0` and `ub = None` unless set in `bounds`. The problem is automatically converted to the form:

Minimize:

```
c @ x
```

Subject to:

```
A @ x == b
    x >= 0
```

for solution. That is, the original problem contains equality, upper-bound and variable constraints whereas the method specific solver requires equality constraints and variable non-negativity. `linprog` converts the original problem to standard form by converting the simple bounds to upper bound constraints, introducing non-negative slack variables for inequality constraints, and expressing unbounded variables as the difference between two non-negative variables. The problem is converted back to the original form before results are reported.

References

[4], [6], [8], [9], [10]

linprog(method='revised simplex')

scipy.optimize.**linprog**(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='revised_simplex'*, *callback=None*, *options={'maxiter': 5000, 'disp': False, 'presolve': True, 'tol': 1e-12, 'autoscale': False, 'rr': True, 'maxupdate': 10, 'mast': False, 'pivot': 'mrc'}*, *x0=None*)

Linear programming: minimize a linear objective function subject to linear equality and inequality constraints using the revised simplex method.

Linear programming solves problems of the following form:

$$\begin{aligned} \min_x \ & c^T x \\ \text{such that } & A_{ub} x \leq b_{ub}, \\ & A_{eq} x = b_{eq}, \\ & l \leq x \leq u, \end{aligned}$$

where x is a vector of decision variables; c, b_{ub}, b_{eq}, l, and u are vectors; and A_{ub} and A_{eq} are matrices.

Alternatively, that's:

minimize:

```
c @ x
```

such that:

```
A_ub @ x <= b_ub
A_eq @ x == b_eq
lb <= x <= ub
```

Note that by default `lb = 0` and `ub = None` unless specified with `bounds`.

Parameters

c [1-D array] The coefficients of the linear objective function to be minimized.

A_ub [2-D array, optional] The inequality constraint matrix. Each row of `A_ub` specifies the coefficients of a linear inequality constraint on `x`.

b_ub [1-D array, optional] The inequality constraint vector. Each element represents an upper bound on the corresponding value of `A_ub @ x`.

A_eq [2-D array, optional] The equality constraint matrix. Each row of `A_eq` specifies the coefficients of a linear equality constraint on `x`.

b_eq [1-D array, optional] The equality constraint vector. Each element of `A_eq @ x` must equal the corresponding element of `b_eq`.

bounds [sequence, optional] A sequence of `(min, max)` pairs for each element in `x`, defining the minimum and maximum values of that decision variable. Use `None` to indicate that there is no bound. By default, bounds are `(0, None)` (all decision variables are non-negative). If a single tuple `(min, max)` is provided, then `min` and `max` will serve as bounds for all decision variables.

method [str] This is the method-specific documentation for 'revised simplex'. *'highs'*, *'highs-ds'*, *'highs-ipm'*, *'interior-point'* (default), and *'simplex'* (legacy) are also available.

callback [callable, optional] Callback function to be executed once per iteration.

x0 [1-D array, optional] Guess values of the decision variables, which will be refined by the optimization algorithm. This argument is currently used only by the 'revised simplex' method, and can only be used if *x0* represents a basic feasible solution.

Returns

res [OptimizeResult] A *scipy.optimize.OptimizeResult* consisting of the fields:

- **x** [1-D array] The values of the decision variables that minimizes the objective function while satisfying the constraints.
- **fun** [float] The optimal value of the objective function `c @ x`.
- **slack** [1-D array] The (nominally positive) values of the slack variables, `b_ub - A_ub @ x`.
- **con** [1-D array] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
- **success** [bool] `True` when the algorithm succeeds in finding an optimal solution.
- **status** [int] An integer representing the exit status of the algorithm.
  - `0` : Optimization terminated successfully.
  - `1` : Iteration limit reached.
  - `2` : Problem appears to be infeasible.
  - `3` : Problem appears to be unbounded.
  - `4` : Numerical difficulties encountered.
  - `5` : Problem has no constraints; turn presolve on.
  - `6` : Invalid guess provided.
- **message** [str] A string descriptor of the exit status of the algorithm.
- **nit** [int] The total number of iterations performed in all phases.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.linprog*

Options

maxiter [int (default: 5000)] The maximum number of iterations to perform in either phase.

disp [bool (default: False)] Set to `True` if indicators of optimization status are to be printed to the console each iteration.

presolve [bool (default: True)] Presolve attempts to identify trivial infeasibilities, identify trivial unboundedness, and simplify the problem before sending it to the main solver. It is generally recommended to keep the default setting `True`; set to `False` if presolve is to be disabled.

tol [float (default: 1e-12)] The tolerance which determines when a solution is "close enough" to zero in Phase 1 to be considered a basic feasible solution or close enough to positive to serve as an optimal solution.

autoscale [bool (default: False)] Set to `True` to automatically perform equilibration. Consider using this option if the numerical values in the constraints are separated by several orders of magnitude.

rr [bool (default: True)] Set to `False` to disable automatic redundancy removal.

maxupdate [int (default: 10)] The maximum number of updates performed on the LU factorization. After this many updates is reached, the basis matrix is factorized from scratch.

mast [bool (default: False)] Minimize Amortized Solve Time. If enabled, the average time to solve a linear system using the basis factorization is measured. Typically, the average solve time will decrease with each successive solve after initial factorization, as factorization takes much more time than the solve operation (and updates). Eventually, however, the updated factorization becomes sufficiently complex that the average solve time begins to increase. When this is detected, the basis is refactorized from scratch. Enable this option to maximize speed at the risk of nondeterministic behavior. Ignored if `maxupdate` is 0.

pivot ["mrc" or "bland" (default: "mrc")] Pivot rule: Minimum Reduced Cost ("mrc") or Bland's rule ("bland"). Choose Bland's rule if iteration limit is reached and cycling is suspected.

unknown_options
[dict] Optional arguments not used by this particular solver. If *unknown_options* is non-empty a warning is issued listing all unused options.

Notes

Method *revised simplex* uses the revised simplex method as described in [9], except that a factorization [11] of the basis matrix, rather than its inverse, is efficiently maintained and used to solve the linear systems at each iteration of the algorithm.

References

[9], [11]

linprog(method='highs-ipm')

`scipy.optimize.linprog`(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='highs-ipm'*, *callback=None*, *options={'maxiter': None, 'disp': False, 'presolve': True, 'time_limit': None, 'dual_feasibility_tolerance': None, 'primal_feasibility_tolerance': None, 'ipm_optimality_tolerance': None}*, *x0=None*)

Linear programming: minimize a linear objective function subject to linear equality and inequality constraints using the HiGHS interior point solver.

Linear programming solves problems of the following form:

$$\begin{aligned} \min_x \ & c^T x \\ \text{such that } & A_{ub} x \leq b_{ub}, \\ & A_{eq} x = b_{eq}, \\ & l \leq x \leq u, \end{aligned}$$

where x is a vector of decision variables; c, b_{ub}, b_{eq}, l, and u are vectors; and A_{ub} and A_{eq} are matrices.

Alternatively, that's:

minimize:

```
c @ x
```

such that:

```
A_ub @ x <= b_ub
A_eq @ x == b_eq
lb <= x <= ub
```

Note that by default `lb = 0` and `ub = None` unless specified with `bounds`.

Parameters

c [1-D array] The coefficients of the linear objective function to be minimized.

A_ub [2-D array, optional] The inequality constraint matrix. Each row of `A_ub` specifies the coefficients of a linear inequality constraint on `x`.

b_ub [1-D array, optional] The inequality constraint vector. Each element represents an upper bound on the corresponding value of `A_ub @ x`.

A_eq [2-D array, optional] The equality constraint matrix. Each row of `A_eq` specifies the coefficients of a linear equality constraint on `x`.

b_eq [1-D array, optional] The equality constraint vector. Each element of `A_eq @ x` must equal the corresponding element of `b_eq`.

bounds [sequence, optional] A sequence of `(min, max)` pairs for each element in `x`, defining the minimum and maximum values of that decision variable. Use `None` to indicate that there is no bound. By default, bounds are `(0, None)` (all decision variables are non-negative). If a single tuple `(min, max)` is provided, then `min` and `max` will serve as bounds for all decision variables.

method [str] This is the method-specific documentation for 'highs-ipm'. *'highs-ipm'*, *'highs-ds'*, *'interior-point'* (default), *'revised simplex'*, and *'simplex'* (legacy) are also available.

Returns

res [OptimizeResult] A *scipy.optimize.OptimizeResult* consisting of the fields:

- **x** [1D array] The values of the decision variables that minimizes the objective function while satisfying the constraints.
- **fun** [float] The optimal value of the objective function `c @ x`.
- **slack** [1D array] The (nominally positive) values of the slack, `b_ub - A_ub @ x`.
- **con** [1D array] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
- **success** [bool] `True` when the algorithm succeeds in finding an optimal solution.
- **status** [int] An integer representing the exit status of the algorithm.
  `0` : Optimization terminated successfully.
  `1` : Iteration or time limit reached.
  `2` : Problem appears to be infeasible.
  `3` : Problem appears to be unbounded.
  `4` : The HiGHS solver ran into a problem.
- **message** [str] A string descriptor of the exit status of the algorithm.
- **nit** [int] The total number of iterations performed. For the HiGHS interior-point method, this does not include crossover iterations.
- **crossover_nit** [int] The number of primal/dual pushes performed during the crossover routine for the HiGHS interior-point method.
- **ineqlin** [OptimizeResult] Solution and sensitivity information corresponding to the inequality constraints, *b_ub*. A dictionary consisting of the fields:
  - **residual** [np.ndnarray] The (nominally positive) values of the slack variables, `b_ub - A_ub @ x`. This quantity is also commonly referred to as "slack".
  - **marginals** [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the right-hand side of the inequality constraints, *b_ub*.
- **eqlin** [OptimizeResult] Solution and sensitivity information corresponding to the equality constraints, *b_eq*. A dictionary consisting of the fields:
  - **residual** [np.ndarray] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
  - **marginals** [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the right-hand side of the equality constraints, *b_eq*.
- **lower, upper** [OptimizeResult] Solution and sensitivity information corresponding to the lower and upper bounds on decision variables, *bounds*.
  - **residual** [np.ndarray] The (nominally positive) values of the quantity `x - lb` (lower) or `ub - x` (upper).

marginals [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the lower and upper *bounds*.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.linprog*

Options

maxiter [int] The maximum number of iterations to perform in either phase. For *'highs-ipm'*, this does not include the number of crossover iterations. Default is the largest possible value for an `int` on the platform.

disp [bool (default: `False`)] Set to `True` if indicators of optimization status are to be printed to the console during optimization.

presolve [bool (default: `True`)] Presolve attempts to identify trivial infeasibilities, identify trivial unboundedness, and simplify the problem before sending it to the main solver. It is generally recommended to keep the default setting `True`; set to `False` if presolve is to be disabled.

time_limit [float] The maximum time in seconds allotted to solve the problem; default is the largest possible value for a `double` on the platform.

dual_feasibility_tolerance
[double (default: 1e-07)] The minimum of this and `primal_feasibility_tolerance` is used for the feasibility tolerance of *'highs-ipm'*.

primal_feasibility_tolerance
[double (default: 1e-07)] The minimum of this and `dual_feasibility_tolerance` is used for the feasibility tolerance of *'highs-ipm'*.

ipm_optimality_tolerance
[double (default: `1e-08`)] Optimality tolerance for *'highs-ipm'*. Minimum allowable value is 1e-12.

unknown_options
[dict] Optional arguments not used by this particular solver. If `unknown_options` is non-empty, a warning is issued listing all unused options.

Notes

Method *'highs-ipm'* is a wrapper of a C++ implementation of an **i**nterior-**p**oint **m**ethod [13]; it features a crossover routine, so it is as accurate as a simplex solver. Method *'highs-ds'* is a wrapper of the C++ high performance dual revised simplex implementation (HSOL) [13], [14]. Method *'highs'* chooses between the two automatically. For new code involving *linprog*, we recommend explicitly choosing one of these three method values instead of *'interior-point'* (default), *'revised simplex'*, and *'simplex'* (legacy).

The result fields *ineqlin*, *eqlin*, *lower*, and *upper* all contain *marginals*, or partial derivatives of the objective function with respect to the right-hand side of each constraint. These partial derivatives are also referred to as "Lagrange multipliers", "dual values", and "shadow prices". The sign convention of *marginals* is opposite that of Lagrange multipliers produced by many nonlinear solvers.

References

[13], [14]

linprog(method='highs-ds')

scipy.optimize.**linprog**(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='highs-ds'*, *callback=None*, *options={'maxiter': None, 'disp': False, 'presolve': True, 'time_limit': None, 'dual_feasibility_tolerance': None, 'primal_feasibility_tolerance': None, 'simplex_dual_edge_weight_strategy': None}*, *x0=None*)

Linear programming: minimize a linear objective function subject to linear equality and inequality constraints using the HiGHS dual simplex solver.

Linear programming solves problems of the following form:

$$\begin{aligned} \min_x \ & c^T x \\ \text{such that } & A_{ub} x \leq b_{ub}, \\ & A_{eq} x = b_{eq}, \\ & l \leq x \leq u, \end{aligned}$$

where x is a vector of decision variables; c, b_{ub}, b_{eq}, l, and u are vectors; and A_{ub} and A_{eq} are matrices.

Alternatively, that's:

minimize:

```
c @ x
```

such that:

```
A_ub @ x <= b_ub
A_eq @ x == b_eq
lb <= x <= ub
```

Note that by default `lb = 0` and `ub = None` unless specified with `bounds`.

Parameters

c [1-D array] The coefficients of the linear objective function to be minimized.

A_ub [2-D array, optional] The inequality constraint matrix. Each row of `A_ub` specifies the coefficients of a linear inequality constraint on `x`.

b_ub [1-D array, optional] The inequality constraint vector. Each element represents an upper bound on the corresponding value of `A_ub @ x`.

A_eq [2-D array, optional] The equality constraint matrix. Each row of `A_eq` specifies the coefficients of a linear equality constraint on `x`.

b_eq [1-D array, optional] The equality constraint vector. Each element of `A_eq @ x` must equal the corresponding element of `b_eq`.

bounds [sequence, optional] A sequence of `(min, max)` pairs for each element in `x`, defining the minimum and maximum values of that decision variable. Use `None` to indicate that there is no bound. By default, bounds are `(0, None)` (all decision variables are non-negative). If a single tuple `(min, max)` is provided, then `min` and `max` will serve as bounds for all decision variables.

method [str] This is the method-specific documentation for 'highs-ds'. *'highs'*, *'highs-ipm'*, *'interior-point'* (default), *'revised simplex'*, and *'simplex'* (legacy) are also available.

Returns

res [OptimizeResult] A *scipy.optimize.OptimizeResult* consisting of the fields:

- **x** [1D array] The values of the decision variables that minimizes the objective function while satisfying the constraints.
- **fun** [float] The optimal value of the objective function `c @ x`.
- **slack** [1D array] The (nominally positive) values of the slack, `b_ub - A_ub @ x`.
- **con** [1D array] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
- **success** [bool] `True` when the algorithm succeeds in finding an optimal solution.
- **status** [int] An integer representing the exit status of the algorithm.
  `0` : Optimization terminated successfully.
  `1` : Iteration or time limit reached.
  `2` : Problem appears to be infeasible.
  `3` : Problem appears to be unbounded.
  `4` : The HiGHS solver ran into a problem.
- **message** [str] A string descriptor of the exit status of the algorithm.
- **nit** [int] The total number of iterations performed. This includes iterations in all phases.
- **crossover_nit** [int] This is always `0` for the HiGHS simplex method. For the HiGHS interior-point method, this is the number of primal/dual pushes performed during the crossover routine.
- **ineqlin** [OptimizeResult] Solution and sensitivity information corresponding to the inequality constraints, *b_ub*. A dictionary consisting of the fields:
  - **residual** [np.ndnarray] The (nominally positive) values of the slack variables, `b_ub - A_ub @ x`. This quantity is also commonly referred to as "slack".
  - **marginals** [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the right-hand side of the inequality constraints, *b_ub*.
- **eqlin** [OptimizeResult] Solution and sensitivity information corresponding to the equality constraints, *b_eq*. A dictionary consisting of the fields:
  - **residual** [np.ndarray] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
  - **marginals** [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the right-hand side of the equality constraints, *b_eq*.
- **lower, upper** [OptimizeResult] Solution and sensitivity information corresponding to the lower and upper bounds on decision variables, *bounds*.
  - **residual** [np.ndarray] The (nominally positive) values of the quantity `x - lb` (lower) or `ub - x` (upper).
  - **marginals** [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the lower and upper *bounds*.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.linprog*

Options

- **maxiter** [int] The maximum number of iterations to perform in either phase. Default is the largest possible value for an `int` on the platform.
- **disp** [bool (default: `False`)] Set to `True` if indicators of optimization status are to be printed to the console during optimization.

presolve [bool (default: `True`)] Presolve attempts to identify trivial infeasibilities, identify trivial unboundedness, and simplify the problem before sending it to the main solver. It is generally recommended to keep the default setting `True`; set to `False` if presolve is to be disabled.

time_limit [float] The maximum time in seconds allotted to solve the problem; default is the largest possible value for a `double` on the platform.

dual_feasibility_tolerance
[double (default: 1e-07)] Dual feasibility tolerance for *'highs-ds'*.

primal_feasibility_tolerance
[double (default: 1e-07)] Primal feasibility tolerance for *'highs-ds'*.

simplex_dual_edge_weight_strategy
[str (default: None)] Strategy for simplex dual edge weights. The default, `None`, automatically selects one of the following.
`'dantzig'` uses Dantzig's original strategy of choosing the most negative reduced cost.
`'devex'` uses the strategy described in [15].
`steepest` uses the exact steepest edge strategy as described in [16].
`'steepest-devex'` begins with the exact steepest edge strategy until the computation is too costly or inexact and then switches to the devex method.
Curently, `None` always selects `'steepest-devex'`, but this may change as new options become available.

unknown_options
[dict] Optional arguments not used by this particular solver. If `unknown_options` is non-empty, a warning is issued listing all unused options.

Notes

Method *'highs-ds'* is a wrapper of the C++ high performance dual revised simplex implementation (HSOL) [13], [14]. Method *'highs-ipm'* is a wrapper of a C++ implementation of an **i**nterior-**p**oint **m**ethod [13]; it features a crossover routine, so it is as accurate as a simplex solver. Method *'highs'* chooses between the two automatically. For new code involving *linprog*, we recommend explicitly choosing one of these three method values instead of *'interior-point'* (default), *'revised simplex'*, and *'simplex'* (legacy).

The result fields *ineqlin*, *eqlin*, *lower*, and *upper* all contain *marginals*, or partial derivatives of the objective function with respect to the right-hand side of each constraint. These partial derivatives are also referred to as "Lagrange multipliers", "dual values", and "shadow prices". The sign convention of *marginals* is opposite that of Lagrange multipliers produced by many nonlinear solvers.

References

[13], [14], [15], [16]

linprog(method='highs')

`scipy.optimize.`**`linprog`**(*c*, *A_ub=None*, *b_ub=None*, *A_eq=None*, *b_eq=None*, *bounds=None*, *method='highs'*, *callback=None*, *options={'maxiter': None, 'disp': False, 'presolve': True, 'time_limit': None, 'dual_feasibility_tolerance': None, 'primal_feasibility_tolerance': None, 'ipm_optimality_tolerance': None, 'simplex_dual_edge_weight_strategy': None}*, *x0=None*)

Linear programming: minimize a linear objective function subject to linear equality and inequality constraints using one of the HiGHS solvers.

Linear programming solves problems of the following form:

$$\min_x c^T x$$
$$\text{such that } A_{ub} x \leq b_{ub},$$
$$A_{eq} x = b_{eq},$$
$$l \leq x \leq u,$$

where x is a vector of decision variables; c, b_{ub}, b_{eq}, l, and u are vectors; and A_{ub} and A_{eq} are matrices.

Alternatively, that's:

minimize:

```
c @ x
```

such that:

```
A_ub @ x <= b_ub
A_eq @ x == b_eq
lb <= x <= ub
```

Note that by default `lb = 0` and `ub = None` unless specified with `bounds`.

Parameters

c [1-D array] The coefficients of the linear objective function to be minimized.

A_ub [2-D array, optional] The inequality constraint matrix. Each row of `A_ub` specifies the coefficients of a linear inequality constraint on `x`.

b_ub [1-D array, optional] The inequality constraint vector. Each element represents an upper bound on the corresponding value of `A_ub @ x`.

A_eq [2-D array, optional] The equality constraint matrix. Each row of `A_eq` specifies the coefficients of a linear equality constraint on `x`.

b_eq [1-D array, optional] The equality constraint vector. Each element of `A_eq @ x` must equal the corresponding element of `b_eq`.

bounds [sequence, optional] A sequence of `(min, max)` pairs for each element in `x`, defining the minimum and maximum values of that decision variable. Use `None` to indicate that there is no bound. By default, bounds are `(0, None)` (all decision variables are non-negative). If a single tuple `(min, max)` is provided, then `min` and `max` will serve as bounds for all decision variables.

method [str] This is the method-specific documentation for 'highs', which chooses automatically between *'highs-ds'* and *'highs-ipm'*. *'interior-point'* (default), *'revised simplex'*, and *'simplex'* (legacy) are also available.

Returns

res [OptimizeResult] A *`scipy.optimize.OptimizeResult`* consisting of the fields:

- **x** [1D array] The values of the decision variables that minimizes the objective function while satisfying the constraints.
- **fun** [float] The optimal value of the objective function `c @ x`.
- **slack** [1D array] The (nominally positive) values of the slack, `b_ub - A_ub @ x`.
- **con** [1D array] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
- **success** [bool] `True` when the algorithm succeeds in finding an optimal solution.
- **status** [int] An integer representing the exit status of the algorithm.
  `0` : Optimization terminated successfully.
  `1` : Iteration or time limit reached.
  `2` : Problem appears to be infeasible.

`3` : Problem appears to be unbounded.
`4` : The HiGHS solver ran into a problem.

message [str] A string descriptor of the exit status of the algorithm.

nit [int] The total number of iterations performed. For the HiGHS simplex method, this includes iterations in all phases. For the HiGHS interior-point method, this does not include crossover iterations.

crossover_nit
[int] The number of primal/dual pushes performed during the crossover routine for the HiGHS interior-point method. This is `0` for the HiGHS simplex method.

ineqlin [OptimizeResult] Solution and sensitivity information corresponding to the inequality constraints, *b_ub*. A dictionary consisting of the fields:

- **residual** [np.ndnarray] The (nominally positive) values of the slack variables, `b_ub - A_ub @ x`. This quantity is also commonly referred to as "slack".
- **marginals** [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the right-hand side of the inequality constraints, *b_ub*.

eqlin [OptimizeResult] Solution and sensitivity information corresponding to the equality constraints, *b_eq*. A dictionary consisting of the fields:

- **residual** [np.ndarray] The (nominally zero) residuals of the equality constraints, `b_eq - A_eq @ x`.
- **marginals** [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the right-hand side of the equality constraints, *b_eq*.

lower, upper
[OptimizeResult] Solution and sensitivity information corresponding to the lower and upper bounds on decision variables, *bounds*.

- **residual** [np.ndarray] The (nominally positive) values of the quantity `x - lb` (lower) or `ub - x` (upper).
- **marginals** [np.ndarray] The sensitivity (partial derivative) of the objective function with respect to the lower and upper *bounds*.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.linprog*

Options

maxiter [int] The maximum number of iterations to perform in either phase. For *'highs-ipm'*, this does not include the number of crossover iterations. Default is the largest possible value for an `int` on the platform.

disp [bool (default: `False`)] Set to `True` if indicators of optimization status are to be printed to the console during optimization.

presolve [bool (default: `True`)] Presolve attempts to identify trivial infeasibilities, identify trivial unboundedness, and simplify the problem before sending it to the main solver. It is generally recommended to keep the default setting `True`; set to `False` if presolve is to be disabled.

time_limit [float] The maximum time in seconds allotted to solve the problem; default is the largest possible value for a `double` on the platform.

dual_feasibility_tolerance
[double (default: 1e-07)] Dual feasibility tolerance for *'highs-ds'*. The minimum of this and `primal_feasibility_tolerance` is used for the feasibility tolerance of *'highs-ipm'*.

primal_feasibility_tolerance
[double (default: 1e-07)] Primal feasibility tolerance for *'highs-ds'*. The minimum of this and `dual_feasibility_tolerance` is used for the feasibility tolerance of *'highs-ipm'*.

ipm_optimality_tolerance
: [double (default: `1e-08`)] Optimality tolerance for *'highs-ipm'*. Minimum allowable value is 1e-12.

simplex_dual_edge_weight_strategy
: [str (default: None)] Strategy for simplex dual edge weights. The default, `None`, automatically selects one of the following.
`'dantzig'` uses Dantzig's original strategy of choosing the most negative reduced cost.
`'devex'` uses the strategy described in [15].
`steepest` uses the exact steepest edge strategy as described in [16].
`'steepest-devex'` begins with the exact steepest edge strategy until the computation is too costly or inexact and then switches to the devex method.
Curently, `None` always selects `'steepest-devex'`, but this may change as new options become available.

unknown_options
: [dict] Optional arguments not used by this particular solver. If `unknown_options` is non-empty, a warning is issued listing all unused options.

Notes

Method *'highs-ds'* is a wrapper of the C++ high performance dual revised simplex implementation (HSOL) [13], [14]. Method *'highs-ipm'* is a wrapper of a C++ implementation of an **i**nterior-**p**oint **m**ethod [13]; it features a crossover routine, so it is as accurate as a simplex solver. Method *'highs'* chooses between the two automatically. For new code involving *linprog*, we recommend explicitly choosing one of these three method values instead of *'interior-point'* (default), *'revised simplex'*, and *'simplex'* (legacy).

The result fields *ineqlin*, *eqlin*, *lower*, and *upper* all contain *marginals*, or partial derivatives of the objective function with respect to the right-hand side of each constraint. These partial derivatives are also referred to as "Lagrange multipliers", "dual values", and "shadow prices". The sign convention of *marginals* is opposite that of Lagrange multipliers produced by many nonlinear solvers.

References

[13], [14], [15], [16]

The simplex, interior-point, and revised simplex methods support callback functions, such as:

linprog_verbose_callback(res)	A sample callback function demonstrating the linprog callback interface.

scipy.optimize.linprog_verbose_callback

scipy.optimize.**linprog_verbose_callback**(*res*)
: A sample callback function demonstrating the linprog callback interface. This callback produces detailed output to sys.stdout before each iteration and after the final iteration of the simplex algorithm.

Parameters

res
: [A *scipy.optimize.OptimizeResult* consisting of the following fields:]

x
: [1-D array] The independent variable vector which optimizes the linear programming problem.

fun
: [float] Value of the objective function.

success
: [bool] True if the algorithm succeeded in finding an optimal solution.

slack
: [1-D array] The values of the slack variables. Each slack variable corresponds to an inequality constraint. If the slack is zero, then the corresponding constraint

is active.

con [1-D array] The (nominally zero) residuals of the equality constraints, that is, `b - A_eq @ x`

phase [int] The phase of the optimization being executed. In phase 1 a basic feasible solution is sought and the T has an additional row representing an alternate objective function.

status [int] An integer representing the exit status of the optimization:

```
0 : Optimization terminated successfully
1 : Iteration limit reached
2 : Problem appears to be infeasible
3 : Problem appears to be unbounded
4 : Serious numerical difficulties encountered
```

nit [int] The number of iterations performed.

message [str] A string descriptor of the exit status of the optimization.

Assignment problems

linear_sum_assignment(cost_matrix[, maximize])	Solve the linear sum assignment problem.
quadratic_assignment(A, B[, method, options])	Approximates solution to the quadratic assignment problem and the graph matching problem.

scipy.optimize.linear_sum_assignment

scipy.optimize.**linear_sum_assignment**(*cost_matrix*, *maximize=False*)

Solve the linear sum assignment problem.

Parameters

cost_matrix
[array] The cost matrix of the bipartite graph.

maximize [bool (default: False)] Calculates a maximum weight matching if true.

Returns

row_ind, col_ind
[array] An array of row indices and one of corresponding column indices giving the optimal assignment. The cost of the assignment can be computed as `cost_matrix[row_ind, col_ind].sum()`. The row indices will be sorted; in the case of a square cost matrix they will be equal to `numpy.arange(cost_matrix.shape[0])`.

See also:

scipy.sparse.csgraph.min_weight_full_bipartite_matching

for sparse inputs

Notes

The linear sum assignment problem [1] is also known as minimum weight matching in bipartite graphs. A problem instance is described by a matrix C, where each C[i,j] is the cost of matching vertex i of the first partite set (a "worker") and vertex j of the second set (a "job"). The goal is to find a complete assignment of workers to jobs of minimal cost.

Formally, let X be a boolean matrix where $X[i,j] = 1$ iff row i is assigned to column j. Then the optimal assignment has cost

$$\min \sum_i \sum_j C_{i,j} X_{i,j}$$

where, in the case where the matrix X is square, each row is assigned to exactly one column, and each column to exactly one row.

This function can also solve a generalization of the classic assignment problem where the cost matrix is rectangular. If it has more rows than columns, then not every row needs to be assigned to a column, and vice versa.

This implementation is a modified Jonker-Volgenant algorithm with no initialization, described in ref. [2].

New in version 0.17.0.

References

[1], [2]

Examples

```
>>> cost = np.array([[4, 1, 3], [2, 0, 5], [3, 2, 2]])
>>> from scipy.optimize import linear_sum_assignment
>>> row_ind, col_ind = linear_sum_assignment(cost)
>>> col_ind
array([1, 0, 2])
>>> cost[row_ind, col_ind].sum()
5
```

scipy.optimize.quadratic_assignment

scipy.optimize.**quadratic_assignment**(*A*, *B*, *method='faq'*, *options=None*)

Approximates solution to the quadratic assignment problem and the graph matching problem.

Quadratic assignment solves problems of the following form:

$$\min_P \ \text{trace}(A^T P B P^T)$$
$$\text{s.t. } P \in \mathcal{P}$$

where $\mathcal{P}$ is the set of all permutation matrices, and A and B are square matrices.

Graph matching tries to *maximize* the same objective function. This algorithm can be thought of as finding the alignment of the nodes of two graphs that minimizes the number of induced edge disagreements, or, in the case of weighted graphs, the sum of squared edge weight differences.

Note that the quadratic assignment problem is NP-hard. The results given here are approximations and are not guaranteed to be optimal.

Parameters

A [2-D array, square] The square matrix A in the objective function above.
B [2-D array, square] The square matrix B in the objective function above.
method [str in {'faq', '2opt'} (default: 'faq')] The algorithm used to solve the problem. *'faq'* (default) and *'2opt'* are available.
options [dict, optional] A dictionary of solver options. All solvers support the following:
maximize [bool (default: False)] Maximizes the objective function if `True`.
partial_match
[2-D array of integers, optional (default: None)] Fixes part of the matching. Also known as a "seed" [2].
Each row of *partial_match* specifies a pair of matched nodes: node `partial_match[i, 0]` of *A* is matched to node `partial_match[i, 1]` of *B*. The array has shape `(m, 2)`, where `m` is not greater than the number of nodes, n.
rng [{None, int, `numpy.random.Generator`,]
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.
For method-specific options, see *`show_options('quadratic_assignment')`*.

Returns

res [OptimizeResult] *`OptimizeResult`* containing the following fields.
col_ind [1-D array] Column indices corresponding to the best permutation found of the nodes of *B*.
fun [float] The objective value of the solution.
nit [int] The number of iterations performed during optimization.

Notes

The default method *'faq'* uses the Fast Approximate QAP algorithm [1]; it typically offers the best combination of speed and accuracy. Method *'2opt'* can be computationally expensive, but may be a useful alternative, or it can be used to refine the solution returned by another method.

References

[1], [2], [3]

Examples

```
>>> from scipy.optimize import quadratic_assignment
>>> A = np.array([[0, 80, 150, 170], [80, 0, 130, 100],
...               [150, 130, 0, 120], [170, 100, 120, 0]])
>>> B = np.array([[0, 5, 2, 7], [0, 0, 3, 8],
...               [0, 0, 0, 3], [0, 0, 0, 0]])
>>> res = quadratic_assignment(A, B)
>>> print(res)
 col_ind: array([0, 3, 2, 1])
     fun: 3260
     nit: 9
```

The see the relationship between the returned `col_ind` and `fun`, use `col_ind` to form the best permutation matrix found, then evaluate the objective function $f(P) = trace(A^T P B P^T)$.

```
>>> perm = res['col_ind']
>>> P = np.eye(len(A), dtype=int)[perm]
>>> fun = np.trace(A.T @ P @ B @ P.T)
>>> print(fun)
3260
```

Alternatively, to avoid constructing the permutation matrix explicitly, directly permute the rows and columns of the distance matrix.

```
>>> fun = np.trace(A.T @ B[perm][:, perm])
>>> print(fun)
3260
```

Although not guaranteed in general, `quadratic_assignment` happens to have found the globally optimal solution.

```
>>> from itertools import permutations
>>> perm_opt, fun_opt = None, np.inf
>>> for perm in permutations([0, 1, 2, 3]):
...     perm = np.array(perm)
...     fun = np.trace(A.T @ B[perm][:, perm])
...     if fun < fun_opt:
...         fun_opt, perm_opt = fun, perm
>>> print(np.array_equal(perm_opt, res['col_ind']))
True
```

Here is an example for which the default method, *'faq'*, does not find the global optimum.

```
>>> A = np.array([[0, 5, 8, 6], [5, 0, 5, 1],
...               [8, 5, 0, 2], [6, 1, 2, 0]])
>>> B = np.array([[0, 1, 8, 4], [1, 0, 5, 2],
...               [8, 5, 0, 5], [4, 2, 5, 0]])
>>> res = quadratic_assignment(A, B)
>>> print(res)
 col_ind: array([1, 0, 3, 2])
     fun: 178
     nit: 13
```

If accuracy is important, consider using *'2opt'* to refine the solution.

```
>>> guess = np.array([np.arange(len(A)), res.col_ind]).T
>>> res = quadratic_assignment(A, B, method="2opt",
...                            options = {'partial_guess': guess})
>>> print(res)
 col_ind: array([1, 2, 3, 0])
     fun: 176
     nit: 17
```

The *quadratic_assignment* function supports the following methods:

quadratic_assignment(method='faq')

scipy.optimize.**quadratic_assignment**(*A*, *B*, *method='faq'*, *options={'maximize': False, 'partial_match': None, 'rng': None, 'P0': 'barycenter', 'shuffle_input': False, 'maxiter': 30, 'tol': 0.03}*)

Solve the quadratic assignment problem (approximately).

This function solves the Quadratic Assignment Problem (QAP) and the Graph Matching Problem (GMP) using the Fast Approximate QAP Algorithm (FAQ) [1].

Quadratic assignment solves problems of the following form:

$$\min_P \ \text{trace}(A^T P B P^T)$$
$$\text{s.t. } P \in \mathcal{P}$$

where $\mathcal{P}$ is the set of all permutation matrices, and A and B are square matrices.

Graph matching tries to *maximize* the same objective function. This algorithm can be thought of as finding the alignment of the nodes of two graphs that minimizes the number of induced edge disagreements, or, in the case of weighted graphs, the sum of squared edge weight differences.

Note that the quadratic assignment problem is NP-hard. The results given here are approximations and are not guaranteed to be optimal.

Parameters

A [2-D array, square] The square matrix A in the objective function above.

B [2-D array, square] The square matrix B in the objective function above.

method [str in {'faq', '2opt'} (default: 'faq')] The algorithm used to solve the problem. This is the method-specific documentation for 'faq'. *'2opt'* is also available.

Returns

res [OptimizeResult] `OptimizeResult` containing the following fields.

- **col_ind** [1-D array] Column indices corresponding to the best permutation found of the nodes of *B*.
- **fun** [float] The objective value of the solution.
- **nit** [int] The number of Frank-Wolfe iterations performed.

See also:

For documentation for the rest of the parameters, see `scipy.optimize.quadratic_assignment`

Options

maximize [bool (default: False)] Maximizes the objective function if `True`.

partial_match
[2-D array of integers, optional (default: None)] Fixes part of the matching. Also known as a "seed" [2].
Each row of *partial_match* specifies a pair of matched nodes: node `partial_match[i, 0]` of *A* is matched to node `partial_match[i, 1]` of *B*. The array has shape `(m, 2)`, where `m` is not greater than the number of nodes, n.

rng [{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

P0 [2-D array, "barycenter", or "randomized" (default: "barycenter")] Initial position. Must be a doubly-stochastic matrix [3].
If the initial position is an array, it must be a doubly stochastic matrix of size $m' \times m'$ where $m' = n - m$.
If `"barycenter"` (default), the initial position is the barycenter of the Birkhoff polytope (the space of doubly stochastic matrices). This is a $m' \times m'$ matrix with all entries equal to $1/m'$.
If `"randomized"` the initial search position is $P_0 = (J+K)/2$, where J is the barycenter and K is a random doubly stochastic matrix.

shuffle_input
[bool (default: False)] Set to *True* to resolve degenerate gradients randomly. For non-degenerate gradients this option has no effect.

maxiter [int, positive (default: 30)] Integer specifying the max number of Frank-Wolfe iterations performed.

tol [float (default: 0.03)] Tolerance for termination. Frank-Wolfe iteration terminates when $\frac{||P_i - P_{i+1}||_F}{\sqrt{m'}} \leq tol$, where i is the iteration number.

Notes

The algorithm may be sensitive to the initial permutation matrix (or search "position") due to the possibility of several local minima within the feasible region. A barycenter initialization is more likely to result in a better solution than a single random initialization. However, calling `quadratic_assignment` several times with different random initializations may result in a better optimum at the cost of longer total execution time.

References

[1], [2], [3]

Examples

As mentioned above, a barycenter initialization often results in a better solution than a single random initialization.

```
>>> from numpy.random import default_rng
>>> rng = default_rng()
>>> n = 15
>>> A = rng.random((n, n))
>>> B = rng.random((n, n))
>>> res = quadratic_assignment(A, B)  # FAQ is default method
>>> print(res.fun)
46.871483385480545  # may vary
```

```
>>> options = {"P0": "randomized"}  # use randomized initialization
>>> res = quadratic_assignment(A, B, options=options)
>>> print(res.fun)
47.224831071310625 # may vary
```

However, consider running from several randomized initializations and keeping the best result.

```
>>> res = min([quadratic_assignment(A, B, options=options)
...             for i in range(30)], key=lambda x: x.fun)
```

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```
>>> print(res.fun)
46.671852533681516 # may vary
```

The '2-opt' method can be used to further refine the results.

```
>>> options = {"partial_guess": np.array([np.arange(n), res.col_ind]).T}
>>> res = quadratic_assignment(A, B, method="2opt", options=options)
>>> print(res.fun)
46.47160735721583 # may vary
```

quadratic_assignment(method='2opt')

scipy.optimize.**quadratic_assignment**(*A*, *B*, *method='2opt'*, *options={'maximize': False, 'rng': None, 'partial_match': None, 'partial_guess': None}*)

Solve the quadratic assignment problem (approximately).

This function solves the Quadratic Assignment Problem (QAP) and the Graph Matching Problem (GMP) using the 2-opt algorithm [1].

Quadratic assignment solves problems of the following form:

$$\min_P \ \text{trace}(A^T P B P^T)$$
$$\text{s.t. } P \in \mathcal{P}$$

where $\mathcal{P}$ is the set of all permutation matrices, and A and B are square matrices.

Graph matching tries to *maximize* the same objective function. This algorithm can be thought of as finding the alignment of the nodes of two graphs that minimizes the number of induced edge disagreements, or, in the case of weighted graphs, the sum of squared edge weight differences.

Note that the quadratic assignment problem is NP-hard. The results given here are approximations and are not guaranteed to be optimal.

Parameters

A [2-D array, square] The square matrix A in the objective function above.
B [2-D array, square] The square matrix B in the objective function above.
method [str in {'faq', '2opt'} (default: 'faq')] The algorithm used to solve the problem. This is the method-specific documentation for '2opt'. *'faq'* is also available.

Returns

res [OptimizeResult] *OptimizeResult* containing the following fields.
- **col_ind** [1-D array] Column indices corresponding to the best permutation found of the nodes of *B*.
- **fun** [float] The objective value of the solution.
- **nit** [int] The number of iterations performed during optimization.

See also:

For documentation for the rest of the parameters, see *scipy.optimize.quadratic_assignment*

Options

maximize [bool (default: False)] Maximizes the objective function if `True`.
rng [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional

If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

partial_match
: [2-D array of integers, optional (default: None)] Fixes part of the matching. Also known as a "seed" [2].
Each row of *partial_match* specifies a pair of matched nodes: node `partial_match[i, 0]` of *A* is matched to node `partial_match[i, 1]` of *B*. The array has shape `(m, 2)`, where `m` is not greater than the number of nodes, n.

partial_guess
: [2-D array of integers, optional (default: None)] A guess for the matching between the two matrices. Unlike *partial_match*, *partial_guess* does not fix the indices; they are still free to be optimized.
Each row of *partial_guess* specifies a pair of matched nodes: node `partial_guess[i, 0]` of *A* is matched to node `partial_guess[i, 1]` of *B*. The array has shape `(m, 2)`, where `m` is not greater than the number of nodes, n.

Notes

This is a greedy algorithm that works similarly to bubble sort: beginning with an initial permutation, it iteratively swaps pairs of indices to improve the objective function until no such improvements are possible.

References

[1], [2]

Utilities

Finite-difference approximation

approx_fprime(xk, f, epsilon, *args)	Finite-difference approximation of the gradient of a scalar function.
check_grad(func, grad, x0, *args, **kwargs)	Check the correctness of a gradient function by comparing it against a (forward) finite-difference approximation of the gradient.

scipy.optimize.approx_fprime

`scipy.optimize.`**`approx_fprime`**(*xk*, *f*, *epsilon*, **args*)
Finite-difference approximation of the gradient of a scalar function.

Parameters

xk [array_like] The coordinate vector at which to determine the gradient of *f*.

f [callable] The function of which to determine the gradient (partial derivatives). Should take *xk* as first argument, other arguments to *f* can be supplied in `*args`. Should return a scalar, the value of the function at *xk*.

epsilon [array_like] Increment to *xk* to use for determining the function gradient. If a scalar, uses the same finite difference delta for all partial derivatives. If an array, should contain one value per element of *xk*.

***args** [args, optional] Any other arguments that are to be passed to *f*.

Returns

grad [ndarray] The partial derivatives of f to xk.

See also:

`check_grad`

Check correctness of gradient function against approx_fprime.

Notes

The function gradient is determined by the forward finite difference formula:

```
             f(xk[i] + epsilon[i]) - f(xk[i])
f'[i] = ---------------------------------
                        epsilon[i]
```

The main use of *approx_fprime* is in scalar function optimizers like *fmin_bfgs*, to determine numerically the Jacobian of a function.

Examples

```
>>> from scipy import optimize
>>> def func(x, c0, c1):
...     "Coordinate vector `x` should be an array of size two."
...     return c0 * x[0]**2 + c1*x[1]**2
```

```
>>> x = np.ones(2)
>>> c0, c1 = (1, 200)
>>> eps = np.sqrt(np.finfo(float).eps)
>>> optimize.approx_fprime(x, func, [eps, np.sqrt(200) * eps], c0, c1)
array([   2.        ,  400.00004198])
```

scipy.optimize.check_grad

scipy.optimize.**check_grad**(*func*, *grad*, *x0*, **args*, ***kwargs*)

Check the correctness of a gradient function by comparing it against a (forward) finite-difference approximation of the gradient.

Parameters

func [callable `func(x0, *args)`] Function whose derivative is to be checked.

grad [callable `grad(x0, *args)`] Gradient of *func*.

x0 [ndarray] Points to check *grad* against forward difference approximation of grad using *func*.

args [*args, optional] Extra arguments passed to *func* and *grad*.

epsilon [float, optional] Step size used for the finite difference approximation. It defaults to `sqrt(np.finfo(float).eps)`, which is approximately 1.49e-08.

Returns

err [float] The square root of the sum of squares (i.e., the 2-norm) of the difference between `grad(x0, *args)` and the finite difference approximation of *grad* using func at the points *x0*.

See also:

`approx_fprime`

Examples

```
>>> def func(x):
...     return x[0]**2 - 0.5 * x[1]**3
>>> def grad(x):
...     return [2 * x[0], -1.5 * x[1]**2]
>>> from scipy.optimize import check_grad
>>> check_grad(func, grad, [1.5, -1.5])
2.9802322387695312e-08
```

Line search

bracket(func[, xa, xb, args, grow_limit, …])	Bracket the minimum of the function.
line_search(f, myfprime, xk, pk[, gfk, …])	Find alpha that satisfies strong Wolfe conditions.

scipy.optimize.bracket

scipy.optimize.**bracket**(*func*, *xa=0.0*, *xb=1.0*, *args=()*, *grow_limit=110.0*, *maxiter=1000*)

Bracket the minimum of the function.

Given a function and distinct initial points, search in the downhill direction (as defined by the initial points) and return new points xa, xb, xc that bracket the minimum of the function f(xa) > f(xb) < f(xc). It doesn't always mean that obtained solution will satisfy xa<=x<=xb.

Parameters

func	[callable f(x,*args)] Objective function to minimize.
xa, xb	[float, optional] Bracketing interval. Defaults *xa* to 0.0, and *xb* to 1.0.
args	[tuple, optional] Additional arguments (if present), passed to *func*.
grow_limit	[float, optional] Maximum grow limit. Defaults to 110.0
maxiter	[int, optional] Maximum number of iterations to perform. Defaults to 1000.

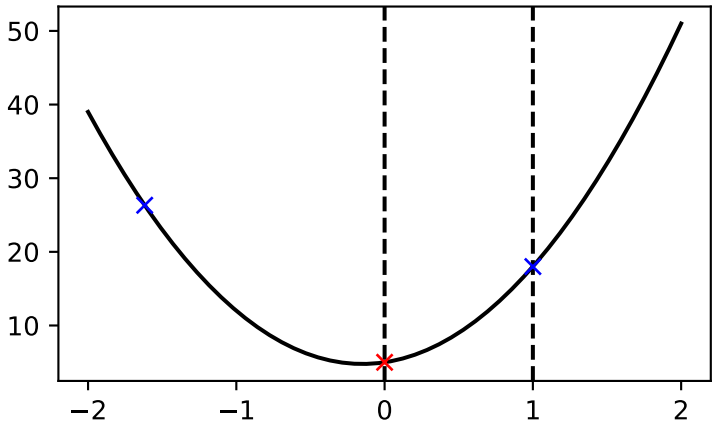
Returns

xa, xb, xc	[float] Bracket.
fa, fb, fc	[float] Objective function values in bracket.
funcalls	[int] Number of function evaluations made.

Examples

This function can find a downward convex region of a function:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.optimize import bracket
>>> def f(x):
...     return 10*x**2 + 3*x + 5
>>> x = np.linspace(-2, 2)
>>> y = f(x)
>>> init_xa, init_xb = 0, 1
>>> xa, xb, xc, fa, fb, fc, funcalls = bracket(f, xa=init_xa, xb=init_xb)
>>> plt.axvline(x=init_xa, color="k", linestyle="--")
>>> plt.axvline(x=init_xb, color="k", linestyle="--")
>>> plt.plot(x, y, "-k")
>>> plt.plot(xa, fa, "bx")
>>> plt.plot(xb, fb, "rx")
>>> plt.plot(xc, fc, "bx")
>>> plt.show()
```



scipy.optimize.line_search

scipy.optimize.**line_search**(*f*, *myfprime*, *xk*, *pk*, *gfk=None*, *old_fval=None*, *old_old_fval=None*, *args=()*, *c1=0.0001*, *c2=0.9*, *amax=None*, *extra_condition=None*, *maxiter=10*)

Find alpha that satisfies strong Wolfe conditions.

Parameters

f	[callable f(x,*args)] Objective function.
myfprime	[callable f'(x,*args)] Objective function gradient.
xk	[ndarray] Starting point.
pk	[ndarray] Search direction.
gfk	[ndarray, optional] Gradient value for x=xk (xk being the current parameter estimate). Will be recomputed if omitted.

old_fval [float, optional] Function value for x=xk. Will be recomputed if omitted.
old_old_fval
[float, optional] Function value for the point preceding x=xk.
args [tuple, optional] Additional arguments passed to objective function.
c1 [float, optional] Parameter for Armijo condition rule.
c2 [float, optional] Parameter for curvature condition rule.
amax [float, optional] Maximum step size
extra_condition
[callable, optional] A callable of the form `extra_condition(alpha, x, f, g)` returning a boolean. Arguments are the proposed step `alpha` and the corresponding `x`, `f` and `g` values. The line search accepts the value of `alpha` only if this callable returns `True`. If the callable returns `False` for the step length, the algorithm will continue with new iterates. The callable is only called for iterates satisfying the strong Wolfe conditions.
maxiter [int, optional] Maximum number of iterations to perform.

Returns

alpha [float or None] Alpha for which `x_new = x0 + alpha * pk`, or None if the line search algorithm did not converge.
fc [int] Number of function evaluations made.
gc [int] Number of gradient evaluations made.
new_fval [float or None] New function value `f(x_new)=f(x0+alpha*pk)`, or None if the line search algorithm did not converge.
old_fval [float] Old function value `f(x0)`.
new_slope [float or None] The local slope along the search direction at the new value `<myfprime(x_new), pk>`, or None if the line search algorithm did not converge.

Notes

Uses the line search algorithm to enforce strong Wolfe conditions. See Wright and Nocedal, 'Numerical Optimization', 1999, pp. 59-61.

Examples

```
>>> from scipy.optimize import line_search
```

A objective function and its gradient are defined.

```
>>> def obj_func(x):
...     return (x[0])**2+(x[1])**2
>>> def obj_grad(x):
...     return [2*x[0], 2*x[1]]
```

We can find alpha that satisfies strong Wolfe conditions.

```
>>> start_point = np.array([1.8, 1.7])
>>> search_gradient = np.array([-1.0, -1.0])
>>> line_search(obj_func, obj_grad, start_point, search_gradient)
(1.0, 2, 1, 1.1300000000000001, 6.13, [1.6, 1.4])
```

Hessian approximation

LbfgsInvHessProduct(*args, **kwargs)	Linear operator for the L-BFGS approximate inverse Hessian.
HessianUpdateStrategy()	Interface for implementing Hessian update strategies.

scipy.optimize.LbfgsInvHessProduct

class scipy.optimize.**LbfgsInvHessProduct**(**args*, ***kwargs*)

Linear operator for the L-BFGS approximate inverse Hessian.

This operator computes the product of a vector with the approximate inverse of the Hessian of the objective function, using the L-BFGS limited memory approximation to the inverse Hessian, accumulated during the optimization.

Objects of this class implement the `scipy.sparse.linalg.LinearOperator` interface.

Parameters

sk [array_like, shape=(n_corr, n)] Array of *n_corr* most recent updates to the solution vector. (See [1]).

yk [array_like, shape=(n_corr, n)] Array of *n_corr* most recent updates to the gradient. (See [1]).

References

[1]

Attributes

H Hermitian adjoint.

T Transpose this linear operator.

Methods

__call__(x)	Call self as a function.
adjoint()	Hermitian adjoint.
dot(x)	Matrix-matrix or matrix-vector multiplication.
matmat(X)	Matrix-matrix multiplication.
matvec(x)	Matrix-vector multiplication.
rmatmat(X)	Adjoint matrix-matrix multiplication.
rmatvec(x)	Adjoint matrix-vector multiplication.
todense()	Return a dense array representation of this operator.
transpose()	Transpose this linear operator.

scipy.optimize.LbfgsInvHessProduct.__call__

LbfgsInvHessProduct.**__call__**(*x*)
Call self as a function.

scipy.optimize.LbfgsInvHessProduct.adjoint

LbfgsInvHessProduct.**adjoint**()
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns

A_H [LinearOperator] Hermitian adjoint of self.

scipy.optimize.LbfgsInvHessProduct.dot

LbfgsInvHessProduct.**dot**(*x*)
Matrix-matrix or matrix-vector multiplication.

Parameters

x [array_like] 1-d or 2-d array, representing a vector or matrix.

Returns

Ax [array] 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

scipy.optimize.LbfgsInvHessProduct.matmat

LbfgsInvHessProduct.**matmat**(*X*)
Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters

X [{matrix, ndarray}] An array with shape (N,K).

Returns

Y [{matrix, ndarray}] A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

scipy.optimize.LbfgsInvHessProduct.matvec

LbfgsInvHessProduct.**matvec**(*x*)

Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters

x [{matrix, ndarray}] An array with shape (N,) or (N,1).

Returns

y [{matrix, ndarray}] A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

scipy.optimize.LbfgsInvHessProduct.rmatmat

LbfgsInvHessProduct.**rmatmat**(*X*)

Adjoint matrix-matrix multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array, or 2-d array. The default implementation defers to the adjoint.

Parameters

X [{matrix, ndarray}] A matrix or 2D array.

Returns

Y [{matrix, ndarray}] A matrix or 2D array depending on the type of the input.

Notes

This rmatmat wraps the user-specified rmatmat routine.

scipy.optimize.LbfgsInvHessProduct.rmatvec

LbfgsInvHessProduct.**rmatvec**(*x*)

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters

x [{matrix, ndarray}] An array with shape (M,) or (M,1).

Returns

y [{matrix, ndarray}] A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

scipy.optimize.LbfgsInvHessProduct.todense

LbfgsInvHessProduct.**todense**()

Return a dense array representation of this operator.

Returns

arr [ndarray, shape=(n, n)] An array with the same shape and containing the same data represented by this *LinearOperator*.

scipy.optimize.LbfgsInvHessProduct.transpose

LbfgsInvHessProduct.**transpose**()

Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

__mul__	

scipy.optimize.HessianUpdateStrategy

class scipy.optimize.**HessianUpdateStrategy**

Interface for implementing Hessian update strategies.

Many optimization methods make use of Hessian (or inverse Hessian) approximations, such as the quasi-Newton methods BFGS, SR1, L-BFGS. Some of these approximations, however, do not actually need to store the entire matrix or can compute the internal matrix product with a given vector in a very efficiently manner. This class serves as an abstract interface between the optimization algorithm and the quasi-Newton update strategies, giving freedom of implementation to store and update the internal matrix as efficiently as possible. Different choices of initialization and update procedure will result in different quasi-Newton strategies.

Four methods should be implemented in derived classes: `initialize`, `update`, `dot` and `get_matrix`.

Notes

Any instance of a class that implements this interface, can be accepted by the method `minimize` and used by the compatible solvers to approximate the Hessian (or inverse Hessian) used by the optimization algorithms.

Methods

dot(p)	Compute the product of the internal matrix with the given vector.
get_matrix()	Return current internal matrix.
initialize(n, approx_type)	Initialize internal matrix.
update(delta_x, delta_grad)	Update internal matrix.

scipy.optimize.HessianUpdateStrategy.dot

HessianUpdateStrategy.**dot**(*p*)

Compute the product of the internal matrix with the given vector.

Parameters

p [array_like] 1-D array representing a vector.

Returns

Hp [array] 1-D represents the result of multiplying the approximation matrix by vector p.

scipy.optimize.HessianUpdateStrategy.get_matrix

HessianUpdateStrategy.**get_matrix**()

Return current internal matrix.

Returns

H [ndarray, shape (n, n)] Dense matrix containing either the Hessian or its inverse (depending on how 'approx_type' is defined).

scipy.optimize.HessianUpdateStrategy.initialize

HessianUpdateStrategy.**initialize**(*n*, *approx_type*)

Initialize internal matrix.

Allocate internal memory for storing and updating the Hessian or its inverse.

Parameters

n [int] Problem dimension.

approx_type

[{'hess', 'inv_hess'}] Selects either the Hessian or the inverse Hessian. When set to 'hess' the Hessian will be stored and updated. When set to 'inv_hess' its inverse will be used instead.

scipy.optimize.HessianUpdateStrategy.update

HessianUpdateStrategy.**update**(*delta_x*, *delta_grad*)

Update internal matrix.

Update Hessian matrix or its inverse (depending on how 'approx_type' is defined) using information about the last evaluated points.

Parameters

delta_x [ndarray] The difference between two points the gradient function have been evaluated at: `delta_x = x2 - x1`.

delta_grad [ndarray] The difference between the gradients: `delta_grad = grad(x2) - grad(x1)`.

Benchmark problems

rosen(x)	The Rosenbrock function.
rosen_der(x)	The derivative (i.e.
rosen_hess(x)	The Hessian matrix of the Rosenbrock function.
rosen_hess_prod(x, p)	Product of the Hessian matrix of the Rosenbrock function with a vector.

scipy.optimize.rosen

scipy.optimize.**rosen**(*x*)

The Rosenbrock function.

The function computed is:

```
sum(100.0*(x[1:] - x[:-1]**2.0)**2.0 + (1 - x[:-1])**2.0)
```

Parameters

x [array_like] 1-D array of points at which the Rosenbrock function is to be computed.

Returns

f [float] The value of the Rosenbrock function.

See also:

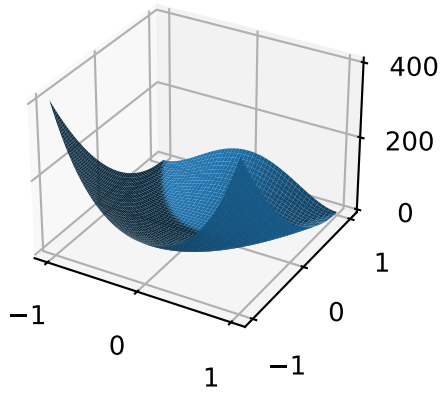
rosen_der, **rosen_hess**, **rosen_hess_prod**

Examples

```
>>> from scipy.optimize import rosen
>>> X = 0.1 * np.arange(10)
>>> rosen(X)
76.56
```

For higher-dimensional input `rosen` broadcasts. In the following example, we use this to plot a 2D landscape. Note that `rosen_hess` does not broadcast in this manner.

```
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.mplot3d import Axes3D
>>> x = np.linspace(-1, 1, 50)
>>> X, Y = np.meshgrid(x, x)
>>> ax = plt.subplot(111, projection='3d')
>>> ax.plot_surface(X, Y, rosen([X, Y]))
>>> plt.show()
```



scipy.optimize.rosen_der

scipy.optimize.**rosen_der**(*x*)

The derivative (i.e. gradient) of the Rosenbrock function.

Parameters

x [array_like] 1-D array of points at which the derivative is to be computed.

Returns

rosen_der [(N,) ndarray] The gradient of the Rosenbrock function at *x*.

See also:

rosen, **rosen_hess**, **rosen_hess_prod**

Examples

```
>>> from scipy.optimize import rosen_der
>>> X = 0.1 * np.arange(9)
>>> rosen_der(X)
array([ -2. ,  10.6,  15.6,  13.4,   6.4,  -3. , -12.4, -19.4,  62. ])
```

scipy.optimize.rosen_hess

scipy.optimize.**rosen_hess**(*x*)

The Hessian matrix of the Rosenbrock function.

Parameters

x [array_like] 1-D array of points at which the Hessian matrix is to be computed.

Returns

rosen_hess [ndarray] The Hessian matrix of the Rosenbrock function at *x*.

See also:

rosen, **rosen_der**, **rosen_hess_prod**

Examples

```
>>> from scipy.optimize import rosen_hess
>>> X = 0.1 * np.arange(4)
>>> rosen_hess(X)
array([[-38.,   0.,   0.,   0.],
       [  0., 134., -40.,   0.],
       [  0., -40., 130., -80.],
       [  0.,   0., -80., 200.]])
```

scipy.optimize.rosen_hess_prod

scipy.optimize.**rosen_hess_prod**(*x*, *p*)

Product of the Hessian matrix of the Rosenbrock function with a vector.

Parameters

x [array_like] 1-D array of points at which the Hessian matrix is to be computed.

p [array_like] 1-D array, the vector to be multiplied by the Hessian matrix.

Returns

rosen_hess_prod [ndarray] The Hessian matrix of the Rosenbrock function at *x* multiplied by the vector *p*.

See also:

rosen, **rosen_der**, **rosen_hess**

Examples

```
>>> from scipy.optimize import rosen_hess_prod
>>> X = 0.1 * np.arange(9)
>>> p = 0.5 * np.arange(9)
>>> rosen_hess_prod(X, p)
array([  -0.,   27.,  -10.,  -95., -192., -265., -278., -195., -180.])
```

Legacy functions

The functions below are not recommended for use in new scripts; all of these methods are accessible via a newer, more consistent interfaces, provided by the interfaces above.

Optimization

General-purpose multivariate methods:

fmin(func, x0[, args, xtol, ftol, maxiter, …])	Minimize a function using the downhill simplex algorithm.
fmin_powell(func, x0[, args, xtol, ftol, …])	Minimize a function using modified Powell's method.
fmin_cg(f, x0[, fprime, args, gtol, norm, …])	Minimize a function using a nonlinear conjugate gradient algorithm.
fmin_bfgs(f, x0[, fprime, args, gtol, norm, …])	Minimize a function using the BFGS algorithm.
fmin_ncg(f, x0, fprime[, fhess_p, fhess, …])	Unconstrained minimization of a function using the Newton-CG method.

scipy.optimize.fmin

scipy.optimize.**fmin**(*func*, *x0*, *args=()*, *xtol=0.0001*, *ftol=0.0001*, *maxiter=None*, *maxfun=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*, *initial_simplex=None*)

Minimize a function using the downhill simplex algorithm.

This algorithm only uses function values, not derivatives or second derivatives.

Parameters

func [callable func(x,*args)] The objective function to be minimized.

x0 [ndarray] Initial guess.

args [tuple, optional] Extra arguments passed to func, i.e., `f(x,*args)`.

xtol [float, optional] Absolute error in xopt between iterations that is acceptable for convergence.

ftol [number, optional] Absolute error in func(xopt) between iterations that is acceptable for convergence.

maxiter [int, optional] Maximum number of iterations to perform.

maxfun [number, optional] Maximum number of function evaluations to make.

full_output [bool, optional] Set to True if fopt and warnflag outputs are desired.

disp [bool, optional] Set to True to print convergence messages.

retall [bool, optional] Set to True to return list of solutions at each iteration.

callback [callable, optional] Called after each iteration, as callback(xk), where xk is the current parameter vector.

initial_simplex

[array_like of shape (N + 1, N), optional] Initial simplex. If given, overrides *x0*. `initial_simplex[j,:]` should contain the coordinates of the jth vertex of the `N+1` vertices in the simplex, where `N` is the dimension.

Returns

xopt	[ndarray] Parameter that minimizes function.
fopt	[float] Value of function at minimum: `fopt = func(xopt)`.
iter	[int] Number of iterations performed.
funcalls	[int] Number of function calls made.
warnflag	[int] 1 : Maximum number of function evaluations made. 2 : Maximum number of iterations reached.
allvecs	[list] Solution at each iteration.

See also:

minimize

Interface to minimization algorithms for multivariate functions. See the 'Nelder-Mead' *method* in particular.

Notes

Uses a Nelder-Mead simplex algorithm to find the minimum of function of one or more variables.

This algorithm has a long history of successful use in applications. But it will usually be slower than an algorithm that uses first or second derivative information. In practice, it can have poor performance in high-dimensional problems and is not robust to minimizing complicated functions. Additionally, there currently is no complete theory describing when the algorithm will successfully converge to the minimum, or how fast it will if it does. Both the ftol and xtol criteria must be met for convergence.

References

[1], [2]

Examples

```
>>> def f(x):
...     return x**2
```

```
>>> from scipy import optimize
```

```
>>> minimum = optimize.fmin(f, 1)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 17
         Function evaluations: 34
>>> minimum[0]
-8.8817841970012523e-16
```

scipy.optimize.fmin_powell

scipy.optimize.**fmin_powell**(*func*, *x0*, *args=()*, *xtol=0.0001*, *ftol=0.0001*, *maxiter=None*, *maxfun=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*, *direc=None*)

Minimize a function using modified Powell's method.

This method only uses function values, not derivatives.

Parameters

func [callable f(x,*args)] Objective function to be minimized.
x0 [ndarray] Initial guess.
args [tuple, optional] Extra arguments passed to func.
xtol [float, optional] Line-search error tolerance.
ftol [float, optional] Relative error in `func(xopt)` acceptable for convergence.
maxiter [int, optional] Maximum number of iterations to perform.
maxfun [int, optional] Maximum number of function evaluations to make.
full_output [bool, optional] If True, `fopt`, `xi`, `direc`, `iter`, `funcalls`, and `warnflag` are returned.
disp [bool, optional] If True, print convergence messages.
retall [bool, optional] If True, return a list of the solution at each iteration.
callback [callable, optional] An optional user-supplied function, called after each iteration. Called as `callback(xk)`, where `xk` is the current parameter vector.
direc [ndarray, optional] Initial fitting step and parameter order set as an (N, N) array, where N is the number of fitting parameters in *x0*. Defaults to step size 1.0 fitting all parameters simultaneously (`np.eye((N, N))`). To prevent initial consideration of values in a step or to change initial step size, set to 0 or desired step size in the Jth position in the Mth block, where J is the position in *x0* and M is the desired evaluation step, with steps being evaluated in index order. Step size and ordering will change freely as minimization proceeds.

Returns

xopt [ndarray] Parameter which minimizes *func*.
fopt [number] Value of function at minimum: `fopt = func(xopt)`.
direc [ndarray] Current direction set.
iter [int] Number of iterations.
funcalls [int] Number of function calls made.
warnflag [int]
Integer warning flag:
1 : Maximum number of function evaluations. 2 : Maximum number of iterations. 3 : NaN result encountered. 4 : The result is out of the provided bounds.
allvecs [list] List of solutions at each iteration.

See also:

minimize

Interface to unconstrained minimization algorithms for multivariate functions. See the 'Powell' method in particular.

Notes

Uses a modification of Powell's method to find the minimum of a function of N variables. Powell's method is a conjugate direction method.

The algorithm has two loops. The outer loop merely iterates over the inner loop. The inner loop minimizes over each current direction in the direction set. At the end of the inner loop, if certain conditions are met, the direction that gave the largest decrease is dropped and replaced with the difference between the current estimated x and the estimated x from the beginning of the inner-loop.

The technical conditions for replacing the direction of greatest increase amount to checking that

1. No further gain can be made along the direction of greatest increase from that iteration.
2. The direction of greatest increase accounted for a large sufficient fraction of the decrease in the function value from that iteration of the inner loop.

References

Powell M.J.D. (1964) An efficient method for finding the minimum of a function of several variables without calculating derivatives, Computer Journal, 7 (2):155-162.

Press W., Teukolsky S.A., Vetterling W.T., and Flannery B.P.: Numerical Recipes (any edition), Cambridge University Press

Examples

```
>>> def f(x):
...     return x**2
```

```
>>> from scipy import optimize
```

```
>>> minimum = optimize.fmin_powell(f, -1)
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 2
         Function evaluations: 18
>>> minimum
array(0.0)
```

scipy.optimize.fmin_cg

scipy.optimize.**fmin_cg**(*f*, *x0*, *fprime=None*, *args=()*, *gtol=1e-05*, *norm=inf*, *epsilon=1.4901161193847656e-08*, *maxiter=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*)

Minimize a function using a nonlinear conjugate gradient algorithm.

Parameters

f [callable, `f(x, *args)`] Objective function to be minimized. Here *x* must be a 1-D array of the variables that are to be changed in the search for a minimum, and *args* are the other (fixed) parameters of *f*.

x0 [ndarray] A user-supplied initial estimate of *xopt*, the optimal value of *x*. It must be a 1-D array of values.

fprime [callable, `fprime(x, *args)`, optional] A function that returns the gradient of *f* at *x*. Here *x* and *args* are as described above for *f*. The returned value must be a 1-D array. Defaults to None, in which case the gradient is approximated numerically (see *epsilon*, below).

args [tuple, optional] Parameter values passed to *f* and *fprime*. Must be supplied whenever additional fixed parameters are needed to completely specify the functions *f* and *fprime*.

gtol [float, optional] Stop when the norm of the gradient is less than *gtol*.

norm [float, optional] Order to use for the norm of the gradient (`-np.Inf` is min, `np.Inf` is max).

epsilon [float or ndarray, optional] Step size(s) to use when *fprime* is approximated numerically. Can be a scalar or a 1-D array. Defaults to `sqrt(eps)`, with eps the floating point machine precision. Usually `sqrt(eps)` is about 1.5e-8.

maxiter [int, optional] Maximum number of iterations to perform. Default is `200 * len(x0)`.

full_output [bool, optional] If True, return *fopt*, *func_calls*, *grad_calls*, and *warnflag* in addition to *xopt*. See the Returns section below for additional information on optional return values.

disp [bool, optional] If True, return a convergence message, followed by *xopt*.

retall [bool, optional] If True, add to the returned values the results of each iteration.

callback [callable, optional] An optional user-supplied function, called after each iteration. Called as `callback(xk)`, where `xk` is the current value of *x0*.

Returns

xopt [ndarray] Parameters which minimize f, i.e., `f(xopt) == fopt`.

fopt [float, optional] Minimum value found, f(xopt). Only returned if *full_output* is True.

func_calls [int, optional] The number of function_calls made. Only returned if *full_output* is True.

grad_calls [int, optional] The number of gradient calls made. Only returned if *full_output* is True.

warnflag [int, optional] Integer value with warning status, only returned if *full_output* is True.
0 : Success.
1 : The maximum number of iterations was exceeded.
2 [Gradient and/or function calls were not changing. May indicate] that precision was lost, i.e., the routine did not converge.
3 : NaN result encountered.

allvecs [list of ndarray, optional] List of arrays, containing the results at each iteration. Only returned if *retall* is True.

See also:

`minimize`

common interface to all *`scipy.optimize`* algorithms for unconstrained and constrained minimization of multivariate functions. It provides an alternative way to call `fmin_cg`, by specifying `method='CG'`.

Notes

This conjugate gradient algorithm is based on that of Polak and Ribiere [1].

Conjugate gradient methods tend to work better when:

1. *f* has a unique global minimizing point, and no local minima or other stationary points,
2. *f* is, at least locally, reasonably well approximated by a quadratic function of the variables,
3. *f* is continuous and has a continuous gradient,
4. *fprime* is not too large, e.g., has a norm less than 1000,
5. The initial guess, *x0*, is reasonably close to *f* 's global minimizing point, *xopt*.

References

[1]

Examples

Example 1: seek the minimum value of the expression `a*u**2 + b*u*v + c*v**2 + d*u + e*v + f` for given values of the parameters and an initial guess `(u, v) = (0, 0)`.

```
>>> args = (2, 3, 7, 8, 9, 10)  # parameter values
>>> def f(x, *args):
...     u, v = x
...     a, b, c, d, e, f = args
...     return a*u**2 + b*u*v + c*v**2 + d*u + e*v + f
>>> def gradf(x, *args):
...     u, v = x
...     a, b, c, d, e, f = args
...     gu = 2*a*u + b*v + d     # u-component of the gradient
...     gv = b*u + 2*c*v + e     # v-component of the gradient
...     return np.asarray((gu, gv))
>>> x0 = np.asarray((0, 0))  # Initial guess.
>>> from scipy import optimize
>>> res1 = optimize.fmin_cg(f, x0, fprime=gradf, args=args)
Optimization terminated successfully.
         Current function value: 1.617021
         Iterations: 4
         Function evaluations: 8
         Gradient evaluations: 8
>>> res1
array([-1.80851064, -0.25531915])
```

Example 2: solve the same problem using the *minimize* function. (This *myopts* dictionary shows all of the available options, although in practice only non-default values would be needed. The returned value will be a dictionary.)

```
>>> opts = {'maxiter' : None,    # default value.
...         'disp' : True,    # non-default value.
...         'gtol' : 1e-5,    # default value.
...         'norm' : np.inf,  # default value.
...         'eps' : 1.4901161193847656e-08}  # default value.
>>> res2 = optimize.minimize(f, x0, jac=gradf, args=args,
...                          method='CG', options=opts)
Optimization terminated successfully.
        Current function value: 1.617021
        Iterations: 4
        Function evaluations: 8
        Gradient evaluations: 8
>>> res2.x  # minimum found
array([-1.80851064, -0.25531915])
```

scipy.optimize.fmin_bfgs

scipy.optimize.**fmin_bfgs**(*f*, *x0*, *fprime=None*, *args=()*, *gtol=1e-05*, *norm=inf*, *epsilon=1.4901161193847656e-08*, *maxiter=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*)

Minimize a function using the BFGS algorithm.

Parameters

f	[callable `f(x,*args)`] Objective function to be minimized.
x0	[ndarray] Initial guess.
fprime	[callable `f'(x,*args)`, optional] Gradient of f.
args	[tuple, optional] Extra arguments passed to f and fprime.
gtol	[float, optional] Gradient norm must be less than *gtol* before successful termination.
norm	[float, optional] Order of norm (Inf is max, -Inf is min)
epsilon	[int or ndarray, optional] If *fprime* is approximated, use this value for the step size.
callback	[callable, optional] An optional user-supplied function to call after each iteration. Called as `callback(xk)`, where `xk` is the current parameter vector.
maxiter	[int, optional] Maximum number of iterations to perform.
full_output	[bool, optional] If True, return `fopt`, `func_calls`, `grad_calls`, and `warnflag` in addition to `xopt`.
disp	[bool, optional] Print convergence message if True.
retall	[bool, optional] Return a list of results at each iteration if True.

Returns

xopt	[ndarray] Parameters which minimize f, i.e., `f(xopt) == fopt`.
fopt	[float] Minimum value.
gopt	[ndarray] Value of gradient at minimum, f'(xopt), which should be near 0.
Bopt	[ndarray] Value of 1/f''(xopt), i.e., the inverse Hessian matrix.
func_calls	[int] Number of function_calls made.
grad_calls	[int] Number of gradient calls made.
warnflag	[integer] 1 : Maximum number of iterations exceeded. 2 : Gradient and/or function calls not changing. 3 : NaN result encountered.
allvecs	[list] The value of *xopt* at each iteration. Only returned if *retall* is True.

See also:

minimize

Interface to minimization algorithms for multivariate functions. See `method='BFGS'` in particular.

Notes

Optimize the function, *f*, whose gradient is given by *fprime* using the quasi-Newton method of Broyden, Fletcher, Goldfarb, and Shanno (BFGS).

References

Wright, and Nocedal 'Numerical Optimization', 1999, p. 198.

Examples

```
>>> from scipy.optimize import fmin_bfgs
>>> def quadratic_cost(x, Q):
...     return x @ Q @ x
...
>>> x0 = np.array([-3, -4])
>>> cost_weight =  np.diag([1., 10.])
>>> # Note that a trailing comma is necessary for a tuple with single␣
 ↪element
>>> fmin_bfgs(quadratic_cost, x0, args=(cost_weight,))
Optimization terminated successfully.
        Current function value: 0.000000
        Iterations: 7                   # may vary
        Function evaluations: 24        # may vary
        Gradient evaluations: 8         # may vary
array([ 2.85169950e-06, -4.61820139e-07])
```

```
>>> def quadratic_cost_grad(x, Q):
...     return 2 * Q @ x
...
>>> fmin_bfgs(quadratic_cost, x0, quadratic_cost_grad, args=(cost_weight,
 ↪))
Optimization terminated successfully.
        Current function value: 0.000000
        Iterations: 7
        Function evaluations: 8
        Gradient evaluations: 8
array([ 2.85916637e-06, -4.54371951e-07])
```

scipy.optimize.fmin_ncg

scipy.optimize.**fmin_ncg**(*f*, *x0*, *fprime*, *fhess_p=None*, *fhess=None*, *args=()*, *avextol=1e-05*, *epsilon=1.4901161193847656e-08*, *maxiter=None*, *full_output=0*, *disp=1*, *retall=0*, *callback=None*)

Unconstrained minimization of a function using the Newton-CG method.

Parameters

f	[callable `f(x, *args)`] Objective function to be minimized.
x0	[ndarray] Initial guess.
fprime	[callable `f'(x, *args)`] Gradient of f.
fhess_p	[callable `fhess_p(x, p, *args)`, optional] Function which computes the Hessian of f times an arbitrary vector, p.
fhess	[callable `fhess(x, *args)`, optional] Function to compute the Hessian matrix of f.
args	[tuple, optional] Extra arguments passed to f, fprime, fhess_p, and fhess (the same set of extra arguments is supplied to all of these functions).
epsilon	[float or ndarray, optional] If fhess is approximated, use this value for the step size.

callback [callable, optional] An optional user-supplied function which is called after each iteration. Called as callback(xk), where xk is the current parameter vector.
avextol [float, optional] Convergence is assumed when the average relative error in the minimizer falls below this amount.
maxiter [int, optional] Maximum number of iterations to perform.
full_output [bool, optional] If True, return the optional outputs.
disp [bool, optional] If True, print convergence message.
retall [bool, optional] If True, return a list of results at each iteration.

Returns

xopt [ndarray] Parameters which minimize f, i.e., `f(xopt) == fopt`.
fopt [float] Value of the function at xopt, i.e., `fopt = f(xopt)`.
fcalls [int] Number of function calls made.
gcalls [int] Number of gradient calls made.
hcalls [int] Number of Hessian calls made.
warnflag [int] Warnings generated by the algorithm. 1 : Maximum number of iterations exceeded. 2 : Line search failure (precision loss). 3 : NaN result encountered.
allvecs [list] The result at each iteration, if retall is True (see below).

See also:

`minimize`

Interface to minimization algorithms for multivariate functions. See the 'Newton-CG' *method* in particular.

Notes

Only one of *fhess_p* or *fhess* need to be given. If *fhess* is provided, then *fhess_p* will be ignored. If neither *fhess* nor *fhess_p* is provided, then the hessian product will be approximated using finite differences on *fprime*. *fhess_p* must compute the hessian times an arbitrary vector. If it is not given, finite-differences on *fprime* are used to compute it.

Newton-CG methods are also called truncated Newton methods. This function differs from scipy.optimize.fmin_tnc because

1. ***scipy.optimize.fmin_ncg is written purely in Python using NumPy***

   and scipy while scipy.optimize.fmin_tnc calls a C function.

2. ***scipy.optimize.fmin_ncg is only for unconstrained minimization***

   while scipy.optimize.fmin_tnc is for unconstrained minimization or box constrained minimization. (Box constraints give lower and upper bounds for each variable separately.)

References

Wright & Nocedal, 'Numerical Optimization', 1999, p. 140.

Constrained multivariate methods:

fmin_l_bfgs_b(func, x0[, fprime, args, …])	Minimize a function func using the L-BFGS-B algorithm.
fmin_tnc(func, x0[, fprime, args, …])	Minimize a function with variables subject to bounds, using gradient information in a truncated Newton algorithm.

continues on next page

Table 146 – continued from previous page

fmin_cobyla(func, x0, cons[, args, …])	Minimize a function using the Constrained Optimization By Linear Approximation (COBYLA) method.
fmin_slsqp(func, x0[, eqcons, f_eqcons, …])	Minimize a function using Sequential Least Squares Programming

scipy.optimize.fmin_l_bfgs_b

scipy.optimize.**fmin_l_bfgs_b**(*func*, *x0*, *fprime=None*, *args=()*, *approx_grad=0*, *bounds=None*, *m=10*, *factr=10000000.0*, *pgtol=1e-05*, *epsilon=1e-08*, *iprint=-1*, *maxfun=15000*, *maxiter=15000*, *disp=None*, *callback=None*, *maxls=20*)

Minimize a function func using the L-BFGS-B algorithm.

Parameters

func [callable f(x,*args)] Function to minimize.

x0 [ndarray] Initial guess.

fprime [callable fprime(x,*args), optional] The gradient of *func*. If None, then *func* returns the function value and the gradient (`f, g = func(x, *args)`), unless *approx_grad* is True in which case *func* returns only `f`.

args [sequence, optional] Arguments to pass to *func* and *fprime*.

approx_grad [bool, optional] Whether to approximate the gradient numerically (in which case *func* returns only the function value).

bounds [list, optional] `(min, max)` pairs for each element in `x`, defining the bounds on that parameter. Use None or +-inf for one of `min` or `max` when there is no bound in that direction.

m [int, optional] The maximum number of variable metric corrections used to define the limited memory matrix. (The limited memory BFGS method does not store the full hessian but uses this many terms in an approximation to it.)

factr [float, optional] The iteration stops when `(f^k - f^{k+1})/max{|f^k|, |f^{k+1}|,1} <= factr * eps`, where `eps` is the machine precision, which is automatically generated by the code. Typical values for *factr* are: 1e12 for low accuracy; 1e7 for moderate accuracy; 10.0 for extremely high accuracy. See Notes for relationship to *ftol*, which is exposed (instead of *factr*) by the *scipy.optimize.minimize* interface to L-BFGS-B.

pgtol [float, optional] The iteration will stop when `max{|proj g_i | i = 1, ..., n} <= pgtol` where `pg_i` is the i-th component of the projected gradient.

epsilon [float, optional] Step size used when *approx_grad* is True, for numerically calculating the gradient

iprint [int, optional] Controls the frequency of output. `iprint < 0` means no output; `iprint = 0` print only one line at the last iteration; `0 < iprint < 99` print also f and `|proj g|` every iprint iterations; `iprint = 99` print details of every iteration except n-vectors; `iprint = 100` print also the changes of active set and final x; `iprint > 100` print details of every iteration including x and g.

disp [int, optional] If zero, then no output. If a positive number, then this over-rides *iprint* (i.e., *iprint* gets the value of *disp*).

maxfun [int, optional] Maximum number of function evaluations.

maxiter [int, optional] Maximum number of iterations.

callback [callable, optional] Called after each iteration, as `callback(xk)`, where `xk` is the current parameter vector.

maxls [int, optional] Maximum number of line search steps (per iteration). Default is 20.

Returns

x [array_like] Estimated position of the minimum.
f [float] Value of *func* at the minimum.
d [dict] Information dictionary.

- d['warnflag'] is
  - 0 if converged,
  - 1 if too many function evaluations or too many iterations,
  - 2 if stopped for another reason, given in d['task']
- d['grad'] is the gradient at the minimum (should be 0 ish)
- d['funcalls'] is the number of function calls made.
- d['nit'] is the number of iterations.

See also:

`minimize`

Interface to minimization algorithms for multivariate functions. See the 'L-BFGS-B' *method* in particular. Note that the *ftol* option is made available via that interface, while *factr* is provided via this interface, where *factr* is the factor multiplying the default machine floating-point precision to arrive at *ftol*: `ftol = factr * numpy.finfo(float).eps`.

Notes

License of L-BFGS-B (FORTRAN code):

The version included here (in fortran code) is 3.0 (released April 25, 2011). It was written by Ciyou Zhu, Richard Byrd, and Jorge Nocedal <nocedal@ece.nwu.edu>. It carries the following condition for use:

This software is freely available, but we expect that all publications describing work using this software, or all commercial products using it, quote at least one of the references given below. This software is released under the BSD License.

References

- R. H. Byrd, P. Lu and J. Nocedal. A Limited Memory Algorithm for Bound Constrained Optimization, (1995), SIAM Journal on Scientific and Statistical Computing, 16, 5, pp. 1190-1208.
- C. Zhu, R. H. Byrd and J. Nocedal. L-BFGS-B: Algorithm 778: L-BFGS-B, FORTRAN routines for large scale bound constrained optimization (1997), ACM Transactions on Mathematical Software, 23, 4, pp. 550 - 560.
- J.L. Morales and J. Nocedal. L-BFGS-B: Remark on Algorithm 778: L-BFGS-B, FORTRAN routines for large scale bound constrained optimization (2011), ACM Transactions on Mathematical Software, 38, 1.

scipy.optimize.fmin_tnc

`scipy.optimize.`**`fmin_tnc`**(*func*, *x0*, *fprime=None*, *args=()*, *approx_grad=0*, *bounds=None*, *epsilon=1e-08*, *scale=None*, *offset=None*, *messages=15*, *maxCGit=- 1*, *maxfun=None*, *eta=- 1*, *stepmx=0*, *accuracy=0*, *fmin=0*, *ftol=- 1*, *xtol=- 1*, *pgtol=- 1*, *rescale=- 1*, *disp=None*, *callback=None*)

Minimize a function with variables subject to bounds, using gradient information in a truncated Newton algorithm. This method wraps a C implementation of the algorithm.

Parameters

func [callable `func(x, *args)`] Function to minimize. Must do one of:

1. Return f and g, where f is the value of the function and g its gradient (a list of floats).
2. Return the function value but supply gradient function separately as *fprime*.
3. Return the function value and set `approx_grad=True`.

If the function returns None, the minimization is aborted.

x0 [array_like] Initial estimate of minimum.

fprime [callable `fprime(x, *args)`, optional] Gradient of *func*. If None, then either *func* must return the function value and the gradient (`f,g = func(x, *args)`) or *approx_grad* must be True.

args [tuple, optional] Arguments to pass to function.

approx_grad [bool, optional] If true, approximate the gradient numerically.

bounds [list, optional] (min, max) pairs for each element in x0, defining the bounds on that parameter. Use None or +/-inf for one of min or max when there is no bound in that direction.

epsilon [float, optional] Used if approx_grad is True. The stepsize in a finite difference approximation for fprime.

scale [array_like, optional] Scaling factors to apply to each variable. If None, the factors are up-low for interval bounded variables and 1+|x| for the others. Defaults to None.

offset [array_like, optional] Value to subtract from each variable. If None, the offsets are (up+low)/2 for interval bounded variables and x for the others.

messages [int, optional] Bit mask used to select messages display during minimization values defined in the MSGS dict. Defaults to MGS_ALL.

disp [int, optional] Integer interface to messages. 0 = no message, 5 = all messages

maxCGit [int, optional] Maximum number of hessian*vector evaluations per main iteration. If maxCGit == 0, the direction chosen is -gradient if maxCGit < 0, maxCGit is set to max(1,min(50,n/2)). Defaults to -1.

maxfun [int, optional] Maximum number of function evaluation. If None, maxfun is set to max(100, 10*len(x0)). Defaults to None.

eta [float, optional] Severity of the line search. If < 0 or > 1, set to 0.25. Defaults to -1.

stepmx [float, optional] Maximum step for the line search. May be increased during call. If too small, it will be set to 10.0. Defaults to 0.

accuracy [float, optional] Relative precision for finite difference calculations. If <= machine_precision, set to sqrt(machine_precision). Defaults to 0.

fmin [float, optional] Minimum function value estimate. Defaults to 0.

ftol [float, optional] Precision goal for the value of f in the stopping criterion. If ftol < 0.0, ftol is set to 0.0 defaults to -1.

xtol [float, optional] Precision goal for the value of x in the stopping criterion (after applying x scaling factors). If xtol < 0.0, xtol is set to sqrt(machine_precision). Defaults to -1.

pgtol [float, optional] Precision goal for the value of the projected gradient in the stopping criterion (after applying x scaling factors). If pgtol < 0.0, pgtol is set to 1e-2 * sqrt(accuracy). Setting it to 0.0 is not recommended. Defaults to -1.

rescale [float, optional] Scaling factor (in log10) used to trigger f value rescaling. If 0, rescale at each iteration. If a large value, never rescale. If < 0, rescale is set to 1.3.

callback [callable, optional] Called after each iteration, as callback(xk), where xk is the current parameter vector.

Returns

x [ndarray] The solution.

nfeval [int] The number of function evaluations.

rc [int] Return code, see below

See also:

minimize

Interface to minimization algorithms for multivariate functions. See the 'TNC' *method* in particular.

Notes

The underlying algorithm is truncated Newton, also called Newton Conjugate-Gradient. This method differs from scipy.optimize.fmin_ncg in that

1. it wraps a C implementation of the algorithm
2. it allows each variable to be given an upper and lower bound.

The algorithm incorporates the bound constraints by determining the descent direction as in an unconstrained truncated Newton, but never taking a step-size large enough to leave the space of feasible x's. The algorithm keeps track of a set of currently active constraints, and ignores them when computing the minimum allowable step size. (The x's associated with the active constraint are kept fixed.) If the maximum allowable step size is zero then a new constraint is added. At the end of each iteration one of the constraints may be deemed no longer active and removed. A constraint is considered no longer active is if it is currently active but the gradient for that variable points inward from the constraint. The specific constraint removed is the one associated with the variable of largest index whose constraint is no longer active.

Return codes are defined as follows:

```
-1 : Infeasible (lower bound > upper bound)
 0 : Local minimum reached (|pg| ~= 0)
 1 : Converged (|f_n-f_(n-1)| ~= 0)
 2 : Converged (|x_n-x_(n-1)| ~= 0)
 3 : Max. number of function evaluations reached
 4 : Linear search failed
 5 : All lower bounds are equal to the upper bounds
 6 : Unable to progress
 7 : User requested end of minimization
```

References

Wright S., Nocedal J. (2006), 'Numerical Optimization'

Nash S.G. (1984), "Newton-Type Minimization Via the Lanczos Method", SIAM Journal of Numerical Analysis 21, pp. 770-778

scipy.optimize.fmin_cobyla

scipy.optimize.**fmin_cobyla**(*func*, *x0*, *cons*, *args=()*, *consargs=None*, *rhobeg=1.0*, *rhoend=0.0001*, *maxfun=1000*, *disp=None*, *catol=0.0002*)

Minimize a function using the Constrained Optimization By Linear Approximation (COBYLA) method. This method wraps a FORTRAN implementation of the algorithm.

Parameters

func	[callable] Function to minimize. In the form func(x, *args).
x0	[ndarray] Initial guess.
cons	[sequence] Constraint functions; must all be `>=0` (a single function if only 1 constraint). Each function takes the parameters *x* as its first argument, and it can return either a single number or an array or list of numbers.
args	[tuple, optional] Extra arguments to pass to function.
consargs	[tuple, optional] Extra arguments to pass to constraint functions (default of None means use same extra arguments as those passed to func). Use `()` for no extra arguments.
rhobeg	[float, optional] Reasonable initial changes to the variables.

rhoend [float, optional] Final accuracy in the optimization (not precisely guaranteed). This is a lower bound on the size of the trust region.
disp [{0, 1, 2, 3}, optional] Controls the frequency of output; 0 implies no output.
maxfun [int, optional] Maximum number of function evaluations.
catol [float, optional] Absolute tolerance for constraint violations.

Returns

x [ndarray] The argument that minimises *f*.

See also:

minimize

Interface to minimization algorithms for multivariate functions. See the 'COBYLA' *method* in particular.

Notes

This algorithm is based on linear approximations to the objective function and each constraint. We briefly describe the algorithm.

Suppose the function is being minimized over k variables. At the jth iteration the algorithm has k+1 points v_1, …, v_(k+1), an approximate solution x_j, and a radius RHO_j. (i.e., linear plus a constant) approximations to the objective function and constraint functions such that their function values agree with the linear approximation on the k+1 points v_1,.., v_(k+1). This gives a linear program to solve (where the linear approximations of the constraint functions are constrained to be non-negative).

However, the linear approximations are likely only good approximations near the current simplex, so the linear program is given the further requirement that the solution, which will become x_(j+1), must be within RHO_j from x_j. RHO_j only decreases, never increases. The initial RHO_j is rhobeg and the final RHO_j is rhoend. In this way COBYLA's iterations behave like a trust region algorithm.

Additionally, the linear program may be inconsistent, or the approximation may give poor improvement. For details about how these issues are resolved, as well as how the points v_i are updated, refer to the source code or the references below.

References

Powell M.J.D. (1994), "A direct search optimization method that models the objective and constraint functions by linear interpolation.", in Advances in Optimization and Numerical Analysis, eds. S. Gomez and J-P Hennart, Kluwer Academic (Dordrecht), pp. 51-67

Powell M.J.D. (1998), "Direct search algorithms for optimization calculations", Acta Numerica 7, 287-336

Powell M.J.D. (2007), "A view of algorithms for optimization without derivatives", Cambridge University Technical Report DAMTP 2007/NA03

Examples

Minimize the objective function f(x,y) = x*y subject to the constraints x**2 + y**2 < 1 and y > 0:

```
>>> def objective(x):
...     return x[0]*x[1]
...
>>> def constr1(x):
...     return 1 - (x[0]**2 + x[1]**2)
...
>>> def constr2(x):
...     return x[1]
...
>>> from scipy.optimize import fmin_cobyla
>>> fmin_cobyla(objective, [0.0, 0.1], [constr1, constr2], rhoend=1e-7)
array([-0.70710685,  0.70710671])
```

The exact solution is (-sqrt(2)/2, sqrt(2)/2).

scipy.optimize.fmin_slsqp

scipy.optimize.**fmin_slsqp**(*func*, *x0*, *eqcons=()*, *f_eqcons=None*, *ieqcons=()*, *f_ieqcons=None*, *bounds=()*, *fprime=None*, *fprime_eqcons=None*, *fprime_ieqcons=None*, *args=()*, *iter=100*, *acc=1e-06*, *iprint=1*, *disp=None*, *full_output=0*, *epsilon=1.4901161193847656e-08*, *callback=None*)

Minimize a function using Sequential Least Squares Programming

Python interface function for the SLSQP Optimization subroutine originally implemented by Dieter Kraft.

Parameters

func [callable f(x,*args)] Objective function. Must return a scalar.

x0 [1-D ndarray of float] Initial guess for the independent variable(s).

eqcons [list, optional] A list of functions of length n such that eqcons[j](x,*args) == 0.0 in a successfully optimized problem.

f_eqcons [callable f(x,*args), optional] Returns a 1-D array in which each element must equal 0.0 in a successfully optimized problem. If f_eqcons is specified, eqcons is ignored.

ieqcons [list, optional] A list of functions of length n such that ieqcons[j](x,*args) >= 0.0 in a successfully optimized problem.

f_ieqcons [callable f(x,*args), optional] Returns a 1-D ndarray in which each element must be greater or equal to 0.0 in a successfully optimized problem. If f_ieqcons is specified, ieqcons is ignored.

bounds [list, optional] A list of tuples specifying the lower and upper bound for each independent variable [(xl0, xu0),(xl1, xu1),…] Infinite values will be interpreted as large floating values.

fprime [callable *f(x,*args)*, optional] A function that evaluates the partial derivatives of func.

fprime_eqcons [callable *f(x,*args)*, optional] A function of the form *f(x, *args)* that returns the m by n array of equality constraint normals. If not provided, the normals will be approximated. The array returned by fprime_eqcons should be sized as (len(eqcons), len(x0)).

fprime_ieqcons [callable *f(x,*args)*, optional] A function of the form *f(x, *args)* that returns the m by n array of inequality constraint normals. If not provided, the normals will be approximated. The array returned by fprime_ieqcons should be sized as (len(ieqcons), len(x0)).

args [sequence, optional] Additional arguments passed to func and fprime.

iter [int, optional] The maximum number of iterations.

acc [float, optional] Requested accuracy.
iprint [int, optional] The verbosity of fmin_slsqp :
- iprint <= 0 : Silent operation
- iprint == 1 : Print summary upon completion (default)
- iprint >= 2 : Print status of each iterate and summary

disp [int, optional] Overrides the iprint interface (preferred).
full_output [bool, optional] If False, return only the minimizer of func (default). Otherwise, output final objective function and summary information.
epsilon [float, optional] The step size for finite-difference derivative estimates.
callback [callable, optional] Called after each iteration, as `callback(x)`, where `x` is the current parameter vector.

Returns

out [ndarray of float] The final minimizer of func.
fx [ndarray of float, if full_output is true] The final value of the objective function.
its [int, if full_output is true] The number of iterations.
imode [int, if full_output is true] The exit mode from the optimizer (see below).
smode [string, if full_output is true] Message describing the exit mode from the optimizer.

See also:

`minimize`

Interface to minimization algorithms for multivariate functions. See the 'SLSQP' *method* in particular.

Notes

Exit modes are defined as follows

```
-1 : Gradient evaluation required (g & a)
 0 : Optimization terminated successfully
 1 : Function evaluation required (f & c)
 2 : More equality constraints than independent variables
 3 : More than 3*n iterations in LSQ subproblem
 4 : Inequality constraints incompatible
 5 : Singular matrix E in LSQ subproblem
 6 : Singular matrix C in LSQ subproblem
 7 : Rank-deficient equality constraint subproblem HFTI
 8 : Positive directional derivative for linesearch
 9 : Iteration limit reached
```

Examples

Examples are given *in the tutorial*.

Univariate (scalar) minimization methods:

fminbound(func, x1, x2[, args, xtol, …])	Bounded minimization for scalar functions.
brent(func[, args, brack, tol, full_output, …])	Given a function of one variable and a possible bracket, return the local minimum of the function isolated to a fractional precision of tol.

continues on next page

Table 147 – continued from previous page

golden(func[, args, brack, tol, …])	Return the minimum of a function of one variable using golden section method.

scipy.optimize.fminbound

scipy.optimize.**fminbound**(*func*, *x1*, *x2*, *args=()*, *xtol=1e-05*, *maxfun=500*, *full_output=0*, *disp=1*)

Bounded minimization for scalar functions.

Parameters

func [callable f(x,*args)] Objective function to be minimized (must accept and return scalars).
x1, x2 [float or array scalar] The optimization bounds.
args [tuple, optional] Extra arguments passed to function.
xtol [float, optional] The convergence tolerance.
maxfun [int, optional] Maximum number of function evaluations allowed.
full_output [bool, optional] If True, return optional outputs.
disp [int, optional] **If non-zero, print messages.** 0 : no message printing. 1 : non-convergence notification messages only. 2 : print a message on convergence too. 3 : print iteration results.

Returns

xopt [ndarray] Parameters (over given interval) which minimize the objective function.
fval [number] The function value at the minimum point.
ierr [int] An error flag (0 if converged, 1 if maximum number of function calls reached).
numfunc [int] The number of function calls made.

See also:

minimize_scalar

Interface to minimization algorithms for scalar univariate functions. See the 'Bounded' *method* in particular.

Notes

Finds a local minimizer of the scalar function *func* in the interval x1 < xopt < x2 using Brent's method. (See *brent* for auto-bracketing.)

Examples

fminbound finds the minimum of the function in the given range. The following examples illustrate the same

```
>>> def f(x):
...     return x**2
```

```
>>> from scipy import optimize
```

```
>>> minimum = optimize.fminbound(f, -1, 2)
>>> minimum
0.0
>>> minimum = optimize.fminbound(f, 1, 2)
>>> minimum
1.0000059608609866
```

scipy.optimize.brent

scipy.optimize.**brent**(*func*, *args=()*, *brack=None*, *tol=1.48e-08*, *full_output=0*, *maxiter=500*)

Given a function of one variable and a possible bracket, return the local minimum of the function isolated to a fractional precision of tol.

Parameters

func	[callable f(x,*args)] Objective function.
args	[tuple, optional] Additional arguments (if present).
brack	[tuple, optional] Either a triple (xa,xb,xc) where xa<xb<xc and func(xb) < func(xa), func(xc) or a pair (xa,xb) which are used as a starting interval for a downhill bracket search (see *bracket*). Providing the pair (xa,xb) does not always mean the obtained solution will satisfy xa<=x<=xb.
tol	[float, optional] Stop if between iteration change is less than *tol*.
full_output	[bool, optional] If True, return all output args (xmin, fval, iter, funcalls).
maxiter	[int, optional] Maximum number of iterations in solution.

Returns

xmin	[ndarray] Optimum point.
fval	[float] Optimum value.
iter	[int] Number of iterations.
funcalls	[int] Number of objective function evaluations made.

See also:

minimize_scalar

Interface to minimization algorithms for scalar univariate functions. See the 'Brent' *method* in particular.

Notes

Uses inverse parabolic interpolation when possible to speed up convergence of golden section method.

Does not ensure that the minimum lies in the range specified by *brack*. See *fminbound*.

Examples

We illustrate the behaviour of the function when *brack* is of size 2 and 3 respectively. In the case where *brack* is of the form (xa,xb), we can see for the given values, the output need not necessarily lie in the range (xa,xb).

```
>>> def f(x):
...     return x**2
```

```
>>> from scipy import optimize
```

```
>>> minimum = optimize.brent(f,brack=(1,2))
>>> minimum
0.0
>>> minimum = optimize.brent(f,brack=(-1,0.5,2))
>>> minimum
-2.7755575615628914e-17
```

scipy.optimize.golden

scipy.optimize.**golden**(*func*, *args=()*, *brack=None*, *tol=1.4901161193847656e-08*, *full_output=0*, *maxiter=5000*)

Return the minimum of a function of one variable using golden section method.

Given a function of one variable and a possible bracketing interval, return the minimum of the function isolated to a fractional precision of tol.

Parameters

func	[callable func(x,*args)] Objective function to minimize.
args	[tuple, optional] Additional arguments (if present), passed to func.
brack	[tuple, optional] Triple (a,b,c), where (a<b<c) and func(b) < func(a),func(c). If bracket consists of two numbers (a, c), then they are assumed to be a starting interval for a downhill bracket search (see *bracket*); it doesn't always mean that obtained solution will satisfy a<=x<=c.
tol	[float, optional] x tolerance stop criterion
full_output	[bool, optional] If True, return optional outputs.
maxiter	[int] Maximum number of iterations to perform.

See also:

minimize_scalar

Interface to minimization algorithms for scalar univariate functions. See the 'Golden' *method* in particular.

Notes

Uses analog of bisection method to decrease the bracketed interval.

Examples

We illustrate the behaviour of the function when *brack* is of size 2 and 3, respectively. In the case where *brack* is of the form (xa,xb), we can see for the given values, the output need not necessarily lie in the range `(xa, xb)`.

```
>>> def f(x):
...     return x**2
```

```
>>> from scipy import optimize
```

```
>>> minimum = optimize.golden(f, brack=(1, 2))
>>> minimum
1.5717277788484873e-162
>>> minimum = optimize.golden(f, brack=(-1, 0.5, 2))
>>> minimum
-1.5717277788484873e-162
```

Least-squares

leastsq(func, x0[, args, Dfun, full_output, …])	Minimize the sum of squares of a set of equations.

scipy.optimize.leastsq

scipy.optimize.**leastsq**(*func*, *x0*, *args=()*, *Dfun=None*, *full_output=0*, *col_deriv=0*, *ftol=1.49012e-08*, *xtol=1.49012e-08*, *gtol=0.0*, *maxfev=0*, *epsfcn=None*, *factor=100*, *diag=None*)

Minimize the sum of squares of a set of equations.

```
x = arg min(sum(func(y)**2,axis=0))
         y
```

Parameters

func [callable] Should take at least one (possibly length `N` vector) argument and returns `M` floating point numbers. It must not return NaNs or fitting might fail. `M` must be greater than or equal to `N`.

x0 [ndarray] The starting estimate for the minimization.

args [tuple, optional] Any extra arguments to func are placed in this tuple.

Dfun [callable, optional] A function or method to compute the Jacobian of func with derivatives across the rows. If this is None, the Jacobian will be estimated.

full_output [bool, optional] non-zero to return all optional outputs.

col_deriv [bool, optional] non-zero to specify that the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

ftol [float, optional] Relative error desired in the sum of squares.

xtol [float, optional] Relative error desired in the approximate solution.

gtol [float, optional] Orthogonality desired between the function vector and the columns of the Jacobian.

maxfev [int, optional] The maximum number of calls to the function. If *Dfun* is provided, then the default *maxfev* is 100*(N+1) where N is the number of elements in x0, otherwise the default *maxfev* is 200*(N+1).

epsfcn [float, optional] A variable used in determining a suitable step length for the forward- difference approximation of the Jacobian (for Dfun=None). Normally the actual step length will be sqrt(epsfcn)*x If epsfcn is less than the machine precision, it is assumed that the relative errors are of the order of the machine precision.

factor [float, optional] A parameter determining the initial step bound (`factor * || diag * x||`). Should be in interval `(0.1, 100)`.

diag [sequence, optional] N positive entries that serve as a scale factors for the variables.

Returns

x [ndarray] The solution (or the result of the last iteration for an unsuccessful call).

cov_x [ndarray] The inverse of the Hessian. *fjac* and *ipvt* are used to construct an estimate of the Hessian. A value of None indicates a singular matrix, which means the curvature in parameters *x* is numerically flat. To obtain the covariance matrix of the parameters *x*, *cov_x* must be multiplied by the variance of the residuals – see curve_fit.

infodict [dict] a dictionary of optional outputs with the keys:

- **`nfev`** The number of function calls
- **`fvec`** The function evaluated at the output
- **`fjac`** A permutation of the R matrix of a QR factorization of the final approximate Jacobian matrix, stored column wise. Together with ipvt, the covariance of the estimate can be approximated.
- **`ipvt`** An integer array of length N which defines a permutation matrix, p, such that fjac*p = q*r, where r is upper triangular with diagonal elements of nonincreasing magnitude. Column j of p is column ipvt(j) of the identity matrix.
- **`qtf`** The vector (transpose(q) * fvec).

mesg [str] A string message giving information about the cause of failure.

ier [int] An integer flag. If it is equal to 1, 2, 3 or 4, the solution was found. Otherwise, the solution was not found. In either case, the optional output variable 'mesg' gives more information.

See also:

`least_squares`

Newer interface to solve nonlinear least-squares problems with bounds on the variables. See `method=='lm'` in particular.

Notes

"leastsq" is a wrapper around MINPACK's lmdif and lmder algorithms.

cov_x is a Jacobian approximation to the Hessian of the least squares objective function. This approximation assumes that the objective function is based on the difference between some observed target data (ydata) and a (non-linear) function of the parameters *f(xdata, params)*

```
func(params) = ydata - f(xdata, params)
```

so that the objective function is

```
  min   sum((ydata - f(xdata, params))**2, axis=0)
params
```

The solution, *x*, is always a 1-D array, regardless of the shape of *x0*, or whether *x0* is a scalar.

Examples

```
>>> from scipy.optimize import leastsq
>>> def func(x):
...     return 2*(x-3)**2+1
>>> leastsq(func, 0)
(array([2.99999999]), 1)
```

Root finding

General nonlinear solvers:

fsolve(func, x0[, args, fprime, …])	Find the roots of a function.
broyden1(F, xin[, iter, alpha, …])	Find a root of a function, using Broyden's first Jacobian approximation.
broyden2(F, xin[, iter, alpha, …])	Find a root of a function, using Broyden's second Jacobian approximation.

scipy.optimize.fsolve

scipy.optimize.**fsolve**(*func*, *x0*, *args=()*, *fprime=None*, *full_output=0*, *col_deriv=0*, *xtol=1.49012e-08*, *maxfev=0*, *band=None*, *epsfcn=None*, *factor=100*, *diag=None*)

Find the roots of a function.

Return the roots of the (non-linear) equations defined by `func(x) = 0` given a starting estimate.

Parameters

func [callable `f(x, *args)`] A function that takes at least one (possibly vector) argument, and returns a value of the same length.

x0 [ndarray] The starting estimate for the roots of `func(x) = 0`.

args [tuple, optional] Any extra arguments to *func*.

fprime [callable `f(x, *args)`, optional] A function to compute the Jacobian of *func* with derivatives across the rows. By default, the Jacobian will be estimated.

full_output [bool, optional] If True, return optional outputs.

col_deriv [bool, optional] Specify whether the Jacobian function computes derivatives down the columns (faster, because there is no transpose operation).

xtol [float, optional] The calculation will terminate if the relative error between two consecutive iterates is at most *xtol*.

maxfev [int, optional] The maximum number of calls to the function. If zero, then `100*(N+1)` is the maximum where N is the number of elements in *x0*.

band [tuple, optional] If set to a two-sequence containing the number of sub- and super-diagonals within the band of the Jacobi matrix, the Jacobi matrix is considered banded (only for `fprime=None`).

epsfcn [float, optional] A suitable step length for the forward-difference approximation of the Jacobian (for `fprime=None`). If *epsfcn* is less than the machine precision, it is assumed that the relative errors in the functions are of the order of the machine precision.

factor [float, optional] A parameter determining the initial step bound (`factor * || diag * x||`). Should be in the interval `(0.1, 100)`.

diag [sequence, optional] N positive entries that serve as a scale factors for the variables.

Returns

x [ndarray] The solution (or the result of the last iteration for an unsuccessful call).

infodict [dict] A dictionary of optional outputs with the keys:

- **nfev** number of function calls
- **njev** number of Jacobian calls
- **fvec** function evaluated at the output
- **fjac** the orthogonal matrix, q, produced by the QR factorization of the final approximate Jacobian matrix, stored column wise
- **r** upper triangular matrix produced by QR factorization of the same matrix
- **qtf** the vector `(transpose(q) * fvec)`

ier [int] An integer flag. Set to 1 if a solution was found, otherwise refer to *mesg* for more information.

mesg [str] If no solution is found, *mesg* details the cause of failure.

See also:

`root`

Interface to root finding algorithms for multivariate functions. See the `method=='hybr'` in particular.

Notes

`fsolve` is a wrapper around MINPACK's hybrd and hybrj algorithms.

Examples

Find a solution to the system of equations: `x0*cos(x1) = 4, x1*x0 - x1 = 5`.

```
>>> from scipy.optimize import fsolve
>>> def func(x):
...     return [x[0] * np.cos(x[1]) - 4,
...             x[1] * x[0] - x[1] - 5]
>>> root = fsolve(func, [1, 1])
>>> root
array([6.50409711, 0.90841421])
>>> np.isclose(func(root), [0.0, 0.0])  # func(root) should be almost 0.0.
array([ True,  True])
```

scipy.optimize.broyden1

scipy.optimize.**broyden1**(*F*, *xin*, *iter=None*, *alpha=None*, *reduction_method='restart'*, *max_rank=None*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using Broyden's first Jacobian approximation.

This method is also known as "Broyden's good method".

Parameters

F [function(x) -> f] Function whose root to find; should take and return an array-like object.

xin [array_like] Initial guess for the solution

alpha [float, optional] Initial guess for the Jacobian is `(-1/alpha)`.

reduction_method

[str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form `(method, param1, param2, ...)` that gives the name of the method and values for additional parameters.

Methods available:

- `restart`: drop all matrix columns. Has no extra parameters.
- `simple`: drop oldest matrix column. Has no extra parameters.
- `svd`: keep only the most significant SVD components. Takes an extra parameter, `to_retain`, which determines the number of SVD components to retain when rank reduction is done. Default is `max_rank - 2`.

max_rank [int, optional] Maximum rank for the Broyden matrix. Default is infinity (i.e., no rank reduction).

iter [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol [float, optional] Relative tolerance for the residual. If omitted, not used.

x_tol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol [float, optional] Relative minimum step size. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search

[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol [ndarray] An array (of similar array type as *x0*) containing the final solution.

Raises

NoConvergence

When a solution was not found.

See also:

root

Interface to root finding algorithms for multivariate functions. See `method=='broyden1'` in particular.

Notes

This algorithm implements the inverse Jacobian Quasi-Newton update

$$H_+ = H + (dx - Hdf)dx^\dagger H/(dx^\dagger Hdf)$$

which corresponds to Broyden's first Jacobian update

$$J_+ = J + (df - Jdx)dx^\dagger/dx^\dagger dx$$

References

[1]

Examples

The following functions define a system of nonlinear equations

```
>>> def fun(x):
...     return [x[0]  + 0.5 * (x[0] - x[1])**3 - 1.0,
...             0.5 * (x[1] - x[0])**3 + x[1]]
```

A solution can be obtained as follows.

```
>>> from scipy import optimize
>>> sol = optimize.broyden1(fun, [0, 0])
>>> sol
array([0.84116396, 0.15883641])
```

scipy.optimize.broyden2

scipy.optimize.**broyden2**(*F*, *xin*, *iter=None*, *alpha=None*, *reduction_method='restart'*, *max_rank=None*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using Broyden's second Jacobian approximation.

This method is also known as "Broyden's bad method".

Parameters

F [function(x) -> f] Function whose root to find; should take and return an array-like object.

xin [array_like] Initial guess for the solution

alpha [float, optional] Initial guess for the Jacobian is `(-1/alpha)`.

reduction_method

[str or tuple, optional] Method used in ensuring that the rank of the Broyden matrix stays low. Can either be a string giving the name of the method, or a tuple of the form `(method, param1, param2, ...)` that gives the name of the method and values for additional parameters.
Methods available:

- `restart`: drop all matrix columns. Has no extra parameters.
- `simple`: drop oldest matrix column. Has no extra parameters.
- `svd`: keep only the most significant SVD components. Takes an extra parameter, `to_retain`, which determines the number of SVD components to retain when rank reduction is done. Default is `max_rank - 2`.

max_rank [int, optional] Maximum rank for the Broyden matrix. Default is infinity (i.e., no rank reduction).

iter [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol [float, optional] Relative tolerance for the residual. If omitted, not used.

x_tol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol [float, optional] Relative minimum step size. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search [{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol [ndarray] An array (of similar array type as *x0*) containing the final solution.

Raises

NoConvergence When a solution was not found.

See also:

root

Interface to root finding algorithms for multivariate functions. See `method=='broyden2'` in particular.

Notes

This algorithm implements the inverse Jacobian Quasi-Newton update

$$H_+ = H + (dx - Hdf)df^\dagger/(df^\dagger df)$$

corresponding to Broyden's second method.

References

[1]

Examples

The following functions define a system of nonlinear equations

```
>>> def fun(x):
...     return [x[0]  + 0.5 * (x[0] - x[1])**3 - 1.0,
...             0.5 * (x[1] - x[0])**3 + x[1]]
```

A solution can be obtained as follows.

```
>>> from scipy import optimize
>>> sol = optimize.broyden2(fun, [0, 0])
>>> sol
array([0.84116365, 0.15883529])
```

Large-scale nonlinear solvers:

newton_krylov(F, xin[, iter, rdiff, method, …])	Find a root of a function, using Krylov approximation for inverse Jacobian.
anderson(F, xin[, iter, alpha, w0, M, …])	Find a root of a function, using (extended) Anderson mixing.

scipy.optimize.newton_krylov

scipy.optimize.**newton_krylov**(*F*, *xin*, *iter=None*, *rdiff=None*, *method='lgmres'*, *inner_maxiter=20*, *inner_M=None*, *outer_k=10*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using Krylov approximation for inverse Jacobian.

This method is suitable for solving large-scale problems.

Parameters

F [function(x) -> f] Function whose root to find; should take and return an array-like object.

xin [array_like] Initial guess for the solution

rdiff [float, optional] Relative step size to use in numerical differentiation.

method [{'lgmres', 'gmres', 'bicgstab', 'cgs', 'minres'} or function] Krylov method to use to approximate the Jacobian. Can be a string, or a function implementing the same interface as the iterative solvers in *scipy.sparse.linalg*.
The default is *scipy.sparse.linalg.lgmres*.

inner_maxiter
[int, optional] Parameter to pass to the "inner" Krylov solver: maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

inner_M [LinearOperator or InverseJacobian] Preconditioner for the inner Krylov iteration. Note that you can use also inverse Jacobians as (adaptive) preconditioners. For example,

```
>>> from scipy.optimize.nonlin import BroydenFirst,␣
↪KrylovJacobian
>>> from scipy.optimize.nonlin import InverseJacobian
>>> jac = BroydenFirst()
>>> kjac = KrylovJacobian(inner_M=InverseJacobian(jac))
```

If the preconditioner has a method named 'update', it will be called as `update(x, f)` after each nonlinear step, with `x` giving the current point, and `f` the current function value.

outer_k [int, optional] Size of the subspace kept across LGMRES nonlinear iterations. See *scipy.sparse.linalg.lgmres* for details.

inner_kwargs
[kwargs] Keyword parameters for the "inner" Krylov solver (defined with *method*). Parameter names must start with the *inner_* prefix which will be stripped before passing on the inner method. See, e.g., *scipy.sparse.linalg.gmres* for details.

iter [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol [float, optional] Relative tolerance for the residual. If omitted, not used.

x_tol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol [float, optional] Relative minimum step size. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search
[{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol [ndarray] An array (of similar array type as *x0*) containing the final solution.

Raises

NoConvergence
When a solution was not found.

See also:

root

Interface to root finding algorithms for multivariate functions. See `method=='krylov'` in particular.

scipy.sparse.linalg.gmres

scipy.sparse.linalg.lgmres

Notes

This function implements a Newton-Krylov solver. The basic idea is to compute the inverse of the Jacobian with an iterative Krylov method. These methods require only evaluating the Jacobian-vector products, which are conveniently approximated by a finite difference:

$$Jv \approx (f(x + \omega * v/|v|) - f(x))/\omega$$

Due to the use of iterative matrix inverses, these methods can deal with large nonlinear problems.

SciPy's *scipy.sparse.linalg* module offers a selection of Krylov solvers to choose from. The default here is *lgmres*, which is a variant of restarted GMRES iteration that reuses some of the information obtained in the previous Newton steps to invert Jacobians in subsequent steps.

For a review on Newton-Krylov methods, see for example [1], and for the LGMRES sparse inverse method, see [2].

References

[1], [2]

Examples

The following functions define a system of nonlinear equations

```
>>> def fun(x):
...     return [x[0] + 0.5 * x[1] - 1.0,
...             0.5 * (x[1] - x[0]) ** 2]
```

A solution can be obtained as follows.

```
>>> from scipy import optimize
>>> sol = optimize.newton_krylov(fun, [0, 0])
>>> sol
array([0.66731771, 0.66536458])
```

scipy.optimize.anderson

scipy.optimize.**anderson**(*F*, *xin*, *iter=None*, *alpha=None*, *w0=0.01*, *M=5*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using (extended) Anderson mixing.

The Jacobian is formed by for a 'best' solution in the space spanned by last *M* vectors. As a result, only a MxM matrix inversions and MxN multiplications are required. [Ey]

Parameters

F	[function(x) -> f] Function whose root to find; should take and return an array-like object.
xin	[array_like] Initial guess for the solution
alpha	[float, optional] Initial guess for the Jacobian is (-1/alpha).
M	[float, optional] Number of previous vectors to retain. Defaults to 5.
w0	[float, optional] Regularization parameter for numerical stability. Compared to unity, good values of the order of 0.01.

iter [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol [float, optional] Relative tolerance for the residual. If omitted, not used.

x_tol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol [float, optional] Relative minimum step size. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search [{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol [ndarray] An array (of similar array type as *x0*) containing the final solution.

Raises

NoConvergence
When a solution was not found.

See also:

`root`

Interface to root finding algorithms for multivariate functions. See `method=='anderson'` in particular.

References

[Ey]

Examples

The following functions define a system of nonlinear equations

```
>>> def fun(x):
...     return [x[0]  + 0.5 * (x[0] - x[1])**3 - 1.0,
...             0.5 * (x[1] - x[0])**3 + x[1]]
```

A solution can be obtained as follows.

```
>>> from scipy import optimize
>>> sol = optimize.anderson(fun, [0, 0])
>>> sol
array([0.84116588, 0.15883789])
```

Simple iteration solvers:

excitingmixing(F, xin[, iter, alpha, …])	Find a root of a function, using a tuned diagonal Jacobian approximation.
linearmixing(F, xin[, iter, alpha, verbose, …])	Find a root of a function, using a scalar Jacobian approximation.
diagbroyden(F, xin[, iter, alpha, verbose, …])	Find a root of a function, using diagonal Broyden Jacobian approximation.

scipy.optimize.excitingmixing

scipy.optimize.**excitingmixing**(*F*, *xin*, *iter=None*, *alpha=None*, *alphamax=1.0*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using a tuned diagonal Jacobian approximation.

The Jacobian matrix is diagonal and is tuned on each iteration.

Warning: This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

Parameters

F [function(x) -> f] Function whose root to find; should take and return an array-like object.
xin [array_like] Initial guess for the solution
alpha [float, optional] Initial Jacobian approximation is (-1/alpha).
alphamax [float, optional] The entries of the diagonal Jacobian are kept in the range `[alpha, alphamax]`.
iter [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
verbose [bool, optional] Print status to stdout on every iteration.
maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.
f_tol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
f_rtol [float, optional] Relative tolerance for the residual. If omitted, not used.
x_tol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
x_rtol [float, optional] Relative minimum step size. If omitted, not used.
tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.
line_search [{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.
callback [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol [ndarray] An array (of similar array type as *x0*) containing the final solution.

Raises

NoConvergence
When a solution was not found.

See also:

`root`

Interface to root finding algorithms for multivariate functions. See `method=='excitingmixing'` in particular.

scipy.optimize.linearmixing

`scipy.optimize.linearmixing(F, xin, iter=None, alpha=None, verbose=False, maxiter=None, f_tol=None, f_rtol=None, x_tol=None, x_rtol=None, tol_norm=None, line_search='armijo', callback=None, **kw)`

Find a root of a function, using a scalar Jacobian approximation.

Warning: This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

Parameters

F [function(x) -> f] Function whose root to find; should take and return an array-like object.
xin [array_like] Initial guess for the solution
alpha [float, optional] The Jacobian approximation is (-1/alpha).
iter [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.
verbose [bool, optional] Print status to stdout on every iteration.
maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.
f_tol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.
f_rtol [float, optional] Relative tolerance for the residual. If omitted, not used.
x_tol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.
x_rtol [float, optional] Relative minimum step size. If omitted, not used.
tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.
line_search [{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.
callback [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol [ndarray] An array (of similar array type as *x0*) containing the final solution.

Raises

NoConvergence
When a solution was not found.

See also:

`root`

Interface to root finding algorithms for multivariate functions. See `method=='linearmixing'` in particular.

scipy.optimize.diagbroyden

scipy.optimize.**diagbroyden**(*F*, *xin*, *iter=None*, *alpha=None*, *verbose=False*, *maxiter=None*, *f_tol=None*, *f_rtol=None*, *x_tol=None*, *x_rtol=None*, *tol_norm=None*, *line_search='armijo'*, *callback=None*, ***kw*)

Find a root of a function, using diagonal Broyden Jacobian approximation.

The Jacobian approximation is derived from previous iterations, by retaining only the diagonal of Broyden matrices.

Warning: This algorithm may be useful for specific problems, but whether it will work may depend strongly on the problem.

Parameters

F [function(x) -> f] Function whose root to find; should take and return an array-like object.

xin [array_like] Initial guess for the solution

alpha [float, optional] Initial guess for the Jacobian is (-1/alpha).

iter [int, optional] Number of iterations to make. If omitted (default), make as many as required to meet tolerances.

verbose [bool, optional] Print status to stdout on every iteration.

maxiter [int, optional] Maximum number of iterations to make. If more are needed to meet convergence, *NoConvergence* is raised.

f_tol [float, optional] Absolute tolerance (in max-norm) for the residual. If omitted, default is 6e-6.

f_rtol [float, optional] Relative tolerance for the residual. If omitted, not used.

x_tol [float, optional] Absolute minimum step size, as determined from the Jacobian approximation. If the step size is smaller than this, optimization is terminated as successful. If omitted, not used.

x_rtol [float, optional] Relative minimum step size. If omitted, not used.

tol_norm [function(vector) -> scalar, optional] Norm to use in convergence check. Default is the maximum norm.

line_search [{None, 'armijo' (default), 'wolfe'}, optional] Which type of a line search to use to determine the step size in the direction given by the Jacobian approximation. Defaults to 'armijo'.

callback [function, optional] Optional callback function. It is called on every iteration as `callback(x, f)` where *x* is the current solution and *f* the corresponding residual.

Returns

sol [ndarray] An array (of similar array type as *x0*) containing the final solution.

Raises

NoConvergence When a solution was not found.

See also:

root

Interface to root finding algorithms for multivariate functions. See `method=='diagbroyden'` in particular.

Examples

The following functions define a system of nonlinear equations

```
>>> def fun(x):
...     return [x[0]  + 0.5 * (x[0] - x[1])**3 - 1.0,
...             0.5 * (x[1] - x[0])**3 + x[1]]
```

A solution can be obtained as follows.

```
>>> from scipy import optimize
>>> sol = optimize.diagbroyden(fun, [0, 0])
>>> sol
array([0.84116403, 0.15883384])
```

Additional information on the nonlinear solvers

3.3.20 Nonlinear solvers

This is a collection of general-purpose nonlinear multidimensional solvers. These solvers find *x* for which *F(x) = 0*. Both *x* and *F* can be multidimensional.

Routines

Large-scale nonlinear solvers:

newton_krylov(F, xin[, iter, rdiff, method, …])	Find a root of a function, using Krylov approximation for inverse Jacobian.
anderson(F, xin[, iter, alpha, w0, M, …])	Find a root of a function, using (extended) Anderson mixing.

General nonlinear solvers:

broyden1(F, xin[, iter, alpha, …])	Find a root of a function, using Broyden's first Jacobian approximation.
broyden2(F, xin[, iter, alpha, …])	Find a root of a function, using Broyden's second Jacobian approximation.

Simple iterations:

excitingmixing(F, xin[, iter, alpha, …])	Find a root of a function, using a tuned diagonal Jacobian approximation.
linearmixing(F, xin[, iter, alpha, verbose, …])	Find a root of a function, using a scalar Jacobian approximation.

continues on next page

Table 154 – continued from previous page

diagbroyden(F, xin[, iter, alpha, verbose, …])	Find a root of a function, using diagonal Broyden Jacobian approximation.

Examples

Small problem

```
>>> def F(x):
...     return np.cos(x) + x[::-1] - [1, 2, 3, 4]
>>> import scipy.optimize
>>> x = scipy.optimize.broyden1(F, [1,1,1,1], f_tol=1e-14)
>>> x
array([ 4.04674914,  3.91158389,  2.71791677,  1.61756251])
>>> np.cos(x) + x[::-1]
array([ 1.,  2.,  3.,  4.])
```

Large problem

Suppose that we needed to solve the following integrodifferential equation on the square $[0,1] \times [0,1]$:

$$\nabla^2 P = 10 \left(\int_0^1 \int_0^1 \cosh(P)\, dx\, dy \right)^2$$

with $P(x,1) = 1$ and $P = 0$ elsewhere on the boundary of the square.

The solution can be found using the *newton_krylov* solver:

```
import numpy as np
from scipy.optimize import newton_krylov
from numpy import cosh, zeros_like, mgrid, zeros

# parameters
nx, ny = 75, 75
hx, hy = 1./(nx-1), 1./(ny-1)

P_left, P_right = 0, 0
P_top, P_bottom = 1, 0

def residual(P):
    d2x = zeros_like(P)
    d2y = zeros_like(P)

    d2x[1:-1] = (P[2:]   - 2*P[1:-1] + P[:-2]) / hx/hx
    d2x[0]    = (P[1]    - 2*P[0]    + P_left)/hx/hx
    d2x[-1]   = (P_right - 2*P[-1]   + P[-2])/hx/hx

    d2y[:,1:-1] = (P[:,2:] - 2*P[:,1:-1] + P[:,:-2])/hy/hy
    d2y[:,0]    = (P[:,1]  - 2*P[:,0]    + P_bottom)/hy/hy
    d2y[:,-1]   = (P_top   - 2*P[:,-1]   + P[:,-2])/hy/hy

    return d2x + d2y - 10*cosh(P).mean()**2

# solve
```

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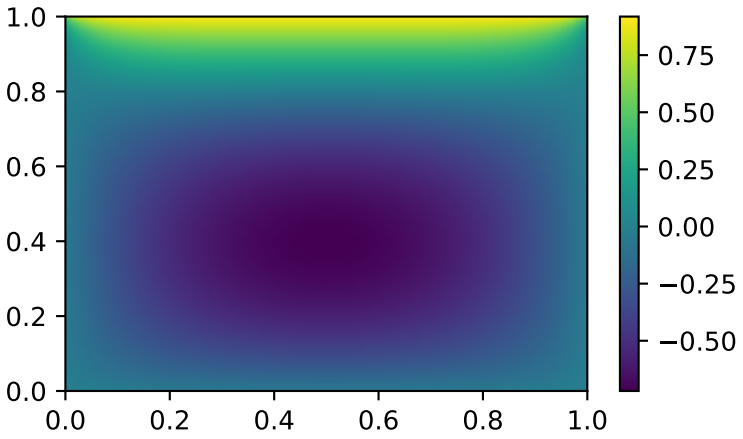
```
guess = zeros((nx, ny), float)
sol = newton_krylov(residual, guess, method='lgmres', verbose=1)
print('Residual: %g' % abs(residual(sol)).max())

# visualize
import matplotlib.pyplot as plt
x, y = mgrid[0:1:(nx*1j), 0:1:(ny*1j)]
plt.pcolormesh(x, y, sol, shading='gouraud')
plt.colorbar()
plt.show()
```



3.3.21 Cython optimize zeros API

The underlying C functions for the following root finders can be accessed directly using Cython:

- *bisect*
- *ridder*
- *brenth*
- *brentq*

The Cython API for the zeros functions is similar except there is no `disp` argument. Import the zeros functions using `cimport` from *scipy.optimize.cython_optimize*.

```
from scipy.optimize.cython_optimize cimport bisect, ridder, brentq, brenth
```

Callback signature

The zeros functions in *cython_optimize* expect a callback that takes a double for the scalar independent variable as the 1st argument and a user defined `struct` with any extra parameters as the 2nd argument.

```
double (*callback_type)(double, void*)
```

Examples

Usage of *cython_optimize* requires Cython to write callbacks that are compiled into C. For more information on compiling Cython, see the Cython Documentation.

These are the basic steps:

1. Create a Cython `.pyx` file, for example: `myexample.pyx`.
2. Import the desired root finder from *cython_optimize*.
3. Write the callback function, and call the selected zeros function passing the callback, any extra arguments, and the other solver parameters.

```
from scipy.optimize.cython_optimize cimport brentq

# import math from Cython
from libc cimport math

myargs = {'C0': 1.0, 'C1': 0.7}  # a dictionary of extra arguments
XLO, XHI = 0.5, 1.0  # lower and upper search boundaries
XTOL, RTOL, MITR = 1e-3, 1e-3, 10  # other solver parameters

# user-defined struct for extra parameters
ctypedef struct test_params:
    double C0
    double C1


# user-defined callback
cdef double f(double x, void *args):
    cdef test_params *myargs = <test_params *> args
    return myargs.C0 - math.exp(-(x - myargs.C1))


# Cython wrapper function
cdef double brentq_wrapper_example(dict args, double xa, double xb,
                                   double xtol, double rtol, int mitr):
    # Cython automatically casts dictionary to struct
    cdef test_params myargs = args
    return brentq(
        f, xa, xb, <test_params *> &myargs, xtol, rtol, mitr, NULL)


# Python function
def brentq_example(args=myargs, xa=XLO, xb=XHI, xtol=XTOL, rtol=RTOL,
                   mitr=MITR):
```

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```
    '''Calls Cython wrapper from Python.'''
    return brentq_wrapper_example(args, xa, xb, xtol, rtol, mitr)
```

4. If you want to call your function from Python, create a Cython wrapper, and a Python function that calls the wrapper, or use `cpdef`. Then, in Python, you can import and run the example.

```
from myexample import brentq_example

x = brentq_example()
# 0.6999942848231314
```

5. Create a Cython `.pxd` file if you need to export any Cython functions.

Full output

The functions in *cython_optimize* can also copy the full output from the solver to a C `struct` that is passed as its last argument. If you don't want the full output, just pass `NULL`. The full output `struct` must be type `zeros_full_output`, which is defined in *scipy.optimize.cython_optimize* with the following fields:

- `int funcalls`: number of function calls
- `int iterations`: number of iterations
- `int error_num`: error number
- `double root`: root of function

The root is copied by *cython_optimize* to the full output `struct`. An error number of -1 means a sign error, -2 means a convergence error, and 0 means the solver converged. Continuing from the previous example:

```
from scipy.optimize.cython_optimize cimport zeros_full_output


# cython brentq solver with full output
cdef brent_full_output brentq_full_output_wrapper_example(
        dict args, double xa, double xb, double xtol, double rtol,
        int mitr):
    cdef test_params myargs = args
    cdef zeros_full_output my_full_output
    # use my_full_output instead of NULL
    brentq(f, xa, xb, &myargs, xtol, rtol, mitr, &my_full_output)
    return my_full_output


# Python function
def brent_full_output_example(args=myargs, xa=XLO, xb=XHI, xtol=XTOL,
                              rtol=RTOL, mitr=MITR):
    '''Returns full output'''
    return brentq_full_output_wrapper_example(args, xa, xb, xtol, rtol,
                                              mitr)

result = brent_full_output_example()
# {'error_num': 0,
#  'funcalls': 6,
```

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```
#  'iterations': 5,
#  'root': 0.6999942848231314}
```

3.3.22 Signal processing (`scipy.signal`)

Convolution

convolve(in1, in2[, mode, method])	Convolve two N-dimensional arrays.
correlate(in1, in2[, mode, method])	Cross-correlate two N-dimensional arrays.
fftconvolve(in1, in2[, mode, axes])	Convolve two N-dimensional arrays using FFT.
oaconvolve(in1, in2[, mode, axes])	Convolve two N-dimensional arrays using the overlap-add method.
convolve2d(in1, in2[, mode, boundary, fillvalue])	Convolve two 2-dimensional arrays.
correlate2d(in1, in2[, mode, boundary, …])	Cross-correlate two 2-dimensional arrays.
sepfir2d(input, hrow, hcol)	Convolve with a 2-D separable FIR filter.
choose_conv_method(in1, in2[, mode, measure])	Find the fastest convolution/correlation method.
correlation_lags(in1_len, in2_len[, mode])	Calculates the lag / displacement indices array for 1D cross-correlation.

scipy.signal.convolve

scipy.signal.**convolve**(*in1*, *in2*, *mode='full'*, *method='auto'*)

Convolve two N-dimensional arrays.

Convolve *in1* and *in2*, with the output size determined by the *mode* argument.

Parameters

in1 [array_like] First input.

in2 [array_like] Second input. Should have the same number of dimensions as *in1*.

mode [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:

- **full** The output is the full discrete linear convolution of the inputs. (Default)
- **valid** The output consists only of those elements that do not rely on the zero-padding. In 'valid' mode, either *in1* or *in2* must be at least as large as the other in every dimension.
- **same** The output is the same size as *in1*, centered with respect to the 'full' output.

method [str {'auto', 'direct', 'fft'}, optional] A string indicating which method to use to calculate the convolution.

- **direct** The convolution is determined directly from sums, the definition of convolution.
- **fft** The Fourier Transform is used to perform the convolution by calling *fftconvolve*.
- **auto** Automatically chooses direct or Fourier method based on an estimate of which is faster (default). See Notes for more detail.
  New in version 0.19.0.

Returns

convolve [array] An N-dimensional array containing a subset of the discrete linear convolution of *in1* with *in2*.

See also:

numpy.polymul

performs polynomial multiplication (same operation, but also accepts poly1d objects)

choose_conv_method

chooses the fastest appropriate convolution method

fftconvolve

Always uses the FFT method.

oaconvolve

Uses the overlap-add method to do convolution, which is generally faster when the input arrays are large and significantly different in size.

Notes

By default, *convolve* and *correlate* use `method='auto'`, which calls *choose_conv_method* to choose the fastest method using pre-computed values (*choose_conv_method* can also measure real-world timing with a keyword argument). Because *fftconvolve* relies on floating point numbers, there are certain constraints that may force *method=direct* (more detail in *choose_conv_method* docstring).

Examples

Smooth a square pulse using a Hann window:

```
>>> from scipy import signal
>>> sig = np.repeat([0., 1., 0.], 100)
>>> win = signal.windows.hann(50)
>>> filtered = signal.convolve(sig, win, mode='same') / sum(win)
```

```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_win, ax_filt) = plt.subplots(3, 1, sharex=True)
>>> ax_orig.plot(sig)
>>> ax_orig.set_title('Original pulse')
>>> ax_orig.margins(0, 0.1)
>>> ax_win.plot(win)
>>> ax_win.set_title('Filter impulse response')
>>> ax_win.margins(0, 0.1)
>>> ax_filt.plot(filtered)
>>> ax_filt.set_title('Filtered signal')
>>> ax_filt.margins(0, 0.1)
>>> fig.tight_layout()
>>> fig.show()
```

scipy.signal.correlate

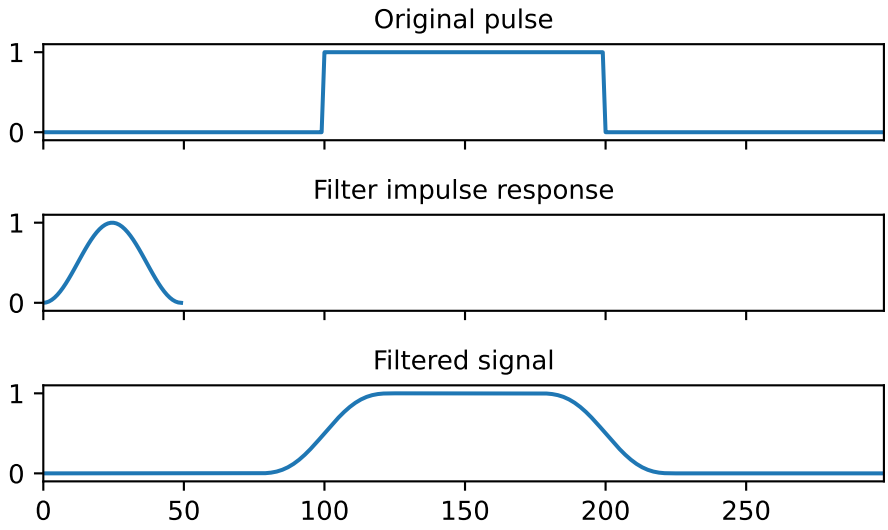
scipy.signal.**correlate**(*in1*, *in2*, *mode='full'*, *method='auto'*)

Cross-correlate two N-dimensional arrays.

Cross-correlate *in1* and *in2*, with the output size determined by the *mode* argument.

Parameters

in1	[array_like] First input.
in2	[array_like] Second input. Should have the same number of dimensions as *in1*.
mode	[str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:



	full	The output is the full discrete linear cross-correlation of the inputs. (Default)
	valid	The output consists only of those elements that do not rely on the zero-padding. In 'valid' mode, either *in1* or *in2* must be at least as large as the other in every dimension.
	same	The output is the same size as *in1*, centered with respect to the 'full' output.
method	[str {'auto', 'direct', 'fft'}, optional] A string indicating which method to use to calculate the correlation.	
	direct	The correlation is determined directly from sums, the definition of correlation.
	fft	The Fast Fourier Transform is used to perform the correlation more quickly (only available for numerical arrays.)
	auto	Automatically chooses direct or Fourier method based on an estimate of which is faster (default). See `convolve` Notes for more detail. New in version 0.19.0.

Returns

correlate	[array] An N-dimensional array containing a subset of the discrete linear cross-correlation of *in1* with *in2*.

See also:

`choose_conv_method`

contains more documentation on *method*.

`correlation_lags`

calculates the lag / displacement indices array for 1D cross-correlation.

Notes

The correlation z of two d-dimensional arrays x and y is defined as:

```
z[...,k,...] = sum[..., i_l, ...] x[..., i_l,...] * conj(y[..., i_l - k,..
↪.])
```

This way, if x and y are 1-D arrays and `z = correlate(x, y, 'full')` then

$$z[k] = (x * y)(k - N + 1) = \sum_{l=0}^{||x||-1} x_l y^*_{l-k+N-1}$$

for $k = 0, 1, ..., ||x|| + ||y|| - 2$

where $||x||$ is the length of `x`, $N = \max(||x||, ||y||)$, and y_m is 0 when m is outside the range of y.

`method='fft'` only works for numerical arrays as it relies on *fftconvolve*. In certain cases (i.e., arrays of objects or when rounding integers can lose precision), `method='direct'` is always used.

When using "same" mode with even-length inputs, the outputs of *correlate* and *correlate2d* differ: There is a 1-index offset between them.

Examples

Implement a matched filter using cross-correlation, to recover a signal that has passed through a noisy channel.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

```
>>> sig = np.repeat([0., 1., 1., 0., 1., 0., 0., 1.], 128)
>>> sig_noise = sig + rng.standard_normal(len(sig))
>>> corr = signal.correlate(sig_noise, np.ones(128), mode='same') / 128
```

```
>>> clock = np.arange(64, len(sig), 128)
>>> fig, (ax_orig, ax_noise, ax_corr) = plt.subplots(3, 1, sharex=True)
>>> ax_orig.plot(sig)
>>> ax_orig.plot(clock, sig[clock], 'ro')
>>> ax_orig.set_title('Original signal')
>>> ax_noise.plot(sig_noise)
>>> ax_noise.set_title('Signal with noise')
>>> ax_corr.plot(corr)
>>> ax_corr.plot(clock, corr[clock], 'ro')
>>> ax_corr.axhline(0.5, ls=':')
>>> ax_corr.set_title('Cross-correlated with rectangular pulse')
>>> ax_orig.margins(0, 0.1)
>>> fig.tight_layout()
>>> plt.show()
```

Compute the cross-correlation of a noisy signal with the original signal.

```
>>> x = np.arange(128) / 128
>>> sig = np.sin(2 * np.pi * x)
>>> sig_noise = sig + rng.standard_normal(len(sig))
```

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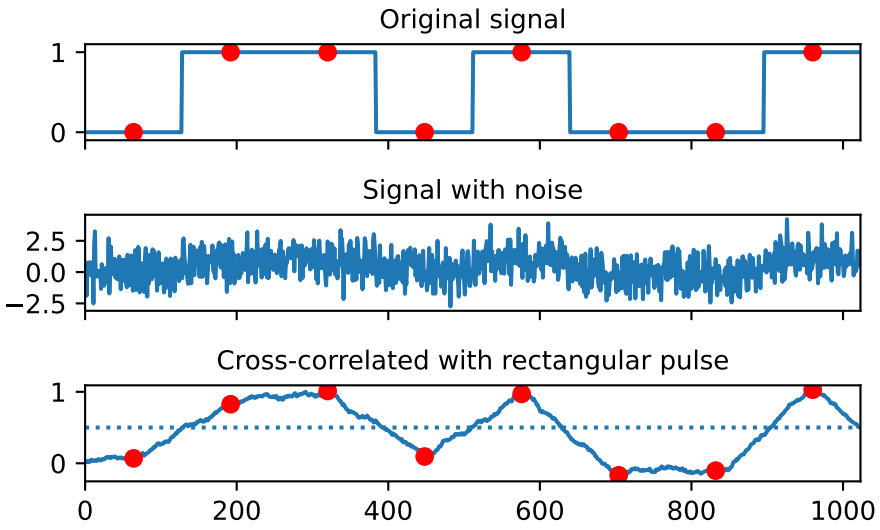


(continued from previous page)

```
>>> corr = signal.correlate(sig_noise, sig)
>>> lags = signal.correlation_lags(len(sig), len(sig_noise))
>>> corr /= np.max(corr)
```

```
>>> fig, (ax_orig, ax_noise, ax_corr) = plt.subplots(3, 1, figsize=(4.8,␣
↪4.8))
>>> ax_orig.plot(sig)
>>> ax_orig.set_title('Original signal')
>>> ax_orig.set_xlabel('Sample Number')
>>> ax_noise.plot(sig_noise)
>>> ax_noise.set_title('Signal with noise')
>>> ax_noise.set_xlabel('Sample Number')
>>> ax_corr.plot(lags, corr)
>>> ax_corr.set_title('Cross-correlated signal')
>>> ax_corr.set_xlabel('Lag')
>>> ax_orig.margins(0, 0.1)
>>> ax_noise.margins(0, 0.1)
>>> ax_corr.margins(0, 0.1)
>>> fig.tight_layout()
>>> plt.show()
```

scipy.signal.fftconvolve

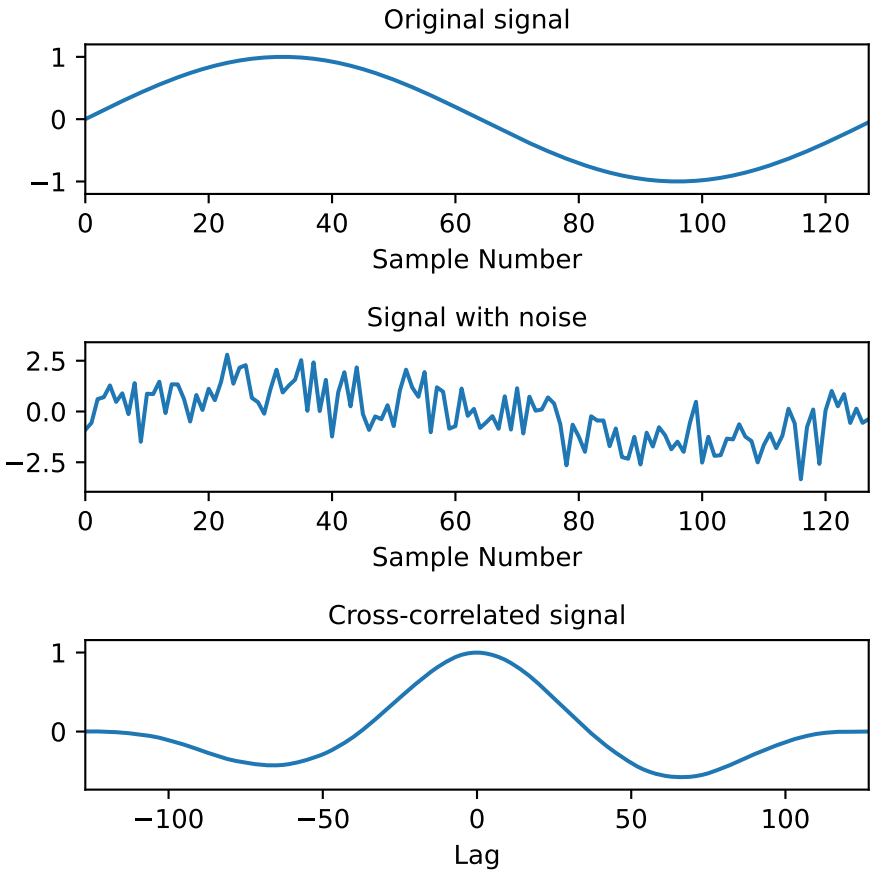
scipy.signal.**fftconvolve**(*in1*, *in2*, *mode='full'*, *axes=None*)

Convolve two N-dimensional arrays using FFT.

Convolve *in1* and *in2* using the fast Fourier transform method, with the output size determined by the *mode* argument.

This is generally much faster than *convolve* for large arrays (n > ~500), but can be slower when only a few output values are needed, and can only output float arrays (int or object array inputs will be cast to float).

As of v0.19, *convolve* automatically chooses this method or the direct method based on an estimation of which is faster.


Original signal
1
0
−1
0
20
40
60
80
100
120
Sample Number
Signal with noise
2.5
0.0
−2.5
0
20
40
60
80
100
120
Sample Number
Cross-correlated signal
1
0
−100
−50
0
50
100
Lag

Parameters

in1 [array_like] First input.

in2 [array_like] Second input. Should have the same number of dimensions as *in1*.

mode [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:

- **full** The output is the full discrete linear convolution of the inputs. (Default)
- **valid** The output consists only of those elements that do not rely on the zero-padding. In 'valid' mode, either *in1* or *in2* must be at least as large as the other in every dimension.
- **same** The output is the same size as *in1*, centered with respect to the 'full' output.

axes [int or array_like of ints or None, optional] Axes over which to compute the convolution. The default is over all axes.

Returns

out [array] An N-dimensional array containing a subset of the discrete linear convolution of *in1* with *in2*.

See also:

convolve

Uses the direct convolution or FFT convolution algorithm depending on which is faster.

oaconvolve

Uses the overlap-add method to do convolution, which is generally faster when the input arrays are large and significantly different in size.

Examples

Autocorrelation of white noise is an impulse.

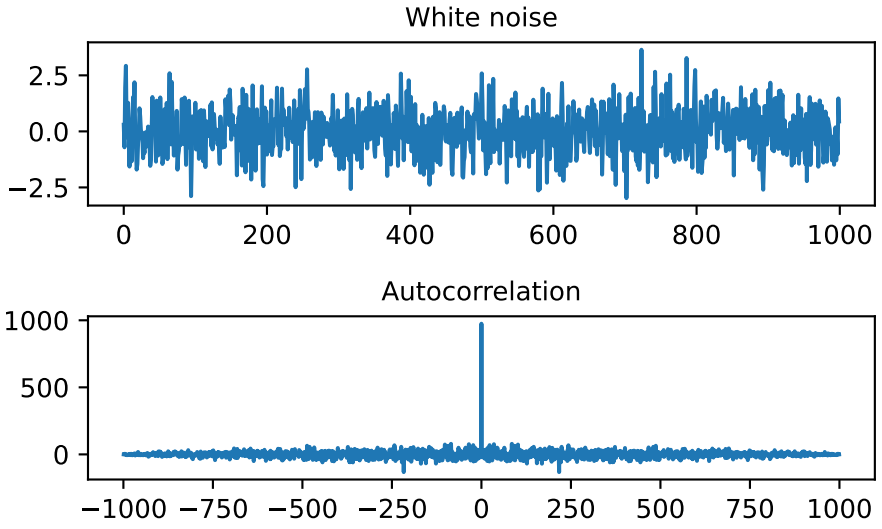
```
>>> from scipy import signal
>>> rng = np.random.default_rng()
>>> sig = rng.standard_normal(1000)
>>> autocorr = signal.fftconvolve(sig, sig[::-1], mode='full')
```

```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_mag) = plt.subplots(2, 1)
>>> ax_orig.plot(sig)
>>> ax_orig.set_title('White noise')
>>> ax_mag.plot(np.arange(-len(sig)+1,len(sig)), autocorr)
>>> ax_mag.set_title('Autocorrelation')
>>> fig.tight_layout()
>>> fig.show()
```

Gaussian blur implemented using FFT convolution. Notice the dark borders around the image, due to the zero-padding beyond its boundaries. The *convolve2d* function allows for other types of image boundaries, but is far slower.

```
>>> from scipy import misc
>>> face = misc.face(gray=True)
>>> kernel = np.outer(signal.windows.gaussian(70, 8),
...                   signal.windows.gaussian(70, 8))
>>> blurred = signal.fftconvolve(face, kernel, mode='same')
```

```
>>> fig, (ax_orig, ax_kernel, ax_blurred) = plt.subplots(3, 1,
...                                                      figsize=(6, 15))
>>> ax_orig.imshow(face, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_kernel.imshow(kernel, cmap='gray')
>>> ax_kernel.set_title('Gaussian kernel')
>>> ax_kernel.set_axis_off()
>>> ax_blurred.imshow(blurred, cmap='gray')
>>> ax_blurred.set_title('Blurred')
>>> ax_blurred.set_axis_off()
>>> fig.show()
```



scipy.signal.oaconvolve

`scipy.signal.`**`oaconvolve`**(*in1*, *in2*, *mode='full'*, *axes=None*)

Convolve two N-dimensional arrays using the overlap-add method.

Convolve *in1* and *in2* using the overlap-add method, with the output size determined by the *mode* argument.

This is generally much faster than *convolve* for large arrays (n > ~500), and generally much faster than *fftconvolve* when one array is much larger than the other, but can be slower when only a few output values are needed or when the arrays are very similar in shape, and can only output float arrays (int or object array inputs will be cast to float).

Parameters

in1 [array_like] First input.

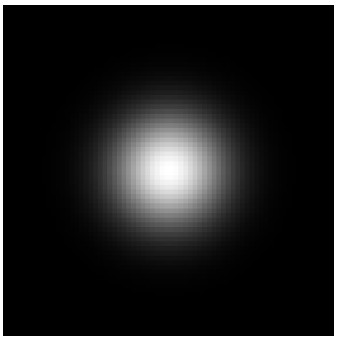
in2 [array_like] Second input. Should have the same number of dimensions as *in1*.

mode [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:

- **full** The output is the full discrete linear convolution of the inputs. (Default)
- **valid** The output consists only of those elements that do not rely on the zero-padding. In 'valid' mode, either *in1* or *in2* must be at least as large as the other in every dimension.
- **same** The output is the same size as *in1*, centered with respect to the 'full' output.

Original

Gaussian kernel



Blurred

axes [int or array_like of ints or None, optional] Axes over which to compute the convolution. The default is over all axes.

Returns

out [array] An N-dimensional array containing a subset of the discrete linear convolution of *in1* with *in2*.

See also:

convolve

Uses the direct convolution or FFT convolution algorithm depending on which is faster.

fftconvolve

An implementation of convolution using FFT.

Notes

New in version 1.4.0.

References

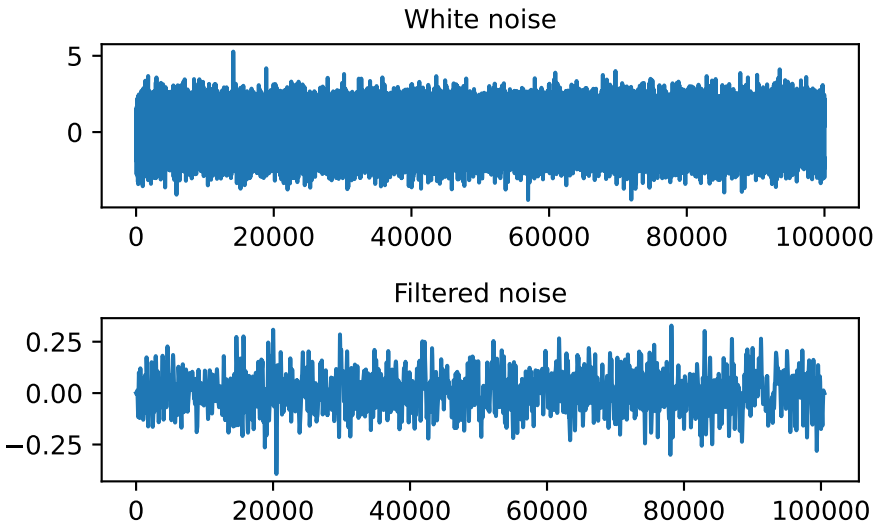
[1], [2]

Examples

Convolve a 100,000 sample signal with a 512-sample filter.

```
>>> from scipy import signal
>>> rng = np.random.default_rng()
>>> sig = rng.standard_normal(100000)
>>> filt = signal.firwin(512, 0.01)
>>> fsig = signal.oaconvolve(sig, filt)
```

```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_mag) = plt.subplots(2, 1)
>>> ax_orig.plot(sig)
>>> ax_orig.set_title('White noise')
>>> ax_mag.plot(fsig)
>>> ax_mag.set_title('Filtered noise')
>>> fig.tight_layout()
>>> fig.show()
```



scipy.signal.convolve2d

`scipy.signal.`**`convolve2d`**(*in1*, *in2*, *mode='full'*, *boundary='fill'*, *fillvalue=0*)

Convolve two 2-dimensional arrays.

Convolve *in1* and *in2* with output size determined by *mode*, and boundary conditions determined by *boundary* and *fillvalue*.

Parameters

in1 [array_like] First input.

in2 [array_like] Second input. Should have the same number of dimensions as *in1*.

mode [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:

- **`full`** The output is the full discrete linear convolution of the inputs. (Default)
- **`valid`** The output consists only of those elements that do not rely on the zero-padding. In 'valid' mode, either *in1* or *in2* must be at least as large as the other in every dimension.
- **`same`** The output is the same size as *in1*, centered with respect to the 'full' output.

boundary [str {'fill', 'wrap', 'symm'}, optional] A flag indicating how to handle boundaries:

- **`fill`** pad input arrays with fillvalue. (default)
- **`wrap`** circular boundary conditions.
- **`symm`** symmetrical boundary conditions.

fillvalue [scalar, optional] Value to fill pad input arrays with. Default is 0.

Returns

out [ndarray] A 2-dimensional array containing a subset of the discrete linear convolution of *in1* with *in2*.

Examples

Compute the gradient of an image by 2D convolution with a complex Scharr operator. (Horizontal operator is real, vertical is imaginary.) Use symmetric boundary condition to avoid creating edges at the image boundaries.

```
>>> from scipy import signal
>>> from scipy import misc
>>> ascent = misc.ascent()
>>> scharr = np.array([[ -3-3j, 0-10j,  +3 -3j],
...                    [-10+0j, 0+ 0j, +10 +0j],
...                    [ -3+3j, 0+10j,  +3 +3j]]) # Gx + j*Gy
>>> grad = signal.convolve2d(ascent, scharr, boundary='symm', mode='same')
```

```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_mag, ax_ang) = plt.subplots(3, 1, figsize=(6, 15))
>>> ax_orig.imshow(ascent, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_mag.imshow(np.absolute(grad), cmap='gray')
>>> ax_mag.set_title('Gradient magnitude')
>>> ax_mag.set_axis_off()
>>> ax_ang.imshow(np.angle(grad), cmap='hsv') # hsv is cyclic, like angles
>>> ax_ang.set_title('Gradient orientation')
>>> ax_ang.set_axis_off()
>>> fig.show()
```

scipy.signal.correlate2d

scipy.signal.**correlate2d**(*in1*, *in2*, *mode='full'*, *boundary='fill'*, *fillvalue=0*)

Cross-correlate two 2-dimensional arrays.

Cross correlate *in1* and *in2* with output size determined by *mode*, and boundary conditions determined by *boundary* and *fillvalue*.

Parameters

in1 [array_like] First input.

in2 [array_like] Second input. Should have the same number of dimensions as *in1*.

mode [str {'full', 'valid', 'same'}, optional] A string indicating the size of the output:

- **full** The output is the full discrete linear cross-correlation of the inputs. (Default)
- **valid** The output consists only of those elements that do not rely on the zero-padding. In 'valid' mode, either *in1* or *in2* must be at least as large as the other in every dimension.
- **same** The output is the same size as *in1*, centered with respect to the 'full' output.

boundary [str {'fill', 'wrap', 'symm'}, optional] A flag indicating how to handle boundaries:

- **fill** pad input arrays with fillvalue. (default)
- **wrap** circular boundary conditions.
- **symm** symmetrical boundary conditions.

fillvalue [scalar, optional] Value to fill pad input arrays with. Default is 0.

Returns

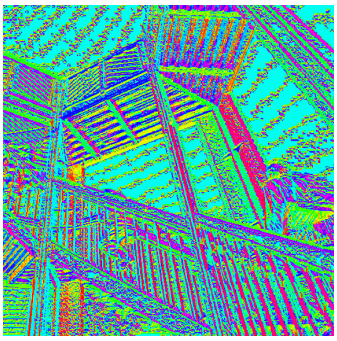
correlate2d

[ndarray] A 2-dimensional array containing a subset of the discrete linear cross-correlation of *in1* with *in2*.

Original

Gradient magnitude

Gradient orientation



Notes

When using "same" mode with even-length inputs, the outputs of *correlate* and *correlate2d* differ: There is a 1-index offset between them.

Examples

Use 2D cross-correlation to find the location of a template in a noisy image:

```
>>> from scipy import signal
>>> from scipy import misc
>>> rng = np.random.default_rng()
>>> face = misc.face(gray=True) - misc.face(gray=True).mean()
>>> template = np.copy(face[300:365, 670:750])  # right eye
>>> template -= template.mean()
>>> face = face + rng.standard_normal(face.shape) * 50  # add noise
>>> corr = signal.correlate2d(face, template, boundary='symm', mode='same
 ↪')
>>> y, x = np.unravel_index(np.argmax(corr), corr.shape)  # find the match
```

```
>>> import matplotlib.pyplot as plt
>>> fig, (ax_orig, ax_template, ax_corr) = plt.subplots(3, 1,
...                                                     figsize=(6, 15))
>>> ax_orig.imshow(face, cmap='gray')
>>> ax_orig.set_title('Original')
>>> ax_orig.set_axis_off()
>>> ax_template.imshow(template, cmap='gray')
>>> ax_template.set_title('Template')
>>> ax_template.set_axis_off()
>>> ax_corr.imshow(corr, cmap='gray')
>>> ax_corr.set_title('Cross-correlation')
>>> ax_corr.set_axis_off()
>>> ax_orig.plot(x, y, 'ro')
>>> fig.show()
```

scipy.signal.sepfir2d

scipy.signal.**sepfir2d**(*input*, *hrow*, *hcol*)

Convolve with a 2-D separable FIR filter.

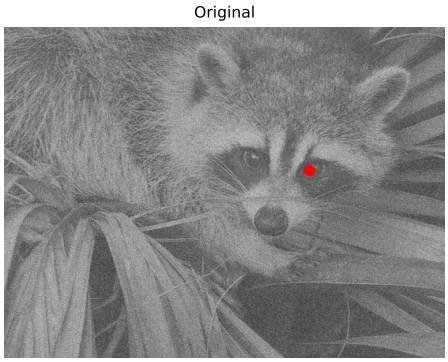
Convolve the rank-2 input array with the separable filter defined by the rank-1 arrays hrow, and hcol. Mirror symmetric boundary conditions are assumed. This function can be used to find an image given its B-spline representation.

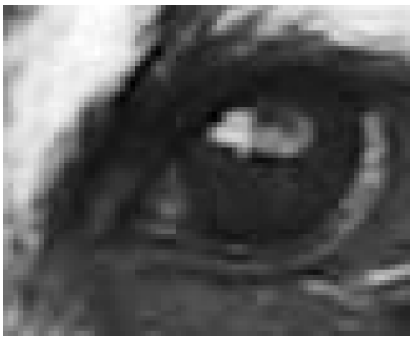
Parameters

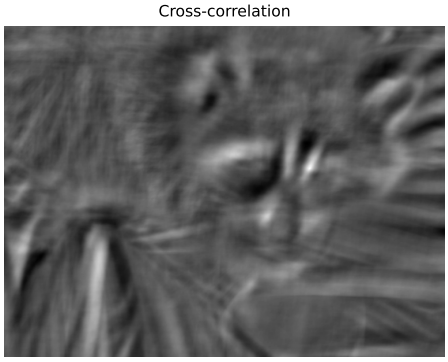
input	[ndarray] The input signal. Must be a rank-2 array.
hrow	[ndarray] A rank-1 array defining the row direction of the filter. Must be odd-length
hcol	[ndarray] A rank-1 array defining the column direction of the filter. Must be odd-length

Returns

output	[ndarray] The filtered signal.


Original


Template


Cross-correlation

Examples

Examples are given *in the tutorial*.

scipy.signal.choose_conv_method

scipy.signal.**choose_conv_method**(*in1*, *in2*, *mode='full'*, *measure=False*)

Find the fastest convolution/correlation method.

This primarily exists to be called during the `method='auto'` option in *convolve* and *correlate*. It can also be used to determine the value of `method` for many different convolutions of the same dtype/shape. In addition, it supports timing the convolution to adapt the value of `method` to a particular set of inputs and/or hardware.

Parameters

in1	[array_like] The first argument passed into the convolution function.
in2	[array_like] The second argument passed into the convolution function.
mode	[str {'full', 'valid', 'same'}, optional] A string indicating the size of the output: **full** The output is the full discrete linear convolution of the inputs. (Default) **valid** The output consists only of those elements that do not rely on the zero-padding. **same** The output is the same size as *in1*, centered with respect to the 'full' output.
measure	[bool, optional] If True, run and time the convolution of *in1* and *in2* with both methods and return the fastest. If False (default), predict the fastest method using precomputed values.

Returns

method	[str] A string indicating which convolution method is fastest, either 'direct' or 'fft'
times	[dict, optional] A dictionary containing the times (in seconds) needed for each method. This value is only returned if `measure=True`.

See also:

convolve

correlate

Notes

Generally, this method is 99% accurate for 2D signals and 85% accurate for 1D signals for randomly chosen input sizes. For precision, use `measure=True` to find the fastest method by timing the convolution. This can be used to avoid the minimal overhead of finding the fastest `method` later, or to adapt the value of `method` to a particular set of inputs.

Experiments were run on an Amazon EC2 r5a.2xlarge machine to test this function. These experiments measured the ratio between the time required when using `method='auto'` and the time required for the fastest method (i.e., `ratio = time_auto / min(time_fft, time_direct)`). In these experiments, we found:

- There is a 95% chance of this ratio being less than 1.5 for 1D signals and a 99% chance of being less than 2.5 for 2D signals.
- The ratio was always less than 2.5/5 for 1D/2D signals respectively.
- This function is most inaccurate for 1D convolutions that take between 1 and 10 milliseconds with `method='direct'`. A good proxy for this (at least in our experiments) is `1e6 <= in1.size * in2.size <= 1e7`.

The 2D results almost certainly generalize to 3D/4D/etc because the implementation is the same (the 1D implementation is different).

All the numbers above are specific to the EC2 machine. However, we did find that this function generalizes fairly decently across hardware. The speed tests were of similar quality (and even slightly better) than the same tests performed on the machine to tune this function's numbers (a mid-2014 15-inch MacBook Pro with 16GB RAM and a 2.5GHz Intel i7 processor).

There are cases when *fftconvolve* supports the inputs but this function returns *direct* (e.g., to protect against floating point integer precision).

New in version 0.19.

Examples

Estimate the fastest method for a given input:

```
>>> from scipy import signal
>>> rng = np.random.default_rng()
>>> img = rng.random((32, 32))
>>> filter = rng.random((8, 8))
>>> method = signal.choose_conv_method(img, filter, mode='same')
>>> method
'fft'
```

This can then be applied to other arrays of the same dtype and shape:

```
>>> img2 = rng.random((32, 32))
>>> filter2 = rng.random((8, 8))
>>> corr2 = signal.correlate(img2, filter2, mode='same', method=method)
>>> conv2 = signal.convolve(img2, filter2, mode='same', method=method)
```

The output of this function (`method`) works with *correlate* and *convolve*.

scipy.signal.correlation_lags

scipy.signal.**correlation_lags**(*in1_len*, *in2_len*, *mode='full'*)

Calculates the lag / displacement indices array for 1D cross-correlation.

Parameters

in1_size	[int] First input size.
in2_size	[int] Second input size.
mode	[str {'full', 'valid', 'same'}, optional] A string indicating the size of the output. See the documentation *correlate* for more information.

Returns

lags	[array] Returns an array containing cross-correlation lag/displacement indices. Indices can be indexed with the np.argmax of the correlation to return the lag/displacement.

See also:

correlate

Compute the N-dimensional cross-correlation.

Notes

Cross-correlation for continuous functions f and g is defined as:

$$(f \star g)(\tau) \triangleq \int_{t_0}^{t_0+T} \overline{f(t)} g(t+\tau)\, dt$$

Where τ is defined as the displacement, also known as the lag.

Cross correlation for discrete functions f and g is defined as:

$$(f \star g)[n] \triangleq \sum_{-\infty}^{\infty} \overline{f[m]} g[m+n]$$

Where n is the lag.

Examples

Cross-correlation of a signal with its time-delayed self.

```
>>> from scipy import signal
>>> from numpy.random import default_rng
>>> rng = default_rng()
>>> x = rng.standard_normal(1000)
>>> y = np.concatenate([rng.standard_normal(100), x])
>>> correlation = signal.correlate(x, y, mode="full")
>>> lags = signal.correlation_lags(x.size, y.size, mode="full")
>>> lag = lags[np.argmax(correlation)]
```

B-splines

bspline(x, n)	B-spline basis function of order n.
cubic(x)	A cubic B-spline.
quadratic(x)	A quadratic B-spline.
gauss_spline(x, n)	Gaussian approximation to B-spline basis function of order n.
cspline1d(signal[, lamb])	Compute cubic spline coefficients for rank-1 array.
qspline1d(signal[, lamb])	Compute quadratic spline coefficients for rank-1 array.
cspline2d(input[, lambda, precision])	Coefficients for 2-D cubic (3rd order) B-spline.
qspline2d(input[, lambda, precision])	Coefficients for 2-D quadratic (2nd order) B-spline:
cspline1d_eval(cj, newx[, dx, x0])	Evaluate a cubic spline at the new set of points.
qspline1d_eval(cj, newx[, dx, x0])	Evaluate a quadratic spline at the new set of points.
spline_filter(Iin[, lmbda])	Smoothing spline (cubic) filtering of a rank-2 array.

scipy.signal.bspline

scipy.signal.**bspline**(*x*, *n*)

B-spline basis function of order n.

Parameters

x	[array_like] a knot vector
n	[int] The order of the spline. Must be non-negative, i.e., n >= 0

Returns

res	[ndarray] B-spline basis function values

See also:

cubic

A cubic B-spline.

quadratic

A quadratic B-spline.

Notes

Uses numpy.piecewise and automatic function-generator.

Examples

We can calculate B-Spline basis function of several orders:

```
>>> from scipy.signal import bspline, cubic, quadratic
>>> bspline(0.0, 1)
1
```

```
>>> knots = [-1.0, 0.0, -1.0]
>>> bspline(knots, 2)
array([0.125, 0.75, 0.125])
```

```
>>> np.array_equal(bspline(knots, 2), quadratic(knots))
True
```

```
>>> np.array_equal(bspline(knots, 3), cubic(knots))
True
```

scipy.signal.cubic

scipy.signal.**cubic**(*x*)

A cubic B-spline.

This is a special case of *bspline*, and equivalent to `bspline(x, 3)`.

Parameters

x	[array_like] a knot vector

Returns

res [ndarray] Cubic B-spline basis function values

See also:

bspline

B-spline basis function of order n

quadratic

A quadratic B-spline.

Examples

We can calculate B-Spline basis function of several orders:

```
>>> from scipy.signal import bspline, cubic, quadratic
>>> bspline(0.0, 1)
1
```

```
>>> knots = [-1.0, 0.0, -1.0]
>>> bspline(knots, 2)
array([0.125, 0.75, 0.125])
```

```
>>> np.array_equal(bspline(knots, 2), quadratic(knots))
True
```

```
>>> np.array_equal(bspline(knots, 3), cubic(knots))
True
```

scipy.signal.quadratic

scipy.signal.**quadratic**(*x*)

A quadratic B-spline.

This is a special case of *bspline*, and equivalent to `bspline(x, 2)`.

Parameters

x [array_like] a knot vector

Returns

res [ndarray] Quadratic B-spline basis function values

See also:

bspline

B-spline basis function of order n

cubic

A cubic B-spline.

Examples

We can calculate B-Spline basis function of several orders:

```
>>> from scipy.signal import bspline, cubic, quadratic
>>> bspline(0.0, 1)
1
```

```
>>> knots = [-1.0, 0.0, -1.0]
>>> bspline(knots, 2)
array([0.125, 0.75, 0.125])
```

```
>>> np.array_equal(bspline(knots, 2), quadratic(knots))
True
```

```
>>> np.array_equal(bspline(knots, 3), cubic(knots))
True
```

scipy.signal.gauss_spline

scipy.signal.**gauss_spline**(*x*, *n*)

Gaussian approximation to B-spline basis function of order n.

Parameters

x	[array_like] a knot vector
n	[int] The order of the spline. Must be non-negative, i.e., n >= 0

Returns

res	[ndarray] B-spline basis function values approximated by a zero-mean Gaussian function.

Notes

The B-spline basis function can be approximated well by a zero-mean Gaussian function with standard-deviation equal to $\sigma = (n+1)/12$ for large n :

$$\frac{1}{\sqrt{2\pi\sigma^2}} exp(-\frac{x^2}{2\sigma})$$

References

[1], [2]

Examples

We can calculate B-Spline basis functions approximated by a gaussian distribution:

```
>>> from scipy.signal import gauss_spline, bspline
>>> knots = np.array([-1.0, 0.0, -1.0])
>>> gauss_spline(knots, 3)
array([0.15418033, 0.6909883, 0.15418033])  # may vary
```

```
>>> bspline(knots, 3)
array([0.16666667, 0.66666667, 0.16666667])  # may vary
```

scipy.signal.cspline1d

scipy.signal.**cspline1d**(*signal*, *lamb=0.0*)

Compute cubic spline coefficients for rank-1 array.

Find the cubic spline coefficients for a 1-D signal assuming mirror-symmetric boundary conditions. To obtain the signal back from the spline representation mirror-symmetric-convolve these coefficients with a length 3 FIR window [1.0, 4.0, 1.0]/ 6.0 .

Parameters

signal	[ndarray] A rank-1 array representing samples of a signal.
lamb	[float, optional] Smoothing coefficient, default is 0.0.

Returns

c	[ndarray] Cubic spline coefficients.

See also:

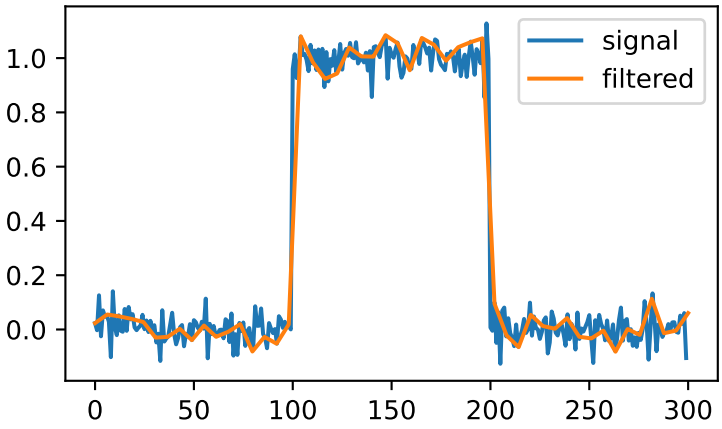
cspline1d_eval

Evaluate a cubic spline at the new set of points.

Examples

We can filter a signal to reduce and smooth out high-frequency noise with a cubic spline:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.signal import cspline1d, cspline1d_eval
>>> rng = np.random.default_rng()
>>> sig = np.repeat([0., 1., 0.], 100)
>>> sig += rng.standard_normal(len(sig))*0.05  # add noise
>>> time = np.linspace(0, len(sig))
>>> filtered = cspline1d_eval(cspline1d(sig), time)
>>> plt.plot(sig, label="signal")
>>> plt.plot(time, filtered, label="filtered")
>>> plt.legend()
>>> plt.show()
```



scipy.signal.qspline1d

`scipy.signal.`**`qspline1d`**(*signal*, *lamb=0.0*)

Compute quadratic spline coefficients for rank-1 array.

Parameters

signal	[ndarray] A rank-1 array representing samples of a signal.
lamb	[float, optional] Smoothing coefficient (must be zero for now).

Returns

c	[ndarray] Quadratic spline coefficients.

See also:

`qspline1d_eval`

Evaluate a quadratic spline at the new set of points.

Notes

Find the quadratic spline coefficients for a 1-D signal assuming mirror-symmetric boundary conditions. To obtain the signal back from the spline representation mirror-symmetric-convolve these coefficients with a length 3 FIR window [1.0, 6.0, 1.0]/ 8.0 .

Examples

We can filter a signal to reduce and smooth out high-frequency noise with a quadratic spline:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.signal import qspline1d, qspline1d_eval
>>> rng = np.random.default_rng()
>>> sig = np.repeat([0., 1., 0.], 100)
>>> sig += rng.standard_normal(len(sig))*0.05  # add noise
>>> time = np.linspace(0, len(sig))
```

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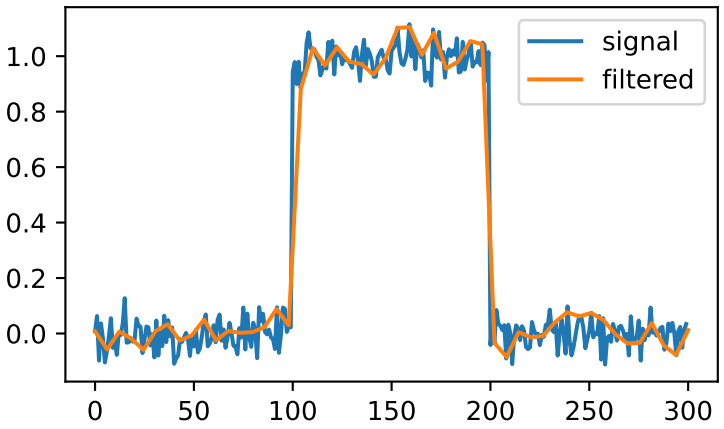
```
>>> filtered = qspline1d_eval(qspline1d(sig), time)
>>> plt.plot(sig, label="signal")
>>> plt.plot(time, filtered, label="filtered")
>>> plt.legend()
>>> plt.show()
```



scipy.signal.cspline2d

`scipy.signal.`**`cspline2d`**(*input*, *lambda=0.0*, *precision=-1.0*)

Coefficients for 2-D cubic (3rd order) B-spline.

Return the third-order B-spline coefficients over a regularly spaced input grid for the two-dimensional input image.

Parameters

input	[ndarray] The input signal.
lambda	[float] Specifies the amount of smoothing in the transfer function.
precision	[float] Specifies the precision for computing the infinite sum needed to apply mirror- symmetric boundary conditions.

Returns

output	[ndarray] The filtered signal.

Examples

Examples are given *in the tutorial*.

scipy.signal.qspline2d

scipy.signal.**qspline2d**(*input*, *lambda=0.0*, *precision=-1.0*)

Coefficients for 2-D quadratic (2nd order) B-spline:

Return the second-order B-spline coefficients over a regularly spaced input grid for the two-dimensional input image.

Parameters

input	[ndarray] The input signal.
lambda	[float] Specifies the amount of smoothing in the transfer function.
precision	[float] Specifies the precision for computing the infinite sum needed to apply mirror- symmetric boundary conditions.

Returns

output	[ndarray] The filtered signal.

Examples

Examples are given *in the tutorial*.

scipy.signal.cspline1d_eval

scipy.signal.**cspline1d_eval**(*cj*, *newx*, *dx=1.0*, *x0=0*)

Evaluate a cubic spline at the new set of points.

dx is the old sample-spacing while *x0* was the old origin. In other-words the old-sample points (knot-points) for which the *cj* represent spline coefficients were at equally-spaced points of:

oldx = x0 + j*dx j=0…N-1, with N=len(cj)

Edges are handled using mirror-symmetric boundary conditions.

Parameters

cj	[ndarray] cublic spline coefficients
newx	[ndarray] New set of points.
dx	[float, optional] Old sample-spacing, the default value is 1.0.
x0	[int, optional] Old origin, the default value is 0.

Returns

res	[ndarray] Evaluated a cubic spline points.

See also:

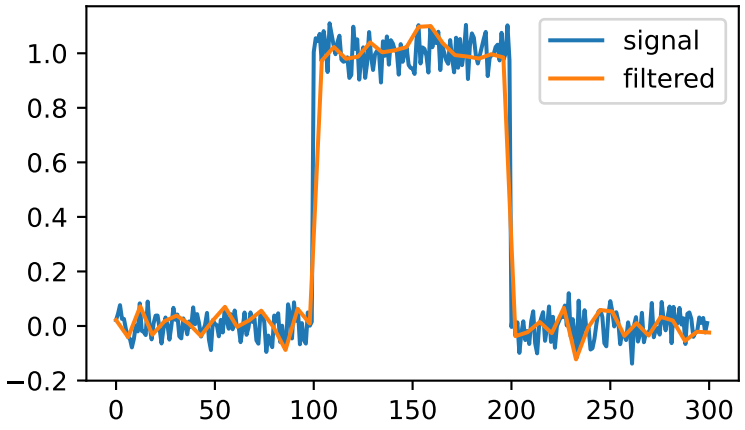
cspline1d

Compute cubic spline coefficients for rank-1 array.

Examples

We can filter a signal to reduce and smooth out high-frequency noise with a cubic spline:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.signal import cspline1d, cspline1d_eval
>>> rng = np.random.default_rng()
>>> sig = np.repeat([0., 1., 0.], 100)
>>> sig += rng.standard_normal(len(sig))*0.05  # add noise
>>> time = np.linspace(0, len(sig))
>>> filtered = cspline1d_eval(cspline1d(sig), time)
>>> plt.plot(sig, label="signal")
>>> plt.plot(time, filtered, label="filtered")
>>> plt.legend()
>>> plt.show()
```



scipy.signal.qspline1d_eval

scipy.signal.**qspline1d_eval**(*cj*, *newx*, *dx=1.0*, *x0=0*)

Evaluate a quadratic spline at the new set of points.

Parameters

cj	[ndarray] Quadratic spline coefficients
newx	[ndarray] New set of points.
dx	[float, optional] Old sample-spacing, the default value is 1.0.
x0	[int, optional] Old origin, the default value is 0.

Returns

res	[ndarray] Evaluated a quadratic spline points.

See also:

qspline1d

Compute quadratic spline coefficients for rank-1 array.

Notes

dx is the old sample-spacing while *x0* was the old origin. In other-words the old-sample points (knot-points) for which the *cj* represent spline coefficients were at equally-spaced points of:

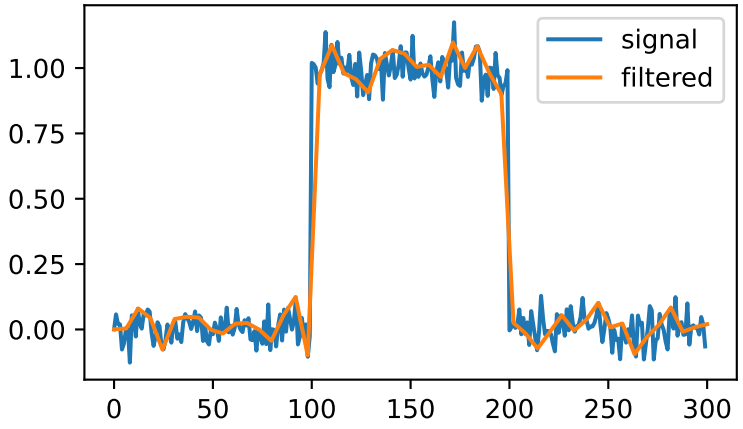
```
oldx = x0 + j*dx  j=0...N-1, with N=len(cj)
```

Edges are handled using mirror-symmetric boundary conditions.

Examples

We can filter a signal to reduce and smooth out high-frequency noise with a quadratic spline:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.signal import qspline1d, qspline1d_eval
>>> rng = np.random.default_rng()
>>> sig = np.repeat([0., 1., 0.], 100)
>>> sig += rng.standard_normal(len(sig))*0.05  # add noise
>>> time = np.linspace(0, len(sig))
>>> filtered = qspline1d_eval(qspline1d(sig), time)
>>> plt.plot(sig, label="signal")
>>> plt.plot(time, filtered, label="filtered")
>>> plt.legend()
>>> plt.show()
```



scipy.signal.spline_filter

scipy.signal.**spline_filter**(*Iin*, *lmbda=5.0*)

Smoothing spline (cubic) filtering of a rank-2 array.

Filter an input data set, *Iin*, using a (cubic) smoothing spline of fall-off *lmbda*.

Parameters

Iin	[array_like] input data set
lmbda	[float, optional] spline smooghing fall-off value, default is *5.0*.

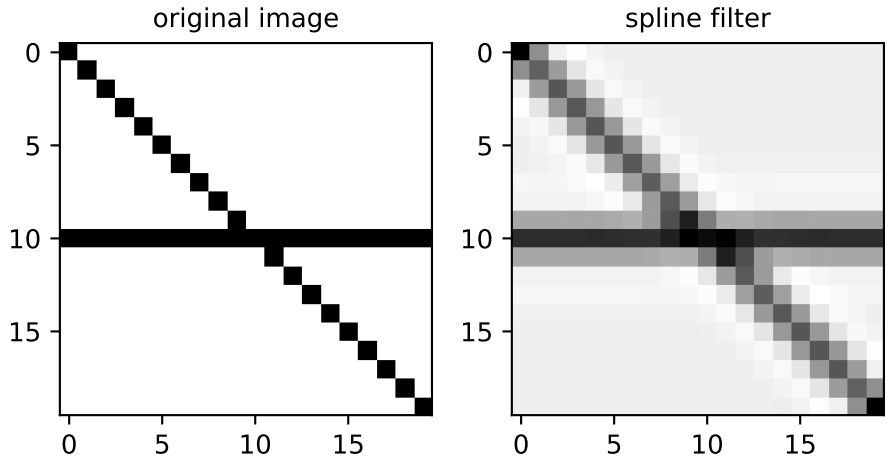
Returns

res	[ndarray] filterd input data

Examples

We can filter an multi dimentional signal (ex: 2D image) using cubic B-spline filter:

```
>>> from scipy.signal import spline_filter
>>> import matplotlib.pyplot as plt
>>> orig_img = np.eye(20)  # create an image
>>> orig_img[10, :] = 1.0
>>> sp_filter = spline_filter(orig_img, lmbda=0.1)
>>> f, ax = plt.subplots(1, 2, sharex=True)
>>> for ind, data in enumerate([[orig_img, "original image"],
...                             [sp_filter, "spline filter"]]):
...     ax[ind].imshow(data[0], cmap='gray_r')
...     ax[ind].set_title(data[1])
>>> plt.tight_layout()
>>> plt.show()
```



Filtering

order_filter(a, domain, rank)	Perform an order filter on an N-D array.
medfilt(volume[, kernel_size])	Perform a median filter on an N-dimensional array.
medfilt2d(input[, kernel_size])	Median filter a 2-dimensional array.
wiener(im[, mysize, noise])	Perform a Wiener filter on an N-dimensional array.
symiirorder1(input, c0, z1[, precision])	Implement a smoothing IIR filter with mirror-symmetric boundary conditions using a cascade of first-order sections. The second section uses a reversed sequence. This implements a system with the following transfer function and mirror-symmetric boundary conditions::.
symiirorder2(input, r, omega[, precision])	Implement a smoothing IIR filter with mirror-symmetric boundary conditions using a cascade of second-order sections. The second section uses a reversed sequence. This implements the following transfer function::.
lfilter(b, a, x[, axis, zi])	Filter data along one-dimension with an IIR or FIR filter.
lfiltic(b, a, y[, x])	Construct initial conditions for lfilter given input and output vectors.
lfilter_zi(b, a)	Construct initial conditions for lfilter for step response steady-state.
filtfilt(b, a, x[, axis, padtype, padlen, …])	Apply a digital filter forward and backward to a signal.
savgol_filter(x, window_length, polyorder[, …])	Apply a Savitzky-Golay filter to an array.
deconvolve(signal, divisor)	Deconvolves `divisor` out of `signal` using inverse filtering.
sosfilt(sos, x[, axis, zi])	Filter data along one dimension using cascaded second-order sections.
sosfilt_zi(sos)	Construct initial conditions for sosfilt for step response steady-state.
sosfiltfilt(sos, x[, axis, padtype, padlen])	A forward-backward digital filter using cascaded second-order sections.
hilbert(x[, N, axis])	Compute the analytic signal, using the Hilbert transform.
hilbert2(x[, N])	Compute the '2-D' analytic signal of *x*
decimate(x, q[, n, ftype, axis, zero_phase])	Downsample the signal after applying an anti-aliasing filter.
detrend(data[, axis, type, bp, overwrite_data])	Remove linear trend along axis from data.
resample(x, num[, t, axis, window, domain])	Resample *x* to *num* samples using Fourier method along the given axis.
resample_poly(x, up, down[, axis, window, …])	Resample *x* along the given axis using polyphase filtering.
upfirdn(h, x[, up, down, axis, mode, cval])	Upsample, FIR filter, and downsample.

scipy.signal.order_filter

scipy.signal.**order_filter**(*a*, *domain*, *rank*)

Perform an order filter on an N-D array.

Perform an order filter on the array in. The domain argument acts as a mask centered over each pixel. The non-zero elements of domain are used to select elements surrounding each input pixel which are placed in a list. The list is sorted, and the output for that pixel is the element corresponding to rank in the sorted list.

Parameters

a [ndarray] The N-dimensional input array.

domain [array_like] A mask array with the same number of dimensions as *a*. Each dimension should have an odd number of elements.

rank [int] A non-negative integer which selects the element from the sorted list (0 corresponds to the smallest element, 1 is the next smallest element, etc.).

Returns

out [ndarray] The results of the order filter in an array with the same shape as *a*.

Examples

```
>>> from scipy import signal
>>> x = np.arange(25).reshape(5, 5)
>>> domain = np.identity(3)
>>> x
array([[ 0,  1,  2,  3,  4],
       [ 5,  6,  7,  8,  9],
       [10, 11, 12, 13, 14],
       [15, 16, 17, 18, 19],
       [20, 21, 22, 23, 24]])
>>> signal.order_filter(x, domain, 0)
array([[  0.,   0.,   0.,   0.,   0.],
       [  0.,   0.,   1.,   2.,   0.],
       [  0.,   5.,   6.,   7.,   0.],
       [  0.,  10.,  11.,  12.,   0.],
       [  0.,   0.,   0.,   0.,   0.]])
>>> signal.order_filter(x, domain, 2)
array([[  6.,   7.,   8.,   9.,   4.],
       [ 11.,  12.,  13.,  14.,   9.],
       [ 16.,  17.,  18.,  19.,  14.],
       [ 21.,  22.,  23.,  24.,  19.],
       [ 20.,  21.,  22.,  23.,  24.]])
```

scipy.signal.medfilt

`scipy.signal.`**`medfilt`**(*volume*, *kernel_size=None*)

Perform a median filter on an N-dimensional array.

Apply a median filter to the input array using a local window-size given by *kernel_size*. The array will automatically be zero-padded.

Parameters

volume [array_like] An N-dimensional input array.

kernel_size [array_like, optional] A scalar or an N-length list giving the size of the median filter window in each dimension. Elements of *kernel_size* should be odd. If *kernel_size* is a scalar, then this scalar is used as the size in each dimension. Default size is 3 for each dimension.

Returns

out [ndarray] An array the same size as input containing the median filtered result.

Warns

UserWarning If array size is smaller than kernel size along any dimension

See also:

scipy.ndimage.median_filter

scipy.signal.medfilt2d

Notes

The more general function *scipy.ndimage.median_filter* has a more efficient implementation of a median filter and therefore runs much faster.

For 2-dimensional images with `uint8`, `float32` or `float64` dtypes, the specialised function *scipy.signal.medfilt2d* may be faster.

scipy.signal.medfilt2d

`scipy.signal.`**`medfilt2d`**(*input*, *kernel_size=3*)

Median filter a 2-dimensional array.

Apply a median filter to the *input* array using a local window-size given by *kernel_size* (must be odd). The array is zero-padded automatically.

Parameters

input [array_like] A 2-dimensional input array.

kernel_size [array_like, optional] A scalar or a list of length 2, giving the size of the median filter window in each dimension. Elements of *kernel_size* should be odd. If *kernel_size* is a scalar, then this scalar is used as the size in each dimension. Default is a kernel of size (3, 3).

Returns

out [ndarray] An array the same size as input containing the median filtered result.

See also:

scipy.ndimage.median_filter

Notes

This is faster than *medfilt* when the input dtype is `uint8`, `float32`, or `float64`; for other types, this falls back to *medfilt*; you should use *scipy.ndimage.median_filter* instead as it is much faster. In some situations, *scipy.ndimage.median_filter* may be faster than this function.

scipy.signal.wiener

`scipy.signal.`**`wiener`**(*im*, *mysize=None*, *noise=None*)

Perform a Wiener filter on an N-dimensional array.

Apply a Wiener filter to the N-dimensional array *im*.

Parameters

im [ndarray] An N-dimensional array.

mysize [int or array_like, optional] A scalar or an N-length list giving the size of the Wiener filter window in each dimension. Elements of mysize should be odd. If mysize is a scalar, then this scalar is used as the size in each dimension.

noise [float, optional] The noise-power to use. If None, then noise is estimated as the average of the local variance of the input.

Returns

out [ndarray] Wiener filtered result with the same shape as *im*.

Notes

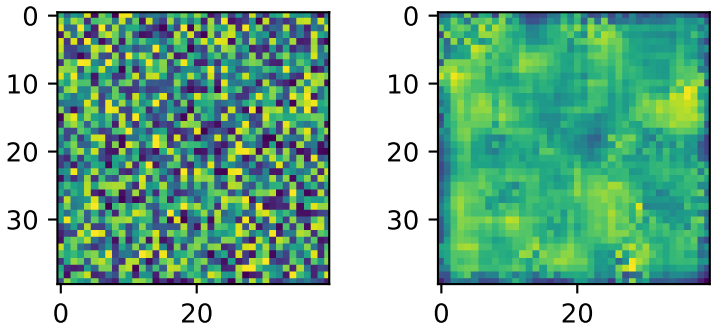
This implementation is similar to wiener2 in Matlab/Octave. For more details see [1]

References

[1]

Examples

```
>>> from scipy.misc import face
>>> from scipy.signal.signaltools import wiener
>>> import matplotlib.pyplot as plt
>>> import numpy as np
>>> rng = np.random.default_rng()
>>> img = rng.random((40, 40))    #Create a random image
>>> filtered_img = wiener(img, (5, 5))  #Filter the image
>>> f, (plot1, plot2) = plt.subplots(1, 2)
>>> plot1.imshow(img)
>>> plot2.imshow(filtered_img)
>>> plt.show()
```



scipy.signal.symiirorder1

scipy.signal.**symiirorder1**(*input*, *c0*, *z1*, *precision=- 1.0*)

Implement a smoothing IIR filter with mirror-symmetric boundary conditions using a cascade of first-order sections. The second section uses a reversed sequence. This implements a system with the following transfer function and mirror-symmetric boundary conditions:

```
                c0
H(z) = ---------------------
        (1-z1/z) (1 - z1 z)
```

The resulting signal will have mirror symmetric boundary conditions as well.

Parameters

input [ndarray] The input signal.
c0, z1 [scalar] Parameters in the transfer function.
precision : Specifies the precision for calculating initial conditions of the recursive filter based on mirror-symmetric input.

Returns

output [ndarray] The filtered signal.

scipy.signal.symiirorder2

scipy.signal.**symiirorder2**(*input*, *r*, *omega*, *precision=- 1.0*)

Implement a smoothing IIR filter with mirror-symmetric boundary conditions using a cascade of second-order sections. The second section uses a reversed sequence. This implements the following transfer function:

```
                            cs^2
H(z) = ---------------------------------------
       (1 - a2/z - a3/z^2) (1 - a2 z - a3 z^2 )
```

where:

```
a2 = (2 r cos omega)
a3 = - r^2
cs = 1 - 2 r cos omega + r^2
```

Parameters

input [ndarray] The input signal.
r, omega [float] Parameters in the transfer function.
precision [float] Specifies the precision for calculating initial conditions of the recursive filter based on mirror-symmetric input.

Returns

output [ndarray] The filtered signal.

scipy.signal.lfilter

scipy.signal.**lfilter**(*b*, *a*, *x*, *axis=- 1*, *zi=None*)

Filter data along one-dimension with an IIR or FIR filter.

Filter a data sequence, *x*, using a digital filter. This works for many fundamental data types (including Object type). The filter is a direct form II transposed implementation of the standard difference equation (see Notes).

The function *sosfilt* (and filter design using `output='sos'`) should be preferred over *lfilter* for most filtering tasks, as second-order sections have fewer numerical problems.

Parameters

b	[array_like] The numerator coefficient vector in a 1-D sequence.
a	[array_like] The denominator coefficient vector in a 1-D sequence. If `a[0]` is not 1, then both *a* and *b* are normalized by `a[0]`.
x	[array_like] An N-dimensional input array.
axis	[int, optional] The axis of the input data array along which to apply the linear filter. The filter is applied to each subarray along this axis. Default is -1.
zi	[array_like, optional] Initial conditions for the filter delays. It is a vector (or array of vectors for an N-dimensional input) of length `max(len(a), len(b)) - 1`. If *zi* is None or is not given then initial rest is assumed. See *lfiltic* for more information.

Returns

y	[array] The output of the digital filter.
zf	[array, optional] If *zi* is None, this is not returned, otherwise, *zf* holds the final filter delay values.

See also:

lfiltic

Construct initial conditions for *lfilter*.

lfilter_zi

Compute initial state (steady state of step response) for *lfilter*.

filtfilt

A forward-backward filter, to obtain a filter with linear phase.

savgol_filter

A Savitzky-Golay filter.

sosfilt

Filter data using cascaded second-order sections.

sosfiltfilt

A forward-backward filter using second-order sections.

Notes

The filter function is implemented as a direct II transposed structure. This means that the filter implements:

```
a[0]*y[n] = b[0]*x[n] + b[1]*x[n-1] + ... + b[M]*x[n-M]
                      - a[1]*y[n-1] - ... - a[N]*y[n-N]
```

where *M* is the degree of the numerator, *N* is the degree of the denominator, and *n* is the sample number. It is implemented using the following difference equations (assuming M = N):

```
a[0]*y[n] = b[0] * x[n]                 + d[0][n-1]
  d[0][n] = b[1] * x[n] - a[1] * y[n] + d[1][n-1]
  d[1][n] = b[2] * x[n] - a[2] * y[n] + d[2][n-1]
...
d[N-2][n] = b[N-1]*x[n] - a[N-1]*y[n] + d[N-1][n-1]
d[N-1][n] = b[N] * x[n] - a[N] * y[n]
```

where *d* are the state variables.

The rational transfer function describing this filter in the z-transform domain is:

```
                     -1              -M
        b[0] + b[1]z  + ... + b[M] z
Y(z) = -------------------------------- X(z)
                     -1              -N
        a[0] + a[1]z  + ... + a[N] z
```

Examples

Generate a noisy signal to be filtered:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> t = np.linspace(-1, 1, 201)
>>> x = (np.sin(2*np.pi*0.75*t*(1-t) + 2.1) +
...      0.1*np.sin(2*np.pi*1.25*t + 1) +
...      0.18*np.cos(2*np.pi*3.85*t))
>>> xn = x + rng.standard_normal(len(t)) * 0.08
```

Create an order 3 lowpass butterworth filter:

```
>>> b, a = signal.butter(3, 0.05)
```

Apply the filter to xn. Use lfilter_zi to choose the initial condition of the filter:

```
>>> zi = signal.lfilter_zi(b, a)
>>> z, _ = signal.lfilter(b, a, xn, zi=zi*xn[0])
```

Apply the filter again, to have a result filtered at an order the same as filtfilt:

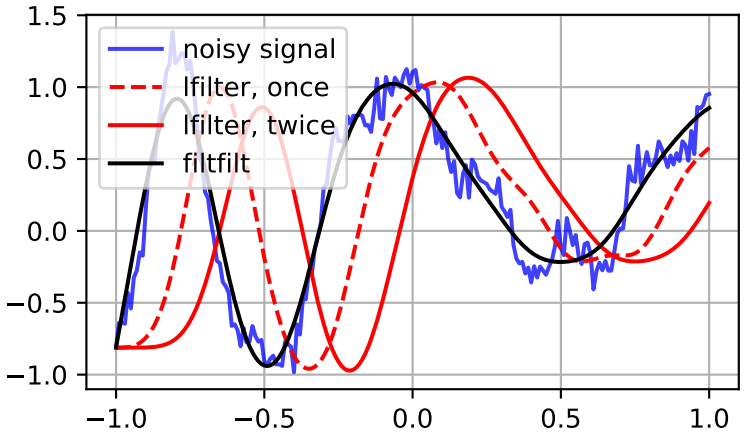
```
>>> z2, _ = signal.lfilter(b, a, z, zi=zi*z[0])
```

Use filtfilt to apply the filter:

```
>>> y = signal.filtfilt(b, a, xn)
```

Plot the original signal and the various filtered versions:

```
>>> plt.figure
>>> plt.plot(t, xn, 'b', alpha=0.75)
>>> plt.plot(t, z, 'r--', t, z2, 'r', t, y, 'k')
>>> plt.legend(('noisy signal', 'lfilter, once', 'lfilter, twice',
...             'filtfilt'), loc='best')
>>> plt.grid(True)
>>> plt.show()
```



scipy.signal.lfiltic

scipy.signal.**lfiltic**(*b*, *a*, *y*, *x=None*)

Construct initial conditions for lfilter given input and output vectors.

Given a linear filter (b, a) and initial conditions on the output *y* and the input *x*, return the initial conditions on the state vector zi which is used by `lfilter` to generate the output given the input.

Parameters

b [array_like] Linear filter term.

a [array_like] Linear filter term.

y [array_like] Initial conditions.
If `N = len(a) - 1`, then `y = {y[-1], y[-2], ..., y[-N]}`.
If *y* is too short, it is padded with zeros.

x [array_like, optional] Initial conditions.
If `M = len(b) - 1`, then `x = {x[-1], x[-2], ..., x[-M]}`.
If *x* is not given, its initial conditions are assumed zero.
If *x* is too short, it is padded with zeros.

Returns

zi [ndarray] The state vector `zi = {z_0[-1], z_1[-1], ..., z_K-1[-1]}`, where `K = max(M, N)`.

See also:

`lfilter`, `lfilter_zi`

scipy.signal.lfilter_zi

scipy.signal.**lfilter_zi**(*b*, *a*)

Construct initial conditions for lfilter for step response steady-state.

Compute an initial state *zi* for the *lfilter* function that corresponds to the steady state of the step response.

A typical use of this function is to set the initial state so that the output of the filter starts at the same value as the first element of the signal to be filtered.

Parameters

b, a [array_like (1-D)] The IIR filter coefficients. See *lfilter* for more information.

Returns

zi [1-D ndarray] The initial state for the filter.

See also:

`lfilter`, `lfiltic`, `filtfilt`

Notes

A linear filter with order m has a state space representation (A, B, C, D), for which the output y of the filter can be expressed as:

```
z(n+1) = A*z(n) + B*x(n)
y(n)   = C*z(n) + D*x(n)
```

where z(n) is a vector of length m, A has shape (m, m), B has shape (m, 1), C has shape (1, m) and D has shape (1, 1) (assuming x(n) is a scalar). lfilter_zi solves:

```
zi = A*zi + B
```

In other words, it finds the initial condition for which the response to an input of all ones is a constant.

Given the filter coefficients *a* and *b*, the state space matrices for the transposed direct form II implementation of the linear filter, which is the implementation used by scipy.signal.lfilter, are:

```
A = scipy.linalg.companion(a).T
B = b[1:] - a[1:]*b[0]
```

assuming *a[0]* is 1.0; if *a[0]* is not 1, *a* and *b* are first divided by a[0].

Examples

The following code creates a lowpass Butterworth filter. Then it applies that filter to an array whose values are all 1.0; the output is also all 1.0, as expected for a lowpass filter. If the *zi* argument of `lfilter` had not been given, the output would have shown the transient signal.

```
>>> from numpy import array, ones
>>> from scipy.signal import lfilter, lfilter_zi, butter
>>> b, a = butter(5, 0.25)
>>> zi = lfilter_zi(b, a)
>>> y, zo = lfilter(b, a, ones(10), zi=zi)
>>> y
array([1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.,  1.])
```

Another example:

```
>>> x = array([0.5, 0.5, 0.5, 0.0, 0.0, 0.0, 0.0])
>>> y, zf = lfilter(b, a, x, zi=zi*x[0])
>>> y
array([ 0.5       ,  0.5       ,  0.5       ,  0.49836039,  0.48610528,
    0.44399389,  0.35505241])
```

Note that the *zi* argument to `lfilter` was computed using `lfilter_zi` and scaled by *x[0]*. Then the output *y* has no transient until the input drops from 0.5 to 0.0.

scipy.signal.filtfilt

`scipy.signal.`**`filtfilt`**(*b*, *a*, *x*, *axis=- 1*, *padtype='odd'*, *padlen=None*, *method='pad'*, *irlen=None*)

Apply a digital filter forward and backward to a signal.

This function applies a linear digital filter twice, once forward and once backwards. The combined filter has zero phase and a filter order twice that of the original.

The function provides options for handling the edges of the signal.

The function `sosfiltfilt` (and filter design using `output='sos'`) should be preferred over `filtfilt` for most filtering tasks, as second-order sections have fewer numerical problems.

Parameters

b	[(N,) array_like] The numerator coefficient vector of the filter.
a	[(N,) array_like] The denominator coefficient vector of the filter. If `a[0]` is not 1, then both *a* and *b* are normalized by `a[0]`.
x	[array_like] The array of data to be filtered.
axis	[int, optional] The axis of *x* to which the filter is applied. Default is -1.
padtype	[str or None, optional] Must be 'odd', 'even', 'constant', or None. This determines the type of extension to use for the padded signal to which the filter is applied. If *padtype* is None, no padding is used. The default is 'odd'.
padlen	[int or None, optional] The number of elements by which to extend *x* at both ends of *axis* before applying the filter. This value must be less than `x.shape[axis] - 1`. `padlen=0` implies no padding. The default value is `3 * max(len(a), len(b))`.
method	[str, optional] Determines the method for handling the edges of the signal, either "pad" or "gust". When *method* is "pad", the signal is padded; the type of padding is determined by *padtype* and *padlen*, and *irlen* is ignored. When *method* is "gust", Gustafsson's method is used, and *padtype* and *padlen* are ignored.

irlen [int or None, optional] When *method* is "gust", *irlen* specifies the length of the impulse response of the filter. If *irlen* is None, no part of the impulse response is ignored. For a long signal, specifying *irlen* can significantly improve the performance of the filter.

Returns

y [ndarray] The filtered output with the same shape as *x*.

See also:

`sosfiltfilt`, `lfilter_zi`, `lfilter`, `lfiltic`, `savgol_filter`, `sosfilt`

Notes

When *method* is "pad", the function pads the data along the given axis in one of three ways: odd, even or constant. The odd and even extensions have the corresponding symmetry about the end point of the data. The constant extension extends the data with the values at the end points. On both the forward and backward passes, the initial condition of the filter is found by using *lfilter_zi* and scaling it by the end point of the extended data.

When *method* is "gust", Gustafsson's method [1] is used. Initial conditions are chosen for the forward and backward passes so that the forward-backward filter gives the same result as the backward-forward filter.

The option to use Gustaffson's method was added in scipy version 0.16.0.

References

[1]

Examples

The examples will use several functions from *scipy.signal*.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

First we create a one second signal that is the sum of two pure sine waves, with frequencies 5 Hz and 250 Hz, sampled at 2000 Hz.

```
>>> t = np.linspace(0, 1.0, 2001)
>>> xlow = np.sin(2 * np.pi * 5 * t)
>>> xhigh = np.sin(2 * np.pi * 250 * t)
>>> x = xlow + xhigh
```

Now create a lowpass Butterworth filter with a cutoff of 0.125 times the Nyquist frequency, or 125 Hz, and apply it to `x` with *filtfilt*. The result should be approximately `xlow`, with no phase shift.

```
>>> b, a = signal.butter(8, 0.125)
>>> y = signal.filtfilt(b, a, x, padlen=150)
>>> np.abs(y - xlow).max()
9.1086182074789912e-06
```

We get a fairly clean result for this artificial example because the odd extension is exact, and with the moderately long padding, the filter's transients have dissipated by the time the actual data is reached. In general, transient effects at the edges are unavoidable.

The following example demonstrates the option `method="gust"`.

First, create a filter.

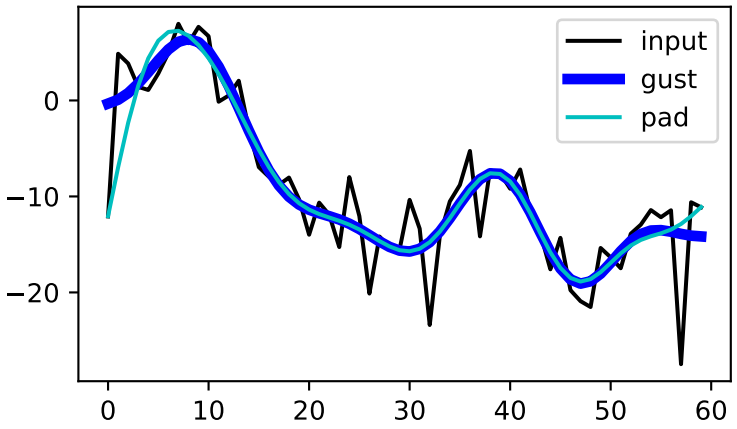
```
>>> b, a = signal.ellip(4, 0.01, 120, 0.125)  # Filter to be applied.
```

sig is a random input signal to be filtered.

```
>>> rng = np.random.default_rng()
>>> n = 60
>>> sig = rng.standard_normal(n)**3 + 3*rng.standard_normal(n).cumsum()
```

Apply *filtfilt* to *sig*, once using the Gustafsson method, and once using padding, and plot the results for comparison.

```
>>> fgust = signal.filtfilt(b, a, sig, method="gust")
>>> fpad = signal.filtfilt(b, a, sig, padlen=50)
>>> plt.plot(sig, 'k-', label='input')
>>> plt.plot(fgust, 'b-', linewidth=4, label='gust')
>>> plt.plot(fpad, 'c-', linewidth=1.5, label='pad')
>>> plt.legend(loc='best')
>>> plt.show()
```



The *irlen* argument can be used to improve the performance of Gustafsson's method.

Estimate the impulse response length of the filter.

```
>>> z, p, k = signal.tf2zpk(b, a)
>>> eps = 1e-9
>>> r = np.max(np.abs(p))
>>> approx_impulse_len = int(np.ceil(np.log(eps) / np.log(r)))
>>> approx_impulse_len
137
```

Apply the filter to a longer signal, with and without the *irlen* argument. The difference between *y1* and *y2* is small. For long signals, using *irlen* gives a significant performance improvement.

```
>>> x = rng.standard_normal(5000)
>>> y1 = signal.filtfilt(b, a, x, method='gust')
>>> y2 = signal.filtfilt(b, a, x, method='gust', irlen=approx_impulse_len)
>>> print(np.max(np.abs(y1 - y2)))
1.80056858312e-10
```

scipy.signal.savgol_filter

scipy.signal.**savgol_filter**(*x*, *window_length*, *polyorder*, *deriv=0*, *delta=1.0*, *axis=- 1*, *mode='interp'*, *cval=0.0*)

Apply a Savitzky-Golay filter to an array.

This is a 1-D filter. If *x* has dimension greater than 1, *axis* determines the axis along which the filter is applied.

Parameters

x [array_like] The data to be filtered. If *x* is not a single or double precision floating point array, it will be converted to type `numpy.float64` before filtering.

window_length [int] The length of the filter window (i.e., the number of coefficients). *window_length* must be a positive odd integer. If *mode* is 'interp', *window_length* must be less than or equal to the size of *x*.

polyorder [int] The order of the polynomial used to fit the samples. *polyorder* must be less than *window_length*.

deriv [int, optional] The order of the derivative to compute. This must be a nonnegative integer. The default is 0, which means to filter the data without differentiating.

delta [float, optional] The spacing of the samples to which the filter will be applied. This is only used if deriv > 0. Default is 1.0.

axis [int, optional] The axis of the array *x* along which the filter is to be applied. Default is -1.

mode [str, optional] Must be 'mirror', 'constant', 'nearest', 'wrap' or 'interp'. This determines the type of extension to use for the padded signal to which the filter is applied. When *mode* is 'constant', the padding value is given by *cval*. See the Notes for more details on 'mirror', 'constant', 'wrap', and 'nearest'. When the 'interp' mode is selected (the default), no extension is used. Instead, a degree *polyorder* polynomial is fit to the last *window_length* values of the edges, and this polynomial is used to evaluate the last *window_length // 2* output values.

cval [scalar, optional] Value to fill past the edges of the input if *mode* is 'constant'. Default is 0.0.

Returns

y [ndarray, same shape as *x*] The filtered data.

See also:

`savgol_coeffs`

Notes

Details on the *mode* options:

'mirror':
Repeats the values at the edges in reverse order. The value closest to the edge is not included.

'nearest':
The extension contains the nearest input value.

'constant':
The extension contains the value given by the *cval* argument.

'wrap':
The extension contains the values from the other end of the array.

For example, if the input is [1, 2, 3, 4, 5, 6, 7, 8], and *window_length* is 7, the following shows the extended data for the various *mode* options (assuming *cval* is 0):

```
mode        |   Ext   |         Input          |   Ext
------------+---------+------------------------+---------
'mirror'    | 4  3  2 | 1  2  3  4  5  6  7  8 | 7  6  5
'nearest'   | 1  1  1 | 1  2  3  4  5  6  7  8 | 8  8  8
'constant'  | 0  0  0 | 1  2  3  4  5  6  7  8 | 0  0  0
'wrap'      | 6  7  8 | 1  2  3  4  5  6  7  8 | 1  2  3
```

New in version 0.14.0.

Examples

```
>>> from scipy.signal import savgol_filter
>>> np.set_printoptions(precision=2)  # For compact display.
>>> x = np.array([2, 2, 5, 2, 1, 0, 1, 4, 9])
```

Filter with a window length of 5 and a degree 2 polynomial. Use the defaults for all other parameters.

```
>>> savgol_filter(x, 5, 2)
array([1.66, 3.17, 3.54, 2.86, 0.66, 0.17, 1.  , 4.  , 9.  ])
```

Note that the last five values in x are samples of a parabola, so when mode='interp' (the default) is used with polyorder=2, the last three values are unchanged. Compare that to, for example, *mode='nearest'*:

```
>>> savgol_filter(x, 5, 2, mode='nearest')
array([1.74, 3.03, 3.54, 2.86, 0.66, 0.17, 1.  , 4.6 , 7.97])
```

scipy.signal.deconvolve

`scipy.signal.`**`deconvolve`**(*signal*, *divisor*)

Deconvolves `divisor` out of `signal` using inverse filtering.

Returns the quotient and remainder such that `signal = convolve(divisor, quotient) + remainder`

Parameters

signal	[array_like] Signal data, typically a recorded signal
divisor	[array_like] Divisor data, typically an impulse response or filter that was applied to the original signal

Returns

quotient	[ndarray] Quotient, typically the recovered original signal
remainder	[ndarray] Remainder

See also:

`numpy.polydiv`

performs polynomial division (same operation, but also accepts poly1d objects)

Examples

Deconvolve a signal that's been filtered:

```
>>> from scipy import signal
>>> original = [0, 1, 0, 0, 1, 1, 0, 0]
>>> impulse_response = [2, 1]
>>> recorded = signal.convolve(impulse_response, original)
>>> recorded
array([0, 2, 1, 0, 2, 3, 1, 0, 0])
>>> recovered, remainder = signal.deconvolve(recorded, impulse_response)
>>> recovered
array([ 0.,  1.,  0.,  0.,  1.,  1.,  0.,  0.])
```

scipy.signal.sosfilt

scipy.signal.**sosfilt**(*sos*, *x*, *axis=- 1*, *zi=None*)

Filter data along one dimension using cascaded second-order sections.

Filter a data sequence, *x*, using a digital IIR filter defined by *sos*.

Parameters

sos [array_like] Array of second-order filter coefficients, must have shape `(n_sections, 6)`. Each row corresponds to a second-order section, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients.

x [array_like] An N-dimensional input array.

axis [int, optional] The axis of the input data array along which to apply the linear filter. The filter is applied to each subarray along this axis. Default is -1.

zi [array_like, optional] Initial conditions for the cascaded filter delays. It is a (at least 2D) vector of shape `(n_sections, ..., 2, ...)`, where `..., 2, ...` denotes the shape of *x*, but with `x.shape[axis]` replaced by 2. If *zi* is None or is not given then initial rest (i.e. all zeros) is assumed. Note that these initial conditions are *not* the same as the initial conditions given by *lfiltic* or *lfilter_zi*.

Returns

y [ndarray] The output of the digital filter.

zf [ndarray, optional] If *zi* is None, this is not returned, otherwise, *zf* holds the final filter delay values.

See also:

zpk2sos, **sos2zpk**, **sosfilt_zi**, **sosfiltfilt**, **sosfreqz**

Notes

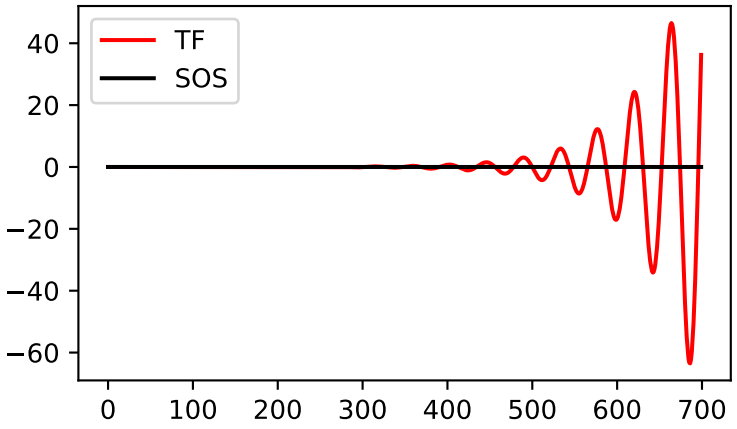
The filter function is implemented as a series of second-order filters with direct-form II transposed structure. It is designed to minimize numerical precision errors for high-order filters.

New in version 0.16.0.

Examples

Plot a 13th-order filter's impulse response using both *lfilter* and *sosfilt*, showing the instability that results from trying to do a 13th-order filter in a single stage (the numerical error pushes some poles outside of the unit circle):

```
>>> import matplotlib.pyplot as plt
>>> from scipy import signal
>>> b, a = signal.ellip(13, 0.009, 80, 0.05, output='ba')
>>> sos = signal.ellip(13, 0.009, 80, 0.05, output='sos')
>>> x = signal.unit_impulse(700)
>>> y_tf = signal.lfilter(b, a, x)
>>> y_sos = signal.sosfilt(sos, x)
>>> plt.plot(y_tf, 'r', label='TF')
>>> plt.plot(y_sos, 'k', label='SOS')
>>> plt.legend(loc='best')
>>> plt.show()
```



scipy.signal.sosfilt_zi

scipy.signal.**sosfilt_zi**(*sos*)

Construct initial conditions for sosfilt for step response steady-state.

Compute an initial state *zi* for the *sosfilt* function that corresponds to the steady state of the step response.

A typical use of this function is to set the initial state so that the output of the filter starts at the same value as the first element of the signal to be filtered.

Parameters

sos [array_like] Array of second-order filter coefficients, must have shape `(n_sections, 6)`. See *sosfilt* for the SOS filter format specification.

Returns

zi [ndarray] Initial conditions suitable for use with `sosfilt`, shape `(n_sections, 2)`.

See also:

sosfilt, **zpk2sos**

Notes

New in version 0.16.0.

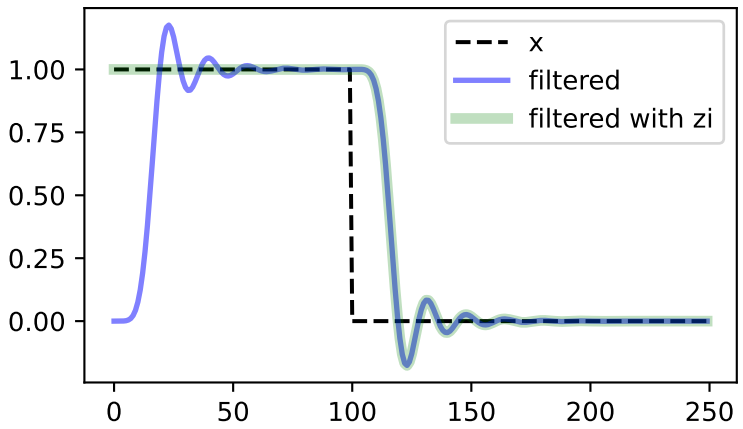
Examples

Filter a rectangular pulse that begins at time 0, with and without the use of the *zi* argument of *scipy.signal.sosfilt*.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> sos = signal.butter(9, 0.125, output='sos')
>>> zi = signal.sosfilt_zi(sos)
>>> x = (np.arange(250) < 100).astype(int)
>>> f1 = signal.sosfilt(sos, x)
>>> f2, zo = signal.sosfilt(sos, x, zi=zi)
```

```
>>> plt.plot(x, 'k--', label='x')
>>> plt.plot(f1, 'b', alpha=0.5, linewidth=2, label='filtered')
>>> plt.plot(f2, 'g', alpha=0.25, linewidth=4, label='filtered with zi')
>>> plt.legend(loc='best')
>>> plt.show()
```



scipy.signal.sosfiltfilt

scipy.signal.**sosfiltfilt**(*sos*, *x*, *axis=- 1*, *padtype='odd'*, *padlen=None*)

A forward-backward digital filter using cascaded second-order sections.

See *filtfilt* for more complete information about this method.

Parameters

sos [array_like] Array of second-order filter coefficients, must have shape `(n_sections, 6)`. Each row corresponds to a second-order section, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients.

x [array_like] The array of data to be filtered.

axis [int, optional] The axis of *x* to which the filter is applied. Default is -1.

padtype [str or None, optional] Must be 'odd', 'even', 'constant', or None. This determines the type of extension to use for the padded signal to which the filter is applied. If *padtype* is None, no padding is used. The default is 'odd'.

padlen [int or None, optional] The number of elements by which to extend *x* at both ends of *axis* before applying the filter. This value must be less than `x.shape[axis] - 1`. `padlen=0` implies no padding. The default value is:

```
3 * (2 * len(sos) + 1 - min((sos[:, 2] == 0).sum(),
                            (sos[:, 5] == 0).sum()))
```

The extra subtraction at the end attempts to compensate for poles and zeros at the origin (e.g. for odd-order filters) to yield equivalent estimates of *padlen* to those of *filtfilt* for second-order section filters built with *scipy.signal* functions.

Returns

y [ndarray] The filtered output with the same shape as *x*.

See also:

filtfilt, **sosfilt**, **sosfilt_zi**, **sosfreqz**

Notes

New in version 0.18.0.

Examples

```
>>> from scipy.signal import sosfiltfilt, butter
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

Create an interesting signal to filter.

```
>>> n = 201
>>> t = np.linspace(0, 1, n)
>>> x = 1 + (t < 0.5) - 0.25*t**2 + 0.05*rng.standard_normal(n)
```

Create a lowpass Butterworth filter, and use it to filter *x*.

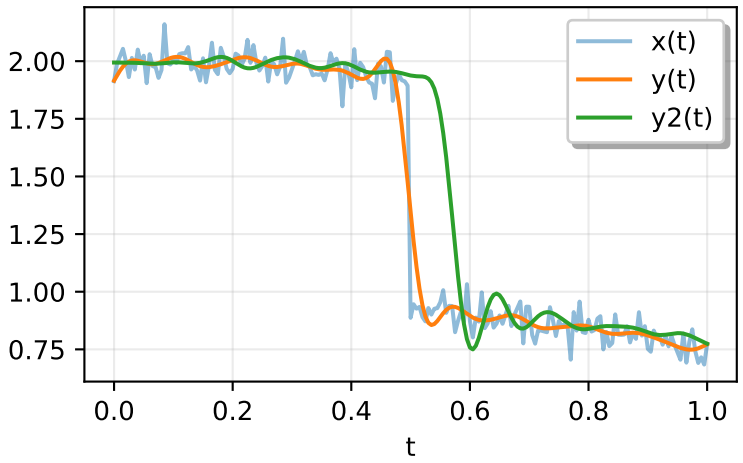
```
>>> sos = butter(4, 0.125, output='sos')
>>> y = sosfiltfilt(sos, x)
```

For comparison, apply an 8th order filter using *sosfilt*. The filter is initialized using the mean of the first four values of *x*.

```
>>> from scipy.signal import sosfilt, sosfilt_zi
>>> sos8 = butter(8, 0.125, output='sos')
>>> zi = x[:4].mean() * sosfilt_zi(sos8)
>>> y2, zo = sosfilt(sos8, x, zi=zi)
```

Plot the results. Note that the phase of *y* matches the input, while *y2* has a significant phase delay.

```
>>> plt.plot(t, x, alpha=0.5, label='x(t)')
>>> plt.plot(t, y, label='y(t)')
>>> plt.plot(t, y2, label='y2(t)')
>>> plt.legend(framealpha=1, shadow=True)
>>> plt.grid(alpha=0.25)
>>> plt.xlabel('t')
>>> plt.show()
```



scipy.signal.hilbert

scipy.signal.**hilbert**(*x*, *N=None*, *axis=- 1*)

Compute the analytic signal, using the Hilbert transform.

The transformation is done along the last axis by default.

Parameters

x	[array_like] Signal data. Must be real.
N	[int, optional] Number of Fourier components. Default: `x.shape[axis]`
axis	[int, optional] Axis along which to do the transformation. Default: -1.

Returns

xa	[ndarray] Analytic signal of *x*, of each 1-D array along *axis*

Notes

The analytic signal `x_a(t)` of signal `x(t)` is:

$$x_a = F^{-1}(F(x)2U) = x + iy$$

where F is the Fourier transform, U the unit step function, and y the Hilbert transform of x. [1]

In other words, the negative half of the frequency spectrum is zeroed out, turning the real-valued signal into a complex signal. The Hilbert transformed signal can be obtained from `np.imag(hilbert(x))`, and the original signal from `np.real(hilbert(x))`.

References

[1], [2], [3]

Examples

In this example we use the Hilbert transform to determine the amplitude envelope and instantaneous frequency of an amplitude-modulated signal.

```
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy.signal import hilbert, chirp
```

```
>>> duration = 1.0
>>> fs = 400.0
>>> samples = int(fs*duration)
>>> t = np.arange(samples) / fs
```

We create a chirp of which the frequency increases from 20 Hz to 100 Hz and apply an amplitude modulation.

```
>>> signal = chirp(t, 20.0, t[-1], 100.0)
>>> signal *= (1.0 + 0.5 * np.sin(2.0*np.pi*3.0*t) )
```

The amplitude envelope is given by magnitude of the analytic signal. The instantaneous frequency can be obtained by differentiating the instantaneous phase in respect to time. The instantaneous phase corresponds to the phase angle of the analytic signal.

```
>>> analytic_signal = hilbert(signal)
>>> amplitude_envelope = np.abs(analytic_signal)
>>> instantaneous_phase = np.unwrap(np.angle(analytic_signal))
>>> instantaneous_frequency = (np.diff(instantaneous_phase) /
...                            (2.0*np.pi) * fs)
```

```
>>> fig, (ax0, ax1) = plt.subplots(nrows=2)
>>> ax0.plot(t, signal, label='signal')
>>> ax0.plot(t, amplitude_envelope, label='envelope')
>>> ax0.set_xlabel("time in seconds")
>>> ax0.legend()
>>> ax1.plot(t[1:], instantaneous_frequency)
>>> ax1.set_xlabel("time in seconds")
```

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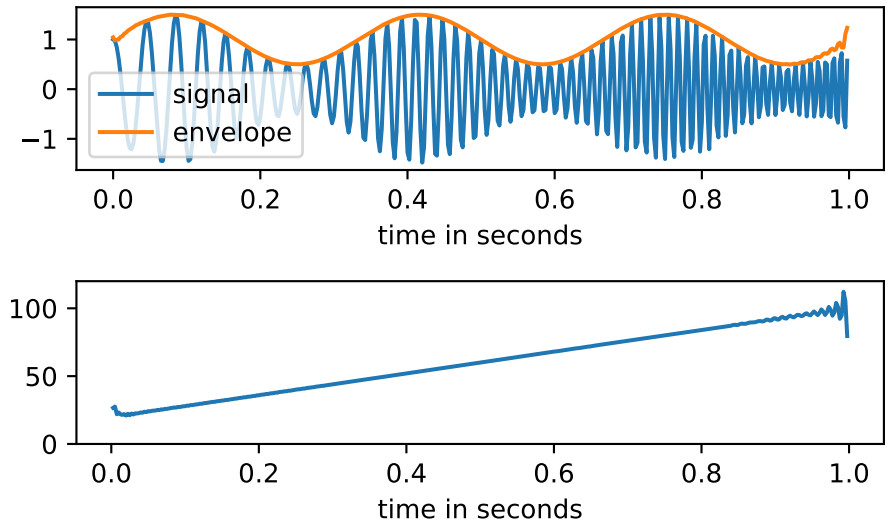
```
>>> ax1.set_ylim(0.0, 120.0)
>>> fig.tight_layout()
```



scipy.signal.hilbert2

`scipy.signal.`**`hilbert2`**(*x*, *N=None*)

Compute the '2-D' analytic signal of *x*

Parameters

x	[array_like] 2-D signal data.
N	[int or tuple of two ints, optional] Number of Fourier components. Default is `x.shape`

Returns

xa	[ndarray] Analytic signal of *x* taken along axes (0,1).

References

[1]

scipy.signal.decimate

`scipy.signal.`**`decimate`**(*x*, *q*, *n=None*, *ftype='iir'*, *axis=- 1*, *zero_phase=True*)

Downsample the signal after applying an anti-aliasing filter.

By default, an order 8 Chebyshev type I filter is used. A 30 point FIR filter with Hamming window is used if *ftype* is 'fir'.

Parameters

x	[array_like] The signal to be downsampled, as an N-dimensional array.
q	[int] The downsampling factor. When using IIR downsampling, it is recommended to call *decimate* multiple times for downsampling factors higher than 13.
n	[int, optional] The order of the filter (1 less than the length for 'fir'). Defaults to 8 for 'iir' and 20 times the downsampling factor for 'fir'.

ftype [str {'iir', 'fir'} or `dlti` instance, optional] If 'iir' or 'fir', specifies the type of lowpass filter. If an instance of an *dlti* object, uses that object to filter before downsampling.

axis [int, optional] The axis along which to decimate.

zero_phase
[bool, optional] Prevent phase shift by filtering with *filtfilt* instead of *lfilter* when using an IIR filter, and shifting the outputs back by the filter's group delay when using an FIR filter. The default value of `True` is recommended, since a phase shift is generally not desired.
New in version 0.18.0.

Returns

y [ndarray] The down-sampled signal.

See also:

resample

Resample up or down using the FFT method.

resample_poly

Resample using polyphase filtering and an FIR filter.

Notes

The `zero_phase` keyword was added in 0.18.0. The possibility to use instances of `dlti` as `ftype` was added in 0.18.0.

scipy.signal.detrend

`scipy.signal.`**`detrend`**(*data*, *axis=-1*, *type='linear'*, *bp=0*, *overwrite_data=False*)

Remove linear trend along axis from data.

Parameters

data [array_like] The input data.

axis [int, optional] The axis along which to detrend the data. By default this is the last axis (-1).

type [{'linear', 'constant'}, optional] The type of detrending. If `type == 'linear'` (default), the result of a linear least-squares fit to *data* is subtracted from *data*. If `type == 'constant'`, only the mean of *data* is subtracted.

bp [array_like of ints, optional] A sequence of break points. If given, an individual linear fit is performed for each part of *data* between two break points. Break points are specified as indices into *data*. This parameter only has an effect when `type == 'linear'`.

overwrite_data
[bool, optional] If True, perform in place detrending and avoid a copy. Default is False

Returns

ret [ndarray] The detrended input data.

Examples

```
>>> from scipy import signal
>>> from numpy.random import default_rng
>>> rng = default_rng()
>>> npoints = 1000
>>> noise = rng.standard_normal(npoints)
>>> x = 3 + 2*np.linspace(0, 1, npoints) + noise
>>> (signal.detrend(x) - noise).max()
0.06  # random
```

scipy.signal.resample

scipy.signal.**resample**(*x*, *num*, *t=None*, *axis=0*, *window=None*, *domain='time'*)

Resample *x* to *num* samples using Fourier method along the given axis.

The resampled signal starts at the same value as *x* but is sampled with a spacing of `len(x) / num * (spacing of x)`. Because a Fourier method is used, the signal is assumed to be periodic.

Parameters

x	[array_like] The data to be resampled.
num	[int] The number of samples in the resampled signal.
t	[array_like, optional] If *t* is given, it is assumed to be the equally spaced sample positions associated with the signal data in *x*.
axis	[int, optional] The axis of *x* that is resampled. Default is 0.
window	[array_like, callable, string, float, or tuple, optional] Specifies the window applied to the signal in the Fourier domain. See below for details.
domain	[string, optional] A string indicating the domain of the input *x*: `time` Consider the input *x* as time-domain (Default), `freq` Consider the input *x* as frequency-domain.

Returns

resampled_x or (resampled_x, resampled_t)
: Either the resampled array, or, if *t* was given, a tuple containing the resampled array and the corresponding resampled positions.

See also:

decimate

Downsample the signal after applying an FIR or IIR filter.

resample_poly

Resample using polyphase filtering and an FIR filter.

Notes

The argument *window* controls a Fourier-domain window that tapers the Fourier spectrum before zero-padding to alleviate ringing in the resampled values for sampled signals you didn't intend to be interpreted as band-limited.

If *window* is a function, then it is called with a vector of inputs indicating the frequency bins (i.e. fftfreq(x.shape[axis])).

If *window* is an array of the same length as *x.shape[axis]* it is assumed to be the window to be applied directly in the Fourier domain (with dc and low-frequency first).

For any other type of *window*, the function *scipy.signal.get_window* is called to generate the window.

The first sample of the returned vector is the same as the first sample of the input vector. The spacing between samples is changed from `dx` to `dx * len(x) / num`.

If *t* is not None, then it is used solely to calculate the resampled positions *resampled_t*

As noted, *resample* uses FFT transformations, which can be very slow if the number of input or output samples is large and prime; see *scipy.fft.fft*.

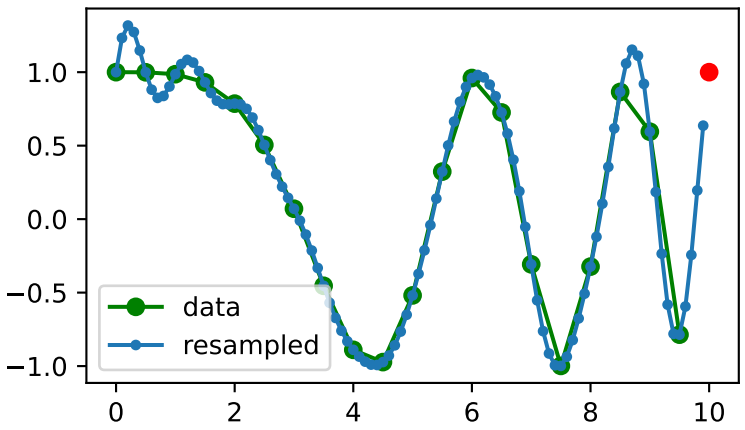
Examples

Note that the end of the resampled data rises to meet the first sample of the next cycle:

```
>>> from scipy import signal
```

```
>>> x = np.linspace(0, 10, 20, endpoint=False)
>>> y = np.cos(-x**2/6.0)
>>> f = signal.resample(y, 100)
>>> xnew = np.linspace(0, 10, 100, endpoint=False)
```

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'go-', xnew, f, '.-', 10, y[0], 'ro')
>>> plt.legend(['data', 'resampled'], loc='best')
>>> plt.show()
```



scipy.signal.resample_poly

scipy.signal.**resample_poly**(*x*, *up*, *down*, *axis=0*, *window=('kaiser', 5.0)*, *padtype='constant'*, *cval=None*)

Resample *x* along the given axis using polyphase filtering.

The signal *x* is upsampled by the factor *up*, a zero-phase low-pass FIR filter is applied, and then it is downsampled by the factor *down*. The resulting sample rate is `up / down` times the original sample rate. By default, values beyond the boundary of the signal are assumed to be zero during the filtering step.

Parameters

x [array_like] The data to be resampled.
up [int] The upsampling factor.
down [int] The downsampling factor.
axis [int, optional] The axis of *x* that is resampled. Default is 0.
window [string, tuple, or array_like, optional] Desired window to use to design the low-pass filter, or the FIR filter coefficients to employ. See below for details.
padtype [string, optional] *constant*, *line*, *mean*, *median*, *maximum*, *minimum* or any of the other signal extension modes supported by `scipy.signal.upfirdn`. Changes assumptions on values beyond the boundary. If *constant*, assumed to be *cval* (default zero). If *line* assumed to continue a linear trend defined by the first and last points. *mean*, *median*, *maximum* and *minimum* work as in *np.pad* and assume that the values beyond the boundary are the mean, median, maximum or minimum respectively of the array along the axis.
New in version 1.4.0.
cval [float, optional] Value to use if *padtype='constant'*. Default is zero.
New in version 1.4.0.

Returns

resampled_x
[array] The resampled array.

See also:

decimate

Downsample the signal after applying an FIR or IIR filter.

resample

Resample up or down using the FFT method.

Notes

This polyphase method will likely be faster than the Fourier method in `scipy.signal.resample` when the number of samples is large and prime, or when the number of samples is large and *up* and *down* share a large greatest common denominator. The length of the FIR filter used will depend on `max(up, down) // gcd(up, down)`, and the number of operations during polyphase filtering will depend on the filter length and *down* (see `scipy.signal.upfirdn` for details).

The argument *window* specifies the FIR low-pass filter design.

If *window* is an array_like it is assumed to be the FIR filter coefficients. Note that the FIR filter is applied after the upsampling step, so it should be designed to operate on a signal at a sampling frequency higher than the original by a factor of *up//gcd(up, down)*. This function's output will be centered with respect to this array, so it is best to pass a symmetric filter with an odd number of samples if, as is usually the case, a zero-phase filter is desired.

For any other type of *window*, the functions `scipy.signal.get_window` and `scipy.signal.firwin` are called to generate the appropriate filter coefficients.

The first sample of the returned vector is the same as the first sample of the input vector. The spacing between samples is changed from `dx` to `dx * down / float(up)`.

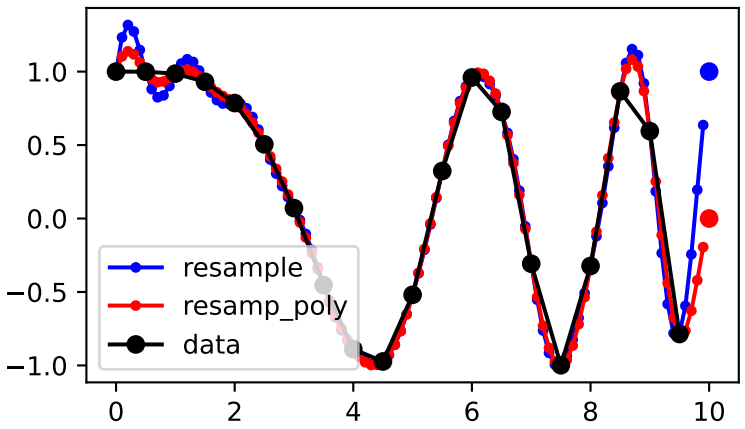
Examples

By default, the end of the resampled data rises to meet the first sample of the next cycle for the FFT method, and gets closer to zero for the polyphase method:

```
>>> from scipy import signal
```

```
>>> x = np.linspace(0, 10, 20, endpoint=False)
>>> y = np.cos(-x**2/6.0)
>>> f_fft = signal.resample(y, 100)
>>> f_poly = signal.resample_poly(y, 100, 20)
>>> xnew = np.linspace(0, 10, 100, endpoint=False)
```

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(xnew, f_fft, 'b.-', xnew, f_poly, 'r.-')
>>> plt.plot(x, y, 'ko-')
>>> plt.plot(10, y[0], 'bo', 10, 0., 'ro')  # boundaries
>>> plt.legend(['resample', 'resamp_poly', 'data'], loc='best')
>>> plt.show()
```



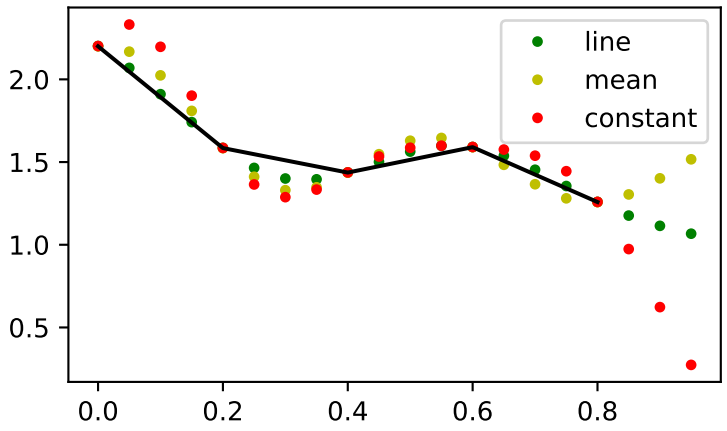
This default behaviour can be changed by using the padtype option:

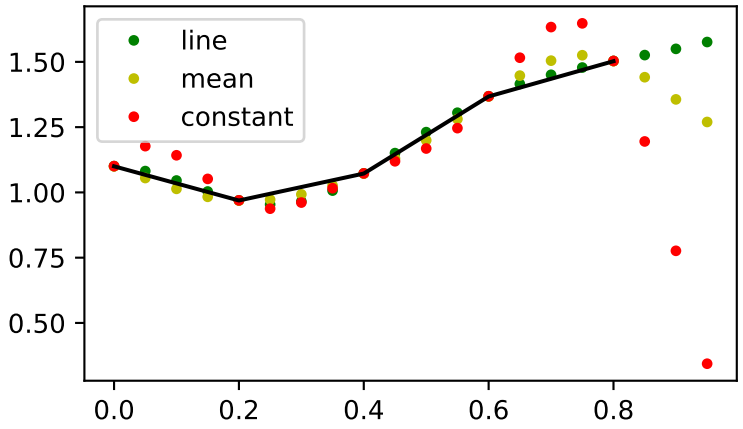
```
>>> import numpy as np
>>> from scipy import signal
```

```
>>> N = 5
>>> x = np.linspace(0, 1, N, endpoint=False)
>>> y = 2 + x**2 - 1.7*np.sin(x) + .2*np.cos(11*x)
>>> y2 = 1 + x**3 + 0.1*np.sin(x) + .1*np.cos(11*x)
>>> Y = np.stack([y, y2], axis=-1)
>>> up = 4
>>> xr = np.linspace(0, 1, N*up, endpoint=False)
```

```
>>> y2 = signal.resample_poly(Y, up, 1, padtype='constant')
>>> y3 = signal.resample_poly(Y, up, 1, padtype='mean')
>>> y4 = signal.resample_poly(Y, up, 1, padtype='line')
```

```
>>> import matplotlib.pyplot as plt
>>> for i in [0,1]:
...     plt.figure()
...     plt.plot(xr, y4[:,i], 'g.', label='line')
...     plt.plot(xr, y3[:,i], 'y.', label='mean')
...     plt.plot(xr, y2[:,i], 'r.', label='constant')
...     plt.plot(x, Y[:,i], 'k-')
...     plt.legend()
>>> plt.show()
```





scipy.signal.upfirdn

scipy.signal.**upfirdn**(*h*, *x*, *up=1*, *down=1*, *axis=- 1*, *mode='constant'*, *cval=0*)

Upsample, FIR filter, and downsample.

Parameters

h [array_like] 1-D FIR (finite-impulse response) filter coefficients.

x [array_like] Input signal array.

up [int, optional] Upsampling rate. Default is 1.

down [int, optional] Downsampling rate. Default is 1.

axis [int, optional] The axis of the input data array along which to apply the linear filter. The filter is applied to each subarray along this axis. Default is -1.

mode [str, optional] The signal extension mode to use. The set `{"constant", "symmetric", "reflect", "edge", "wrap"}` correspond to modes provided by `numpy.pad`. `"smooth"` implements a smooth extension by extending based on the slope of the last 2 points at each end of the array. `"antireflect"` and `"antisymmetric"` are anti-symmetric versions of `"reflect"` and `"symmetric"`. The mode *"line"* extends the signal based on a linear trend defined by the first and last points along the `axis`.
New in version 1.4.0.

cval [float, optional] The constant value to use when `mode == "constant"`.
New in version 1.4.0.

Returns

y [ndarray] The output signal array. Dimensions will be the same as *x* except for along *axis*, which will change size according to the *h*, *up*, and *down* parameters.

Notes

The algorithm is an implementation of the block diagram shown on page 129 of the Vaidyanathan text [1] (Figure 4.3-8d).

The direct approach of upsampling by factor of P with zero insertion, FIR filtering of length `N`, and downsampling by factor of Q is O(N*Q) per output sample. The polyphase implementation used here is O(N/P).

New in version 0.18.

References

[1]

Examples

Simple operations:

```
>>> from scipy.signal import upfirdn
>>> upfirdn([1, 1, 1], [1, 1, 1])   # FIR filter
array([ 1.,  2.,  3.,  2.,  1.])
>>> upfirdn([1], [1, 2, 3], 3)  # upsampling with zeros insertion
array([ 1.,  0.,  0.,  2.,  0.,  0.,  3.,  0.,  0.])
>>> upfirdn([1, 1, 1], [1, 2, 3], 3)  # upsampling with sample-and-hold
array([ 1.,  1.,  1.,  2.,  2.,  2.,  3.,  3.,  3.])
```

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```
>>> upfirdn([.5, 1, .5], [1, 1, 1], 2)  # linear interpolation
array([ 0.5,  1. ,  1. ,  1. ,  1. ,  1. ,  0.5,  0. ])
>>> upfirdn([1], np.arange(10), 1, 3)  # decimation by 3
array([ 0.,  3.,  6.,  9.])
>>> upfirdn([.5, 1, .5], np.arange(10), 2, 3)  # linear interp, rate 2/3
array([ 0. ,  1. ,  2.5,  4. ,  5.5,  7. ,  8.5,  0. ])
```

Apply a single filter to multiple signals:

```
>>> x = np.reshape(np.arange(8), (4, 2))
>>> x
array([[0, 1],
       [2, 3],
       [4, 5],
       [6, 7]])
```

Apply along the last dimension of `x`:

```
>>> h = [1, 1]
>>> upfirdn(h, x, 2)
array([[ 0.,  0.,  1.,  1.],
       [ 2.,  2.,  3.,  3.],
       [ 4.,  4.,  5.,  5.],
       [ 6.,  6.,  7.,  7.]])
```

Apply along the 0th dimension of `x`:

```
>>> upfirdn(h, x, 2, axis=0)
array([[ 0.,  1.],
       [ 0.,  1.],
       [ 2.,  3.],
       [ 2.,  3.],
       [ 4.,  5.],
       [ 4.,  5.],
       [ 6.,  7.],
       [ 6.,  7.]])
```

Filter design

bilinear(b, a[, fs])	Return a digital IIR filter from an analog one using a bilinear transform.
bilinear_zpk(z, p, k, fs)	Return a digital IIR filter from an analog one using a bilinear transform.
findfreqs(num, den, N[, kind])	Find array of frequencies for computing the response of an analog filter.
firls(numtaps, bands, desired[, weight, nyq, fs])	FIR filter design using least-squares error minimization.
firwin(numtaps, cutoff[, width, window, …])	FIR filter design using the window method.
firwin2(numtaps, freq, gain[, nfreqs, …])	FIR filter design using the window method.
freqs(b, a[, worN, plot])	Compute frequency response of analog filter.
freqs_zpk(z, p, k[, worN])	Compute frequency response of analog filter.

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Table 158 – continued from previous page

freqz(b[, a, worN, whole, plot, fs, …])	Compute the frequency response of a digital filter.
freqz_zpk(z, p, k[, worN, whole, fs])	Compute the frequency response of a digital filter in ZPK form.
sosfreqz(sos[, worN, whole, fs])	Compute the frequency response of a digital filter in SOS format.
gammatone(freq, ftype[, order, numtaps, fs])	Gammatone filter design.
group_delay(system[, w, whole, fs])	Compute the group delay of a digital filter.
iirdesign(wp, ws, gpass, gstop[, analog, …])	Complete IIR digital and analog filter design.
iirfilter(N, Wn[, rp, rs, btype, analog, …])	IIR digital and analog filter design given order and critical points.
kaiser_atten(numtaps, width)	Compute the attenuation of a Kaiser FIR filter.
kaiser_beta(a)	Compute the Kaiser parameter *beta*, given the attenuation *a*.
kaiserord(ripple, width)	Determine the filter window parameters for the Kaiser window method.
minimum_phase(h[, method, n_fft])	Convert a linear-phase FIR filter to minimum phase
savgol_coeffs(window_length, polyorder[, …])	Compute the coefficients for a 1-D Savitzky-Golay FIR filter.
remez(numtaps, bands, desired[, weight, Hz, …])	Calculate the minimax optimal filter using the Remez exchange algorithm.
unique_roots(p[, tol, rtype])	Determine unique roots and their multiplicities from a list of roots.
residue(b, a[, tol, rtype])	Compute partial-fraction expansion of b(s) / a(s).
residuez(b, a[, tol, rtype])	Compute partial-fraction expansion of b(z) / a(z).
invres(r, p, k[, tol, rtype])	Compute b(s) and a(s) from partial fraction expansion.
invresz(r, p, k[, tol, rtype])	Compute b(z) and a(z) from partial fraction expansion.
BadCoefficients	Warning about badly conditioned filter coefficients

scipy.signal.bilinear

scipy.signal.**bilinear**(*b*, *a*, *fs=1.0*)

Return a digital IIR filter from an analog one using a bilinear transform.

Transform a set of poles and zeros from the analog s-plane to the digital z-plane using Tustin's method, which substitutes `(z-1) / (z+1)` for `s`, maintaining the shape of the frequency response.

Parameters

b [array_like] Numerator of the analog filter transfer function.

a [array_like] Denominator of the analog filter transfer function.

fs [float] Sample rate, as ordinary frequency (e.g., hertz). No prewarping is done in this function.

Returns

z [ndarray] Numerator of the transformed digital filter transfer function.

p [ndarray] Denominator of the transformed digital filter transfer function.

See also:

lp2lp, **lp2hp**, **lp2bp**, **lp2bs**

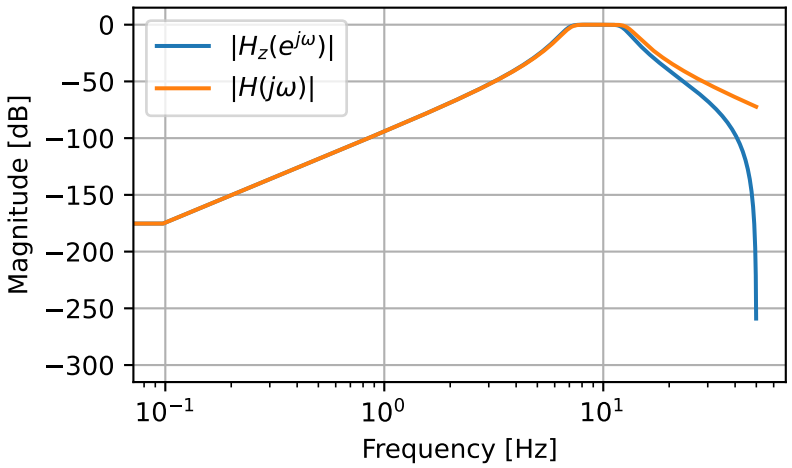
bilinear_zpk

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> fs = 100
>>> bf = 2 * np.pi * np.array([7, 13])
>>> filts = signal.lti(*signal.butter(4, bf, btype='bandpass',
...                                   analog=True))
>>> filtz = signal.lti(*signal.bilinear(filts.num, filts.den, fs))
>>> wz, hz = signal.freqz(filtz.num, filtz.den)
>>> ws, hs = signal.freqs(filts.num, filts.den, worN=fs*wz)
```

```
>>> plt.semilogx(wz*fs/(2*np.pi), 20*np.log10(np.abs(hz).clip(1e-15)),
...              label=r'$|H_z(e^{j \omega})|$')
>>> plt.semilogx(wz*fs/(2*np.pi), 20*np.log10(np.abs(hs).clip(1e-15)),
...              label=r'$|H(j \omega)|$')
>>> plt.legend()
>>> plt.xlabel('Frequency [Hz]')
>>> plt.ylabel('Magnitude [dB]')
>>> plt.grid()
```



scipy.signal.bilinear_zpk

`scipy.signal.`**`bilinear_zpk`**(*z*, *p*, *k*, *fs*)

Return a digital IIR filter from an analog one using a bilinear transform.

Transform a set of poles and zeros from the analog s-plane to the digital z-plane using Tustin's method, which substitutes `(z-1) / (z+1)` for `s`, maintaining the shape of the frequency response.

Parameters

z	[array_like] Zeros of the analog filter transfer function.
p	[array_like] Poles of the analog filter transfer function.
k	[float] System gain of the analog filter transfer function.

fs [float] Sample rate, as ordinary frequency (e.g., hertz). No prewarping is done in this function.

Returns

z [ndarray] Zeros of the transformed digital filter transfer function.
p [ndarray] Poles of the transformed digital filter transfer function.
k [float] System gain of the transformed digital filter.

See also:

lp2lp_zpk, **lp2hp_zpk**, **lp2bp_zpk**, **lp2bs_zpk**

bilinear

Notes

New in version 1.1.0.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> fs = 100
>>> bf = 2 * np.pi * np.array([7, 13])
>>> filts = signal.lti(*signal.butter(4, bf, btype='bandpass',␣
↪analog=True,
...                                    output='zpk'))
>>> filtz = signal.lti(*signal.bilinear_zpk(filts.zeros, filts.poles,
...                                         filts.gain, fs))
>>> wz, hz = signal.freqz_zpk(filtz.zeros, filtz.poles, filtz.gain)
>>> ws, hs = signal.freqs_zpk(filts.zeros, filts.poles, filts.gain,
...                           worN=fs*wz)
>>> plt.semilogx(wz*fs/(2*np.pi), 20*np.log10(np.abs(hz).clip(1e-15)),
...              label=r'$|H_z(e^{j \omega})|$')
>>> plt.semilogx(wz*fs/(2*np.pi), 20*np.log10(np.abs(hs).clip(1e-15)),
...              label=r'$|H(j \omega)|$')
>>> plt.legend()
>>> plt.xlabel('Frequency [Hz]')
>>> plt.ylabel('Magnitude [dB]')
>>> plt.grid()
```

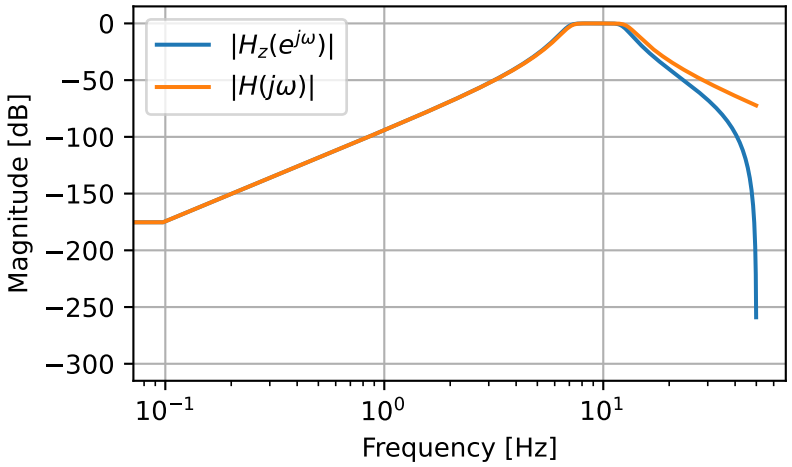
scipy.signal.findfreqs

scipy.signal.**findfreqs**(*num*, *den*, *N*, *kind='ba'*)

Find array of frequencies for computing the response of an analog filter.

Parameters

num, den [array_like, 1-D] The polynomial coefficients of the numerator and denominator of the transfer function of the filter or LTI system, where the coefficients are ordered from highest to lowest degree. Or, the roots of the transfer function numerator and denominator (i.e., zeroes and poles).
N [int] The length of the array to be computed.



kind [str {'ba', 'zp'}, optional] Specifies whether the numerator and denominator are specified by their polynomial coefficients ('ba'), or their roots ('zp').

Returns

w [(N,) ndarray] A 1-D array of frequencies, logarithmically spaced.

Examples

Find a set of nine frequencies that span the "interesting part" of the frequency response for the filter with the transfer function

H(s) = s / (s^2 + 8s + 25)

```
>>> from scipy import signal
>>> signal.findfreqs([1, 0], [1, 8, 25], N=9)
array([  1.00000000e-02,   3.16227766e-02,   1.00000000e-01,
         3.16227766e-01,   1.00000000e+00,   3.16227766e+00,
         1.00000000e+01,   3.16227766e+01,   1.00000000e+02])
```

scipy.signal.firls

`scipy.signal.`**`firls`**(*numtaps*, *bands*, *desired*, *weight=None*, *nyq=None*, *fs=None*)

FIR filter design using least-squares error minimization.

Calculate the filter coefficients for the linear-phase finite impulse response (FIR) filter which has the best approximation to the desired frequency response described by *bands* and *desired* in the least squares sense (i.e., the integral of the weighted mean-squared error within the specified bands is minimized).

Parameters

numtaps [int] The number of taps in the FIR filter. *numtaps* must be odd.

bands [array_like] A monotonic nondecreasing sequence containing the band edges in Hz. All elements must be non-negative and less than or equal to the Nyquist frequency given by *nyq*.

desired [array_like] A sequence the same size as *bands* containing the desired gain at the start and end point of each band.

weight [array_like, optional] A relative weighting to give to each band region when solving the least squares problem. *weight* has to be half the size of *bands*.

nyq [float, optional] *Deprecated. Use `fs` instead.* Nyquist frequency. Each frequency in *bands* must be between 0 and *nyq* (inclusive). Default is 1.

fs [float, optional] The sampling frequency of the signal. Each frequency in *bands* must be between 0 and `fs/2` (inclusive). Default is 2.

Returns

coeffs [ndarray] Coefficients of the optimal (in a least squares sense) FIR filter.

See also:

`firwin`

`firwin2`

`minimum_phase`

`remez`

Notes

This implementation follows the algorithm given in [1]. As noted there, least squares design has multiple advantages:

1. Optimal in a least-squares sense.
2. Simple, non-iterative method.
3. The general solution can obtained by solving a linear system of equations.
4. Allows the use of a frequency dependent weighting function.

This function constructs a Type I linear phase FIR filter, which contains an odd number of *coeffs* satisfying for $n < numtaps$:

$$coeffs(n) = coeffs(numtaps - 1 - n)$$

The odd number of coefficients and filter symmetry avoid boundary conditions that could otherwise occur at the Nyquist and 0 frequencies (e.g., for Type II, III, or IV variants).

New in version 0.18.

References

[1]

Examples

We want to construct a band-pass filter. Note that the behavior in the frequency ranges between our stop bands and pass bands is unspecified, and thus may overshoot depending on the parameters of our filter:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> fig, axs = plt.subplots(2)
>>> fs = 10.0  # Hz
>>> desired = (0, 0, 1, 1, 0, 0)
```

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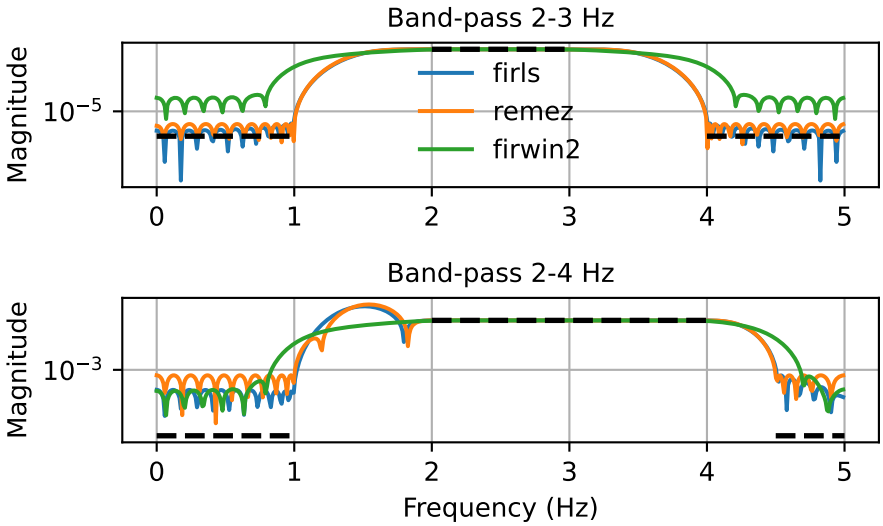
```
>>> for bi, bands in enumerate(((0, 1, 2, 3, 4, 5), (0, 1, 2, 4, 4.5,␣
↪5))):
...     fir_firls = signal.firls(73, bands, desired, fs=fs)
...     fir_remez = signal.remez(73, bands, desired[::2], fs=fs)
...     fir_firwin2 = signal.firwin2(73, bands, desired, fs=fs)
...     hs = list()
...     ax = axs[bi]
...     for fir in (fir_firls, fir_remez, fir_firwin2):
...         freq, response = signal.freqz(fir)
...         hs.append(ax.semilogy(0.5*fs*freq/np.pi, np.abs(response))[0])
...     for band, gains in zip(zip(bands[::2], bands[1::2]),
...                            zip(desired[::2], desired[1::2])):
...         ax.semilogy(band, np.maximum(gains, 1e-7), 'k--', linewidth=2)
...     if bi == 0:
...         ax.legend(hs, ('firls', 'remez', 'firwin2'),
...                   loc='lower center', frameon=False)
...     else:
...         ax.set_xlabel('Frequency (Hz)')
...     ax.grid(True)
...     ax.set(title='Band-pass %d-%d Hz' % bands[2:4], ylabel='Magnitude
↪')
...
>>> fig.tight_layout()
>>> plt.show()
```



scipy.signal.firwin

scipy.signal.**firwin**(*numtaps*, *cutoff*, *width=None*, *window='hamming'*, *pass_zero=True*, *scale=True*, *nyq=None*, *fs=None*)

FIR filter design using the window method.

This function computes the coefficients of a finite impulse response filter. The filter will have linear phase; it will be Type I if *numtaps* is odd and Type II if *numtaps* is even.

Type II filters always have zero response at the Nyquist frequency, so a ValueError exception is raised if firwin is called with *numtaps* even and having a passband whose right end is at the Nyquist frequency.

Parameters

numtaps [int] Length of the filter (number of coefficients, i.e. the filter order + 1). *numtaps* must be odd if a passband includes the Nyquist frequency.

cutoff [float or 1-D array_like] Cutoff frequency of filter (expressed in the same units as *fs*) OR an array of cutoff frequencies (that is, band edges). In the latter case, the frequencies in *cutoff* should be positive and monotonically increasing between 0 and *fs/2*. The values 0 and *fs/2* must not be included in *cutoff*.

width [float or None, optional] If *width* is not None, then assume it is the approximate width of the transition region (expressed in the same units as *fs*) for use in Kaiser FIR filter design. In this case, the *window* argument is ignored.

window [string or tuple of string and parameter values, optional] Desired window to use. See *scipy.signal.get_window* for a list of windows and required parameters.

pass_zero [{True, False, 'bandpass', 'lowpass', 'highpass', 'bandstop'}, optional] If True, the gain at the frequency 0 (i.e., the "DC gain") is 1. If False, the DC gain is 0. Can also be a string argument for the desired filter type (equivalent to `btype` in IIR design functions).
New in version 1.3.0: Support for string arguments.

scale [bool, optional] Set to True to scale the coefficients so that the frequency response is exactly unity at a certain frequency. That frequency is either:
- 0 (DC) if the first passband starts at 0 (i.e. pass_zero is True)
- *fs/2* (the Nyquist frequency) if the first passband ends at *fs/2* (i.e the filter is a single band highpass filter); center of first passband otherwise

nyq [float, optional] *Deprecated. Use `fs` instead.* This is the Nyquist frequency. Each frequency in *cutoff* must be between 0 and *nyq*. Default is 1.

fs [float, optional] The sampling frequency of the signal. Each frequency in *cutoff* must be between 0 and `fs/2`. Default is 2.

Returns

h [(numtaps,) ndarray] Coefficients of length *numtaps* FIR filter.

Raises

ValueError

If any value in *cutoff* is less than or equal to 0 or greater than or equal to `fs/2`, if the values in *cutoff* are not strictly monotonically increasing, or if *numtaps* is even but a passband includes the Nyquist frequency.

See also:

firwin2

firls

minimum_phase

remez

Examples

Low-pass from 0 to f:

```
>>> from scipy import signal
>>> numtaps = 3
>>> f = 0.1
>>> signal.firwin(numtaps, f)
array([ 0.06799017,  0.86401967,  0.06799017])
```

Use a specific window function:

```
>>> signal.firwin(numtaps, f, window='nuttall')
array([  3.56607041e-04,   9.99286786e-01,   3.56607041e-04])
```

High-pass ('stop' from 0 to f):

```
>>> signal.firwin(numtaps, f, pass_zero=False)
array([-0.00859313,  0.98281375, -0.00859313])
```

Band-pass:

```
>>> f1, f2 = 0.1, 0.2
>>> signal.firwin(numtaps, [f1, f2], pass_zero=False)
array([ 0.06301614,  0.88770441,  0.06301614])
```

Band-stop:

```
>>> signal.firwin(numtaps, [f1, f2])
array([-0.00801395,  1.0160279 , -0.00801395])
```

Multi-band (passbands are [0, f1], [f2, f3] and [f4, 1]):

```
>>> f3, f4 = 0.3, 0.4
>>> signal.firwin(numtaps, [f1, f2, f3, f4])
array([-0.01376344,  1.02752689, -0.01376344])
```

Multi-band (passbands are [f1, f2] and [f3,f4]):

```
>>> signal.firwin(numtaps, [f1, f2, f3, f4], pass_zero=False)
array([ 0.04890915,  0.91284326,  0.04890915])
```

scipy.signal.firwin2

scipy.signal.**firwin2**(*numtaps*, *freq*, *gain*, *nfreqs=None*, *window='hamming'*, *nyq=None*, *antisymmetric=False*, *fs=None*)

FIR filter design using the window method.

From the given frequencies *freq* and corresponding gains *gain*, this function constructs an FIR filter with linear phase and (approximately) the given frequency response.

Parameters

numtaps [int] The number of taps in the FIR filter. *numtaps* must be less than *nfreqs*.

freq [array_like, 1-D] The frequency sampling points. Typically 0.0 to 1.0 with 1.0 being Nyquist. The Nyquist frequency is half *fs*. The values in *freq* must be nondecreasing. A value can be

repeated once to implement a discontinuity. The first value in *freq* must be 0, and the last value must be `fs/2`. Values 0 and `fs/2` must not be repeated.

gain [array_like] The filter gains at the frequency sampling points. Certain constraints to gain values, depending on the filter type, are applied, see Notes for details.

nfreqs [int, optional] The size of the interpolation mesh used to construct the filter. For most efficient behavior, this should be a power of 2 plus 1 (e.g, 129, 257, etc). The default is one more than the smallest power of 2 that is not less than *numtaps*. *nfreqs* must be greater than *numtaps*.

window [string or (string, float) or float, or None, optional] Window function to use. Default is "hamming". See *scipy.signal.get_window* for the complete list of possible values. If None, no window function is applied.

nyq [float, optional] *Deprecated. Use `fs` instead.* This is the Nyquist frequency. Each frequency in *freq* must be between 0 and *nyq*. Default is 1.

antisymmetric

[bool, optional] Whether resulting impulse response is symmetric/antisymmetric. See Notes for more details.

fs [float, optional] The sampling frequency of the signal. Each frequency in *cutoff* must be between 0 and `fs/2`. Default is 2.

Returns

taps [ndarray] The filter coefficients of the FIR filter, as a 1-D array of length *numtaps*.

See also:

firls

firwin

minimum_phase

remez

Notes

From the given set of frequencies and gains, the desired response is constructed in the frequency domain. The inverse FFT is applied to the desired response to create the associated convolution kernel, and the first *numtaps* coefficients of this kernel, scaled by *window*, are returned.

The FIR filter will have linear phase. The type of filter is determined by the value of 'numtaps` and *antisymmetric* flag. There are four possible combinations:

- odd *numtaps*, *antisymmetric* is False, type I filter is produced
- even *numtaps*, *antisymmetric* is False, type II filter is produced
- odd *numtaps*, *antisymmetric* is True, type III filter is produced
- even *numtaps*, *antisymmetric* is True, type IV filter is produced

Magnitude response of all but type I filters are subjects to following constraints:

- type II – zero at the Nyquist frequency
- type III – zero at zero and Nyquist frequencies
- type IV – zero at zero frequency

New in version 0.9.0.

References

[1], [2]

Examples

A lowpass FIR filter with a response that is 1 on [0.0, 0.5], and that decreases linearly on [0.5, 1.0] from 1 to 0:

```
>>> from scipy import signal
>>> taps = signal.firwin2(150, [0.0, 0.5, 1.0], [1.0, 1.0, 0.0])
>>> print(taps[72:78])
[-0.02286961 -0.06362756  0.57310236  0.57310236 -0.06362756 -0.02286961]
```

scipy.signal.freqs

scipy.signal.**freqs**(*b*, *a*, *worN=200*, *plot=None*)

Compute frequency response of analog filter.

Given the M-order numerator *b* and N-order denominator *a* of an analog filter, compute its frequency response:

```
         b[0]*(jw)**M + b[1]*(jw)**(M-1) + ... + b[M]
H(w) = ----------------------------------------------
         a[0]*(jw)**N + a[1]*(jw)**(N-1) + ... + a[N]
```

Parameters

b	[array_like] Numerator of a linear filter.
a	[array_like] Denominator of a linear filter.
worN	[{None, int, array_like}, optional] If None, then compute at 200 frequencies around the interesting parts of the response curve (determined by pole-zero locations). If a single integer, then compute at that many frequencies. Otherwise, compute the response at the angular frequencies (e.g., rad/s) given in *worN*.
plot	[callable, optional] A callable that takes two arguments. If given, the return parameters *w* and *h* are passed to plot. Useful for plotting the frequency response inside *freqs*.

Returns

w	[ndarray] The angular frequencies at which *h* was computed.
h	[ndarray] The frequency response.

See also:

freqz

Compute the frequency response of a digital filter.

Notes

Using Matplotlib's "plot" function as the callable for *plot* produces unexpected results, this plots the real part of the complex transfer function, not the magnitude. Try `lambda w, h: plot(w, abs(h))`.

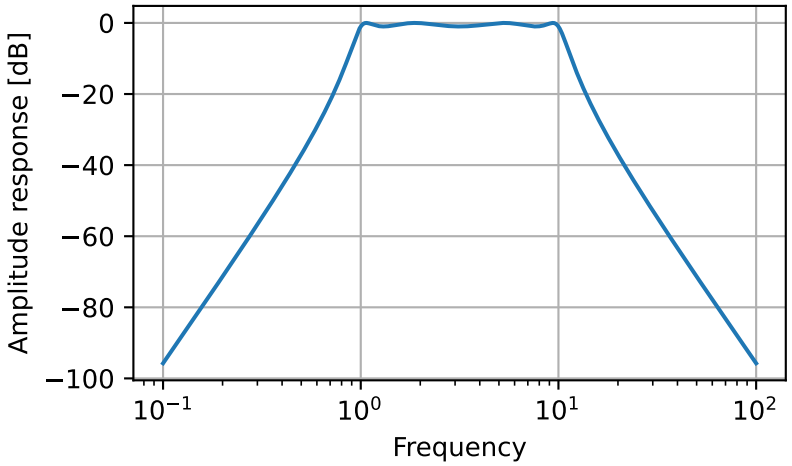
Examples

```
>>> from scipy.signal import freqs, iirfilter
```

```
>>> b, a = iirfilter(4, [1, 10], 1, 60, analog=True, ftype='cheby1')
```

```
>>> w, h = freqs(b, a, worN=np.logspace(-1, 2, 1000))
```

```
>>> import matplotlib.pyplot as plt
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.xlabel('Frequency')
>>> plt.ylabel('Amplitude response [dB]')
>>> plt.grid()
>>> plt.show()
```



scipy.signal.freqs_zpk

`scipy.signal.`**`freqs_zpk`**(*z*, *p*, *k*, *worN=200*)

Compute frequency response of analog filter.

Given the zeros *z*, poles *p*, and gain *k* of a filter, compute its frequency response:

```
             (jw-z[0]) * (jw-z[1]) * ... * (jw-z[-1])
H(w) = k * ----------------------------------------
             (jw-p[0]) * (jw-p[1]) * ... * (jw-p[-1])
```

Parameters

z	[array_like] Zeroes of a linear filter
p	[array_like] Poles of a linear filter
k	[scalar] Gain of a linear filter
worN	[{None, int, array_like}, optional] If None, then compute at 200 frequencies around the interesting parts of the response curve (determined by pole-zero locations). If a single integer, then compute at that many frequencies. Otherwise, compute the response at the angular frequencies (e.g., rad/s) given in *worN*.

Returns

w	[ndarray] The angular frequencies at which *h* was computed.
h	[ndarray] The frequency response.

See also:

freqs

Compute the frequency response of an analog filter in TF form

freqz

Compute the frequency response of a digital filter in TF form

freqz_zpk

Compute the frequency response of a digital filter in ZPK form

Notes

New in version 0.19.0.

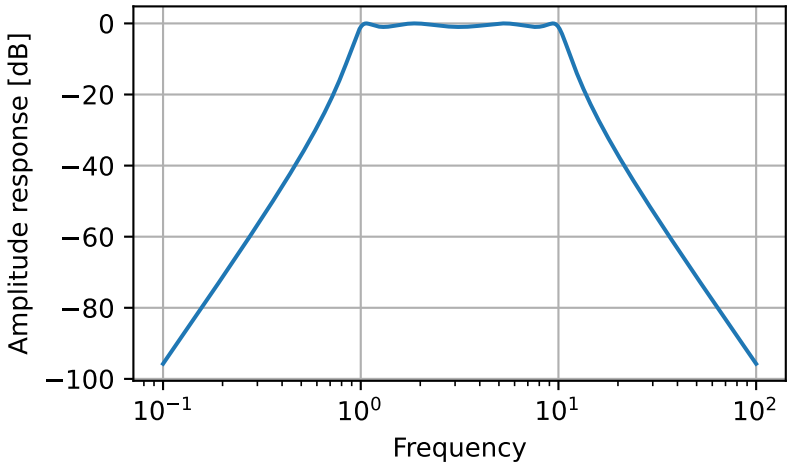
Examples

```
>>> from scipy.signal import freqs_zpk, iirfilter
```

```
>>> z, p, k = iirfilter(4, [1, 10], 1, 60, analog=True, ftype='cheby1',
...                     output='zpk')
```

```
>>> w, h = freqs_zpk(z, p, k, worN=np.logspace(-1, 2, 1000))
```

```
>>> import matplotlib.pyplot as plt
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.xlabel('Frequency')
>>> plt.ylabel('Amplitude response [dB]')
>>> plt.grid()
>>> plt.show()
```



scipy.signal.freqz

`scipy.signal.`**`freqz`**(*b*, *a=1*, *worN=512*, *whole=False*, *plot=None*, *fs=6.283185307179586*, *include_nyquist=False*)

Compute the frequency response of a digital filter.

Given the M-order numerator *b* and N-order denominator *a* of a digital filter, compute its frequency response:

```
             jw                 -jw              -jwM
   jw     B(e  )     b[0] + b[1]e    + ... + b[M]e
H(e  ) = ------ = ----------------------------------
             jw                 -jw              -jwN
          A(e  )     a[0] + a[1]e    + ... + a[N]e
```

Parameters

b [array_like] Numerator of a linear filter. If *b* has dimension greater than 1, it is assumed that the coefficients are stored in the first dimension, and `b.shape[1:]`, `a.shape[1:]`, and the shape of the frequencies array must be compatible for broadcasting.

a [array_like] Denominator of a linear filter. If *b* has dimension greater than 1, it is assumed that the coefficients are stored in the first dimension, and `b.shape[1:]`, `a.shape[1:]`, and the shape of the frequencies array must be compatible for broadcasting.

worN [{None, int, array_like}, optional] If a single integer, then compute at that many frequencies (default is N=512). This is a convenient alternative to:

```
np.linspace(0, fs if whole else fs/2, N, endpoint=include_
↪nyquist)
```

Using a number that is fast for FFT computations can result in faster computations (see Notes).
If an array_like, compute the response at the frequencies given. These are in the same units as *fs*.

whole [bool, optional] Normally, frequencies are computed from 0 to the Nyquist frequency, fs/2 (upper-half of unit-circle). If *whole* is True, compute frequencies from 0 to fs. Ignored if worN is array_like.

plot [callable] A callable that takes two arguments. If given, the return parameters *w* and *h* are passed to plot. Useful for plotting the frequency response inside `freqz`.

fs [float, optional] The sampling frequency of the digital system. Defaults to 2*pi radians/sample (so w is from 0 to pi).
New in version 1.2.0.

include_nyquist
[bool, optional] If *whole* is False and *worN* is an integer, setting *include_nyquist* to True will include the last frequency (Nyquist frequency) and is otherwise ignored.
New in version 1.5.0.

Returns

w [ndarray] The frequencies at which *h* was computed, in the same units as *fs*. By default, *w* is normalized to the range [0, pi) (radians/sample).

h [ndarray] The frequency response, as complex numbers.

See also:

`freqz_zpk`

`sosfreqz`

Notes

Using Matplotlib's `matplotlib.pyplot.plot` function as the callable for *plot* produces unexpected results, as this plots the real part of the complex transfer function, not the magnitude. Try `lambda w, h: plot(w, np.abs(h))`.

A direct computation via (R)FFT is used to compute the frequency response when the following conditions are met:

1. An integer value is given for *worN*.
2. *worN* is fast to compute via FFT (i.e., `next_fast_len(worN)` equals *worN*).
3. The denominator coefficients are a single value (`a.shape[0] == 1`).
4. *worN* is at least as long as the numerator coefficients (`worN >= b.shape[0]`).
5. If `b.ndim > 1`, then `b.shape[-1] == 1`.

For long FIR filters, the FFT approach can have lower error and be much faster than the equivalent direct polynomial calculation.

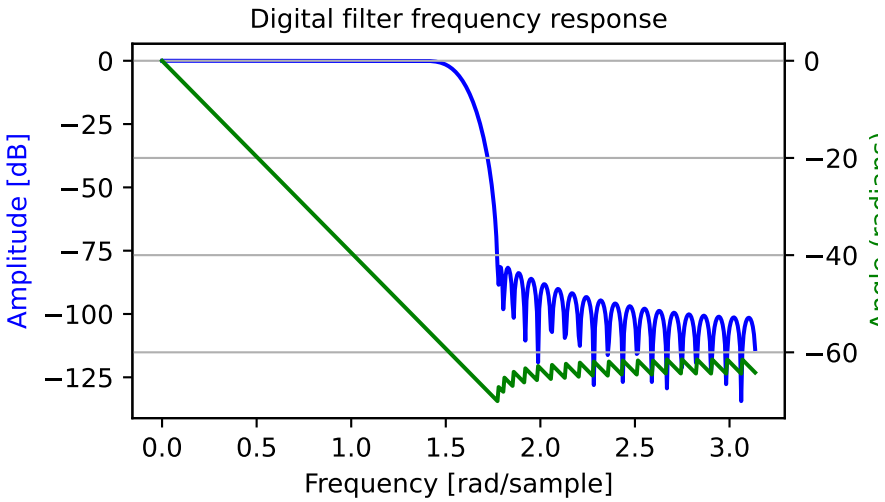
Examples

```
>>> from scipy import signal
>>> b = signal.firwin(80, 0.5, window=('kaiser', 8))
>>> w, h = signal.freqz(b)
```

```
>>> import matplotlib.pyplot as plt
>>> fig, ax1 = plt.subplots()
>>> ax1.set_title('Digital filter frequency response')
```

```
>>> ax1.plot(w, 20 * np.log10(abs(h)), 'b')
>>> ax1.set_ylabel('Amplitude [dB]', color='b')
>>> ax1.set_xlabel('Frequency [rad/sample]')
```

```
>>> ax2 = ax1.twinx()
>>> angles = np.unwrap(np.angle(h))
>>> ax2.plot(w, angles, 'g')
>>> ax2.set_ylabel('Angle (radians)', color='g')
>>> ax2.grid()
>>> ax2.axis('tight')
>>> plt.show()
```



Broadcasting Examples

Suppose we have two FIR filters whose coefficients are stored in the rows of an array with shape (2, 25). For this demonstration, we'll use random data:

```
>>> rng = np.random.default_rng()
>>> b = rng.random((2, 25))
```

To compute the frequency response for these two filters with one call to *freqz*, we must pass in `b.T`, because *freqz* expects the first axis to hold the coefficients. We must then extend the shape with a trivial dimension of length 1 to allow broadcasting with the array of frequencies. That is, we pass in `b.T[..., np.newaxis]`, which has shape (25, 2, 1):

```
>>> w, h = signal.freqz(b.T[..., np.newaxis], worN=1024)
>>> w.shape
(1024,)
>>> h.shape
(2, 1024)
```

Now, suppose we have two transfer functions, with the same numerator coefficients `b = [0.5, 0.5]`. The coefficients for the two denominators are stored in the first dimension of the 2-D array *a*:

```
a = [    1       1   ]
    [ -0.25, -0.5 ]
```

```
>>> b = np.array([0.5, 0.5])
>>> a = np.array([[1, 1], [-0.25, -0.5]])
```

Only *a* is more than 1-D. To make it compatible for broadcasting with the frequencies, we extend it with a trivial dimension in the call to *freqz*:

```
>>> w, h = signal.freqz(b, a[..., np.newaxis], worN=1024)
>>> w.shape
(1024,)
>>> h.shape
(2, 1024)
```

scipy.signal.freqz_zpk

scipy.signal.**freqz_zpk**(*z*, *p*, *k*, *worN=512*, *whole=False*, *fs=6.283185307179586*)

Compute the frequency response of a digital filter in ZPK form.

Given the Zeros, Poles and Gain of a digital filter, compute its frequency response:

$H(z) = k \prod_i (z - Z[i]) / \prod_j (z - P[j])$

where k is the *gain*, Z are the *zeros* and P are the *poles*.

Parameters

z	[array_like] Zeroes of a linear filter
p	[array_like] Poles of a linear filter
k	[scalar] Gain of a linear filter
worN	[{None, int, array_like}, optional] If a single integer, then compute at that many frequencies (default is N=512). If an array_like, compute the response at the frequencies given. These are in the same units as *fs*.
whole	[bool, optional] Normally, frequencies are computed from 0 to the Nyquist frequency, fs/2 (upper-half of unit-circle). If *whole* is True, compute frequencies from 0 to fs. Ignored if w is array_like.
fs	[float, optional] The sampling frequency of the digital system. Defaults to 2*pi radians/sample (so w is from 0 to pi). New in version 1.2.0.

Returns

w	[ndarray] The frequencies at which *h* was computed, in the same units as *fs*. By default, *w* is normalized to the range [0, pi) (radians/sample).
h	[ndarray] The frequency response, as complex numbers.

See also:

freqs

Compute the frequency response of an analog filter in TF form

freqs_zpk

Compute the frequency response of an analog filter in ZPK form

freqz

Compute the frequency response of a digital filter in TF form

Notes

New in version 0.19.0.

Examples

Design a 4th-order digital Butterworth filter with cut-off of 100 Hz in a system with sample rate of 1000 Hz, and plot the frequency response:

```
>>> from scipy import signal
>>> z, p, k = signal.butter(4, 100, output='zpk', fs=1000)
>>> w, h = signal.freqz_zpk(z, p, k, fs=1000)
```

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(1, 1, 1)
>>> ax1.set_title('Digital filter frequency response')
```

```
>>> ax1.plot(w, 20 * np.log10(abs(h)), 'b')
>>> ax1.set_ylabel('Amplitude [dB]', color='b')
>>> ax1.set_xlabel('Frequency [Hz]')
>>> ax1.grid()
```

```
>>> ax2 = ax1.twinx()
>>> angles = np.unwrap(np.angle(h))
>>> ax2.plot(w, angles, 'g')
>>> ax2.set_ylabel('Angle [radians]', color='g')
```

```
>>> plt.axis('tight')
>>> plt.show()
```

scipy.signal.sosfreqz

scipy.signal.**sosfreqz**(*sos*, *worN=512*, *whole=False*, *fs=6.283185307179586*)

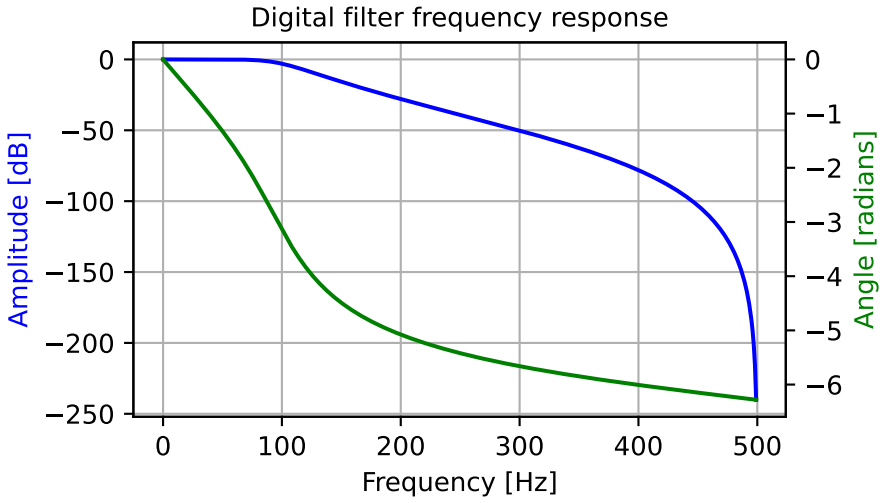
Compute the frequency response of a digital filter in SOS format.

Given *sos*, an array with shape (n, 6) of second order sections of a digital filter, compute the frequency response of the system function:

```
       B0(z)   B1(z)         B{n-1}(z)
H(z) = ----- * ----- * ... * ---------
       A0(z)   A1(z)         A{n-1}(z)
```

for z = exp(omega*1j), where B{k}(z) and A{k}(z) are numerator and denominator of the transfer function of the k-th second order section.

Parameters



sos [array_like] Array of second-order filter coefficients, must have shape `(n_sections, 6)`. Each row corresponds to a second-order section, with the first three columns providing the numerator coefficients and the last three providing the denominator coefficients.

worN [{None, int, array_like}, optional] If a single integer, then compute at that many frequencies (default is N=512). Using a number that is fast for FFT computations can result in faster computations (see Notes of *freqz*).
If an array_like, compute the response at the frequencies given (must be 1-D). These are in the same units as *fs*.

whole [bool, optional] Normally, frequencies are computed from 0 to the Nyquist frequency, fs/2 (upper-half of unit-circle). If *whole* is True, compute frequencies from 0 to fs.

fs [float, optional] The sampling frequency of the digital system. Defaults to 2*pi radians/sample (so w is from 0 to pi).
New in version 1.2.0.

Returns

w [ndarray] The frequencies at which *h* was computed, in the same units as *fs*. By default, *w* is normalized to the range [0, pi) (radians/sample).

h [ndarray] The frequency response, as complex numbers.

See also:

freqz, **sosfilt**

Notes

New in version 0.19.0.

Examples

Design a 15th-order bandpass filter in SOS format.

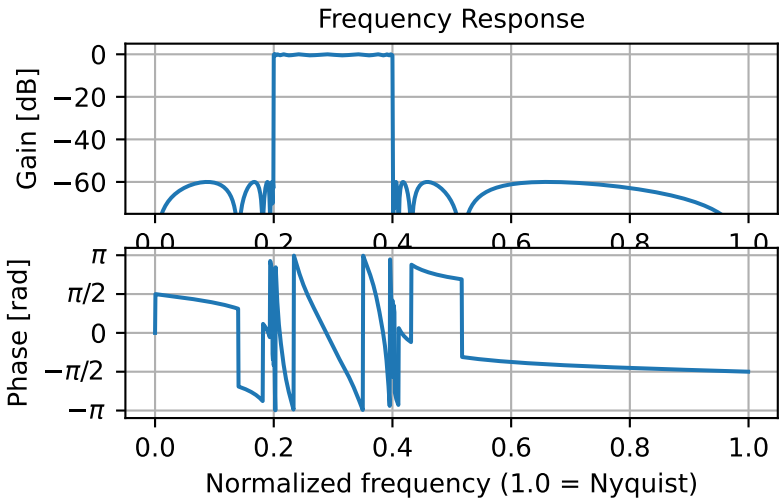
```
>>> from scipy import signal
>>> sos = signal.ellip(15, 0.5, 60, (0.2, 0.4), btype='bandpass',
...                    output='sos')
```

Compute the frequency response at 1500 points from DC to Nyquist.

```
>>> w, h = signal.sosfreqz(sos, worN=1500)
```

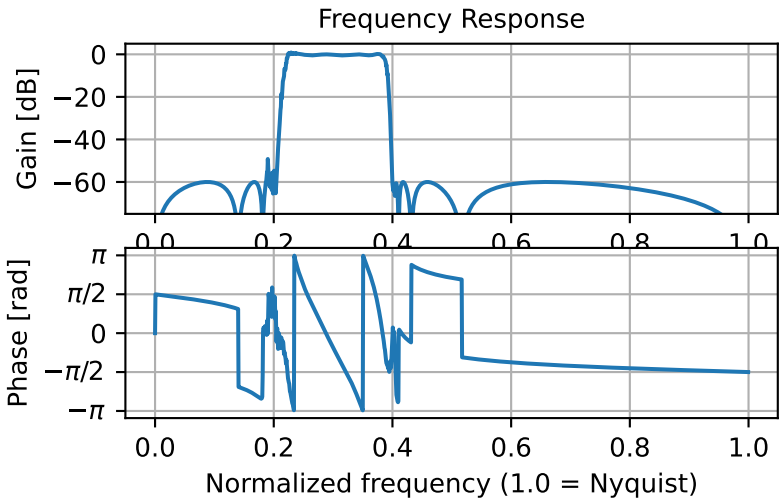
Plot the response.

```
>>> import matplotlib.pyplot as plt
>>> plt.subplot(2, 1, 1)
>>> db = 20*np.log10(np.maximum(np.abs(h), 1e-5))
>>> plt.plot(w/np.pi, db)
>>> plt.ylim(-75, 5)
>>> plt.grid(True)
>>> plt.yticks([0, -20, -40, -60])
>>> plt.ylabel('Gain [dB]')
>>> plt.title('Frequency Response')
>>> plt.subplot(2, 1, 2)
>>> plt.plot(w/np.pi, np.angle(h))
>>> plt.grid(True)
>>> plt.yticks([-np.pi, -0.5*np.pi, 0, 0.5*np.pi, np.pi],
...            [r'$-\pi$', r'$-\pi/2$', '0', r'$\pi/2$', r'$\pi$'])
>>> plt.ylabel('Phase [rad]')
>>> plt.xlabel('Normalized frequency (1.0 = Nyquist)')
>>> plt.show()
```



If the same filter is implemented as a single transfer function, numerical error corrupts the frequency response:

```
>>> b, a = signal.ellip(15, 0.5, 60, (0.2, 0.4), btype='bandpass',
...                     output='ba')
>>> w, h = signal.freqz(b, a, worN=1500)
>>> plt.subplot(2, 1, 1)
>>> db = 20*np.log10(np.maximum(np.abs(h), 1e-5))
>>> plt.plot(w/np.pi, db)
>>> plt.ylim(-75, 5)
>>> plt.grid(True)
>>> plt.yticks([0, -20, -40, -60])
>>> plt.ylabel('Gain [dB]')
>>> plt.title('Frequency Response')
>>> plt.subplot(2, 1, 2)
>>> plt.plot(w/np.pi, np.angle(h))
>>> plt.grid(True)
>>> plt.yticks([-np.pi, -0.5*np.pi, 0, 0.5*np.pi, np.pi],
...            [r'$-\pi$', r'$-\pi/2$', '0', r'$\pi/2$', r'$\pi$'])
>>> plt.ylabel('Phase [rad]')
>>> plt.xlabel('Normalized frequency (1.0 = Nyquist)')
>>> plt.show()
```



scipy.signal.gammatone

`scipy.signal.`**`gammatone`**(*freq*, *ftype*, *order=None*, *numtaps=None*, *fs=None*)

Gammatone filter design.

This function computes the coefficients of an FIR or IIR gammatone digital filter [1].

Parameters

freq [float] Center frequency of the filter (expressed in the same units as *fs*).

ftype [{'fir', 'iir'}] The type of filter the function generates. If 'fir', the function will generate an Nth order FIR gammatone filter. If 'iir', the function will generate an 8th order digital IIR filter, modeled as as 4th order gammatone filter.

order [int, optional] The order of the filter. Only used when `ftype='fir'`. Default is 4 to model the human auditory system. Must be between 0 and 24.

numtaps [int, optional] Length of the filter. Only used when `ftype='fir'`. Default is `fs*0.015` if *fs* is greater than 1000, 15 if *fs* is less than or equal to 1000.

fs [float, optional] The sampling frequency of the signal. *freq* must be between 0 and `fs/2`. Default is 2.

Returns

b, a [ndarray, ndarray] Numerator (`b`) and denominator (`a`) polynomials of the filter.

Raises

ValueError

If *freq* is less than or equal to 0 or greater than or equal to `fs/2`, if *ftype* is not 'fir' or 'iir', if *order* is less than or equal to 0 or greater than 24 when `ftype='fir'`

See also:

`firwin`

`iirfilter`

References

[1]

Examples

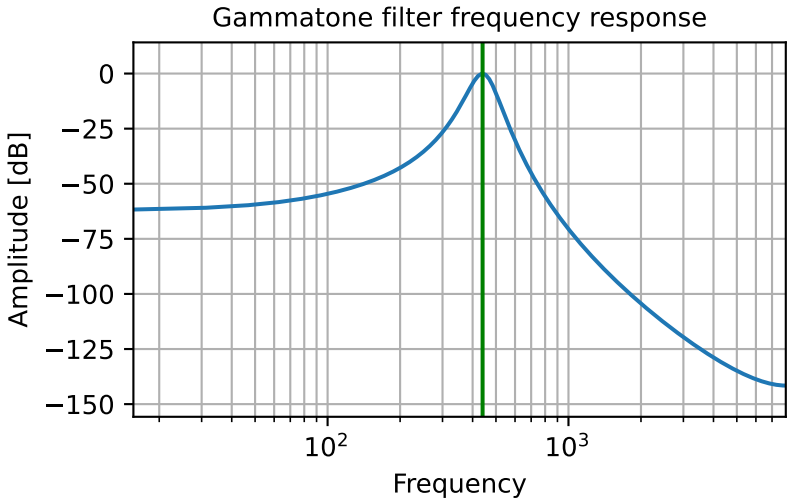
16-sample 4th order FIR Gammatone filter centered at 440 Hz

```
>>> from scipy import signal
>>> signal.gammatone(440, 'fir', numtaps=16, fs=16000)
(array([ 0.00000000e+00,  2.22196719e-07,  1.64942101e-06,  4.99298227e-
↪06,
    1.01993969e-05,  1.63125770e-05,  2.14648940e-05,  2.29947263e-05,
    1.76776931e-05,  2.04980537e-06, -2.72062858e-05, -7.28455299e-05,
   -1.36651076e-04, -2.19066855e-04, -3.18905076e-04, -4.33156712e-04]),
   [1.0])
```

IIR Gammatone filter centered at 440 Hz

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.gammatone(440, 'iir', fs=16000)
>>> w, h = signal.freqz(b, a)
>>> plt.plot(w / ((2 * np.pi) / 16000), 20 * np.log10(abs(h)))
>>> plt.xscale('log')
>>> plt.title('Gammatone filter frequency response')
>>> plt.xlabel('Frequency')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(440, color='green') # cutoff frequency
>>> plt.show()
```



scipy.signal.group_delay

scipy.signal.**group_delay**(*system*, *w=512*, *whole=False*, *fs=6.283185307179586*)

Compute the group delay of a digital filter.

The group delay measures by how many samples amplitude envelopes of various spectral components of a signal are delayed by a filter. It is formally defined as the derivative of continuous (unwrapped) phase:

```
            d        jw
D(w) = - -- arg H(e)
           dw
```

Parameters

system [tuple of array_like (b, a)] Numerator and denominator coefficients of a filter transfer function.

w [{None, int, array_like}, optional] If a single integer, then compute at that many frequencies (default is N=512).
If an array_like, compute the delay at the frequencies given. These are in the same units as *fs*.

whole [bool, optional] Normally, frequencies are computed from 0 to the Nyquist frequency, fs/2 (upper-half of unit-circle). If *whole* is True, compute frequencies from 0 to fs. Ignored if w is array_like.

fs [float, optional] The sampling frequency of the digital system. Defaults to 2*pi radians/sample (so w is from 0 to pi).
New in version 1.2.0.

Returns

w [ndarray] The frequencies at which group delay was computed, in the same units as *fs*. By default, *w* is normalized to the range [0, pi) (radians/sample).

gd [ndarray] The group delay.

See also:

freqz

Frequency response of a digital filter

Notes

The similar function in MATLAB is called *grpdelay*.

If the transfer function $H(z)$ has zeros or poles on the unit circle, the group delay at corresponding frequencies is undefined. When such a case arises the warning is raised and the group delay is set to 0 at those frequencies.

For the details of numerical computation of the group delay refer to [1].

New in version 0.16.0.

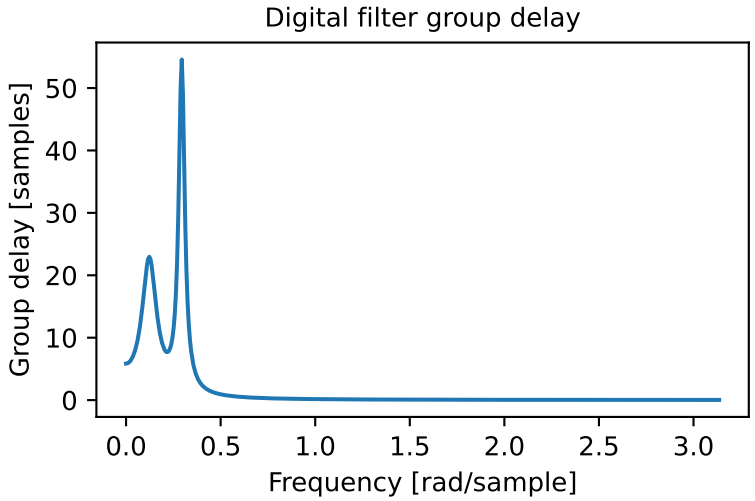
References

[1]

Examples

```
>>> from scipy import signal
>>> b, a = signal.iirdesign(0.1, 0.3, 5, 50, ftype='cheby1')
>>> w, gd = signal.group_delay((b, a))
```

```
>>> import matplotlib.pyplot as plt
>>> plt.title('Digital filter group delay')
>>> plt.plot(w, gd)
>>> plt.ylabel('Group delay [samples]')
>>> plt.xlabel('Frequency [rad/sample]')
>>> plt.show()
```



scipy.signal.iirdesign

scipy.signal.**iirdesign**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*, *ftype='ellip'*, *output='ba'*, *fs=None*)

Complete IIR digital and analog filter design.

Given passband and stopband frequencies and gains, construct an analog or digital IIR filter of minimum order for a given basic type. Return the output in numerator, denominator ('ba'), pole-zero ('zpk') or second order sections ('sos') form.

Parameters

wp, ws [float or array like, shape (2,)] Passband and stopband edge frequencies. Possible values are scalars (for lowpass and highpass filters) or ranges (for bandpass and bandstop filters). For digital filters, these are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. For example:
- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g., rad/s). Note, that for bandpass and bandstop filters passband must lie strictly inside stopband or vice versa.

gpass [float] The maximum loss in the passband (dB).

gstop [float] The minimum attenuation in the stopband (dB).

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

ftype [str, optional] The type of IIR filter to design:
- Butterworth : 'butter'
- Chebyshev I : 'cheby1'
- Chebyshev II : 'cheby2'
- Cauer/elliptic: 'ellip'
- Bessel/Thomson: 'bessel'

output [{'ba', 'zpk', 'sos'}, optional] Filter form of the output:
- second-order sections (recommended): 'sos'
- numerator/denominator (default) : 'ba'
- pole-zero : 'zpk'

In general the second-order sections ('sos') form is recommended because inferring the coefficients for the numerator/denominator form ('ba') suffers from numerical instabilities. For reasons of backward compatibility the default form is the numerator/denominator form ('ba'), where the 'b' and the 'a' in 'ba' refer to the commonly used names of the coefficients used.
Note: Using the second-order sections form ('sos') is sometimes associated with additional computational costs: for data-intense use cases it is therefore recommended to also investigate the numerator/denominator form ('ba').

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos [ndarray] Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

butter

Filter design using order and critical points

cheby1, **cheby2**, **ellip**, **bessel**

buttord

Find order and critical points from passband and stopband spec

cheb1ord, **cheb2ord**, **ellipord**

iirfilter

General filter design using order and critical frequencies

Notes

The `'sos'` output parameter was added in 0.16.0.

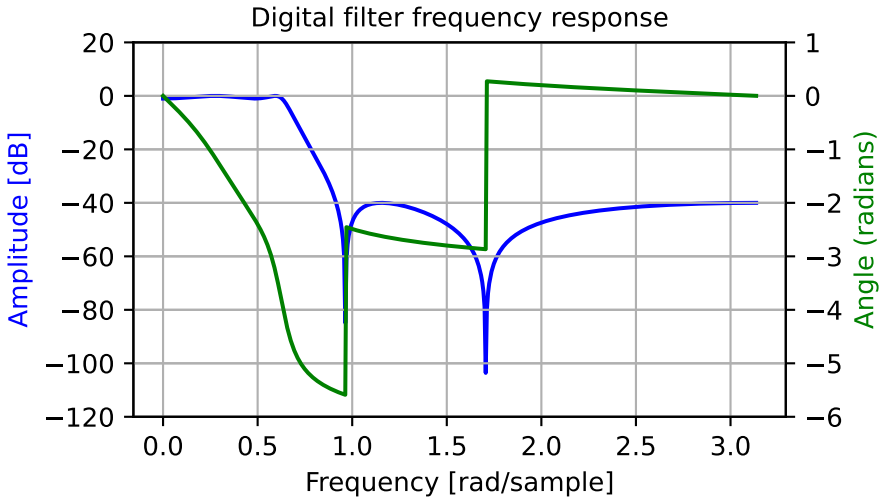
Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> import matplotlib.ticker
```

```
>>> wp = 0.2
>>> ws = 0.3
>>> gpass = 1
>>> gstop = 40
```

```
>>> system = signal.iirdesign(wp, ws, gpass, gstop)
>>> w, h = signal.freqz(*system)
```

```
>>> fig, ax1 = plt.subplots()
>>> ax1.set_title('Digital filter frequency response')
>>> ax1.plot(w, 20 * np.log10(abs(h)), 'b')
>>> ax1.set_ylabel('Amplitude [dB]', color='b')
>>> ax1.set_xlabel('Frequency [rad/sample]')
>>> ax1.grid()
>>> ax1.set_ylim([-120, 20])
>>> ax2 = ax1.twinx()
>>> angles = np.unwrap(np.angle(h))
>>> ax2.plot(w, angles, 'g')
>>> ax2.set_ylabel('Angle (radians)', color='g')
>>> ax2.grid()
>>> ax2.axis('tight')
>>> ax2.set_ylim([-6, 1])
>>> nticks = 8
>>> ax1.yaxis.set_major_locator(matplotlib.ticker.LinearLocator(nticks))
>>> ax2.yaxis.set_major_locator(matplotlib.ticker.LinearLocator(nticks))
```



scipy.signal.iirfilter

`scipy.signal.`**`iirfilter`**(*N*, *Wn*, *rp=None*, *rs=None*, *btype='band'*, *analog=False*, *ftype='butter'*, *output='ba'*, *fs=None*)

IIR digital and analog filter design given order and critical points.

Design an Nth-order digital or analog filter and return the filter coefficients.

Parameters

N [int] The order of the filter.

Wn [array_like] A scalar or length-2 sequence giving the critical frequencies.
For digital filters, *Wn* are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*Wn* is thus in half-cycles / sample.)
For analog filters, *Wn* is an angular frequency (e.g., rad/s).

rp [float, optional] For Chebyshev and elliptic filters, provides the maximum ripple in the passband. (dB)

rs [float, optional] For Chebyshev and elliptic filters, provides the minimum attenuation in the stop band. (dB)

btype [{'bandpass', 'lowpass', 'highpass', 'bandstop'}, optional] The type of filter. Default is 'bandpass'.

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

ftype [str, optional] The type of IIR filter to design:
- Butterworth : 'butter'
- Chebyshev I : 'cheby1'
- Chebyshev II : 'cheby2'
- Cauer/elliptic: 'ellip'
- Bessel/Thomson: 'bessel'

output [{'ba', 'zpk', 'sos'}, optional] Filter form of the output:
- second-order sections (recommended): 'sos'
- numerator/denominator (default) : 'ba'
- pole-zero : 'zpk'

In general the second-order sections ('sos') form is recommended because inferring the coefficients for the numerator/denominator form ('ba') suffers from numerical instabilities. For

reasons of backward compatibility the default form is the numerator/denominator form ('ba'), where the 'b' and the 'a' in 'ba' refer to the commonly used names of the coefficients used. Note: Using the second-order sections form ('sos') is sometimes associated with additional computational costs: for data-intense use cases it is therefore recommended to also investigate the numerator/denominator form ('ba').

fs [float, optional] The sampling frequency of the digital system. New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos [ndarray] Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

butter

Filter design using order and critical points

cheby1, **cheby2**, **ellip**, **bessel**

buttord

Find order and critical points from passband and stopband spec

cheb1ord, **cheb2ord**, **ellipord**

iirdesign

General filter design using passband and stopband spec

Notes

The `'sos'` output parameter was added in 0.16.0.

Examples

Generate a 17th-order Chebyshev II analog bandpass filter from 50 Hz to 200 Hz and plot the frequency response:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.iirfilter(17, [2*np.pi*50, 2*np.pi*200], rs=60,
...                         btype='band', analog=True, ftype='cheby2')
>>> w, h = signal.freqs(b, a, 1000)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(1, 1, 1)
>>> ax.semilogx(w / (2*np.pi), 20 * np.log10(np.maximum(abs(h), 1e-5)))
>>> ax.set_title('Chebyshev Type II bandpass frequency response')
>>> ax.set_xlabel('Frequency [Hz]')
>>> ax.set_ylabel('Amplitude [dB]')
>>> ax.axis((10, 1000, -100, 10))
```

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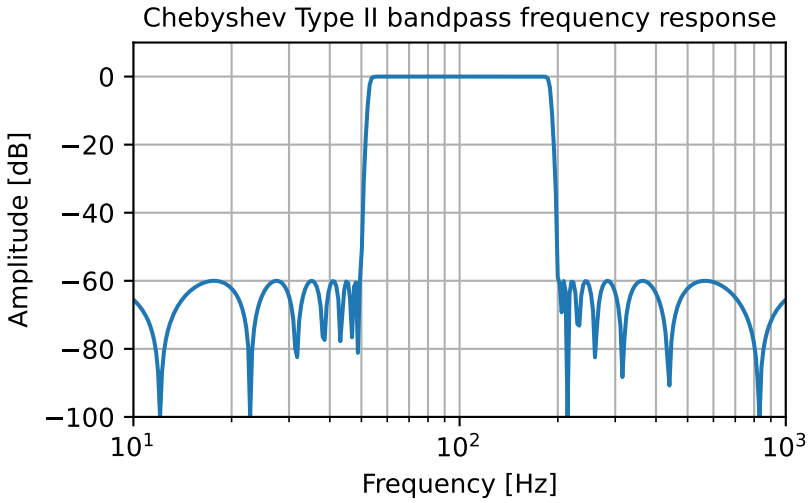
```
>>> ax.grid(which='both', axis='both')
>>> plt.show()
```



Create a digital filter with the same properties, in a system with sampling rate of 2000 Hz, and plot the frequency response. (Second-order sections implementation is required to ensure stability of a filter of this order):

```
>>> sos = signal.iirfilter(17, [50, 200], rs=60, btype='band',
...                        analog=False, ftype='cheby2', fs=2000,
...                        output='sos')
>>> w, h = signal.sosfreqz(sos, 2000, fs=2000)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(1, 1, 1)
>>> ax.semilogx(w, 20 * np.log10(np.maximum(abs(h), 1e-5)))
>>> ax.set_title('Chebyshev Type II bandpass frequency response')
>>> ax.set_xlabel('Frequency [Hz]')
>>> ax.set_ylabel('Amplitude [dB]')
>>> ax.axis((10, 1000, -100, 10))
>>> ax.grid(which='both', axis='both')
>>> plt.show()
```

scipy.signal.kaiser_atten

scipy.signal.**kaiser_atten**(*numtaps*, *width*)

Compute the attenuation of a Kaiser FIR filter.

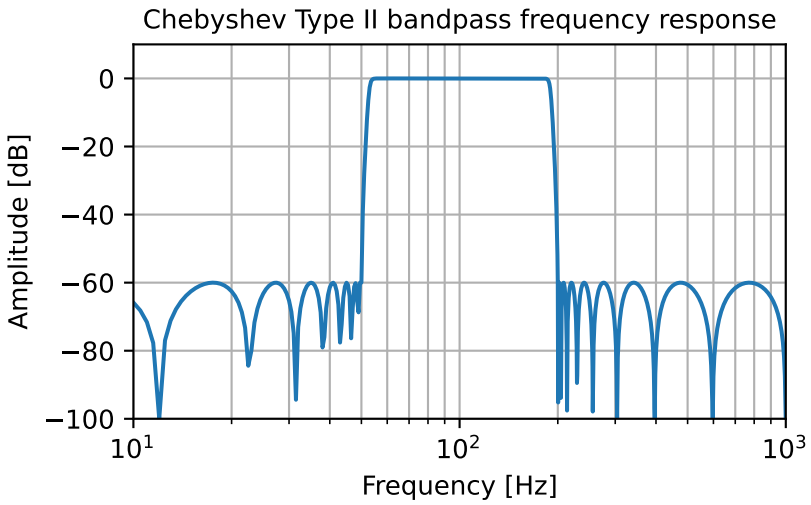
Given the number of taps *N* and the transition width *width*, compute the attenuation *a* in dB, given by Kaiser's formula:

a = 2.285 * (N - 1) * pi * width + 7.95

Parameters

numtaps [int] The number of taps in the FIR filter.

width [float] The desired width of the transition region between passband and stopband (or, in general, at any discontinuity) for the filter, expressed as a fraction of the Nyquist frequency.



Returns

a [float] The attenuation of the ripple, in dB.

See also:

kaiserord, **kaiser_beta**

Examples

Suppose we want to design a FIR filter using the Kaiser window method that will have 211 taps and a transition width of 9 Hz for a signal that is sampled at 480 Hz. Expressed as a fraction of the Nyquist frequency, the width is 9/(0.5*480) = 0.0375. The approximate attenuation (in dB) is computed as follows:

```
>>> from scipy.signal import kaiser_atten
>>> kaiser_atten(211, 0.0375)
64.48099630593983
```

scipy.signal.kaiser_beta

scipy.signal.**kaiser_beta**(*a*)

Compute the Kaiser parameter *beta*, given the attenuation *a*.

Parameters

a [float] The desired attenuation in the stopband and maximum ripple in the passband, in dB. This should be a *positive* number.

Returns

beta [float] The *beta* parameter to be used in the formula for a Kaiser window.

References

Oppenheim, Schafer, "Discrete-Time Signal Processing", p.475-476.

Examples

Suppose we want to design a lowpass filter, with 65 dB attenuation in the stop band. The Kaiser window parameter to be used in the window method is computed by *kaiser_beta(65)*:

```
>>> from scipy.signal import kaiser_beta
>>> kaiser_beta(65)
6.20426
```

scipy.signal.kaiserord

scipy.signal.**kaiserord**(*ripple*, *width*)

Determine the filter window parameters for the Kaiser window method.

The parameters returned by this function are generally used to create a finite impulse response filter using the window method, with either *firwin* or *firwin2*.

Parameters

ripple [float] Upper bound for the deviation (in dB) of the magnitude of the filter's frequency response from that of the desired filter (not including frequencies in any transition intervals). That is, if w is the frequency expressed as a fraction of the Nyquist frequency, A(w) is the actual frequency response of the filter and D(w) is the desired frequency response, the design requirement is that:

```
abs(A(w) - D(w)) < 10**(-ripple/20)
```

for 0 <= w <= 1 and w not in a transition interval.

width [float] Width of transition region, normalized so that 1 corresponds to pi radians / sample. That is, the frequency is expressed as a fraction of the Nyquist frequency.

Returns

numtaps [int] The length of the Kaiser window.

beta [float] The beta parameter for the Kaiser window.

See also:

kaiser_beta, **kaiser_atten**

Notes

There are several ways to obtain the Kaiser window:

- `signal.windows.kaiser(numtaps, beta, sym=True)`
- `signal.get_window(beta, numtaps)`
- `signal.get_window(('kaiser', beta), numtaps)`

The empirical equations discovered by Kaiser are used.

References

Oppenheim, Schafer, "Discrete-Time Signal Processing", pp.475-476.

Examples

We will use the Kaiser window method to design a lowpass FIR filter for a signal that is sampled at 1000 Hz.

We want at least 65 dB rejection in the stop band, and in the pass band the gain should vary no more than 0.5%.

We want a cutoff frequency of 175 Hz, with a transition between the pass band and the stop band of 24 Hz. That is, in the band [0, 163], the gain varies no more than 0.5%, and in the band [187, 500], the signal is attenuated by at least 65 dB.

```
>>> from scipy.signal import kaiserord, firwin, freqz
>>> import matplotlib.pyplot as plt
>>> fs = 1000.0
>>> cutoff = 175
>>> width = 24
```

The Kaiser method accepts just a single parameter to control the pass band ripple and the stop band rejection, so we use the more restrictive of the two. In this case, the pass band ripple is 0.005, or 46.02 dB, so we will use 65 dB as the design parameter.

Use *kaiserord* to determine the length of the filter and the parameter for the Kaiser window.

```
>>> numtaps, beta = kaiserord(65, width/(0.5*fs))
>>> numtaps
167
>>> beta
6.20426
```

Use *firwin* to create the FIR filter.

```
>>> taps = firwin(numtaps, cutoff, window=('kaiser', beta),
...               scale=False, nyq=0.5*fs)
```

Compute the frequency response of the filter. `w` is the array of frequencies, and `h` is the corresponding complex array of frequency responses.

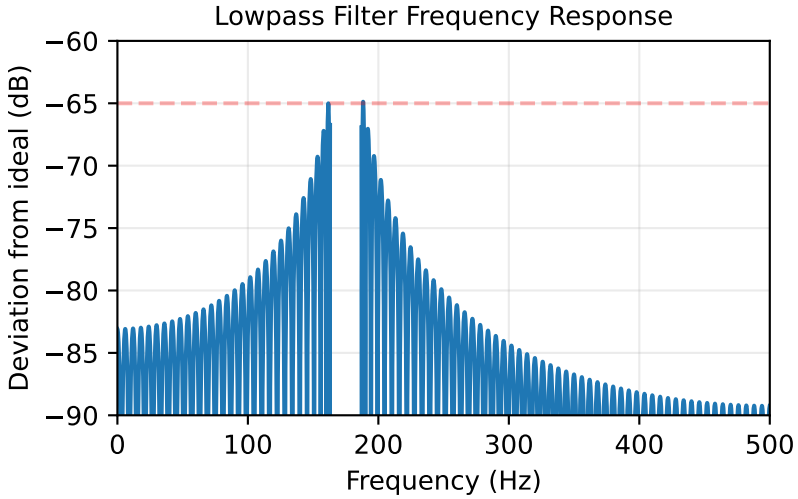
```
>>> w, h = freqz(taps, worN=8000)
>>> w *= 0.5*fs/np.pi  # Convert w to Hz.
```

Compute the deviation of the magnitude of the filter's response from that of the ideal lowpass filter. Values in the transition region are set to `nan`, so they won't appear in the plot.

```
>>> ideal = w < cutoff  # The "ideal" frequency response.
>>> deviation = np.abs(np.abs(h) - ideal)
>>> deviation[(w > cutoff - 0.5*width) & (w < cutoff + 0.5*width)] = np.
↪nan
```

Plot the deviation. A close look at the left end of the stop band shows that the requirement for 65 dB attenuation is violated in the first lobe by about 0.125 dB. This is not unusual for the Kaiser window method.

```
>>> plt.plot(w, 20*np.log10(np.abs(deviation)))
>>> plt.xlim(0, 0.5*fs)
>>> plt.ylim(-90, -60)
>>> plt.grid(alpha=0.25)
>>> plt.axhline(-65, color='r', ls='--', alpha=0.3)
>>> plt.xlabel('Frequency (Hz)')
>>> plt.ylabel('Deviation from ideal (dB)')
>>> plt.title('Lowpass Filter Frequency Response')
>>> plt.show()
```



scipy.signal.minimum_phase

scipy.signal.**minimum_phase**(*h*, *method='homomorphic'*, *n_fft=None*)

Convert a linear-phase FIR filter to minimum phase

Parameters

h [array] Linear-phase FIR filter coefficients.

method [{'hilbert', 'homomorphic'}] The method to use:

'homomorphic' (default)
This method [4] [5] works best with filters with an odd number of taps, and the resulting minimum phase filter will have a magnitude response that approximates the square root of the the original filter's magnitude response.

'hilbert' This method [1] is designed to be used with equiripple filters (e.g., from *remez*) with unity or zero gain regions.

n_fft [int] The number of points to use for the FFT. Should be at least a few times larger than the signal length (see Notes).

Returns

h_minimum
[array] The minimum-phase version of the filter, with length `(length(h) + 1) // 2`.

See also:

firwin

firwin2

remez

Notes

Both the Hilbert [1] or homomorphic [4] [5] methods require selection of an FFT length to estimate the complex cepstrum of the filter.

In the case of the Hilbert method, the deviation from the ideal spectrum `epsilon` is related to the number of stopband zeros `n_stop` and FFT length `n_fft` as:

```
epsilon = 2. * n_stop / n_fft
```

For example, with 100 stopband zeros and a FFT length of 2048, `epsilon = 0.0976`. If we conservatively assume that the number of stopband zeros is one less than the filter length, we can take the FFT length to be the next power of 2 that satisfies `epsilon=0.01` as:

```
n_fft = 2 ** int(np.ceil(np.log2(2 * (len(h) - 1) / 0.01)))
```

This gives reasonable results for both the Hilbert and homomorphic methods, and gives the value used when `n_fft=None`.

Alternative implementations exist for creating minimum-phase filters, including zero inversion [2] and spectral factorization [3] [4]. For more information, see:

http://dspguru.com/dsp/howtos/how-to-design-minimum-phase-fir-filters

References

[1], [2], [3], [4], [5]

Examples

Create an optimal linear-phase filter, then convert it to minimum phase:

```
>>> from scipy.signal import remez, minimum_phase, freqz, group_delay
>>> import matplotlib.pyplot as plt
>>> freq = [0, 0.2, 0.3, 1.0]
>>> desired = [1, 0]
>>> h_linear = remez(151, freq, desired, Hz=2.)
```

Convert it to minimum phase:

```
>>> h_min_hom = minimum_phase(h_linear, method='homomorphic')
>>> h_min_hil = minimum_phase(h_linear, method='hilbert')
```

Compare the three filters:

```
>>> fig, axs = plt.subplots(4, figsize=(4, 8))
>>> for h, style, color in zip((h_linear, h_min_hom, h_min_hil),
...                            ('-', '-', '--'), ('k', 'r', 'c')):
...     w, H = freqz(h)
...     w, gd = group_delay((h, 1))
```

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```
...     w /= np.pi
...     axs[0].plot(h, color=color, linestyle=style)
...     axs[1].plot(w, np.abs(H), color=color, linestyle=style)
...     axs[2].plot(w, 20 * np.log10(np.abs(H)), color=color,␣
↪linestyle=style)
...     axs[3].plot(w, gd, color=color, linestyle=style)
>>> for ax in axs:
...     ax.grid(True, color='0.5')
...     ax.fill_between(freq[1:3], *ax.get_ylim(), color='#ffeeaa',␣
↪zorder=1)
>>> axs[0].set(xlim=[0, len(h_linear) - 1], ylabel='Amplitude', xlabel=
↪'Samples')
>>> axs[1].legend(['Linear', 'Min-Hom', 'Min-Hil'], title='Phase')
>>> for ax, ylim in zip(axs[1:], ([0, 1.1], [-150, 10], [-60, 60])):
...     ax.set(xlim=[0, 1], ylim=ylim, xlabel='Frequency')
>>> axs[1].set(ylabel='Magnitude')
>>> axs[2].set(ylabel='Magnitude (dB)')
>>> axs[3].set(ylabel='Group delay')
>>> plt.tight_layout()
```

scipy.signal.savgol_coeffs

scipy.signal.**savgol_coeffs**(*window_length*, *polyorder*, *deriv=0*, *delta=1.0*, *pos=None*, *use='conv'*)

Compute the coefficients for a 1-D Savitzky-Golay FIR filter.

Parameters

window_length
: [int] The length of the filter window (i.e., the number of coefficients). *window_length* must be an odd positive integer.

polyorder
: [int] The order of the polynomial used to fit the samples. *polyorder* must be less than *window_length*.

deriv
: [int, optional] The order of the derivative to compute. This must be a nonnegative integer. The default is 0, which means to filter the data without differentiating.

delta
: [float, optional] The spacing of the samples to which the filter will be applied. This is only used if deriv > 0.

pos
: [int or None, optional] If pos is not None, it specifies evaluation position within the window. The default is the middle of the window.

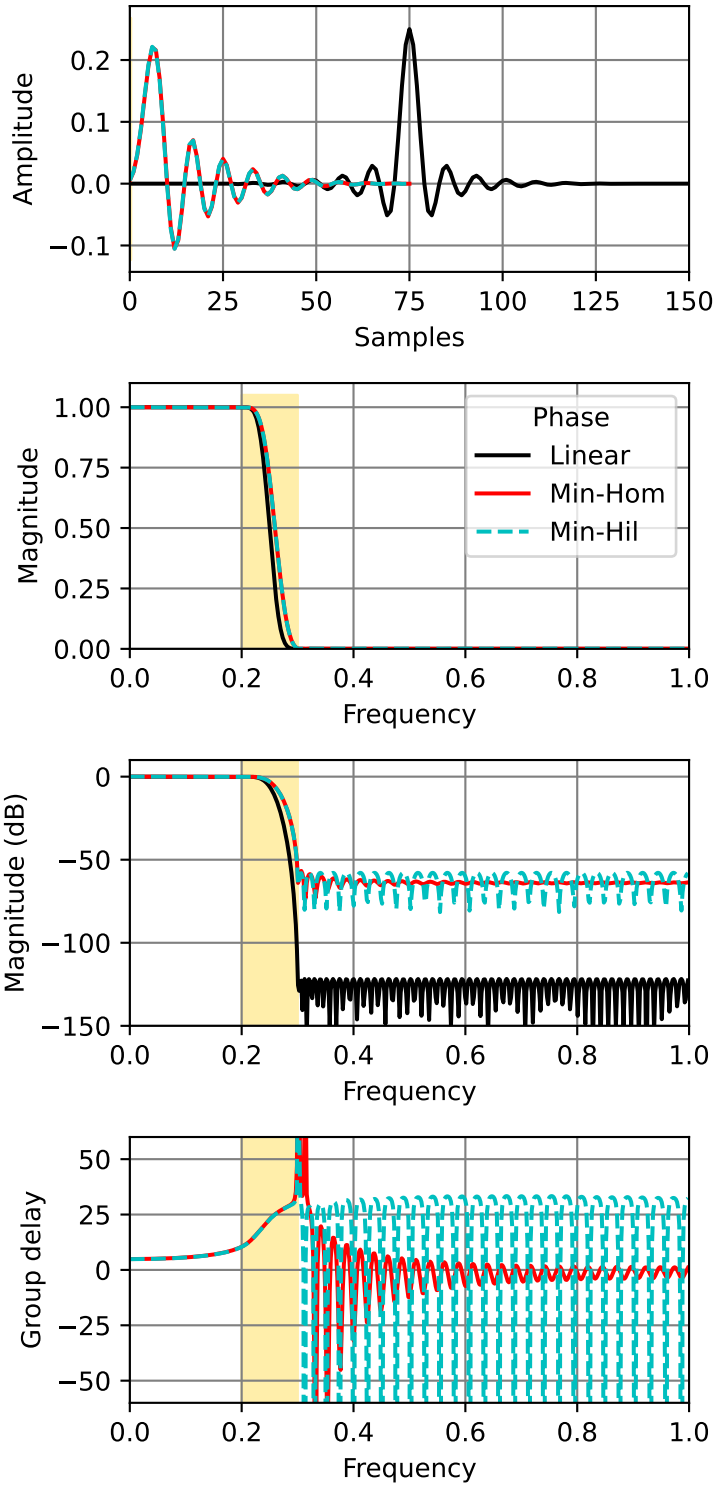
use
: [str, optional] Either 'conv' or 'dot'. This argument chooses the order of the coefficients. The default is 'conv', which means that the coefficients are ordered to be used in a convolution. With use='dot', the order is reversed, so the filter is applied by dotting the coefficients with the data set.

Returns

coeffs
: [1-D ndarray] The filter coefficients.

See also:

savgol_filter


Amplitude
0.2
0.1
0.0
−0.1
0
25
50
75
100
125
150
Samples
Magnitude
1.00
0.75
0.50
0.25
0.00
0.0
0.2
0.4
0.6
0.8
1.0
Frequency
Phase
Linear
Min-Hom
Min-Hil
Magnitude (dB)
0
−50
−100
−150
0.0
0.2
0.4
0.6
0.8
1.0
Frequency
Group delay
50
25
0
−25
−50
0.0
0.2
0.4
0.6
0.8
1.0
Frequency

Notes

New in version 0.14.0.

References

A. Savitzky, M. J. E. Golay, Smoothing and Differentiation of Data by Simplified Least Squares Procedures. Analytical Chemistry, 1964, 36 (8), pp 1627-1639.

Examples

```
>>> from scipy.signal import savgol_coeffs
>>> savgol_coeffs(5, 2)
array([-0.08571429,  0.34285714,  0.48571429,  0.34285714, -0.08571429])
>>> savgol_coeffs(5, 2, deriv=1)
array([ 2.00000000e-01,  1.00000000e-01,  2.07548111e-16, -1.00000000e-01,
       -2.00000000e-01])
```

Note that use='dot' simply reverses the coefficients.

```
>>> savgol_coeffs(5, 2, pos=3)
array([ 0.25714286,  0.37142857,  0.34285714,  0.17142857, -0.14285714])
>>> savgol_coeffs(5, 2, pos=3, use='dot')
array([-0.14285714,  0.17142857,  0.34285714,  0.37142857,  0.25714286])
```

x contains data from the parabola x = t**2, sampled at t = -1, 0, 1, 2, 3. *c* holds the coefficients that will compute the derivative at the last position. When dotted with *x* the result should be 6.

```
>>> x = np.array([1, 0, 1, 4, 9])
>>> c = savgol_coeffs(5, 2, pos=4, deriv=1, use='dot')
>>> c.dot(x)
6.0
```

scipy.signal.remez

scipy.signal.**remez**(*numtaps*, *bands*, *desired*, *weight=None*, *Hz=None*, *type='bandpass'*, *maxiter=25*, *grid_density=16*, *fs=None*)

Calculate the minimax optimal filter using the Remez exchange algorithm.

Calculate the filter-coefficients for the finite impulse response (FIR) filter whose transfer function minimizes the maximum error between the desired gain and the realized gain in the specified frequency bands using the Remez exchange algorithm.

Parameters

numtaps [int] The desired number of taps in the filter. The number of taps is the number of terms in the filter, or the filter order plus one.

bands [array_like] A monotonic sequence containing the band edges. All elements must be non-negative and less than half the sampling frequency as given by *fs*.

desired [array_like] A sequence half the size of bands containing the desired gain in each of the specified bands.

weight [array_like, optional] A relative weighting to give to each band region. The length of *weight* has to be half the length of *bands*.

Hz [scalar, optional] *Deprecated. Use `fs` instead.* The sampling frequency in Hz. Default is 1.

type [{'bandpass', 'differentiator', 'hilbert'}, optional] The type of filter:
- 'bandpass' : flat response in bands. This is the default.
- 'differentiator' : frequency proportional response in bands.
- **'hilbert'** [filter with odd symmetry, that is, type III] (for even order) or type IV (for odd order) linear phase filters.

maxiter [int, optional] Maximum number of iterations of the algorithm. Default is 25.

grid_density [int, optional] Grid density. The dense grid used in *remez* is of size `(numtaps + 1) * grid_density`. Default is 16.

fs [float, optional] The sampling frequency of the signal. Default is 1.

Returns

out [ndarray] A rank-1 array containing the coefficients of the optimal (in a minimax sense) filter.

See also:

firls

firwin

firwin2

minimum_phase

References

[1], [2]

Examples

In these examples *remez* gets used creating a bandpass, bandstop, lowpass and highpass filter. The used parameters are the filter order, an array with according frequency boundaries, the desired attenuation values and the sampling frequency. Using *freqz* the corresponding frequency response gets calculated and plotted.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> def plot_response(fs, w, h, title):
...     "Utility function to plot response functions"
...     fig = plt.figure()
...     ax = fig.add_subplot(111)
...     ax.plot(0.5*fs*w/np.pi, 20*np.log10(np.abs(h)))
...     ax.set_ylim(-40, 5)
...     ax.set_xlim(0, 0.5*fs)
...     ax.grid(True)
...     ax.set_xlabel('Frequency (Hz)')
...     ax.set_ylabel('Gain (dB)')
...     ax.set_title(title)
```

This example shows a steep low pass transition according to the small transition width and high filter order:

```
>>> fs = 22050.0       # Sample rate, Hz
>>> cutoff = 8000.0    # Desired cutoff frequency, Hz
>>> trans_width = 100  # Width of transition from pass band to stop band,␣
↪Hz
>>> numtaps = 400      # Size of the FIR filter.
>>> taps = signal.remez(numtaps, [0, cutoff, cutoff + trans_width, 0.
↪5*fs], [1, 0], Hz=fs)
>>> w, h = signal.freqz(taps, [1], worN=2000)
>>> plot_response(fs, w, h, "Low-pass Filter")
```

This example shows a high pass filter:

```
>>> fs = 22050.0       # Sample rate, Hz
>>> cutoff = 2000.0    # Desired cutoff frequency, Hz
>>> trans_width = 250  # Width of transition from pass band to stop band,␣
↪Hz
>>> numtaps = 125      # Size of the FIR filter.
>>> taps = signal.remez(numtaps, [0, cutoff - trans_width, cutoff, 0.
↪5*fs],
...                     [0, 1], Hz=fs)
>>> w, h = signal.freqz(taps, [1], worN=2000)
>>> plot_response(fs, w, h, "High-pass Filter")
```

For a signal sampled with 22 kHz a bandpass filter with a pass band of 2-5 kHz gets calculated using the Remez algorithm. The transition width is 260 Hz and the filter order 10:

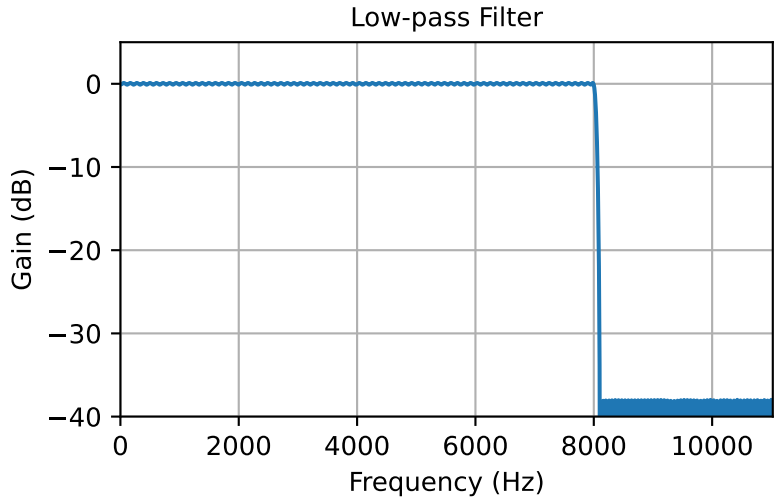
```
>>> fs = 22000.0         # Sample rate, Hz
>>> band = [2000, 5000]  # Desired pass band, Hz
>>> trans_width = 260    # Width of transition from pass band to stop␣
↪band, Hz
>>> numtaps = 10        # Size of the FIR filter.
>>> edges = [0, band[0] - trans_width, band[0], band[1],
...          band[1] + trans_width, 0.5*fs]
>>> taps = signal.remez(numtaps, edges, [0, 1, 0], Hz=fs)
>>> w, h = signal.freqz(taps, [1], worN=2000)
>>> plot_response(fs, w, h, "Band-pass Filter")
```

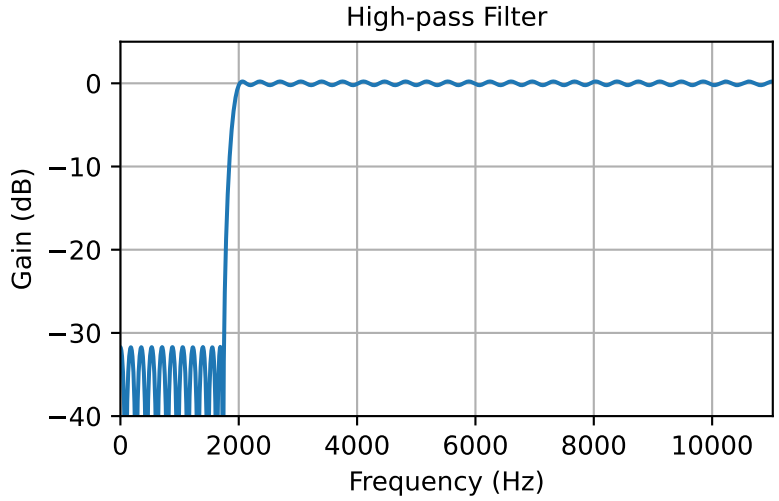
It can be seen that for this bandpass filter, the low order leads to higher ripple and less steep transitions. There is very low attenuation in the stop band and little overshoot in the pass band. Of course the desired gain can be better approximated with a higher filter order.

The next example shows a bandstop filter. Because of the high filter order the transition is quite steep:

```
>>> fs = 20000.0         # Sample rate, Hz
>>> band = [6000, 8000]  # Desired stop band, Hz
>>> trans_width = 200    # Width of transition from pass band to stop␣
↪band, Hz
>>> numtaps = 175        # Size of the FIR filter.
>>> edges = [0, band[0] - trans_width, band[0], band[1], band[1] + trans_
↪width, 0.5*fs]
>>> taps = signal.remez(numtaps, edges, [1, 0, 1], Hz=fs)
>>> w, h = signal.freqz(taps, [1], worN=2000)
>>> plot_response(fs, w, h, "Band-stop Filter")
```

```
>>> plt.show()
```





scipy.signal.unique_roots

`scipy.signal.`**`unique_roots`**(*p*, *tol=0.001*, *rtype='min'*)

Determine unique roots and their multiplicities from a list of roots.

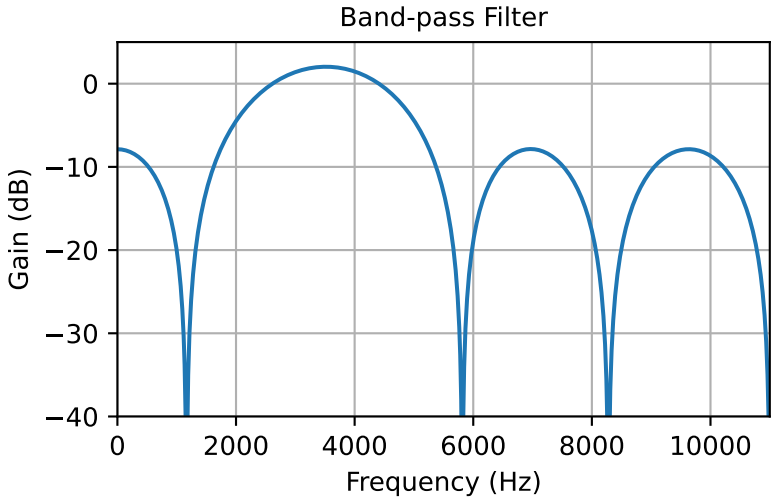
Parameters

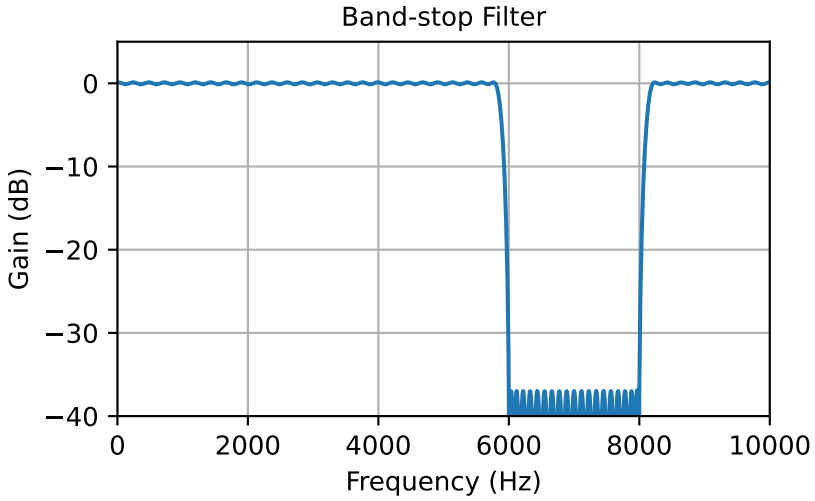
p [array_like] The list of roots.

tol [float, optional] The tolerance for two roots to be considered equal in terms of the distance between them. Default is 1e-3. Refer to Notes about the details on roots grouping.

rtype [{'max', 'maximum', 'min', 'minimum', 'avg', 'mean'}, optional] How to determine the returned root if multiple roots are within *tol* of each other.

- 'max', 'maximum': pick the maximum of those roots
- 'min', 'minimum': pick the minimum of those roots


Band-pass Filter
Gain (dB)
0
−10
−20
−30
−40
0
2000
4000
6000
8000
10000
Frequency (Hz)


Band-stop Filter
Gain (dB)
0
−10
−20
−30
−40
0
2000
4000
6000
8000
10000
Frequency (Hz)

- 'avg', 'mean': take the average of those roots

When finding minimum or maximum among complex roots they are compared first by the real part and then by the imaginary part.

Returns

unique [ndarray] The list of unique roots.

multiplicity [ndarray] The multiplicity of each root.

Notes

If we have 3 roots `a`, `b` and `c`, such that `a` is close to `b` and `b` is close to `c` (distance is less than *tol*), then it doesn't necessarily mean that `a` is close to `c`. It means that roots grouping is not unique. In this function we use "greedy" grouping going through the roots in the order they are given in the input *p*.

This utility function is not specific to roots but can be used for any sequence of values for which uniqueness and multiplicity has to be determined. For a more general routine, see `numpy.unique`.

Examples

```
>>> from scipy import signal
>>> vals = [0, 1.3, 1.31, 2.8, 1.25, 2.2, 10.3]
>>> uniq, mult = signal.unique_roots(vals, tol=2e-2, rtype='avg')
```

Check which roots have multiplicity larger than 1:

```
>>> uniq[mult > 1]
array([ 1.305])
```

scipy.signal.residue

`scipy.signal.`**`residue`**(*b*, *a*, *tol=0.001*, *rtype='avg'*)

Compute partial-fraction expansion of b(s) / a(s).

If *M* is the degree of numerator *b* and *N* the degree of denominator *a*:

```
        b(s)     b[0] s**(M) + b[1] s**(M-1) + ... + b[M]
H(s) = ------ = ----------------------------------------
        a(s)     a[0] s**(N) + a[1] s**(N-1) + ... + a[N]
```

then the partial-fraction expansion H(s) is defined as:

```
    r[0]        r[1]              r[-1]
= -------- + -------- + ... + --------- + k(s)
  (s-p[0])    (s-p[1])          (s-p[-1])
```

If there are any repeated roots (closer together than *tol*), then H(s) has terms like:

```
  r[i]       r[i+1]               r[i+n-1]
-------- + ----------- + ... + -----------
(s-p[i])   (s-p[i])**2           (s-p[i])**n
```

This function is used for polynomials in positive powers of s or z, such as analog filters or digital filters in controls engineering. For negative powers of z (typical for digital filters in DSP), use *residuez*.

See Notes for details about the algorithm.

Parameters

b	[array_like] Numerator polynomial coefficients.
a	[array_like] Denominator polynomial coefficients.
tol	[float, optional] The tolerance for two roots to be considered equal in terms of the distance between them. Default is 1e-3. See *unique_roots* for further details.
rtype	[{'avg', 'min', 'max'}, optional] Method for computing a root to represent a group of identical roots. Default is 'avg'. See *unique_roots* for further details.

Returns

r	[ndarray] Residues corresponding to the poles. For repeated poles, the residues are ordered to correspond to ascending by power fractions.
p	[ndarray] Poles ordered by magnitude in ascending order.
k	[ndarray] Coefficients of the direct polynomial term.

See also:

invres, **residuez**, ***numpy.poly***, **unique_roots**

Notes

The "deflation through subtraction" algorithm is used for computations — method 6 in [1].

The form of partial fraction expansion depends on poles multiplicity in the exact mathematical sense. However there is no way to exactly determine multiplicity of roots of a polynomial in numerical computing. Thus you should think of the result of *residue* with given *tol* as partial fraction expansion computed for the denominator composed of the computed poles with empirically determined multiplicity. The choice of *tol* can drastically change the result if there are close poles.

References

[1]

scipy.signal.residuez

scipy.signal.**residuez**(*b*, *a*, *tol=0.001*, *rtype='avg'*)

Compute partial-fraction expansion of b(z) / a(z).

If *M* is the degree of numerator *b* and *N* the degree of denominator *a*:

```
        b(z)     b[0] + b[1] z**(-1) + ... + b[M] z**(-M)
H(z) = ------ = ------------------------------------------
        a(z)     a[0] + a[1] z**(-1) + ... + a[N] z**(-N)
```

then the partial-fraction expansion H(z) is defined as:

```
         r[0]                   r[-1]
= --------------- + ... + ---------------- + k[0] + k[1]z**(-1) ...
  (1-p[0]z**(-1))         (1-p[-1]z**(-1))
```

If there are any repeated roots (closer than *tol*), then the partial fraction expansion has terms like:

```
     r[i]               r[i+1]                      r[i+n-1]
-------------- + ------------------ + ... + ------------------
(1-p[i]z**(-1))   (1-p[i]z**(-1))**2          (1-p[i]z**(-1))**n
```

This function is used for polynomials in negative powers of z, such as digital filters in DSP. For positive powers, use *residue*.

See Notes of *residue* for details about the algorithm.

Parameters

b	[array_like] Numerator polynomial coefficients.
a	[array_like] Denominator polynomial coefficients.
tol	[float, optional] The tolerance for two roots to be considered equal in terms of the distance between them. Default is 1e-3. See *unique_roots* for further details.
rtype	[{'avg', 'min', 'max'}, optional] Method for computing a root to represent a group of identical roots. Default is 'avg'. See *unique_roots* for further details.

Returns

r	[ndarray] Residues corresponding to the poles. For repeated poles, the residues are ordered to correspond to ascending by power fractions.
p	[ndarray] Poles ordered by magnitude in ascending order.
k	[ndarray] Coefficients of the direct polynomial term.

See also:

invresz, **residue**, **unique_roots**

scipy.signal.invres

scipy.signal.**invres**(*r*, *p*, *k*, *tol=0.001*, *rtype='avg'*)

Compute b(s) and a(s) from partial fraction expansion.

If *M* is the degree of numerator *b* and *N* the degree of denominator *a*:

```
        b(s)     b[0] s**(M) + b[1] s**(M-1) + ... + b[M]
H(s) = ------ = ----------------------------------------
        a(s)     a[0] s**(N) + a[1] s**(N-1) + ... + a[N]
```

then the partial-fraction expansion H(s) is defined as:

```
    r[0]        r[1]              r[-1]
= -------- + -------- + ... + --------- + k(s)
  (s-p[0])    (s-p[1])          (s-p[-1])
```

If there are any repeated roots (closer together than *tol*), then H(s) has terms like:

```
  r[i]       r[i+1]               r[i+n-1]
-------- + ----------- + ... + -----------
(s-p[i])   (s-p[i])**2           (s-p[i])**n
```

This function is used for polynomials in positive powers of s or z, such as analog filters or digital filters in controls engineering. For negative powers of z (typical for digital filters in DSP), use *invresz*.

Parameters

r	[array_like] Residues corresponding to the poles. For repeated poles, the residues must be ordered to correspond to ascending by power fractions.

p [array_like] Poles. Equal poles must be adjacent.
k [array_like] Coefficients of the direct polynomial term.
tol [float, optional] The tolerance for two roots to be considered equal in terms of the distance between them. Default is 1e-3. See *unique_roots* for further details.
rtype [{'avg', 'min', 'max'}, optional] Method for computing a root to represent a group of identical roots. Default is 'avg'. See *unique_roots* for further details.

Returns

b [ndarray] Numerator polynomial coefficients.
a [ndarray] Denominator polynomial coefficients.

See also:

residue, invresz, unique_roots

scipy.signal.invresz

scipy.signal.**invresz**(*r*, *p*, *k*, *tol=0.001*, *rtype='avg'*)

Compute b(z) and a(z) from partial fraction expansion.

If *M* is the degree of numerator *b* and *N* the degree of denominator *a*:

```
        b(z)     b[0] + b[1] z**(-1) + ... + b[M] z**(-M)
H(z) = ------ = ----------------------------------------
        a(z)     a[0] + a[1] z**(-1) + ... + a[N] z**(-N)
```

then the partial-fraction expansion H(z) is defined as:

```
         r[0]                   r[-1]
= ---------------- + ... + ---------------- + k[0] + k[1]z**(-1) ...
  (1-p[0]z**(-1))         (1-p[-1]z**(-1))
```

If there are any repeated roots (closer than *tol*), then the partial fraction expansion has terms like:

```
     r[i]              r[i+1]                    r[i+n-1]
-------------- + ------------------ + ... + ------------------
(1-p[i]z**(-1))  (1-p[i]z**(-1))**2          (1-p[i]z**(-1))**n
```

This function is used for polynomials in negative powers of z, such as digital filters in DSP. For positive powers, use *invres*.

Parameters

r [array_like] Residues corresponding to the poles. For repeated poles, the residues must be ordered to correspond to ascending by power fractions.
p [array_like] Poles. Equal poles must be adjacent.
k [array_like] Coefficients of the direct polynomial term.
tol [float, optional] The tolerance for two roots to be considered equal in terms of the distance between them. Default is 1e-3. See *unique_roots* for further details.
rtype [{'avg', 'min', 'max'}, optional] Method for computing a root to represent a group of identical roots. Default is 'avg'. See *unique_roots* for further details.

Returns

b [ndarray] Numerator polynomial coefficients.
a [ndarray] Denominator polynomial coefficients.

See also:

residuez, **unique_roots**, **invres**

scipy.signal.BadCoefficients

exception scipy.signal.**BadCoefficients**
Warning about badly conditioned filter coefficients

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

Lower-level filter design functions:

abcd_normalize([A, B, C, D])	Check state-space matrices and ensure they are 2-D.
band_stop_obj(wp, ind, passb, stopb, gpass, …)	Band Stop Objective Function for order minimization.
besselap(N[, norm])	Return (z,p,k) for analog prototype of an Nth-order Bessel filter.
buttap(N)	Return (z,p,k) for analog prototype of Nth-order Butterworth filter.
cheb1ap(N, rp)	Return (z,p,k) for Nth-order Chebyshev type I analog lowpass filter.
cheb2ap(N, rs)	Return (z,p,k) for Nth-order Chebyshev type I analog lowpass filter.
cmplx_sort(p)	Sort roots based on magnitude.
ellipap(N, rp, rs)	Return (z,p,k) of Nth-order elliptic analog lowpass filter.
lp2bp(b, a[, wo, bw])	Transform a lowpass filter prototype to a bandpass filter.
lp2bp_zpk(z, p, k[, wo, bw])	Transform a lowpass filter prototype to a bandpass filter.
lp2bs(b, a[, wo, bw])	Transform a lowpass filter prototype to a bandstop filter.
lp2bs_zpk(z, p, k[, wo, bw])	Transform a lowpass filter prototype to a bandstop filter.
lp2hp(b, a[, wo])	Transform a lowpass filter prototype to a highpass filter.
lp2hp_zpk(z, p, k[, wo])	Transform a lowpass filter prototype to a highpass filter.
lp2lp(b, a[, wo])	Transform a lowpass filter prototype to a different frequency.
lp2lp_zpk(z, p, k[, wo])	Transform a lowpass filter prototype to a different frequency.
normalize(b, a)	Normalize numerator/denominator of a continuous-time transfer function.

scipy.signal.abcd_normalize

scipy.signal.**abcd_normalize**(*A=None*, *B=None*, *C=None*, *D=None*)
Check state-space matrices and ensure they are 2-D.

If enough information on the system is provided, that is, enough properly-shaped arrays are passed to the function, the missing ones are built from this information, ensuring the correct number of rows and columns. Otherwise a ValueError is raised.

Parameters

A, B, C, D [array_like, optional] State-space matrices. All of them are None (missing) by default. See *ss2tf* for format.

Returns

A, B, C, D [array] Properly shaped state-space matrices.

Raises

ValueError

If not enough information on the system was provided.

scipy.signal.band_stop_obj

scipy.signal.**band_stop_obj**(*wp*, *ind*, *passb*, *stopb*, *gpass*, *gstop*, *type*)

Band Stop Objective Function for order minimization.

Returns the non-integer order for an analog band stop filter.

Parameters

wp	[scalar] Edge of passband *passb*.
ind	[int, {0, 1}] Index specifying which *passb* edge to vary (0 or 1).
passb	[ndarray] Two element sequence of fixed passband edges.
stopb	[ndarray] Two element sequence of fixed stopband edges.
gstop	[float] Amount of attenuation in stopband in dB.
gpass	[float] Amount of ripple in the passband in dB.
type	[{'butter', 'cheby', 'ellip'}] Type of filter.

Returns

n	[scalar] Filter order (possibly non-integer).

scipy.signal.besselap

scipy.signal.**besselap**(*N*, *norm='phase'*)

Return (z,p,k) for analog prototype of an Nth-order Bessel filter.

Parameters

N	[int] The order of the filter.
norm	[{'phase', 'delay', 'mag'}, optional] Frequency normalization:
	phase The filter is normalized such that the phase response reaches its midpoint at an angular (e.g., rad/s) cutoff frequency of 1. This happens for both low-pass and high-pass filters, so this is the "phase-matched" case. [6] The magnitude response asymptotes are the same as a Butterworth filter of the same order with a cutoff of *Wn*. This is the default, and matches MATLAB's implementation.
	delay The filter is normalized such that the group delay in the passband is 1 (e.g., 1 second). This is the "natural" type obtained by solving Bessel polynomials
	mag The filter is normalized such that the gain magnitude is -3 dB at angular frequency 1. This is called "frequency normalization" by Bond. [1]
	New in version 0.18.0.

Returns

z	[ndarray] Zeros of the transfer function. Is always an empty array.
p	[ndarray] Poles of the transfer function.
k	[scalar] Gain of the transfer function. For phase-normalized, this is always 1.

See also:

bessel

Filter design function using this prototype

Notes

To find the pole locations, approximate starting points are generated [2] for the zeros of the ordinary Bessel polynomial [3], then the Aberth-Ehrlich method [4] [5] is used on the Kv(x) Bessel function to calculate more accurate zeros, and these locations are then inverted about the unit circle.

References

[1], [2], [3], [4], [5], [6]

scipy.signal.buttap

`scipy.signal.`**`buttap`**(*N*)

Return (z,p,k) for analog prototype of Nth-order Butterworth filter.

The filter will have an angular (e.g., rad/s) cutoff frequency of 1.

See also:

`butter`

Filter design function using this prototype

scipy.signal.cheb1ap

`scipy.signal.`**`cheb1ap`**(*N*, *rp*)

Return (z,p,k) for Nth-order Chebyshev type I analog lowpass filter.

The returned filter prototype has *rp* decibels of ripple in the passband.

The filter's angular (e.g. rad/s) cutoff frequency is normalized to 1, defined as the point at which the gain first drops below `-rp`.

See also:

`cheby1`

Filter design function using this prototype

scipy.signal.cheb2ap

`scipy.signal.`**`cheb2ap`**(*N*, *rs*)

Return (z,p,k) for Nth-order Chebyshev type I analog lowpass filter.

The returned filter prototype has *rs* decibels of ripple in the stopband.

The filter's angular (e.g. rad/s) cutoff frequency is normalized to 1, defined as the point at which the gain first reaches `-rs`.

See also:

`cheby2`

Filter design function using this prototype

scipy.signal.cmplx_sort

scipy.signal.**cmplx_sort**(*p*)

Sort roots based on magnitude.

Parameters

p [array_like] The roots to sort, as a 1-D array.

Returns

p_sorted [ndarray] Sorted roots.
indx [ndarray] Array of indices needed to sort the input *p*.

Examples

```
>>> from scipy import signal
>>> vals = [1, 4, 1+1.j, 3]
>>> p_sorted, indx = signal.cmplx_sort(vals)
>>> p_sorted
array([1.+0.j, 1.+1.j, 3.+0.j, 4.+0.j])
>>> indx
array([0, 2, 3, 1])
```

scipy.signal.ellipap

scipy.signal.**ellipap**(*N*, *rp*, *rs*)

Return (z,p,k) of Nth-order elliptic analog lowpass filter.

The filter is a normalized prototype that has *rp* decibels of ripple in the passband and a stopband *rs* decibels down.

The filter's angular (e.g., rad/s) cutoff frequency is normalized to 1, defined as the point at which the gain first drops below `-rp`.

See also:

ellip

Filter design function using this prototype

References

[1], [2]

scipy.signal.lp2bp

scipy.signal.**lp2bp**(*b*, *a*, *wo=1.0*, *bw=1.0*)

Transform a lowpass filter prototype to a bandpass filter.

Return an analog band-pass filter with center frequency *wo* and bandwidth *bw* from an analog low-pass filter prototype with unity cutoff frequency, in transfer function ('ba') representation.

Parameters

b [array_like] Numerator polynomial coefficients.
a [array_like] Denominator polynomial coefficients.
wo [float] Desired passband center, as angular frequency (e.g., rad/s). Defaults to no change.
bw [float] Desired passband width, as angular frequency (e.g., rad/s). Defaults to 1.

Returns

b	[array_like] Numerator polynomial coefficients of the transformed band-pass filter.
a	[array_like] Denominator polynomial coefficients of the transformed band-pass filter.

See also:

lp2lp, **lp2hp**, **lp2bs**, **bilinear**

lp2bp_zpk

Notes

This is derived from the s-plane substitution

$$s \to \frac{s^2 + {\omega_0}^2}{s \cdot \mathrm{BW}}$$

This is the "wideband" transformation, producing a passband with geometric (log frequency) symmetry about *wo*.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> lp = signal.lti([1.0], [1.0, 1.0])
>>> bp = signal.lti(*signal.lp2bp(lp.num, lp.den))
>>> w, mag_lp, p_lp = lp.bode()
>>> w, mag_bp, p_bp = bp.bode(w)
```

```
>>> plt.plot(w, mag_lp, label='Lowpass')
>>> plt.plot(w, mag_bp, label='Bandpass')
>>> plt.semilogx()
>>> plt.grid()
>>> plt.xlabel('Frequency [rad/s]')
>>> plt.ylabel('Magnitude [dB]')
>>> plt.legend()
```

scipy.signal.lp2bp_zpk

scipy.signal.**lp2bp_zpk**(*z*, *p*, *k*, *wo=1.0*, *bw=1.0*)

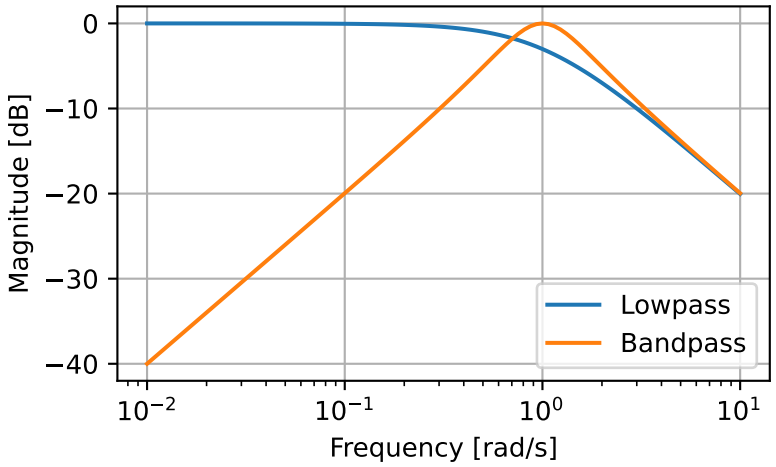
Transform a lowpass filter prototype to a bandpass filter.

Return an analog band-pass filter with center frequency *wo* and bandwidth *bw* from an analog low-pass filter prototype with unity cutoff frequency, using zeros, poles, and gain ('zpk') representation.

Parameters

z	[array_like] Zeros of the analog filter transfer function.
p	[array_like] Poles of the analog filter transfer function.
k	[float] System gain of the analog filter transfer function.
wo	[float] Desired passband center, as angular frequency (e.g., rad/s). Defaults to no change.
bw	[float] Desired passband width, as angular frequency (e.g., rad/s). Defaults to 1.

Returns



z	[ndarray] Zeros of the transformed band-pass filter transfer function.
p	[ndarray] Poles of the transformed band-pass filter transfer function.
k	[float] System gain of the transformed band-pass filter.

See also:

`lp2lp_zpk`, `lp2hp_zpk`, `lp2bs_zpk`, `bilinear`

`lp2bp`

Notes

This is derived from the s-plane substitution

$$s \rightarrow \frac{s^2 + {\omega_0}^2}{s \cdot \mathrm{BW}}$$

This is the “wideband” transformation, producing a passband with geometric (log frequency) symmetry about *wo*.

New in version 1.1.0.

scipy.signal.lp2bs

`scipy.signal.`**`lp2bs`**(*b*, *a*, *wo=1.0*, *bw=1.0*)

Transform a lowpass filter prototype to a bandstop filter.

Return an analog band-stop filter with center frequency *wo* and bandwidth *bw* from an analog low-pass filter prototype with unity cutoff frequency, in transfer function (‘ba’) representation.

Parameters

b	[array_like] Numerator polynomial coefficients.
a	[array_like] Denominator polynomial coefficients.
wo	[float] Desired stopband center, as angular frequency (e.g., rad/s). Defaults to no change.
bw	[float] Desired stopband width, as angular frequency (e.g., rad/s). Defaults to 1.

Returns

b	[array_like] Numerator polynomial coefficients of the transformed band-stop filter.

a [array_like] Denominator polynomial coefficients of the transformed band-stop filter.

See also:

`lp2lp`, `lp2hp`, `lp2bp`, `bilinear`

`lp2bs_zpk`

Notes

This is derived from the s-plane substitution

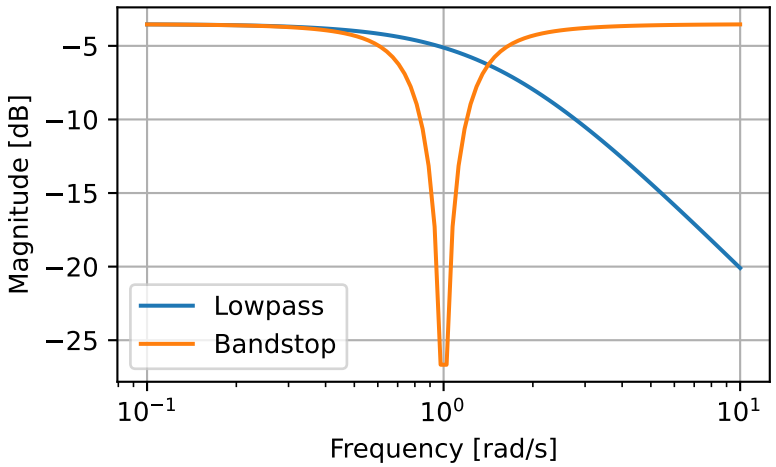
$$s \rightarrow \frac{s \cdot \mathrm{BW}}{s^2 + {\omega_0}^2}$$

This is the "wideband" transformation, producing a stopband with geometric (log frequency) symmetry about *wo*.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> lp = signal.lti([1.0], [1.0, 1.5])
>>> bs = signal.lti(*signal.lp2bs(lp.num, lp.den))
>>> w, mag_lp, p_lp = lp.bode()
>>> w, mag_bs, p_bs = bs.bode(w)
>>> plt.plot(w, mag_lp, label='Lowpass')
>>> plt.plot(w, mag_bs, label='Bandstop')
>>> plt.semilogx()
>>> plt.grid()
>>> plt.xlabel('Frequency [rad/s]')
>>> plt.ylabel('Magnitude [dB]')
>>> plt.legend()
```



scipy.signal.lp2bs_zpk

scipy.signal.**lp2bs_zpk**(*z*, *p*, *k*, *wo=1.0*, *bw=1.0*)

Transform a lowpass filter prototype to a bandstop filter.

Return an analog band-stop filter with center frequency *wo* and stopband width *bw* from an analog low-pass filter prototype with unity cutoff frequency, using zeros, poles, and gain ('zpk') representation.

Parameters

z	[array_like] Zeros of the analog filter transfer function.
p	[array_like] Poles of the analog filter transfer function.
k	[float] System gain of the analog filter transfer function.
wo	[float] Desired stopband center, as angular frequency (e.g., rad/s). Defaults to no change.
bw	[float] Desired stopband width, as angular frequency (e.g., rad/s). Defaults to 1.

Returns

z	[ndarray] Zeros of the transformed band-stop filter transfer function.
p	[ndarray] Poles of the transformed band-stop filter transfer function.
k	[float] System gain of the transformed band-stop filter.

See also:

lp2lp_zpk, **lp2hp_zpk**, **lp2bp_zpk**, **bilinear**

lp2bs

Notes

This is derived from the s-plane substitution

$$s \rightarrow \frac{s \cdot \mathrm{BW}}{s^2 + \omega_0{}^2}$$

This is the "wideband" transformation, producing a stopband with geometric (log frequency) symmetry about *wo*.

New in version 1.1.0.

scipy.signal.lp2hp

scipy.signal.**lp2hp**(*b*, *a*, *wo=1.0*)

Transform a lowpass filter prototype to a highpass filter.

Return an analog high-pass filter with cutoff frequency *wo* from an analog low-pass filter prototype with unity cutoff frequency, in transfer function ('ba') representation.

Parameters

b	[array_like] Numerator polynomial coefficients.
a	[array_like] Denominator polynomial coefficients.
wo	[float] Desired cutoff, as angular frequency (e.g., rad/s). Defaults to no change.

Returns

b	[array_like] Numerator polynomial coefficients of the transformed high-pass filter.
a	[array_like] Denominator polynomial coefficients of the transformed high-pass filter.

See also:

lp2lp, **lp2bp**, **lp2bs**, **bilinear**

lp2hp_zpk

Notes

This is derived from the s-plane substitution

$$s \to \frac{\omega_0}{s}$$

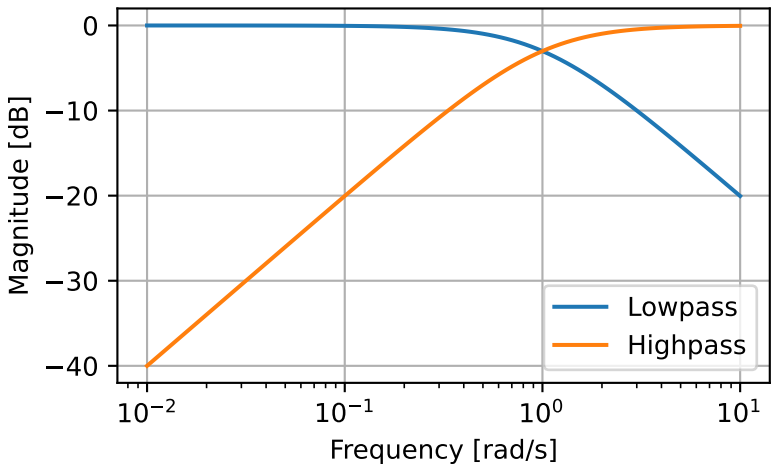
This maintains symmetry of the lowpass and highpass responses on a logarithmic scale.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> lp = signal.lti([1.0], [1.0, 1.0])
>>> hp = signal.lti(*signal.lp2hp(lp.num, lp.den))
>>> w, mag_lp, p_lp = lp.bode()
>>> w, mag_hp, p_hp = hp.bode(w)
```

```
>>> plt.plot(w, mag_lp, label='Lowpass')
>>> plt.plot(w, mag_hp, label='Highpass')
>>> plt.semilogx()
>>> plt.grid()
>>> plt.xlabel('Frequency [rad/s]')
>>> plt.ylabel('Magnitude [dB]')
>>> plt.legend()
```



scipy.signal.lp2hp_zpk

scipy.signal.**lp2hp_zpk**(*z*, *p*, *k*, *wo=1.0*)

Transform a lowpass filter prototype to a highpass filter.

Return an analog high-pass filter with cutoff frequency *wo* from an analog low-pass filter prototype with unity cutoff frequency, using zeros, poles, and gain ('zpk') representation.

Parameters

z	[array_like] Zeros of the analog filter transfer function.
p	[array_like] Poles of the analog filter transfer function.
k	[float] System gain of the analog filter transfer function.
wo	[float] Desired cutoff, as angular frequency (e.g., rad/s). Defaults to no change.

Returns

z	[ndarray] Zeros of the transformed high-pass filter transfer function.
p	[ndarray] Poles of the transformed high-pass filter transfer function.
k	[float] System gain of the transformed high-pass filter.

See also:

lp2lp_zpk, **lp2bp_zpk**, **lp2bs_zpk**, **bilinear**

lp2hp

Notes

This is derived from the s-plane substitution

$$s \rightarrow \frac{\omega_0}{s}$$

This maintains symmetry of the lowpass and highpass responses on a logarithmic scale.

New in version 1.1.0.

scipy.signal.lp2lp

scipy.signal.**lp2lp**(*b*, *a*, *wo=1.0*)

Transform a lowpass filter prototype to a different frequency.

Return an analog low-pass filter with cutoff frequency *wo* from an analog low-pass filter prototype with unity cutoff frequency, in transfer function ('ba') representation.

Parameters

b	[array_like] Numerator polynomial coefficients.
a	[array_like] Denominator polynomial coefficients.
wo	[float] Desired cutoff, as angular frequency (e.g. rad/s). Defaults to no change.

Returns

b	[array_like] Numerator polynomial coefficients of the transformed low-pass filter.
a	[array_like] Denominator polynomial coefficients of the transformed low-pass filter.

See also:

lp2hp, **lp2bp**, **lp2bs**, **bilinear**

lp2lp_zpk

Notes

This is derived from the s-plane substitution

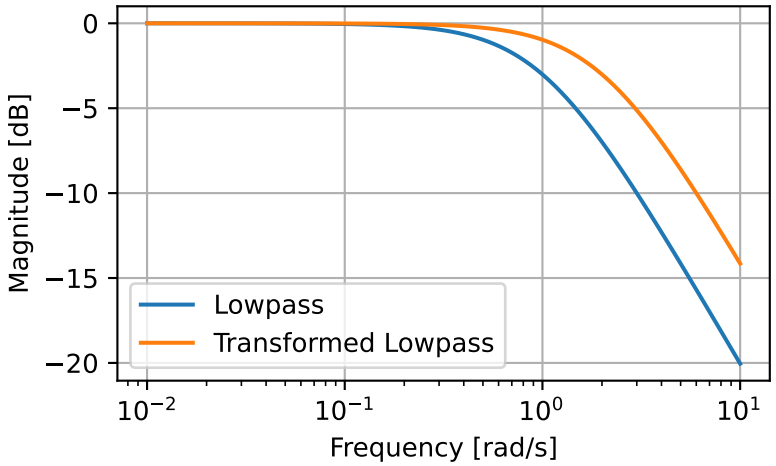
$$s \rightarrow \frac{s}{\omega_0}$$

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> lp = signal.lti([1.0], [1.0, 1.0])
>>> lp2 = signal.lti(*signal.lp2lp(lp.num, lp.den, 2))
>>> w, mag_lp, p_lp = lp.bode()
>>> w, mag_lp2, p_lp2 = lp2.bode(w)
```

```
>>> plt.plot(w, mag_lp, label='Lowpass')
>>> plt.plot(w, mag_lp2, label='Transformed Lowpass')
>>> plt.semilogx()
>>> plt.grid()
>>> plt.xlabel('Frequency [rad/s]')
>>> plt.ylabel('Magnitude [dB]')
>>> plt.legend()
```



scipy.signal.lp2lp_zpk

scipy.signal.**lp2lp_zpk**(*z*, *p*, *k*, *wo=1.0*)

Transform a lowpass filter prototype to a different frequency.

Return an analog low-pass filter with cutoff frequency *wo* from an analog low-pass filter prototype with unity cutoff frequency, using zeros, poles, and gain ('zpk') representation.

Parameters

z	[array_like] Zeros of the analog filter transfer function.
p	[array_like] Poles of the analog filter transfer function.
k	[float] System gain of the analog filter transfer function.
wo	[float] Desired cutoff, as angular frequency (e.g., rad/s). Defaults to no change.

Returns

z	[ndarray] Zeros of the transformed low-pass filter transfer function.
p	[ndarray] Poles of the transformed low-pass filter transfer function.
k	[float] System gain of the transformed low-pass filter.

See also:

lp2hp_zpk, **lp2bp_zpk**, **lp2bs_zpk**, **bilinear**

lp2lp

Notes

This is derived from the s-plane substitution

$$s \rightarrow \frac{s}{\omega_0}$$

New in version 1.1.0.

scipy.signal.normalize

scipy.signal.**normalize**(*b*, *a*)

Normalize numerator/denominator of a continuous-time transfer function.

If values of *b* are too close to 0, they are removed. In that case, a BadCoefficients warning is emitted.

Parameters

b: array_like
: Numerator of the transfer function. Can be a 2-D array to normalize multiple transfer functions.

a: array_like
: Denominator of the transfer function. At most 1-D.

Returns

num: array
: The numerator of the normalized transfer function. At least a 1-D array. A 2-D array if the input *num* is a 2-D array.

den: 1-D array
: The denominator of the normalized transfer function.

Notes

Coefficients for both the numerator and denominator should be specified in descending exponent order (e.g., `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

Matlab-style IIR filter design

butter(N, Wn[, btype, analog, output, fs])	Butterworth digital and analog filter design.
buttord(wp, ws, gpass, gstop[, analog, fs])	Butterworth filter order selection.
cheby1(N, rp, Wn[, btype, analog, output, fs])	Chebyshev type I digital and analog filter design.
cheb1ord(wp, ws, gpass, gstop[, analog, fs])	Chebyshev type I filter order selection.
cheby2(N, rs, Wn[, btype, analog, output, fs])	Chebyshev type II digital and analog filter design.
cheb2ord(wp, ws, gpass, gstop[, analog, fs])	Chebyshev type II filter order selection.
ellip(N, rp, rs, Wn[, btype, analog, output, fs])	Elliptic (Cauer) digital and analog filter design.
ellipord(wp, ws, gpass, gstop[, analog, fs])	Elliptic (Cauer) filter order selection.
bessel(N, Wn[, btype, analog, output, norm, fs])	Bessel/Thomson digital and analog filter design.
iirnotch(w0, Q[, fs])	Design second-order IIR notch digital filter.
iirpeak(w0, Q[, fs])	Design second-order IIR peak (resonant) digital filter.
iircomb(w0, Q[, ftype, fs])	Design IIR notching or peaking digital comb filter.

scipy.signal.butter

`scipy.signal.`**`butter`**(*N*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*, *fs=None*)

Butterworth digital and analog filter design.

Design an Nth-order digital or analog Butterworth filter and return the filter coefficients.

Parameters

N [int] The order of the filter.

Wn [array_like] The critical frequency or frequencies. For lowpass and highpass filters, Wn is a scalar; for bandpass and bandstop filters, Wn is a length-2 sequence.
For a Butterworth filter, this is the point at which the gain drops to 1/sqrt(2) that of the passband (the "-3 dB point").
For digital filters, *Wn* are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*Wn* is thus in half-cycles / sample.)
For analog filters, *Wn* is an angular frequency (e.g. rad/s).

btype [{'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional] The type of filter. Default is 'lowpass'.

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

output [{'ba', 'zpk', 'sos'}, optional] Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba' for backwards compatibility, but 'sos' should be used for general-purpose filtering.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos [ndarray] Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

`buttord`, `buttap`

Notes

The Butterworth filter has maximally flat frequency response in the passband.

The `'sos'` output parameter was added in 0.16.0.

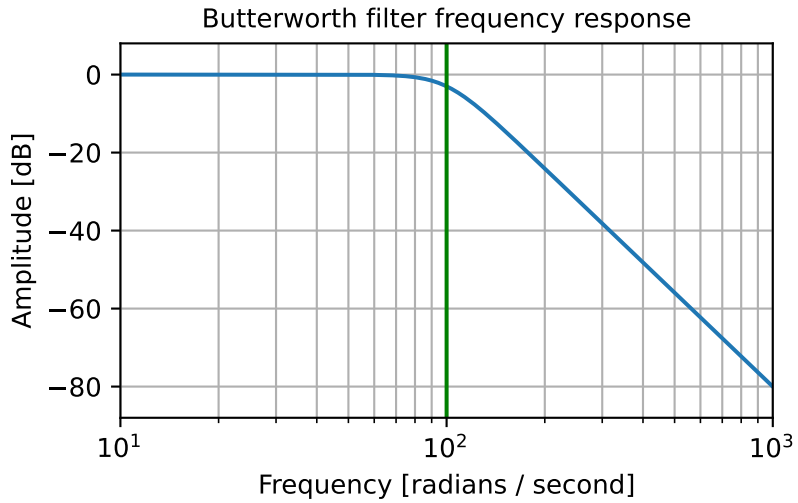
If the transfer function form `[b, a]` is requested, numerical problems can occur since the conversion between roots and the polynomial coefficients is a numerically sensitive operation, even for N >= 4. It is recommended to work with the SOS representation.

Examples

Design an analog filter and plot its frequency response, showing the critical points:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.butter(4, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Butterworth filter frequency response')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.show()
```

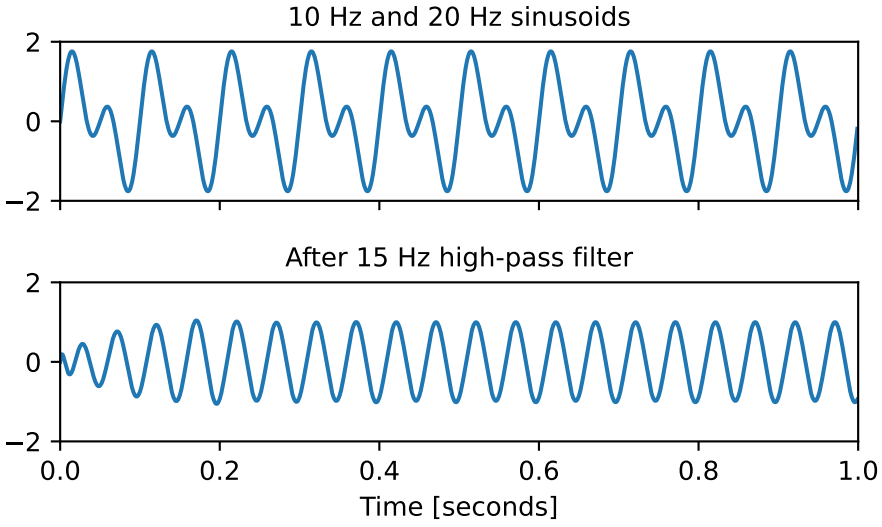


Generate a signal made up of 10 Hz and 20 Hz, sampled at 1 kHz

```
>>> t = np.linspace(0, 1, 1000, False)  # 1 second
>>> sig = np.sin(2*np.pi*10*t) + np.sin(2*np.pi*20*t)
>>> fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
>>> ax1.plot(t, sig)
>>> ax1.set_title('10 Hz and 20 Hz sinusoids')
>>> ax1.axis([0, 1, -2, 2])
```

Design a digital high-pass filter at 15 Hz to remove the 10 Hz tone, and apply it to the signal. (It's recommended to use second-order sections format when filtering, to avoid numerical error with transfer function (`ba`) format):

```
>>> sos = signal.butter(10, 15, 'hp', fs=1000, output='sos')
>>> filtered = signal.sosfilt(sos, sig)
>>> ax2.plot(t, filtered)
>>> ax2.set_title('After 15 Hz high-pass filter')
>>> ax2.axis([0, 1, -2, 2])
>>> ax2.set_xlabel('Time [seconds]')
>>> plt.tight_layout()
>>> plt.show()
```



scipy.signal.buttord

`scipy.signal.`**`buttord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*, *fs=None*)

Butterworth filter order selection.

Return the order of the lowest order digital or analog Butterworth filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

Parameters

wp, ws [float] Passband and stopband edge frequencies.
For digital filters, these are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*wp* and *ws* are thus in half-cycles / sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]

- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g., rad/s).

gpass [float] The maximum loss in the passband (dB).

gstop [float] The minimum attenuation in the stopband (dB).

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

ord [int] The lowest order for a Butterworth filter which meets specs.

wn [ndarray or float] The Butterworth natural frequency (i.e. the "3dB frequency"). Should be used with `butter` to give filter results. If *fs* is specified, this is in the same units, and *fs* must also be passed to `butter`.

See also:

butter

Filter design using order and critical points

cheb1ord

Find order and critical points from passband and stopband spec

cheb2ord, **ellipord**

iirfilter

General filter design using order and critical frequencies

iirdesign

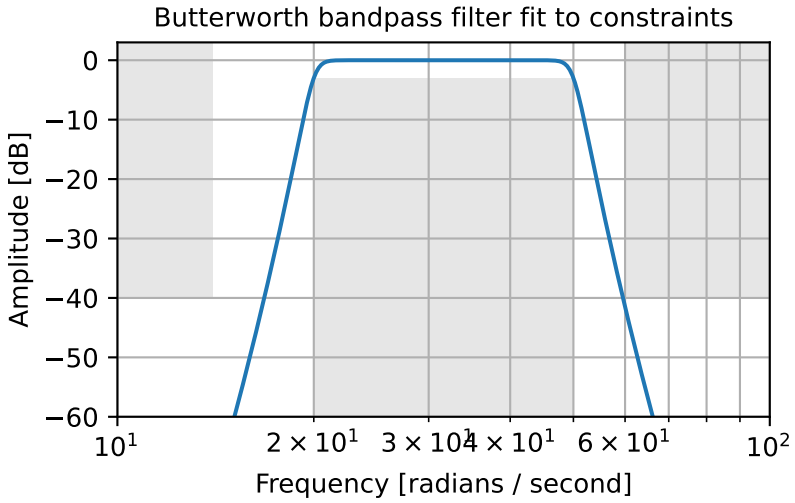
General filter design using passband and stopband spec

Examples

Design an analog bandpass filter with passband within 3 dB from 20 to 50 rad/s, while rejecting at least -40 dB below 14 and above 60 rad/s. Plot its frequency response, showing the passband and stopband constraints in gray.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> N, Wn = signal.buttord([20, 50], [14, 60], 3, 40, True)
>>> b, a = signal.butter(N, Wn, 'band', True)
>>> w, h = signal.freqs(b, a, np.logspace(1, 2, 500))
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Butterworth bandpass filter fit to constraints')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([1,  14,  14,   1], [-40, -40, 99, 99], '0.9', lw=0) # stop
>>> plt.fill([20, 20,  50,  50], [-99, -3, -3, -99], '0.9', lw=0) # pass
>>> plt.fill([60, 60, 1e9, 1e9], [99, -40, -40, 99], '0.9', lw=0) # stop
>>> plt.axis([10, 100, -60, 3])
>>> plt.show()
```



scipy.signal.cheby1

`scipy.signal.`**`cheby1`**(*N*, *rp*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*, *fs=None*)

Chebyshev type I digital and analog filter design.

Design an Nth-order digital or analog Chebyshev type I filter and return the filter coefficients.

Parameters

N	[int] The order of the filter.
rp	[float] The maximum ripple allowed below unity gain in the passband. Specified in decibels, as a positive number.
Wn	[array_like] A scalar or length-2 sequence giving the critical frequencies. For Type I filters, this is the point in the transition band at which the gain first drops below *-rp*. For digital filters, *Wn* are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*Wn* is thus in half-cycles / sample.) For analog filters, *Wn* is an angular frequency (e.g., rad/s).
btype	[{'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional] The type of filter. Default is 'lowpass'.
analog	[bool, optional] When True, return an analog filter, otherwise a digital filter is returned.
output	[{'ba', 'zpk', 'sos'}, optional] Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba' for backwards compatibility, but 'sos' should be used for general-purpose filtering.
fs	[float, optional] The sampling frequency of the digital system. New in version 1.2.0.

Returns

b, a	[ndarray, ndarray] Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.
z, p, k	[ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.
sos	[ndarray] Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

cheb1ord, **cheb1ap**

Notes

The Chebyshev type I filter maximizes the rate of cutoff between the frequency response's passband and stopband, at the expense of ripple in the passband and increased ringing in the step response.

Type I filters roll off faster than Type II (*cheby2*), but Type II filters do not have any ripple in the passband.

The equiripple passband has N maxima or minima (for example, a 5th-order filter has 3 maxima and 2 minima). Consequently, the DC gain is unity for odd-order filters, or -rp dB for even-order filters.

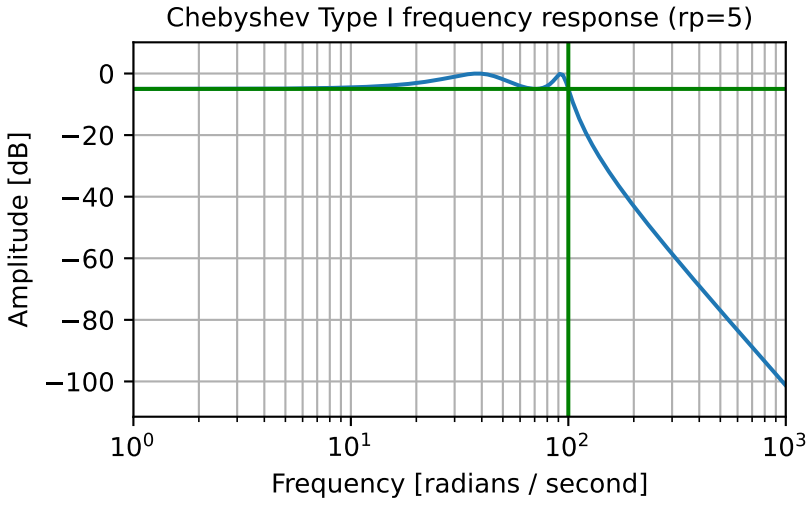
The `'sos'` output parameter was added in 0.16.0.

Examples

Design an analog filter and plot its frequency response, showing the critical points:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.cheby1(4, 5, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev Type I frequency response (rp=5)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.axhline(-5, color='green') # rp
>>> plt.show()
```

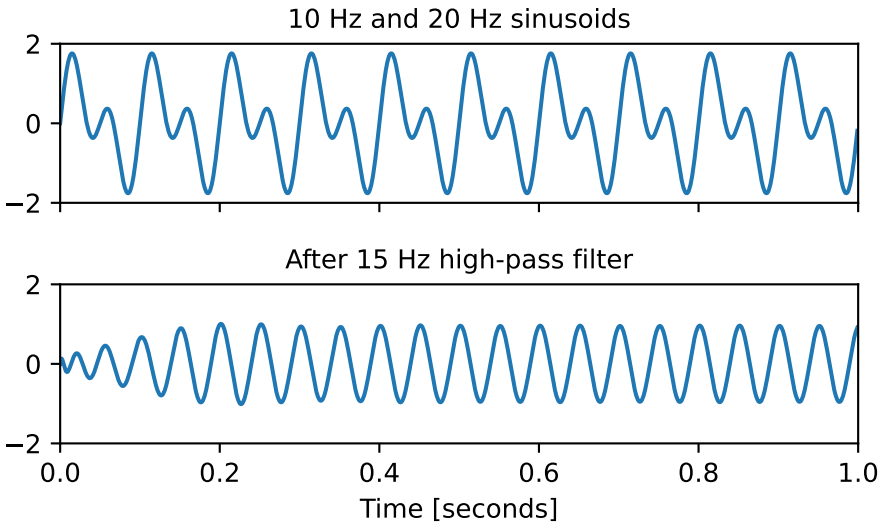


Generate a signal made up of 10 Hz and 20 Hz, sampled at 1 kHz

```
>>> t = np.linspace(0, 1, 1000, False)  # 1 second
>>> sig = np.sin(2*np.pi*10*t) + np.sin(2*np.pi*20*t)
>>> fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
>>> ax1.plot(t, sig)
>>> ax1.set_title('10 Hz and 20 Hz sinusoids')
>>> ax1.axis([0, 1, -2, 2])
```

Design a digital high-pass filter at 15 Hz to remove the 10 Hz tone, and apply it to the signal. (It's recommended to use second-order sections format when filtering, to avoid numerical error with transfer function (`ba`) format):

```
>>> sos = signal.cheby1(10, 1, 15, 'hp', fs=1000, output='sos')
>>> filtered = signal.sosfilt(sos, sig)
>>> ax2.plot(t, filtered)
>>> ax2.set_title('After 15 Hz high-pass filter')
>>> ax2.axis([0, 1, -2, 2])
>>> ax2.set_xlabel('Time [seconds]')
>>> plt.tight_layout()
>>> plt.show()
```



scipy.signal.cheb1ord

`scipy.signal.`**`cheb1ord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*, *fs=None*)

Chebyshev type I filter order selection.

Return the order of the lowest order digital or analog Chebyshev Type I filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

Parameters

wp, ws [float] Passband and stopband edge frequencies.
For digital filters, these are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*wp* and *ws* are thus in half-cycles / sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]

- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g., rad/s).

gpass [float] The maximum loss in the passband (dB).

gstop [float] The minimum attenuation in the stopband (dB).

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

ord [int] The lowest order for a Chebyshev type I filter that meets specs.

wn [ndarray or float] The Chebyshev natural frequency (the "3dB frequency") for use with *cheby1* to give filter results. If *fs* is specified, this is in the same units, and *fs* must also be passed to *cheby1*.

See also:

cheby1

Filter design using order and critical points

buttord

Find order and critical points from passband and stopband spec

cheb2ord, **ellipord**

iirfilter

General filter design using order and critical frequencies

iirdesign

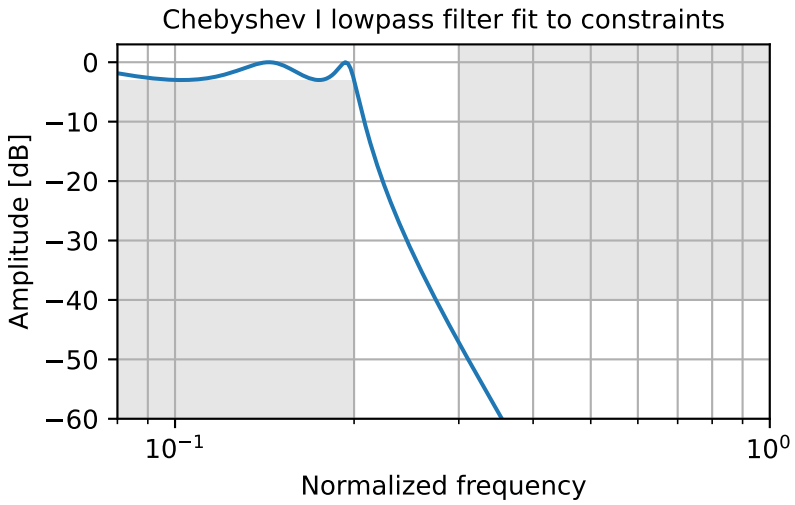
General filter design using passband and stopband spec

Examples

Design a digital lowpass filter such that the passband is within 3 dB up to 0.2*(fs/2), while rejecting at least -40 dB above 0.3*(fs/2). Plot its frequency response, showing the passband and stopband constraints in gray.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> N, Wn = signal.cheb1ord(0.2, 0.3, 3, 40)
>>> b, a = signal.cheby1(N, 3, Wn, 'low')
>>> w, h = signal.freqz(b, a)
>>> plt.semilogx(w / np.pi, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev I lowpass filter fit to constraints')
>>> plt.xlabel('Normalized frequency')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([.01, 0.2, 0.2, .01], [-3, -3, -99, -99], '0.9', lw=0) # stop
>>> plt.fill([0.3, 0.3,   2,   2], [ 9, -40, -40,  9], '0.9', lw=0) # pass
>>> plt.axis([0.08, 1, -60, 3])
>>> plt.show()
```



scipy.signal.cheby2

`scipy.signal.`**cheby2**(*N*, *rs*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*, *fs=None*)

Chebyshev type II digital and analog filter design.

Design an Nth-order digital or analog Chebyshev type II filter and return the filter coefficients.

Parameters

N [int] The order of the filter.

rs [float] The minimum attenuation required in the stop band. Specified in decibels, as a positive number.

Wn [array_like] A scalar or length-2 sequence giving the critical frequencies. For Type II filters, this is the point in the transition band at which the gain first reaches *-rs*.
For digital filters, *Wn* are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*Wn* is thus in half-cycles / sample.)
For analog filters, *Wn* is an angular frequency (e.g., rad/s).

btype [{'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional] The type of filter. Default is 'lowpass'.

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

output [{'ba', 'zpk', 'sos'}, optional] Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba' for backwards compatibility, but 'sos' should be used for general-purpose filtering.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos [ndarray] Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

cheb2ord, **cheb2ap**

Notes

The Chebyshev type II filter maximizes the rate of cutoff between the frequency response's passband and stopband, at the expense of ripple in the stopband and increased ringing in the step response.

Type II filters do not roll off as fast as Type I (*cheby1*).

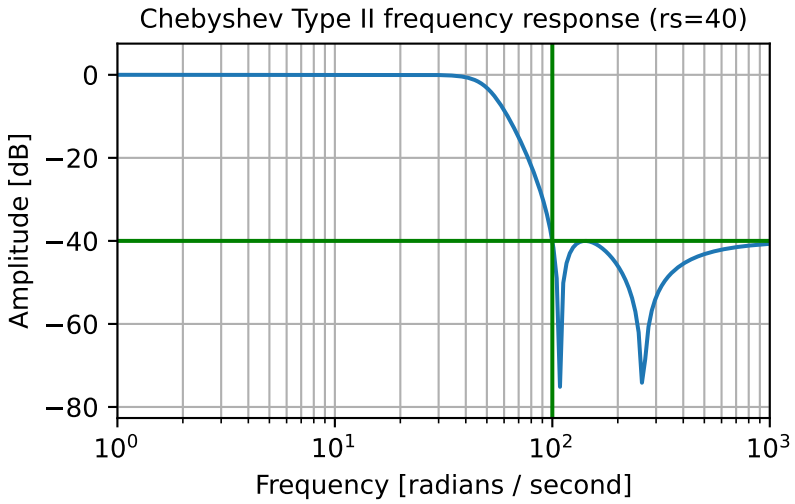
The `'sos'` output parameter was added in 0.16.0.

Examples

Design an analog filter and plot its frequency response, showing the critical points:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.cheby2(4, 40, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev Type II frequency response (rs=40)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.axhline(-40, color='green') # rs
>>> plt.show()
```

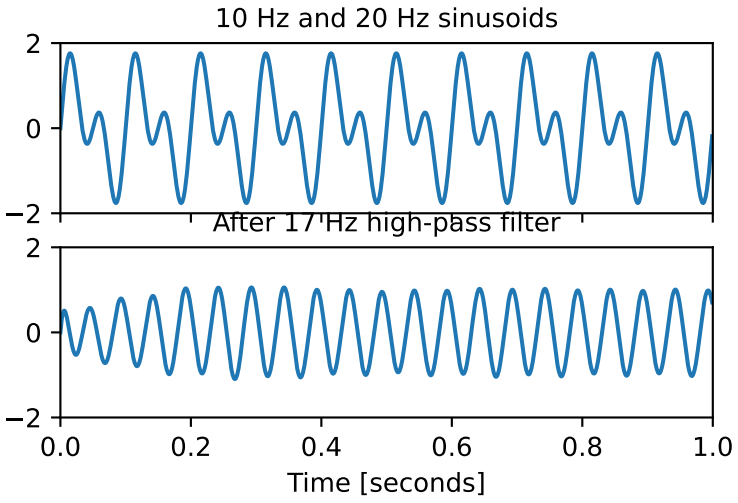


Generate a signal made up of 10 Hz and 20 Hz, sampled at 1 kHz

```
>>> t = np.linspace(0, 1, 1000, False)  # 1 second
>>> sig = np.sin(2*np.pi*10*t) + np.sin(2*np.pi*20*t)
>>> fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
>>> ax1.plot(t, sig)
>>> ax1.set_title('10 Hz and 20 Hz sinusoids')
>>> ax1.axis([0, 1, -2, 2])
```

Design a digital high-pass filter at 17 Hz to remove the 10 Hz tone, and apply it to the signal. (It's recommended to use second-order sections format when filtering, to avoid numerical error with transfer function (`ba`) format):

```
>>> sos = signal.cheby2(12, 20, 17, 'hp', fs=1000, output='sos')
>>> filtered = signal.sosfilt(sos, sig)
>>> ax2.plot(t, filtered)
>>> ax2.set_title('After 17 Hz high-pass filter')
>>> ax2.axis([0, 1, -2, 2])
>>> ax2.set_xlabel('Time [seconds]')
>>> plt.show()
```



scipy.signal.cheb2ord

`scipy.signal.`**`cheb2ord`**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*, *fs=None*)

Chebyshev type II filter order selection.

Return the order of the lowest order digital or analog Chebyshev Type II filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

Parameters

wp, ws [float] Passband and stopband edge frequencies.
For digital filters, these are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*wp* and *ws* are thus in half-cycles / sample.) For example:

- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g., rad/s).

gpass [float] The maximum loss in the passband (dB).

gstop [float] The minimum attenuation in the stopband (dB).

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

ord [int] The lowest order for a Chebyshev type II filter that meets specs.

wn [ndarray or float] The Chebyshev natural frequency (the "3dB frequency") for use with `cheby2` to give filter results. If *fs* is specified, this is in the same units, and *fs* must also be passed to `cheby2`.

See also:

cheby2

Filter design using order and critical points

buttord

Find order and critical points from passband and stopband spec

cheb1ord, **ellipord**

iirfilter

General filter design using order and critical frequencies

iirdesign

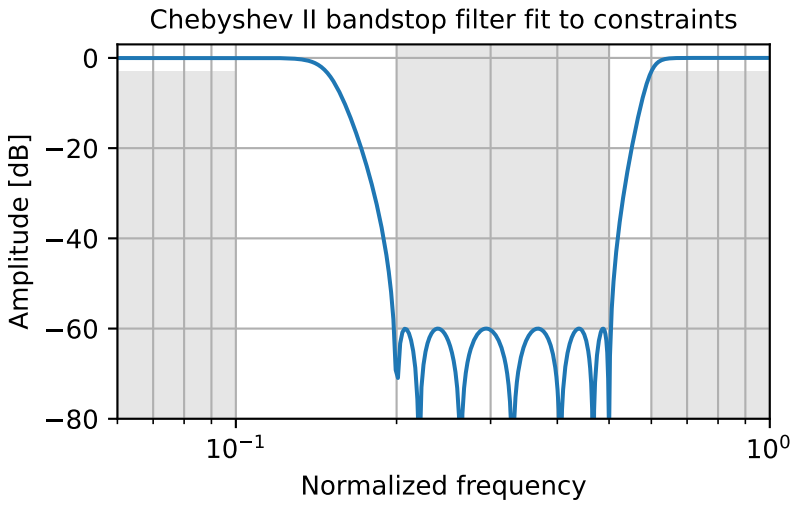
General filter design using passband and stopband spec

Examples

Design a digital bandstop filter which rejects -60 dB from 0.2*(fs/2) to 0.5*(fs/2), while staying within 3 dB below 0.1*(fs/2) or above 0.6*(fs/2). Plot its frequency response, showing the passband and stopband constraints in gray.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> N, Wn = signal.cheb2ord([0.1, 0.6], [0.2, 0.5], 3, 60)
>>> b, a = signal.cheby2(N, 60, Wn, 'stop')
>>> w, h = signal.freqz(b, a)
>>> plt.semilogx(w / np.pi, 20 * np.log10(abs(h)))
>>> plt.title('Chebyshev II bandstop filter fit to constraints')
>>> plt.xlabel('Normalized frequency')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([.01, .1, .1, .01], [-3,  -3, -99, -99], '0.9', lw=0) # stop
>>> plt.fill([.2,  .2, .5,  .5], [ 9, -60, -60,   9], '0.9', lw=0) # pass
>>> plt.fill([.6,  .6,  2,   2], [-99, -3,  -3, -99], '0.9', lw=0) # stop
>>> plt.axis([0.06, 1, -80, 3])
>>> plt.show()
```



scipy.signal.ellip

`scipy.signal.`**`ellip`**(*N*, *rp*, *rs*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*, *fs=None*)

Elliptic (Cauer) digital and analog filter design.

Design an Nth-order digital or analog elliptic filter and return the filter coefficients.

Parameters

N [int] The order of the filter.

rp [float] The maximum ripple allowed below unity gain in the passband. Specified in decibels, as a positive number.

rs [float] The minimum attenuation required in the stop band. Specified in decibels, as a positive number.

Wn [array_like] A scalar or length-2 sequence giving the critical frequencies. For elliptic filters, this is the point in the transition band at which the gain first drops below *-rp*.
For digital filters, *Wn* are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*Wn* is thus in half-cycles / sample.)
For analog filters, *Wn* is an angular frequency (e.g., rad/s).

btype [{'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional] The type of filter. Default is 'lowpass'.

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

output [{'ba', 'zpk', 'sos'}, optional] Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba' for backwards compatibility, but 'sos' should be used for general-purpose filtering.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos [ndarray] Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

See also:

ellipord, **ellipap**

Notes

Also known as Cauer or Zolotarev filters, the elliptical filter maximizes the rate of transition between the frequency response's passband and stopband, at the expense of ripple in both, and increased ringing in the step response.

As *rp* approaches 0, the elliptical filter becomes a Chebyshev type II filter (*cheby2*). As *rs* approaches 0, it becomes a Chebyshev type I filter (*cheby1*). As both approach 0, it becomes a Butterworth filter (*butter*).

The equiripple passband has N maxima or minima (for example, a 5th-order filter has 3 maxima and 2 minima). Consequently, the DC gain is unity for odd-order filters, or -rp dB for even-order filters.

The `'sos'` output parameter was added in 0.16.0.

Examples

Design an analog filter and plot its frequency response, showing the critical points:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.ellip(4, 5, 40, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Elliptic filter frequency response (rp=5, rs=40)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green') # cutoff frequency
>>> plt.axhline(-40, color='green') # rs
>>> plt.axhline(-5, color='green') # rp
>>> plt.show()
```

Generate a signal made up of 10 Hz and 20 Hz, sampled at 1 kHz

```
>>> t = np.linspace(0, 1, 1000, False)  # 1 second
>>> sig = np.sin(2*np.pi*10*t) + np.sin(2*np.pi*20*t)
>>> fig, (ax1, ax2) = plt.subplots(2, 1, sharex=True)
>>> ax1.plot(t, sig)
>>> ax1.set_title('10 Hz and 20 Hz sinusoids')
>>> ax1.axis([0, 1, -2, 2])
```

Design a digital high-pass filter at 17 Hz to remove the 10 Hz tone, and apply it to the signal. (It's recommended to use second-order sections format when filtering, to avoid numerical error with transfer function (`ba`) format):

```
>>> sos = signal.ellip(8, 1, 100, 17, 'hp', fs=1000, output='sos')
>>> filtered = signal.sosfilt(sos, sig)
>>> ax2.plot(t, filtered)
>>> ax2.set_title('After 17 Hz high-pass filter')
```

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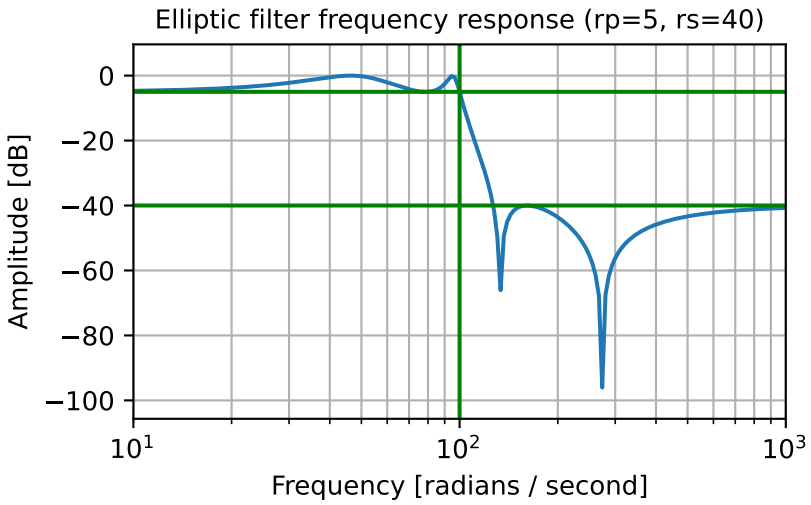

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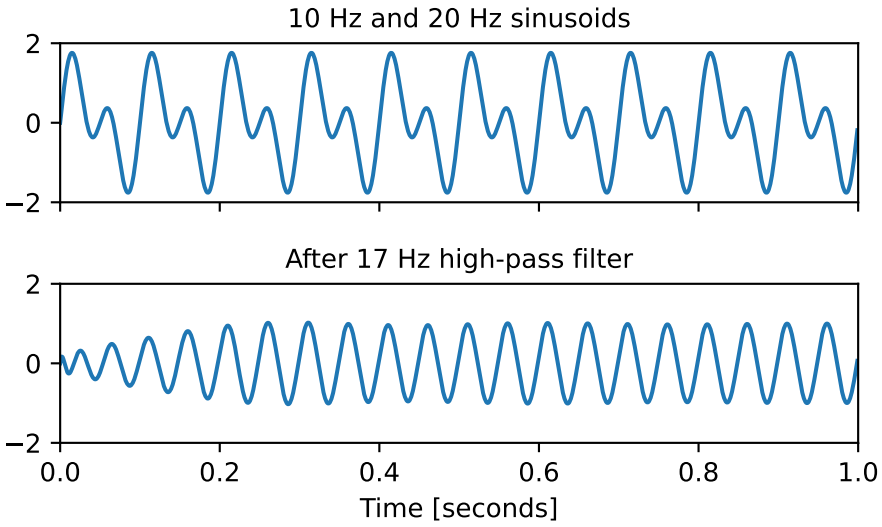
```
>>> ax2.axis([0, 1, -2, 2])
>>> ax2.set_xlabel('Time [seconds]')
>>> plt.tight_layout()
>>> plt.show()
```



scipy.signal.ellipord

scipy.signal.**ellipord**(*wp*, *ws*, *gpass*, *gstop*, *analog=False*, *fs=None*)

Elliptic (Cauer) filter order selection.

Return the order of the lowest order digital or analog elliptic filter that loses no more than *gpass* dB in the passband and has at least *gstop* dB attenuation in the stopband.

Parameters

wp, ws [float] Passband and stopband edge frequencies.
For digital filters, these are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*wp* and *ws* are thus in half-cycles / sample.) For example:
- Lowpass: wp = 0.2, ws = 0.3
- Highpass: wp = 0.3, ws = 0.2
- Bandpass: wp = [0.2, 0.5], ws = [0.1, 0.6]
- Bandstop: wp = [0.1, 0.6], ws = [0.2, 0.5]

For analog filters, *wp* and *ws* are angular frequencies (e.g., rad/s).

gpass [float] The maximum loss in the passband (dB).

gstop [float] The minimum attenuation in the stopband (dB).

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

ord [int] The lowest order for an Elliptic (Cauer) filter that meets specs.

wn [ndarray or float] The Chebyshev natural frequency (the "3dB frequency") for use with *ellip* to give filter results. If *fs* is specified, this is in the same units, and *fs* must also be passed to *ellip*.

See also:

ellip

Filter design using order and critical points

buttord

Find order and critical points from passband and stopband spec

cheb1ord, **cheb2ord**

iirfilter

General filter design using order and critical frequencies

iirdesign

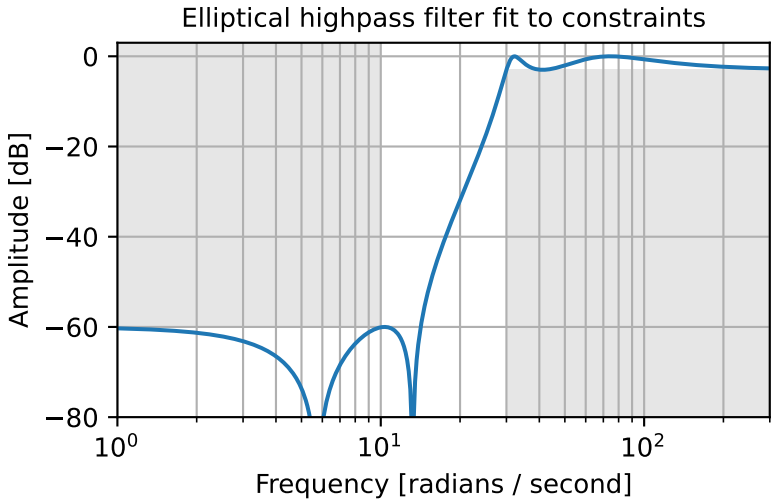
General filter design using passband and stopband spec

Examples

Design an analog highpass filter such that the passband is within 3 dB above 30 rad/s, while rejecting -60 dB at 10 rad/s. Plot its frequency response, showing the passband and stopband constraints in gray.

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> N, Wn = signal.ellipord(30, 10, 3, 60, True)
>>> b, a = signal.ellip(N, 3, 60, Wn, 'high', True)
>>> w, h = signal.freqs(b, a, np.logspace(0, 3, 500))
>>> plt.semilogx(w, 20 * np.log10(abs(h)))
>>> plt.title('Elliptical highpass filter fit to constraints')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.grid(which='both', axis='both')
>>> plt.fill([.1, 10,  10,  .1], [1e4, 1e4, -60, -60], '0.9', lw=0) # stop
>>> plt.fill([30, 30, 1e9, 1e9], [-99,  -3,  -3, -99], '0.9', lw=0) # pass
>>> plt.axis([1, 300, -80, 3])
>>> plt.show()
```



scipy.signal.bessel

`scipy.signal.`**`bessel`**(*N*, *Wn*, *btype='low'*, *analog=False*, *output='ba'*, *norm='phase'*, *fs=None*)

Bessel/Thomson digital and analog filter design.

Design an Nth-order digital or analog Bessel filter and return the filter coefficients.

Parameters

N [int] The order of the filter.

Wn [array_like] A scalar or length-2 sequence giving the critical frequencies (defined by the *norm* parameter). For analog filters, *Wn* is an angular frequency (e.g., rad/s).
For digital filters, *Wn* are in the same units as *fs*. By default, *fs* is 2 half-cycles/sample, so these are normalized from 0 to 1, where 1 is the Nyquist frequency. (*Wn* is thus in half-cycles / sample.)

btype [{'lowpass', 'highpass', 'bandpass', 'bandstop'}, optional] The type of filter. Default is 'lowpass'.

analog [bool, optional] When True, return an analog filter, otherwise a digital filter is returned. (See Notes.)

output [{'ba', 'zpk', 'sos'}, optional] Type of output: numerator/denominator ('ba'), pole-zero ('zpk'), or second-order sections ('sos'). Default is 'ba'.

norm [{'phase', 'delay', 'mag'}, optional] Critical frequency normalization:

`phase` The filter is normalized such that the phase response reaches its midpoint at angular (e.g. rad/s) frequency *Wn*. This happens for both low-pass and high-pass filters, so this is the "phase-matched" case.
The magnitude response asymptotes are the same as a Butterworth filter of the same order with a cutoff of *Wn*.
This is the default, and matches MATLAB's implementation.

`delay` The filter is normalized such that the group delay in the passband is 1/*Wn* (e.g., seconds). This is the "natural" type obtained by solving Bessel polynomials.

`mag` The filter is normalized such that the gain magnitude is -3 dB at angular frequency *Wn*.

New in version 0.18.0.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (*b*) and denominator (*a*) polynomials of the IIR filter. Only returned if `output='ba'`.

z, p, k [ndarray, ndarray, float] Zeros, poles, and system gain of the IIR filter transfer function. Only returned if `output='zpk'`.

sos [ndarray] Second-order sections representation of the IIR filter. Only returned if `output=='sos'`.

Notes

Also known as a Thomson filter, the analog Bessel filter has maximally flat group delay and maximally linear phase response, with very little ringing in the step response. [1]

The Bessel is inherently an analog filter. This function generates digital Bessel filters using the bilinear transform, which does not preserve the phase response of the analog filter. As such, it is only approximately correct at frequencies below about fs/4. To get maximally-flat group delay at higher frequencies, the analog Bessel filter must be transformed using phase-preserving techniques.

See *`besselap`* for implementation details and references.

The `'sos'` output parameter was added in 0.16.0.

References

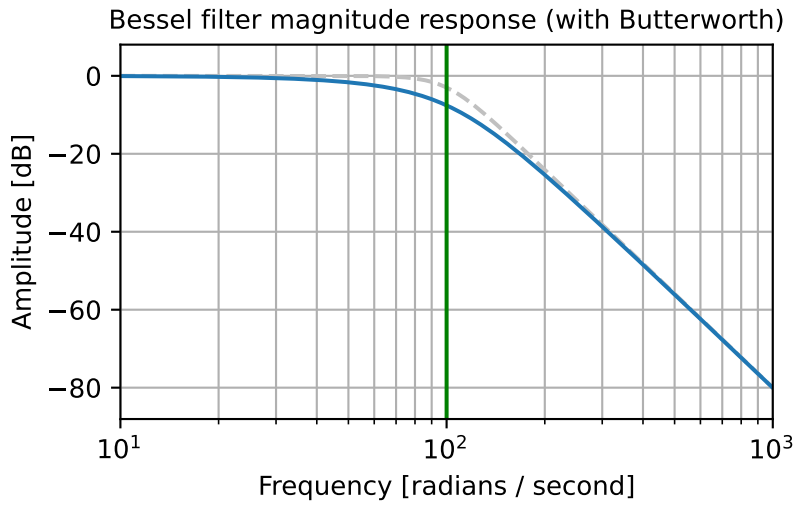
[1]

Examples

Plot the phase-normalized frequency response, showing the relationship to the Butterworth's cutoff frequency (green):

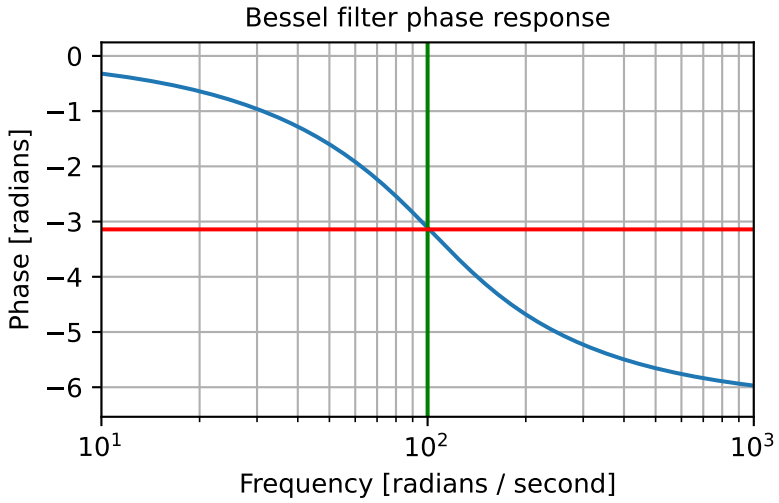
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> b, a = signal.butter(4, 100, 'low', analog=True)
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(np.abs(h)), color='silver', ls='dashed')
>>> b, a = signal.bessel(4, 100, 'low', analog=True, norm='phase')
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(np.abs(h)))
>>> plt.title('Bessel filter magnitude response (with Butterworth)')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.axvline(100, color='green')  # cutoff frequency
>>> plt.show()
```



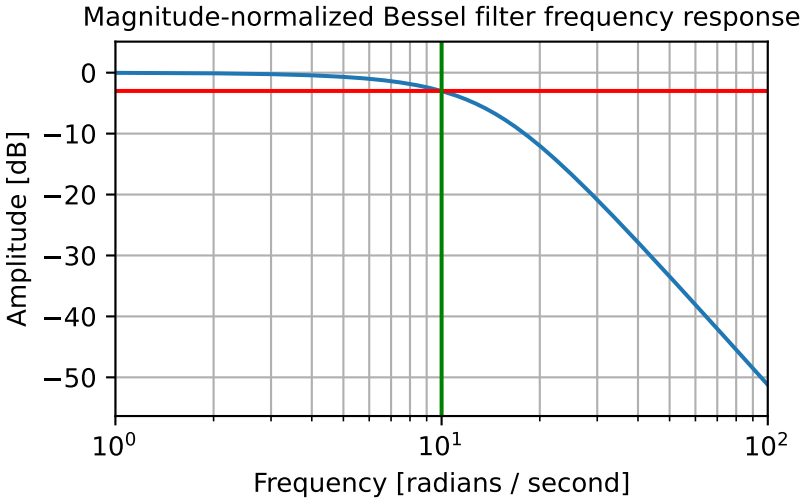
and the phase midpoint:

```
>>> plt.figure()
>>> plt.semilogx(w, np.unwrap(np.angle(h)))
>>> plt.axvline(100, color='green')  # cutoff frequency
>>> plt.axhline(-np.pi, color='red')  # phase midpoint
>>> plt.title('Bessel filter phase response')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Phase [radians]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.show()
```



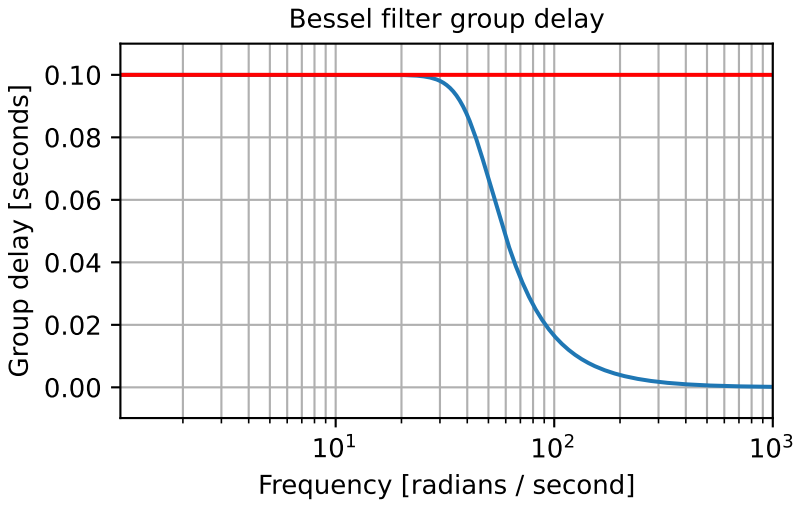
Plot the magnitude-normalized frequency response, showing the -3 dB cutoff:

```
>>> b, a = signal.bessel(3, 10, 'low', analog=True, norm='mag')
>>> w, h = signal.freqs(b, a)
>>> plt.semilogx(w, 20 * np.log10(np.abs(h)))
>>> plt.axhline(-3, color='red')  # -3 dB magnitude
>>> plt.axvline(10, color='green')  # cutoff frequency
>>> plt.title('Magnitude-normalized Bessel filter frequency response')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Amplitude [dB]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.show()
```



Plot the delay-normalized filter, showing the maximally-flat group delay at 0.1 seconds:

```
>>> b, a = signal.bessel(5, 1/0.1, 'low', analog=True, norm='delay')
>>> w, h = signal.freqs(b, a)
>>> plt.figure()
>>> plt.semilogx(w[1:], -np.diff(np.unwrap(np.angle(h)))/np.diff(w))
>>> plt.axhline(0.1, color='red')  # 0.1 seconds group delay
>>> plt.title('Bessel filter group delay')
>>> plt.xlabel('Frequency [radians / second]')
>>> plt.ylabel('Group delay [seconds]')
>>> plt.margins(0, 0.1)
>>> plt.grid(which='both', axis='both')
>>> plt.show()
```



scipy.signal.iirnotch

scipy.signal.**iirnotch**(*w0*, *Q*, *fs=2.0*)

Design second-order IIR notch digital filter.

A notch filter is a band-stop filter with a narrow bandwidth (high quality factor). It rejects a narrow frequency band and leaves the rest of the spectrum little changed.

Parameters

w0 [float] Frequency to remove from a signal. If *fs* is specified, this is in the same units as *fs*. By default, it is a normalized scalar that must satisfy `0 < w0 < 1`, with `w0 = 1` corresponding to half of the sampling frequency.

Q [float] Quality factor. Dimensionless parameter that characterizes notch filter -3 dB bandwidth `bw` relative to its center frequency, `Q = w0/bw`.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (`b`) and denominator (`a`) polynomials of the IIR filter.

See also:

`iirpeak`

Notes

New in version 0.19.0.

References

[1]

Examples

Design and plot filter to remove the 60 Hz component from a signal sampled at 200 Hz, using a quality factor Q = 30

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> fs = 200.0  # Sample frequency (Hz)
>>> f0 = 60.0  # Frequency to be removed from signal (Hz)
>>> Q = 30.0  # Quality factor
>>> # Design notch filter
>>> b, a = signal.iirnotch(f0, Q, fs)
```

```
>>> # Frequency response
>>> freq, h = signal.freqz(b, a, fs=fs)
>>> # Plot
>>> fig, ax = plt.subplots(2, 1, figsize=(8, 6))
>>> ax[0].plot(freq, 20*np.log10(abs(h)), color='blue')
>>> ax[0].set_title("Frequency Response")
>>> ax[0].set_ylabel("Amplitude (dB)", color='blue')
>>> ax[0].set_xlim([0, 100])
>>> ax[0].set_ylim([-25, 10])
>>> ax[0].grid()
>>> ax[1].plot(freq, np.unwrap(np.angle(h))*180/np.pi, color='green')
>>> ax[1].set_ylabel("Angle (degrees)", color='green')
>>> ax[1].set_xlabel("Frequency (Hz)")
>>> ax[1].set_xlim([0, 100])
>>> ax[1].set_yticks([-90, -60, -30, 0, 30, 60, 90])
>>> ax[1].set_ylim([-90, 90])
>>> ax[1].grid()
>>> plt.show()
```

scipy.signal.iirpeak

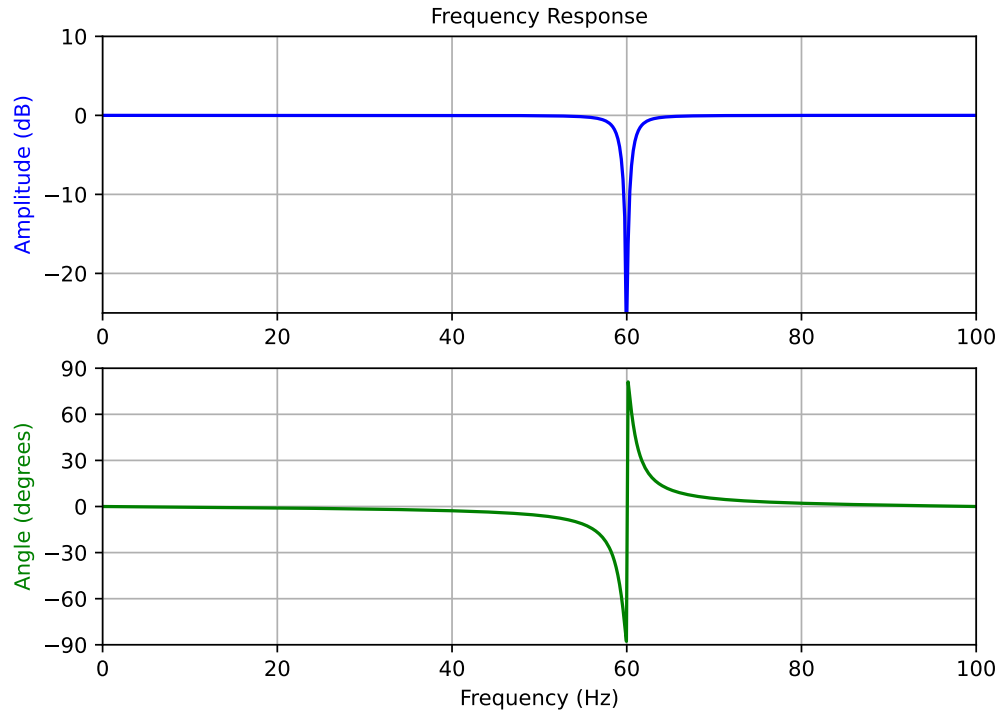
scipy.signal.**iirpeak**(*w0*, *Q*, *fs=2.0*)

Design second-order IIR peak (resonant) digital filter.

A peak filter is a band-pass filter with a narrow bandwidth (high quality factor). It rejects components outside a narrow frequency band.

Parameters

w0 [float] Frequency to be retained in a signal. If *fs* is specified, this is in the same units as *fs*. By default, it is a normalized scalar that must satisfy `0 < w0 < 1`, with `w0 = 1` corresponding to half of the sampling frequency.


Frequency Response
Amplitude (dB)
10
0
−10
−20
0
20
40
60
80
100
Angle (degrees)
90
60
30
0
−30
−60
−90
0
20
40
60
80
100
Frequency (Hz)

Q [float] Quality factor. Dimensionless parameter that characterizes peak filter -3 dB bandwidth `bw` relative to its center frequency, `Q = w0/bw`.

fs [float, optional] The sampling frequency of the digital system.
New in version 1.2.0.

Returns

b, a [ndarray, ndarray] Numerator (`b`) and denominator (`a`) polynomials of the IIR filter.

See also:

`iirnotch`

Notes

New in version 0.19.0.

References

[1]

Examples

Design and plot filter to remove the frequencies other than the 300 Hz component from a signal sampled at 1000 Hz, using a quality factor Q = 30

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> fs = 1000.0  # Sample frequency (Hz)
>>> f0 = 300.0  # Frequency to be retained (Hz)
>>> Q = 30.0  # Quality factor
>>> # Design peak filter
>>> b, a = signal.iirpeak(f0, Q, fs)
```

```
>>> # Frequency response
>>> freq, h = signal.freqz(b, a, fs=fs)
>>> # Plot
>>> fig, ax = plt.subplots(2, 1, figsize=(8, 6))
>>> ax[0].plot(freq, 20*np.log10(np.maximum(abs(h), 1e-5)), color='blue')
>>> ax[0].set_title("Frequency Response")
>>> ax[0].set_ylabel("Amplitude (dB)", color='blue')
>>> ax[0].set_xlim([0, 500])
>>> ax[0].set_ylim([-50, 10])
>>> ax[0].grid()
>>> ax[1].plot(freq, np.unwrap(np.angle(h))*180/np.pi, color='green')
>>> ax[1].set_ylabel("Angle (degrees)", color='green')
>>> ax[1].set_xlabel("Frequency (Hz)")
>>> ax[1].set_xlim([0, 500])
>>> ax[1].set_yticks([-90, -60, -30, 0, 30, 60, 90])
>>> ax[1].set_ylim([-90, 90])
```

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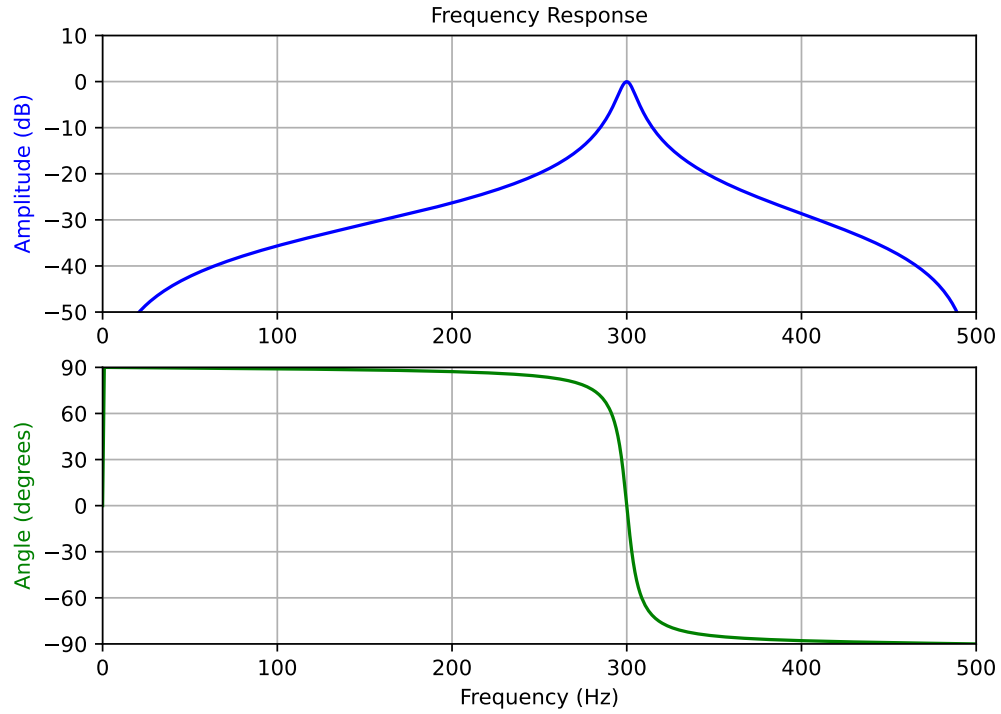
```
>>> ax[1].grid()
>>> plt.show()
```



scipy.signal.iircomb

`scipy.signal.`**`iircomb`**(*w0*, *Q*, *ftype='notch'*, *fs=2.0*)

Design IIR notching or peaking digital comb filter.

A notching comb filter is a band-stop filter with a narrow bandwidth (high quality factor). It rejects a narrow frequency band and leaves the rest of the spectrum little changed.

A peaking comb filter is a band-pass filter with a narrow bandwidth (high quality factor). It rejects components outside a narrow frequency band.

Parameters

w0 [float] Frequency to attenuate (notching) or boost (peaking). If *fs* is specified, this is in the same units as *fs*. By default, it is a normalized scalar that must satisfy `0 < w0 < 1`, with `w0 = 1` corresponding to half of the sampling frequency.

Q [float] Quality factor. Dimensionless parameter that characterizes notch filter -3 dB bandwidth `bw` relative to its center frequency, `Q = w0/bw`.

ftype [{'notch', 'peak'}] The type of comb filter generated by the function. If 'notch', then it returns a filter with notches at frequencies `0`, `w0`, `2 * w0`, etc. If 'peak', then it returns a filter with peaks at frequencies `0.5 * w0`, `1.5 * w0`, `2.5 * w0`, etc. Default is 'notch'.

fs [float, optional] The sampling frequency of the signal. Default is 2.0.

Returns

b, a [ndarray, ndarray] Numerator (`b`) and denominator (`a`) polynomials of the IIR filter.

Raises

ValueError
If *w0* is less than or equal to 0 or greater than or equal to `fs/2`, if *fs* is not divisible by *w0*, if *ftype* is not 'notch' or 'peak'

See also:

iirnotch

iirpeak

Notes

For implementation details, see [1]. The TF implementation of the comb filter is numerically stable even at higher orders due to the use of a single repeated pole, which won't suffer from precision loss.

References

[1]

Examples

Design and plot notching comb filter at 20 Hz for a signal sampled at 200 Hz, using quality factor Q = 30

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> fs = 200.0  # Sample frequency (Hz)
>>> f0 = 20.0  # Frequency to be removed from signal (Hz)
>>> Q = 30.0  # Quality factor
>>> # Design notching comb filter
>>> b, a = signal.iircomb(f0, Q, ftype='notch', fs=fs)
```

```
>>> # Frequency response
>>> freq, h = signal.freqz(b, a, fs=fs)
>>> response = abs(h)
>>> # To avoid divide by zero when graphing
>>> response[response == 0] = 1e-20
>>> # Plot
>>> fig, ax = plt.subplots(2, 1, figsize=(8, 6))
>>> ax[0].plot(freq, 20*np.log10(abs(response)), color='blue')
>>> ax[0].set_title("Frequency Response")
>>> ax[0].set_ylabel("Amplitude (dB)", color='blue')
>>> ax[0].set_xlim([0, 100])
>>> ax[0].set_ylim([-30, 10])
>>> ax[0].grid()
```

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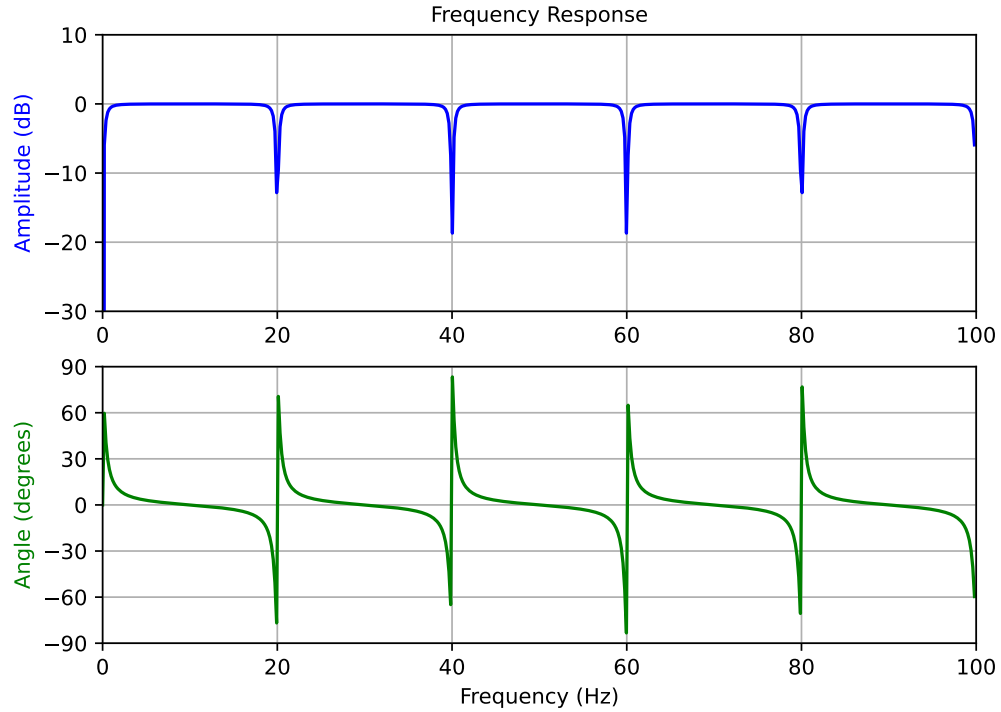
```
>>> ax[1].plot(freq, np.unwrap(np.angle(h))*180/np.pi, color='green')
>>> ax[1].set_ylabel("Angle (degrees)", color='green')
>>> ax[1].set_xlabel("Frequency (Hz)")
>>> ax[1].set_xlim([0, 100])
>>> ax[1].set_yticks([-90, -60, -30, 0, 30, 60, 90])
>>> ax[1].set_ylim([-90, 90])
>>> ax[1].grid()
>>> plt.show()
```



Design and plot peaking comb filter at 250 Hz for a signal sampled at 1000 Hz, using quality factor Q = 30

```
>>> fs = 1000.0  # Sample frequency (Hz)
>>> f0 = 250.0  # Frequency to be retained (Hz)
>>> Q = 30.0  # Quality factor
>>> # Design peaking filter
>>> b, a = signal.iircomb(f0, Q, ftype='peak', fs=fs)
```

```
>>> # Frequency response
>>> freq, h = signal.freqz(b, a, fs=fs)
>>> response = abs(h)
>>> # To avoid divide by zero when graphing
```

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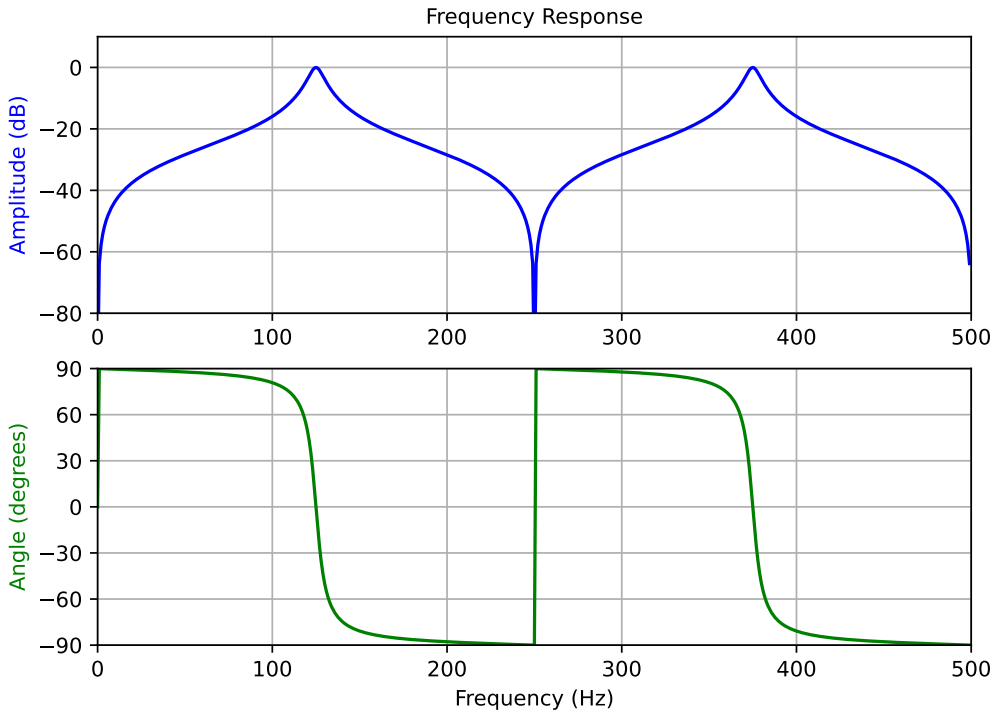
```
>>> response[response == 0] = 1e-20
>>> # Plot
>>> fig, ax = plt.subplots(2, 1, figsize=(8, 6))
>>> ax[0].plot(freq, 20*np.log10(np.maximum(abs(h), 1e-5)), color='blue')
>>> ax[0].set_title("Frequency Response")
>>> ax[0].set_ylabel("Amplitude (dB)", color='blue')
>>> ax[0].set_xlim([0, 500])
>>> ax[0].set_ylim([-80, 10])
>>> ax[0].grid()
>>> ax[1].plot(freq, np.unwrap(np.angle(h))*180/np.pi, color='green')
>>> ax[1].set_ylabel("Angle (degrees)", color='green')
>>> ax[1].set_xlabel("Frequency (Hz)")
>>> ax[1].set_xlim([0, 500])
>>> ax[1].set_yticks([-90, -60, -30, 0, 30, 60, 90])
>>> ax[1].set_ylim([-90, 90])
>>> ax[1].grid()
>>> plt.show()
```



Continuous-time linear systems

lti(*system)	Continuous-time linear time invariant system base class.
StateSpace(*system, **kwargs)	Linear Time Invariant system in state-space form.
TransferFunction(*system, **kwargs)	Linear Time Invariant system class in transfer function form.
ZerosPolesGain(*system, **kwargs)	Linear Time Invariant system class in zeros, poles, gain form.
lsim(system, U, T[, X0, interp])	Simulate output of a continuous-time linear system.
lsim2(system[, U, T, X0])	Simulate output of a continuous-time linear system, by using the ODE solver *scipy.integrate.odeint*.
impulse(system[, X0, T, N])	Impulse response of continuous-time system.
impulse2(system[, X0, T, N])	Impulse response of a single-input, continuous-time linear system.
step(system[, X0, T, N])	Step response of continuous-time system.
step2(system[, X0, T, N])	Step response of continuous-time system.
freqresp(system[, w, n])	Calculate the frequency response of a continuous-time system.
bode(system[, w, n])	Calculate Bode magnitude and phase data of a continuous-time system.

scipy.signal.lti

class scipy.signal.**lti**(**system*)

Continuous-time linear time invariant system base class.

Parameters

***system** [arguments] The *lti* class can be instantiated with either 2, 3 or 4 arguments. The following gives the number of arguments and the corresponding continuous-time subclass that is created:
- 2: *TransferFunction*: (numerator, denominator)
- 3: *ZerosPolesGain*: (zeros, poles, gain)
- 4: *StateSpace*: (A, B, C, D)

Each argument can be an array or a sequence.

See also:

ZerosPolesGain, **StateSpace**, **TransferFunction**, **dlti**

Notes

lti instances do not exist directly. Instead, *lti* creates an instance of one of its subclasses: *StateSpace*, *TransferFunction* or *ZerosPolesGain*.

If (numerator, denominator) is passed in for `*system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g., `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

Changing the value of properties that are not directly part of the current system representation (such as the `zeros` of a *StateSpace* system) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call `sys = sys.to_zpk()` before accessing/changing the zeros, poles or gain.

Examples

```
>>> from scipy import signal
```

```
>>> signal.lti(1, 2, 3, 4)
StateSpaceContinuous(
array([[1]]),
array([[2]]),
array([[3]]),
array([[4]]),
dt: None
)
```

Construct the transfer function $H(s) = \frac{5(s-1)(s-2)}{(s-3)(s-4)}$:

```
>>> signal.lti([1, 2], [3, 4], 5)
ZerosPolesGainContinuous(
array([1, 2]),
array([3, 4]),
5,
dt: None
)
```

Construct the transfer function $H(s) = \frac{3s+4}{1s+2}$:

```
>>> signal.lti([3, 4], [1, 2])
TransferFunctionContinuous(
array([3., 4.]),
array([1., 2.]),
dt: None
)
```

Attributes

dt	Return the sampling time of the system, *None* for `lti` systems.
poles	Poles of the system.
zeros	Zeros of the system.

Methods

`bode`([w, n])	Calculate Bode magnitude and phase data of a continuous-time system.
`freqresp`([w, n])	Calculate the frequency response of a continuous-time system.
`impulse`([X0, T, N])	Return the impulse response of a continuous-time system.
`output`(U, T[, X0])	Return the response of a continuous-time system to input *U*.
`step`([X0, T, N])	Return the step response of a continuous-time system.
`to_discrete`(dt[, method, alpha])	Return a discretized version of the current system.

scipy.signal.lti.bode

lti.**bode**(*w=None*, *n=100*)

Calculate Bode magnitude and phase data of a continuous-time system.

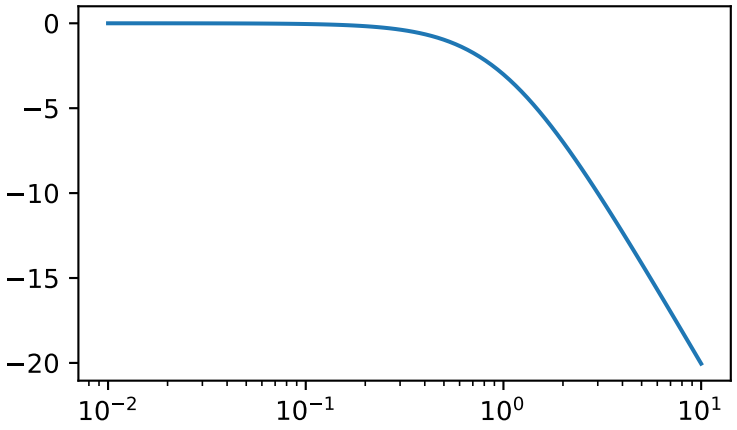
Returns a 3-tuple containing arrays of frequencies [rad/s], magnitude [dB] and phase [deg]. See *bode* for details.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> sys = signal.TransferFunction([1], [1, 1])
>>> w, mag, phase = sys.bode()
```

```
>>> plt.figure()
>>> plt.semilogx(w, mag)    # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

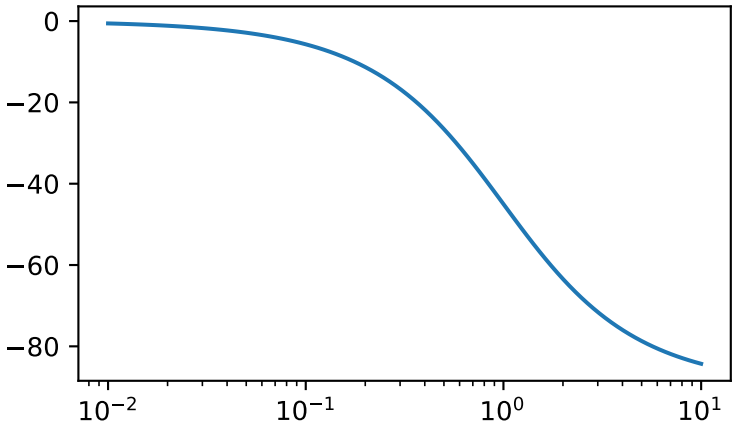


scipy.signal.lti.freqresp

lti.**freqresp**(*w=None*, *n=10000*)

Calculate the frequency response of a continuous-time system.

Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See *freqresp* for details.



scipy.signal.lti.impulse

`lti.`**`impulse`**(*X0=None*, *T=None*, *N=None*)
Return the impulse response of a continuous-time system. See *impulse* for details.

scipy.signal.lti.output

`lti.`**`output`**(*U*, *T*, *X0=None*)
Return the response of a continuous-time system to input *U*. See *lsim* for details.

scipy.signal.lti.step

`lti.`**`step`**(*X0=None*, *T=None*, *N=None*)
Return the step response of a continuous-time system. See *step* for details.

scipy.signal.lti.to_discrete

`lti.`**`to_discrete`**(*dt*, *method='zoh'*, *alpha=None*)
Return a discretized version of the current system.

Parameters: See *cont2discrete* for details.

Returns

sys: instance of *dlti*

scipy.signal.StateSpace

class scipy.signal.**StateSpace**(**system*, ***kwargs*)

Linear Time Invariant system in state-space form.

Represents the system as the continuous-time, first order differential equation $\dot{x} = Ax + Bu$ or the discrete-time difference equation $x[k+1] = Ax[k] + Bu[k]$. *StateSpace* systems inherit additional functionality from the *lti*, respectively the *dlti* classes, depending on which system representation is used.

Parameters

***system: arguments**

The *StateSpace* class can be instantiated with 1 or 4 arguments. The following gives the number of input arguments and their interpretation:

- 1: *lti* or *dlti* system: (*StateSpace*, *TransferFunction* or *ZerosPolesGain*)
- 4: array_like: (A, B, C, D)

dt: float, optional

Sampling time [s] of the discrete-time systems. Defaults to *None* (continuous-time). Must be specified as a keyword argument, for example, `dt=0.1`.

See also:

TransferFunction, **ZerosPolesGain**, **lti**, **dlti**

ss2zpk, **ss2tf**, **zpk2sos**

Notes

Changing the value of properties that are not part of the *StateSpace* system representation (such as `zeros` or `poles`) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call `sys = sys.to_zpk()` before accessing/changing the zeros, poles or gain.

Examples

```
>>> from scipy import signal
```

```
>>> a = np.array([[0, 1], [0, 0]])
>>> b = np.array([[0], [1]])
>>> c = np.array([[1, 0]])
>>> d = np.array([[0]])
```

```
>>> sys = signal.StateSpace(a, b, c, d)
>>> print(sys)
StateSpaceContinuous(
array([[0, 1],
       [0, 0]]),
array([[0],
       [1]]),
array([[1, 0]]),
array([[0]]),
dt: None
)
```

```
>>> sys.to_discrete(0.1)
StateSpaceDiscrete(
array([[1. , 0.1],
       [0. , 1. ]]),
array([[0.005],
       [0.1  ]]),
array([[1, 0]]),
array([[0]]),
dt: 0.1
)
```

```
>>> a = np.array([[1, 0.1], [0, 1]])
>>> b = np.array([[0.005], [0.1]])
```

```
>>> signal.StateSpace(a, b, c, d, dt=0.1)
StateSpaceDiscrete(
array([[1. , 0.1],
       [0. , 1. ]]),
array([[0.005],
       [0.1  ]]),
array([[1, 0]]),
array([[0]]),
dt: 0.1
)
```

Attributes

A	State matrix of the *StateSpace* system.
B	Input matrix of the *StateSpace* system.
C	Output matrix of the *StateSpace* system.
D	Feedthrough matrix of the *StateSpace* system.
dt	Return the sampling time of the system, *None* for *lti* systems.
poles	Poles of the system.
zeros	Zeros of the system.

Methods

__mul__(other)	Post-multiply another system or a scalar
to_ss()	Return a copy of the current *StateSpace* system.
to_tf(**kwargs)	Convert system representation to *TransferFunction*.
to_zpk(**kwargs)	Convert system representation to *ZerosPolesGain*.

scipy.signal.StateSpace.__mul__

StateSpace.**__mul__**(*other*)
Post-multiply another system or a scalar

Handles multiplication of systems in the sense of a frequency domain multiplication. That means, given two systems E1(s) and E2(s), their multiplication, H(s) = E1(s) * E2(s), means that applying H(s) to U(s) is equivalent to first applying E2(s), and then E1(s).

Notes

For SISO systems the order of system application does not matter. However, for MIMO systems, where the two systems are matrices, the order above ensures standard Matrix multiplication rules apply.

scipy.signal.StateSpace.to_ss

StateSpace.**to_ss**()
Return a copy of the current *StateSpace* system.

Returns

sys [instance of *StateSpace*] The current system (copy)

scipy.signal.StateSpace.to_tf

StateSpace.**to_tf**(***kwargs*)
Convert system representation to *TransferFunction*.

Parameters

kwargs [dict, optional] Additional keywords passed to *ss2zpk*

Returns

sys [instance of *TransferFunction*] Transfer function of the current system

scipy.signal.StateSpace.to_zpk

StateSpace.**to_zpk**(***kwargs*)
Convert system representation to *ZerosPolesGain*.

Parameters

kwargs [dict, optional] Additional keywords passed to *ss2zpk*

Returns

sys [instance of *ZerosPolesGain*] Zeros, poles, gain representation of the current system

scipy.signal.TransferFunction

class scipy.signal.**TransferFunction**(**system*, ***kwargs*)

Linear Time Invariant system class in transfer function form.

Represents the system as the continuous-time transfer function $H(s) = \sum_{i=0}^{N} b[N-i]s^i / \sum_{j=0}^{M} a[M-j]s^j$ or the discrete-time transfer function $H(s) = \sum_{i=0}^{N} b[N-i]z^i / \sum_{j=0}^{M} a[M-j]z^j$, where b are elements of the numerator `num`, a are elements of the denominator `den`, and `N == len(b) - 1`, `M == len(a) - 1`. *TransferFunction* systems inherit additional functionality from the *lti*, respectively the *dlti* classes, depending on which system representation is used.

Parameters

***system: arguments**

The *TransferFunction* class can be instantiated with 1 or 2 arguments. The following gives the number of input arguments and their interpretation:

- 1: *lti* or *dlti* system: (*StateSpace*, *TransferFunction* or *ZerosPolesGain*)
- 2: array_like: (numerator, denominator)

dt: float, optional

Sampling time [s] of the discrete-time systems. Defaults to *None* (continuous-time). Must be specified as a keyword argument, for example, `dt=0.1`.

See also:

ZerosPolesGain, **StateSpace**, **lti**, **dlti**

tf2ss, **tf2zpk**, **tf2sos**

Notes

Changing the value of properties that are not part of the *TransferFunction* system representation (such as the *A*, *B*, *C*, *D* state-space matrices) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call `sys = sys.to_ss()` before accessing/changing the A, B, C, D system matrices.

If (numerator, denominator) is passed in for `*system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` or `z^2 + 3z + 5` would be represented as `[1, 3, 5]`)

Examples

Construct the transfer function $H(s) = \frac{s^2+3s+3}{s^2+2s+1}$:

```
>>> from scipy import signal
```

```
>>> num = [1, 3, 3]
>>> den = [1, 2, 1]
```

```
>>> signal.TransferFunction(num, den)
TransferFunctionContinuous(
array([1., 3., 3.]),
array([1., 2., 1.]),
dt: None
)
```

Construct the transfer function $H(z) = \frac{z^2+3z+3}{z^2+2z+1}$ with a sampling time of 0.1 seconds:

```
>>> signal.TransferFunction(num, den, dt=0.1)
TransferFunctionDiscrete(
array([1., 3., 3.]),
array([1., 2., 1.]),
dt: 0.1
)
```

Attributes

den	Denominator of the *TransferFunction* system.
dt	Return the sampling time of the system, *None* for *lti* systems.
num	Numerator of the *TransferFunction* system.
poles	Poles of the system.
zeros	Zeros of the system.

Methods

to_ss()	Convert system representation to *StateSpace*.
to_tf()	Return a copy of the current *TransferFunction* system.
to_zpk()	Convert system representation to *ZerosPoles-Gain*.

scipy.signal.TransferFunction.to_ss

TransferFunction.**to_ss**()
Convert system representation to *StateSpace*.

Returns

sys [instance of *StateSpace*] State space model of the current system

scipy.signal.TransferFunction.to_tf

TransferFunction.**to_tf**()
Return a copy of the current *TransferFunction* system.

Returns

sys [instance of *TransferFunction*] The current system (copy)

scipy.signal.TransferFunction.to_zpk

TransferFunction.**to_zpk**()
Convert system representation to *ZerosPolesGain*.

Returns

sys [instance of *ZerosPolesGain*] Zeros, poles, gain representation of the current system

scipy.signal.ZerosPolesGain

class scipy.signal.**ZerosPolesGain**(**system*, ***kwargs*)
Linear Time Invariant system class in zeros, poles, gain form.

Represents the system as the continuous- or discrete-time transfer function $H(s) = k \prod_i (s - z[i]) / \prod_j (s - p[j])$, where k is the `gain`, z are the `zeros` and p are the `poles`. *ZerosPolesGain* systems inherit additional functionality from the *lti*, respectively the *dlti* classes, depending on which system representation is used.

Parameters

***system** [arguments] The *ZerosPolesGain* class can be instantiated with 1 or 3 arguments. The following gives the number of input arguments and their interpretation:
- 1: *lti* or *dlti* system: (*StateSpace*, *TransferFunction* or *ZerosPolesGain*)
- 3: array_like: (zeros, poles, gain)

dt: float, optional
Sampling time [s] of the discrete-time systems. Defaults to *None* (continuous-time). Must be specified as a keyword argument, for example, `dt=0.1`.

See also:

TransferFunction, **StateSpace**, **lti**, **dlti**

zpk2ss, **zpk2tf**, **zpk2sos**

Notes

Changing the value of properties that are not part of the *ZerosPolesGain* system representation (such as the *A*, *B*, *C*, *D* state-space matrices) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call `sys = sys.to_ss()` before accessing/changing the A, B, C, D system matrices.

Examples

Construct the transfer function $H(s) = \frac{5(s-1)(s-2)}{(s-3)(s-4)}$:

```
>>> from scipy import signal
```

```
>>> signal.ZerosPolesGain([1, 2], [3, 4], 5)
ZerosPolesGainContinuous(
array([1, 2]),
array([3, 4]),
5,
```

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```
dt: None
)
```

Construct the transfer function $H(z) = \frac{5(z-1)(z-2)}{(z-3)(z-4)}$ with a sampling time of 0.1 seconds:

```
>>> signal.ZerosPolesGain([1, 2], [3, 4], 5, dt=0.1)
ZerosPolesGainDiscrete(
array([1, 2]),
array([3, 4]),
5,
dt: 0.1
)
```

Attributes

dt	Return the sampling time of the system, *None* for *lti* systems.
gain	Gain of the *ZerosPolesGain* system.
poles	Poles of the *ZerosPolesGain* system.
zeros	Zeros of the *ZerosPolesGain* system.

Methods

to_ss()	Convert system representation to *StateSpace*.
to_tf()	Convert system representation to *TransferFunction*.
to_zpk()	Return a copy of the current 'ZerosPolesGain' system.

scipy.signal.ZerosPolesGain.to_ss

ZerosPolesGain.**to_ss**()
Convert system representation to *StateSpace*.

Returns

sys [instance of *StateSpace*] State space model of the current system

scipy.signal.ZerosPolesGain.to_tf

ZerosPolesGain.**to_tf**()
Convert system representation to *TransferFunction*.

Returns

sys [instance of *TransferFunction*] Transfer function of the current system

scipy.signal.ZerosPolesGain.to_zpk

ZerosPolesGain.**to_zpk**()
Return a copy of the current 'ZerosPolesGain' system.

Returns

sys [instance of *ZerosPolesGain*] The current system (copy)

scipy.signal.lsim

scipy.signal.**lsim**(*system*, *U*, *T*, *X0=None*, *interp=True*)
Simulate output of a continuous-time linear system.

Parameters

system [an instance of the LTI class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
- 1: (instance of *lti*)
- 2: (num, den)
- 3: (zeros, poles, gain)
- 4: (A, B, C, D)

U [array_like] An input array describing the input at each time *T* (interpolation is assumed between given times). If there are multiple inputs, then each column of the rank-2 array represents an input. If U = 0 or None, a zero input is used.

T [array_like] The time steps at which the input is defined and at which the output is desired. Must be nonnegative, increasing, and equally spaced.

X0 [array_like, optional] The initial conditions on the state vector (zero by default).

interp [bool, optional] Whether to use linear (True, the default) or zero-order-hold (False) interpolation for the input array.

Returns

T [1D ndarray] Time values for the output.

yout [1D ndarray] System response.

xout [ndarray] Time evolution of the state vector.

Notes

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

Examples

We'll use *lsim* to simulate an analog Bessel filter applied to a signal.

```
>>> from scipy.signal import bessel, lsim
>>> import matplotlib.pyplot as plt
```

Create a low-pass Bessel filter with a cutoff of 12 Hz.

```
>>> b, a = bessel(N=5, Wn=2*np.pi*12, btype='lowpass', analog=True)
```

Generate data to which the filter is applied.

```
>>> t = np.linspace(0, 1.25, 500, endpoint=False)
```

The input signal is the sum of three sinusoidal curves, with frequencies 4 Hz, 40 Hz, and 80 Hz. The filter should mostly eliminate the 40 Hz and 80 Hz components, leaving just the 4 Hz signal.

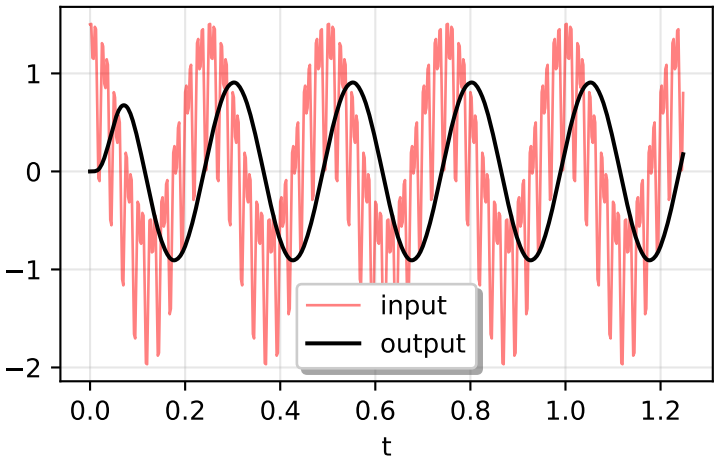
```
>>> u = (np.cos(2*np.pi*4*t) + 0.6*np.sin(2*np.pi*40*t) +
...      0.5*np.cos(2*np.pi*80*t))
```

Simulate the filter with *lsim*.

```
>>> tout, yout, xout = lsim((b, a), U=u, T=t)
```

Plot the result.

```
>>> plt.plot(t, u, 'r', alpha=0.5, linewidth=1, label='input')
>>> plt.plot(tout, yout, 'k', linewidth=1.5, label='output')
>>> plt.legend(loc='best', shadow=True, framealpha=1)
>>> plt.grid(alpha=0.3)
>>> plt.xlabel('t')
>>> plt.show()
```



In a second example, we simulate a double integrator `y'' = u`, with a constant input `u = 1`. We'll use the state space representation of the integrator.

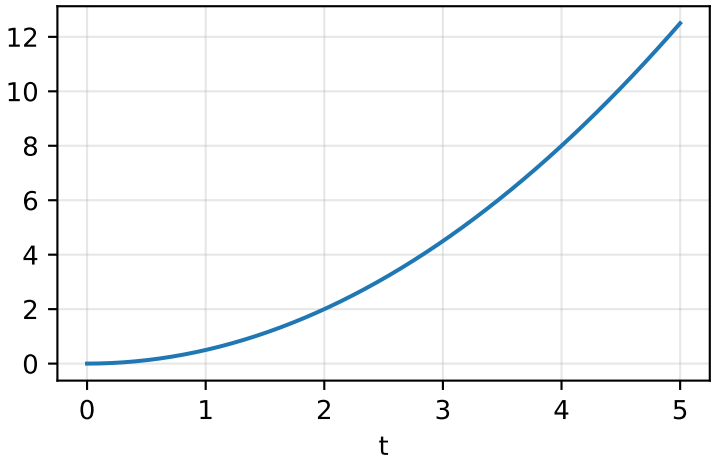
```
>>> from scipy.signal import lti
>>> A = np.array([[0.0, 1.0], [0.0, 0.0]])
>>> B = np.array([[0.0], [1.0]])
>>> C = np.array([[1.0, 0.0]])
>>> D = 0.0
>>> system = lti(A, B, C, D)
```

t and *u* define the time and input signal for the system to be simulated.

```
>>> t = np.linspace(0, 5, num=50)
>>> u = np.ones_like(t)
```

Compute the simulation, and then plot *y*. As expected, the plot shows the curve `y = 0.5*t**2`.

```
>>> tout, y, x = lsim(system, u, t)
>>> plt.plot(t, y)
>>> plt.grid(alpha=0.3)
>>> plt.xlabel('t')
>>> plt.show()
```



scipy.signal.lsim2

`scipy.signal.`**`lsim2`**(*system*, *U=None*, *T=None*, *X0=None*, ***kwargs*)

Simulate output of a continuous-time linear system, by using the ODE solver *scipy.integrate.odeint*.

Parameters

system [an instance of the *lti* class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
- 1: (instance of *lti*)
- 2: (num, den)
- 3: (zeros, poles, gain)
- 4: (A, B, C, D)

U [array_like (1D or 2D), optional] An input array describing the input at each time T. Linear interpolation is used between given times. If there are multiple inputs, then each column of the rank-2 array represents an input. If U is not given, the input is assumed to be zero.

T [array_like (1D or 2D), optional] The time steps at which the input is defined and at which the output is desired. The default is 101 evenly spaced points on the interval [0,10.0].

X0 [array_like (1D), optional] The initial condition of the state vector. If *X0* is not given, the initial conditions are assumed to be 0.

kwargs [dict] Additional keyword arguments are passed on to the function *odeint*. See the notes below for more details.

Returns

T [1D ndarray] The time values for the output.

yout [ndarray] The response of the system.

xout [ndarray] The time-evolution of the state-vector.

See also:

`lsim`

Notes

This function uses *scipy.integrate.odeint* to solve the system's differential equations. Additional keyword arguments given to *lsim2* are passed on to *odeint*. See the documentation for *scipy.integrate.odeint* for the full list of arguments.

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

Examples

We'll use *lsim2* to simulate an analog Bessel filter applied to a signal.

```
>>> from scipy.signal import bessel, lsim2
>>> import matplotlib.pyplot as plt
```

Create a low-pass Bessel filter with a cutoff of 12 Hz.

```
>>> b, a = bessel(N=5, Wn=2*np.pi*12, btype='lowpass', analog=True)
```

Generate data to which the filter is applied.

```
>>> t = np.linspace(0, 1.25, 500, endpoint=False)
```

The input signal is the sum of three sinusoidal curves, with frequencies 4 Hz, 40 Hz, and 80 Hz. The filter should mostly eliminate the 40 Hz and 80 Hz components, leaving just the 4 Hz signal.

```
>>> u = (np.cos(2*np.pi*4*t) + 0.6*np.sin(2*np.pi*40*t) +
...      0.5*np.cos(2*np.pi*80*t))
```

Simulate the filter with *lsim2*.

```
>>> tout, yout, xout = lsim2((b, a), U=u, T=t)
```

Plot the result.

```
>>> plt.plot(t, u, 'r', alpha=0.5, linewidth=1, label='input')
>>> plt.plot(tout, yout, 'k', linewidth=1.5, label='output')
>>> plt.legend(loc='best', shadow=True, framealpha=1)
>>> plt.grid(alpha=0.3)
>>> plt.xlabel('t')
>>> plt.show()
```

In a second example, we simulate a double integrator `y'' = u`, with a constant input `u = 1`. We'll use the state space representation of the integrator.

```
>>> from scipy.signal import lti
>>> A = np.array([[0, 1], [0, 0]])
>>> B = np.array([[0], [1]])
```

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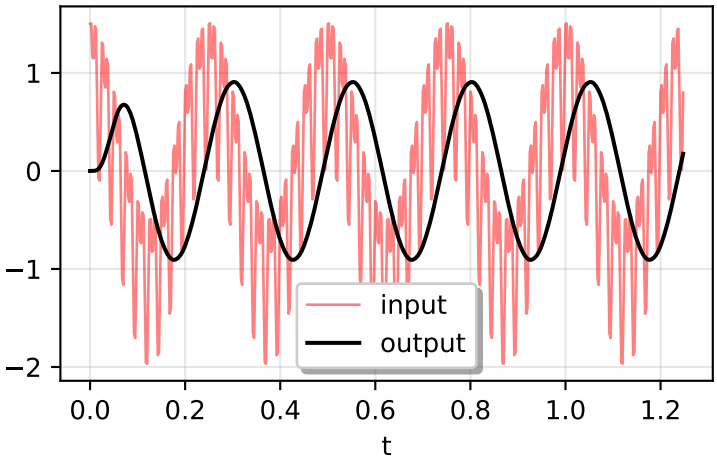

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```
>>> C = np.array([[1, 0]])
>>> D = 0
>>> system = lti(A, B, C, D)
```

t and *u* define the time and input signal for the system to be simulated.

```
>>> t = np.linspace(0, 5, num=50)
>>> u = np.ones_like(t)
```

Compute the simulation, and then plot *y*. As expected, the plot shows the curve `y = 0.5*t**2`.

```
>>> tout, y, x = lsim2(system, u, t)
>>> plt.plot(t, y)
>>> plt.grid(alpha=0.3)
>>> plt.xlabel('t')
>>> plt.show()
```

scipy.signal.impulse

`scipy.signal.`**`impulse`**(*system*, *X0=None*, *T=None*, *N=None*)

Impulse response of continuous-time system.

Parameters

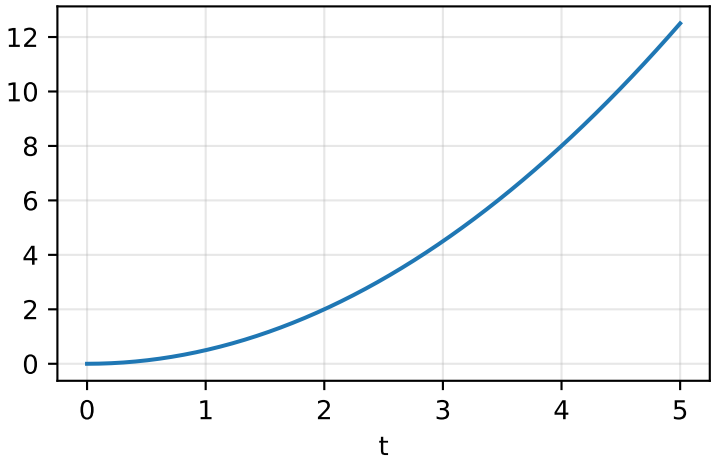
system [an instance of the LTI class or a tuple of array_like] describing the system. The following gives the number of elements in the tuple and the interpretation:
- 1 (instance of *lti*)
- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

X0 [array_like, optional] Initial state-vector. Defaults to zero.

T [array_like, optional] Time points. Computed if not given.

N [int, optional] The number of time points to compute (if *T* is not given).

Returns



T [ndarray] A 1-D array of time points.
yout [ndarray] A 1-D array containing the impulse response of the system (except for singularities at zero).

Notes

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

Examples

Compute the impulse response of a second order system with a repeated root: `x''(t) + 2*x'(t) + x(t) = u(t)`

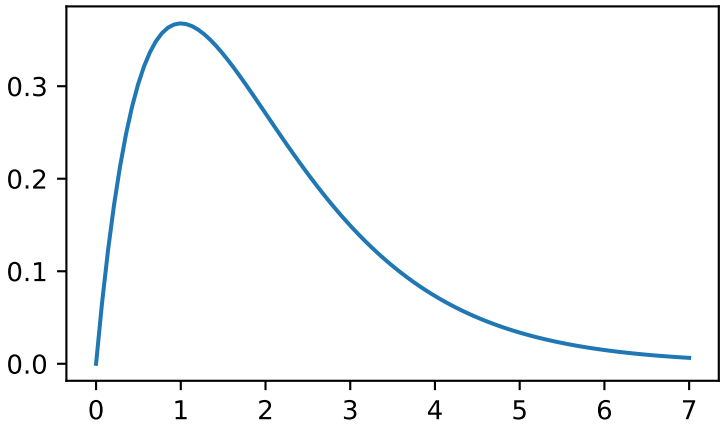
```
>>> from scipy import signal
>>> system = ([1.0], [1.0, 2.0, 1.0])
>>> t, y = signal.impulse(system)
>>> import matplotlib.pyplot as plt
>>> plt.plot(t, y)
```

scipy.signal.impulse2

`scipy.signal.`**`impulse2`**(*system*, *X0=None*, *T=None*, *N=None*, ***kwargs*)
Impulse response of a single-input, continuous-time linear system.

Parameters

system [an instance of the LTI class or a tuple of array_like] describing the system. The following gives the number of elements in the tuple and the interpretation:
- 1 (instance of *lti*)
- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)



X0	[1-D array_like, optional] The initial condition of the state vector. Default: 0 (the zero vector).
T	[1-D array_like, optional] The time steps at which the input is defined and at which the output is desired. If *T* is not given, the function will generate a set of time samples automatically.
N	[int, optional] Number of time points to compute. Default: 100.
kwargs	[various types] Additional keyword arguments are passed on to the function *scipy.signal.lsim2*, which in turn passes them on to *scipy.integrate.odeint*; see the latter's documentation for information about these arguments.

Returns

T	[ndarray] The time values for the output.
yout	[ndarray] The output response of the system.

See also:

impulse, **lsim2**, **scipy.integrate.odeint**

Notes

The solution is generated by calling *scipy.signal.lsim2*, which uses the differential equation solver *scipy.integrate.odeint*.

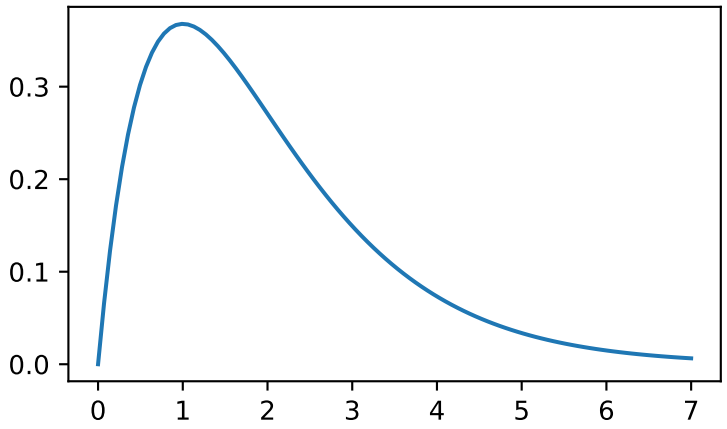
If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

New in version 0.8.0.

Examples

Compute the impulse response of a second order system with a repeated root: `x''(t) + 2*x'(t) + x(t) = u(t)`

```
>>> from scipy import signal
>>> system = ([1.0], [1.0, 2.0, 1.0])
>>> t, y = signal.impulse2(system)
>>> import matplotlib.pyplot as plt
>>> plt.plot(t, y)
```



scipy.signal.step

`scipy.signal.`**`step`**(*system*, *X0=None*, *T=None*, *N=None*)

Step response of continuous-time system.

Parameters

system [an instance of the LTI class or a tuple of array_like] describing the system. The following gives the number of elements in the tuple and the interpretation:
- 1 (instance of *lti*)
- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

X0 [array_like, optional] Initial state-vector (default is zero).

T [array_like, optional] Time points (computed if not given).

N [int, optional] Number of time points to compute if *T* is not given.

Returns

T [1D ndarray] Output time points.

yout [1D ndarray] Step response of system.

See also:

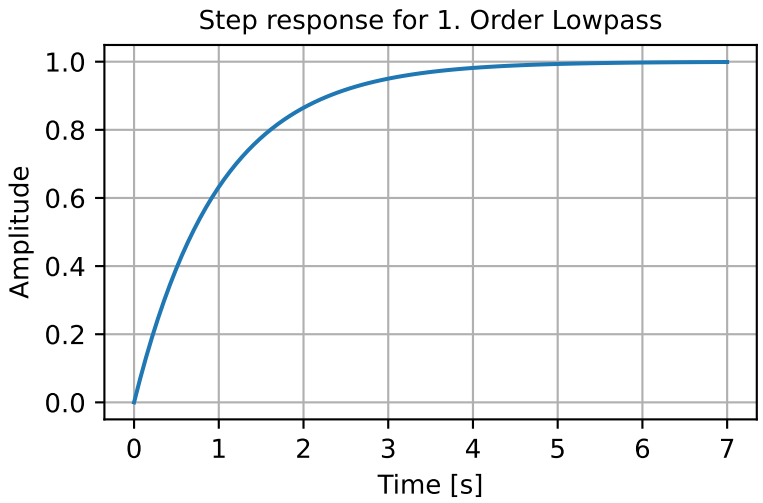
scipy.signal.step2

Notes

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> lti = signal.lti([1.0], [1.0, 1.0])
>>> t, y = signal.step(lti)
>>> plt.plot(t, y)
>>> plt.xlabel('Time [s]')
>>> plt.ylabel('Amplitude')
>>> plt.title('Step response for 1. Order Lowpass')
>>> plt.grid()
```



scipy.signal.step2

`scipy.signal.`**`step2`**(*system*, *X0=None*, *T=None*, *N=None*, ***kwargs*)

Step response of continuous-time system.

This function is functionally the same as *`scipy.signal.step`*, but it uses the function *`scipy.signal.lsim2`* to compute the step response.

Parameters

system [an instance of the LTI class or a tuple of array_like] describing the system. The following gives the number of elements in the tuple and the interpretation:
- 1 (instance of *`lti`*)
- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

X0 [array_like, optional] Initial state-vector (default is zero).

T [array_like, optional] Time points (computed if not given).

N [int, optional] Number of time points to compute if *T* is not given.
kwargs [various types] Additional keyword arguments are passed on the function *scipy.signal.lsim2*, which in turn passes them on to *scipy.integrate.odeint*. See the documentation for *scipy.integrate.odeint* for information about these arguments.

Returns

T [1D ndarray] Output time points.
yout [1D ndarray] Step response of system.

See also:

scipy.signal.step

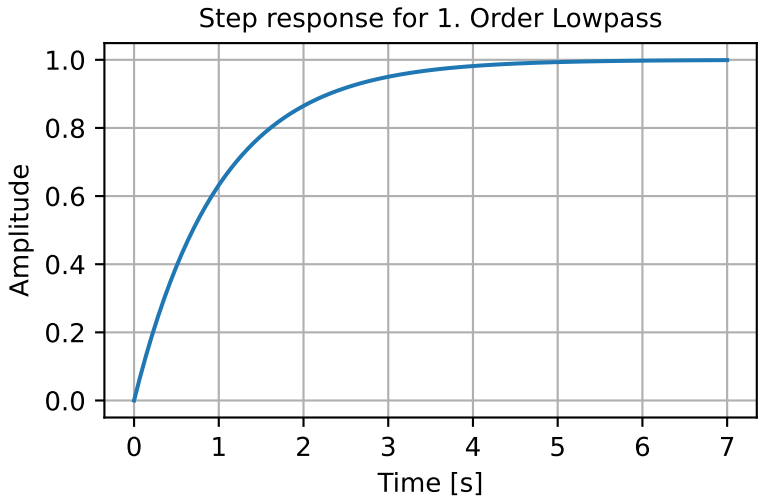
Notes

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

New in version 0.8.0.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> lti = signal.lti([1.0], [1.0, 1.0])
>>> t, y = signal.step2(lti)
>>> plt.plot(t, y)
>>> plt.xlabel('Time [s]')
>>> plt.ylabel('Amplitude')
>>> plt.title('Step response for 1. Order Lowpass')
>>> plt.grid()
```



scipy.signal.freqresp

scipy.signal.**freqresp**(*system*, *w=None*, *n=10000*)

Calculate the frequency response of a continuous-time system.

Parameters

system [an instance of the `lti` class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
- 1 (instance of `lti`)
- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

w [array_like, optional] Array of frequencies (in rad/s). Magnitude and phase data is calculated for every value in this array. If not given, a reasonable set will be calculated.

n [int, optional] Number of frequency points to compute if *w* is not given. The *n* frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

Returns

w [1D ndarray] Frequency array [rad/s]

H [1D ndarray] Array of complex magnitude values

Notes

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

Examples

Generating the Nyquist plot of a transfer function

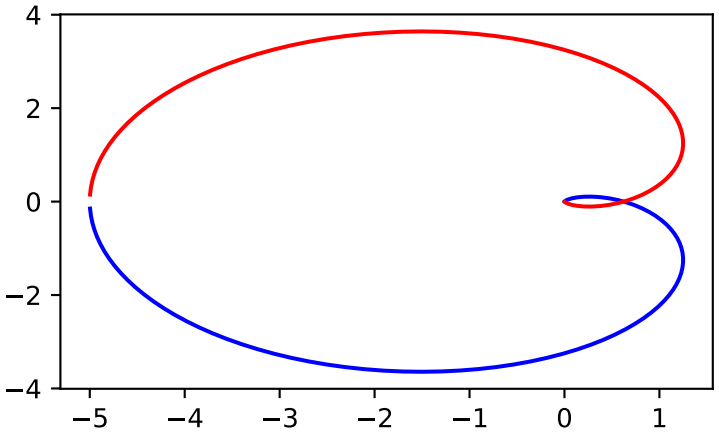
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Construct the transfer function $H(s) = \frac{5}{(s-1)^3}$:

```
>>> s1 = signal.ZerosPolesGain([], [1, 1, 1], [5])
```

```
>>> w, H = signal.freqresp(s1)
```

```
>>> plt.figure()
>>> plt.plot(H.real, H.imag, "b")
>>> plt.plot(H.real, -H.imag, "r")
>>> plt.show()
```



scipy.signal.bode

`scipy.signal.`**bode**(*system*, *w=None*, *n=100*)

Calculate Bode magnitude and phase data of a continuous-time system.

Parameters

system [an instance of the LTI class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
- 1 (instance of `lti`)
- 2 (num, den)
- 3 (zeros, poles, gain)
- 4 (A, B, C, D)

w [array_like, optional] Array of frequencies (in rad/s). Magnitude and phase data is calculated for every value in this array. If not given a reasonable set will be calculated.

n [int, optional] Number of frequency points to compute if *w* is not given. The *n* frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

Returns

w [1D ndarray] Frequency array [rad/s]

mag [1D ndarray] Magnitude array [dB]

phase [1D ndarray] Phase array [deg]

Notes

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `s^2 + 3s + 5` would be represented as `[1, 3, 5]`).

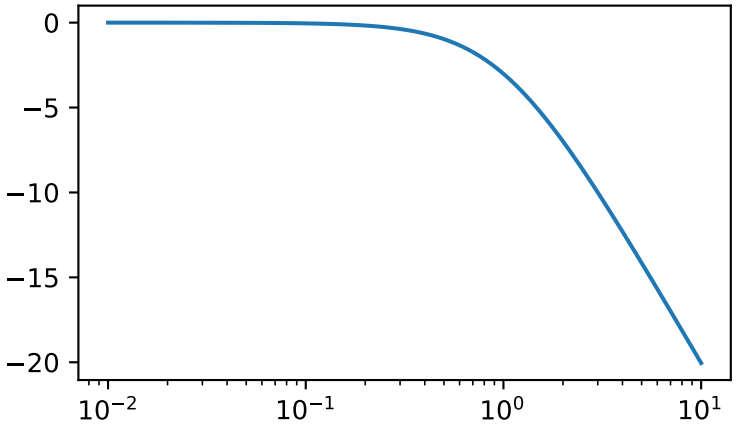
New in version 0.11.0.

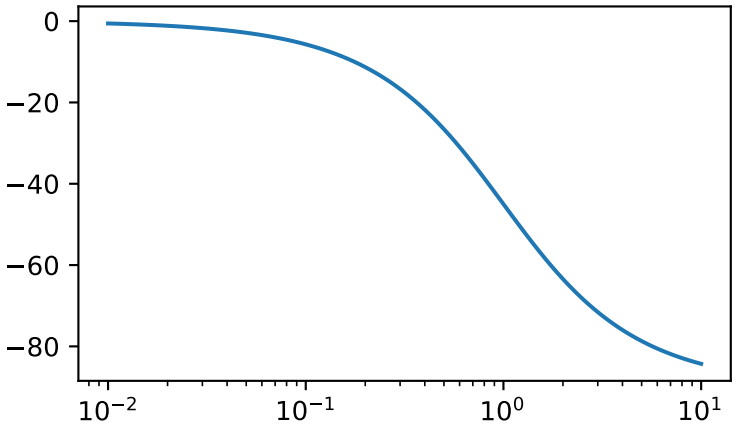
Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> sys = signal.TransferFunction([1], [1, 1])
>>> w, mag, phase = signal.bode(sys)
```

```
>>> plt.figure()
>>> plt.semilogx(w, mag)    # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```





Discrete-time linear systems

dlti(*system, **kwargs)	Discrete-time linear time invariant system base class.
StateSpace(*system, **kwargs)	Linear Time Invariant system in state-space form.
TransferFunction(*system, **kwargs)	Linear Time Invariant system class in transfer function form.
ZerosPolesGain(*system, **kwargs)	Linear Time Invariant system class in zeros, poles, gain form.
dlsim(system, u[, t, x0])	Simulate output of a discrete-time linear system.
dimpulse(system[, x0, t, n])	Impulse response of discrete-time system.
dstep(system[, x0, t, n])	Step response of discrete-time system.
dfreqresp(system[, w, n, whole])	Calculate the frequency response of a discrete-time system.
dbode(system[, w, n])	Calculate Bode magnitude and phase data of a discrete-time system.

scipy.signal.dlti

class scipy.signal.**dlti**(**system*, ***kwargs*)

Discrete-time linear time invariant system base class.

Parameters

***system: arguments**

The *dlti* class can be instantiated with either 2, 3 or 4 arguments. The following gives the number of arguments and the corresponding discrete-time subclass that is created:

- 2: *TransferFunction*: (numerator, denominator)
- 3: *ZerosPolesGain*: (zeros, poles, gain)
- 4: *StateSpace*: (A, B, C, D)

Each argument can be an array or a sequence.

dt: float, optional

Sampling time [s] of the discrete-time systems. Defaults to `True` (unspecified sampling time). Must be specified as a keyword argument, for example, `dt=0.1`.

See also:

ZerosPolesGain, **StateSpace**, **TransferFunction**, **lti**

Notes

dlti instances do not exist directly. Instead, *dlti* creates an instance of one of its subclasses: *StateSpace*, *TransferFunction* or *ZerosPolesGain*.

Changing the value of properties that are not directly part of the current system representation (such as the `zeros` of a *StateSpace* system) is very inefficient and may lead to numerical inaccuracies. It is better to convert to the specific system representation first. For example, call `sys = sys.to_zpk()` before accessing/changing the zeros, poles or gain.

If (numerator, denominator) is passed in for `*system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g., `z^2 + 3z + 5` would be represented as `[1, 3, 5]`).

New in version 0.18.0.

Examples

```
>>> from scipy import signal
```

```
>>> signal.dlti(1, 2, 3, 4)
StateSpaceDiscrete(
array([[1]]),
array([[2]]),
array([[3]]),
array([[4]]),
dt: True
)
```

```
>>> signal.dlti(1, 2, 3, 4, dt=0.1)
StateSpaceDiscrete(
array([[1]]),
array([[2]]),
array([[3]]),
array([[4]]),
dt: 0.1
)
```

Construct the transfer function $H(z) = \frac{5(z-1)(z-2)}{(z-3)(z-4)}$ with a sampling time of 0.1 seconds:

```
>>> signal.dlti([1, 2], [3, 4], 5, dt=0.1)
ZerosPolesGainDiscrete(
array([1, 2]),
array([3, 4]),
5,
dt: 0.1
)
```

Construct the transfer function $H(z) = \frac{3z+4}{1z+2}$ with a sampling time of 0.1 seconds:

```
>>> signal.dlti([3, 4], [1, 2], dt=0.1)
TransferFunctionDiscrete(
array([3., 4.]),
array([1., 2.]),
dt: 0.1
)
```

Attributes

dt	Return the sampling time of the system.
poles	Poles of the system.
zeros	Zeros of the system.

Methods

bode([w, n])	Calculate Bode magnitude and phase data of a discrete-time system.
freqresp([w, n, whole])	Calculate the frequency response of a discrete-time system.
impulse([x0, t, n])	Return the impulse response of the discrete-time *dlti* system.
output(u, t[, x0])	Return the response of the discrete-time system to input *u*.
step([x0, t, n])	Return the step response of the discrete-time *dlti* system.

scipy.signal.dlti.bode

dlti.**bode**(*w=None*, *n=100*)

Calculate Bode magnitude and phase data of a discrete-time system.

Returns a 3-tuple containing arrays of frequencies [rad/s], magnitude [dB] and phase [deg]. See *dbode* for details.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Construct the transfer function $H(z) = \frac{1}{z^2+2z+3}$ with sampling time 0.5s:

```
>>> sys = signal.TransferFunction([1], [1, 2, 3], dt=0.5)
```

Equivalent: signal.dbode(sys)

```
>>> w, mag, phase = sys.bode()
```

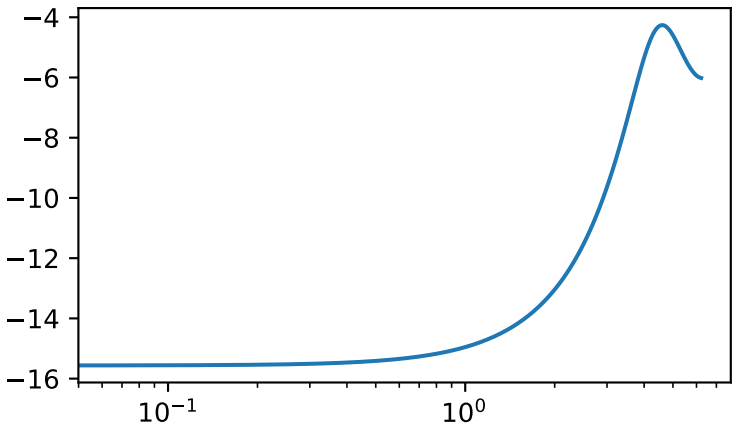
```
>>> plt.figure()
>>> plt.semilogx(w, mag)    # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```

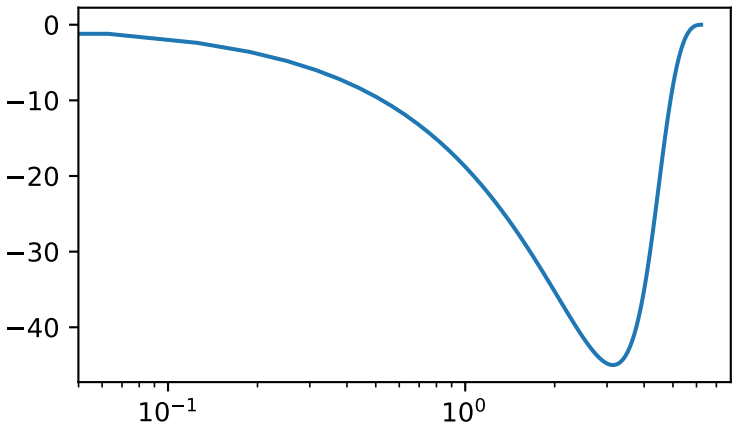
scipy.signal.dlti.freqresp

dlti.**freqresp**(*w=None*, *n=10000*, *whole=False*)

Calculate the frequency response of a discrete-time system.

Returns a 2-tuple containing arrays of frequencies [rad/s] and complex magnitude. See *dfreqresp* for details.


−4
−6
−8
−10
−12
−14
−16
10^{-1}
10^{0}


0
−10
−20
−30
−40
10^{-1}
10^{0}

scipy.signal.dlti.impulse

dlti.**impulse**(*x0=None*, *t=None*, *n=None*)
Return the impulse response of the discrete-time *dlti* system. See *dimpulse* for details.

scipy.signal.dlti.output

dlti.**output**(*u*, *t*, *x0=None*)
Return the response of the discrete-time system to input *u*. See *dlsim* for details.

scipy.signal.dlti.step

dlti.**step**(*x0=None*, *t=None*, *n=None*)
Return the step response of the discrete-time *dlti* system. See *dstep* for details.

scipy.signal.dlsim

scipy.signal.**dlsim**(*system*, *u*, *t=None*, *x0=None*)
Simulate output of a discrete-time linear system.

Parameters

system [tuple of array_like or instance of *dlti*] A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:
- 1: (instance of *dlti*)
- 3: (num, den, dt)
- 4: (zeros, poles, gain, dt)
- 5: (A, B, C, D, dt)

u [array_like] An input array describing the input at each time *t* (interpolation is assumed between given times). If there are multiple inputs, then each column of the rank-2 array represents an input.

t [array_like, optional] The time steps at which the input is defined. If *t* is given, it must be the same length as *u*, and the final value in *t* determines the number of steps returned in the output.

x0 [array_like, optional] The initial conditions on the state vector (zero by default).

Returns

tout [ndarray] Time values for the output, as a 1-D array.

yout [ndarray] System response, as a 1-D array.

xout [ndarray, optional] Time-evolution of the state-vector. Only generated if the input is a *StateSpace* system.

See also:

lsim, **dstep**, **dimpulse**, **cont2discrete**

Examples

A simple integrator transfer function with a discrete time step of 1.0 could be implemented as:

```
>>> from scipy import signal
>>> tf = ([1.0,], [1.0, -1.0], 1.0)
>>> t_in = [0.0, 1.0, 2.0, 3.0]
>>> u = np.asarray([0.0, 0.0, 1.0, 1.0])
>>> t_out, y = signal.dlsim(tf, u, t=t_in)
>>> y.T
array([[ 0.,  0.,  0.,  1.]])
```

scipy.signal.dimpulse

scipy.signal.**dimpulse**(*system*, *x0=None*, *t=None*, *n=None*)

Impulse response of discrete-time system.

Parameters

system [tuple of array_like or instance of *dlti*] A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:
- 1: (instance of *dlti*)
- 3: (num, den, dt)
- 4: (zeros, poles, gain, dt)
- 5: (A, B, C, D, dt)

x0 [array_like, optional] Initial state-vector. Defaults to zero.

t [array_like, optional] Time points. Computed if not given.

n [int, optional] The number of time points to compute (if *t* is not given).

Returns

tout [ndarray] Time values for the output, as a 1-D array.

yout [tuple of ndarray] Impulse response of system. Each element of the tuple represents the output of the system based on an impulse in each input.

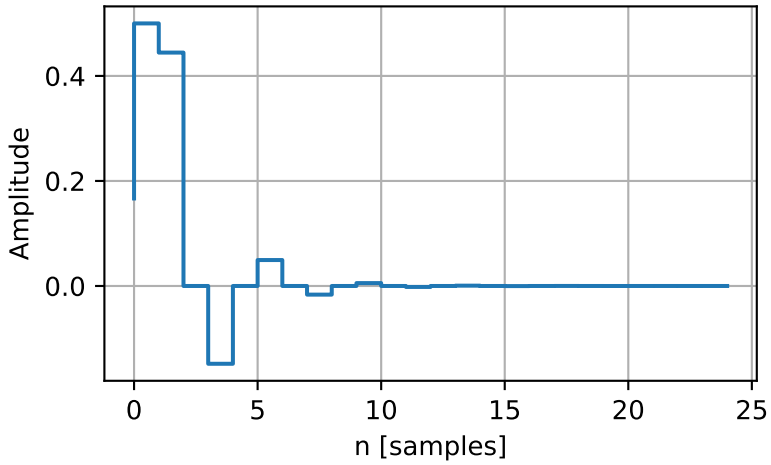
See also:

impulse, **dstep**, **dlsim**, **cont2discrete**

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> butter = signal.dlti(*signal.butter(3, 0.5))
>>> t, y = signal.dimpulse(butter, n=25)
>>> plt.step(t, np.squeeze(y))
>>> plt.grid()
>>> plt.xlabel('n [samples]')
>>> plt.ylabel('Amplitude')
```



scipy.signal.dstep

scipy.signal.**dstep**(*system*, *x0=None*, *t=None*, *n=None*)

Step response of discrete-time system.

Parameters

system [tuple of array_like] A tuple describing the system. The following gives the number of elements in the tuple and the interpretation:
- 1: (instance of *dlti*)
- 3: (num, den, dt)
- 4: (zeros, poles, gain, dt)
- 5: (A, B, C, D, dt)

x0 [array_like, optional] Initial state-vector. Defaults to zero.

t [array_like, optional] Time points. Computed if not given.

n [int, optional] The number of time points to compute (if *t* is not given).

Returns

tout [ndarray] Output time points, as a 1-D array.

yout [tuple of ndarray] Step response of system. Each element of the tuple represents the output of the system based on a step response to each input.

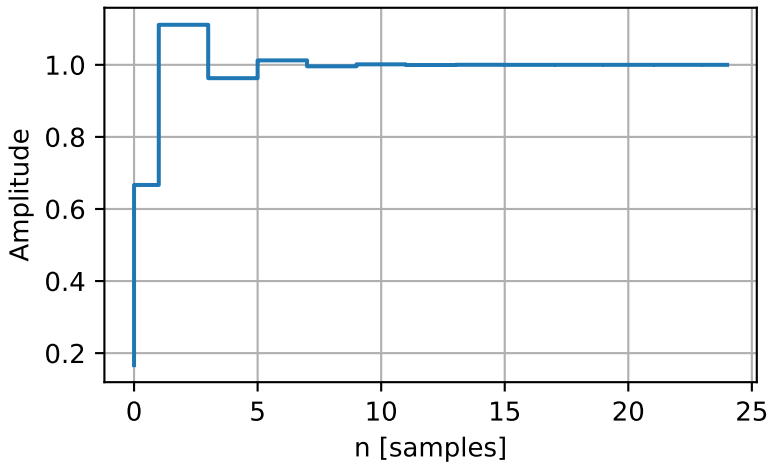
See also:

step, **dimpulse**, **dlsim**, **cont2discrete**

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> butter = signal.dlti(*signal.butter(3, 0.5))
>>> t, y = signal.dstep(butter, n=25)
>>> plt.step(t, np.squeeze(y))
>>> plt.grid()
>>> plt.xlabel('n [samples]')
>>> plt.ylabel('Amplitude')
```



scipy.signal.dfreqresp

scipy.signal.**dfreqresp**(*system*, *w=None*, *n=10000*, *whole=False*)

Calculate the frequency response of a discrete-time system.

Parameters

system [an instance of the *dlti* class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
- 1 (instance of *dlti*)
- 2 (numerator, denominator, dt)
- 3 (zeros, poles, gain, dt)
- 4 (A, B, C, D, dt)

w [array_like, optional] Array of frequencies (in radians/sample). Magnitude and phase data is calculated for every value in this array. If not given a reasonable set will be calculated.

n [int, optional] Number of frequency points to compute if *w* is not given. The *n* frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

whole [bool, optional] Normally, if 'w' is not given, frequencies are computed from 0 to the Nyquist frequency, pi radians/sample (upper-half of unit-circle). If *whole* is True, compute frequencies from 0 to 2*pi radians/sample.

Returns

w	[1D ndarray] Frequency array [radians/sample]
H	[1D ndarray] Array of complex magnitude values

Notes

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `z^2 + 3z + 5` would be represented as `[1, 3, 5]`).

New in version 0.18.0.

Examples

Generating the Nyquist plot of a transfer function

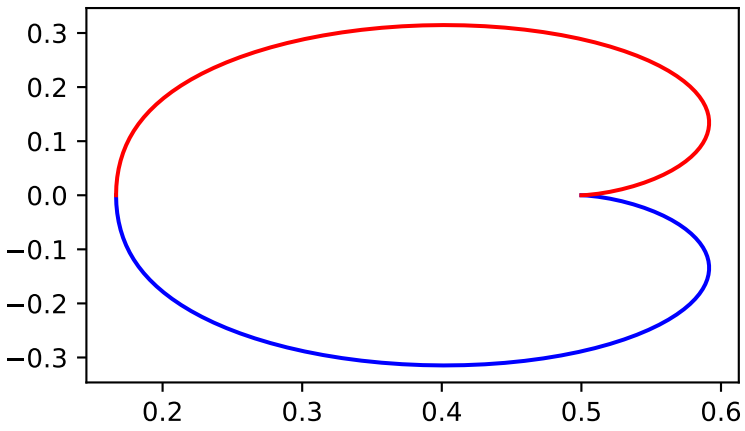
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

Construct the transfer function $H(z) = \frac{1}{z^2+2z+3}$ with a sampling time of 0.05 seconds:

```
>>> sys = signal.TransferFunction([1], [1, 2, 3], dt=0.05)
```

```
>>> w, H = signal.dfreqresp(sys)
```

```
>>> plt.figure()
>>> plt.plot(H.real, H.imag, "b")
>>> plt.plot(H.real, -H.imag, "r")
>>> plt.show()
```



scipy.signal.dbode

scipy.signal.**dbode**(*system*, *w=None*, *n=100*)

Calculate Bode magnitude and phase data of a discrete-time system.

Parameters

system [an instance of the LTI class or a tuple describing the system.] The following gives the number of elements in the tuple and the interpretation:
- 1 (instance of *dlti*)
- 2 (num, den, dt)
- 3 (zeros, poles, gain, dt)
- 4 (A, B, C, D, dt)

w [array_like, optional] Array of frequencies (in radians/sample). Magnitude and phase data is calculated for every value in this array. If not given a reasonable set will be calculated.

n [int, optional] Number of frequency points to compute if *w* is not given. The *n* frequencies are logarithmically spaced in an interval chosen to include the influence of the poles and zeros of the system.

Returns

w [1D ndarray] Frequency array [rad/time_unit]

mag [1D ndarray] Magnitude array [dB]

phase [1D ndarray] Phase array [deg]

Notes

If (num, den) is passed in for `system`, coefficients for both the numerator and denominator should be specified in descending exponent order (e.g. `z^2 + 3z + 5` would be represented as `[1, 3, 5]`).

New in version 0.18.0.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

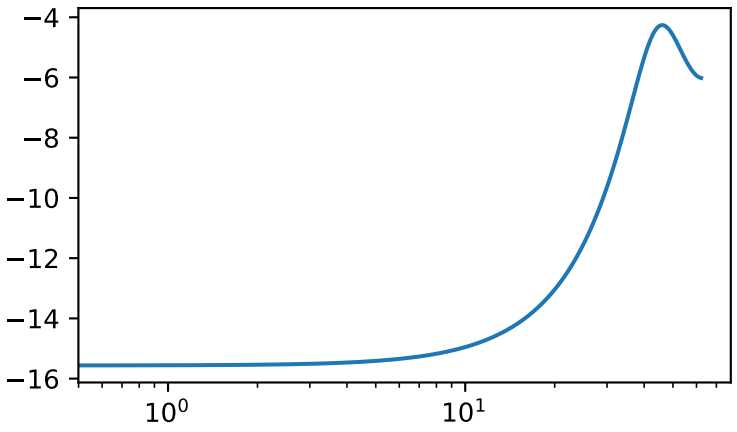
Construct the transfer function $H(z) = \frac{1}{z^2+2z+3}$ with a sampling time of 0.05 seconds:

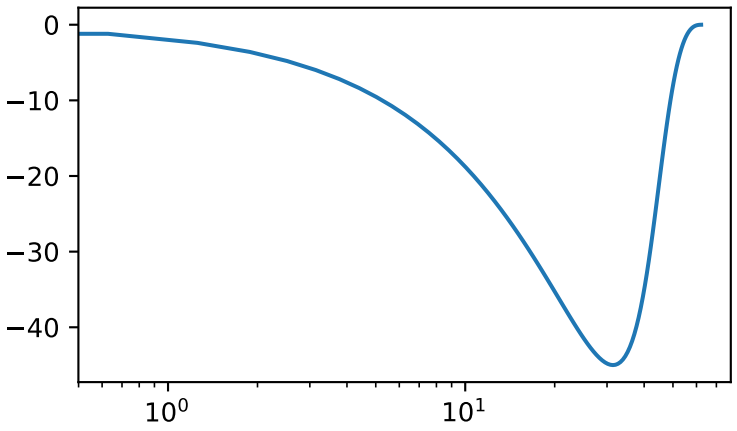
```
>>> sys = signal.TransferFunction([1], [1, 2, 3], dt=0.05)
```

Equivalent: sys.bode()

```
>>> w, mag, phase = signal.dbode(sys)
```

```
>>> plt.figure()
>>> plt.semilogx(w, mag)    # Bode magnitude plot
>>> plt.figure()
>>> plt.semilogx(w, phase)  # Bode phase plot
>>> plt.show()
```


−4
−6
−8
−10
−12
−14
−16
10^0
10^1


0
−10
−20
−30
−40
10^0
10^1

LTI representations

tf2zpk(b, a)	Return zero, pole, gain (z, p, k) representation from a numerator, denominator representation of a linear filter.
tf2sos(b, a[, pairing])	Return second-order sections from transfer function representation
tf2ss(num, den)	Transfer function to state-space representation.
zpk2tf(z, p, k)	Return polynomial transfer function representation from zeros and poles
zpk2sos(z, p, k[, pairing])	Return second-order sections from zeros, poles, and gain of a system
zpk2ss(z, p, k)	Zero-pole-gain representation to state-space representation
ss2tf(A, B, C, D[, input])	State-space to transfer function.
ss2zpk(A, B, C, D[, input])	State-space representation to zero-pole-gain representation.
sos2zpk(sos)	Return zeros, poles, and gain of a series of second-order sections
sos2tf(sos)	Return a single transfer function from a series of second-order sections
cont2discrete(system, dt[, method, alpha])	Transform a continuous to a discrete state-space system.
place_poles(A, B, poles[, method, rtol, maxiter])	Compute K such that eigenvalues (A - dot(B, K))=poles.

scipy.signal.tf2zpk

scipy.signal.**tf2zpk**(*b*, *a*)

Return zero, pole, gain (z, p, k) representation from a numerator, denominator representation of a linear filter.

Parameters

b [array_like] Numerator polynomial coefficients.

a [array_like] Denominator polynomial coefficients.

Returns

z [ndarray] Zeros of the transfer function.

p [ndarray] Poles of the transfer function.

k [float] System gain.

Notes

If some values of *b* are too close to 0, they are removed. In that case, a BadCoefficients warning is emitted.

The *b* and *a* arrays are interpreted as coefficients for positive, descending powers of the transfer function variable. So the inputs $b = [b_0, b_1, ..., b_M]$ and $a = [a_0, a_1, ..., a_N]$ can represent an analog filter of the form:

$$H(s) = \frac{b_0 s^M + b_1 s^{(M-1)} + \cdots + b_M}{a_0 s^N + a_1 s^{(N-1)} + \cdots + a_N}$$

or a discrete-time filter of the form:

$$H(z) = \frac{b_0 z^M + b_1 z^{(M-1)} + \cdots + b_M}{a_0 z^N + a_1 z^{(N-1)} + \cdots + a_N}$$

This "positive powers" form is found more commonly in controls engineering. If *M* and *N* are equal (which is true for all filters generated by the bilinear transform), then this happens to be equivalent to the "negative powers" discrete-time form preferred in DSP:

$$H(z) = \frac{b_0 + b_1 z^{-1} + \cdots + b_M z^{-M}}{a_0 + a_1 z^{-1} + \cdots + a_N z^{-N}}$$

Although this is true for common filters, remember that this is not true in the general case. If *M* and *N* are not equal, the discrete-time transfer function coefficients must first be converted to the "positive powers" form before finding the poles and zeros.

scipy.signal.tf2sos

`scipy.signal.`**`tf2sos`**(*b*, *a*, *pairing='nearest'*)

Return second-order sections from transfer function representation

Parameters

b [array_like] Numerator polynomial coefficients.

a [array_like] Denominator polynomial coefficients.

pairing [{'nearest', 'keep_odd'}, optional] The method to use to combine pairs of poles and zeros into sections. See *zpk2sos*.

Returns

sos [ndarray] Array of second-order filter coefficients, with shape `(n_sections, 6)`. See *sosfilt* for the SOS filter format specification.

See also:

zpk2sos, **sosfilt**

Notes

It is generally discouraged to convert from TF to SOS format, since doing so usually will not improve numerical precision errors. Instead, consider designing filters in ZPK format and converting directly to SOS. TF is converted to SOS by first converting to ZPK format, then converting ZPK to SOS.

New in version 0.16.0.

scipy.signal.tf2ss

`scipy.signal.`**`tf2ss`**(*num*, *den*)

Transfer function to state-space representation.

Parameters

num, den [array_like] Sequences representing the coefficients of the numerator and denominator polynomials, in order of descending degree. The denominator needs to be at least as long as the numerator.

Returns

A, B, C, D [ndarray] State space representation of the system, in controller canonical form.

Examples

Convert the transfer function:

$$H(s) = \frac{s^2 + 3s + 3}{s^2 + 2s + 1}$$

```
>>> num = [1, 3, 3]
>>> den = [1, 2, 1]
```

to the state-space representation:

$$\dot{\mathbf{x}}(t) = \begin{bmatrix} -2 & -1 \\ 1 & 0 \end{bmatrix} \mathbf{x}(t) + \begin{bmatrix} 1 \\ 0 \end{bmatrix} \mathbf{u}(t)$$

$$\mathbf{y}(t) = \begin{bmatrix} 1 & 2 \end{bmatrix} \mathbf{x}(t) + \begin{bmatrix} 1 \end{bmatrix} \mathbf{u}(t)$$

```
>>> from scipy.signal import tf2ss
>>> A, B, C, D = tf2ss(num, den)
>>> A
array([[-2., -1.],
       [ 1.,  0.]])
>>> B
array([[ 1.],
       [ 0.]])
>>> C
array([[ 1.,  2.]])
>>> D
array([[ 1.]])
```

scipy.signal.zpk2tf

scipy.signal.**zpk2tf**(*z*, *p*, *k*)

Return polynomial transfer function representation from zeros and poles

Parameters

z	[array_like] Zeros of the transfer function.
p	[array_like] Poles of the transfer function.
k	[float] System gain.

Returns

b	[ndarray] Numerator polynomial coefficients.
a	[ndarray] Denominator polynomial coefficients.

scipy.signal.zpk2sos

scipy.signal.**zpk2sos**(*z*, *p*, *k*, *pairing='nearest'*)

Return second-order sections from zeros, poles, and gain of a system

Parameters

z	[array_like] Zeros of the transfer function.
p	[array_like] Poles of the transfer function.
k	[float] System gain.

pairing [{'nearest', 'keep_odd'}, optional] The method to use to combine pairs of poles and zeros into sections. See Notes below.

Returns

sos [ndarray] Array of second-order filter coefficients, with shape `(n_sections, 6)`. See *`sosfilt`* for the SOS filter format specification.

See also:

`sosfilt`

Notes

The algorithm used to convert ZPK to SOS format is designed to minimize errors due to numerical precision issues. The pairing algorithm attempts to minimize the peak gain of each biquadratic section. This is done by pairing poles with the nearest zeros, starting with the poles closest to the unit circle.

Algorithms

The current algorithms are designed specifically for use with digital filters. (The output coefficients are not correct for analog filters.)

The steps in the `pairing='nearest'` and `pairing='keep_odd'` algorithms are mostly shared. The `nearest` algorithm attempts to minimize the peak gain, while `'keep_odd'` minimizes peak gain under the constraint that odd-order systems should retain one section as first order. The algorithm steps and are as follows:

As a pre-processing step, add poles or zeros to the origin as necessary to obtain the same number of poles and zeros for pairing. If `pairing == 'nearest'` and there are an odd number of poles, add an additional pole and a zero at the origin.

The following steps are then iterated over until no more poles or zeros remain:

1. Take the (next remaining) pole (complex or real) closest to the unit circle to begin a new filter section.
2. If the pole is real and there are no other remaining real poles[1], add the closest real zero to the section and leave it as a first order section. Note that after this step we are guaranteed to be left with an even number of real poles, complex poles, real zeros, and complex zeros for subsequent pairing iterations.
3. Else:
    1. If the pole is complex and the zero is the only remaining real zero*, then pair the pole with the *next* closest zero (guaranteed to be complex). This is necessary to ensure that there will be a real zero remaining to eventually create a first-order section (thus keeping the odd order).
    2. Else pair the pole with the closest remaining zero (complex or real).
    3. Proceed to complete the second-order section by adding another pole and zero to the current pole and zero in the section:
        1. If the current pole and zero are both complex, add their conjugates.
        2. Else if the pole is complex and the zero is real, add the conjugate pole and the next closest real zero.
        3. Else if the pole is real and the zero is complex, add the conjugate zero and the real pole closest to those zeros.
        4. Else (we must have a real pole and real zero) add the next real pole closest to the unit circle, and then add the real zero closest to that pole.

New in version 0.16.0.

[1] This conditional can only be met for specific odd-order inputs with the `pairing == 'keep_odd'` method.

Examples

Design a 6th order low-pass elliptic digital filter for a system with a sampling rate of 8000 Hz that has a pass-band corner frequency of 1000 Hz. The ripple in the pass-band should not exceed 0.087 dB, and the attenuation in the stop-band should be at least 90 dB.

In the following call to *signal.ellip*, we could use `output='sos'`, but for this example, we'll use `output='zpk'`, and then convert to SOS format with *zpk2sos*:

```
>>> from scipy import signal
>>> z, p, k = signal.ellip(6, 0.087, 90, 1000/(0.5*8000), output='zpk')
```

Now convert to SOS format.

```
>>> sos = signal.zpk2sos(z, p, k)
```

The coefficients of the numerators of the sections:

```
>>> sos[:, :3]
array([[ 0.0014154 ,  0.00248707,  0.0014154 ],
       [ 1.        ,  0.72965193,  1.        ],
       [ 1.        ,  0.17594966,  1.        ]])
```

The symmetry in the coefficients occurs because all the zeros are on the unit circle.

The coefficients of the denominators of the sections:

```
>>> sos[:, 3:]
array([[ 1.        , -1.32543251,  0.46989499],
       [ 1.        , -1.26117915,  0.6262586 ],
       [ 1.        , -1.25707217,  0.86199667]])
```

The next example shows the effect of the *pairing* option. We have a system with three poles and three zeros, so the SOS array will have shape (2, 6). The means there is, in effect, an extra pole and an extra zero at the origin in the SOS representation.

```
>>> z1 = np.array([-1, -0.5-0.5j, -0.5+0.5j])
>>> p1 = np.array([0.75, 0.8+0.1j, 0.8-0.1j])
```

With `pairing='nearest'` (the default), we obtain

```
>>> signal.zpk2sos(z1, p1, 1)
array([[ 1.  ,  1.  ,  0.5 ,  1.  , -0.75,  0.  ],
       [ 1.  ,  1.  ,  0.  ,  1.  , -1.6 ,  0.65]])
```

The first section has the zeros {-0.5-0.05j, -0.5+0.5j} and the poles {0, 0.75}, and the second section has the zeros {-1, 0} and poles {0.8+0.1j, 0.8-0.1j}. Note that the extra pole and zero at the origin have been assigned to different sections.

With `pairing='keep_odd'`, we obtain:

```
>>> signal.zpk2sos(z1, p1, 1, pairing='keep_odd')
array([[ 1.  ,  1.  ,  0.  ,  1.  , -0.75,  0.  ],
       [ 1.  ,  1.  ,  0.5 ,  1.  , -1.6 ,  0.65]])
```

The extra pole and zero at the origin are in the same section. The first section is, in effect, a first-order section.

scipy.signal.zpk2ss

scipy.signal.**zpk2ss**(*z*, *p*, *k*)

Zero-pole-gain representation to state-space representation

Parameters

z, p	[sequence] Zeros and poles.
k	[float] System gain.

Returns

A, B, C, D	[ndarray] State space representation of the system, in controller canonical form.

scipy.signal.ss2tf

scipy.signal.**ss2tf**(*A*, *B*, *C*, *D*, *input=0*)

State-space to transfer function.

A, B, C, D defines a linear state-space system with *p* inputs, *q* outputs, and *n* state variables.

Parameters

A	[array_like] State (or system) matrix of shape `(n, n)`
B	[array_like] Input matrix of shape `(n, p)`
C	[array_like] Output matrix of shape `(q, n)`
D	[array_like] Feedthrough (or feedforward) matrix of shape `(q, p)`
input	[int, optional] For multiple-input systems, the index of the input to use.

Returns

num	[2-D ndarray] Numerator(s) of the resulting transfer function(s). *num* has one row for each of the system's outputs. Each row is a sequence representation of the numerator polynomial.
den	[1-D ndarray] Denominator of the resulting transfer function(s). *den* is a sequence representation of the denominator polynomial.

Examples

Convert the state-space representation:

$$\dot{\mathbf{x}}(t) = \begin{bmatrix} -2 & -1 \\ 1 & 0 \end{bmatrix} \mathbf{x}(t) + \begin{bmatrix} 1 \\ 0 \end{bmatrix} \mathbf{u}(t)$$

$$\mathbf{y}(t) = \begin{bmatrix} 1 & 2 \end{bmatrix} \mathbf{x}(t) + \begin{bmatrix} 1 \end{bmatrix} \mathbf{u}(t)$$

```
>>> A = [[-2, -1], [1, 0]]
>>> B = [[1], [0]]  # 2-D column vector
>>> C = [[1, 2]]    # 2-D row vector
>>> D = 1
```

to the transfer function:

$$H(s) = \frac{s^2 + 3s + 3}{s^2 + 2s + 1}$$

```
>>> from scipy.signal import ss2tf
>>> ss2tf(A, B, C, D)
(array([[1., 3., 3.]]), array([ 1.,  2.,  1.]))
```

scipy.signal.ss2zpk

scipy.signal.**ss2zpk**(*A*, *B*, *C*, *D*, *input=0*)

State-space representation to zero-pole-gain representation.

A, B, C, D defines a linear state-space system with *p* inputs, *q* outputs, and *n* state variables.

Parameters

A	[array_like] State (or system) matrix of shape `(n, n)`
B	[array_like] Input matrix of shape `(n, p)`
C	[array_like] Output matrix of shape `(q, n)`
D	[array_like] Feedthrough (or feedforward) matrix of shape `(q, p)`
input	[int, optional] For multiple-input systems, the index of the input to use.

Returns

z, p	[sequence] Zeros and poles.
k	[float] System gain.

scipy.signal.sos2zpk

scipy.signal.**sos2zpk**(*sos*)

Return zeros, poles, and gain of a series of second-order sections

Parameters

sos	[array_like] Array of second-order filter coefficients, must have shape `(n_sections, 6)`. See *sosfilt* for the SOS filter format specification.

Returns

z	[ndarray] Zeros of the transfer function.
p	[ndarray] Poles of the transfer function.
k	[float] System gain.

Notes

The number of zeros and poles returned will be `n_sections * 2` even if some of these are (effectively) zero.

New in version 0.16.0.

scipy.signal.sos2tf

scipy.signal.**sos2tf**(*sos*)

Return a single transfer function from a series of second-order sections

Parameters

sos	[array_like] Array of second-order filter coefficients, must have shape `(n_sections, 6)`. See *sosfilt* for the SOS filter format specification.

Returns

b	[ndarray] Numerator polynomial coefficients.
a	[ndarray] Denominator polynomial coefficients.

Notes

New in version 0.16.0.

scipy.signal.cont2discrete

scipy.signal.**cont2discrete**(*system*, *dt*, *method='zoh'*, *alpha=None*)

Transform a continuous to a discrete state-space system.

Parameters

system [a tuple describing the system or an instance of `lti`] The following gives the number of elements in the tuple and the interpretation:
- 1: (instance of `lti`)
- 2: (num, den)
- 3: (zeros, poles, gain)
- 4: (A, B, C, D)

dt [float] The discretization time step.

method [str, optional] Which method to use:
- gbt: generalized bilinear transformation
- bilinear: Tustin's approximation ("gbt" with alpha=0.5)
- euler: Euler (or forward differencing) method ("gbt" with alpha=0)
- backward_diff: Backwards differencing ("gbt" with alpha=1.0)
- zoh: zero-order hold (default)
- foh: first-order hold (*versionadded: 1.3.0*)
- impulse: equivalent impulse response (*versionadded: 1.3.0*)

alpha [float within [0, 1], optional] The generalized bilinear transformation weighting parameter, which should only be specified with method="gbt", and is ignored otherwise

Returns

sysd [tuple containing the discrete system] Based on the input type, the output will be of the form
- (num, den, dt) for transfer function input
- (zeros, poles, gain, dt) for zeros-poles-gain input
- (A, B, C, D, dt) for state-space system input

Notes

By default, the routine uses a Zero-Order Hold (zoh) method to perform the transformation. Alternatively, a generalized bilinear transformation may be used, which includes the common Tustin's bilinear approximation, an Euler's method technique, or a backwards differencing technique.

The Zero-Order Hold (zoh) method is based on [1], the generalized bilinear approximation is based on [2] and [3], the First-Order Hold (foh) method is based on [4].

References

[1], [2], [3], [4]

Examples

We can transform a continuous state-space system to a discrete one:

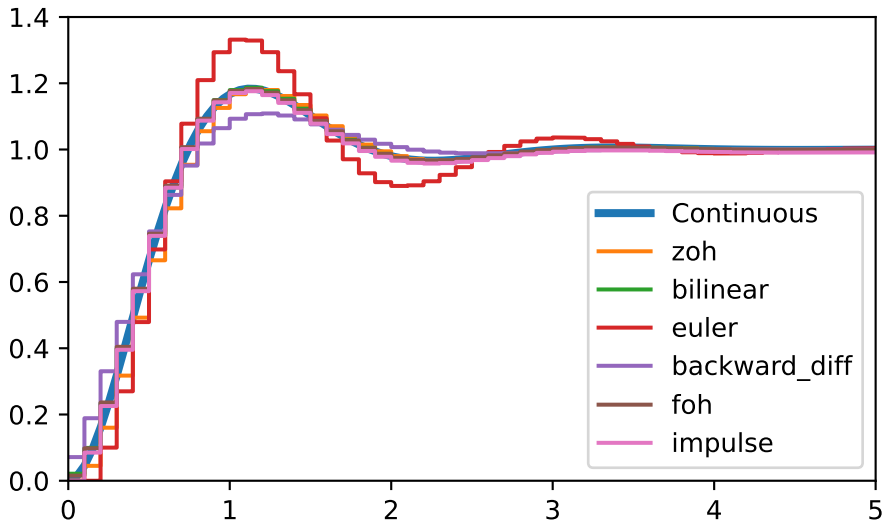
```
>>> import matplotlib.pyplot as plt
>>> from scipy.signal import cont2discrete, lti, dlti, dstep
```

Define a continuous state-space system.

```
>>> A = np.array([[0, 1],[-10., -3]])
>>> B = np.array([[0],[10.]])
>>> C = np.array([[1., 0]])
>>> D = np.array([[0.]])
>>> l_system = lti(A, B, C, D)
>>> t, x = l_system.step(T=np.linspace(0, 5, 100))
>>> fig, ax = plt.subplots()
>>> ax.plot(t, x, label='Continuous', linewidth=3)
```

Transform it to a discrete state-space system using several methods.

```
>>> dt = 0.1
>>> for method in ['zoh', 'bilinear', 'euler', 'backward_diff', 'foh',
↪'impulse']:
...     d_system = cont2discrete((A, B, C, D), dt, method=method)
...     s, x_d = dstep(d_system)
...     ax.step(s, np.squeeze(x_d), label=method, where='post')
>>> ax.axis([t[0], t[-1], x[0], 1.4])
>>> ax.legend(loc='best')
>>> fig.tight_layout()
>>> plt.show()
```



scipy.signal.place_poles

scipy.signal.**place_poles**(*A*, *B*, *poles*, *method='YT'*, *rtol=0.001*, *maxiter=30*)

Compute K such that eigenvalues (A - dot(B, K))=poles.

K is the gain matrix such as the plant described by the linear system `AX+BU` will have its closed-loop poles, i.e the eigenvalues `A - B*K`, as close as possible to those asked for in poles.

SISO, MISO and MIMO systems are supported.

Parameters

A, B [ndarray] State-space representation of linear system `AX + BU`.

poles [array_like] Desired real poles and/or complex conjugates poles. Complex poles are only supported with `method="YT"` (default).

method: {'YT', 'KNV0'}, optional

Which method to choose to find the gain matrix K. One of:

- 'YT': Yang Tits
- 'KNV0': Kautsky, Nichols, Van Dooren update method 0

See References and Notes for details on the algorithms.

rtol: float, optional

After each iteration the determinant of the eigenvectors of `A - B*K` is compared to its previous value, when the relative error between these two values becomes lower than *rtol* the algorithm stops. Default is 1e-3.

maxiter: int, optional

Maximum number of iterations to compute the gain matrix. Default is 30.

Returns

full_state_feedback

[Bunch object]

full_state_feedback is composed of:

gain_matrix

[1-D ndarray] The closed loop matrix K such as the eigenvalues of `A-BK` are as close as possible to the requested poles.

computed_poles

[1-D ndarray] The poles corresponding to `A-BK` sorted as first the real poles in increasing order, then the complex congugates in lexicographic order.

requested_poles

[1-D ndarray] The poles the algorithm was asked to place sorted as above, they may differ from what was achieved.

X [2-D ndarray] The transfer matrix such as `X * diag(poles) = (A - B*K)*X` (see Notes)

rtol [float] The relative tolerance achieved on `det(X)` (see Notes). *rtol* will be NaN if it is possible to solve the system `diag(poles) = (A - B*K)`, or 0 when the optimization algorithms can't do anything i.e when `B.shape[1] == 1`.

nb_iter [int] The number of iterations performed before converging. *nb_iter* will be NaN if it is possible to solve the system `diag(poles) = (A - B*K)`, or 0 when the optimization algorithms can't do anything i.e when `B.shape[1] == 1`.

Notes

The Tits and Yang (YT), [2] paper is an update of the original Kautsky et al. (KNV) paper [1]. KNV relies on rank-1 updates to find the transfer matrix X such that `X * diag(poles) = (A - B*K)*X`, whereas YT uses rank-2 updates. This yields on average more robust solutions (see [2] pp 21-22), furthermore the YT algorithm supports complex poles whereas KNV does not in its original version. Only update method 0 proposed by KNV has been implemented here, hence the name `'KNV0'`.

KNV extended to complex poles is used in Matlab's `place` function, YT is distributed under a non-free licence by Slicot under the name `robpole`. It is unclear and undocumented how KNV0 has been extended to complex poles (Tits and Yang claim on page 14 of their paper that their method can not be used to extend KNV to complex poles), therefore only YT supports them in this implementation.

As the solution to the problem of pole placement is not unique for MIMO systems, both methods start with a tentative transfer matrix which is altered in various way to increase its determinant. Both methods have been proven to converge to a stable solution, however depending on the way the initial transfer matrix is chosen they will converge to different solutions and therefore there is absolutely no guarantee that using `'KNV0'` will yield results similar to Matlab's or any other implementation of these algorithms.

Using the default method `'YT'` should be fine in most cases; `'KNV0'` is only provided because it is needed by `'YT'` in some specific cases. Furthermore `'YT'` gives on average more robust results than `'KNV0'` when `abs(det(X))` is used as a robustness indicator.

[2] is available as a technical report on the following URL: https://hdl.handle.net/1903/5598

References

[1], [2]

Examples

A simple example demonstrating real pole placement using both KNV and YT algorithms. This is example number 1 from section 4 of the reference KNV publication ([1]):

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> A = np.array([[ 1.380,  -0.2077,  6.715, -5.676  ],
...               [-0.5814, -4.290,   0,      0.6750 ],
...               [ 1.067,   4.273,  -6.654,  5.893  ],
...               [ 0.0480,  4.273,   1.343, -2.104  ]])
>>> B = np.array([[ 0,      5.679 ],
...               [ 1.136,  1.136 ],
...               [ 0,      0,    ],
...               [-3.146,  0     ]])
>>> P = np.array([-0.2, -0.5, -5.0566, -8.6659])
```

Now compute K with KNV method 0, with the default YT method and with the YT method while forcing 100 iterations of the algorithm and print some results after each call.

```
>>> fsf1 = signal.place_poles(A, B, P, method='KNV0')
>>> fsf1.gain_matrix
array([[ 0.20071427, -0.96665799,  0.24066128, -0.10279785],
       [ 0.50587268,  0.57779091,  0.51795763, -0.41991442]])
```

```
>>> fsf2 = signal.place_poles(A, B, P)  # uses YT method
>>> fsf2.computed_poles
array([-8.6659, -5.0566, -0.5   , -0.2   ])
```

```
>>> fsf3 = signal.place_poles(A, B, P, rtol=-1, maxiter=100)
>>> fsf3.X
array([[ 0.52072442+0.j, -0.08409372+0.j, -0.56847937+0.j,  0.74823657+0.
↪j],
       [-0.04977751+0.j, -0.80872954+0.j,  0.13566234+0.j, -0.29322906+0.
↪j],
       [-0.82266932+0.j, -0.19168026+0.j, -0.56348322+0.j, -0.43815060+0.
↪j],
       [ 0.22267347+0.j,  0.54967577+0.j, -0.58387806+0.j, -0.40271926+0.
↪j]])
```

The absolute value of the determinant of X is a good indicator to check the robustness of the results, both `'KNV0'` and `'YT'` aim at maximizing it. Below a comparison of the robustness of the results above:

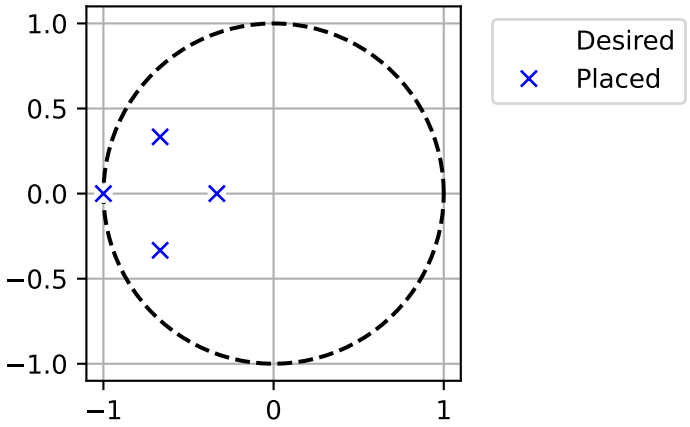
```
>>> abs(np.linalg.det(fsf1.X)) < abs(np.linalg.det(fsf2.X))
True
>>> abs(np.linalg.det(fsf2.X)) < abs(np.linalg.det(fsf3.X))
True
```

Now a simple example for complex poles:

```
>>> A = np.array([[ 0,  7/3.,  0,   0   ],
...               [ 0,   0,    0,  7/9. ],
...               [ 0,   0,    0,   0   ],
...               [ 0,   0,    0,   0   ]])
>>> B = np.array([[ 0,  0 ],
...               [ 0,  0 ],
...               [ 1,  0 ],
...               [ 0,  1 ]])
>>> P = np.array([-3, -1, -2-1j, -2+1j]) / 3.
>>> fsf = signal.place_poles(A, B, P, method='YT')
```

We can plot the desired and computed poles in the complex plane:

```
>>> t = np.linspace(0, 2*np.pi, 401)
>>> plt.plot(np.cos(t), np.sin(t), 'k--')  # unit circle
>>> plt.plot(fsf.requested_poles.real, fsf.requested_poles.imag,
...          'wo', label='Desired')
>>> plt.plot(fsf.computed_poles.real, fsf.computed_poles.imag, 'bx',
...          label='Placed')
>>> plt.grid()
>>> plt.axis('image')
>>> plt.axis([-1.1, 1.1, -1.1, 1.1])
>>> plt.legend(bbox_to_anchor=(1.05, 1), loc=2, numpoints=1)
```



Waveforms

chirp(t, f0, t1, f1[, method, phi, vertex_zero])	Frequency-swept cosine generator.
gausspulse(t[, fc, bw, bwr, tpr, retquad, …])	Return a Gaussian modulated sinusoid:
max_len_seq(nbits[, state, length, taps])	Maximum length sequence (MLS) generator.
sawtooth(t[, width])	Return a periodic sawtooth or triangle waveform.
square(t[, duty])	Return a periodic square-wave waveform.
sweep_poly(t, poly[, phi])	Frequency-swept cosine generator, with a time-dependent frequency.
unit_impulse(shape[, idx, dtype])	Unit impulse signal (discrete delta function) or unit basis vector.

scipy.signal.chirp

scipy.signal.**chirp**(*t*, *f0*, *t1*, *f1*, *method='linear'*, *phi=0*, *vertex_zero=True*)

Frequency-swept cosine generator.

In the following, 'Hz' should be interpreted as 'cycles per unit'; there is no requirement here that the unit is one second. The important distinction is that the units of rotation are cycles, not radians. Likewise, *t* could be a measurement of space instead of time.

Parameters

t [array_like] Times at which to evaluate the waveform.

f0 [float] Frequency (e.g. Hz) at time t=0.

t1 [float] Time at which *f1* is specified.

f1 [float] Frequency (e.g. Hz) of the waveform at time *t1*.

method [{'linear', 'quadratic', 'logarithmic', 'hyperbolic'}, optional] Kind of frequency sweep. If not given, *linear* is assumed. See Notes below for more details.

phi [float, optional] Phase offset, in degrees. Default is 0.

vertex_zero [bool, optional] This parameter is only used when *method* is 'quadratic'. It determines whether the vertex of the parabola that is the graph of the frequency is at t=0 or t=t1.

Returns

y [ndarray] A numpy array containing the signal evaluated at *t* with the requested time-varying frequency. More precisely, the function returns `cos(phase + (pi/180)*phi)` where *phase* is the integral (from 0 to *t*) of `2*pi*f(t)`. `f(t)` is defined below.

See also:

sweep_poly

The graph of the frequency f(t) is a parabola through (0, f0) and (t1, f1). By default, the vertex of the parabola is at (0, f0). If *vertex_zero* is False, then the vertex is at (t1, f1). The formula is:
if vertex_zero is True:

```
f(t) = f0 + (f1 - f0) * t**2 / t1**2
```

else:

```
f(t) = f1 - (f1 - f0) * (t1 - t)**2 / t1**2
```

To use a more general quadratic function, or an arbitrary polynomial, use the function *scipy.signal.sweep_poly*.

logarithmic, log, lo:

```
f(t) = f0 * (f1/f0)**(t/t1)
```

f0 and f1 must be nonzero and have the same sign.
This signal is also known as a geometric or exponential chirp.

hyperbolic, hyp:

```
f(t) = f0*f1*t1 / ((f0 - f1)*t + f1*t1)
```

f0 and f1 must be nonzero.

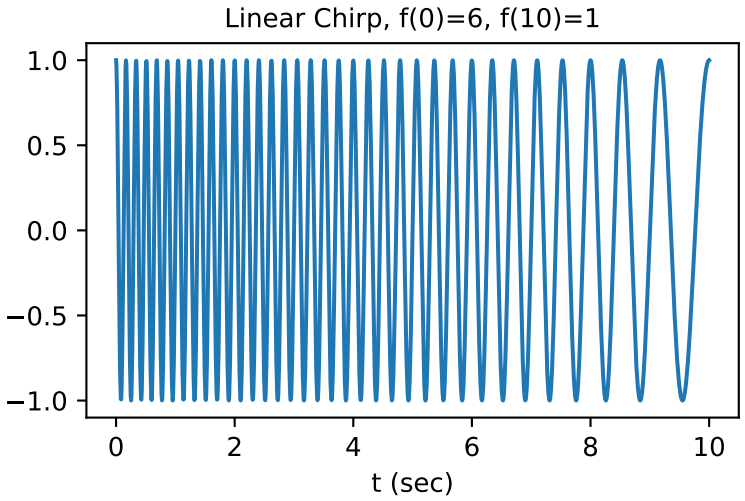
Examples

The following will be used in the examples:

```
>>> from scipy.signal import chirp, spectrogram
>>> import matplotlib.pyplot as plt
```

For the first example, we'll plot the waveform for a linear chirp from 6 Hz to 1 Hz over 10 seconds:

```
>>> t = np.linspace(0, 10, 1500)
>>> w = chirp(t, f0=6, f1=1, t1=10, method='linear')
>>> plt.plot(t, w)
>>> plt.title("Linear Chirp, f(0)=6, f(10)=1")
>>> plt.xlabel('t (sec)')
>>> plt.show()
```



For the remaining examples, we'll use higher frequency ranges, and demonstrate the result using *scipy.signal.spectrogram*. We'll use a 4 second interval sampled at 7200 Hz.

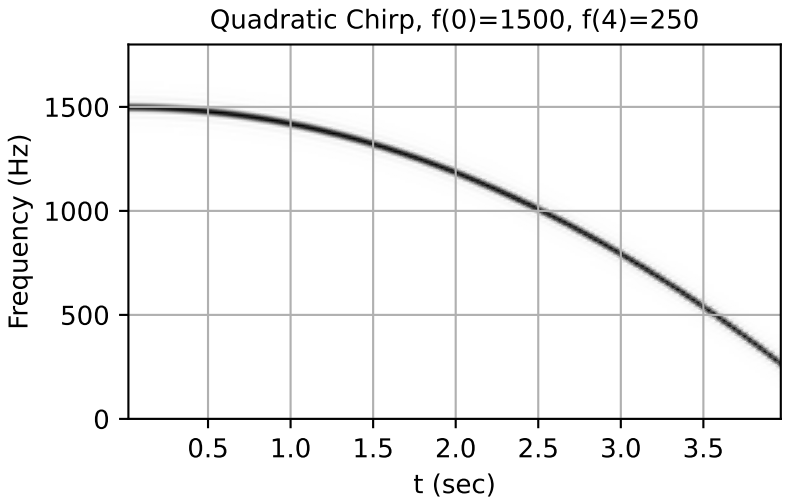
```
>>> fs = 7200
>>> T = 4
>>> t = np.arange(0, int(T*fs)) / fs
```

We'll use this function to plot the spectrogram in each example.

```
>>> def plot_spectrogram(title, w, fs):
...     ff, tt, Sxx = spectrogram(w, fs=fs, nperseg=256, nfft=576)
...     plt.pcolormesh(tt, ff[:145], Sxx[:145], cmap='gray_r', shading=
↪'gouraud')
...     plt.title(title)
...     plt.xlabel('t (sec)')
...     plt.ylabel('Frequency (Hz)')
...     plt.grid()
...
```

Quadratic chirp from 1500 Hz to 250 Hz (vertex of the parabolic curve of the frequency is at t=0):

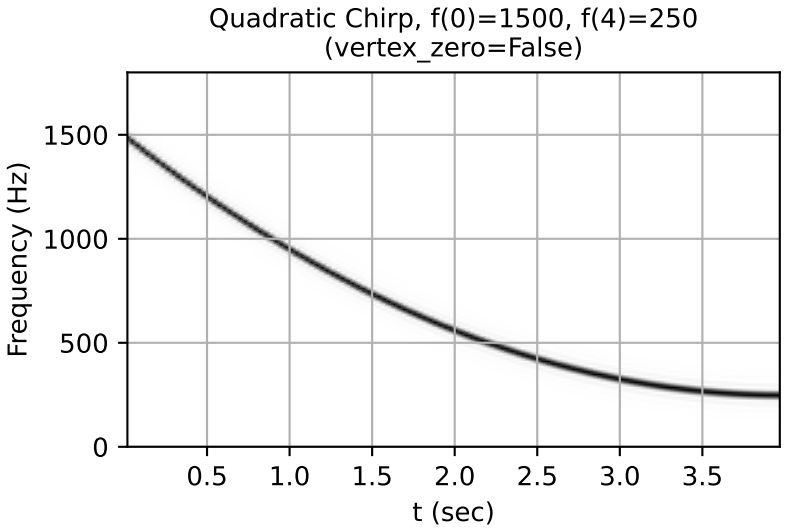
```
>>> w = chirp(t, f0=1500, f1=250, t1=T, method='quadratic')
>>> plot_spectrogram(f'Quadratic Chirp, f(0)=1500, f({T})=250', w, fs)
>>> plt.show()
```



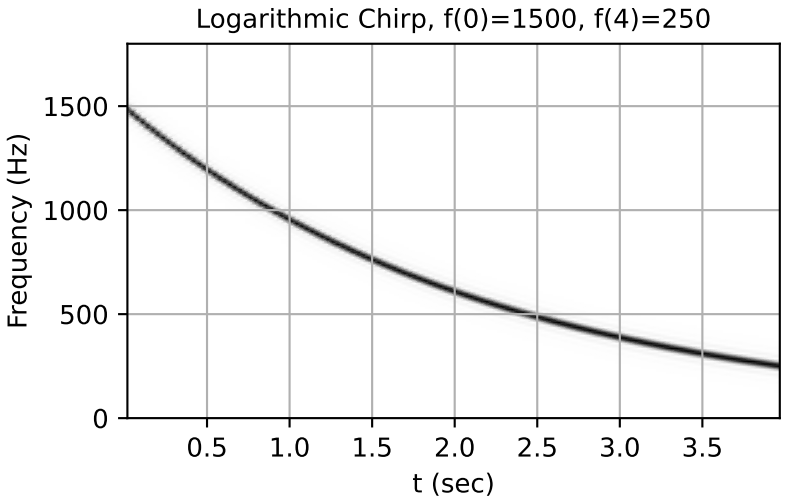
Quadratic chirp from 1500 Hz to 250 Hz (vertex of the parabolic curve of the frequency is at t=T):

```
>>> w = chirp(t, f0=1500, f1=250, t1=T, method='quadratic',
...           vertex_zero=False)
>>> plot_spectrogram(f'Quadratic Chirp, f(0)=1500, f({T})=250\n' +
...                  '(vertex_zero=False)', w, fs)
>>> plt.show()
```

Logarithmic chirp from 1500 Hz to 250 Hz:

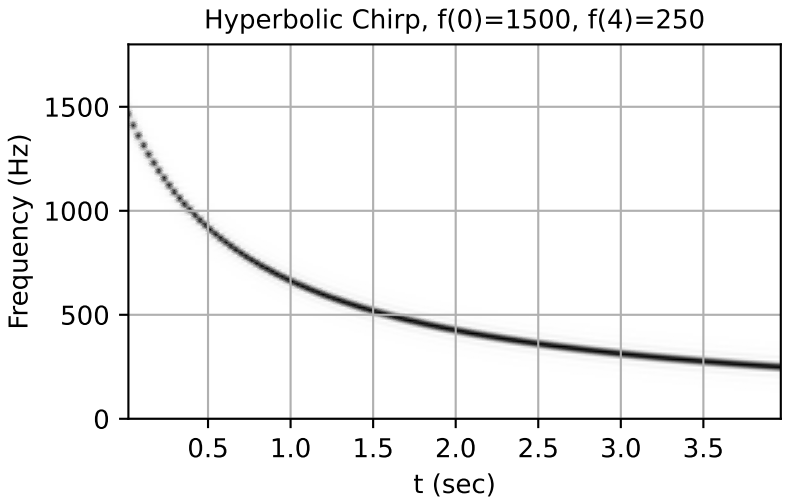



```
>>> w = chirp(t, f0=1500, f1=250, t1=T, method='logarithmic')
>>> plot_spectrogram(f'Logarithmic Chirp, f(0)=1500, f({T})=250', w, fs)
>>> plt.show()
```



Hyperbolic chirp from 1500 Hz to 250 Hz:

```
>>> w = chirp(t, f0=1500, f1=250, t1=T, method='hyperbolic')
>>> plot_spectrogram(f'Hyperbolic Chirp, f(0)=1500, f({T})=250', w, fs)
>>> plt.show()
```



scipy.signal.gausspulse

`scipy.signal.`**`gausspulse`**(*t*, *fc=1000*, *bw=0.5*, *bwr=- 6*, *tpr=- 60*, *retquad=False*, *retenv=False*)

Return a Gaussian modulated sinusoid:

```
exp(-a t^2) exp(1j*2*pi*fc*t).
```

If *retquad* is True, then return the real and imaginary parts (in-phase and quadrature). If *retenv* is True, then return the envelope (unmodulated signal). Otherwise, return the real part of the modulated sinusoid.

Parameters

t	[ndarray or the string 'cutoff'] Input array.
fc	[float, optional] Center frequency (e.g. Hz). Default is 1000.
bw	[float, optional] Fractional bandwidth in frequency domain of pulse (e.g. Hz). Default is 0.5.
bwr	[float, optional] Reference level at which fractional bandwidth is calculated (dB). Default is -6.
tpr	[float, optional] If *t* is 'cutoff', then the function returns the cutoff time for when the pulse amplitude falls below *tpr* (in dB). Default is -60.
retquad	[bool, optional] If True, return the quadrature (imaginary) as well as the real part of the signal. Default is False.
retenv	[bool, optional] If True, return the envelope of the signal. Default is False.

Returns

yI	[ndarray] Real part of signal. Always returned.
yQ	[ndarray] Imaginary part of signal. Only returned if *retquad* is True.
yenv	[ndarray] Envelope of signal. Only returned if *retenv* is True.

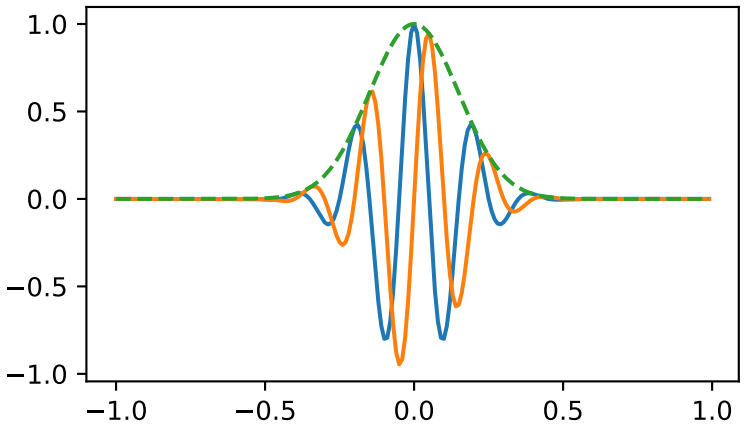
See also:

`scipy.signal.morlet`

Examples

Plot real component, imaginary component, and envelope for a 5 Hz pulse, sampled at 100 Hz for 2 seconds:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(-1, 1, 2 * 100, endpoint=False)
>>> i, q, e = signal.gausspulse(t, fc=5, retquad=True, retenv=True)
>>> plt.plot(t, i, t, q, t, e, '--')
```



scipy.signal.max_len_seq

scipy.signal.**max_len_seq**(*nbits*, *state=None*, *length=None*, *taps=None*)

Maximum length sequence (MLS) generator.

Parameters

nbits [int] Number of bits to use. Length of the resulting sequence will be `(2**nbits) - 1`. Note that generating long sequences (e.g., greater than `nbits == 16`) can take a long time.

state [array_like, optional] If array, must be of length `nbits`, and will be cast to binary (bool) representation. If None, a seed of ones will be used, producing a repeatable representation. If `state` is all zeros, an error is raised as this is invalid. Default: None.

length [int, optional] Number of samples to compute. If None, the entire length `(2**nbits) - 1` is computed.

taps [array_like, optional] Polynomial taps to use (e.g., `[7, 6, 1]` for an 8-bit sequence). If None, taps will be automatically selected (for up to `nbits == 32`).

Returns

seq [array] Resulting MLS sequence of 0's and 1's.

state [array] The final state of the shift register.

Notes

The algorithm for MLS generation is generically described in:

https://en.wikipedia.org/wiki/Maximum_length_sequence

The default values for taps are specifically taken from the first option listed for each value of `nbits` in:

https://web.archive.org/web/20181001062252/http://www.newwaveinstruments.com/resources/articles/m_sequence_linear_feedback_shift_register_lfsr.htm

New in version 0.15.0.

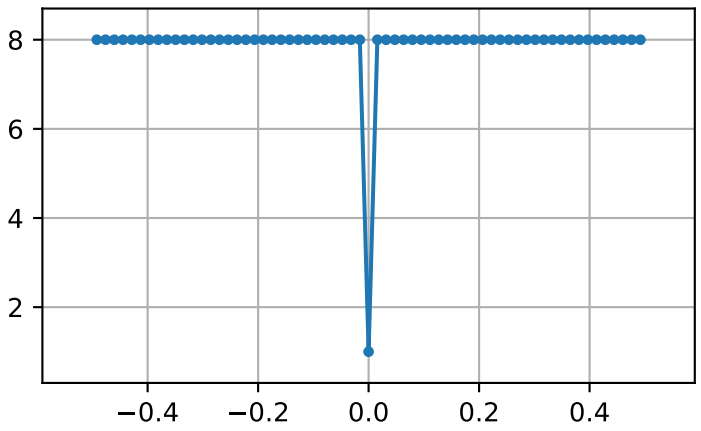
Examples

MLS uses binary convention:

```
>>> from scipy.signal import max_len_seq
>>> max_len_seq(4)[0]
array([1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 0], dtype=int8)
```

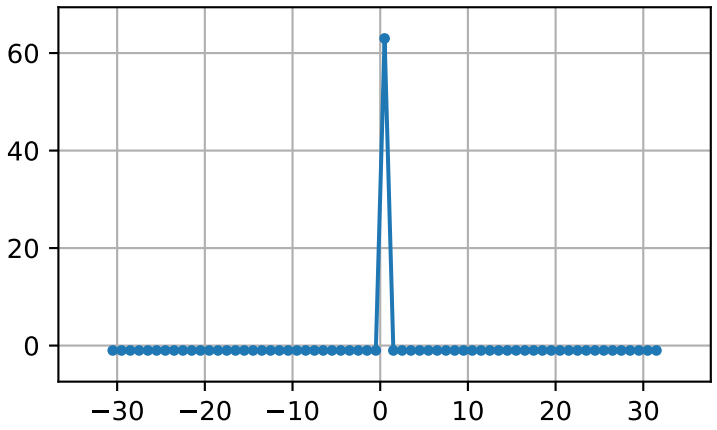
MLS has a white spectrum (except for DC):

```
>>> import matplotlib.pyplot as plt
>>> from numpy.fft import fft, ifft, fftshift, fftfreq
>>> seq = max_len_seq(6)[0]*2-1  # +1 and -1
>>> spec = fft(seq)
>>> N = len(seq)
>>> plt.plot(fftshift(fftfreq(N)), fftshift(np.abs(spec)), '.-')
>>> plt.margins(0.1, 0.1)
>>> plt.grid(True)
>>> plt.show()
```



Circular autocorrelation of MLS is an impulse:

```
>>> acorrcirc = ifft(spec * np.conj(spec)).real
>>> plt.figure()
>>> plt.plot(np.arange(-N/2+1, N/2+1), fftshift(acorrcirc), '.-')
>>> plt.margins(0.1, 0.1)
>>> plt.grid(True)
>>> plt.show()
```



Linear autocorrelation of MLS is approximately an impulse:

```
>>> acorr = np.correlate(seq, seq, 'full')
>>> plt.figure()
>>> plt.plot(np.arange(-N+1, N), acorr, '.-')
>>> plt.margins(0.1, 0.1)
>>> plt.grid(True)
>>> plt.show()
```

scipy.signal.sawtooth

`scipy.signal.`**`sawtooth`**(*t*, *width=1*)

Return a periodic sawtooth or triangle waveform.

The sawtooth waveform has a period `2*pi`, rises from -1 to 1 on the interval 0 to `width*2*pi`, then drops from 1 to -1 on the interval `width*2*pi` to `2*pi`. *width* must be in the interval [0, 1].

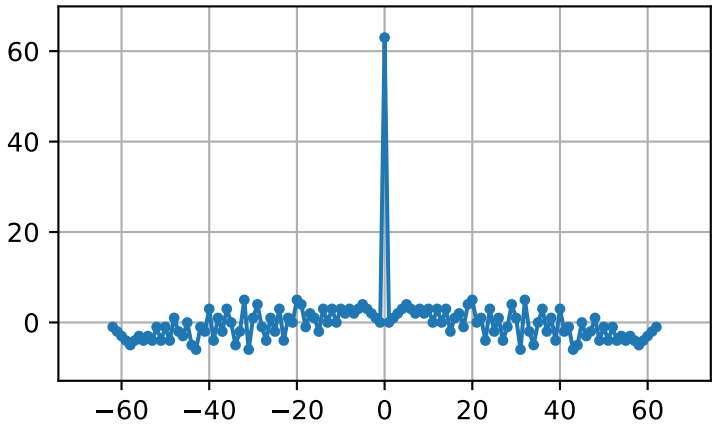
Note that this is not band-limited. It produces an infinite number of harmonics, which are aliased back and forth across the frequency spectrum.

Parameters

t	[array_like] Time.
width	[array_like, optional] Width of the rising ramp as a proportion of the total cycle. Default is 1, producing a rising ramp, while 0 produces a falling ramp. *width* = 0.5 produces a triangle wave. If an array, causes wave shape to change over time, and must be the same length as t.

Returns

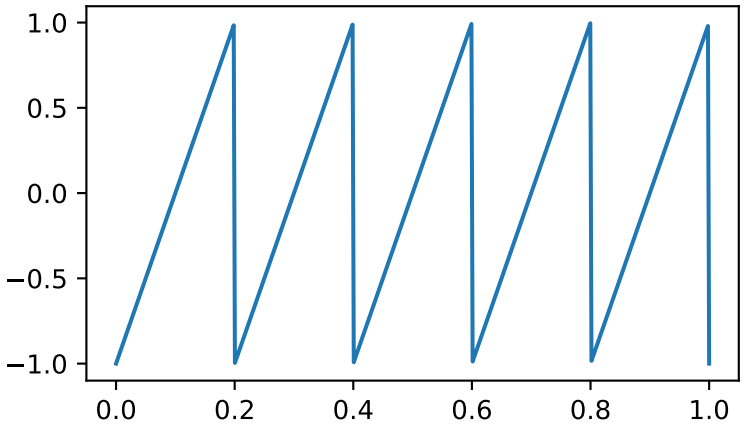
y	[ndarray] Output array containing the sawtooth waveform.



Examples

A 5 Hz waveform sampled at 500 Hz for 1 second:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(0, 1, 500)
>>> plt.plot(t, signal.sawtooth(2 * np.pi * 5 * t))
```



scipy.signal.square

scipy.signal.**square**(*t*, *duty=0.5*)

Return a periodic square-wave waveform.

The square wave has a period `2*pi`, has value +1 from 0 to `2*pi*duty` and -1 from `2*pi*duty` to `2*pi`. *duty* must be in the interval [0,1].

Note that this is not band-limited. It produces an infinite number of harmonics, which are aliased back and forth across the frequency spectrum.

Parameters

t	[array_like] The input time array.
duty	[array_like, optional] Duty cycle. Default is 0.5 (50% duty cycle). If an array, causes wave shape to change over time, and must be the same length as t.

Returns

y	[ndarray] Output array containing the square waveform.

Examples

A 5 Hz waveform sampled at 500 Hz for 1 second:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(0, 1, 500, endpoint=False)
>>> plt.plot(t, signal.square(2 * np.pi * 5 * t))
>>> plt.ylim(-2, 2)
```

A pulse-width modulated sine wave:

```
>>> plt.figure()
>>> sig = np.sin(2 * np.pi * t)
>>> pwm = signal.square(2 * np.pi * 30 * t, duty=(sig + 1)/2)
>>> plt.subplot(2, 1, 1)
>>> plt.plot(t, sig)
>>> plt.subplot(2, 1, 2)
>>> plt.plot(t, pwm)
>>> plt.ylim(-1.5, 1.5)
```

scipy.signal.sweep_poly

scipy.signal.**sweep_poly**(*t*, *poly*, *phi=0*)

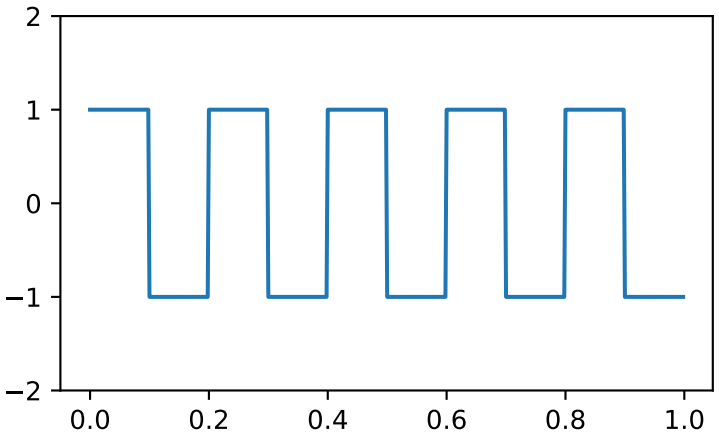
Frequency-swept cosine generator, with a time-dependent frequency.

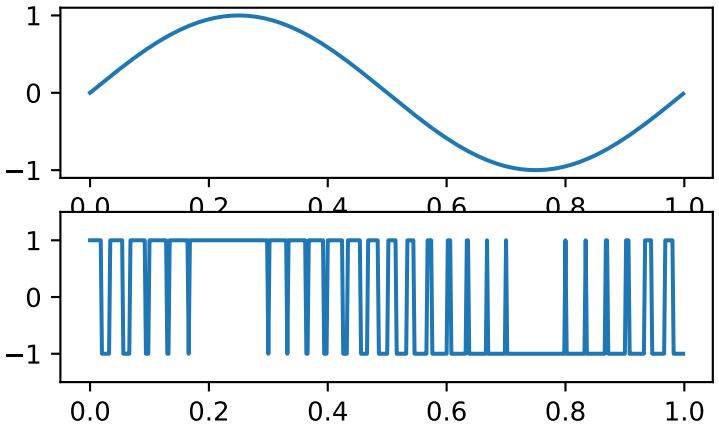
This function generates a sinusoidal function whose instantaneous frequency varies with time. The frequency at time *t* is given by the polynomial *poly*.

Parameters

t	[ndarray] Times at which to evaluate the waveform.

poly	[1-D array_like or instance of numpy.poly1d] The desired frequency expressed as a polynomial. If *poly* is a list or ndarray of length n, then the elements of *poly* are the coefficients of the polynomial, and the instantaneous frequency is
	`f(t) = poly[0]*t**(n-1) + poly[1]*t**(n-2) + ... + poly[n-1]`
	If *poly* is an instance of numpy.poly1d, then the instantaneous frequency is
	`f(t) = poly(t)`


2
1
0
−1
−2
0.0
0.2
0.4
0.6
0.8
1.0


1
0
−1
1
0
−1
0.0
0.2
0.4
0.6
0.8
1.0

phi [float, optional] Phase offset, in degrees, Default: 0.

Returns

sweep_poly

[ndarray] A numpy array containing the signal evaluated at *t* with the requested time-varying frequency. More precisely, the function returns `cos(phase + (pi/180)*phi)`, where *phase* is the integral (from 0 to t) of `2 * pi * f(t)`; `f(t)` is defined above.

See also:

`chirp`

Notes

New in version 0.8.0.

If *poly* is a list or ndarray of length *n*, then the elements of *poly* are the coefficients of the polynomial, and the instantaneous frequency is:

```
f(t) = poly[0]*t**(n-1) + poly[1]*t**(n-2) + ... + poly[n-1]
```

If *poly* is an instance of `numpy.poly1d`, then the instantaneous frequency is:

```
f(t) = poly(t)
```

Finally, the output *s* is:

```
cos(phase + (pi/180)*phi)
```

where *phase* is the integral from 0 to *t* of `2 * pi * f(t)`, `f(t)` as defined above.

Examples

Compute the waveform with instantaneous frequency:

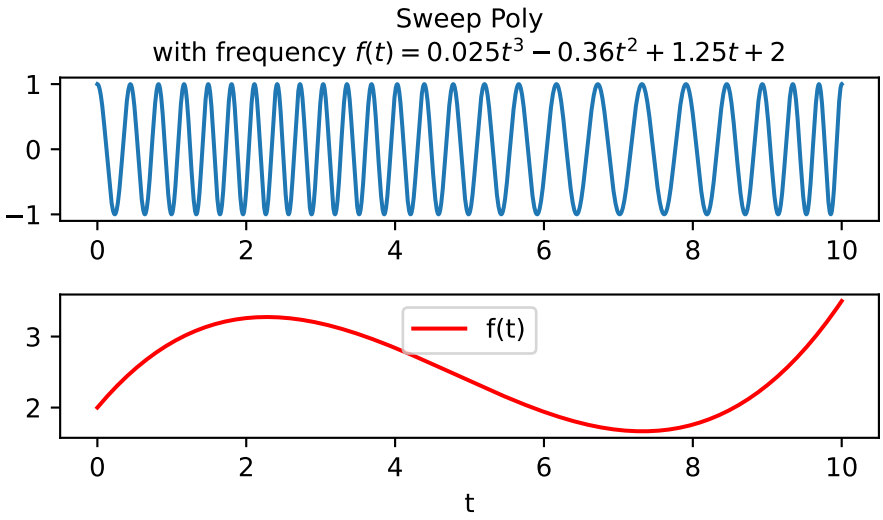
```
f(t) = 0.025*t**3 - 0.36*t**2 + 1.25*t + 2
```

over the interval 0 <= t <= 10.

```
>>> from scipy.signal import sweep_poly
>>> p = np.poly1d([0.025, -0.36, 1.25, 2.0])
>>> t = np.linspace(0, 10, 5001)
>>> w = sweep_poly(t, p)
```

Plot it:

```
>>> import matplotlib.pyplot as plt
>>> plt.subplot(2, 1, 1)
>>> plt.plot(t, w)
>>> plt.title("Sweep Poly\nwith frequency " +
...           "$f(t) = 0.025t^3 - 0.36t^2 + 1.25t + 2$")
>>> plt.subplot(2, 1, 2)
>>> plt.plot(t, p(t), 'r', label='f(t)')
>>> plt.legend()
>>> plt.xlabel('t')
>>> plt.tight_layout()
>>> plt.show()
```



scipy.signal.unit_impulse

`scipy.signal.`**`unit_impulse`**(*shape*, *idx=None*, *dtype=<class 'float'>*)

Unit impulse signal (discrete delta function) or unit basis vector.

Parameters

shape [int or tuple of int] Number of samples in the output (1-D), or a tuple that represents the shape of the output (N-D).

idx [None or int or tuple of int or 'mid', optional] Index at which the value is 1. If None, defaults to the 0th element. If `idx='mid'`, the impulse will be centered at `shape // 2` in all dimensions. If an int, the impulse will be at *idx* in all dimensions.

dtype [data-type, optional] The desired data-type for the array, e.g., `numpy.int8`. Default is `numpy.float64`.

Returns

y [ndarray] Output array containing an impulse signal.

Notes

The 1D case is also known as the Kronecker delta.

New in version 0.19.0.

Examples

An impulse at the 0th element ($\delta[n]$):

```
>>> from scipy import signal
>>> signal.unit_impulse(8)
array([ 1.,  0.,  0.,  0.,  0.,  0.,  0.,  0.])
```

Impulse offset by 2 samples ($\delta[n-2]$):

```
>>> signal.unit_impulse(7, 2)
array([ 0.,  0.,  1.,  0.,  0.,  0.,  0.])
```

2-dimensional impulse, centered:

```
>>> signal.unit_impulse((3, 3), 'mid')
array([[ 0.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  0.]])
```

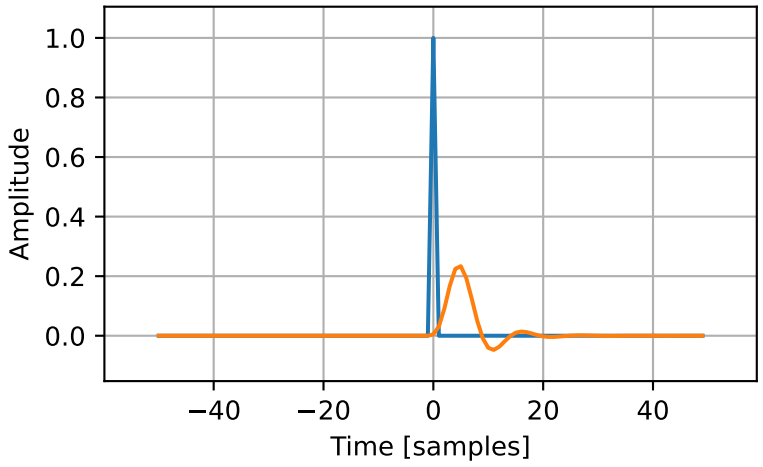
Impulse at (2, 2), using broadcasting:

```
>>> signal.unit_impulse((4, 4), 2)
array([[ 0.,  0.,  0.,  0.],
       [ 0.,  0.,  0.,  0.],
       [ 0.,  0.,  1.,  0.],
       [ 0.,  0.,  0.,  0.]])
```

Plot the impulse response of a 4th-order Butterworth lowpass filter:

```
>>> imp = signal.unit_impulse(100, 'mid')
>>> b, a = signal.butter(4, 0.2)
>>> response = signal.lfilter(b, a, imp)
```

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(np.arange(-50, 50), imp)
>>> plt.plot(np.arange(-50, 50), response)
>>> plt.margins(0.1, 0.1)
>>> plt.xlabel('Time [samples]')
>>> plt.ylabel('Amplitude')
>>> plt.grid(True)
>>> plt.show()
```



Window functions

For window functions, see the `scipy.signal.windows` namespace.

In the *scipy.signal* namespace, there is a convenience function to obtain these windows by name:

get_window(window, Nx[, fftbins])	Return a window of a given length and type.

scipy.signal.get_window

scipy.signal.**get_window**(*window*, *Nx*, *fftbins=True*)

Return a window of a given length and type.

Parameters

window [string, float, or tuple] The type of window to create. See below for more details.

Nx [int] The number of samples in the window.

fftbins [bool, optional] If True (default), create a "periodic" window, ready to use with *ifftshift* and be multiplied by the result of an FFT (see also *fftfreq*). If False, create a "symmetric" window, for use in filter design.

Returns

get_window

[ndarray] Returns a window of length *Nx* and type *window*

Notes

Window types:

- `boxcar`
- `triang`
- `blackman`
- `hamming`
- `hann`
- `bartlett`
- `flattop`
- `parzen`
- `bohman`
- `blackmanharris`
- `nuttall`
- `barthann`
- `cosine`
- `exponential`
- `tukey`
- `taylor`
- `kaiser` (needs beta)

- `gaussian` (needs standard deviation)
- `general_cosine` (needs weighting coefficients)
- `general_gaussian` (needs power, width)
- `general_hamming` (needs window coefficient)
- `dpss` (needs normalized half-bandwidth)
- `chebwin` (needs attenuation)

If the window requires no parameters, then *window* can be a string.

If the window requires parameters, then *window* must be a tuple with the first argument the string name of the window, and the next arguments the needed parameters.

If *window* is a floating point number, it is interpreted as the beta parameter of the `kaiser` window.

Each of the window types listed above is also the name of a function that can be called directly to create a window of that type.

Examples

```
>>> from scipy import signal
>>> signal.get_window('triang', 7)
array([ 0.125,  0.375,  0.625,  0.875,  0.875,  0.625,  0.375])
>>> signal.get_window(('kaiser', 4.0), 9)
array([ 0.08848053,  0.29425961,  0.56437221,  0.82160913,  0.97885093,
        0.97885093,  0.82160913,  0.56437221,  0.29425961])
>>> signal.get_window(('exponential', None, 1.), 9)
array([ 0.011109  ,  0.03019738,  0.082085  ,  0.22313016,  0.60653066,
        0.60653066,  0.22313016,  0.082085  ,  0.03019738])
>>> signal.get_window(4.0, 9)
array([ 0.08848053,  0.29425961,  0.56437221,  0.82160913,  0.97885093,
        0.97885093,  0.82160913,  0.56437221,  0.29425961])
```

Wavelets

cascade(hk[, J])	Return (x, phi, psi) at dyadic points `K/2**J` from filter coefficients.
daub(p)	The coefficients for the FIR low-pass filter producing Daubechies wavelets.
morlet(M[, w, s, complete])	Complex Morlet wavelet.
qmf(hk)	Return high-pass qmf filter from low-pass
ricker(points, a)	Return a Ricker wavelet, also known as the “Mexican hat wavelet”.
morlet2(M, s[, w])	Complex Morlet wavelet, designed to work with *cwt*.
cwt(data, wavelet, widths[, dtype])	Continuous wavelet transform.

scipy.signal.cascade

scipy.signal.**cascade**(*hk*, *J=7*)

Return (x, phi, psi) at dyadic points `K/2**J` from filter coefficients.

Parameters

hk	[array_like] Coefficients of low-pass filter.
J	[int, optional] Values will be computed at grid points `K/2**J`. Default is 7.

Returns

x	[ndarray] The dyadic points `K/2**J` for `K=0...N * (2**J)-1` where `len(hk) = len(gk) = N+1`.
phi	[ndarray] The scaling function `phi(x)` at *x*: `phi(x) = sum(hk * phi(2x-k))`, where k is from 0 to N.
psi	[ndarray, optional] The wavelet function `psi(x)` at *x*: `phi(x) = sum(gk * phi(2x-k))`, where k is from 0 to N. *psi* is only returned if *gk* is not None.

Notes

The algorithm uses the vector cascade algorithm described by Strang and Nguyen in "Wavelets and Filter Banks". It builds a dictionary of values and slices for quick reuse. Then inserts vectors into final vector at the end.

scipy.signal.daub

scipy.signal.**daub**(*p*)

The coefficients for the FIR low-pass filter producing Daubechies wavelets.

p>=1 gives the order of the zero at f=1/2. There are 2p filter coefficients.

Parameters

p	[int] Order of the zero at f=1/2, can have values from 1 to 34.

Returns

daub	[ndarray] Return

scipy.signal.morlet

scipy.signal.**morlet**(*M*, *w=5.0*, *s=1.0*, *complete=True*)

Complex Morlet wavelet.

Parameters

M	[int] Length of the wavelet.
w	[float, optional] Omega0. Default is 5
s	[float, optional] Scaling factor, windowed from `-s*2*pi` to `+s*2*pi`. Default is 1.
complete	[bool, optional] Whether to use the complete or the standard version.

Returns

morlet	[(M,) ndarray]

See also:

morlet2

Implementation of Morlet wavelet, compatible with *cwt*.

scipy.signal.gausspulse

Notes

The standard version:

```
pi**-0.25 * exp(1j*w*x) * exp(-0.5*(x**2))
```

This commonly used wavelet is often referred to simply as the Morlet wavelet. Note that this simplified version can cause admissibility problems at low values of *w*.

The complete version:

```
pi**-0.25 * (exp(1j*w*x) - exp(-0.5*(w**2))) * exp(-0.5*(x**2))
```

This version has a correction term to improve admissibility. For *w* greater than 5, the correction term is negligible.

Note that the energy of the return wavelet is not normalised according to *s*.

The fundamental frequency of this wavelet in Hz is given by `f = 2*s*w*r / M` where *r* is the sampling rate.

Note: This function was created before *cwt* and is not compatible with it.

scipy.signal.qmf

`scipy.signal.`**`qmf`**(*hk*)

Return high-pass qmf filter from low-pass

Parameters

hk [array_like] Coefficients of high-pass filter.

scipy.signal.ricker

`scipy.signal.`**`ricker`**(*points*, *a*)

Return a Ricker wavelet, also known as the "Mexican hat wavelet".

It models the function:

```
A * (1 - (x/a)**2) * exp(-0.5*(x/a)**2),
```

where `A = 2/(sqrt(3*a)*(pi**0.25))`.

Parameters

points [int] Number of points in *vector*. Will be centered around 0.
a [scalar] Width parameter of the wavelet.

Returns

vector [(N,) ndarray] Array of length *points* in shape of ricker curve.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> points = 100
>>> a = 4.0
>>> vec2 = signal.ricker(points, a)
>>> print(len(vec2))
100
```

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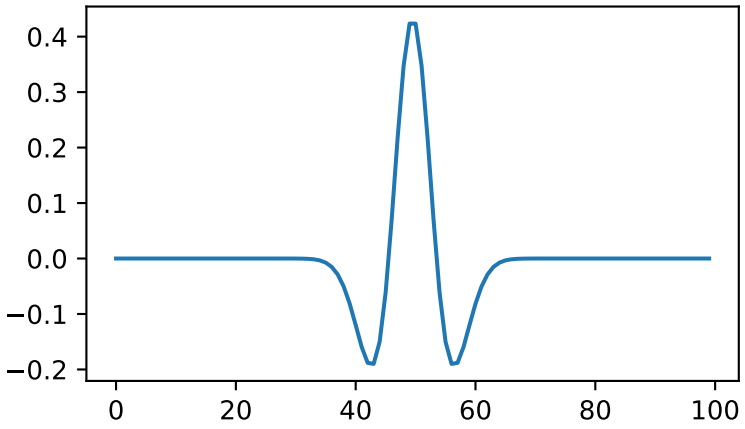
```
>>> plt.plot(vec2)
>>> plt.show()
```



scipy.signal.morlet2

scipy.signal.**morlet2**(*M*, *s*, *w=5*)

Complex Morlet wavelet, designed to work with *cwt*.

Returns the complete version of morlet wavelet, normalised according to *s*:

```
exp(1j*w*x/s) * exp(-0.5*(x/s)**2) * pi**(-0.25) * sqrt(1/s)
```

Parameters

M	[int] Length of the wavelet.
s	[float] Width parameter of the wavelet.
w	[float, optional] Omega0. Default is 5

Returns

morlet	[(M,) ndarray]

See also:

morlet

Implementation of Morlet wavelet, incompatible with *cwt*

Notes

New in version 1.4.0.

This function was designed to work with *cwt*. Because *morlet2* returns an array of complex numbers, the *dtype* argument of *cwt* should be set to *complex128* for best results.

Note the difference in implementation with *morlet*. The fundamental frequency of this wavelet in Hz is given by:

```
f = w*fs / (2*s*np.pi)
```

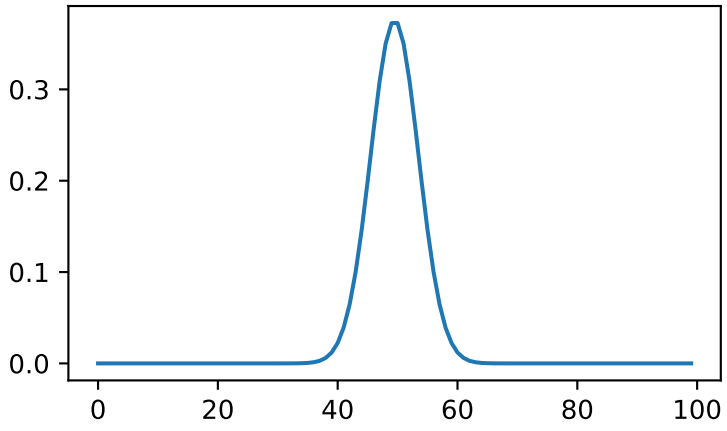
where `fs` is the sampling rate and *s* is the wavelet width parameter. Similarly we can get the wavelet width parameter at `f`:

```
s = w*fs / (2*f*np.pi)
```

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

```
>>> M = 100
>>> s = 4.0
>>> w = 2.0
>>> wavelet = signal.morlet2(M, s, w)
>>> plt.plot(abs(wavelet))
>>> plt.show()
```



This example shows basic use of *morlet2* with *cwt* in time-frequency analysis:

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
```

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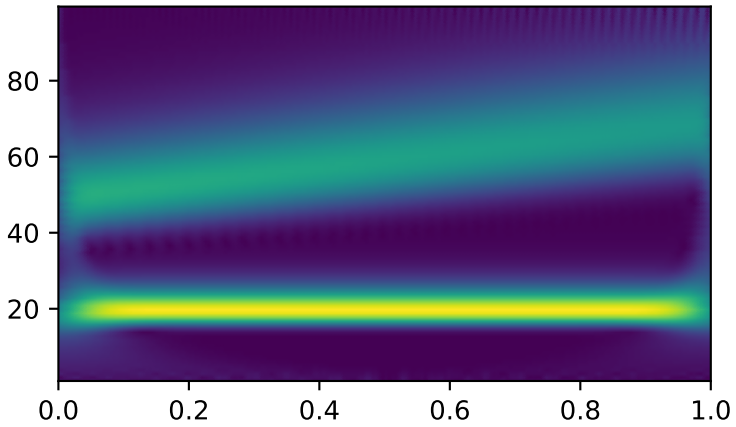
```
>>> t, dt = np.linspace(0, 1, 200, retstep=True)
>>> fs = 1/dt
>>> w = 6.
>>> sig = np.cos(2*np.pi*(50 + 10*t)*t) + np.sin(40*np.pi*t)
>>> freq = np.linspace(1, fs/2, 100)
>>> widths = w*fs / (2*freq*np.pi)
>>> cwtm = signal.cwt(sig, signal.morlet2, widths, w=w)
>>> plt.pcolormesh(t, freq, np.abs(cwtm), cmap='viridis', shading='gouraud
↪')
>>> plt.show()
```



scipy.signal.cwt

`scipy.signal.`**`cwt`**(*data*, *wavelet*, *widths*, *dtype=None*, ***kwargs*)

Continuous wavelet transform.

Performs a continuous wavelet transform on *data*, using the *wavelet* function. A CWT performs a convolution with *data* using the *wavelet* function, which is characterized by a width parameter and length parameter. The *wavelet* function is allowed to be complex.

Parameters

data	[(N,) ndarray] data on which to perform the transform.
wavelet	[function] Wavelet function, which should take 2 arguments. The first argument is the number of points that the returned vector will have (len(wavelet(length,width)) == length). The second is a width parameter, defining the size of the wavelet (e.g. standard deviation of a gaussian). See *ricker*, which satisfies these requirements.
widths	[(M,) sequence] Widths to use for transform.
dtype	[data-type, optional] The desired data type of output. Defaults to `float64` if the output of *wavelet* is real and `complex128` if it is complex. New in version 1.4.0.
kwargs	Keyword arguments passed to wavelet function. New in version 1.4.0.

Returns

cwt: (M, N) ndarray
Will have shape of (len(widths), len(data)).

Notes

New in version 1.4.0.

For non-symmetric, complex-valued wavelets, the input signal is convolved with the time-reversed complex-conjugate of the wavelet data [1].

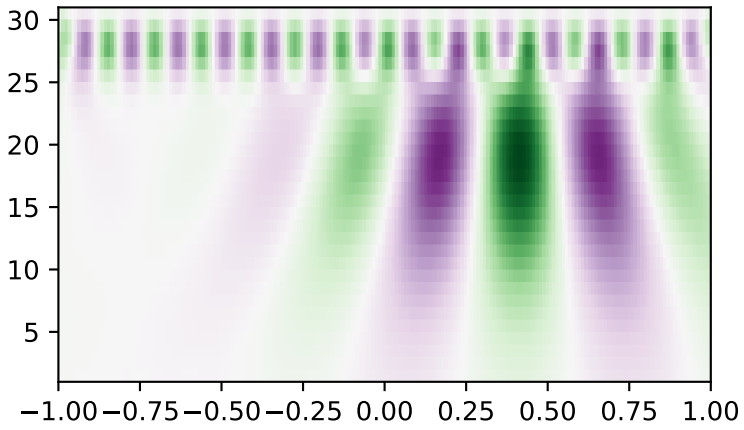
```
length = min(10 * width[ii], len(data))
cwt[ii,:] = signal.convolve(data, np.conj(wavelet(length, width[ii],
                                    **kwargs))[::-1], mode='same')
```

References

[1]

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> t = np.linspace(-1, 1, 200, endpoint=False)
>>> sig  = np.cos(2 * np.pi * 7 * t) + signal.gausspulse(t - 0.4, fc=2)
>>> widths = np.arange(1, 31)
>>> cwtmatr = signal.cwt(sig, signal.ricker, widths)
>>> plt.imshow(cwtmatr, extent=[-1, 1, 1, 31], cmap='PRGn', aspect='auto',
...            vmax=abs(cwtmatr).max(), vmin=-abs(cwtmatr).max())
>>> plt.show()
```



Peak finding

argrelmin(data[, axis, order, mode])	Calculate the relative minima of *data*.
argrelmax(data[, axis, order, mode])	Calculate the relative maxima of *data*.
argrelextrema(data, comparator[, axis, …])	Calculate the relative extrema of *data*.
find_peaks(x[, height, threshold, distance, …])	Find peaks inside a signal based on peak properties.
find_peaks_cwt(vector, widths[, wavelet, …])	Find peaks in a 1-D array with wavelet transformation.
peak_prominences(x, peaks[, wlen])	Calculate the prominence of each peak in a signal.
peak_widths(x, peaks[, rel_height, …])	Calculate the width of each peak in a signal.

scipy.signal.argrelmin

scipy.signal.**argrelmin**(*data*, *axis=0*, *order=1*, *mode='clip'*)

Calculate the relative minima of *data*.

Parameters

data [ndarray] Array in which to find the relative minima.

axis [int, optional] Axis over which to select from *data*. Default is 0.

order [int, optional] How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.

mode [str, optional] How the edges of the vector are treated. Available options are 'wrap' (wrap around) or 'clip' (treat overflow as the same as the last (or first) element). Default 'clip'. See numpy.take.

Returns

extrema [tuple of ndarrays] Indices of the minima in arrays of integers. `extrema[k]` is the array of indices of axis *k* of *data*. Note that the return value is a tuple even when *data* is 1-D.

See also:

argrelextrema, **argrelmax**, **find_peaks**

Notes

This function uses *argrelextrema* with np.less as comparator. Therefore, it requires a strict inequality on both sides of a value to consider it a minimum. This means flat minima (more than one sample wide) are not detected. In case of 1-D *data* *find_peaks* can be used to detect all local minima, including flat ones, by calling it with negated *data*.

New in version 0.11.0.

Examples

```
>>> from scipy.signal import argrelmin
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelmin(x)
(array([1, 5]),)
>>> y = np.array([[1, 2, 1, 2],
...               [2, 2, 0, 0],
...               [5, 3, 4, 4]])
...
```

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```
>>> argrelmin(y, axis=1)
(array([0, 2]), array([2, 1]))
```

scipy.signal.argrelmax

scipy.signal.**argrelmax**(*data*, *axis=0*, *order=1*, *mode='clip'*)

Calculate the relative maxima of *data*.

Parameters

data	[ndarray] Array in which to find the relative maxima.
axis	[int, optional] Axis over which to select from *data*. Default is 0.
order	[int, optional] How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.
mode	[str, optional] How the edges of the vector are treated. Available options are 'wrap' (wrap around) or 'clip' (treat overflow as the same as the last (or first) element). Default 'clip'. See `numpy.take`.

Returns

extrema	[tuple of ndarrays] Indices of the maxima in arrays of integers. `extrema[k]` is the array of indices of axis *k* of *data*. Note that the return value is a tuple even when *data* is 1-D.

See also:

argrelextrema, **argrelmin**, **find_peaks**

Notes

This function uses *argrelextrema* with np.greater as comparator. Therefore, it requires a strict inequality on both sides of a value to consider it a maximum. This means flat maxima (more than one sample wide) are not detected. In case of 1-D *data* *find_peaks* can be used to detect all local maxima, including flat ones.

New in version 0.11.0.

Examples

```
>>> from scipy.signal import argrelmax
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelmax(x)
(array([3, 6]),)
>>> y = np.array([[1, 2, 1, 2],
...               [2, 2, 0, 0],
...               [5, 3, 4, 4]])
...
>>> argrelmax(y, axis=1)
(array([0]), array([1]))
```

scipy.signal.argrelextrema

scipy.signal.**argrelextrema**(*data*, *comparator*, *axis=0*, *order=1*, *mode='clip'*)

Calculate the relative extrema of *data*.

Parameters

data [ndarray] Array in which to find the relative extrema.

comparator [callable] Function to use to compare two data points. Should take two arrays as arguments.

axis [int, optional] Axis over which to select from *data*. Default is 0.

order [int, optional] How many points on each side to use for the comparison to consider `comparator(n, n+x)` to be True.

mode [str, optional] How the edges of the vector are treated. 'wrap' (wrap around) or 'clip' (treat overflow as the same as the last (or first) element). Default is 'clip'. See `numpy.take`.

Returns

extrema [tuple of ndarrays] Indices of the maxima in arrays of integers. `extrema[k]` is the array of indices of axis *k* of *data*. Note that the return value is a tuple even when *data* is 1-D.

See also:

argrelmin, **argrelmax**

Notes

New in version 0.11.0.

Examples

```
>>> from scipy.signal import argrelextrema
>>> x = np.array([2, 1, 2, 3, 2, 0, 1, 0])
>>> argrelextrema(x, np.greater)
(array([3, 6]),)
>>> y = np.array([[1, 2, 1, 2],
...               [2, 2, 0, 0],
...               [5, 3, 4, 4]])
...
>>> argrelextrema(y, np.less, axis=1)
(array([0, 2]), array([2, 1]))
```

scipy.signal.find_peaks

scipy.signal.**find_peaks**(*x*, *height=None*, *threshold=None*, *distance=None*, *prominence=None*, *width=None*, *wlen=None*, *rel_height=0.5*, *plateau_size=None*)

Find peaks inside a signal based on peak properties.

This function takes a 1-D array and finds all local maxima by simple comparison of neighboring values. Optionally, a subset of these peaks can be selected by specifying conditions for a peak's properties.

Parameters

x [sequence] A signal with peaks.

height [number or ndarray or sequence, optional] Required height of peaks. Either a number, `None`, an array matching *x* or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied, as the maximal required height.

threshold [number or ndarray or sequence, optional] Required threshold of peaks, the vertical distance to its neighboring samples. Either a number, `None`, an array matching *x* or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied, as the maximal required threshold.

distance [number, optional] Required minimal horizontal distance (>= 1) in samples between neighbouring peaks. Smaller peaks are removed first until the condition is fulfilled for all remaining peaks.

prominence
[number or ndarray or sequence, optional] Required prominence of peaks. Either a number, `None`, an array matching *x* or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied, as the maximal required prominence.

width [number or ndarray or sequence, optional] Required width of peaks in samples. Either a number, `None`, an array matching *x* or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied, as the maximal required width.

wlen [int, optional] Used for calculation of the peaks prominences, thus it is only used if one of the arguments *prominence* or *width* is given. See argument *wlen* in `peak_prominences` for a full description of its effects.

rel_height [float, optional] Used for calculation of the peaks width, thus it is only used if *width* is given. See argument *rel_height* in `peak_widths` for a full description of its effects.

plateau_size
[number or ndarray or sequence, optional] Required size of the flat top of peaks in samples. Either a number, `None`, an array matching *x* or a 2-element sequence of the former. The first element is always interpreted as the minimal and the second, if supplied as the maximal required plateau size.
New in version 1.2.0.

Returns

peaks [ndarray] Indices of peaks in *x* that satisfy all given conditions.

properties [dict] A dictionary containing properties of the returned peaks which were calculated as intermediate results during evaluation of the specified conditions:

- **'peak_heights'**
  If *height* is given, the height of each peak in *x*.
- **'left_thresholds', 'right_thresholds'**
  If *threshold* is given, these keys contain a peaks vertical distance to its neighbouring samples.
- **'prominences', 'right_bases', 'left_bases'**
  If *prominence* is given, these keys are accessible. See `peak_prominences` for a description of their content.
- **'width_heights', 'left_ips', 'right_ips'**
  If *width* is given, these keys are accessible. See `peak_widths` for a description of their content.
- **'plateau_sizes', left_edges', 'right_edges'**
  If *plateau_size* is given, these keys are accessible and contain the indices of a peak's edges (edges are still part of the plateau) and the calculated plateau sizes.
  New in version 1.2.0.

To calculate and return properties without excluding peaks, provide the open interval `(None, None)` as a value to the appropriate argument (excluding *distance*).

Warns

PeakPropertyWarning
Raised if a peak's properties have unexpected values (see `peak_prominences` and `peak_widths`).

Warning: This function may return unexpected results for data containing NaNs. To avoid this, NaNs should either be removed or replaced.

See also:

`find_peaks_cwt`

Find peaks using the wavelet transformation.

`peak_prominences`

Directly calculate the prominence of peaks.

`peak_widths`

Directly calculate the width of peaks.

Notes

In the context of this function, a peak or local maximum is defined as any sample whose two direct neighbours have a smaller amplitude. For flat peaks (more than one sample of equal amplitude wide) the index of the middle sample is returned (rounded down in case the number of samples is even). For noisy signals the peak locations can be off because the noise might change the position of local maxima. In those cases consider smoothing the signal before searching for peaks or use other peak finding and fitting methods (like *find_peaks_cwt*).

Some additional comments on specifying conditions:

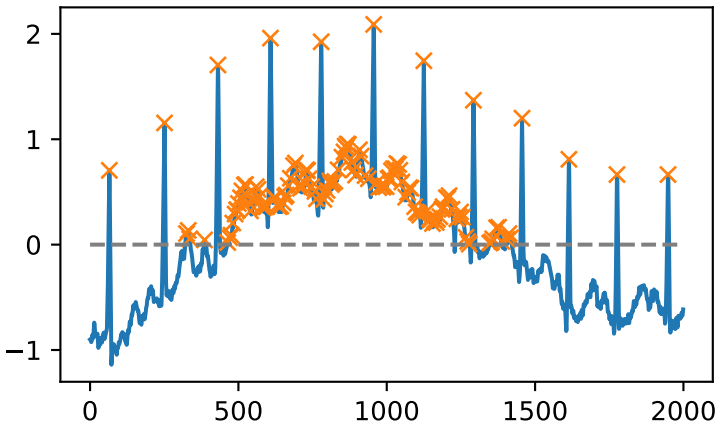
- Almost all conditions (excluding *distance*) can be given as half-open or closed intervals, e.g., `1` or `(1, None)` defines the half-open interval $[1, \infty]$ while `(None, 1)` defines the interval $[-\infty, 1]$. The open interval `(None, None)` can be specified as well, which returns the matching properties without exclusion of peaks.
- The border is always included in the interval used to select valid peaks.
- For several conditions the interval borders can be specified with arrays matching *x* in shape which enables dynamic constrains based on the sample position.
- The conditions are evaluated in the following order: *plateau_size*, *height*, *threshold*, *distance*, *prominence*, *width*. In most cases this order is the fastest one because faster operations are applied first to reduce the number of peaks that need to be evaluated later.
- While indices in *peaks* are guaranteed to be at least *distance* samples apart, edges of flat peaks may be closer than the allowed *distance*.
- Use *wlen* to reduce the time it takes to evaluate the conditions for *prominence* or *width* if *x* is large or has many local maxima (see *peak_prominences*).

New in version 1.1.0.

Examples

To demonstrate this function's usage we use a signal *x* supplied with SciPy (see *scipy.misc.electrocardiogram*). Let's find all peaks (local maxima) in *x* whose amplitude lies above 0.

```
>>> import matplotlib.pyplot as plt
>>> from scipy.misc import electrocardiogram
>>> from scipy.signal import find_peaks
>>> x = electrocardiogram()[2000:4000]
>>> peaks, _ = find_peaks(x, height=0)
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.plot(np.zeros_like(x), "--", color="gray")
>>> plt.show()
```



We can select peaks below 0 with `height=(None, 0)` or use arrays matching *x* in size to reflect a changing condition for different parts of the signal.

```
>>> border = np.sin(np.linspace(0, 3 * np.pi, x.size))
>>> peaks, _ = find_peaks(x, height=(-border, border))
>>> plt.plot(x)
>>> plt.plot(-border, "--", color="gray")
>>> plt.plot(border, ":", color="gray")
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.show()
```

Another useful condition for periodic signals can be given with the *distance* argument. In this case, we can easily select the positions of QRS complexes within the electrocardiogram (ECG) by demanding a distance of at least 150 samples.

```
>>> peaks, _ = find_peaks(x, distance=150)
>>> np.diff(peaks)
array([186, 180, 177, 171, 177, 169, 167, 164, 158, 162, 172])
>>> plt.plot(x)
```

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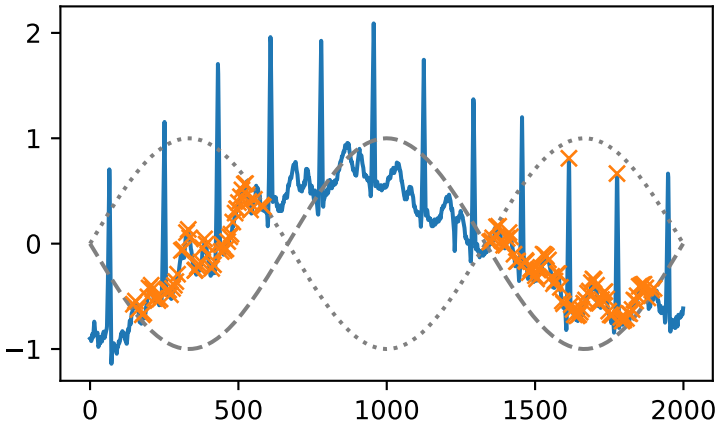

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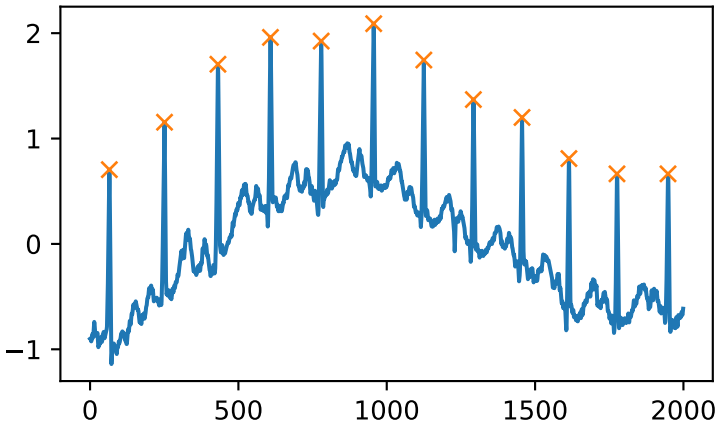
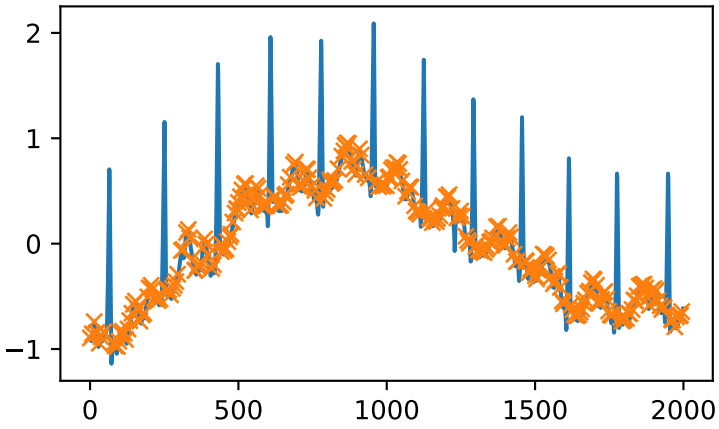
```
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.show()
```



Especially for noisy signals peaks can be easily grouped by their prominence (see *peak_prominences*). E.g., we can select all peaks except for the mentioned QRS complexes by limiting the allowed prominence to 0.6.

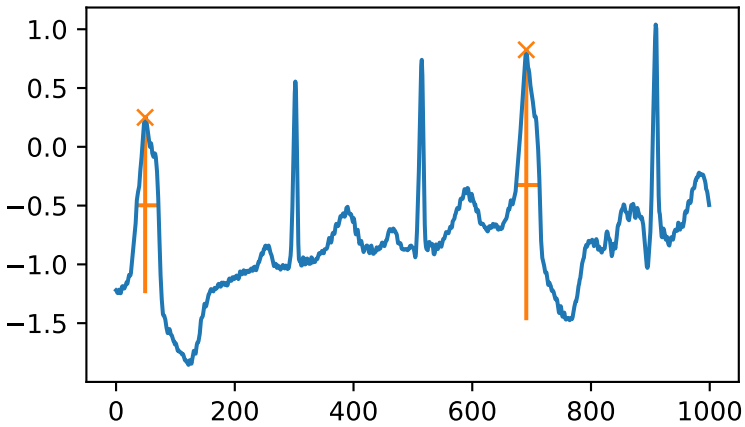
```
>>> peaks, properties = find_peaks(x, prominence=(None, 0.6))
>>> properties["prominences"].max()
0.5049999999999999
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.show()
```

And, finally, let's examine a different section of the ECG which contains beat forms of different shape. To select



only the atypical heart beats, we combine two conditions: a minimal prominence of 1 and width of at least 20 samples.

```
>>> x = electrocardiogram()[17000:18000]
>>> peaks, properties = find_peaks(x, prominence=1, width=20)
>>> properties["prominences"], properties["widths"]
(array([1.495, 2.3  ]), array([36.93773946, 39.32723577]))
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.vlines(x=peaks, ymin=x[peaks] - properties["prominences"],
...            ymax = x[peaks], color = "C1")
>>> plt.hlines(y=properties["width_heights"], xmin=properties["left_ips"],
...            xmax=properties["right_ips"], color = "C1")
>>> plt.show()
```



scipy.signal.find_peaks_cwt

scipy.signal.**find_peaks_cwt**(*vector*, *widths*, *wavelet=None*, *max_distances=None*, *gap_thresh=None*, *min_length=None*, *min_snr=1*, *noise_perc=10*, *window_size=None*)

Find peaks in a 1-D array with wavelet transformation.

The general approach is to smooth *vector* by convolving it with *wavelet(width)* for each width in *widths*. Relative maxima which appear at enough length scales, and with sufficiently high SNR, are accepted.

Parameters

vector [ndarray] 1-D array in which to find the peaks.

widths [float or sequence] Single width or 1-D array-like of widths to use for calculating the CWT matrix. In general, this range should cover the expected width of peaks of interest.

wavelet [callable, optional] Should take two parameters and return a 1-D array to convolve with *vector*. The first parameter determines the number of points of the returned wavelet array, the second parameter is the scale (*width*) of the wavelet. Should be normalized and symmetric. Default is the ricker wavelet.

max_distances
[ndarray, optional] At each row, a ridge line is only connected if the relative max at row[n] is within `max_distances[n]` from the relative max at `row[n+1]`. Default value is `widths/4`.

gap_thresh
[float, optional] If a relative maximum is not found within *max_distances*, there will be a gap. A ridge line is discontinued if there are more than *gap_thresh* points without connecting a new relative maximum. Default is the first value of the widths array i.e. widths[0].

min_length
[int, optional] Minimum length a ridge line needs to be acceptable. Default is `cwt.shape[0] / 4`, ie 1/4-th the number of widths.

min_snr [float, optional] Minimum SNR ratio. Default 1. The signal is the value of the cwt matrix at the shortest length scale (`cwt[0, loc]`), the noise is the *noise_perc`th percentile of datapoints contained within a window of `window_size* around `cwt[0, loc]`.

noise_perc
[float, optional] When calculating the noise floor, percentile of data points examined below which to consider noise. Calculated using *stats.scoreatpercentile*. Default is 10.

window_size
[int, optional] Size of window to use to calculate noise floor. Default is `cwt.shape[1] / 20`.

Returns

peaks_indices
[ndarray] Indices of the locations in the *vector* where peaks were found. The list is sorted.

See also:

cwt

Continuous wavelet transform.

find_peaks

Find peaks inside a signal based on peak properties.

Notes

This approach was designed for finding sharp peaks among noisy data, however with proper parameter selection it should function well for different peak shapes.

The algorithm is as follows:

1. Perform a continuous wavelet transform on *vector*, for the supplied *widths*. This is a convolution of *vector* with *wavelet(width)* for each width in *widths*. See `cwt`.
2. Identify "ridge lines" in the cwt matrix. These are relative maxima at each row, connected across adjacent rows. See identify_ridge_lines
3. Filter the ridge_lines using filter_ridge_lines.

New in version 0.11.0.

References

[1]

Examples

```
>>> from scipy import signal
>>> xs = np.arange(0, np.pi, 0.05)
>>> data = np.sin(xs)
>>> peakind = signal.find_peaks_cwt(data, np.arange(1,10))
>>> peakind, xs[peakind], data[peakind]
([32], array([ 1.6]), array([ 0.9995736]))
```

scipy.signal.peak_prominences

`scipy.signal.`**`peak_prominences`**(*x*, *peaks*, *wlen=None*)

Calculate the prominence of each peak in a signal.

The prominence of a peak measures how much a peak stands out from the surrounding baseline of the signal and is defined as the vertical distance between the peak and its lowest contour line.

Parameters

x [sequence] A signal with peaks.

peaks [sequence] Indices of peaks in *x*.

wlen [int, optional] A window length in samples that optionally limits the evaluated area for each peak to a subset of *x*. The peak is always placed in the middle of the window therefore the given length is rounded up to the next odd integer. This parameter can speed up the calculation (see Notes).

Returns

prominences
[ndarray] The calculated prominences for each peak in *peaks*.

left_bases, right_bases
[ndarray] The peaks' bases as indices in *x* to the left and right of each peak. The higher base of each pair is a peak's lowest contour line.

Raises

ValueError
If a value in *peaks* is an invalid index for *x*.

Warns

PeakPropertyWarning
For indices in *peaks* that don't point to valid local maxima in *x*, the returned prominence will be 0 and this warning is raised. This also happens if *wlen* is smaller than the plateau size of a peak.

Warning: This function may return unexpected results for data containing NaNs. To avoid this, NaNs should either be removed or replaced.

See also:

`find_peaks`

Find peaks inside a signal based on peak properties.

`peak_widths`

Calculate the width of peaks.

Notes

Strategy to compute a peak's prominence:

1. Extend a horizontal line from the current peak to the left and right until the line either reaches the window border (see *wlen*) or intersects the signal again at the slope of a higher peak. An intersection with a peak of the same height is ignored.
2. On each side find the minimal signal value within the interval defined above. These points are the peak's bases.
3. The higher one of the two bases marks the peak's lowest contour line. The prominence can then be calculated as the vertical difference between the peaks height itself and its lowest contour line.

Searching for the peak's bases can be slow for large *x* with periodic behavior because large chunks or even the full signal need to be evaluated for the first algorithmic step. This evaluation area can be limited with the parameter *wlen* which restricts the algorithm to a window around the current peak and can shorten the calculation time if the window length is short in relation to *x*. However, this may stop the algorithm from finding the true global contour line if the peak's true bases are outside this window. Instead, a higher contour line is found within the restricted window leading to a smaller calculated prominence. In practice, this is only relevant for the highest set of peaks in *x*. This behavior may even be used intentionally to calculate "local" prominences.

New in version 1.1.0.

References

[1]

Examples

```
>>> from scipy.signal import find_peaks, peak_prominences
>>> import matplotlib.pyplot as plt
```

Create a test signal with two overlayed harmonics

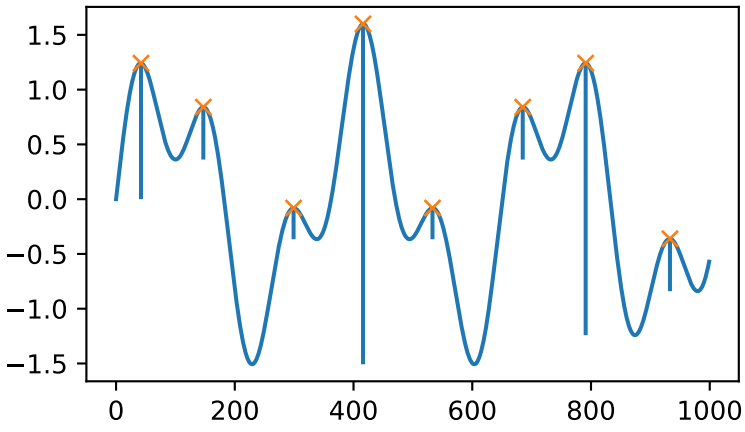
```
>>> x = np.linspace(0, 6 * np.pi, 1000)
>>> x = np.sin(x) + 0.6 * np.sin(2.6 * x)
```

Find all peaks and calculate prominences

```
>>> peaks, _ = find_peaks(x)
>>> prominences = peak_prominences(x, peaks)[0]
>>> prominences
array([1.24159486, 0.47840168, 0.28470524, 3.10716793, 0.284603  ,
       0.47822491, 2.48340261, 0.47822491])
```

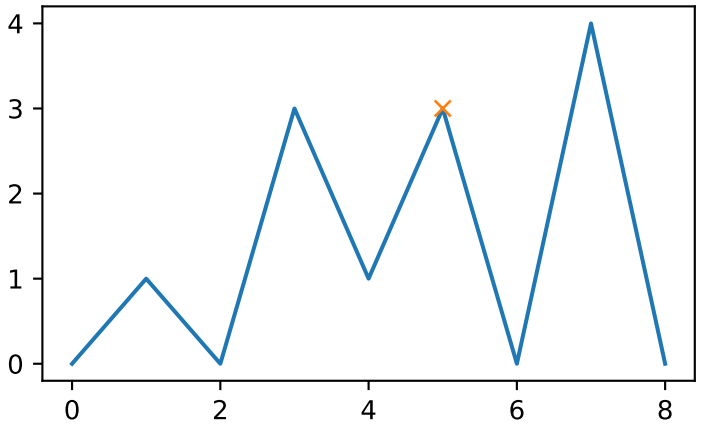
Calculate the height of each peak's contour line and plot the results

```
>>> contour_heights = x[peaks] - prominences
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.vlines(x=peaks, ymin=contour_heights, ymax=x[peaks])
>>> plt.show()
```



Let's evaluate a second example that demonstrates several edge cases for one peak at index 5.

```
>>> x = np.array([0, 1, 0, 3, 1, 3, 0, 4, 0])
>>> peaks = np.array([5])
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.show()
```




```
>>> peak_prominences(x, peaks)  # -> (prominences, left_bases, right_
↪bases)
(array([3.]), array([2]), array([6]))
```

Note how the peak at index 3 of the same height is not considered as a border while searching for the left base. Instead, two minima at 0 and 2 are found in which case the one closer to the evaluated peak is always chosen. On the right side, however, the base must be placed at 6 because the higher peak represents the right border to the evaluated area.

```
>>> peak_prominences(x, peaks, wlen=3.1)
(array([2.]), array([4]), array([6]))
```

Here, we restricted the algorithm to a window from 3 to 7 (the length is 5 samples because *wlen* was rounded up to the next odd integer). Thus, the only two candidates in the evaluated area are the two neighboring samples and a smaller prominence is calculated.

scipy.signal.peak_widths

`scipy.signal.`**`peak_widths`**(*x*, *peaks*, *rel_height=0.5*, *prominence_data=None*, *wlen=None*)

Calculate the width of each peak in a signal.

This function calculates the width of a peak in samples at a relative distance to the peak's height and prominence.

Parameters

x	[sequence] A signal with peaks.
peaks	[sequence] Indices of peaks in *x*.
rel_height	[float, optional] Chooses the relative height at which the peak width is measured as a percentage of its prominence. 1.0 calculates the width of the peak at its lowest contour line

while 0.5 evaluates at half the prominence height. Must be at least 0. See notes for further explanation.

prominence_data
: [tuple, optional] A tuple of three arrays matching the output of `peak_prominences` when called with the same arguments *x* and *peaks*. This data are calculated internally if not provided.

wlen
: [int, optional] A window length in samples passed to `peak_prominences` as an optional argument for internal calculation of *prominence_data*. This argument is ignored if *prominence_data* is given.

Returns

widths
: [ndarray] The widths for each peak in samples.

width_heights
: [ndarray] The height of the contour lines at which the *widths* where evaluated.

left_ips, right_ips
: [ndarray] Interpolated positions of left and right intersection points of a horizontal line at the respective evaluation height.

Raises

ValueError
: If *prominence_data* is supplied but doesn't satisfy the condition `0 <= left_base <= peak <= right_base < x.shape[0]` for each peak, has the wrong dtype, is not C-contiguous or does not have the same shape.

Warns

PeakPropertyWarning
: Raised if any calculated width is 0. This may stem from the supplied *prominence_data* or if *rel_height* is set to 0.

Warning: This function may return unexpected results for data containing NaNs. To avoid this, NaNs should either be removed or replaced.

See also:

`find_peaks`

Find peaks inside a signal based on peak properties.

`peak_prominences`

Calculate the prominence of peaks.

Notes

The basic algorithm to calculate a peak's width is as follows:

- Calculate the evaluation height h_{eval} with the formula $h_{eval} = h_{Peak} - P \cdot R$, where h_{Peak} is the height of the peak itself, P is the peak's prominence and R a positive ratio specified with the argument *rel_height*.
- Draw a horizontal line at the evaluation height to both sides, starting at the peak's current vertical position until the lines either intersect a slope, the signal border or cross the vertical position of the peak's base (see `peak_prominences` for an definition). For the first case, intersection with the signal, the true intersection point is estimated with linear interpolation.

- Calculate the width as the horizontal distance between the chosen endpoints on both sides. As a consequence of this the maximal possible width for each peak is the horizontal distance between its bases.

As shown above to calculate a peak's width its prominence and bases must be known. You can supply these yourself with the argument *prominence_data*. Otherwise, they are internally calculated (see *peak_prominences*).

New in version 1.1.0.

Examples

```
>>> from scipy.signal import chirp, find_peaks, peak_widths
>>> import matplotlib.pyplot as plt
```

Create a test signal with two overlayed harmonics

```
>>> x = np.linspace(0, 6 * np.pi, 1000)
>>> x = np.sin(x) + 0.6 * np.sin(2.6 * x)
```

Find all peaks and calculate their widths at the relative height of 0.5 (contour line at half the prominence height) and 1 (at the lowest contour line at full prominence height).

```
>>> peaks, _ = find_peaks(x)
>>> results_half = peak_widths(x, peaks, rel_height=0.5)
>>> results_half[0]  # widths
array([ 64.25172825,  41.29465463,  35.46943289, 104.71586081,
        35.46729324,  41.30429622, 181.93835853,  45.37078546])
>>> results_full = peak_widths(x, peaks, rel_height=1)
>>> results_full[0]  # widths
array([181.9396084 ,  72.99284945,  61.28657872, 373.84622694,
    61.78404617,  72.48822812, 253.09161876,  79.36860878])
```

Plot signal, peaks and contour lines at which the widths where calculated

```
>>> plt.plot(x)
>>> plt.plot(peaks, x[peaks], "x")
>>> plt.hlines(*results_half[1:], color="C2")
>>> plt.hlines(*results_full[1:], color="C3")
>>> plt.show()
```

Spectral analysis

periodogram(x[, fs, window, nfft, detrend, …])	Estimate power spectral density using a periodogram.
welch(x[, fs, window, nperseg, noverlap, …])	Estimate power spectral density using Welch's method.
csd(x, y[, fs, window, nperseg, noverlap, …])	Estimate the cross power spectral density, Pxy, using Welch's method.
coherence(x, y[, fs, window, nperseg, …])	Estimate the magnitude squared coherence estimate, Cxy, of discrete-time signals X and Y using Welch's method.
spectrogram(x[, fs, window, nperseg, …])	Compute a spectrogram with consecutive Fourier transforms.
lombscargle(x, y, freqs)	Computes the Lomb-Scargle periodogram.

continues on next page

Table 173 – continued from previous page

`vectorstrength`(events, period)	Determine the vector strength of the events corresponding to the given period.
`stft`(x[, fs, window, nperseg, noverlap, …])	Compute the Short Time Fourier Transform (STFT).
`istft`(Zxx[, fs, window, nperseg, noverlap, …])	Perform the inverse Short Time Fourier transform (iSTFT).
`check_COLA`(window, nperseg, noverlap[, tol])	Check whether the Constant OverLap Add (COLA) constraint is met.
`check_NOLA`(window, nperseg, noverlap[, tol])	Check whether the Nonzero Overlap Add (NOLA) constraint is met.

scipy.signal.periodogram

scipy.signal.**periodogram**(*x*, *fs=1.0*, *window='boxcar'*, *nfft=None*, *detrend='constant'*, *return_onesided=True*, *scaling='density'*, *axis=- 1*)

Estimate power spectral density using a periodogram.

Parameters

x [array_like] Time series of measurement values

fs [float, optional] Sampling frequency of the *x* time series. Defaults to 1.0.

window [str or tuple or array_like, optional] Desired window to use. If *window* is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg. Defaults to 'boxcar'.

nfft [int, optional] Length of the FFT used. If *None* the length of *x* will be used.

detrend [str or function or *False*, optional] Specifies how to detrend each segment. If `detrend` is a string, it is passed as the *type* argument to the `detrend` function. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is *False*, no detrending is done. Defaults to 'constant'.

return_onesided [bool, optional] If *True*, return a one-sided spectrum for real data. If *False* return a two-sided spectrum. Defaults to *True*, but for complex data, a two-sided spectrum is always returned.

scaling [{ 'density', 'spectrum' }, optional] Selects between computing the power spectral density ('density') where *Pxx* has units of V**2/Hz and computing the power spectrum ('spectrum') where *Pxx* has units of V**2, if *x* is measured in V and *fs* is measured in Hz. Defaults to 'density'

axis [int, optional] Axis along which the periodogram is computed; the default is over the last axis (i.e. `axis=-1`).

Returns

f [ndarray] Array of sample frequencies.

Pxx [ndarray] Power spectral density or power spectrum of *x*.

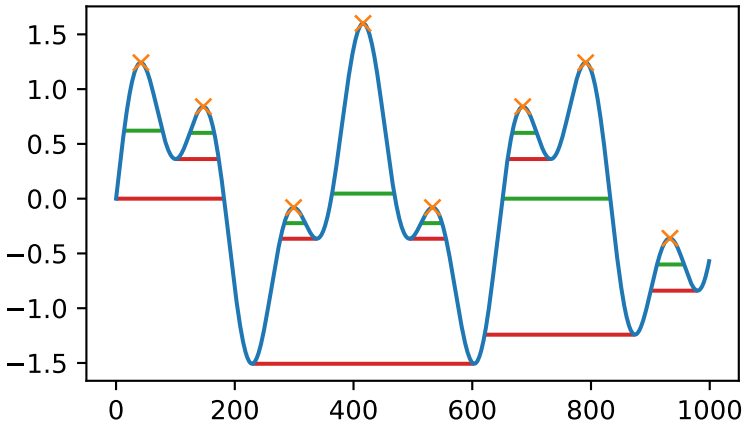
See also:

welch

Estimate power spectral density using Welch's method

lombscargle

Lomb-Scargle periodogram for unevenly sampled data



Notes

New in version 0.12.0.

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

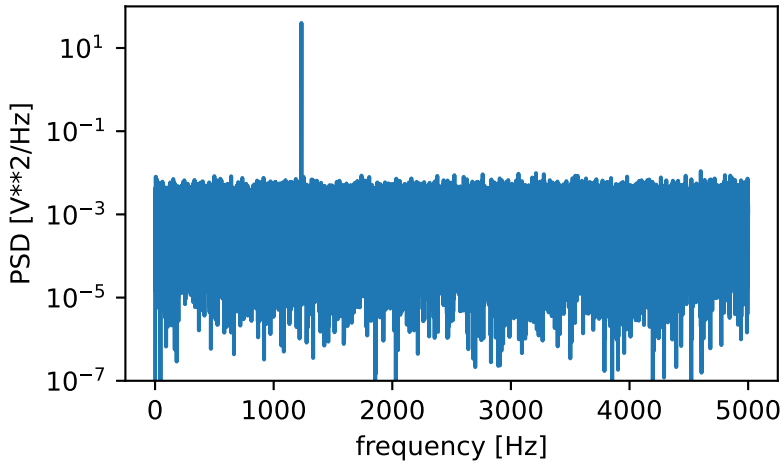
Generate a test signal, a 2 Vrms sine wave at 1234 Hz, corrupted by 0.001 V**2/Hz of white noise sampled at 10 kHz.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += rng.normal(scale=np.sqrt(noise_power), size=time.shape)
```

Compute and plot the power spectral density.

```
>>> f, Pxx_den = signal.periodogram(x, fs)
>>> plt.semilogy(f, Pxx_den)
>>> plt.ylim([1e-7, 1e2])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD [V**2/Hz]')
>>> plt.show()
```

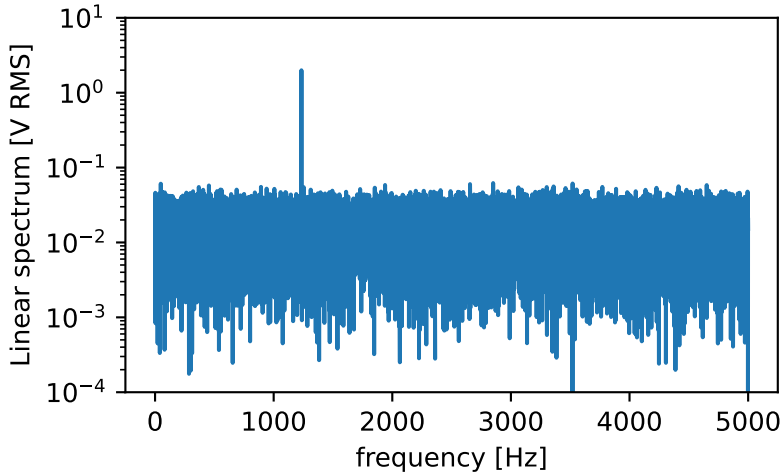
If we average the last half of the spectral density, to exclude the peak, we can recover the noise power on the signal.




```
>>> np.mean(Pxx_den[25000:])
0.000985320699252543
```

Now compute and plot the power spectrum.

```
>>> f, Pxx_spec = signal.periodogram(x, fs, 'flattop', scaling='spectrum')
>>> plt.figure()
>>> plt.semilogy(f, np.sqrt(Pxx_spec))
>>> plt.ylim([1e-4, 1e1])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Linear spectrum [V RMS]')
>>> plt.show()
```



The peak height in the power spectrum is an estimate of the RMS amplitude.

```
>>> np.sqrt(Pxx_spec.max())
2.0077340678640727
```

scipy.signal.welch

scipy.signal.**welch**(*x*, *fs=1.0*, *window='hann'*, *nperseg=None*, *noverlap=None*, *nfft=None*, *detrend='constant'*, *return_onesided=True*, *scaling='density'*, *axis=-1*, *average='mean'*)

Estimate power spectral density using Welch's method.

Welch's method [1] computes an estimate of the power spectral density by dividing the data into overlapping segments, computing a modified periodogram for each segment and averaging the periodograms.

Parameters

x [array_like] Time series of measurement values

fs [float, optional] Sampling frequency of the *x* time series. Defaults to 1.0.

window [str or tuple or array_like, optional] Desired window to use. If *window* is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg. Defaults to a Hann window.

nperseg [int, optional] Length of each segment. Defaults to None, but if window is str or tuple, is set to 256, and if window is array_like, is set to the length of the window.

noverlap [int, optional] Number of points to overlap between segments. If *None*, `noverlap = nperseg // 2`. Defaults to *None*.

nfft [int, optional] Length of the FFT used, if a zero padded FFT is desired. If *None*, the FFT length is *nperseg*. Defaults to *None*.

detrend [str or function or *False*, optional] Specifies how to detrend each segment. If `detrend` is a string, it is passed as the *type* argument to the `detrend` function. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is *False*, no detrending is done. Defaults to 'constant'.

return_onesided [bool, optional] If *True*, return a one-sided spectrum for real data. If *False* return a two-sided spectrum. Defaults to *True*, but for complex data, a two-sided spectrum is always returned.

scaling [{ 'density', 'spectrum' }, optional] Selects between computing the power spectral density ('density') where *Pxx* has units of V**2/Hz and computing the power spectrum ('spectrum') where *Pxx* has units of V**2, if *x* is measured in V and *fs* is measured in Hz. Defaults to 'density'

axis [int, optional] Axis along which the periodogram is computed; the default is over the last axis (i.e. `axis=-1`).

average [{ 'mean', 'median' }, optional] Method to use when averaging periodograms. Defaults to 'mean'.
New in version 1.2.0.

Returns

f [ndarray] Array of sample frequencies.

Pxx [ndarray] Power spectral density or power spectrum of x.

See also:

`periodogram`

Simple, optionally modified periodogram

lombscargle

Lomb-Scargle periodogram for unevenly sampled data

Notes

An appropriate amount of overlap will depend on the choice of window and on your requirements. For the default Hann window an overlap of 50% is a reasonable trade off between accurately estimating the signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

If *noverlap* is 0, this method is equivalent to Bartlett's method [2].

New in version 0.12.0.

References

[1], [2]

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

Generate a test signal, a 2 Vrms sine wave at 1234 Hz, corrupted by 0.001 V**2/Hz of white noise sampled at 10 kHz.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2*np.sqrt(2)
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> x = amp*np.sin(2*np.pi*freq*time)
>>> x += rng.normal(scale=np.sqrt(noise_power), size=time.shape)
```

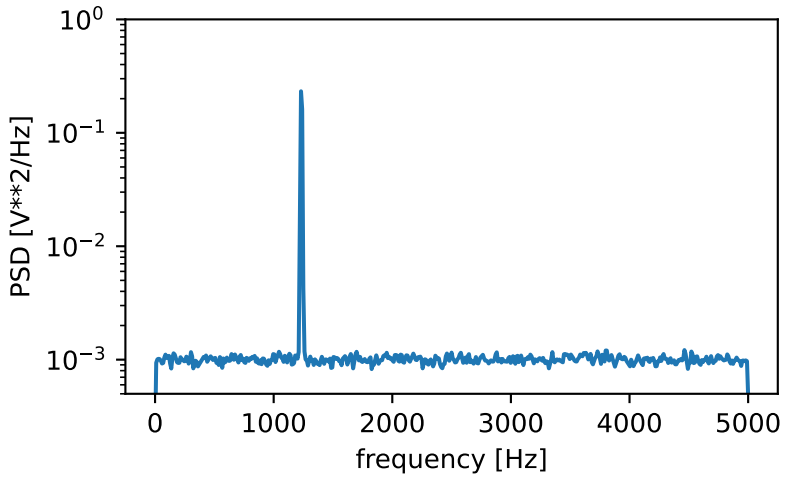
Compute and plot the power spectral density.

```
>>> f, Pxx_den = signal.welch(x, fs, nperseg=1024)
>>> plt.semilogy(f, Pxx_den)
>>> plt.ylim([0.5e-3, 1])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD [V**2/Hz]')
>>> plt.show()
```

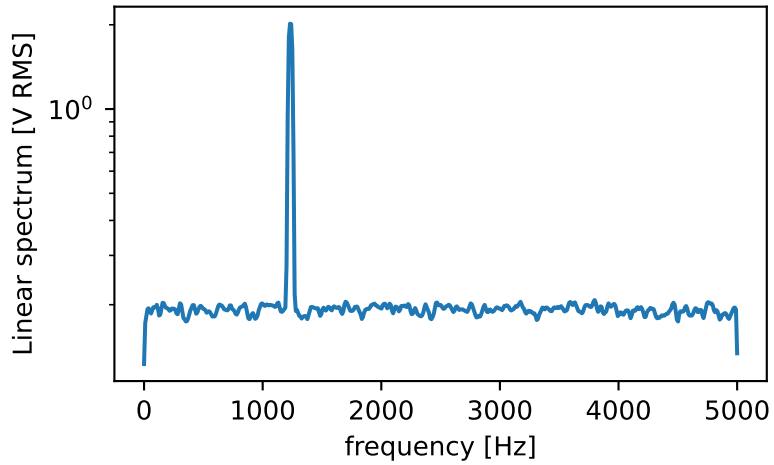
If we average the last half of the spectral density, to exclude the peak, we can recover the noise power on the signal.

```
>>> np.mean(Pxx_den[256:])
0.0009924865443739191
```

Now compute and plot the power spectrum.




```
>>> f, Pxx_spec = signal.welch(x, fs, 'flattop', 1024, scaling='spectrum')
>>> plt.figure()
>>> plt.semilogy(f, np.sqrt(Pxx_spec))
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Linear spectrum [V RMS]')
>>> plt.show()
```

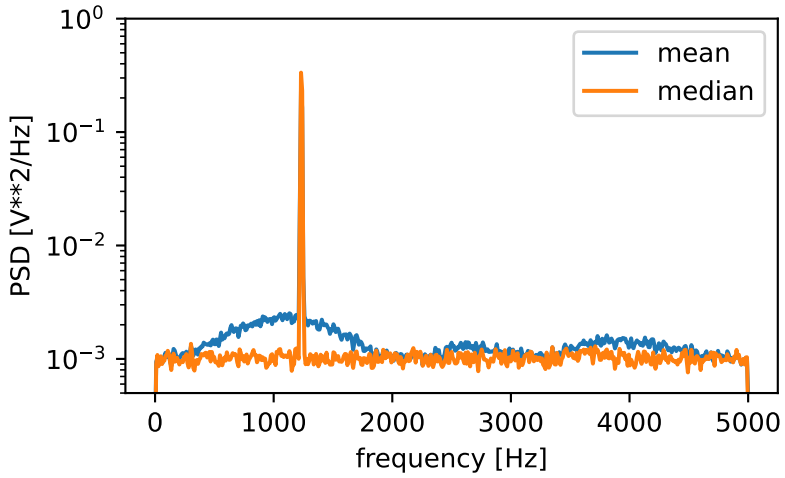


The peak height in the power spectrum is an estimate of the RMS amplitude.

```
>>> np.sqrt(Pxx_spec.max())
2.0077340678640727
```

If we now introduce a discontinuity in the signal, by increasing the amplitude of a small portion of the signal by 50, we can see the corruption of the mean average power spectral density, but using a median average better estimates the normal behaviour.

```
>>> x[int(N//2):int(N//2)+10] *= 50.
>>> f, Pxx_den = signal.welch(x, fs, nperseg=1024)
>>> f_med, Pxx_den_med = signal.welch(x, fs, nperseg=1024, average='median
↪')
>>> plt.semilogy(f, Pxx_den, label='mean')
>>> plt.semilogy(f_med, Pxx_den_med, label='median')
>>> plt.ylim([0.5e-3, 1])
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('PSD [V**2/Hz]')
>>> plt.legend()
>>> plt.show()
```



scipy.signal.csd

scipy.signal.**csd**(*x*, *y*, *fs=1.0*, *window='hann'*, *nperseg=None*, *noverlap=None*, *nfft=None*, *detrend='constant'*, *return_onesided=True*, *scaling='density'*, *axis=- 1*, *average='mean'*)

Estimate the cross power spectral density, Pxy, using Welch's method.

Parameters

x [array_like] Time series of measurement values

y [array_like] Time series of measurement values

fs [float, optional] Sampling frequency of the *x* and *y* time series. Defaults to 1.0.

window [str or tuple or array_like, optional] Desired window to use. If *window* is a string or tuple, it is passed to *get_window* to generate the window values, which are DFT-even by default. See *get_window* for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg. Defaults to a Hann window.

nperseg [int, optional] Length of each segment. Defaults to None, but if window is str or tuple, is set to 256, and if window is array_like, is set to the length of the window.

noverlap: int, optional

Number of points to overlap between segments. If *None*, `noverlap = nperseg // 2`. Defaults to *None*.

nfft [int, optional] Length of the FFT used, if a zero padded FFT is desired. If *None*, the FFT length is *nperseg*. Defaults to *None*.

detrend [str or function or *False*, optional] Specifies how to detrend each segment. If `detrend` is a string, it is passed as the *type* argument to the `detrend` function. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is *False*, no detrending is done. Defaults to 'constant'.

return_onesided [bool, optional] If *True*, return a one-sided spectrum for real data. If *False* return a two-sided spectrum. Defaults to *True*, but for complex data, a two-sided spectrum is always returned.

scaling [{ 'density', 'spectrum' }, optional] Selects between computing the cross spectral density ('density') where *Pxy* has units of V**2/Hz and computing the cross spectrum ('spectrum') where *Pxy* has units of V**2, if *x* and *y* are measured in V and *fs* is measured in Hz. Defaults to 'density'

axis [int, optional] Axis along which the CSD is computed for both inputs; the default is over the last axis (i.e. `axis=-1`).

average [{ 'mean', 'median' }, optional] Method to use when averaging periodograms. If the spectrum is complex, the average is computed separately for the real and imaginary parts. Defaults to 'mean'.
New in version 1.2.0.

Returns

f [ndarray] Array of sample frequencies.

Pxy [ndarray] Cross spectral density or cross power spectrum of x,y.

See also:

periodogram

Simple, optionally modified periodogram

lombscargle

Lomb-Scargle periodogram for unevenly sampled data

welch

Power spectral density by Welch's method. [Equivalent to csd(x,x)]

coherence

Magnitude squared coherence by Welch's method.

Notes

By convention, Pxy is computed with the conjugate FFT of X multiplied by the FFT of Y.

If the input series differ in length, the shorter series will be zero-padded to match.

An appropriate amount of overlap will depend on the choice of window and on your requirements. For the default Hann window an overlap of 50% is a reasonable trade off between accurately estimating the signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

New in version 0.16.0.

References

[1], [2]

Examples

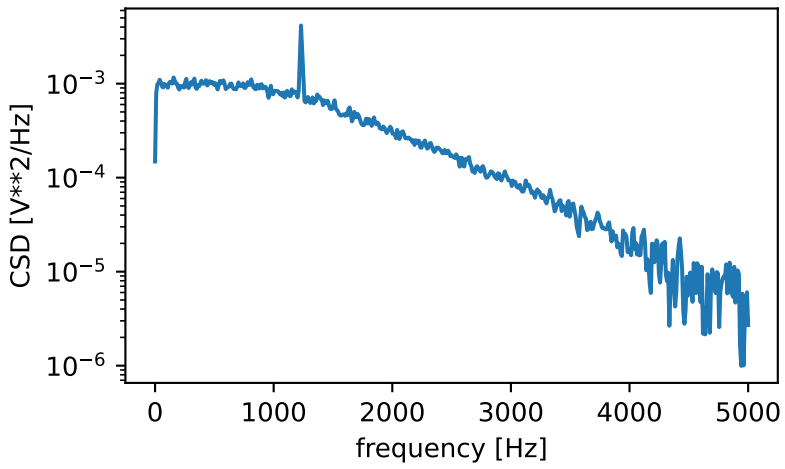
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

Generate two test signals with some common features.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 20
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> b, a = signal.butter(2, 0.25, 'low')
>>> x = rng.normal(scale=np.sqrt(noise_power), size=time.shape)
>>> y = signal.lfilter(b, a, x)
>>> x += amp*np.sin(2*np.pi*freq*time)
>>> y += rng.normal(scale=0.1*np.sqrt(noise_power), size=time.shape)
```

Compute and plot the magnitude of the cross spectral density.

```
>>> f, Pxy = signal.csd(x, y, fs, nperseg=1024)
>>> plt.semilogy(f, np.abs(Pxy))
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('CSD [V**2/Hz]')
>>> plt.show()
```



scipy.signal.coherence

scipy.signal.**coherence**(*x*, *y*, *fs=1.0*, *window='hann'*, *nperseg=None*, *noverlap=None*, *nfft=None*, *detrend='constant'*, *axis=- 1*)

Estimate the magnitude squared coherence estimate, Cxy, of discrete-time signals X and Y using Welch's method.

`Cxy = abs(Pxy)**2/(Pxx*Pyy)`, where *Pxx* and *Pyy* are power spectral density estimates of X and Y, and *Pxy* is the cross spectral density estimate of X and Y.

Parameters

x [array_like] Time series of measurement values

y [array_like] Time series of measurement values

fs [float, optional] Sampling frequency of the *x* and *y* time series. Defaults to 1.0.

window [str or tuple or array_like, optional] Desired window to use. If *window* is a string or tuple, it is passed to *get_window* to generate the window values, which are DFT-even by default. See *get_window* for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg. Defaults to a Hann window.

nperseg [int, optional] Length of each segment. Defaults to None, but if window is str or tuple, is set to 256, and if window is array_like, is set to the length of the window.

noverlap: int, optional
Number of points to overlap between segments. If *None*, `noverlap = nperseg // 2`. Defaults to *None*.

nfft [int, optional] Length of the FFT used, if a zero padded FFT is desired. If *None*, the FFT length is *nperseg*. Defaults to *None*.

detrend [str or function or *False*, optional] Specifies how to detrend each segment. If *detrend* is a string, it is passed as the *type* argument to the *detrend* function. If it is a function, it takes a segment and returns a detrended segment. If *detrend* is *False*, no detrending is done. Defaults to 'constant'.

axis [int, optional] Axis along which the coherence is computed for both inputs; the default is over the last axis (i.e. `axis=-1`).

Returns

f [ndarray] Array of sample frequencies.

Cxy [ndarray] Magnitude squared coherence of x and y.

See also:

periodogram

Simple, optionally modified periodogram

lombscargle

Lomb-Scargle periodogram for unevenly sampled data

welch

Power spectral density by Welch's method.

csd

Cross spectral density by Welch's method.

Notes

An appropriate amount of overlap will depend on the choice of window and on your requirements. For the default Hann window an overlap of 50% is a reasonable trade off between accurately estimating the signal power, while not over counting any of the data. Narrower windows may require a larger overlap.

New in version 0.16.0.

References

[1], [2]

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

Generate two test signals with some common features.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 20
>>> freq = 1234.0
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / fs
>>> b, a = signal.butter(2, 0.25, 'low')
>>> x = rng.normal(scale=np.sqrt(noise_power), size=time.shape)
>>> y = signal.lfilter(b, a, x)
>>> x += amp*np.sin(2*np.pi*freq*time)
>>> y += rng.normal(scale=0.1*np.sqrt(noise_power), size=time.shape)
```

Compute and plot the coherence.

```
>>> f, Cxy = signal.coherence(x, y, fs, nperseg=1024)
>>> plt.semilogy(f, Cxy)
>>> plt.xlabel('frequency [Hz]')
>>> plt.ylabel('Coherence')
>>> plt.show()
```

scipy.signal.spectrogram

scipy.signal.**spectrogram**(*x*, *fs=1.0*, *window=('tukey', 0.25)*, *nperseg=None*, *noverlap=None*, *nfft=None*, *detrend='constant'*, *return_onesided=True*, *scaling='density'*, *axis=- 1*, *mode='psd'*)

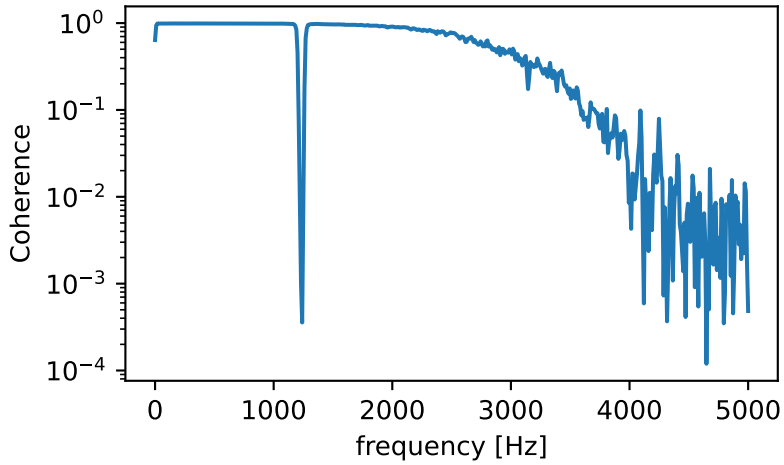
Compute a spectrogram with consecutive Fourier transforms.

Spectrograms can be used as a way of visualizing the change of a nonstationary signal's frequency content over time.

Parameters

x [array_like] Time series of measurement values

fs [float, optional] Sampling frequency of the *x* time series. Defaults to 1.0.



window [str or tuple or array_like, optional] Desired window to use. If *window* is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg. Defaults to a Tukey window with shape parameter of 0.25.

nperseg [int, optional] Length of each segment. Defaults to None, but if window is str or tuple, is set to 256, and if window is array_like, is set to the length of the window.

noverlap [int, optional] Number of points to overlap between segments. If *None*, `noverlap = nperseg // 8`. Defaults to *None*.

nfft [int, optional] Length of the FFT used, if a zero padded FFT is desired. If *None*, the FFT length is *nperseg*. Defaults to *None*.

detrend [str or function or *False*, optional] Specifies how to detrend each segment. If `detrend` is a string, it is passed as the *type* argument to the `detrend` function. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is *False*, no detrending is done. Defaults to 'constant'.

return_onesided [bool, optional] If *True*, return a one-sided spectrum for real data. If *False* return a two-sided spectrum. Defaults to *True*, but for complex data, a two-sided spectrum is always returned.

scaling [{ 'density', 'spectrum' }, optional] Selects between computing the power spectral density ('density') where *Sxx* has units of V**2/Hz and computing the power spectrum ('spectrum') where *Sxx* has units of V**2, if *x* is measured in V and *fs* is measured in Hz. Defaults to 'density'.

axis [int, optional] Axis along which the spectrogram is computed; the default is over the last axis (i.e. `axis=-1`).

mode [str, optional] Defines what kind of return values are expected. Options are ['psd', 'complex', 'magnitude', 'angle', 'phase']. 'complex' is equivalent to the output of `stft` with no padding or boundary extension. 'magnitude' returns the absolute magnitude of the STFT. 'angle' and 'phase' return the complex angle of the STFT, with and without unwrapping, respectively.

Returns

f [ndarray] Array of sample frequencies.

t [ndarray] Array of segment times.

Sxx [ndarray] Spectrogram of x. By default, the last axis of Sxx corresponds to the segment times.

See also:

periodogram

Simple, optionally modified periodogram

lombscargle

Lomb-Scargle periodogram for unevenly sampled data

welch

Power spectral density by Welch's method.

csd

Cross spectral density by Welch's method.

Notes

An appropriate amount of overlap will depend on the choice of window and on your requirements. In contrast to welch's method, where the entire data stream is averaged over, one may wish to use a smaller overlap (or perhaps none at all) when computing a spectrogram, to maintain some statistical independence between individual segments. It is for this reason that the default window is a Tukey window with 1/8th of a window's length overlap at each end.

New in version 0.16.0.

References

[1]

Examples

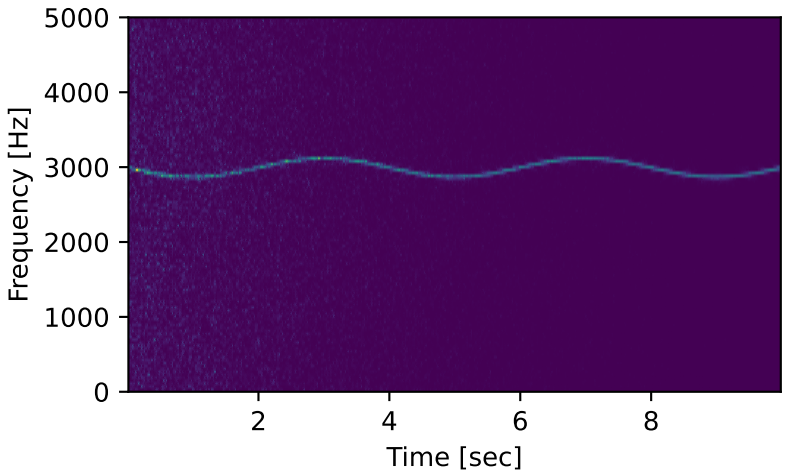
```
>>> from scipy import signal
>>> from scipy.fft import fftshift
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

Generate a test signal, a 2 Vrms sine wave whose frequency is slowly modulated around 3kHz, corrupted by white noise of exponentially decreasing magnitude sampled at 10 kHz.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2 * np.sqrt(2)
>>> noise_power = 0.01 * fs / 2
>>> time = np.arange(N) / float(fs)
>>> mod = 500*np.cos(2*np.pi*0.25*time)
>>> carrier = amp * np.sin(2*np.pi*3e3*time + mod)
>>> noise = rng.normal(scale=np.sqrt(noise_power), size=time.shape)
>>> noise *= np.exp(-time/5)
>>> x = carrier + noise
```

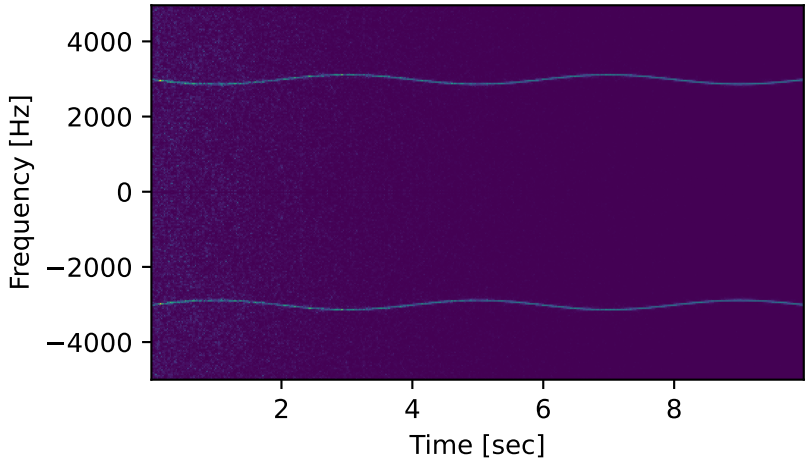
Compute and plot the spectrogram.

```
>>> f, t, Sxx = signal.spectrogram(x, fs)
>>> plt.pcolormesh(t, f, Sxx, shading='gouraud')
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.show()
```



Note, if using output that is not one sided, then use the following:

```
>>> f, t, Sxx = signal.spectrogram(x, fs, return_onesided=False)
>>> plt.pcolormesh(t, fftshift(f), fftshift(Sxx, axes=0), shading='gouraud
↪')
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.show()
```



scipy.signal.lombscargle

scipy.signal.**lombscargle**(*x*, *y*, *freqs*)

Computes the Lomb-Scargle periodogram.

The Lomb-Scargle periodogram was developed by Lomb [1] and further extended by Scargle [2] to find, and test the significance of weak periodic signals with uneven temporal sampling.

When *normalize* is False (default) the computed periodogram is unnormalized, it takes the value `(A**2) * N/4` for a harmonic signal with amplitude A for sufficiently large N.

When *normalize* is True the computed periodogram is normalized by the residuals of the data around a constant reference model (at zero).

Input arrays should be 1-D and will be cast to float64.

Parameters

x	[array_like] Sample times.
y	[array_like] Measurement values.
freqs	[array_like] Angular frequencies for output periodogram.
precenter	[bool, optional] Pre-center measurement values by subtracting the mean.
normalize	[bool, optional] Compute normalized periodogram.

Returns

pgram	[array_like] Lomb-Scargle periodogram.

Raises

ValueError
: If the input arrays *x* and *y* do not have the same shape.

See also:

istft

Inverse Short Time Fourier Transform

check_COLA

Check whether the Constant OverLap Add (COLA) constraint is met

welch

Power spectral density by Welch's method

spectrogram

Spectrogram by Welch's method

csd

Cross spectral density by Welch's method

Notes

This subroutine calculates the periodogram using a slightly modified algorithm due to Townsend [3] which allows the periodogram to be calculated using only a single pass through the input arrays for each frequency.

The algorithm running time scales roughly as O(x * freqs) or O(N^2) for a large number of samples and frequencies.

References

[1], [2], [3]

Examples

```
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

First define some input parameters for the signal:

```
>>> A = 2.
>>> w = 1.
>>> phi = 0.5 * np.pi
>>> nin = 1000
>>> nout = 100000
>>> frac_points = 0.9  # Fraction of points to select
```

Randomly select a fraction of an array with timesteps:

```
>>> r = rng.standard_normal(nin)
>>> x = np.linspace(0.01, 10*np.pi, nin)
>>> x = x[r >= frac_points]
```

Plot a sine wave for the selected times:

```
>>> y = A * np.sin(w*x+phi)
```

Define the array of frequencies for which to compute the periodogram:

```
>>> f = np.linspace(0.01, 10, nout)
```

Calculate Lomb-Scargle periodogram:

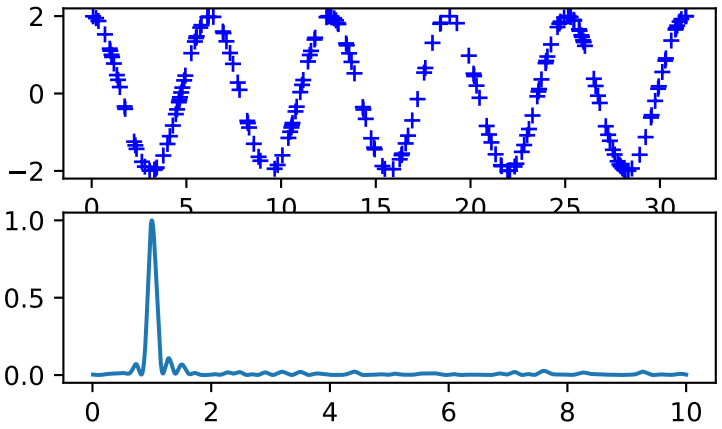
```
>>> import scipy.signal as signal
>>> pgram = signal.lombscargle(x, y, f, normalize=True)
```

Now make a plot of the input data:

```
>>> plt.subplot(2, 1, 1)
>>> plt.plot(x, y, 'b+')
```

Then plot the normalized periodogram:

```
>>> plt.subplot(2, 1, 2)
>>> plt.plot(f, pgram)
>>> plt.show()
```



scipy.signal.vectorstrength

scipy.signal.**vectorstrength**(*events*, *period*)

Determine the vector strength of the events corresponding to the given period.

The vector strength is a measure of phase synchrony, how well the timing of the events is synchronized to a single period of a periodic signal.

If multiple periods are used, calculate the vector strength of each. This is called the "resonating vector strength".

Parameters

events [1D array_like] An array of time points containing the timing of the events.

period [float or array_like] The period of the signal that the events should synchronize to. The period is in the same units as *events*. It can also be an array of periods, in which case the outputs are arrays of the same length.

Returns

strength [float or 1D array] The strength of the synchronization. 1.0 is perfect synchronization and 0.0 is no synchronization. If *period* is an array, this is also an array with each element containing the vector strength at the corresponding period.

phase [float or array] The phase that the events are most strongly synchronized to in radians. If *period* is an array, this is also an array with each element containing the phase for the corresponding period.

References

van Hemmen, JL, Longtin, A, and Vollmayr, AN. Testing resonating vector

strength: Auditory system, electric fish, and noise. Chaos 21, 047508 (2011); DOI:10.1063/1.3670512.

van Hemmen, JL. Vector strength after Goldberg, Brown, and von Mises:

biological and mathematical perspectives. Biol Cybern. 2013 Aug;107(4):385-96. DOI:10.1007/s00422-013-0561-7.

van Hemmen, JL and Vollmayr, AN. Resonating vector strength: what happens

when we vary the "probing" frequency while keeping the spike times fixed. Biol Cybern. 2013 Aug;107(4):491-94. DOI:10.1007/s00422-013-0560-8.

scipy.signal.stft

scipy.signal.**stft**(*x*, *fs=1.0*, *window='hann'*, *nperseg=256*, *noverlap=None*, *nfft=None*, *detrend=False*, *return_onesided=True*, *boundary='zeros'*, *padded=True*, *axis=- 1*)

Compute the Short Time Fourier Transform (STFT).

STFTs can be used as a way of quantifying the change of a nonstationary signal's frequency and phase content over time.

Parameters

x [array_like] Time series of measurement values

fs [float, optional] Sampling frequency of the *x* time series. Defaults to 1.0.

window [str or tuple or array_like, optional] Desired window to use. If *window* is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg. Defaults to a Hann window.

nperseg [int, optional] Length of each segment. Defaults to 256.

noverlap [int, optional] Number of points to overlap between segments. If *None*, `noverlap = nperseg // 2`. Defaults to *None*. When specified, the COLA constraint must be met (see Notes below).

nfft [int, optional] Length of the FFT used, if a zero padded FFT is desired. If *None*, the FFT length is *nperseg*. Defaults to *None*.

detrend [str or function or *False*, optional] Specifies how to detrend each segment. If `detrend` is a string, it is passed as the *type* argument to the `detrend` function. If it is a function, it takes a segment and returns a detrended segment. If `detrend` is *False*, no detrending is done. Defaults to *False*.

return_onesided [bool, optional] If *True*, return a one-sided spectrum for real data. If *False* return a two-sided spectrum. Defaults to *True*, but for complex data, a two-sided spectrum is always returned.

boundary [str or None, optional] Specifies whether the input signal is extended at both ends, and how to generate the new values, in order to center the first windowed segment on the first input point. This has the benefit of enabling reconstruction of the first input point when the employed window function starts at zero. Valid options are `['even', 'odd', 'constant', 'zeros', None]`. Defaults to 'zeros', for zero padding extension. I.e. `[1, 2, 3, 4]` is extended to `[0, 1, 2, 3, 4, 0]` for `nperseg=3`.

padded [bool, optional] Specifies whether the input signal is zero-padded at the end to make the signal fit exactly into an integer number of window segments, so that all of the signal is included in the output. Defaults to *True*. Padding occurs after boundary extension, if *boundary* is not *None*, and *padded* is *True*, as is the default.

axis [int, optional] Axis along which the STFT is computed; the default is over the last axis (i.e. `axis=-1`).

Returns

f [ndarray] Array of sample frequencies.

t [ndarray] Array of segment times.

Zxx [ndarray] STFT of *x*. By default, the last axis of *Zxx* corresponds to the segment times.

See also:

`istft`

Inverse Short Time Fourier Transform

check_COLA

Check whether the Constant OverLap Add (COLA) constraint is met

check_NOLA

Check whether the Nonzero Overlap Add (NOLA) constraint is met

welch

Power spectral density by Welch's method.

spectrogram

Spectrogram by Welch's method.

csd

Cross spectral density by Welch's method.

lombscargle

Lomb-Scargle periodogram for unevenly sampled data

Notes

In order to enable inversion of an STFT via the inverse STFT in *istft*, the signal windowing must obey the constraint of "Nonzero OverLap Add" (NOLA), and the input signal must have complete windowing coverage (i.e. `(x.shape[axis] - nperseg) % (nperseg-noverlap) == 0`). The *padded* argument may be used to accomplish this.

Given a time-domain signal $x[n]$, a window $w[n]$, and a hop size H = *nperseg - noverlap*, the windowed frame at time index t is given by

$$x_t[n] = x[n]w[n - tH]$$

The overlap-add (OLA) reconstruction equation is given by

$$x[n] = \frac{\sum_t x_t[n]w[n - tH]}{\sum_t w^2[n - tH]}$$

The NOLA constraint ensures that every normalization term that appears in the denomimator of the OLA reconstruction equation is nonzero. Whether a choice of *window*, *nperseg*, and *noverlap* satisfy this constraint can be tested with *check_NOLA*.

New in version 0.19.0.

References

[1], [2]

Examples

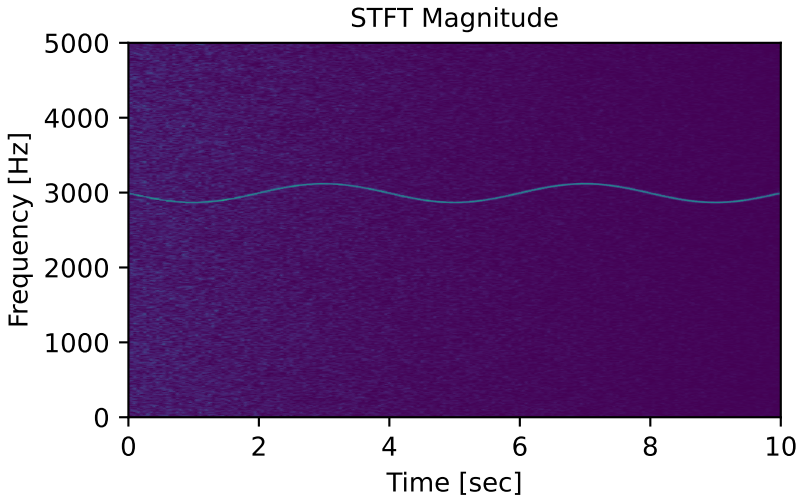
```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

Generate a test signal, a 2 Vrms sine wave whose frequency is slowly modulated around 3kHz, corrupted by white noise of exponentially decreasing magnitude sampled at 10 kHz.

```
>>> fs = 10e3
>>> N = 1e5
>>> amp = 2 * np.sqrt(2)
>>> noise_power = 0.01 * fs / 2
>>> time = np.arange(N) / float(fs)
>>> mod = 500*np.cos(2*np.pi*0.25*time)
>>> carrier = amp * np.sin(2*np.pi*3e3*time + mod)
>>> noise = rng.normal(scale=np.sqrt(noise_power),
...                    size=time.shape)
>>> noise *= np.exp(-time/5)
>>> x = carrier + noise
```

Compute and plot the STFT's magnitude.

```
>>> f, t, Zxx = signal.stft(x, fs, nperseg=1000)
>>> plt.pcolormesh(t, f, np.abs(Zxx), vmin=0, vmax=amp, shading='gouraud')
>>> plt.title('STFT Magnitude')
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.show()
```



scipy.signal.istft

scipy.signal.**istft**(*Zxx*, *fs=1.0*, *window='hann'*, *nperseg=None*, *noverlap=None*, *nfft=None*, *input_onesided=True*, *boundary=True*, *time_axis=-1*, *freq_axis=-2*)

Perform the inverse Short Time Fourier transform (iSTFT).

Parameters

Zxx [array_like] STFT of the signal to be reconstructed. If a purely real array is passed, it will be cast to a complex data type.

fs [float, optional] Sampling frequency of the time series. Defaults to 1.0.

window [str or tuple or array_like, optional] Desired window to use. If *window* is a string or tuple, it is passed to `get_window` to generate the window values, which are DFT-even by default. See `get_window` for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg. Defaults to a Hann window. Must match the window used to generate the STFT for faithful inversion.

nperseg [int, optional] Number of data points corresponding to each STFT segment. This parameter must be specified if the number of data points per segment is odd, or if the STFT was padded via `nfft > nperseg`. If *None*, the value depends on the shape of *Zxx* and *input_onesided*. If *input_onesided* is *True*, `nperseg=2*(Zxx.shape[freq_axis] - 1)`. Otherwise, `nperseg=Zxx.shape[freq_axis]`. Defaults to *None*.

noverlap [int, optional] Number of points to overlap between segments. If *None*, half of the segment length. Defaults to *None*. When specified, the COLA constraint must be met (see Notes below), and should match the parameter used to generate the STFT. Defaults to *None*.

nfft [int, optional] Number of FFT points corresponding to each STFT segment. This parameter must be specified if the STFT was padded via `nfft > nperseg`. If *None*, the default values are the same as for *nperseg*, detailed above, with one exception: if *input_onesided* is True and `nperseg==2*Zxx.shape[freq_axis] - 1`, *nfft* also takes on that value. This case allows the proper inversion of an odd-length unpadded STFT using `nfft=None`. Defaults to *None*.

input_onesided [bool, optional] If *True*, interpret the input array as one-sided FFTs, such as is returned by `stft` with `return_onesided=True` and `numpy.fft.rfft`. If *False*, interpret the input as a a two-sided FFT. Defaults to *True*.

boundary [bool, optional] Specifies whether the input signal was extended at its boundaries by supplying a non-*None* `boundary` argument to `stft`. Defaults to *True*.

time_axis [int, optional] Where the time segments of the STFT is located; the default is the last axis (i.e. `axis=-1`).

freq_axis [int, optional] Where the frequency axis of the STFT is located; the default is the penultimate axis (i.e. `axis=-2`).

Returns

t [ndarray] Array of output data times.

x [ndarray] iSTFT of *Zxx*.

See also:

stft

Short Time Fourier Transform

check_COLA

Check whether the Constant OverLap Add (COLA) constraint is met

check_NOLA

Check whether the Nonzero Overlap Add (NOLA) constraint is met

Notes

In order to enable inversion of an STFT via the inverse STFT with *istft*, the signal windowing must obey the constraint of "nonzero overlap add" (NOLA):

$$\sum_t w^2[n - tH] \neq 0$$

This ensures that the normalization factors that appear in the denominator of the overlap-add reconstruction equation

$$x[n] = \frac{\sum_t x_t[n] w[n - tH]}{\sum_t w^2[n - tH]}$$

are not zero. The NOLA constraint can be checked with the *check_NOLA* function.

An STFT which has been modified (via masking or otherwise) is not guaranteed to correspond to a exactly realizible signal. This function implements the iSTFT via the least-squares estimation algorithm detailed in [2], which produces a signal that minimizes the mean squared error between the STFT of the returned signal and the modified STFT.

New in version 0.19.0.

References

[1], [2]

Examples

```
>>> from scipy import signal
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
```

Generate a test signal, a 2 Vrms sine wave at 50Hz corrupted by 0.001 V**2/Hz of white noise sampled at 1024 Hz.

```
>>> fs = 1024
>>> N = 10*fs
>>> nperseg = 512
>>> amp = 2 * np.sqrt(2)
>>> noise_power = 0.001 * fs / 2
>>> time = np.arange(N) / float(fs)
>>> carrier = amp * np.sin(2*np.pi*50*time)
>>> noise = rng.normal(scale=np.sqrt(noise_power),
...                    size=time.shape)
>>> x = carrier + noise
```

Compute the STFT, and plot its magnitude

```
>>> f, t, Zxx = signal.stft(x, fs=fs, nperseg=nperseg)
>>> plt.figure()
>>> plt.pcolormesh(t, f, np.abs(Zxx), vmin=0, vmax=amp, shading='gouraud')
>>> plt.ylim([f[1], f[-1]])
>>> plt.title('STFT Magnitude')
```

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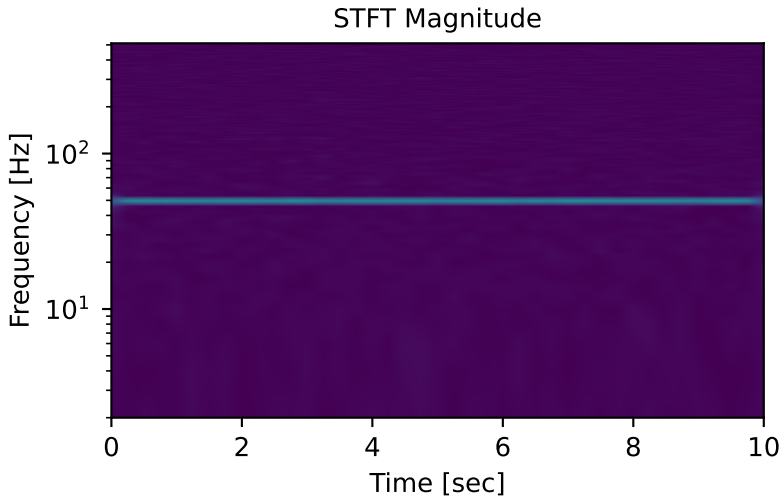
```
>>> plt.ylabel('Frequency [Hz]')
>>> plt.xlabel('Time [sec]')
>>> plt.yscale('log')
>>> plt.show()
```



Zero the components that are 10% or less of the carrier magnitude, then convert back to a time series via inverse STFT

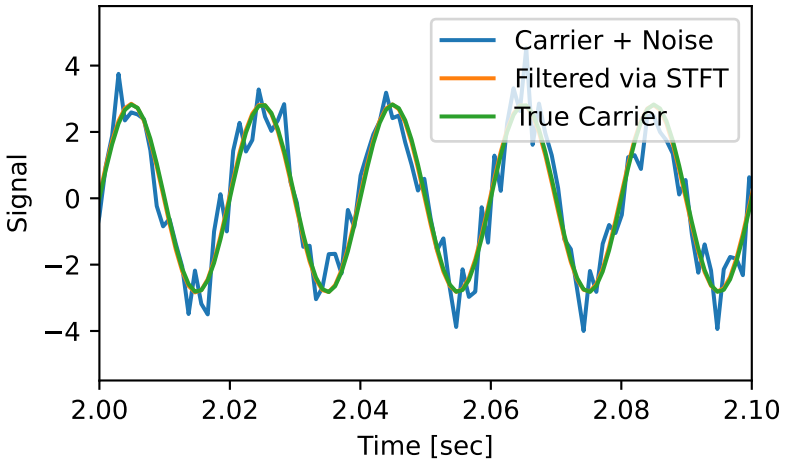
```
>>> Zxx = np.where(np.abs(Zxx) >= amp/10, Zxx, 0)
>>> _, xrec = signal.istft(Zxx, fs)
```

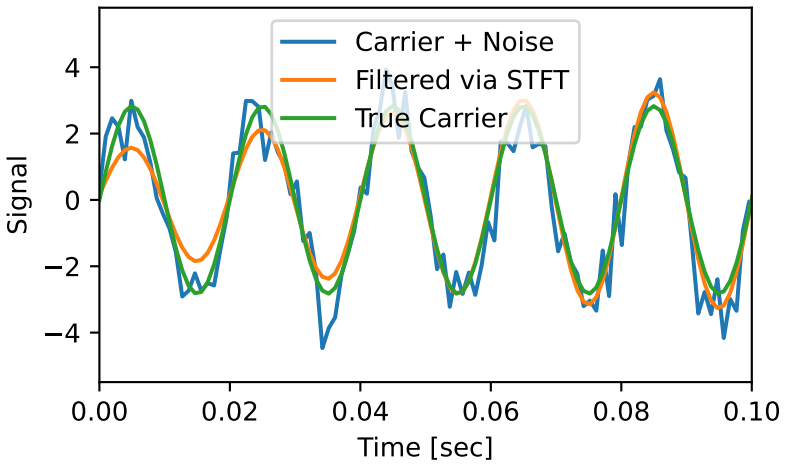
Compare the cleaned signal with the original and true carrier signals.

```
>>> plt.figure()
>>> plt.plot(time, x, time, xrec, time, carrier)
>>> plt.xlim([2, 2.1])
>>> plt.xlabel('Time [sec]')
>>> plt.ylabel('Signal')
>>> plt.legend(['Carrier + Noise', 'Filtered via STFT', 'True Carrier'])
>>> plt.show()
```

Note that the cleaned signal does not start as abruptly as the original, since some of the coefficients of the transient were also removed:

```
>>> plt.figure()
>>> plt.plot(time, x, time, xrec, time, carrier)
>>> plt.xlim([0, 0.1])
>>> plt.xlabel('Time [sec]')
>>> plt.ylabel('Signal')
>>> plt.legend(['Carrier + Noise', 'Filtered via STFT', 'True Carrier'])
>>> plt.show()
```


Carrier + Noise
Filtered via STFT
True Carrier
Signal
4
2
0
−2
−4
2.00
2.02
2.04
2.06
2.08
2.10
Time [sec]


Carrier + Noise
Filtered via STFT
True Carrier
Signal
4
2
0
−2
−4
0.00
0.02
0.04
0.06
0.08
0.10
Time [sec]

scipy.signal.check_COLA

scipy.signal.**check_COLA**(*window*, *nperseg*, *noverlap*, *tol=1e-10*)

Check whether the Constant OverLap Add (COLA) constraint is met.

Parameters

window [str or tuple or array_like] Desired window to use. If *window* is a string or tuple, it is passed to *get_window* to generate the window values, which are DFT-even by default. See *get_window* for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg.

nperseg [int] Length of each segment.

noverlap [int] Number of points to overlap between segments.

tol [float, optional] The allowed variance of a bin's weighted sum from the median bin sum.

Returns

verdict [bool] *True* if chosen combination satisfies COLA within *tol*, *False* otherwise

See also:

check_NOLA

Check whether the Nonzero Overlap Add (NOLA) constraint is met

stft

Short Time Fourier Transform

istft

Inverse Short Time Fourier Transform

Notes

In order to enable inversion of an STFT via the inverse STFT in *istft*, it is sufficient that the signal windowing obeys the constraint of "Constant OverLap Add" (COLA). This ensures that every point in the input data is equally weighted, thereby avoiding aliasing and allowing full reconstruction.

Some examples of windows that satisfy COLA:

- Rectangular window at overlap of 0, 1/2, 2/3, 3/4, …
- Bartlett window at overlap of 1/2, 3/4, 5/6, …
- Hann window at 1/2, 2/3, 3/4, …
- Any Blackman family window at 2/3 overlap
- Any window with `noverlap = nperseg-1`

A very comprehensive list of other windows may be found in [2], wherein the COLA condition is satisfied when the "Amplitude Flatness" is unity.

New in version 0.19.0.

References

[1], [2]

Examples

```
>>> from scipy import signal
```

Confirm COLA condition for rectangular window of 75% (3/4) overlap:

```
>>> signal.check_COLA(signal.windows.boxcar(100), 100, 75)
True
```

COLA is not true for 25% (1/4) overlap, though:

```
>>> signal.check_COLA(signal.windows.boxcar(100), 100, 25)
False
```

"Symmetrical" Hann window (for filter design) is not COLA:

```
>>> signal.check_COLA(signal.windows.hann(120, sym=True), 120, 60)
False
```

"Periodic" or "DFT-even" Hann window (for FFT analysis) is COLA for overlap of 1/2, 2/3, 3/4, etc.:

```
>>> signal.check_COLA(signal.windows.hann(120, sym=False), 120, 60)
True
```

```
>>> signal.check_COLA(signal.windows.hann(120, sym=False), 120, 80)
True
```

```
>>> signal.check_COLA(signal.windows.hann(120, sym=False), 120, 90)
True
```

scipy.signal.check_NOLA

scipy.signal.**check_NOLA**(*window*, *nperseg*, *noverlap*, *tol=1e-10*)

Check whether the Nonzero Overlap Add (NOLA) constraint is met.

Parameters

window [str or tuple or array_like] Desired window to use. If *window* is a string or tuple, it is passed to *get_window* to generate the window values, which are DFT-even by default. See *get_window* for a list of windows and required parameters. If *window* is array_like it will be used directly as the window and its length must be nperseg.

nperseg [int] Length of each segment.

noverlap [int] Number of points to overlap between segments.

tol [float, optional] The allowed variance of a bin's weighted sum from the median bin sum.

Returns

verdict [bool] *True* if chosen combination satisfies the NOLA constraint within *tol*, *False* otherwise

See also:

check_COLA

Check whether the Constant OverLap Add (COLA) constraint is met

stft

Short Time Fourier Transform

istft

Inverse Short Time Fourier Transform

Notes

In order to enable inversion of an STFT via the inverse STFT in *istft*, the signal windowing must obey the constraint of "nonzero overlap add" (NOLA):

$$\sum_{t} w^2[n - tH] \neq 0$$

for all n, where w is the window function, t is the frame index, and H is the hop size (H = *nperseg* - *noverlap*).

This ensures that the normalization factors in the denominator of the overlap-add inversion equation are not zero. Only very pathological windows will fail the NOLA constraint.

New in version 1.2.0.

References

[1], [2]

Examples

```
>>> from scipy import signal
```

Confirm NOLA condition for rectangular window of 75% (3/4) overlap:

```
>>> signal.check_NOLA(signal.windows.boxcar(100), 100, 75)
True
```

NOLA is also true for 25% (1/4) overlap:

```
>>> signal.check_NOLA(signal.windows.boxcar(100), 100, 25)
True
```

"Symmetrical" Hann window (for filter design) is also NOLA:

```
>>> signal.check_NOLA(signal.windows.hann(120, sym=True), 120, 60)
True
```

As long as there is overlap, it takes quite a pathological window to fail NOLA:

```
>>> w = np.ones(64, dtype="float")
>>> w[::2] = 0
>>> signal.check_NOLA(w, 64, 32)
False
```

If there is not enough overlap, a window with zeros at the ends will not work:

```
>>> signal.check_NOLA(signal.windows.hann(64), 64, 0)
False
>>> signal.check_NOLA(signal.windows.hann(64), 64, 1)
False
>>> signal.check_NOLA(signal.windows.hann(64), 64, 2)
True
```

3.3.23 Sparse matrices (`scipy.sparse`)

SciPy 2-D sparse matrix package for numeric data.

Contents

Sparse matrix classes

bsr_matrix(arg1[, shape, dtype, copy, blocksize])	Block Sparse Row matrix
coo_matrix(arg1[, shape, dtype, copy])	A sparse matrix in COOrdinate format.
csc_matrix(arg1[, shape, dtype, copy])	Compressed Sparse Column matrix
csr_matrix(arg1[, shape, dtype, copy])	Compressed Sparse Row matrix
dia_matrix(arg1[, shape, dtype, copy])	Sparse matrix with DIAgonal storage
dok_matrix(arg1[, shape, dtype, copy])	Dictionary Of Keys based sparse matrix.
lil_matrix(arg1[, shape, dtype, copy])	Row-based list of lists sparse matrix
spmatrix([maxprint])	This class provides a base class for all sparse matrices.

scipy.sparse.bsr_matrix

class scipy.sparse.**bsr_matrix**(*arg1*, *shape=None*, *dtype=None*, *copy=False*, *blocksize=None*)

Block Sparse Row matrix

This can be instantiated in several ways:

bsr_matrix(D, [blocksize=(R,C)])

where D is a dense matrix or 2-D ndarray.

bsr_matrix(S, [blocksize=(R,C)])

with another sparse matrix S (equivalent to S.tobsr())

bsr_matrix((M, N), [blocksize=(R,C), dtype])

to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

bsr_matrix((data, ij), [blocksize=(R,C), shape=(M, N)])

where `data` and `ij` satisfy `a[ij[0, k], ij[1, k]] = data[k]`

bsr_matrix((data, indices, indptr), [shape=(M, N)])

is the standard BSR representation where the block column indices for row i are stored in `indices[indptr[i]:indptr[i+1]]` and their corresponding block values are stored in `data[ indptr[i]: indptr[i+1] ]`. If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Summary of BSR format

The Block Compressed Row (BSR) format is very similar to the Compressed Sparse Row (CSR) format. BSR is appropriate for sparse matrices with dense sub matrices like the last example below. Block matrices often arise in vector-valued finite element discretizations. In such cases, BSR is considerably more efficient than CSR and CSC for many sparse arithmetic operations.

Blocksize

The blocksize (R,C) must evenly divide the shape of the matrix (M,N). That is, R and C must satisfy the relationship `M % R = 0` and `N % C = 0`.

If no blocksize is specified, a simple heuristic is applied to determine an appropriate blocksize.

Examples

```
>>> from scipy.sparse import bsr_matrix
>>> bsr_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> row = np.array([0, 0, 1, 2, 2, 2])
>>> col = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3 ,4, 5, 6])
>>> bsr_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])
```

```
>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6]).repeat(4).reshape(6, 2, 2)
>>> bsr_matrix((data,indices,indptr), shape=(6, 6)).toarray()
array([[1, 1, 0, 0, 2, 2],
       [1, 1, 0, 0, 2, 2],
       [0, 0, 0, 0, 3, 3],
       [0, 0, 0, 0, 3, 3],
       [4, 4, 5, 5, 6, 6],
       [4, 4, 5, 5, 6, 6]])
```

Attributes

dtype	[dtype] Data type of the matrix
shape	[2-tuple] Get shape of a matrix.
ndim	[int] Number of dimensions (this is always 2)
nnz	Number of stored values, including explicit zeros.
data	Data array of the matrix
indices	BSR format index array
indptr	BSR format index pointer array

blocksize Block size of the matrix

has_sorted_indices
Determine whether the matrix has sorted indices

Methods

__len__()	
__mul__(other)	interpret other and call one of the following
arcsin()	Element-wise arcsin.
arcsinh()	Element-wise arcsinh.
arctan()	Element-wise arctan.
arctanh()	Element-wise arctanh.
argmax([axis, out])	Return indices of maximum elements along an axis.
argmin([axis, out])	Return indices of minimum elements along an axis.
asformat(format[, copy])	Return this matrix in the passed format.
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(dtype[, casting, copy])	Cast the matrix elements to a specified type.
ceil()	Element-wise ceil.
check_format([full_check])	check whether the matrix format is valid
conj([copy])	Element-wise complex conjugation.
conjugate([copy])	Element-wise complex conjugation.
copy()	Returns a copy of this matrix.
count_nonzero()	Number of non-zero entries, equivalent to
deg2rad()	Element-wise deg2rad.
diagonal([k])	Returns the kth diagonal of the matrix.
dot(other)	Ordinary dot product
eliminate_zeros()	Remove zero elements in-place.
expm1()	Element-wise expm1.
floor()	Element-wise floor.
getH()	Return the Hermitian transpose of this matrix.
get_shape()	Get shape of a matrix.
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
getformat()	Format of a matrix representation as a string.
getmaxprint()	Maximum number of elements to display when printed.
getnnz([axis])	Number of stored values, including explicit zeros.
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
log1p()	Element-wise log1p.
matmat(**kwds)	matmat is deprecated! BSR matmat is deprecated in SciPy 0.19.0.
matvec(**kwds)	matvec is deprecated! BSR matvec is deprecated in SciPy 0.19.0.
max([axis, out])	Return the maximum of the matrix or maximum along an axis.
maximum(other)	Element-wise maximum between this and another matrix.
mean([axis, dtype, out])	Compute the arithmetic mean along the specified axis.

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min([axis, out])	Return the minimum of the matrix or maximum along an axis.
minimum(other)	Element-wise minimum between this and another matrix.
multiply(other)	Point-wise multiplication by another matrix, vector, or scalar.
nonzero()	nonzero indices
power(n[, dtype])	This function performs element-wise power.
prune()	Remove empty space after all non-zero elements.
rad2deg()	Element-wise rad2deg.
reshape(self, shape[, order, copy])	Gives a new shape to a sparse matrix without changing its data.
resize(*shape)	Resize the matrix in-place to dimensions given by `shape`
rint()	Element-wise rint.
set_shape(shape)	See *reshape*.
setdiag(values[, k])	Set diagonal or off-diagonal elements of the array.
sign()	Element-wise sign.
sin()	Element-wise sin.
sinh()	Element-wise sinh.
sort_indices()	Sort the indices of this matrix *in place*
sorted_indices()	Return a copy of this matrix with sorted indices
sqrt()	Element-wise sqrt.
sum([axis, dtype, out])	Sum the matrix elements over a given axis.
sum_duplicates()	Eliminate duplicate matrix entries by adding them together
tan()	Element-wise tan.
tanh()	Element-wise tanh.
toarray([order, out])	Return a dense ndarray representation of this matrix.
tobsr([blocksize, copy])	Convert this matrix into Block Sparse Row Format.
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc([copy])	Convert this matrix to Compressed Sparse Column format.
tocsr([copy])	Convert this matrix to Compressed Sparse Row format.
todense([order, out])	Return a dense matrix representation of this matrix.
todia([copy])	Convert this matrix to sparse DIAgonal format.
todok([copy])	Convert this matrix to Dictionary Of Keys format.
tolil([copy])	Convert this matrix to List of Lists format.
transpose([axes, copy])	Reverses the dimensions of the sparse matrix.
trunc()	Element-wise trunc.

scipy.sparse.bsr_matrix.__len__

bsr_matrix.**__len__**()

scipy.sparse.bsr_matrix.__mul__

bsr_matrix.**__mul__**(*other*)
interpret other and call one of the following

self._mul_scalar() self._mul_vector() self._mul_multivector() self._mul_sparse_matrix()

scipy.sparse.bsr_matrix.arcsin

bsr_matrix.**arcsin**()
Element-wise arcsin.

See numpy.arcsin for more information.

scipy.sparse.bsr_matrix.arcsinh

bsr_matrix.**arcsinh**()
Element-wise arcsinh.

See numpy.arcsinh for more information.

scipy.sparse.bsr_matrix.arctan

bsr_matrix.**arctan**()
Element-wise arctan.

See numpy.arctan for more information.

scipy.sparse.bsr_matrix.arctanh

bsr_matrix.**arctanh**()
Element-wise arctanh.

See numpy.arctanh for more information.

scipy.sparse.bsr_matrix.argmax

bsr_matrix.**argmax**(*axis=None*, *out=None*)
Return indices of maximum elements along an axis.

Implicit zero elements are also taken into account. If there are several maximum values, the index of the first occurrence is returned.

Parameters

axis [{-2, -1, 0, 1, None}, optional] Axis along which the argmax is computed. If None (default), index of the maximum element in the flatten data is returned.

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind [numpy.matrix or int] Indices of maximum elements. If matrix, its size along *axis* is 1.

scipy.sparse.bsr_matrix.argmin

bsr_matrix.**argmin**(*axis=None*, *out=None*)

Return indices of minimum elements along an axis.

Implicit zero elements are also taken into account. If there are several minimum values, the index of the first occurrence is returned.

Parameters

axis [{-2, -1, 0, 1, None}, optional] Axis along which the argmin is computed. If None (default), index of the minimum element in the flatten data is returned.

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind [numpy.matrix or int] Indices of minimum elements. If matrix, its size along *axis* is 1.

scipy.sparse.bsr_matrix.asformat

bsr_matrix.**asformat**(*format*, *copy=False*)

Return this matrix in the passed format.

Parameters

format [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", …) or None for no conversion.

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [This matrix in the passed format.]

scipy.sparse.bsr_matrix.asfptype

bsr_matrix.**asfptype**()

Upcast matrix to a floating point format (if necessary)

scipy.sparse.bsr_matrix.astype

bsr_matrix.**astype**(*dtype*, *casting='unsafe'*, *copy=True*)

Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. 'no' means the data types should not be cast at all. 'equiv' means only byte-order changes are allowed. 'safe' means only casts which can preserve values are allowed. 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed. 'unsafe' means any data conversions may be done.

copy [bool, optional] If *copy* is *False*, the result might share some memory with this matrix. If *copy* is *True*, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.bsr_matrix.ceil

bsr_matrix.**ceil**()

Element-wise ceil.

See numpy.ceil for more information.

scipy.sparse.bsr_matrix.check_format

bsr_matrix.**check_format**(*full_check=True*)

check whether the matrix format is valid

Parameters*:*

full_check:

True - rigorous check, O(N) operations : default False - basic check, O(1) operations

scipy.sparse.bsr_matrix.conj

bsr_matrix.**conj**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.bsr_matrix.conjugate

bsr_matrix.**conjugate**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.bsr_matrix.copy

bsr_matrix.**copy**()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.bsr_matrix.count_nonzero

bsr_matrix.**count_nonzero**()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.bsr_matrix.deg2rad

bsr_matrix.**deg2rad**()

Element-wise deg2rad.

See numpy.deg2rad for more information.

scipy.sparse.bsr_matrix.diagonal

bsr_matrix.**diagonal**(*k=0*)

Returns the kth diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to get, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.bsr_matrix.dot

bsr_matrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.bsr_matrix.eliminate_zeros

bsr_matrix.**eliminate_zeros**()
Remove zero elements in-place.

scipy.sparse.bsr_matrix.expm1

bsr_matrix.**expm1**()
Element-wise expm1.

See numpy.expm1 for more information.

scipy.sparse.bsr_matrix.floor

bsr_matrix.**floor**()
Element-wise floor.

See numpy.floor for more information.

scipy.sparse.bsr_matrix.getH

bsr_matrix.**getH**()
Return the Hermitian transpose of this matrix.

See also:

numpy.matrix.getH

NumPy's implementation of *getH* for matrices

scipy.sparse.bsr_matrix.get_shape

bsr_matrix.**get_shape**()
Get shape of a matrix.

scipy.sparse.bsr_matrix.getcol

bsr_matrix.**getcol**(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

scipy.sparse.bsr_matrix.getformat

bsr_matrix.**getformat**()
Format of a matrix representation as a string.

scipy.sparse.bsr_matrix.getmaxprint

bsr_matrix.**getmaxprint**()
Maximum number of elements to display when printed.

scipy.sparse.bsr_matrix.getnnz

bsr_matrix.**getnnz**(*axis=None*)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero

Number of non-zero entries

scipy.sparse.bsr_matrix.getrow

bsr_matrix.**getrow**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

scipy.sparse.bsr_matrix.log1p

bsr_matrix.**log1p**()
Element-wise log1p.

See numpy.log1p for more information.

scipy.sparse.bsr_matrix.matmat

bsr_matrix.**matmat**(***kwds*)
matmat is deprecated! BSR matmat is deprecated in SciPy 0.19.0. Use * operator instead.

Multiply this sparse matrix by other matrix.

scipy.sparse.bsr_matrix.matvec

bsr_matrix.**matvec**(***kwds*)
matvec is deprecated! BSR matvec is deprecated in SciPy 0.19.0. Use * operator instead.

Multiply matrix by vector.

scipy.sparse.bsr_matrix.max

bsr_matrix.**max**(*axis=None*, *out=None*)
Return the maximum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the maximum over all the matrix elements, returning a scalar (i.e., *axis* = *None*).

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amax [coo_matrix or scalar] Maximum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension `a.ndim - 1`.

See also:

min

The minimum value of a sparse matrix along a given axis.

numpy.matrix.max

NumPy's implementation of 'max' for matrices

scipy.sparse.bsr_matrix.maximum

bsr_matrix.**maximum**(*other*)
Element-wise maximum between this and another matrix.

scipy.sparse.bsr_matrix.mean

bsr_matrix.**mean**(*axis=None*, *dtype=None*, *out=None*)
Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e., *axis* = *None*).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]

See also:

numpy.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.bsr_matrix.min

bsr_matrix.**min**(*axis=None*, *out=None*)
Return the minimum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the minimum over all the matrix elements, returning a scalar (i.e., *axis* = *None*).

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amin [coo_matrix or scalar] Minimum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension `a.ndim - 1`.

See also:

max

The maximum value of a sparse matrix along a given axis.

numpy.matrix.min

NumPy's implementation of 'min' for matrices

scipy.sparse.bsr_matrix.minimum

bsr_matrix.**minimum**(*other*)
Element-wise minimum between this and another matrix.

scipy.sparse.bsr_matrix.multiply

bsr_matrix.**multiply**(*other*)
Point-wise multiplication by another matrix, vector, or scalar.

scipy.sparse.bsr_matrix.nonzero

bsr_matrix.**nonzero**()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.bsr_matrix.power

bsr_matrix.**power**(*n*, *dtype=None*)
This function performs element-wise power.

Parameters

n	[n is a scalar]
dtype	[If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.bsr_matrix.prune

bsr_matrix.**prune**()
Remove empty space after all non-zero elements.

scipy.sparse.bsr_matrix.rad2deg

bsr_matrix.**rad2deg**()
Element-wise rad2deg.

See numpy.rad2deg for more information.

scipy.sparse.bsr_matrix.reshape

bsr_matrix.**reshape**(*self*, *shape*, *order='C'*, *copy=False*)
Gives a new shape to a sparse matrix without changing its data.

Parameters

shape [length-2 tuple of ints] The new shape should be compatible with the original shape.
order [{'C', 'F'}, optional] Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. 'F' means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.
copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix
[sparse matrix] A sparse matrix with the given shape, not necessarily of the same format as the current object.

See also:

numpy.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.bsr_matrix.resize

bsr_matrix.**resize**(**shape*)
Resize the matrix in-place to dimensions given by shape

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.bsr_matrix.rint

bsr_matrix.**rint**()
Element-wise rint.

See `numpy.rint` for more information.

scipy.sparse.bsr_matrix.set_shape

bsr_matrix.**set_shape**(*shape*)
See *reshape*.

scipy.sparse.bsr_matrix.setdiag

bsr_matrix.**setdiag**(*values*, *k=0*)
Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values are longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.bsr_matrix.sign

bsr_matrix.**sign**()
Element-wise sign.

See `numpy.sign` for more information.

scipy.sparse.bsr_matrix.sin

bsr_matrix.**sin**()
Element-wise sin.

See numpy.sin for more information.

scipy.sparse.bsr_matrix.sinh

bsr_matrix.**sinh**()
Element-wise sinh.

See numpy.sinh for more information.

scipy.sparse.bsr_matrix.sort_indices

bsr_matrix.**sort_indices**()
Sort the indices of this matrix *in place*

scipy.sparse.bsr_matrix.sorted_indices

bsr_matrix.**sorted_indices**()
Return a copy of this matrix with sorted indices

scipy.sparse.bsr_matrix.sqrt

bsr_matrix.**sqrt**()
Element-wise sqrt.

See numpy.sqrt for more information.

scipy.sparse.bsr_matrix.sum

bsr_matrix.**sum**(*axis=None*, *dtype=None*, *out=None*)
Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e., *axis* = *None*).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

sum_along_axis
[np.matrix] A matrix with the same shape as *self*, with the specified axis removed.

See also:

numpy.matrix.sum

NumPy's implementation of 'sum' for matrices

scipy.sparse.bsr_matrix.sum_duplicates

bsr_matrix.**sum_duplicates**()
Eliminate duplicate matrix entries by adding them together

The is an *in place* operation

scipy.sparse.bsr_matrix.tan

bsr_matrix.**tan**()
Element-wise tan.

See numpy.tan for more information.

scipy.sparse.bsr_matrix.tanh

bsr_matrix.**tanh**()
Element-wise tanh.

See numpy.tanh for more information.

scipy.sparse.bsr_matrix.toarray

bsr_matrix.**toarray**(*order=None*, *out=None*)
Return a dense ndarray representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multidimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns

arr [ndarray, 2-D] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

scipy.sparse.bsr_matrix.tobsr

bsr_matrix.**tobsr**(*blocksize=None*, *copy=False*)
Convert this matrix into Block Sparse Row Format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

If blocksize=(R, C) is provided, it will be used for determining block size of the bsr_matrix.

scipy.sparse.bsr_matrix.tocoo

bsr_matrix.**tocoo**(*copy=True*)
Convert this matrix to COOrdinate format.

When copy=False the data array will be shared between this matrix and the resultant coo_matrix.

scipy.sparse.bsr_matrix.tocsc

bsr_matrix.**tocsc**(*copy=False*)
Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.bsr_matrix.tocsr

bsr_matrix.**tocsr**(*copy=False*)
Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.bsr_matrix.todense

bsr_matrix.**todense**(*order=None*, *out=None*)
Return a dense matrix representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-D] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

scipy.sparse.bsr_matrix.todia

bsr_matrix.**todia**(*copy=False*)
Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.bsr_matrix.todok

bsr_matrix.**todok**(*copy=False*)
Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.bsr_matrix.tolil

bsr_matrix.**tolil**(*copy=False*)
Convert this matrix to List of Lists format.

With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.bsr_matrix.transpose

bsr_matrix.**transpose**(*axes=None*, *copy=False*)
Reverses the dimensions of the sparse matrix.

Parameters

axes [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.

copy [bool, optional] Indicates whether or not attributes of *self* should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p [*self* with the dimensions reversed.]

See also:

numpy.matrix.transpose

NumPy's implementation of 'transpose' for matrices

scipy.sparse.bsr_matrix.trunc

bsr_matrix.**trunc**()
Element-wise trunc.

See numpy.trunc for more information.

__getitem__	

scipy.sparse.coo_matrix

class scipy.sparse.**coo_matrix**(*arg1*, *shape=None*, *dtype=None*, *copy=False*)

A sparse matrix in COOrdinate format.

Also known as the 'ijv' or 'triplet' format.

This can be instantiated in several ways:

coo_matrix(D)

with a dense matrix D

coo_matrix(S)

with another sparse matrix S (equivalent to S.tocoo())

coo_matrix((M, N), [dtype])

to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

coo_matrix((data, (i, j)), [shape=(M, N)])

to construct from three arrays:

1. data[:] the entries of the matrix, in any order
2. i[:] the row indices of the matrix entries
3. j[:] the column indices of the matrix entries

Where `A[i[k], j[k]] = data[k]`. When shape is not specified, it is inferred from the index arrays

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the COO format

- facilitates fast conversion among sparse formats
- permits duplicate entries (see example)
- very fast conversion to and from CSR/CSC formats

Disadvantages of the COO format

- **does not directly support:**
  - arithmetic operations
  - slicing

Intended Usage

- COO is a fast format for constructing sparse matrices

- Once a matrix has been constructed, convert to CSR or CSC format for fast arithmetic and matrix vector operations
- By default when converting to CSR or CSC format, duplicate (i,j) entries will be summed together. This facilitates efficient construction of finite element matrices and the like. (see example)

Examples

```
>>> # Constructing an empty matrix
>>> from scipy.sparse import coo_matrix
>>> coo_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> # Constructing a matrix using ijv format
>>> row  = np.array([0, 3, 1, 0])
>>> col  = np.array([0, 3, 1, 2])
>>> data = np.array([4, 5, 7, 9])
>>> coo_matrix((data, (row, col)), shape=(4, 4)).toarray()
array([[4, 0, 9, 0],
       [0, 7, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 5]])
```

```
>>> # Constructing a matrix with duplicate indices
>>> row  = np.array([0, 0, 1, 3, 1, 0, 0])
>>> col  = np.array([0, 2, 1, 3, 1, 0, 0])
>>> data = np.array([1, 1, 1, 1, 1, 1, 1])
>>> coo = coo_matrix((data, (row, col)), shape=(4, 4))
>>> # Duplicate indices are maintained until implicitly or explicitly␣
 ↪summed
>>> np.max(coo.data)
1
>>> coo.toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])
```

Attributes

dtype	[dtype] Data type of the matrix
shape	[2-tuple] Get shape of a matrix.
ndim	[int] Number of dimensions (this is always 2)
nnz	Number of stored values, including explicit zeros.
data	COO format data array of the matrix
row	COO format row index array of the matrix
col	COO format column index array of the matrix

Methods

__len__()	

__mul__(other)	interpret other and call one of the following
arcsin()	Element-wise arcsin.
arcsinh()	Element-wise arcsinh.
arctan()	Element-wise arctan.
arctanh()	Element-wise arctanh.
argmax([axis, out])	Return indices of maximum elements along an axis.
argmin([axis, out])	Return indices of minimum elements along an axis.
asformat(format[, copy])	Return this matrix in the passed format.
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(dtype[, casting, copy])	Cast the matrix elements to a specified type.
ceil()	Element-wise ceil.
conj([copy])	Element-wise complex conjugation.
conjugate([copy])	Element-wise complex conjugation.
copy()	Returns a copy of this matrix.
count_nonzero()	Number of non-zero entries, equivalent to
deg2rad()	Element-wise deg2rad.
diagonal([k])	Returns the kth diagonal of the matrix.
dot(other)	Ordinary dot product
eliminate_zeros()	Remove zero entries from the matrix
expm1()	Element-wise expm1.
floor()	Element-wise floor.
getH()	Return the Hermitian transpose of this matrix.
get_shape()	Get shape of a matrix.
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
getformat()	Format of a matrix representation as a string.
getmaxprint()	Maximum number of elements to display when printed.
getnnz([axis])	Number of stored values, including explicit zeros.
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
log1p()	Element-wise log1p.
max([axis, out])	Return the maximum of the matrix or maximum along an axis.
maximum(other)	Element-wise maximum between this and another matrix.
mean([axis, dtype, out])	Compute the arithmetic mean along the specified axis.
min([axis, out])	Return the minimum of the matrix or maximum along an axis.
minimum(other)	Element-wise minimum between this and another matrix.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
power(n[, dtype])	This function performs element-wise power.
rad2deg()	Element-wise rad2deg.
reshape(self, shape[, order, copy])	Gives a new shape to a sparse matrix without changing its data.

continues on next page

Table 176 – continued from previous page

resize(*shape)	Resize the matrix in-place to dimensions given by `shape`
rint()	Element-wise rint.
set_shape(shape)	See *reshape*.
setdiag(values[, k])	Set diagonal or off-diagonal elements of the array.
sign()	Element-wise sign.
sin()	Element-wise sin.
sinh()	Element-wise sinh.
sqrt()	Element-wise sqrt.
sum([axis, dtype, out])	Sum the matrix elements over a given axis.
sum_duplicates()	Eliminate duplicate matrix entries by adding them together
tan()	Element-wise tan.
tanh()	Element-wise tanh.
toarray([order, out])	See the docstring for *spmatrix.toarray*.
tobsr([blocksize, copy])	Convert this matrix to Block Sparse Row format.
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc([copy])	Convert this matrix to Compressed Sparse Column format
tocsr([copy])	Convert this matrix to Compressed Sparse Row format
todense([order, out])	Return a dense matrix representation of this matrix.
todia([copy])	Convert this matrix to sparse DIAgonal format.
todok([copy])	Convert this matrix to Dictionary Of Keys format.
tolil([copy])	Convert this matrix to List of Lists format.
transpose([axes, copy])	Reverses the dimensions of the sparse matrix.
trunc()	Element-wise trunc.

scipy.sparse.coo_matrix.__len__

coo_matrix.**__len__**()

scipy.sparse.coo_matrix.__mul__

coo_matrix.**__mul__**(*other*)

interpret other and call one of the following

self._mul_scalar() self._mul_vector() self._mul_multivector() self._mul_sparse_matrix()

scipy.sparse.coo_matrix.arcsin

coo_matrix.**arcsin**()

Element-wise arcsin.

See `numpy.arcsin` for more information.

scipy.sparse.coo_matrix.arcsinh

coo_matrix.**arcsinh**()
Element-wise arcsinh.

See numpy.arcsinh for more information.

scipy.sparse.coo_matrix.arctan

coo_matrix.**arctan**()
Element-wise arctan.

See numpy.arctan for more information.

scipy.sparse.coo_matrix.arctanh

coo_matrix.**arctanh**()
Element-wise arctanh.

See numpy.arctanh for more information.

scipy.sparse.coo_matrix.argmax

coo_matrix.**argmax**(*axis=None*, *out=None*)
Return indices of maximum elements along an axis.

Implicit zero elements are also taken into account. If there are several maximum values, the index of the first occurrence is returned.

Parameters

axis [{-2, -1, 0, 1, None}, optional] Axis along which the argmax is computed. If None (default), index of the maximum element in the flatten data is returned.

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind [numpy.matrix or int] Indices of maximum elements. If matrix, its size along *axis* is 1.

scipy.sparse.coo_matrix.argmin

coo_matrix.**argmin**(*axis=None*, *out=None*)
Return indices of minimum elements along an axis.

Implicit zero elements are also taken into account. If there are several minimum values, the index of the first occurrence is returned.

Parameters

axis [{-2, -1, 0, 1, None}, optional] Axis along which the argmin is computed. If None (default), index of the minimum element in the flatten data is returned.

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind [numpy.matrix or int] Indices of minimum elements. If matrix, its size along *axis* is 1.

scipy.sparse.coo_matrix.asformat

coo_matrix.**asformat**(*format*, *copy=False*)

Return this matrix in the passed format.

Parameters

format [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", …) or None for no conversion.

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [This matrix in the passed format.]

scipy.sparse.coo_matrix.asfptype

coo_matrix.**asfptype**()

Upcast matrix to a floating point format (if necessary)

scipy.sparse.coo_matrix.astype

coo_matrix.**astype**(*dtype*, *casting='unsafe'*, *copy=True*)

Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. 'no' means the data types should not be cast at all. 'equiv' means only byte-order changes are allowed. 'safe' means only casts which can preserve values are allowed. 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed. 'unsafe' means any data conversions may be done.

copy [bool, optional] If *copy* is *False*, the result might share some memory with this matrix. If *copy* is *True*, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.coo_matrix.ceil

coo_matrix.**ceil**()

Element-wise ceil.

See numpy.ceil for more information.

scipy.sparse.coo_matrix.conj

coo_matrix.**conj**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.coo_matrix.conjugate

coo_matrix.**conjugate**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.coo_matrix.copy

coo_matrix.**copy**()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.coo_matrix.count_nonzero

coo_matrix.**count_nonzero**()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.coo_matrix.deg2rad

coo_matrix.**deg2rad**()
Element-wise deg2rad.

See numpy.deg2rad for more information.

scipy.sparse.coo_matrix.diagonal

coo_matrix.**diagonal**(*k=0*)
Returns the kth diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to get, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.coo_matrix.dot

coo_matrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.coo_matrix.eliminate_zeros

coo_matrix.**eliminate_zeros**()
Remove zero entries from the matrix

This is an *in place* operation

scipy.sparse.coo_matrix.expm1

coo_matrix.**expm1**()
Element-wise expm1.

See numpy.expm1 for more information.

scipy.sparse.coo_matrix.floor

coo_matrix.**floor**()
Element-wise floor.

See numpy.floor for more information.

scipy.sparse.coo_matrix.getH

coo_matrix.**getH**()
Return the Hermitian transpose of this matrix.

See also:

numpy.matrix.getH

NumPy's implementation of *getH* for matrices

scipy.sparse.coo_matrix.get_shape

coo_matrix.**get_shape**()
Get shape of a matrix.

scipy.sparse.coo_matrix.getcol

coo_matrix.**getcol**(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

scipy.sparse.coo_matrix.getformat

coo_matrix.**getformat**()
Format of a matrix representation as a string.

scipy.sparse.coo_matrix.getmaxprint

coo_matrix.**getmaxprint**()
Maximum number of elements to display when printed.

scipy.sparse.coo_matrix.getnnz

coo_matrix.**getnnz**(*axis=None*)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero

Number of non-zero entries

scipy.sparse.coo_matrix.getrow

coo_matrix.**getrow**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

scipy.sparse.coo_matrix.log1p

coo_matrix.**log1p**()
Element-wise log1p.

See numpy.log1p for more information.

scipy.sparse.coo_matrix.max

coo_matrix.**max**(*axis=None*, *out=None*)
Return the maximum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the maximum over all the matrix elements, returning a scalar (i.e., *axis* = *None*).

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amax [coo_matrix or scalar] Maximum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension `a.ndim - 1`.

See also:

`min`

The minimum value of a sparse matrix along a given axis.

`numpy.matrix.max`

NumPy's implementation of 'max' for matrices

scipy.sparse.coo_matrix.maximum

`coo_matrix.`**`maximum`**(*other*)

Element-wise maximum between this and another matrix.

scipy.sparse.coo_matrix.mean

`coo_matrix.`**`mean`**(*axis=None*, *dtype=None*, *out=None*)

Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e., *axis* = *None*).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]

See also:

`numpy.matrix.mean`

NumPy's implementation of 'mean' for matrices

scipy.sparse.coo_matrix.min

coo_matrix.**min**(*axis=None*, *out=None*)

Return the minimum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the minimum over all the matrix elements, returning a scalar (i.e., *axis* = *None*).

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amin [coo_matrix or scalar] Minimum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension `a.ndim - 1`.

See also:

max

The maximum value of a sparse matrix along a given axis.

numpy.matrix.min

NumPy's implementation of 'min' for matrices

scipy.sparse.coo_matrix.minimum

coo_matrix.**minimum**(*other*)

Element-wise minimum between this and another matrix.

scipy.sparse.coo_matrix.multiply

coo_matrix.**multiply**(*other*)

Point-wise multiplication by another matrix

scipy.sparse.coo_matrix.nonzero

coo_matrix.**nonzero**()

nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.coo_matrix.power

coo_matrix.**power**(*n*, *dtype=None*)

This function performs element-wise power.

Parameters

n [n is a scalar]

dtype [If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.coo_matrix.rad2deg

coo_matrix.**rad2deg**()

Element-wise rad2deg.

See numpy.rad2deg for more information.

scipy.sparse.coo_matrix.reshape

coo_matrix.**reshape**(*self*, *shape*, *order='C'*, *copy=False*)

Gives a new shape to a sparse matrix without changing its data.

Parameters

shape [length-2 tuple of ints] The new shape should be compatible with the original shape.

order [{'C', 'F'}, optional] Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. 'F' means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.

copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix

[sparse matrix] A sparse matrix with the given shape, not necessarily of the same format as the current object.

See also:

numpy.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.coo_matrix.resize

coo_matrix.**resize**(**shape*)
Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.coo_matrix.rint

coo_matrix.**rint**()
Element-wise rint.

See `numpy.rint` for more information.

scipy.sparse.coo_matrix.set_shape

coo_matrix.**set_shape**(*shape*)
See *reshape*.

scipy.sparse.coo_matrix.setdiag

coo_matrix.**setdiag**(*values*, *k=0*)
Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values are longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.coo_matrix.sign

coo_matrix.**sign**()
Element-wise sign.

See numpy.sign for more information.

scipy.sparse.coo_matrix.sin

coo_matrix.**sin**()
Element-wise sin.

See numpy.sin for more information.

scipy.sparse.coo_matrix.sinh

coo_matrix.**sinh**()
Element-wise sinh.

See numpy.sinh for more information.

scipy.sparse.coo_matrix.sqrt

coo_matrix.**sqrt**()
Element-wise sqrt.

See numpy.sqrt for more information.

scipy.sparse.coo_matrix.sum

coo_matrix.**sum**(*axis=None*, *dtype=None*, *out=None*)
Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e., *axis* = *None*).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

sum_along_axis
[np.matrix] A matrix with the same shape as *self*, with the specified axis removed.

See also:

numpy.matrix.sum

NumPy's implementation of 'sum' for matrices

scipy.sparse.coo_matrix.sum_duplicates

coo_matrix.**sum_duplicates**()
Eliminate duplicate matrix entries by adding them together

This is an *in place* operation

scipy.sparse.coo_matrix.tan

coo_matrix.**tan**()
Element-wise tan.

See numpy.tan for more information.

scipy.sparse.coo_matrix.tanh

coo_matrix.**tanh**()
Element-wise tanh.

See numpy.tanh for more information.

scipy.sparse.coo_matrix.toarray

coo_matrix.**toarray**(*order=None*, *out=None*)
See the docstring for *spmatrix.toarray*.

scipy.sparse.coo_matrix.tobsr

coo_matrix.**tobsr**(*blocksize=None*, *copy=False*)
Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.coo_matrix.tocoo

coo_matrix.**tocoo**(*copy=False*)
Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.coo_matrix.tocsc

coo_matrix.**tocsc**(*copy=False*)

Convert this matrix to Compressed Sparse Column format

Duplicate entries will be summed together.

Examples

```
>>> from numpy import array
>>> from scipy.sparse import coo_matrix
>>> row  = array([0, 0, 1, 3, 1, 0, 0])
>>> col  = array([0, 2, 1, 3, 1, 0, 0])
>>> data = array([1, 1, 1, 1, 1, 1, 1])
>>> A = coo_matrix((data, (row, col)), shape=(4, 4)).tocsc()
>>> A.toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])
```

scipy.sparse.coo_matrix.tocsr

coo_matrix.**tocsr**(*copy=False*)

Convert this matrix to Compressed Sparse Row format

Duplicate entries will be summed together.

Examples

```
>>> from numpy import array
>>> from scipy.sparse import coo_matrix
>>> row  = array([0, 0, 1, 3, 1, 0, 0])
>>> col  = array([0, 2, 1, 3, 1, 0, 0])
>>> data = array([1, 1, 1, 1, 1, 1, 1])
>>> A = coo_matrix((data, (row, col)), shape=(4, 4)).tocsr()
>>> A.toarray()
array([[3, 0, 1, 0],
       [0, 2, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 1]])
```

scipy.sparse.coo_matrix.todense

coo_matrix.**todense**(*order=None*, *out=None*)

Return a dense matrix representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-D] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

scipy.sparse.coo_matrix.todia

coo_matrix.**todia**(*copy=False*)

Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.coo_matrix.todok

coo_matrix.**todok**(*copy=False*)

Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.coo_matrix.tolil

coo_matrix.**tolil**(*copy=False*)

Convert this matrix to List of Lists format.

With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.coo_matrix.transpose

coo_matrix.**transpose**(*axes=None*, *copy=False*)

Reverses the dimensions of the sparse matrix.

Parameters

axes [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.

copy [bool, optional] Indicates whether or not attributes of *self* should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p [*self* with the dimensions reversed.]

See also:

numpy.matrix.transpose

NumPy's implementation of 'transpose' for matrices

scipy.sparse.coo_matrix.trunc

coo_matrix.**trunc**()
Element-wise trunc.

See numpy.trunc for more information.

scipy.sparse.csc_matrix

class scipy.sparse.**csc_matrix**(*arg1*, *shape=None*, *dtype=None*, *copy=False*)
Compressed Sparse Column matrix

This can be instantiated in several ways:

csc_matrix(D)
with a dense matrix or rank-2 ndarray D
csc_matrix(S)
with another sparse matrix S (equivalent to S.tocsc())
csc_matrix((M, N), [dtype])
to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.
csc_matrix((data, (row_ind, col_ind)), [shape=(M, N)])
where `data`, `row_ind` and `col_ind` satisfy the relationship `a[row_ind[k], col_ind[k]] = data[k]`.
csc_matrix((data, indices, indptr), [shape=(M, N)])
is the standard CSC representation where the row indices for column i are stored in `indices[indptr[i]:indptr[i+1]]` and their corresponding values are stored in `data[indptr[i]:indptr[i+1]]`. If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the CSC format

- efficient arithmetic operations CSC + CSC, CSC * CSC, etc.
- efficient column slicing
- fast matrix vector products (CSR, BSR may be faster)

Disadvantages of the CSC format

- slow row slicing operations (consider CSR)
- changes to the sparsity structure are expensive (consider LIL or DOK)

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csc_matrix
>>> csc_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> row = np.array([0, 2, 2, 0, 1, 2])
>>> col = np.array([0, 0, 1, 2, 2, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csc_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 4],
       [0, 0, 5],
       [2, 3, 6]])
```

```
>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csc_matrix((data, indices, indptr), shape=(3, 3)).toarray()
array([[1, 0, 4],
       [0, 0, 5],
       [2, 3, 6]])
```

Attributes

dtype	[dtype] Data type of the matrix
shape	[2-tuple] Get shape of a matrix.
ndim	[int] Number of dimensions (this is always 2)
nnz	Number of stored values, including explicit zeros.
data	Data array of the matrix
indices	CSC format index array
indptr	CSC format index pointer array
has_sorted_indices	Determine whether the matrix has sorted indices

Methods

`__len__`()	

`__mul__`(other)	interpret other and call one of the following
`arcsin`()	Element-wise arcsin.
`arcsinh`()	Element-wise arcsinh.
`arctan`()	Element-wise arctan.
`arctanh`()	Element-wise arctanh.
`argmax`([axis, out])	Return indices of maximum elements along an axis.
`argmin`([axis, out])	Return indices of minimum elements along an axis.
`asformat`(format[, copy])	Return this matrix in the passed format.
`asfptype`()	Upcast matrix to a floating point format (if necessary)
`astype`(dtype[, casting, copy])	Cast the matrix elements to a specified type.
`ceil`()	Element-wise ceil.
`check_format`([full_check])	check whether the matrix format is valid
`conj`([copy])	Element-wise complex conjugation.
`conjugate`([copy])	Element-wise complex conjugation.
`copy`()	Returns a copy of this matrix.
`count_nonzero`()	Number of non-zero entries, equivalent to
`deg2rad`()	Element-wise deg2rad.
`diagonal`([k])	Returns the kth diagonal of the matrix.
`dot`(other)	Ordinary dot product
`eliminate_zeros`()	Remove zero entries from the matrix
`expm1`()	Element-wise expm1.
`floor`()	Element-wise floor.
`getH`()	Return the Hermitian transpose of this matrix.
`get_shape`()	Get shape of a matrix.
`getcol`(i)	Returns a copy of column i of the matrix, as a (m x 1) CSC matrix (column vector).
`getformat`()	Format of a matrix representation as a string.
`getmaxprint`()	Maximum number of elements to display when printed.
`getnnz`([axis])	Number of stored values, including explicit zeros.
`getrow`(i)	Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).
`log1p`()	Element-wise log1p.
`max`([axis, out])	Return the maximum of the matrix or maximum along an axis.
`maximum`(other)	Element-wise maximum between this and another matrix.
`mean`([axis, dtype, out])	Compute the arithmetic mean along the specified axis.
`min`([axis, out])	Return the minimum of the matrix or maximum along an axis.
`minimum`(other)	Element-wise minimum between this and another matrix.
`multiply`(other)	Point-wise multiplication by another matrix, vector, or scalar.
`nonzero`()	nonzero indices
`power`(n[, dtype])	This function performs element-wise power.
`prune`()	Remove empty space after all non-zero elements.

continues on next page

Table 177 – continued from previous page

rad2deg()	Element-wise rad2deg.
reshape(self, shape[, order, copy])	Gives a new shape to a sparse matrix without changing its data.
resize(*shape)	Resize the matrix in-place to dimensions given by `shape`
rint()	Element-wise rint.
set_shape(shape)	See *reshape*.
setdiag(values[, k])	Set diagonal or off-diagonal elements of the array.
sign()	Element-wise sign.
sin()	Element-wise sin.
sinh()	Element-wise sinh.
sort_indices()	Sort the indices of this matrix *in place*
sorted_indices()	Return a copy of this matrix with sorted indices
sqrt()	Element-wise sqrt.
sum([axis, dtype, out])	Sum the matrix elements over a given axis.
sum_duplicates()	Eliminate duplicate matrix entries by adding them together
tan()	Element-wise tan.
tanh()	Element-wise tanh.
toarray([order, out])	Return a dense ndarray representation of this matrix.
tobsr([blocksize, copy])	Convert this matrix to Block Sparse Row format.
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc([copy])	Convert this matrix to Compressed Sparse Column format.
tocsr([copy])	Convert this matrix to Compressed Sparse Row format.
todense([order, out])	Return a dense matrix representation of this matrix.
todia([copy])	Convert this matrix to sparse DIAgonal format.
todok([copy])	Convert this matrix to Dictionary Of Keys format.
tolil([copy])	Convert this matrix to List of Lists format.
transpose([axes, copy])	Reverses the dimensions of the sparse matrix.
trunc()	Element-wise trunc.

scipy.sparse.csc_matrix.__len__

csc_matrix.**__len__**()

scipy.sparse.csc_matrix.__mul__

csc_matrix.**__mul__**(*other*)
interpret other and call one of the following

self._mul_scalar() self._mul_vector() self._mul_multivector() self._mul_sparse_matrix()

scipy.sparse.csc_matrix.arcsin

csc_matrix.**arcsin**()
Element-wise arcsin.

See numpy.arcsin for more information.

scipy.sparse.csc_matrix.arcsinh

csc_matrix.**arcsinh**()
Element-wise arcsinh.

See numpy.arcsinh for more information.

scipy.sparse.csc_matrix.arctan

csc_matrix.**arctan**()
Element-wise arctan.

See numpy.arctan for more information.

scipy.sparse.csc_matrix.arctanh

csc_matrix.**arctanh**()
Element-wise arctanh.

See numpy.arctanh for more information.

scipy.sparse.csc_matrix.argmax

csc_matrix.**argmax**(*axis=None*, *out=None*)
Return indices of maximum elements along an axis.

Implicit zero elements are also taken into account. If there are several maximum values, the index of the first occurrence is returned.

Parameters

axis [{-2, -1, 0, 1, None}, optional] Axis along which the argmax is computed. If None (default), index of the maximum element in the flatten data is returned.

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind [numpy.matrix or int] Indices of maximum elements. If matrix, its size along *axis* is 1.

scipy.sparse.csc_matrix.argmin

csc_matrix.**argmin**(*axis=None*, *out=None*)

Return indices of minimum elements along an axis.

Implicit zero elements are also taken into account. If there are several minimum values, the index of the first occurrence is returned.

Parameters

axis [{-2, -1, 0, 1, None}, optional] Axis along which the argmin is computed. If None (default), index of the minimum element in the flatten data is returned.

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind [numpy.matrix or int] Indices of minimum elements. If matrix, its size along *axis* is 1.

scipy.sparse.csc_matrix.asformat

csc_matrix.**asformat**(*format*, *copy=False*)

Return this matrix in the passed format.

Parameters

format [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", ...) or None for no conversion.

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [This matrix in the passed format.]

scipy.sparse.csc_matrix.asfptype

csc_matrix.**asfptype**()

Upcast matrix to a floating point format (if necessary)

scipy.sparse.csc_matrix.astype

csc_matrix.**astype**(*dtype*, *casting='unsafe'*, *copy=True*)

Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. 'no' means the data types should not be cast at all. 'equiv' means only byte-order changes are allowed. 'safe' means only casts which can preserve values are allowed. 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed. 'unsafe' means any data conversions may be done.

copy [bool, optional] If *copy* is *False*, the result might share some memory with this matrix. If *copy* is *True*, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.csc_matrix.ceil

csc_matrix.**ceil**()
Element-wise ceil.

See numpy.ceil for more information.

scipy.sparse.csc_matrix.check_format

csc_matrix.**check_format**(*full_check=True*)
check whether the matrix format is valid

Parameters

full_check [bool, optional] If *True*, rigorous check, O(N) operations. Otherwise basic check, O(1) operations (default True).

scipy.sparse.csc_matrix.conj

csc_matrix.**conj**(*copy=True*)
Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.csc_matrix.conjugate

csc_matrix.**conjugate**(*copy=True*)
Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.csc_matrix.copy

csc_matrix.**copy**()
Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.csc_matrix.count_nonzero

csc_matrix.**count_nonzero**()
Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.csc_matrix.deg2rad

csc_matrix.**deg2rad**()
Element-wise deg2rad.

See numpy.deg2rad for more information.

scipy.sparse.csc_matrix.diagonal

csc_matrix.**diagonal**(*k=0*)
Returns the kth diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to get, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.csc_matrix.dot

csc_matrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.csc_matrix.eliminate_zeros

csc_matrix.**eliminate_zeros**()
Remove zero entries from the matrix

This is an *in place* operation.

scipy.sparse.csc_matrix.expm1

csc_matrix.**expm1**()
Element-wise expm1.

See numpy.expm1 for more information.

scipy.sparse.csc_matrix.floor

csc_matrix.**floor**()
Element-wise floor.

See numpy.floor for more information.

scipy.sparse.csc_matrix.getH

csc_matrix.**getH**()
Return the Hermitian transpose of this matrix.

See also:

numpy.matrix.getH

NumPy's implementation of *getH* for matrices

scipy.sparse.csc_matrix.get_shape

csc_matrix.**get_shape**()
Get shape of a matrix.

scipy.sparse.csc_matrix.getcol

csc_matrix.**getcol**(*i*)
Returns a copy of column i of the matrix, as a (m x 1) CSC matrix (column vector).

scipy.sparse.csc_matrix.getformat

csc_matrix.**getformat**()
Format of a matrix representation as a string.

scipy.sparse.csc_matrix.getmaxprint

csc_matrix.**getmaxprint**()
Maximum number of elements to display when printed.

scipy.sparse.csc_matrix.getnnz

csc_matrix.**getnnz**(*axis=None*)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero

Number of non-zero entries

scipy.sparse.csc_matrix.getrow

csc_matrix.**getrow**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).

scipy.sparse.csc_matrix.log1p

csc_matrix.**log1p**()
Element-wise log1p.

See numpy.log1p for more information.

scipy.sparse.csc_matrix.max

csc_matrix.**max**(*axis=None*, *out=None*)
Return the maximum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the maximum over all the matrix elements, returning a scalar (i.e., *axis* = *None*).

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amax [coo_matrix or scalar] Maximum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension `a.ndim - 1`.

See also:

min

The minimum value of a sparse matrix along a given axis.

numpy.matrix.max

NumPy's implementation of 'max' for matrices

scipy.sparse.csc_matrix.maximum

csc_matrix.**maximum**(*other*)
Element-wise maximum between this and another matrix.

scipy.sparse.csc_matrix.mean

csc_matrix.**mean**(*axis=None*, *dtype=None*, *out=None*)
Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e., *axis* = *None*).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]

See also:

numpy.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.csc_matrix.min

csc_matrix.**min**(*axis=None*, *out=None*)

Return the minimum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the minimum over all the matrix elements, returning a scalar (i.e., *axis* = *None*).

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amin [coo_matrix or scalar] Minimum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension `a.ndim - 1`.

See also:

max

The maximum value of a sparse matrix along a given axis.

numpy.matrix.min

NumPy's implementation of 'min' for matrices

scipy.sparse.csc_matrix.minimum

csc_matrix.**minimum**(*other*)

Element-wise minimum between this and another matrix.

scipy.sparse.csc_matrix.multiply

csc_matrix.**multiply**(*other*)
Point-wise multiplication by another matrix, vector, or scalar.

scipy.sparse.csc_matrix.nonzero

csc_matrix.**nonzero**()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.csc_matrix.power

csc_matrix.**power**(*n*, *dtype=None*)
This function performs element-wise power.

Parameters

n	[n is a scalar]
dtype	[If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.csc_matrix.prune

csc_matrix.**prune**()
Remove empty space after all non-zero elements.

scipy.sparse.csc_matrix.rad2deg

csc_matrix.**rad2deg**()
Element-wise rad2deg.

See numpy.rad2deg for more information.

scipy.sparse.csc_matrix.reshape

csc_matrix.**reshape**(*self*, *shape*, *order='C'*, *copy=False*)

Gives a new shape to a sparse matrix without changing its data.

Parameters

shape [length-2 tuple of ints] The new shape should be compatible with the original shape.

order [{'C', 'F'}, optional] Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. 'F' means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.

copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix

[sparse matrix] A sparse matrix with the given `shape`, not necessarily of the same format as the current object.

See also:

numpy.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.csc_matrix.resize

csc_matrix.**resize**(**shape*)

Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.csc_matrix.rint

csc_matrix.**rint**()
Element-wise rint.

See numpy.rint for more information.

scipy.sparse.csc_matrix.set_shape

csc_matrix.**set_shape**(*shape*)
See *reshape*.

scipy.sparse.csc_matrix.setdiag

csc_matrix.**setdiag**(*values*, *k=0*)
Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values are longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.csc_matrix.sign

csc_matrix.**sign**()
Element-wise sign.

See numpy.sign for more information.

scipy.sparse.csc_matrix.sin

csc_matrix.**sin**()
Element-wise sin.

See numpy.sin for more information.

scipy.sparse.csc_matrix.sinh

csc_matrix.**sinh**()
Element-wise sinh.

See numpy.sinh for more information.

scipy.sparse.csc_matrix.sort_indices

csc_matrix.**sort_indices**()
Sort the indices of this matrix *in place*

scipy.sparse.csc_matrix.sorted_indices

csc_matrix.**sorted_indices**()
Return a copy of this matrix with sorted indices

scipy.sparse.csc_matrix.sqrt

csc_matrix.**sqrt**()
Element-wise sqrt.

See numpy.sqrt for more information.

scipy.sparse.csc_matrix.sum

csc_matrix.**sum**(*axis=None*, *dtype=None*, *out=None*)
Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e., *axis* = *None*).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

sum_along_axis
[np.matrix] A matrix with the same shape as *self*, with the specified axis removed.

See also:

numpy.matrix.sum

NumPy's implementation of 'sum' for matrices

scipy.sparse.csc_matrix.sum_duplicates

csc_matrix.**sum_duplicates**()
Eliminate duplicate matrix entries by adding them together

This is an *in place* operation.

scipy.sparse.csc_matrix.tan

csc_matrix.**tan**()
Element-wise tan.

See numpy.tan for more information.

scipy.sparse.csc_matrix.tanh

csc_matrix.**tanh**()
Element-wise tanh.

See numpy.tanh for more information.

scipy.sparse.csc_matrix.toarray

csc_matrix.**toarray**(*order=None*, *out=None*)
Return a dense ndarray representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multidimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns

arr [ndarray, 2-D] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

scipy.sparse.csc_matrix.tobsr

csc_matrix.**tobsr**(*blocksize=None*, *copy=False*)
Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.csc_matrix.tocoo

csc_matrix.**tocoo**(*copy=True*)
Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.csc_matrix.tocsc

csc_matrix.**tocsc**(*copy=False*)
Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.csc_matrix.tocsr

csc_matrix.**tocsr**(*copy=False*)
Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.csc_matrix.todense

csc_matrix.**todense**(*order=None*, *out=None*)
Return a dense matrix representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-D] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

scipy.sparse.csc_matrix.todia

csc_matrix.**todia**(*copy=False*)
Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.csc_matrix.todok

csc_matrix.**todok**(*copy=False*)
Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.csc_matrix.tolil

csc_matrix.**tolil**(*copy=False*)
Convert this matrix to List of Lists format.

With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.csc_matrix.transpose

csc_matrix.**transpose**(*axes=None*, *copy=False*)
Reverses the dimensions of the sparse matrix.

Parameters

axes [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.

copy [bool, optional] Indicates whether or not attributes of *self* should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p [*self* with the dimensions reversed.]

See also:

numpy.matrix.transpose

NumPy's implementation of 'transpose' for matrices

scipy.sparse.csc_matrix.trunc

csc_matrix.**trunc**()
Element-wise trunc.

See numpy.trunc for more information.

__getitem__	

scipy.sparse.csr_matrix

class scipy.sparse.**csr_matrix**(*arg1*, *shape=None*, *dtype=None*, *copy=False*)

Compressed Sparse Row matrix

This can be instantiated in several ways:

csr_matrix(D)

with a dense matrix or rank-2 ndarray D

csr_matrix(S)

with another sparse matrix S (equivalent to S.tocsr())

csr_matrix((M, N), [dtype])

to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

csr_matrix((data, (row_ind, col_ind)), [shape=(M, N)])

where `data`, `row_ind` and `col_ind` satisfy the relationship `a[row_ind[k], col_ind[k]] = data[k]`.

csr_matrix((data, indices, indptr), [shape=(M, N)])

is the standard CSR representation where the column indices for row i are stored in `indices[indptr[i]:indptr[i+1]]` and their corresponding values are stored in `data[indptr[i]:indptr[i+1]]`. If the shape parameter is not supplied, the matrix dimensions are inferred from the index arrays.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the CSR format

- efficient arithmetic operations CSR + CSR, CSR * CSR, etc.
- efficient row slicing
- fast matrix vector products

Disadvantages of the CSR format

- slow column slicing operations (consider CSC)
- changes to the sparsity structure are expensive (consider LIL or DOK)

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> csr_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> row = np.array([0, 0, 1, 2, 2, 2])
>>> col = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csr_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])
```

```
>>> indptr = np.array([0, 2, 3, 6])
>>> indices = np.array([0, 2, 2, 0, 1, 2])
>>> data = np.array([1, 2, 3, 4, 5, 6])
>>> csr_matrix((data, indices, indptr), shape=(3, 3)).toarray()
array([[1, 0, 2],
       [0, 0, 3],
       [4, 5, 6]])
```

Duplicate entries are summed together:

```
>>> row = np.array([0, 1, 2, 0])
>>> col = np.array([0, 1, 1, 0])
>>> data = np.array([1, 2, 4, 8])
>>> csr_matrix((data, (row, col)), shape=(3, 3)).toarray()
array([[9, 0, 0],
       [0, 2, 0],
       [0, 4, 0]])
```

As an example of how to construct a CSR matrix incrementally, the following snippet builds a term-document matrix from texts:

```
>>> docs = [["hello", "world", "hello"], ["goodbye", "cruel", "world"]]
>>> indptr = [0]
>>> indices = []
>>> data = []
>>> vocabulary = {}
>>> for d in docs:
...     for term in d:
...         index = vocabulary.setdefault(term, len(vocabulary))
...         indices.append(index)
...         data.append(1)
...     indptr.append(len(indices))
...
>>> csr_matrix((data, indices, indptr), dtype=int).toarray()
array([[2, 1, 0, 0],
       [0, 1, 1, 1]])
```

Attributes

dtype [dtype] Data type of the matrix
shape [2-tuple] Get shape of a matrix.
ndim [int] Number of dimensions (this is always 2)
nnz Number of stored values, including explicit zeros.
data CSR format data array of the matrix
indices CSR format index array of the matrix
indptr CSR format index pointer array of the matrix
has_sorted_indices
Determine whether the matrix has sorted indices

Methods

__len__()	
__mul__(other)	interpret other and call one of the following
arcsin()	Element-wise arcsin.
arcsinh()	Element-wise arcsinh.
arctan()	Element-wise arctan.
arctanh()	Element-wise arctanh.
argmax([axis, out])	Return indices of maximum elements along an axis.
argmin([axis, out])	Return indices of minimum elements along an axis.
asformat(format[, copy])	Return this matrix in the passed format.
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(dtype[, casting, copy])	Cast the matrix elements to a specified type.
ceil()	Element-wise ceil.
check_format([full_check])	check whether the matrix format is valid
conj([copy])	Element-wise complex conjugation.
conjugate([copy])	Element-wise complex conjugation.
copy()	Returns a copy of this matrix.
count_nonzero()	Number of non-zero entries, equivalent to
deg2rad()	Element-wise deg2rad.
diagonal([k])	Returns the kth diagonal of the matrix.
dot(other)	Ordinary dot product
eliminate_zeros()	Remove zero entries from the matrix
expm1()	Element-wise expm1.
floor()	Element-wise floor.
getH()	Return the Hermitian transpose of this matrix.
get_shape()	Get shape of a matrix.
getcol(i)	Returns a copy of column i of the matrix, as a (m x 1) CSR matrix (column vector).
getformat()	Format of a matrix representation as a string.
getmaxprint()	Maximum number of elements to display when printed.
getnnz([axis])	Number of stored values, including explicit zeros.
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).
log1p()	Element-wise log1p.
max([axis, out])	Return the maximum of the matrix or maximum along an axis.

continues on next page

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maximum(other)	Element-wise maximum between this and another matrix.
mean([axis, dtype, out])	Compute the arithmetic mean along the specified axis.
min([axis, out])	Return the minimum of the matrix or maximum along an axis.
minimum(other)	Element-wise minimum between this and another matrix.
multiply(other)	Point-wise multiplication by another matrix, vector, or scalar.
nonzero()	nonzero indices
power(n[, dtype])	This function performs element-wise power.
prune()	Remove empty space after all non-zero elements.
rad2deg()	Element-wise rad2deg.
reshape(self, shape[, order, copy])	Gives a new shape to a sparse matrix without changing its data.
resize(*shape)	Resize the matrix in-place to dimensions given by `shape`
rint()	Element-wise rint.
set_shape(shape)	See *reshape*.
setdiag(values[, k])	Set diagonal or off-diagonal elements of the array.
sign()	Element-wise sign.
sin()	Element-wise sin.
sinh()	Element-wise sinh.
sort_indices()	Sort the indices of this matrix *in place*
sorted_indices()	Return a copy of this matrix with sorted indices
sqrt()	Element-wise sqrt.
sum([axis, dtype, out])	Sum the matrix elements over a given axis.
sum_duplicates()	Eliminate duplicate matrix entries by adding them together
tan()	Element-wise tan.
tanh()	Element-wise tanh.
toarray([order, out])	Return a dense ndarray representation of this matrix.
tobsr([blocksize, copy])	Convert this matrix to Block Sparse Row format.
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc([copy])	Convert this matrix to Compressed Sparse Column format.
tocsr([copy])	Convert this matrix to Compressed Sparse Row format.
todense([order, out])	Return a dense matrix representation of this matrix.
todia([copy])	Convert this matrix to sparse DIAgonal format.
todok([copy])	Convert this matrix to Dictionary Of Keys format.
tolil([copy])	Convert this matrix to List of Lists format.
transpose([axes, copy])	Reverses the dimensions of the sparse matrix.
trunc()	Element-wise trunc.

scipy.sparse.csr_matrix.__len__

csr_matrix.**__len__**()

scipy.sparse.csr_matrix.__mul__

csr_matrix.**__mul__**(*other*)
interpret other and call one of the following

self._mul_scalar() self._mul_vector() self._mul_multivector() self._mul_sparse_matrix()

scipy.sparse.csr_matrix.arcsin

csr_matrix.**arcsin**()
Element-wise arcsin.

See numpy.arcsin for more information.

scipy.sparse.csr_matrix.arcsinh

csr_matrix.**arcsinh**()
Element-wise arcsinh.

See numpy.arcsinh for more information.

scipy.sparse.csr_matrix.arctan

csr_matrix.**arctan**()
Element-wise arctan.

See numpy.arctan for more information.

scipy.sparse.csr_matrix.arctanh

csr_matrix.**arctanh**()
Element-wise arctanh.

See numpy.arctanh for more information.

scipy.sparse.csr_matrix.argmax

csr_matrix.**argmax**(*axis=None*, *out=None*)
Return indices of maximum elements along an axis.

Implicit zero elements are also taken into account. If there are several maximum values, the index of the first occurrence is returned.

Parameters

axis [{-2, -1, 0, 1, None}, optional] Axis along which the argmax is computed. If None (default), index of the maximum element in the flatten data is returned.

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind [numpy.matrix or int] Indices of maximum elements. If matrix, its size along *axis* is 1.

scipy.sparse.csr_matrix.argmin

csr_matrix.**argmin**(*axis=None*, *out=None*)

Return indices of minimum elements along an axis.

Implicit zero elements are also taken into account. If there are several minimum values, the index of the first occurrence is returned.

Parameters

axis [{-2, -1, 0, 1, None}, optional] Axis along which the argmin is computed. If None (default), index of the minimum element in the flatten data is returned.

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

ind [numpy.matrix or int] Indices of minimum elements. If matrix, its size along *axis* is 1.

scipy.sparse.csr_matrix.asformat

csr_matrix.**asformat**(*format*, *copy=False*)

Return this matrix in the passed format.

Parameters

format [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", …) or None for no conversion.

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [This matrix in the passed format.]

scipy.sparse.csr_matrix.asfptype

csr_matrix.**asfptype**()

Upcast matrix to a floating point format (if necessary)

scipy.sparse.csr_matrix.astype

csr_matrix.**astype**(*dtype*, *casting='unsafe'*, *copy=True*)

Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. 'no' means the data types should not be cast at all. 'equiv' means only byte-order changes are allowed. 'safe' means only casts which can preserve values are allowed. 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed. 'unsafe' means any data conversions may be done.

copy [bool, optional] If *copy* is *False*, the result might share some memory with this matrix. If *copy* is *True*, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.csr_matrix.ceil

csr_matrix.**ceil**()

Element-wise ceil.

See numpy.ceil for more information.

scipy.sparse.csr_matrix.check_format

csr_matrix.**check_format**(*full_check=True*)

check whether the matrix format is valid

Parameters

full_check [bool, optional] If *True*, rigorous check, O(N) operations. Otherwise basic check, O(1) operations (default True).

scipy.sparse.csr_matrix.conj

csr_matrix.**conj**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.csr_matrix.conjugate

csr_matrix.**conjugate**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.csr_matrix.copy

csr_matrix.**copy**()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.csr_matrix.count_nonzero

csr_matrix.**count_nonzero**()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.csr_matrix.deg2rad

csr_matrix.**deg2rad**()

Element-wise deg2rad.

See numpy.deg2rad for more information.

scipy.sparse.csr_matrix.diagonal

csr_matrix.**diagonal**(*k=0*)

Returns the kth diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to get, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.csr_matrix.dot

csr_matrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.csr_matrix.eliminate_zeros

csr_matrix.**eliminate_zeros**()
Remove zero entries from the matrix

This is an *in place* operation.

scipy.sparse.csr_matrix.expm1

csr_matrix.**expm1**()
Element-wise expm1.

See numpy.expm1 for more information.

scipy.sparse.csr_matrix.floor

csr_matrix.**floor**()
Element-wise floor.

See numpy.floor for more information.

scipy.sparse.csr_matrix.getH

csr_matrix.**getH**()
Return the Hermitian transpose of this matrix.

See also:

numpy.matrix.getH

NumPy's implementation of *getH* for matrices

scipy.sparse.csr_matrix.get_shape

csr_matrix.**get_shape**()
Get shape of a matrix.

scipy.sparse.csr_matrix.getcol

csr_matrix.**getcol**(*i*)
Returns a copy of column i of the matrix, as a (m x 1) CSR matrix (column vector).

scipy.sparse.csr_matrix.getformat

csr_matrix.**getformat**()
Format of a matrix representation as a string.

scipy.sparse.csr_matrix.getmaxprint

csr_matrix.**getmaxprint**()
Maximum number of elements to display when printed.

scipy.sparse.csr_matrix.getnnz

csr_matrix.**getnnz**(*axis=None*)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero

Number of non-zero entries

scipy.sparse.csr_matrix.getrow

csr_matrix.**getrow**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) CSR matrix (row vector).

scipy.sparse.csr_matrix.log1p

csr_matrix.**log1p**()
Element-wise log1p.

See numpy.log1p for more information.

scipy.sparse.csr_matrix.max

csr_matrix.**max**(*axis=None*, *out=None*)
Return the maximum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the maximum over all the matrix elements, returning a scalar (i.e., *axis* = *None*).

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amax [coo_matrix or scalar] Maximum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension a.ndim - 1.

See also:

min

The minimum value of a sparse matrix along a given axis.

numpy.matrix.max

NumPy's implementation of 'max' for matrices

scipy.sparse.csr_matrix.maximum

csr_matrix.**maximum**(*other*)
Element-wise maximum between this and another matrix.

scipy.sparse.csr_matrix.mean

csr_matrix.**mean**(*axis=None*, *dtype=None*, *out=None*)

Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e., *axis* = *None*).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]

See also:

numpy.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.csr_matrix.min

csr_matrix.**min**(*axis=None*, *out=None*)

Return the minimum of the matrix or maximum along an axis. This takes all elements into account, not just the non-zero ones.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the minimum over all the matrix elements, returning a scalar (i.e., *axis* = *None*).

out [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value, as this argument is not used.

Returns

amin [coo_matrix or scalar] Minimum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is a sparse.coo_matrix of dimension `a.ndim - 1`.

See also:

max

The maximum value of a sparse matrix along a given axis.

numpy.matrix.min

NumPy's implementation of 'min' for matrices

scipy.sparse.csr_matrix.minimum

csr_matrix.**minimum**(*other*)
Element-wise minimum between this and another matrix.

scipy.sparse.csr_matrix.multiply

csr_matrix.**multiply**(*other*)
Point-wise multiplication by another matrix, vector, or scalar.

scipy.sparse.csr_matrix.nonzero

csr_matrix.**nonzero**()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.csr_matrix.power

csr_matrix.**power**(*n*, *dtype=None*)
This function performs element-wise power.

Parameters

n	[n is a scalar]
dtype	[If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.csr_matrix.prune

csr_matrix.**prune**()
Remove empty space after all non-zero elements.

scipy.sparse.csr_matrix.rad2deg

csr_matrix.**rad2deg**()
Element-wise rad2deg.

See numpy.rad2deg for more information.

scipy.sparse.csr_matrix.reshape

csr_matrix.**reshape**(*self*, *shape*, *order='C'*, *copy=False*)

Gives a new shape to a sparse matrix without changing its data.

Parameters

shape [length-2 tuple of ints] The new shape should be compatible with the original shape.

order [{'C', 'F'}, optional] Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. 'F' means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.

copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix

[sparse matrix] A sparse matrix with the given `shape`, not necessarily of the same format as the current object.

See also:

numpy.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.csr_matrix.resize

csr_matrix.**resize**(**shape*)

Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.csr_matrix.rint

csr_matrix.**rint**()
Element-wise rint.

See numpy.rint for more information.

scipy.sparse.csr_matrix.set_shape

csr_matrix.**set_shape**(*shape*)
See *reshape*.

scipy.sparse.csr_matrix.setdiag

csr_matrix.**setdiag**(*values*, *k=0*)
Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values are longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.csr_matrix.sign

csr_matrix.**sign**()
Element-wise sign.

See numpy.sign for more information.

scipy.sparse.csr_matrix.sin

csr_matrix.**sin**()
Element-wise sin.

See numpy.sin for more information.

scipy.sparse.csr_matrix.sinh

csr_matrix.**sinh**()
Element-wise sinh.

See numpy.sinh for more information.

scipy.sparse.csr_matrix.sort_indices

csr_matrix.**sort_indices**()
Sort the indices of this matrix *in place*

scipy.sparse.csr_matrix.sorted_indices

csr_matrix.**sorted_indices**()
Return a copy of this matrix with sorted indices

scipy.sparse.csr_matrix.sqrt

csr_matrix.**sqrt**()
Element-wise sqrt.

See numpy.sqrt for more information.

scipy.sparse.csr_matrix.sum

csr_matrix.**sum**(*axis=None*, *dtype=None*, *out=None*)
Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e., *axis* = *None*).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

sum_along_axis
[np.matrix] A matrix with the same shape as *self*, with the specified axis removed.

See also:

numpy.matrix.sum

NumPy's implementation of 'sum' for matrices

scipy.sparse.csr_matrix.sum_duplicates

csr_matrix.**sum_duplicates**()
Eliminate duplicate matrix entries by adding them together

This is an *in place* operation.

scipy.sparse.csr_matrix.tan

csr_matrix.**tan**()
Element-wise tan.

See numpy.tan for more information.

scipy.sparse.csr_matrix.tanh

csr_matrix.**tanh**()
Element-wise tanh.

See numpy.tanh for more information.

scipy.sparse.csr_matrix.toarray

csr_matrix.**toarray**(*order=None*, *out=None*)
Return a dense ndarray representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multidimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns

arr [ndarray, 2-D] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

scipy.sparse.csr_matrix.tobsr

csr_matrix.**tobsr**(*blocksize=None*, *copy=True*)
Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.csr_matrix.tocoo

csr_matrix.**tocoo**(*copy=True*)
Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.csr_matrix.tocsc

csr_matrix.**tocsc**(*copy=False*)
Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.csr_matrix.tocsr

csr_matrix.**tocsr**(*copy=False*)
Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.csr_matrix.todense

csr_matrix.**todense**(*order=None*, *out=None*)
Return a dense matrix representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-D] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

scipy.sparse.csr_matrix.todia

csr_matrix.**todia**(*copy=False*)
Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.csr_matrix.todok

csr_matrix.**todok**(*copy=False*)

Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.csr_matrix.tolil

csr_matrix.**tolil**(*copy=False*)

Convert this matrix to List of Lists format.

With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.csr_matrix.transpose

csr_matrix.**transpose**(*axes=None*, *copy=False*)

Reverses the dimensions of the sparse matrix.

Parameters

axes [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.

copy [bool, optional] Indicates whether or not attributes of *self* should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p [*self* with the dimensions reversed.]

See also:

numpy.matrix.transpose

NumPy's implementation of 'transpose' for matrices

scipy.sparse.csr_matrix.trunc

csr_matrix.**trunc**()

Element-wise trunc.

See numpy.trunc for more information.

__getitem__	

scipy.sparse.dia_matrix

class scipy.sparse.**dia_matrix**(*arg1*, *shape=None*, *dtype=None*, *copy=False*)

Sparse matrix with DIAgonal storage

This can be instantiated in several ways:

dia_matrix(D)

with a dense matrix

dia_matrix(S)

with another sparse matrix S (equivalent to S.todia())

dia_matrix((M, N), [dtype])

to construct an empty matrix with shape (M, N), dtype is optional, defaulting to dtype='d'.

dia_matrix((data, offsets), shape=(M, N))

where the `data[k,:]` stores the diagonal entries for diagonal `offsets[k]` (See example below)

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Examples

```
>>> import numpy as np
>>> from scipy.sparse import dia_matrix
>>> dia_matrix((3, 4), dtype=np.int8).toarray()
array([[0, 0, 0, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]], dtype=int8)
```

```
>>> data = np.array([[1, 2, 3, 4]]).repeat(3, axis=0)
>>> offsets = np.array([0, -1, 2])
>>> dia_matrix((data, offsets), shape=(4, 4)).toarray()
array([[1, 0, 3, 0],
       [1, 2, 0, 4],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

```
>>> from scipy.sparse import dia_matrix
>>> n = 10
>>> ex = np.ones(n)
>>> data = np.array([ex, 2 * ex, ex])
>>> offsets = np.array([-1, 0, 1])
>>> dia_matrix((data, offsets), shape=(n, n)).toarray()
array([[2., 1., 0., ..., 0., 0., 0.],
       [1., 2., 1., ..., 0., 0., 0.],
```

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```
       [0., 1., 2., ..., 0., 0., 0.],
       ...,
       [0., 0., 0., ..., 2., 1., 0.],
       [0., 0., 0., ..., 1., 2., 1.],
       [0., 0., 0., ..., 0., 1., 2.]])
```

Attributes

dtype	[dtype] Data type of the matrix
shape	[2-tuple] Get shape of a matrix.
ndim	[int] Number of dimensions (this is always 2)
nnz	Number of stored values, including explicit zeros.
data	DIA format data array of the matrix
offsets	DIA format offset array of the matrix

Methods

__len__()	
__mul__(other)	interpret other and call one of the following
arcsin()	Element-wise arcsin.
arcsinh()	Element-wise arcsinh.
arctan()	Element-wise arctan.
arctanh()	Element-wise arctanh.
asformat(format[, copy])	Return this matrix in the passed format.
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(dtype[, casting, copy])	Cast the matrix elements to a specified type.
ceil()	Element-wise ceil.
conj([copy])	Element-wise complex conjugation.
conjugate([copy])	Element-wise complex conjugation.
copy()	Returns a copy of this matrix.
count_nonzero()	Number of non-zero entries, equivalent to
deg2rad()	Element-wise deg2rad.
diagonal([k])	Returns the kth diagonal of the matrix.
dot(other)	Ordinary dot product
expm1()	Element-wise expm1.
floor()	Element-wise floor.
getH()	Return the Hermitian transpose of this matrix.
get_shape()	Get shape of a matrix.
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
getformat()	Format of a matrix representation as a string.
getmaxprint()	Maximum number of elements to display when printed.
getnnz([axis])	Number of stored values, including explicit zeros.
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
log1p()	Element-wise log1p.

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maximum(other)	Element-wise maximum between this and another matrix.
mean([axis, dtype, out])	Compute the arithmetic mean along the specified axis.
minimum(other)	Element-wise minimum between this and another matrix.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
power(n[, dtype])	This function performs element-wise power.
rad2deg()	Element-wise rad2deg.
reshape(self, shape[, order, copy])	Gives a new shape to a sparse matrix without changing its data.
resize(*shape)	Resize the matrix in-place to dimensions given by `shape`
rint()	Element-wise rint.
set_shape(shape)	See *reshape*.
setdiag(values[, k])	Set diagonal or off-diagonal elements of the array.
sign()	Element-wise sign.
sin()	Element-wise sin.
sinh()	Element-wise sinh.
sqrt()	Element-wise sqrt.
sum([axis, dtype, out])	Sum the matrix elements over a given axis.
tan()	Element-wise tan.
tanh()	Element-wise tanh.
toarray([order, out])	Return a dense ndarray representation of this matrix.
tobsr([blocksize, copy])	Convert this matrix to Block Sparse Row format.
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc([copy])	Convert this matrix to Compressed Sparse Column format.
tocsr([copy])	Convert this matrix to Compressed Sparse Row format.
todense([order, out])	Return a dense matrix representation of this matrix.
todia([copy])	Convert this matrix to sparse DIAgonal format.
todok([copy])	Convert this matrix to Dictionary Of Keys format.
tolil([copy])	Convert this matrix to List of Lists format.
transpose([axes, copy])	Reverses the dimensions of the sparse matrix.
trunc()	Element-wise trunc.

scipy.sparse.dia_matrix.__len__

dia_matrix.**__len__**()

scipy.sparse.dia_matrix.__mul__

dia_matrix.**__mul__**(*other*)
interpret other and call one of the following

self._mul_scalar() self._mul_vector() self._mul_multivector() self._mul_sparse_matrix()

scipy.sparse.dia_matrix.arcsin

dia_matrix.**arcsin**()
Element-wise arcsin.

See numpy.arcsin for more information.

scipy.sparse.dia_matrix.arcsinh

dia_matrix.**arcsinh**()
Element-wise arcsinh.

See numpy.arcsinh for more information.

scipy.sparse.dia_matrix.arctan

dia_matrix.**arctan**()
Element-wise arctan.

See numpy.arctan for more information.

scipy.sparse.dia_matrix.arctanh

dia_matrix.**arctanh**()
Element-wise arctanh.

See numpy.arctanh for more information.

scipy.sparse.dia_matrix.asformat

dia_matrix.**asformat**(*format*, *copy=False*)
Return this matrix in the passed format.

Parameters

format [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", …) or None for no conversion.

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [This matrix in the passed format.]

scipy.sparse.dia_matrix.asfptype

dia_matrix.**asfptype**()
Upcast matrix to a floating point format (if necessary)

scipy.sparse.dia_matrix.astype

dia_matrix.**astype**(*dtype*, *casting='unsafe'*, *copy=True*)
Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.
casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. 'no' means the data types should not be cast at all. 'equiv' means only byte-order changes are allowed. 'safe' means only casts which can preserve values are allowed. 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed. 'unsafe' means any data conversions may be done.
copy [bool, optional] If *copy* is *False*, the result might share some memory with this matrix. If *copy* is *True*, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.dia_matrix.ceil

dia_matrix.**ceil**()
Element-wise ceil.

See numpy.ceil for more information.

scipy.sparse.dia_matrix.conj

dia_matrix.**conj**(*copy=True*)
Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.dia_matrix.conjugate

dia_matrix.**conjugate**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.dia_matrix.copy

dia_matrix.**copy**()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.dia_matrix.count_nonzero

dia_matrix.**count_nonzero**()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.dia_matrix.deg2rad

dia_matrix.**deg2rad**()

Element-wise deg2rad.

See numpy.deg2rad for more information.

scipy.sparse.dia_matrix.diagonal

dia_matrix.**diagonal**(*k=0*)

Returns the kth diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to get, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.dia_matrix.dot

dia_matrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.dia_matrix.expm1

dia_matrix.**expm1**()
Element-wise expm1.

See numpy.expm1 for more information.

scipy.sparse.dia_matrix.floor

dia_matrix.**floor**()
Element-wise floor.

See numpy.floor for more information.

scipy.sparse.dia_matrix.getH

dia_matrix.**getH**()
Return the Hermitian transpose of this matrix.

See also:

numpy.matrix.getH

NumPy's implementation of *getH* for matrices

scipy.sparse.dia_matrix.get_shape

dia_matrix.**get_shape**()
Get shape of a matrix.

scipy.sparse.dia_matrix.getcol

dia_matrix.**getcol**(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

scipy.sparse.dia_matrix.getformat

dia_matrix.**getformat**()
Format of a matrix representation as a string.

scipy.sparse.dia_matrix.getmaxprint

dia_matrix.**getmaxprint**()
Maximum number of elements to display when printed.

scipy.sparse.dia_matrix.getnnz

dia_matrix.**getnnz**(*axis=None*)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero

Number of non-zero entries

scipy.sparse.dia_matrix.getrow

dia_matrix.**getrow**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

scipy.sparse.dia_matrix.log1p

dia_matrix.**log1p**()
Element-wise log1p.

See numpy.log1p for more information.

scipy.sparse.dia_matrix.maximum

dia_matrix.**maximum**(*other*)
Element-wise maximum between this and another matrix.

scipy.sparse.dia_matrix.mean

dia_matrix.**mean**(*axis=None*, *dtype=None*, *out=None*)
Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e., *axis* = *None*).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]

See also:

numpy.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.dia_matrix.minimum

dia_matrix.**minimum**(*other*)
Element-wise minimum between this and another matrix.

scipy.sparse.dia_matrix.multiply

dia_matrix.**multiply**(*other*)
Point-wise multiplication by another matrix

scipy.sparse.dia_matrix.nonzero

dia_matrix.**nonzero**()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.dia_matrix.power

dia_matrix.**power**(*n*, *dtype=None*)
This function performs element-wise power.

Parameters

n	[n is a scalar]
dtype	[If dtype is not specified, the current dtype will be preserved.]

scipy.sparse.dia_matrix.rad2deg

dia_matrix.**rad2deg**()
Element-wise rad2deg.

See numpy.rad2deg for more information.

scipy.sparse.dia_matrix.reshape

dia_matrix.**reshape**(*self*, *shape*, *order='C'*, *copy=False*)
Gives a new shape to a sparse matrix without changing its data.

Parameters

shape	[length-2 tuple of ints] The new shape should be compatible with the original shape.
order	[{'C', 'F'}, optional] Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. 'F' means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.
copy	[bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix
[sparse matrix] A sparse matrix with the given `shape`, not necessarily of the same format as the current object.

See also:

numpy.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.dia_matrix.resize

`dia_matrix.`**`resize`**`(*shape)`
Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.dia_matrix.rint

`dia_matrix.`**`rint`**`()`
Element-wise rint.

See `numpy.rint` for more information.

scipy.sparse.dia_matrix.set_shape

`dia_matrix.`**`set_shape`**`(shape)`
See *reshape*.

scipy.sparse.dia_matrix.setdiag

dia_matrix.**setdiag**(*values*, *k=0*)

Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values are longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.dia_matrix.sign

dia_matrix.**sign**()

Element-wise sign.

See numpy.sign for more information.

scipy.sparse.dia_matrix.sin

dia_matrix.**sin**()

Element-wise sin.

See numpy.sin for more information.

scipy.sparse.dia_matrix.sinh

dia_matrix.**sinh**()

Element-wise sinh.

See numpy.sinh for more information.

scipy.sparse.dia_matrix.sqrt

dia_matrix.**sqrt**()

Element-wise sqrt.

See numpy.sqrt for more information.

scipy.sparse.dia_matrix.sum

dia_matrix.**sum**(*axis=None*, *dtype=None*, *out=None*)

Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e., *axis* = *None*).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

sum_along_axis
[np.matrix] A matrix with the same shape as *self*, with the specified axis removed.

See also:

numpy.matrix.sum

NumPy's implementation of 'sum' for matrices

scipy.sparse.dia_matrix.tan

dia_matrix.**tan**()

Element-wise tan.

See numpy.tan for more information.

scipy.sparse.dia_matrix.tanh

dia_matrix.**tanh**()

Element-wise tanh.

See numpy.tanh for more information.

scipy.sparse.dia_matrix.toarray

dia_matrix.**toarray**(*order=None*, *out=None*)

Return a dense ndarray representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multidimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns

arr [ndarray, 2-D] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

scipy.sparse.dia_matrix.tobsr

dia_matrix.**tobsr**(*blocksize=None*, *copy=False*)

Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.dia_matrix.tocoo

dia_matrix.**tocoo**(*copy=False*)

Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.dia_matrix.tocsc

dia_matrix.**tocsc**(*copy=False*)

Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.dia_matrix.tocsr

dia_matrix.**tocsr**(*copy=False*)

Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.dia_matrix.todense

dia_matrix.**todense**(*order=None*, *out=None*)

Return a dense matrix representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-D] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

scipy.sparse.dia_matrix.todia

dia_matrix.**todia**(*copy=False*)

Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.dia_matrix.todok

dia_matrix.**todok**(*copy=False*)

Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.dia_matrix.tolil

dia_matrix.**tolil**(*copy=False*)

Convert this matrix to List of Lists format.

With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.dia_matrix.transpose

dia_matrix.**transpose**(*axes=None*, *copy=False*)

Reverses the dimensions of the sparse matrix.

Parameters

axes [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.

copy [bool, optional] Indicates whether or not attributes of *self* should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p [*self* with the dimensions reversed.]

See also:

numpy.matrix.transpose

NumPy's implementation of 'transpose' for matrices

scipy.sparse.dia_matrix.trunc

dia_matrix.**trunc**()

Element-wise trunc.

See numpy.trunc for more information.

scipy.sparse.dok_matrix

class scipy.sparse.**dok_matrix**(*arg1*, *shape=None*, *dtype=None*, *copy=False*)

Dictionary Of Keys based sparse matrix.

This is an efficient structure for constructing sparse matrices incrementally.

This can be instantiated in several ways:

dok_matrix(D)

with a dense matrix, D

dok_matrix(S)

with a sparse matrix, S

dok_matrix((M,N), [dtype])

create the matrix with initial shape (M,N) dtype is optional, defaulting to dtype='d'

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Allows for efficient O(1) access of individual elements. Duplicates are not allowed. Can be efficiently converted to a coo_matrix once constructed.

Examples

```
>>> import numpy as np
>>> from scipy.sparse import dok_matrix
>>> S = dok_matrix((5, 5), dtype=np.float32)
>>> for i in range(5):
...     for j in range(5):
...         S[i, j] = i + j     # Update element
```

Attributes

dtype	[dtype] Data type of the matrix
shape	[2-tuple] Get shape of a matrix.
ndim	[int] Number of dimensions (this is always 2)
nnz	Number of stored values, including explicit zeros.

Methods

__len__()	Return len(self).
__mul__(other)	interpret other and call one of the following
asformat(format[, copy])	Return this matrix in the passed format.
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(dtype[, casting, copy])	Cast the matrix elements to a specified type.
clear()	
conj([copy])	Element-wise complex conjugation.
conjtransp()	Return the conjugate transpose.
conjugate([copy])	Element-wise complex conjugation.
copy()	Returns a copy of this matrix.
count_nonzero()	Number of non-zero entries, equivalent to
diagonal([k])	Returns the kth diagonal of the matrix.
dot(other)	Ordinary dot product
fromkeys(iterable[, value])	Create a new dictionary with keys from iterable and values set to value.
get(key[, default])	This overrides the dict.get method, providing type checking but otherwise equivalent functionality.
getH()	Return the Hermitian transpose of this matrix.
get_shape()	Get shape of a matrix.
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
getformat()	Format of a matrix representation as a string.

continues on next page

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getmaxprint()	Maximum number of elements to display when printed.
getnnz([axis])	Number of stored values, including explicit zeros.
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
items()	
keys()	
maximum(other)	Element-wise maximum between this and another matrix.
mean([axis, dtype, out])	Compute the arithmetic mean along the specified axis.
minimum(other)	Element-wise minimum between this and another matrix.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
pop(k[,d])	If key is not found, d is returned if given, otherwise KeyError is raised
popitem(/)	Remove and return a (key, value) pair as a 2-tuple.
power(n[, dtype])	Element-wise power.
reshape(self, shape[, order, copy])	Gives a new shape to a sparse matrix without changing its data.
resize(*shape)	Resize the matrix in-place to dimensions given by `shape`
set_shape(shape)	See reshape.
setdefault(key[, default])	Insert key with a value of default if key is not in the dictionary.
setdiag(values[, k])	Set diagonal or off-diagonal elements of the array.
sum([axis, dtype, out])	Sum the matrix elements over a given axis.
toarray([order, out])	Return a dense ndarray representation of this matrix.
tobsr([blocksize, copy])	Convert this matrix to Block Sparse Row format.
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc([copy])	Convert this matrix to Compressed Sparse Column format.
tocsr([copy])	Convert this matrix to Compressed Sparse Row format.
todense([order, out])	Return a dense matrix representation of this matrix.
todia([copy])	Convert this matrix to sparse DIAgonal format.
todok([copy])	Convert this matrix to Dictionary Of Keys format.
tolil([copy])	Convert this matrix to List of Lists format.
transpose([axes, copy])	Reverses the dimensions of the sparse matrix.
update([E,]**F)	If E is present and has a .keys() method, then does: for k in E: D[k] = E[k] If E is present and lacks a .keys() method, then does: for k, v in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]
values()	

scipy.sparse.dok_matrix.__len__

dok_matrix.**__len__**()
Return len(self).

scipy.sparse.dok_matrix.__mul__

dok_matrix.**__mul__**(*other*)
interpret other and call one of the following

self._mul_scalar() self._mul_vector() self._mul_multivector() self._mul_sparse_matrix()

scipy.sparse.dok_matrix.asformat

dok_matrix.**asformat**(*format*, *copy=False*)
Return this matrix in the passed format.

Parameters

format [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", …) or None for no conversion.
copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [This matrix in the passed format.]

scipy.sparse.dok_matrix.asfptype

dok_matrix.**asfptype**()
Upcast matrix to a floating point format (if necessary)

scipy.sparse.dok_matrix.astype

dok_matrix.**astype**(*dtype*, *casting='unsafe'*, *copy=True*)
Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.
casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. 'no' means the data types should not be cast at all. 'equiv' means only byte-order changes are allowed. 'safe' means only casts which can preserve values are allowed. 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed. 'unsafe' means any data conversions may be done.
copy [bool, optional] If `copy` is *False*, the result might share some memory with this matrix. If `copy` is *True*, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.dok_matrix.clear

dok_matrix.**clear**() → None. Remove all items from D.

scipy.sparse.dok_matrix.conj

dok_matrix.**conj**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.dok_matrix.conjtransp

dok_matrix.**conjtransp**()

Return the conjugate transpose.

scipy.sparse.dok_matrix.conjugate

dok_matrix.**conjugate**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.dok_matrix.copy

dok_matrix.**copy**()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.dok_matrix.count_nonzero

dok_matrix.**count_nonzero**()
Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.dok_matrix.diagonal

dok_matrix.**diagonal**(*k=0*)
Returns the kth diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to get, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.dok_matrix.dot

dok_matrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.dok_matrix.fromkeys

dok_matrix.**fromkeys**(*iterable*, *value=None*, */*)
Create a new dictionary with keys from iterable and values set to value.

scipy.sparse.dok_matrix.get

dok_matrix.**get**(*key*, *default=0.0*)
This overrides the dict.get method, providing type checking but otherwise equivalent functionality.

scipy.sparse.dok_matrix.getH

dok_matrix.**getH**()
Return the Hermitian transpose of this matrix.

See also:

numpy.matrix.getH

NumPy's implementation of *getH* for matrices

scipy.sparse.dok_matrix.get_shape

dok_matrix.**get_shape**()
Get shape of a matrix.

scipy.sparse.dok_matrix.getcol

dok_matrix.**getcol**(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

scipy.sparse.dok_matrix.getformat

dok_matrix.**getformat**()
Format of a matrix representation as a string.

scipy.sparse.dok_matrix.getmaxprint

dok_matrix.**getmaxprint**()
Maximum number of elements to display when printed.

scipy.sparse.dok_matrix.getnnz

dok_matrix.**getnnz**(*axis=None*)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero

Number of non-zero entries

scipy.sparse.dok_matrix.getrow

dok_matrix.**getrow**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

scipy.sparse.dok_matrix.items

dok_matrix.**items**() → a set-like object providing a view on D's items

scipy.sparse.dok_matrix.keys

dok_matrix.**keys**() → a set-like object providing a view on D's keys

scipy.sparse.dok_matrix.maximum

dok_matrix.**maximum**(*other*)
Element-wise maximum between this and another matrix.

scipy.sparse.dok_matrix.mean

dok_matrix.**mean**(*axis=None*, *dtype=None*, *out=None*)
Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e., *axis* = *None*).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]

See also:

numpy.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.dok_matrix.minimum

dok_matrix.**minimum**(*other*)
Element-wise minimum between this and another matrix.

scipy.sparse.dok_matrix.multiply

dok_matrix.**multiply**(*other*)
Point-wise multiplication by another matrix

scipy.sparse.dok_matrix.nonzero

dok_matrix.**nonzero**()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.dok_matrix.pop

dok_matrix.**pop**($k[, d]$) $\rightarrow$ v, remove specified key and return the corresponding value.
If key is not found, d is returned if given, otherwise KeyError is raised

scipy.sparse.dok_matrix.popitem

dok_matrix.**popitem**(/)
Remove and return a (key, value) pair as a 2-tuple.

Pairs are returned in LIFO (last-in, first-out) order. Raises KeyError if the dict is empty.

scipy.sparse.dok_matrix.power

dok_matrix.**power**(*n*, *dtype=None*)
Element-wise power.

scipy.sparse.dok_matrix.reshape

dok_matrix.**reshape**(*self*, *shape*, *order='C'*, *copy=False*)
Gives a new shape to a sparse matrix without changing its data.

Parameters

shape [length-2 tuple of ints] The new shape should be compatible with the original shape.
order [{'C', 'F'}, optional] Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. 'F' means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.
copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix
[sparse matrix] A sparse matrix with the given `shape`, not necessarily of the same format as the current object.

See also:

numpy.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.dok_matrix.resize

dok_matrix.**resize**(**shape*)
Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.dok_matrix.set_shape

dok_matrix.**set_shape**(*shape*)
See *reshape*.

scipy.sparse.dok_matrix.setdefault

dok_matrix.**setdefault**(*key*, *default=None*, */*)
Insert key with a value of default if key is not in the dictionary.

Return the value for key if key is in the dictionary, else default.

scipy.sparse.dok_matrix.setdiag

dok_matrix.**setdiag**(*values*, *k=0*)
Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values are longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.dok_matrix.sum

dok_matrix.**sum**(*axis=None*, *dtype=None*, *out=None*)
Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e., *axis* = *None*).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

sum_along_axis
[np.matrix] A matrix with the same shape as *self*, with the specified axis removed.

See also:

numpy.matrix.sum

NumPy's implementation of 'sum' for matrices

scipy.sparse.dok_matrix.toarray

dok_matrix.**toarray**(*order=None*, *out=None*)
Return a dense ndarray representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multidimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns

arr [ndarray, 2-D] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

scipy.sparse.dok_matrix.tobsr

dok_matrix.**tobsr**(*blocksize=None*, *copy=False*)
Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.dok_matrix.tocoo

dok_matrix.**tocoo**(*copy=False*)
Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.dok_matrix.tocsc

dok_matrix.**tocsc**(*copy=False*)

Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.dok_matrix.tocsr

dok_matrix.**tocsr**(*copy=False*)

Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.dok_matrix.todense

dok_matrix.**todense**(*order=None*, *out=None*)

Return a dense matrix representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-D] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

scipy.sparse.dok_matrix.todia

dok_matrix.**todia**(*copy=False*)

Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.dok_matrix.todok

dok_matrix.**todok**(*copy=False*)

Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.dok_matrix.tolil

dok_matrix.**tolil**(*copy=False*)
Convert this matrix to List of Lists format.

With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.dok_matrix.transpose

dok_matrix.**transpose**(*axes=None*, *copy=False*)
Reverses the dimensions of the sparse matrix.

Parameters

axes [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.

copy [bool, optional] Indicates whether or not attributes of *self* should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p [*self* with the dimensions reversed.]

See also:

numpy.matrix.transpose

NumPy's implementation of 'transpose' for matrices

scipy.sparse.dok_matrix.update

dok_matrix.**update**(*[E]*, ***F*) → None. Update D from dict/iterable E and F.
If E is present and has a .keys() method, then does: for k in E: D[k] = E[k] If E is present and lacks a .keys() method, then does: for k, v in E: D[k] = v In either case, this is followed by: for k in F: D[k] = F[k]

scipy.sparse.dok_matrix.values

dok_matrix.**values**() → an object providing a view on D's values

__getitem__	

scipy.sparse.lil_matrix

class scipy.sparse.**lil_matrix**(*arg1*, *shape=None*, *dtype=None*, *copy=False*)
Row-based list of lists sparse matrix

This is a structure for constructing sparse matrices incrementally. Note that inserting a single item can take linear time in the worst case; to construct a matrix efficiently, make sure the items are pre-sorted by index, per row.

This can be instantiated in several ways:

lil_matrix(D)

with a dense matrix or rank-2 ndarray D

lil_matrix(S)

with another sparse matrix S (equivalent to S.tolil())

lil_matrix((M, N), [dtype])

to construct an empty matrix with shape (M, N) dtype is optional, defaulting to dtype='d'.

Notes

Sparse matrices can be used in arithmetic operations: they support addition, subtraction, multiplication, division, and matrix power.

Advantages of the LIL format

- supports flexible slicing
- changes to the matrix sparsity structure are efficient

Disadvantages of the LIL format

- arithmetic operations LIL + LIL are slow (consider CSR or CSC)
- slow column slicing (consider CSC)
- slow matrix vector products (consider CSR or CSC)

Intended Usage

- LIL is a convenient format for constructing sparse matrices
- once a matrix has been constructed, convert to CSR or CSC format for fast arithmetic and matrix vector operations
- consider using the COO format when constructing large matrices

Data Structure

- An array (`self.rows`) of rows, each of which is a sorted list of column indices of non-zero elements.
- The corresponding nonzero values are stored in similar fashion in `self.data`.

Attributes

dtype	[dtype] Data type of the matrix
shape	[2-tuple] Get shape of a matrix.
ndim	[int] Number of dimensions (this is always 2)
nnz	Number of stored values, including explicit zeros.
data	LIL format data array of the matrix
rows	LIL format row index array of the matrix

Methods

__len__()	

__mul__(other)	interpret other and call one of the following
asformat(format[, copy])	Return this matrix in the passed format.
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(dtype[, casting, copy])	Cast the matrix elements to a specified type.
conj([copy])	Element-wise complex conjugation.
conjugate([copy])	Element-wise complex conjugation.
copy()	Returns a copy of this matrix.
count_nonzero()	Number of non-zero entries, equivalent to
diagonal([k])	Returns the kth diagonal of the matrix.
dot(other)	Ordinary dot product
getH()	Return the Hermitian transpose of this matrix.
get_shape()	Get shape of a matrix.
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
getformat()	Format of a matrix representation as a string.
getmaxprint()	Maximum number of elements to display when printed.
getnnz([axis])	Number of stored values, including explicit zeros.
getrow(i)	Returns a copy of the ‘i’th row.
getrowview(i)	Returns a view of the ‘i’th row (without copying).
maximum(other)	Element-wise maximum between this and another matrix.
mean([axis, dtype, out])	Compute the arithmetic mean along the specified axis.
minimum(other)	Element-wise minimum between this and another matrix.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
power(n[, dtype])	Element-wise power.
reshape(self, shape[, order, copy])	Gives a new shape to a sparse matrix without changing its data.
resize(*shape)	Resize the matrix in-place to dimensions given by `shape`
set_shape(shape)	See *reshape*.
setdiag(values[, k])	Set diagonal or off-diagonal elements of the array.
sum([axis, dtype, out])	Sum the matrix elements over a given axis.
toarray([order, out])	Return a dense ndarray representation of this matrix.
tobsr([blocksize, copy])	Convert this matrix to Block Sparse Row format.
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc([copy])	Convert this matrix to Compressed Sparse Column format.
tocsr([copy])	Convert this matrix to Compressed Sparse Row format.
todense([order, out])	Return a dense matrix representation of this matrix.
todia([copy])	Convert this matrix to sparse DIAgonal format.
todok([copy])	Convert this matrix to Dictionary Of Keys format.
tolil([copy])	Convert this matrix to List of Lists format.
transpose([axes, copy])	Reverses the dimensions of the sparse matrix.

scipy.sparse.lil_matrix.__len__

lil_matrix.**__len__**()

scipy.sparse.lil_matrix.__mul__

lil_matrix.**__mul__**(*other*)

interpret other and call one of the following

self._mul_scalar() self._mul_vector() self._mul_multivector() self._mul_sparse_matrix()

scipy.sparse.lil_matrix.asformat

lil_matrix.**asformat**(*format*, *copy=False*)

Return this matrix in the passed format.

Parameters

format [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", …) or None for no conversion.

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [This matrix in the passed format.]

scipy.sparse.lil_matrix.asfptype

lil_matrix.**asfptype**()

Upcast matrix to a floating point format (if necessary)

scipy.sparse.lil_matrix.astype

lil_matrix.**astype**(*dtype*, *casting='unsafe'*, *copy=True*)

Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. 'no' means the data types should not be cast at all. 'equiv' means only byte-order changes are allowed. 'safe' means only casts which can preserve values are allowed. 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed. 'unsafe' means any data conversions may be done.

copy [bool, optional] If `copy` is *False*, the result might share some memory with this matrix. If `copy` is *True*, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.lil_matrix.conj

lil_matrix.**conj**(*copy=True*)
Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.lil_matrix.conjugate

lil_matrix.**conjugate**(*copy=True*)
Element-wise complex conjugation.

If the matrix is of non-complex data type and *copy* is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.lil_matrix.copy

lil_matrix.**copy**()
Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.lil_matrix.count_nonzero

lil_matrix.**count_nonzero**()
Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.lil_matrix.diagonal

lil_matrix.**diagonal**(*k=0*)
Returns the kth diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to get, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.lil_matrix.dot

lil_matrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.lil_matrix.getH

lil_matrix.**getH**()
Return the Hermitian transpose of this matrix.

See also:

numpy.matrix.getH

NumPy's implementation of *getH* for matrices

scipy.sparse.lil_matrix.get_shape

lil_matrix.**get_shape**()
Get shape of a matrix.

scipy.sparse.lil_matrix.getcol

lil_matrix.**getcol**(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

scipy.sparse.lil_matrix.getformat

lil_matrix.**getformat**()
Format of a matrix representation as a string.

scipy.sparse.lil_matrix.getmaxprint

lil_matrix.**getmaxprint**()
Maximum number of elements to display when printed.

scipy.sparse.lil_matrix.getnnz

lil_matrix.**getnnz**(*axis=None*)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero

Number of non-zero entries

scipy.sparse.lil_matrix.getrow

lil_matrix.**getrow**(*i*)
Returns a copy of the ‘i’th row.

scipy.sparse.lil_matrix.getrowview

lil_matrix.**getrowview**(*i*)
Returns a view of the 'i'th row (without copying).

scipy.sparse.lil_matrix.maximum

lil_matrix.**maximum**(*other*)
Element-wise maximum between this and another matrix.

scipy.sparse.lil_matrix.mean

lil_matrix.**mean**(*axis=None*, *dtype=None*, *out=None*)
Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e., *axis = None*).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]

See also:

numpy.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.lil_matrix.minimum

lil_matrix.**minimum**(*other*)
Element-wise minimum between this and another matrix.

scipy.sparse.lil_matrix.multiply

lil_matrix.**multiply**(*other*)
Point-wise multiplication by another matrix

scipy.sparse.lil_matrix.nonzero

lil_matrix.**nonzero**()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.lil_matrix.power

lil_matrix.**power**(*n*, *dtype=None*)
Element-wise power.

scipy.sparse.lil_matrix.reshape

lil_matrix.**reshape**(*self*, *shape*, *order='C'*, *copy=False*)
Gives a new shape to a sparse matrix without changing its data.

Parameters

shape [length-2 tuple of ints] The new shape should be compatible with the original shape.
order [{'C', 'F'}, optional] Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. 'F' means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.
copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix
[sparse matrix] A sparse matrix with the given `shape`, not necessarily of the same format as the current object.

See also:

numpy.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.lil_matrix.resize

lil_matrix.**resize**(**shape*)
Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.lil_matrix.set_shape

lil_matrix.**set_shape**(*shape*)
See *reshape*.

scipy.sparse.lil_matrix.setdiag

lil_matrix.**setdiag**(*values*, *k=0*)
Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values are longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.lil_matrix.sum

lil_matrix.**sum**(*axis=None*, *dtype=None*, *out=None*)
Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e., *axis* = *None*).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

sum_along_axis
[np.matrix] A matrix with the same shape as *self*, with the specified axis removed.

See also:

numpy.matrix.sum

NumPy's implementation of 'sum' for matrices

scipy.sparse.lil_matrix.toarray

lil_matrix.**toarray**(*order=None*, *out=None*)
Return a dense ndarray representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multidimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns

arr [ndarray, 2-D] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

scipy.sparse.lil_matrix.tobsr

lil_matrix.**tobsr**(*blocksize=None*, *copy=False*)
Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.lil_matrix.tocoo

lil_matrix.**tocoo**(*copy=False*)
Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.lil_matrix.tocsc

lil_matrix.**tocsc**(*copy=False*)
Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.lil_matrix.tocsr

lil_matrix.**tocsr**(*copy=False*)
Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.lil_matrix.todense

lil_matrix.**todense**(*order=None*, *out=None*)
Return a dense matrix representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-D] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

scipy.sparse.lil_matrix.todia

lil_matrix.**todia**(*copy=False*)
Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.lil_matrix.todok

lil_matrix.**todok**(*copy=False*)

Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.lil_matrix.tolil

lil_matrix.**tolil**(*copy=False*)

Convert this matrix to List of Lists format.

With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.lil_matrix.transpose

lil_matrix.**transpose**(*axes=None*, *copy=False*)

Reverses the dimensions of the sparse matrix.

Parameters

axes	[None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.
copy	[bool, optional] Indicates whether or not attributes of *self* should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p	[*self* with the dimensions reversed.]

See also:

numpy.matrix.transpose

NumPy's implementation of 'transpose' for matrices

__getitem__	

scipy.sparse.spmatrix

class scipy.sparse.**spmatrix**(*maxprint=50*)

This class provides a base class for all sparse matrices. It cannot be instantiated. Most of the work is provided by subclasses.

Attributes

nnz	Number of stored values, including explicit zeros.
shape	Get shape of a matrix.

Methods

__len__()	

__mul__(other)	interpret other and call one of the following
asformat(format[, copy])	Return this matrix in the passed format.
asfptype()	Upcast matrix to a floating point format (if necessary)
astype(dtype[, casting, copy])	Cast the matrix elements to a specified type.
conj([copy])	Element-wise complex conjugation.
conjugate([copy])	Element-wise complex conjugation.
copy()	Returns a copy of this matrix.
count_nonzero()	Number of non-zero entries, equivalent to
diagonal([k])	Returns the kth diagonal of the matrix.
dot(other)	Ordinary dot product
getH()	Return the Hermitian transpose of this matrix.
get_shape()	Get shape of a matrix.
getcol(j)	Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).
getformat()	Format of a matrix representation as a string.
getmaxprint()	Maximum number of elements to display when printed.
getnnz([axis])	Number of stored values, including explicit zeros.
getrow(i)	Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).
maximum(other)	Element-wise maximum between this and another matrix.
mean([axis, dtype, out])	Compute the arithmetic mean along the specified axis.
minimum(other)	Element-wise minimum between this and another matrix.
multiply(other)	Point-wise multiplication by another matrix
nonzero()	nonzero indices
power(n[, dtype])	Element-wise power.
reshape(self, shape[, order, copy])	Gives a new shape to a sparse matrix without changing its data.
resize(shape)	Resize the matrix in-place to dimensions given by `shape`
set_shape(shape)	See *reshape*.
setdiag(values[, k])	Set diagonal or off-diagonal elements of the array.
sum([axis, dtype, out])	Sum the matrix elements over a given axis.
toarray([order, out])	Return a dense ndarray representation of this matrix.
tobsr([blocksize, copy])	Convert this matrix to Block Sparse Row format.
tocoo([copy])	Convert this matrix to COOrdinate format.
tocsc([copy])	Convert this matrix to Compressed Sparse Column format.
tocsr([copy])	Convert this matrix to Compressed Sparse Row format.
todense([order, out])	Return a dense matrix representation of this matrix.
todia([copy])	Convert this matrix to sparse DIAgonal format.
todok([copy])	Convert this matrix to Dictionary Of Keys format.
tolil([copy])	Convert this matrix to List of Lists format.
transpose([axes, copy])	Reverses the dimensions of the sparse matrix.

scipy.sparse.spmatrix.__len__

spmatrix.**__len__**()

scipy.sparse.spmatrix.__mul__

spmatrix.**__mul__**(*other*)

interpret other and call one of the following

self._mul_scalar() self._mul_vector() self._mul_multivector() self._mul_sparse_matrix()

scipy.sparse.spmatrix.asformat

spmatrix.**asformat**(*format*, *copy=False*)

Return this matrix in the passed format.

Parameters

format [{str, None}] The desired matrix format ("csr", "csc", "lil", "dok", "array", …) or None for no conversion.

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [This matrix in the passed format.]

scipy.sparse.spmatrix.asfptype

spmatrix.**asfptype**()

Upcast matrix to a floating point format (if necessary)

scipy.sparse.spmatrix.astype

spmatrix.**astype**(*dtype*, *casting='unsafe'*, *copy=True*)

Cast the matrix elements to a specified type.

Parameters

dtype [string or numpy dtype] Typecode or data-type to which to cast the data.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility. 'no' means the data types should not be cast at all. 'equiv' means only byte-order changes are allowed. 'safe' means only casts which can preserve values are allowed. 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed. 'unsafe' means any data conversions may be done.

copy [bool, optional] If `copy` is *False*, the result might share some memory with this matrix. If `copy` is *True*, it is guaranteed that the result and this matrix do not share any memory.

scipy.sparse.spmatrix.conj

spmatrix.**conj**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and `copy` is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.spmatrix.conjugate

spmatrix.**conjugate**(*copy=True*)

Element-wise complex conjugation.

If the matrix is of non-complex data type and `copy` is False, this method does nothing and the data is not copied.

Parameters

copy [bool, optional] If True, the result is guaranteed to not share data with self.

Returns

A [The element-wise complex conjugate.]

scipy.sparse.spmatrix.copy

spmatrix.**copy**()

Returns a copy of this matrix.

No data/indices will be shared between the returned value and current matrix.

scipy.sparse.spmatrix.count_nonzero

spmatrix.**count_nonzero**()

Number of non-zero entries, equivalent to

np.count_nonzero(a.toarray())

Unlike getnnz() and the nnz property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

scipy.sparse.spmatrix.diagonal

spmatrix.**diagonal**(*k=0*)
Returns the kth diagonal of the matrix.

Parameters

k [int, optional] Which diagonal to get, corresponding to elements a[i, i+k]. Default: 0 (the main diagonal).
New in version 1.0.

See also:

numpy.diagonal

Equivalent numpy function.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> A.diagonal()
array([1, 0, 5])
>>> A.diagonal(k=1)
array([2, 3])
```

scipy.sparse.spmatrix.dot

spmatrix.**dot**(*other*)
Ordinary dot product

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

scipy.sparse.spmatrix.getH

spmatrix.**getH**()
Return the Hermitian transpose of this matrix.

See also:

numpy.matrix.getH

NumPy's implementation of *getH* for matrices

scipy.sparse.spmatrix.get_shape

spmatrix.**get_shape**()
Get shape of a matrix.

scipy.sparse.spmatrix.getcol

spmatrix.**getcol**(*j*)
Returns a copy of column j of the matrix, as an (m x 1) sparse matrix (column vector).

scipy.sparse.spmatrix.getformat

spmatrix.**getformat**()
Format of a matrix representation as a string.

scipy.sparse.spmatrix.getmaxprint

spmatrix.**getmaxprint**()
Maximum number of elements to display when printed.

scipy.sparse.spmatrix.getnnz

spmatrix.**getnnz**(*axis=None*)
Number of stored values, including explicit zeros.

Parameters

axis [None, 0, or 1] Select between the number of values across the whole matrix, in each column, or in each row.

See also:

count_nonzero

Number of non-zero entries

scipy.sparse.spmatrix.getrow

spmatrix.**getrow**(*i*)
Returns a copy of row i of the matrix, as a (1 x n) sparse matrix (row vector).

scipy.sparse.spmatrix.maximum

spmatrix.**maximum**(*other*)
Element-wise maximum between this and another matrix.

scipy.sparse.spmatrix.mean

spmatrix.**mean**(*axis=None*, *dtype=None*, *out=None*)
Compute the arithmetic mean along the specified axis.

Returns the average of the matrix elements. The average is taken over all elements in the matrix by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the mean is computed. The default is to compute the mean of all elements in the matrix (i.e., *axis* = *None*).

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

m [np.matrix]

See also:

numpy.matrix.mean

NumPy's implementation of 'mean' for matrices

scipy.sparse.spmatrix.minimum

spmatrix.**minimum**(*other*)
Element-wise minimum between this and another matrix.

scipy.sparse.spmatrix.multiply

spmatrix.**multiply**(*other*)
Point-wise multiplication by another matrix

scipy.sparse.spmatrix.nonzero

spmatrix.**nonzero**()
nonzero indices

Returns a tuple of arrays (row,col) containing the indices of the non-zero elements of the matrix.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1,2,0],[0,0,3],[4,0,5]])
>>> A.nonzero()
(array([0, 0, 1, 2, 2]), array([0, 1, 2, 0, 2]))
```

scipy.sparse.spmatrix.power

spmatrix.**power**(*n*, *dtype=None*)
Element-wise power.

scipy.sparse.spmatrix.reshape

spmatrix.**reshape**(*self*, *shape*, *order='C'*, *copy=False*)
Gives a new shape to a sparse matrix without changing its data.

Parameters

shape [length-2 tuple of ints] The new shape should be compatible with the original shape.
order [{'C', 'F'}, optional] Read the elements using this index order. 'C' means to read and write the elements using C-like index order; e.g., read entire first row, then second row, etc. 'F' means to read and write the elements using Fortran-like index order; e.g., read entire first column, then second column, etc.
copy [bool, optional] Indicates whether or not attributes of self should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

reshaped_matrix
[sparse matrix] A sparse matrix with the given `shape`, not necessarily of the same format as the current object.

See also:

numpy.matrix.reshape

NumPy's implementation of 'reshape' for matrices

scipy.sparse.spmatrix.resize

spmatrix.**resize**(*shape*)

Resize the matrix in-place to dimensions given by `shape`

Any elements that lie within the new shape will remain at the same indices, while non-zero elements lying outside the new shape are removed.

Parameters

shape [(int, int)] number of rows and columns in the new matrix

Notes

The semantics are not identical to `numpy.ndarray.resize` or `numpy.resize`. Here, the same data will be maintained at each index before and after reshape, if that index is within the new bounds. In numpy, resizing maintains contiguity of the array, moving elements around in the logical matrix but not within a flattened representation.

We give no guarantees about whether the underlying data attributes (arrays, etc.) will be modified in place or replaced with new objects.

scipy.sparse.spmatrix.set_shape

spmatrix.**set_shape**(*shape*)

See *reshape*.

scipy.sparse.spmatrix.setdiag

spmatrix.**setdiag**(*values*, *k=0*)

Set diagonal or off-diagonal elements of the array.

Parameters

values [array_like] New values of the diagonal elements.
Values may have any length. If the diagonal is longer than values, then the remaining diagonal entries will not be set. If values are longer than the diagonal, then the remaining values are ignored.
If a scalar value is given, all of the diagonal is set to it.

k [int, optional] Which off-diagonal to set, corresponding to elements a[i,i+k]. Default: 0 (the main diagonal).

scipy.sparse.spmatrix.sum

spmatrix.**sum**(*axis=None*, *dtype=None*, *out=None*)

Sum the matrix elements over a given axis.

Parameters

axis [{-2, -1, 0, 1, None} optional] Axis along which the sum is computed. The default is to compute the sum of all the matrix elements, returning a scalar (i.e., *axis* = *None*).

dtype [dtype, optional] The type of the returned matrix and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.
New in version 0.18.0.

out [np.matrix, optional] Alternative output matrix in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.
New in version 0.18.0.

Returns

sum_along_axis
[np.matrix] A matrix with the same shape as *self*, with the specified axis removed.

See also:

numpy.matrix.sum

NumPy's implementation of 'sum' for matrices

scipy.sparse.spmatrix.toarray

spmatrix.**toarray**(*order=None*, *out=None*)

Return a dense ndarray representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multidimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method. For most sparse types, *out* is required to be memory contiguous (either C or Fortran ordered).

Returns

arr [ndarray, 2-D] An array with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed, the same object is returned after being modified in-place to contain the appropriate values.

scipy.sparse.spmatrix.tobsr

spmatrix.**tobsr**(*blocksize=None*, *copy=False*)

Convert this matrix to Block Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant bsr_matrix.

When blocksize=(R, C) is provided, it will be used for construction of the bsr_matrix.

scipy.sparse.spmatrix.tocoo

spmatrix.**tocoo**(*copy=False*)

Convert this matrix to COOrdinate format.

With copy=False, the data/indices may be shared between this matrix and the resultant coo_matrix.

scipy.sparse.spmatrix.tocsc

spmatrix.**tocsc**(*copy=False*)

Convert this matrix to Compressed Sparse Column format.

With copy=False, the data/indices may be shared between this matrix and the resultant csc_matrix.

scipy.sparse.spmatrix.tocsr

spmatrix.**tocsr**(*copy=False*)

Convert this matrix to Compressed Sparse Row format.

With copy=False, the data/indices may be shared between this matrix and the resultant csr_matrix.

scipy.sparse.spmatrix.todense

spmatrix.**todense**(*order=None*, *out=None*)

Return a dense matrix representation of this matrix.

Parameters

order [{'C', 'F'}, optional] Whether to store multi-dimensional data in C (row-major) or Fortran (column-major) order in memory. The default is 'None', indicating the NumPy default of C-ordered. Cannot be specified in conjunction with the *out* argument.

out [ndarray, 2-D, optional] If specified, uses this array (or `numpy.matrix`) as the output buffer instead of allocating a new array to return. The provided array must have the same shape and dtype as the sparse matrix on which you are calling the method.

Returns

arr [numpy.matrix, 2-D] A NumPy matrix object with the same shape and containing the same data represented by the sparse matrix, with the requested memory order. If *out* was passed and was an array (rather than a `numpy.matrix`), it will be filled with the appropriate values and returned wrapped in a `numpy.matrix` object that shares the same memory.

scipy.sparse.spmatrix.todia

spmatrix.**todia**(*copy=False*)

Convert this matrix to sparse DIAgonal format.

With copy=False, the data/indices may be shared between this matrix and the resultant dia_matrix.

scipy.sparse.spmatrix.todok

spmatrix.**todok**(*copy=False*)

Convert this matrix to Dictionary Of Keys format.

With copy=False, the data/indices may be shared between this matrix and the resultant dok_matrix.

scipy.sparse.spmatrix.tolil

spmatrix.**tolil**(*copy=False*)

Convert this matrix to List of Lists format.

With copy=False, the data/indices may be shared between this matrix and the resultant lil_matrix.

scipy.sparse.spmatrix.transpose

spmatrix.**transpose**(*axes=None*, *copy=False*)

Reverses the dimensions of the sparse matrix.

Parameters

axes [None, optional] This argument is in the signature *solely* for NumPy compatibility reasons. Do not pass in anything except for the default value.

copy [bool, optional] Indicates whether or not attributes of *self* should be copied whenever possible. The degree to which attributes are copied varies depending on the type of sparse matrix being used.

Returns

p [*self* with the dimensions reversed.]

See also:

numpy.matrix.transpose

NumPy's implementation of 'transpose' for matrices

Functions

Building sparse matrices:

eye(m[, n, k, dtype, format])	Sparse matrix with ones on diagonal
identity(n[, dtype, format])	Identity matrix in sparse format
kron(A, B[, format])	kronecker product of sparse matrices A and B
kronsum(A, B[, format])	kronecker sum of sparse matrices A and B
diags(diagonals[, offsets, shape, format, dtype])	Construct a sparse matrix from diagonals.
spdiags(data, diags, m, n[, format])	Return a sparse matrix from diagonals.
block_diag(mats[, format, dtype])	Build a block diagonal sparse matrix from provided matrices.
tril(A[, k, format])	Return the lower triangular portion of a matrix in sparse format
triu(A[, k, format])	Return the upper triangular portion of a matrix in sparse format
bmat(blocks[, format, dtype])	Build a sparse matrix from sparse sub-blocks

continues on next page

Table 183 – continued from previous page

hstack(blocks[, format, dtype])	Stack sparse matrices horizontally (column wise)
vstack(blocks[, format, dtype])	Stack sparse matrices vertically (row wise)
rand(m, n[, density, format, dtype, …])	Generate a sparse matrix of the given shape and density with uniformly distributed values.
random(m, n[, density, format, dtype, …])	Generate a sparse matrix of the given shape and density with randomly distributed values.

scipy.sparse.eye

scipy.sparse.**eye**(*m*, *n=None*, *k=0*, *dtype=<class 'float'>*, *format=None*)

Sparse matrix with ones on diagonal

Returns a sparse (m x n) matrix where the kth diagonal is all ones and everything else is zeros.

Parameters

m	[int] Number of rows in the matrix.
n	[int, optional] Number of columns. Default: *m*.
k	[int, optional] Diagonal to place ones on. Default: 0 (main diagonal).
dtype	[dtype, optional] Data type of the matrix.
format	[str, optional] Sparse format of the result, e.g., format="csr", etc.

Examples

```
>>> from scipy import sparse
>>> sparse.eye(3).toarray()
array([[ 1.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  1.]])
>>> sparse.eye(3, dtype=np.int8)
<3x3 sparse matrix of type '<class 'numpy.int8'>'
    with 3 stored elements (1 diagonals) in DIAgonal format>
```

scipy.sparse.identity

scipy.sparse.**identity**(*n*, *dtype='d'*, *format=None*)

Identity matrix in sparse format

Returns an identity matrix with shape (n,n) using a given sparse format and dtype.

Parameters

n	[int] Shape of the identity matrix.
dtype	[dtype, optional] Data type of the matrix
format	[str, optional] Sparse format of the result, e.g., format="csr", etc.

Examples

```
>>> from scipy.sparse import identity
>>> identity(3).toarray()
array([[ 1.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  1.]])
>>> identity(3, dtype='int8', format='dia')
<3x3 sparse matrix of type '<class 'numpy.int8'>'
        with 3 stored elements (1 diagonals) in DIAgonal format>
```

scipy.sparse.kron

scipy.sparse.**kron**(*A*, *B*, *format=None*)

kronecker product of sparse matrices A and B

Parameters

A	[sparse or dense matrix] first matrix of the product
B	[sparse or dense matrix] second matrix of the product
format	[str, optional] format of the result (e.g. “csr”)

Returns

kronecker product in a sparse matrix format

Examples

```
>>> from scipy import sparse
>>> A = sparse.csr_matrix(np.array([[0, 2], [5, 0]]))
>>> B = sparse.csr_matrix(np.array([[1, 2], [3, 4]]))
>>> sparse.kron(A, B).toarray()
array([[ 0,  0,  2,  4],
       [ 0,  0,  6,  8],
       [ 5, 10,  0,  0],
       [15, 20,  0,  0]])
```

```
>>> sparse.kron(A, [[1, 2], [3, 4]]).toarray()
array([[ 0,  0,  2,  4],
       [ 0,  0,  6,  8],
       [ 5, 10,  0,  0],
       [15, 20,  0,  0]])
```

scipy.sparse.kronsum

scipy.sparse.**kronsum**(*A*, *B*, *format=None*)

kronecker sum of sparse matrices A and B

Kronecker sum of two sparse matrices is a sum of two Kronecker products kron(I_n,A) + kron(B,I_m) where A has shape (m,m) and B has shape (n,n) and I_m and I_n are identity matrices of shape (m,m) and (n,n), respectively.

Parameters

A	square matrix
B	square matrix
format	[str] format of the result (e.g. "csr")

Returns

kronecker sum in a sparse matrix format

scipy.sparse.diags

scipy.sparse.**diags**(*diagonals*, *offsets=0*, *shape=None*, *format=None*, *dtype=None*)

Construct a sparse matrix from diagonals.

Parameters

diagonals	[sequence of array_like] Sequence of arrays containing the matrix diagonals, corresponding to *offsets*.
offsets	[sequence of int or an int, optional] **Diagonals to set:** • k = 0 the main diagonal (default) • k > 0 the kth upper diagonal • k < 0 the kth lower diagonal
shape	[tuple of int, optional] Shape of the result. If omitted, a square matrix large enough to contain the diagonals is returned.
format	[{"dia", "csr", "csc", "lil", …}, optional] Matrix format of the result. By default (format=None) an appropriate sparse matrix format is returned. This choice is subject to change.
dtype	[dtype, optional] Data type of the matrix.

See also:

spdiags

construct matrix from diagonals

Notes

This function differs from *spdiags* in the way it handles off-diagonals.

The result from *diags* is the sparse equivalent of:

```
np.diag(diagonals[0], offsets[0])
+ ...
+ np.diag(diagonals[k], offsets[k])
```

Repeated diagonal offsets are disallowed.

New in version 0.11.

Examples

```
>>> from scipy.sparse import diags
>>> diagonals = [[1, 2, 3, 4], [1, 2, 3], [1, 2]]
>>> diags(diagonals, [0, -1, 2]).toarray()
array([[1, 0, 1, 0],
       [1, 2, 0, 2],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

Broadcasting of scalars is supported (but shape needs to be specified):

```
>>> diags([1, -2, 1], [-1, 0, 1], shape=(4, 4)).toarray()
array([[-2.,  1.,  0.,  0.],
       [ 1., -2.,  1.,  0.],
       [ 0.,  1., -2.,  1.],
       [ 0.,  0.,  1., -2.]])
```

If only one diagonal is wanted (as in `numpy.diag`), the following works as well:

```
>>> diags([1, 2, 3], 1).toarray()
array([[ 0.,  1.,  0.,  0.],
       [ 0.,  0.,  2.,  0.],
       [ 0.,  0.,  0.,  3.],
       [ 0.,  0.,  0.,  0.]])
```

scipy.sparse.spdiags

scipy.sparse.**spdiags**(*data*, *diags*, *m*, *n*, *format=None*)

Return a sparse matrix from diagonals.

Parameters

data	[array_like] matrix diagonals stored row-wise
diags	[diagonals to set] • k = 0 the main diagonal • k > 0 the k-th upper diagonal • k < 0 the k-th lower diagonal
m, n	[int] shape of the result
format	[str, optional] Format of the result. By default (format=None) an appropriate sparse matrix format is returned. This choice is subject to change.

See also:

diags

more convenient form of this function

dia_matrix

the sparse DIAgonal format.

Examples

```
>>> from scipy.sparse import spdiags
>>> data = np.array([[1, 2, 3, 4], [1, 2, 3, 4], [1, 2, 3, 4]])
>>> diags = np.array([0, -1, 2])
>>> spdiags(data, diags, 4, 4).toarray()
array([[1, 0, 3, 0],
       [1, 2, 0, 4],
       [0, 2, 3, 0],
       [0, 0, 3, 4]])
```

scipy.sparse.block_diag

scipy.sparse.**block_diag**(*mats*, *format=None*, *dtype=None*)

Build a block diagonal sparse matrix from provided matrices.

Parameters

mats [sequence of matrices] Input matrices.

format [str, optional] The sparse format of the result (e.g., "csr"). If not given, the matrix is returned in "coo" format.

dtype [dtype specifier, optional] The data-type of the output matrix. If not given, the dtype is determined from that of *blocks*.

Returns

res [sparse matrix]

See also:

bmat, **diags**

Notes

New in version 0.11.0.

Examples

```
>>> from scipy.sparse import coo_matrix, block_diag
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5], [6]])
>>> C = coo_matrix([[7]])
>>> block_diag((A, B, C)).toarray()
array([[1, 2, 0, 0],
       [3, 4, 0, 0],
       [0, 0, 5, 0],
       [0, 0, 6, 0],
       [0, 0, 0, 7]])
```

scipy.sparse.tril

scipy.sparse.**tril**(*A*, *k=0*, *format=None*)

Return the lower triangular portion of a matrix in sparse format

Returns the elements on or below the k-th diagonal of the matrix A.

- k = 0 corresponds to the main diagonal
- k > 0 is above the main diagonal
- k < 0 is below the main diagonal

Parameters

A	[dense or sparse matrix] Matrix whose lower trianglar portion is desired.
k	[integer] The top-most diagonal of the lower triangle.
format	[string] Sparse format of the result, e.g. format="csr", etc.

Returns

L	[sparse matrix] Lower triangular portion of A in sparse format.

See also:

triu

upper triangle in sparse format

Examples

```
>>> from scipy.sparse import csr_matrix, tril
>>> A = csr_matrix([[1, 2, 0, 0, 3], [4, 5, 0, 6, 7], [0, 0, 8, 9, 0]],
...                dtype='int32')
>>> A.toarray()
array([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> tril(A).toarray()
array([[1, 0, 0, 0, 0],
       [4, 5, 0, 0, 0],
       [0, 0, 8, 0, 0]])
>>> tril(A).nnz
4
>>> tril(A, k=1).toarray()
array([[1, 2, 0, 0, 0],
       [4, 5, 0, 0, 0],
       [0, 0, 8, 9, 0]])
>>> tril(A, k=-1).toarray()
array([[0, 0, 0, 0, 0],
       [4, 0, 0, 0, 0],
       [0, 0, 0, 0, 0]])
>>> tril(A, format='csc')
<3x5 sparse matrix of type '<class 'numpy.int32'>'
        with 4 stored elements in Compressed Sparse Column format>
```

scipy.sparse.triu

scipy.sparse.**triu**(*A*, *k=0*, *format=None*)

Return the upper triangular portion of a matrix in sparse format

Returns the elements on or above the k-th diagonal of the matrix A.

- k = 0 corresponds to the main diagonal
- k > 0 is above the main diagonal
- k < 0 is below the main diagonal

Parameters

A	[dense or sparse matrix] Matrix whose upper trianglar portion is desired.
k	[integer] The bottom-most diagonal of the upper triangle.
format	[string] Sparse format of the result, e.g. format="csr", etc.

Returns

L	[sparse matrix] Upper triangular portion of A in sparse format.

See also:

tril

lower triangle in sparse format

Examples

```
>>> from scipy.sparse import csr_matrix, triu
>>> A = csr_matrix([[1, 2, 0, 0, 3], [4, 5, 0, 6, 7], [0, 0, 8, 9, 0]],
...                dtype='int32')
>>> A.toarray()
array([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A).toarray()
array([[1, 2, 0, 0, 3],
       [0, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A).nnz
8
>>> triu(A, k=1).toarray()
array([[0, 2, 0, 0, 3],
       [0, 0, 0, 6, 7],
       [0, 0, 0, 9, 0]])
>>> triu(A, k=-1).toarray()
array([[1, 2, 0, 0, 3],
       [4, 5, 0, 6, 7],
       [0, 0, 8, 9, 0]])
>>> triu(A, format='csc')
<3x5 sparse matrix of type '<class 'numpy.int32'>'
        with 8 stored elements in Compressed Sparse Column format>
```

scipy.sparse.bmat

scipy.sparse.**bmat**(*blocks*, *format=None*, *dtype=None*)

Build a sparse matrix from sparse sub-blocks

Parameters

blocks [array_like] Grid of sparse matrices with compatible shapes. An entry of None implies an all-zero matrix.

format [{'bsr', 'coo', 'csc', 'csr', 'dia', 'dok', 'lil'}, optional] The sparse format of the result (e.g. "csr"). By default an appropriate sparse matrix format is returned. This choice is subject to change.

dtype [dtype, optional] The data-type of the output matrix. If not given, the dtype is determined from that of *blocks*.

Returns

bmat [sparse matrix]

See also:

block_diag, **diags**

Examples

```
>>> from scipy.sparse import coo_matrix, bmat
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5], [6]])
>>> C = coo_matrix([[7]])
>>> bmat([[A, B], [None, C]]).toarray()
array([[1, 2, 5],
       [3, 4, 6],
       [0, 0, 7]])
```

```
>>> bmat([[A, None], [None, C]]).toarray()
array([[1, 2, 0],
       [3, 4, 0],
       [0, 0, 7]])
```

scipy.sparse.hstack

scipy.sparse.**hstack**(*blocks*, *format=None*, *dtype=None*)

Stack sparse matrices horizontally (column wise)

Parameters

blocks sequence of sparse matrices with compatible shapes

format [str] sparse format of the result (e.g., "csr") by default an appropriate sparse matrix format is returned. This choice is subject to change.

dtype [dtype, optional] The data-type of the output matrix. If not given, the dtype is determined from that of *blocks*.

See also:

vstack

stack sparse matrices vertically (row wise)

Examples

```
>>> from scipy.sparse import coo_matrix, hstack
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5], [6]])
>>> hstack([A,B]).toarray()
array([[1, 2, 5],
       [3, 4, 6]])
```

scipy.sparse.vstack

scipy.sparse.**vstack**(*blocks*, *format=None*, *dtype=None*)

Stack sparse matrices vertically (row wise)

Parameters

blocks	sequence of sparse matrices with compatible shapes
format	[str, optional] sparse format of the result (e.g., "csr") by default an appropriate sparse matrix format is returned. This choice is subject to change.
dtype	[dtype, optional] The data-type of the output matrix. If not given, the dtype is determined from that of *blocks*.

See also:

hstack

stack sparse matrices horizontally (column wise)

Examples

```
>>> from scipy.sparse import coo_matrix, vstack
>>> A = coo_matrix([[1, 2], [3, 4]])
>>> B = coo_matrix([[5, 6]])
>>> vstack([A, B]).toarray()
array([[1, 2],
       [3, 4],
       [5, 6]])
```

scipy.sparse.rand

scipy.sparse.**rand**(*m*, *n*, *density=0.01*, *format='coo'*, *dtype=None*, *random_state=None*)

Generate a sparse matrix of the given shape and density with uniformly distributed values.

Parameters

m, n	[int] shape of the matrix
density	[real, optional] density of the generated matrix: density equal to one means a full matrix, density of 0 means a matrix with no non-zero items.

format [str, optional] sparse matrix format.
dtype [dtype, optional] type of the returned matrix values.
random_state
[{None, int, numpy.random.Generator,]
numpy.random.RandomState}, optional
If *seed* is None (or *np.random*), the numpy.random.RandomState singleton is used. If *seed* is an int, a new RandomState instance is used, seeded with *seed*. If *seed* is already a Generator or RandomState instance then that instance is used.

Returns

res [sparse matrix]

See also:

scipy.sparse.random

Similar function that allows a user-specified random data source.

Notes

Only float types are supported for now.

Examples

```
>>> from scipy.sparse import rand
>>> matrix = rand(3, 4, density=0.25, format="csr", random_state=42)
>>> matrix
<3x4 sparse matrix of type '<class 'numpy.float64'>'
   with 3 stored elements in Compressed Sparse Row format>
>>> matrix.todense()
matrix([[0.05641158, 0.        , 0.        , 0.65088847],
        [0.        , 0.        , 0.        , 0.14286682],
        [0.        , 0.        , 0.        , 0.        ]])
```

scipy.sparse.random

scipy.sparse.**random**(*m*, *n*, *density=0.01*, *format='coo'*, *dtype=None*, *random_state=None*, *data_rvs=None*)

Generate a sparse matrix of the given shape and density with randomly distributed values.

Parameters

m, n [int] shape of the matrix
density [real, optional] density of the generated matrix: density equal to one means a full matrix, density of 0 means a matrix with no non-zero items.
format [str, optional] sparse matrix format.
dtype [dtype, optional] type of the returned matrix values.
random_state
[{None, int, numpy.random.Generator,]
numpy.random.RandomState}, optional

If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used. This random state will be used for sampling the sparsity structure, but not necessarily for sampling the values of the structurally nonzero entries of the matrix.

data_rvs [callable, optional] Samples a requested number of random values. This function should take a single argument specifying the length of the ndarray that it will return. The structurally nonzero entries of the sparse random matrix will be taken from the array sampled by this function. By default, uniform [0, 1) random values will be sampled using the same random state as is used for sampling the sparsity structure.

Returns

res [sparse matrix]

Notes

Only float types are supported for now.

Examples

```
>>> from scipy.sparse import random
>>> from scipy import stats
>>> from numpy.random import default_rng
>>> rng = default_rng()
>>> rvs = stats.poisson(25, loc=10).rvs
>>> S = random(3, 4, density=0.25, random_state=rng, data_rvs=rvs)
>>> S.A
array([[ 36.,   0.,  33.,   0.],   # random
       [  0.,   0.,   0.,   0.],
       [  0.,   0.,  36.,   0.]])
```

```
>>> from scipy.sparse import random
>>> from scipy.stats import rv_continuous
>>> class CustomDistribution(rv_continuous):
...     def _rvs(self,  size=None, random_state=None):
...         return random_state.standard_normal(size)
>>> X = CustomDistribution(seed=rng)
>>> Y = X()  # get a frozen version of the distribution
>>> S = random(3, 4, density=0.25, random_state=rng, data_rvs=Y.rvs)
>>> S.A
array([[ 0.        ,  0.        ,  0.        ,  0.        ],   # random
       [ 0.13569738,  1.9467163 , -0.81205367,  0.        ],
       [ 0.        ,  0.        ,  0.        ,  0.        ]])
```

Save and load sparse matrices:

save_npz(file, matrix[, compressed])	Save a sparse matrix to a file using `.npz` format.
load_npz(file)	Load a sparse matrix from a file using `.npz` format.

scipy.sparse.save_npz

scipy.sparse.**save_npz**(*file*, *matrix*, *compressed=True*)

Save a sparse matrix to a file using `.npz` format.

Parameters

file [str or file-like object] Either the file name (string) or an open file (file-like object) where the data will be saved. If file is a string, the `.npz` extension will be appended to the file name if it is not already there.

matrix: spmatrix (format: ``csc``, ``csr``, ``bsr``, ``dia`` or coo``)
The sparse matrix to save.

compressed
[bool, optional] Allow compressing the file. Default: True

See also:

scipy.sparse.load_npz

Load a sparse matrix from a file using `.npz` format.

numpy.savez

Save several arrays into a `.npz` archive.

numpy.savez_compressed

Save several arrays into a compressed `.npz` archive.

Examples

Store sparse matrix to disk, and load it again:

```
>>> import scipy.sparse
>>> sparse_matrix = scipy.sparse.csc_matrix(np.array([[0, 0, 3], [4, 0,␣
↪0]]))
>>> sparse_matrix
<2x3 sparse matrix of type '<class 'numpy.int64'>'
   with 2 stored elements in Compressed Sparse Column format>
>>> sparse_matrix.todense()
matrix([[0, 0, 3],
        [4, 0, 0]], dtype=int64)
```

```
>>> scipy.sparse.save_npz('/tmp/sparse_matrix.npz', sparse_matrix)
>>> sparse_matrix = scipy.sparse.load_npz('/tmp/sparse_matrix.npz')
```

```
>>> sparse_matrix
<2x3 sparse matrix of type '<class 'numpy.int64'>'
   with 2 stored elements in Compressed Sparse Column format>
>>> sparse_matrix.todense()
matrix([[0, 0, 3],
        [4, 0, 0]], dtype=int64)
```

scipy.sparse.load_npz

scipy.sparse.**load_npz**(*file*)

Load a sparse matrix from a file using `.npz` format.

Parameters

file [str or file-like object] Either the file name (string) or an open file (file-like object) where the data will be loaded.

Returns

result [csc_matrix, csr_matrix, bsr_matrix, dia_matrix or coo_matrix] A sparse matrix containing the loaded data.

Raises

IOError If the input file does not exist or cannot be read.

See also:

scipy.sparse.save_npz

Save a sparse matrix to a file using `.npz` format.

numpy.load

Load several arrays from a `.npz` archive.

Examples

Store sparse matrix to disk, and load it again:

```
>>> import scipy.sparse
>>> sparse_matrix = scipy.sparse.csc_matrix(np.array([[0, 0, 3], [4, 0,␣
↪0]]))
>>> sparse_matrix
<2x3 sparse matrix of type '<class 'numpy.int64'>'
   with 2 stored elements in Compressed Sparse Column format>
>>> sparse_matrix.todense()
matrix([[0, 0, 3],
        [4, 0, 0]], dtype=int64)
```

```
>>> scipy.sparse.save_npz('/tmp/sparse_matrix.npz', sparse_matrix)
>>> sparse_matrix = scipy.sparse.load_npz('/tmp/sparse_matrix.npz')
```

```
>>> sparse_matrix
<2x3 sparse matrix of type '<class 'numpy.int64'>'
    with 2 stored elements in Compressed Sparse Column format>
>>> sparse_matrix.todense()
matrix([[0, 0, 3],
        [4, 0, 0]], dtype=int64)
```

Sparse matrix tools:

find(A)	Return the indices and values of the nonzero elements of a matrix

scipy.sparse.find

scipy.sparse.**find**(*A*)

Return the indices and values of the nonzero elements of a matrix

Parameters

A [dense or sparse matrix] Matrix whose nonzero elements are desired.

Returns

(I,J,V) [tuple of arrays] I,J, and V contain the row indices, column indices, and values of the nonzero matrix entries.

Examples

```
>>> from scipy.sparse import csr_matrix, find
>>> A = csr_matrix([[7.0, 8.0, 0],[0, 0, 9.0]])
>>> find(A)
(array([0, 0, 1], dtype=int32), array([0, 1, 2], dtype=int32), array([ 7.,
↪  8.,  9.]))
```

Identifying sparse matrices:

issparse(x)	Is x of a sparse matrix type?
isspmatrix(x)	Is x of a sparse matrix type?
isspmatrix_csc(x)	Is x of csc_matrix type?
isspmatrix_csr(x)	Is x of csr_matrix type?
isspmatrix_bsr(x)	Is x of a bsr_matrix type?
isspmatrix_lil(x)	Is x of lil_matrix type?
isspmatrix_dok(x)	Is x of dok_matrix type?
isspmatrix_coo(x)	Is x of coo_matrix type?
isspmatrix_dia(x)	Is x of dia_matrix type?

scipy.sparse.issparse

scipy.sparse.**issparse**(*x*)

Is x of a sparse matrix type?

Parameters

x object to check for being a sparse matrix

Returns

bool True if x is a sparse matrix, False otherwise

Notes

issparse and isspmatrix are aliases for the same function.

Examples

```
>>> from scipy.sparse import csr_matrix, isspmatrix
>>> isspmatrix(csr_matrix([[5]]))
True
```

```
>>> from scipy.sparse import isspmatrix
>>> isspmatrix(5)
False
```

scipy.sparse.isspmatrix

scipy.sparse.**isspmatrix**(*x*)

Is x of a sparse matrix type?

Parameters

x object to check for being a sparse matrix

Returns

bool True if x is a sparse matrix, False otherwise

Notes

issparse and isspmatrix are aliases for the same function.

Examples

```
>>> from scipy.sparse import csr_matrix, isspmatrix
>>> isspmatrix(csr_matrix([[5]]))
True
```

```
>>> from scipy.sparse import isspmatrix
>>> isspmatrix(5)
False
```

scipy.sparse.isspmatrix_csc

scipy.sparse.**isspmatrix_csc**(*x*)

Is x of csc_matrix type?

Parameters

x object to check for being a csc matrix

Returns

bool True if x is a csc matrix, False otherwise

Examples

```
>>> from scipy.sparse import csc_matrix, isspmatrix_csc
>>> isspmatrix_csc(csc_matrix([[5]]))
True
```

```
>>> from scipy.sparse import csc_matrix, csr_matrix, isspmatrix_csc
>>> isspmatrix_csc(csr_matrix([[5]]))
False
```

scipy.sparse.isspmatrix_csr

scipy.sparse.**isspmatrix_csr**(*x*)

Is x of csr_matrix type?

Parameters

x object to check for being a csr matrix

Returns

bool True if x is a csr matrix, False otherwise

Examples

```
>>> from scipy.sparse import csr_matrix, isspmatrix_csr
>>> isspmatrix_csr(csr_matrix([[5]]))
True
```

```
>>> from scipy.sparse import csc_matrix, csr_matrix, isspmatrix_csc
>>> isspmatrix_csr(csc_matrix([[5]]))
False
```

scipy.sparse.isspmatrix_bsr

scipy.sparse.**isspmatrix_bsr**(*x*)

Is x of a bsr_matrix type?

Parameters

x object to check for being a bsr matrix

Returns

bool True if x is a bsr matrix, False otherwise

Examples

```
>>> from scipy.sparse import bsr_matrix, isspmatrix_bsr
>>> isspmatrix_bsr(bsr_matrix([[5]]))
True
```

```
>>> from scipy.sparse import bsr_matrix, csr_matrix, isspmatrix_bsr
>>> isspmatrix_bsr(csr_matrix([[5]]))
False
```

scipy.sparse.isspmatrix_lil

scipy.sparse.**isspmatrix_lil**(*x*)

Is x of lil_matrix type?

Parameters

x object to check for being a lil matrix

Returns

bool True if x is a lil matrix, False otherwise

Examples

```
>>> from scipy.sparse import lil_matrix, isspmatrix_lil
>>> isspmatrix_lil(lil_matrix([[5]]))
True
```

```
>>> from scipy.sparse import lil_matrix, csr_matrix, isspmatrix_lil
>>> isspmatrix_lil(csr_matrix([[5]]))
False
```

scipy.sparse.isspmatrix_dok

scipy.sparse.**isspmatrix_dok**(*x*)

Is x of dok_matrix type?

Parameters

x object to check for being a dok matrix

Returns

bool True if x is a dok matrix, False otherwise

Examples

```
>>> from scipy.sparse import dok_matrix, isspmatrix_dok
>>> isspmatrix_dok(dok_matrix([[5]]))
True
```

```
>>> from scipy.sparse import dok_matrix, csr_matrix, isspmatrix_dok
>>> isspmatrix_dok(csr_matrix([[5]]))
False
```

scipy.sparse.isspmatrix_coo

scipy.sparse.**isspmatrix_coo**(*x*)

Is x of coo_matrix type?

Parameters

x object to check for being a coo matrix

Returns

bool True if x is a coo matrix, False otherwise

Examples

```
>>> from scipy.sparse import coo_matrix, isspmatrix_coo
>>> isspmatrix_coo(coo_matrix([[5]]))
True
```

```
>>> from scipy.sparse import coo_matrix, csr_matrix, isspmatrix_coo
>>> isspmatrix_coo(csr_matrix([[5]]))
False
```

scipy.sparse.isspmatrix_dia

scipy.sparse.**isspmatrix_dia**(*x*)

Is x of dia_matrix type?

Parameters

x object to check for being a dia matrix

Returns

bool True if x is a dia matrix, False otherwise

Examples

```
>>> from scipy.sparse import dia_matrix, isspmatrix_dia
>>> isspmatrix_dia(dia_matrix([[5]]))
True
```

```
>>> from scipy.sparse import dia_matrix, csr_matrix, isspmatrix_dia
>>> isspmatrix_dia(csr_matrix([[5]]))
False
```

Submodules

csgraph	Compressed sparse graph routines (*scipy.sparse.csgraph*)
linalg	Sparse linear algebra (*scipy.sparse.linalg*)

Exceptions

SparseEfficiencyWarning
SparseWarning

scipy.sparse.SparseEfficiencyWarning

exception scipy.sparse.**SparseEfficiencyWarning**

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.sparse.SparseWarning

exception scipy.sparse.**SparseWarning**

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

Usage information

There are seven available sparse matrix types:

1. csc_matrix: Compressed Sparse Column format
2. csr_matrix: Compressed Sparse Row format
3. bsr_matrix: Block Sparse Row format
4. lil_matrix: List of Lists format
5. dok_matrix: Dictionary of Keys format
6. coo_matrix: COOrdinate format (aka IJV, triplet format)
7. dia_matrix: DIAgonal format

To construct a matrix efficiently, use either dok_matrix or lil_matrix. The lil_matrix class supports basic slicing and fancy indexing with a similar syntax to NumPy arrays. As illustrated below, the COO format may also be used to efficiently construct matrices. Despite their similarity to NumPy arrays, it is **strongly discouraged** to use NumPy functions directly on these matrices because NumPy may not properly convert them for computations, leading to unexpected (and incorrect) results. If you do want to apply a NumPy function to these matrices, first check if SciPy has its own implementation for the given sparse matrix class, or **convert the sparse matrix to a NumPy array** (e.g., using the *toarray()* method of the class) first before applying the method.

To perform manipulations such as multiplication or inversion, first convert the matrix to either CSC or CSR format. The lil_matrix format is row-based, so conversion to CSR is efficient, whereas conversion to CSC is less so.

All conversions among the CSR, CSC, and COO formats are efficient, linear-time operations.

Matrix vector product

To do a vector product between a sparse matrix and a vector simply use the matrix *dot* method, as described in its docstring:

```
>>> import numpy as np
>>> from scipy.sparse import csr_matrix
>>> A = csr_matrix([[1, 2, 0], [0, 0, 3], [4, 0, 5]])
>>> v = np.array([1, 0, -1])
>>> A.dot(v)
array([ 1, -3, -1], dtype=int64)
```

Warning: As of NumPy 1.7, *np.dot* is not aware of sparse matrices, therefore using it will result on unexpected results or errors. The corresponding dense array should be obtained first instead:

```
>>> np.dot(A.toarray(), v)
array([ 1, -3, -1], dtype=int64)
```

but then all the performance advantages would be lost.

The CSR format is specially suitable for fast matrix vector products.

Example 1

Construct a 1000x1000 lil_matrix and add some values to it:

```
>>> from scipy.sparse import lil_matrix
>>> from scipy.sparse.linalg import spsolve
>>> from numpy.linalg import solve, norm
>>> from numpy.random import rand
```

```
>>> A = lil_matrix((1000, 1000))
>>> A[0, :100] = rand(100)
>>> A[1, 100:200] = A[0, :100]
>>> A.setdiag(rand(1000))
```

Now convert it to CSR format and solve A x = b for x:

```
>>> A = A.tocsr()
>>> b = rand(1000)
>>> x = spsolve(A, b)
```

Convert it to a dense matrix and solve, and check that the result is the same:

```
>>> x_ = solve(A.toarray(), b)
```

Now we can compute norm of the error with:

```
>>> err = norm(x-x_)
>>> err < 1e-10
True
```

It should be small :)

Example 2

Construct a matrix in COO format:

```
>>> from scipy import sparse
>>> from numpy import array
>>> I = array([0,3,1,0])
>>> J = array([0,3,1,2])
>>> V = array([4,5,7,9])
>>> A = sparse.coo_matrix((V,(I,J)),shape=(4,4))
```

Notice that the indices do not need to be sorted.

Duplicate (i,j) entries are summed when converting to CSR or CSC.

```
>>> I = array([0,0,1,3,1,0,0])
>>> J = array([0,2,1,3,1,0,0])
>>> V = array([1,1,1,1,1,1,1])
>>> B = sparse.coo_matrix((V,(I,J)),shape=(4,4)).tocsr()
```

This is useful for constructing finite-element stiffness and mass matrices.

Further details

CSR column indices are not necessarily sorted. Likewise for CSC row indices. Use the .sorted_indices() and .sort_indices() methods when sorted indices are required (e.g., when passing data to other libraries).

3.3.24 Sparse linear algebra (`scipy.sparse.linalg`)

Abstract linear operators

LinearOperator(*args, **kwargs)	Common interface for performing matrix vector products
aslinearoperator(A)	Return A as a LinearOperator.

scipy.sparse.linalg.LinearOperator

class scipy.sparse.linalg.**LinearOperator**(**args*, ***kwargs*)

Common interface for performing matrix vector products

Many iterative methods (e.g. cg, gmres) do not need to know the individual entries of a matrix to solve a linear system A*x=b. Such solvers only require the computation of matrix vector products, A*v where v is a dense vector. This class serves as an abstract interface between iterative solvers and matrix-like objects.

To construct a concrete LinearOperator, either pass appropriate callables to the constructor of this class, or subclass it.

A subclass must implement either one of the methods `_matvec` and `_matmat`, and the attributes/properties `shape` (pair of integers) and `dtype` (may be None). It may call the `__init__` on this class to have these attributes validated. Implementing `_matvec` automatically implements `_matmat` (using a naive algorithm) and vice-versa.

Optionally, a subclass may implement `_rmatvec` or `_adjoint` to implement the Hermitian adjoint (conjugate transpose). As with `_matvec` and `_matmat`, implementing either `_rmatvec` or `_adjoint` implements the other automatically. Implementing `_adjoint` is preferable; `_rmatvec` is mostly there for backwards compatibility.

Parameters

shape	[tuple] Matrix dimensions (M, N).
matvec	[callable f(v)] Returns returns A * v.
rmatvec	[callable f(v)] Returns A^H * v, where A^H is the conjugate transpose of A.
matmat	[callable f(V)] Returns A * V, where V is a dense matrix with dimensions (N, K).
dtype	[dtype] Data type of the matrix.
rmatmat	[callable f(V)] Returns A^H * V, where V is a dense matrix with dimensions (M, K).

See also:

aslinearoperator

Construct LinearOperators

Notes

The user-defined matvec() function must properly handle the case where v has shape (N,) as well as the (N,1) case. The shape of the return type is handled internally by LinearOperator.

LinearOperator instances can also be multiplied, added with each other and exponentiated, all lazily: the result of these operations is always a new, composite LinearOperator, that defers linear operations to the original operators and combines the results.

More details regarding how to subclass a LinearOperator and several examples of concrete LinearOperator instances can be found in the external project PyLops.

Examples

```
>>> import numpy as np
>>> from scipy.sparse.linalg import LinearOperator
>>> def mv(v):
...     return np.array([2*v[0], 3*v[1]])
...
>>> A = LinearOperator((2,2), matvec=mv)
>>> A
<2x2 _CustomLinearOperator with dtype=float64>
>>> A.matvec(np.ones(2))
array([ 2.,  3.])
>>> A * np.ones(2)
array([ 2.,  3.])
```

Attributes

args [tuple] For linear operators describing products etc. of other linear operators, the operands of the binary operation.

ndim [int] Number of dimensions (this is always 2)

Methods

__call__(x)	Call self as a function.
adjoint()	Hermitian adjoint.
dot(x)	Matrix-matrix or matrix-vector multiplication.
matmat(X)	Matrix-matrix multiplication.
matvec(x)	Matrix-vector multiplication.
rmatmat(X)	Adjoint matrix-matrix multiplication.
rmatvec(x)	Adjoint matrix-vector multiplication.
transpose()	Transpose this linear operator.

scipy.sparse.linalg.LinearOperator.__call__

LinearOperator.**__call__**(*x*)
Call self as a function.

scipy.sparse.linalg.LinearOperator.adjoint

LinearOperator.**adjoint**()
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns

A_H [LinearOperator] Hermitian adjoint of self.

scipy.sparse.linalg.LinearOperator.dot

LinearOperator.**dot**(*x*)
Matrix-matrix or matrix-vector multiplication.

Parameters

x [array_like] 1-d or 2-d array, representing a vector or matrix.

Returns

Ax [array] 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

scipy.sparse.linalg.LinearOperator.matmat

LinearOperator.**matmat**(*X*)
Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters

X [{matrix, ndarray}] An array with shape (N,K).

Returns

Y [{matrix, ndarray}] A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

scipy.sparse.linalg.LinearOperator.matvec

LinearOperator.**matvec**(*x*)

Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters

x [{matrix, ndarray}] An array with shape (N,) or (N,1).

Returns

y [{matrix, ndarray}] A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

scipy.sparse.linalg.LinearOperator.rmatmat

LinearOperator.**rmatmat**(*X*)

Adjoint matrix-matrix multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array, or 2-d array. The default implementation defers to the adjoint.

Parameters

X [{matrix, ndarray}] A matrix or 2D array.

Returns

Y [{matrix, ndarray}] A matrix or 2D array depending on the type of the input.

Notes

This rmatmat wraps the user-specified rmatmat routine.

scipy.sparse.linalg.LinearOperator.rmatvec

LinearOperator.**rmatvec**(*x*)

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters

x [{matrix, ndarray}] An array with shape (M,) or (M,1).

Returns

y [{matrix, ndarray}] A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

scipy.sparse.linalg.LinearOperator.transpose

LinearOperator.**transpose**()

Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

__mul__	

scipy.sparse.linalg.aslinearoperator

scipy.sparse.linalg.**aslinearoperator**(*A*)

Return A as a LinearOperator.

'A' may be any of the following types:

- ndarray
- matrix
- sparse matrix (e.g. csr_matrix, lil_matrix, etc.)
- LinearOperator
- An object with .shape and .matvec attributes

See the LinearOperator documentation for additional information.

Notes

If 'A' has no .dtype attribute, the data type is determined by calling *LinearOperator.matvec* - set the .dtype attribute to prevent this call upon the linear operator creation.

Examples

```
>>> from scipy.sparse.linalg import aslinearoperator
>>> M = np.array([[1,2,3],[4,5,6]], dtype=np.int32)
>>> aslinearoperator(M)
<2x3 MatrixLinearOperator with dtype=int32>
```

Matrix Operations

inv(A)	Compute the inverse of a sparse matrix
expm(A)	Compute the matrix exponential using Pade approximation.
expm_multiply(A, B[, start, stop, num, endpoint])	Compute the action of the matrix exponential of A on B.

scipy.sparse.linalg.inv

scipy.sparse.linalg.**inv**(*A*)

Compute the inverse of a sparse matrix

Parameters

A [(M,M) ndarray or sparse matrix] square matrix to be inverted

Returns

Ainv [(M,M) ndarray or sparse matrix] inverse of *A*

Notes

This computes the sparse inverse of *A*. If the inverse of *A* is expected to be non-sparse, it will likely be faster to convert *A* to dense and use scipy.linalg.inv.

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import inv
>>> A = csc_matrix([[1., 0.], [1., 2.]])
>>> Ainv = inv(A)
>>> Ainv
<2x2 sparse matrix of type '<class 'numpy.float64'>'
    with 3 stored elements in Compressed Sparse Column format>
>>> A.dot(Ainv)
<2x2 sparse matrix of type '<class 'numpy.float64'>'
    with 2 stored elements in Compressed Sparse Column format>
>>> A.dot(Ainv).todense()
```

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```
matrix([[ 1.,  0.],
        [ 0.,  1.]])
```

New in version 0.12.0.

scipy.sparse.linalg.expm

scipy.sparse.linalg.**expm**(*A*)

Compute the matrix exponential using Pade approximation.

Parameters

A [(M,M) array_like or sparse matrix] 2D Array or Matrix (sparse or dense) to be exponentiated

Returns

expA [(M,M) ndarray] Matrix exponential of *A*

Notes

This is algorithm (6.1) which is a simplification of algorithm (5.1).

New in version 0.12.0.

References

[1]

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import expm
>>> A = csc_matrix([[1, 0, 0], [0, 2, 0], [0, 0, 3]])
>>> A.todense()
matrix([[1, 0, 0],
        [0, 2, 0],
        [0, 0, 3]], dtype=int64)
>>> Aexp = expm(A)
>>> Aexp
<3x3 sparse matrix of type '<class 'numpy.float64'>'
    with 3 stored elements in Compressed Sparse Column format>
>>> Aexp.todense()
matrix([[  2.71828183,   0.        ,   0.        ],
        [  0.        ,   7.3890561 ,   0.        ],
        [  0.        ,   0.        ,  20.08553692]])
```

scipy.sparse.linalg.expm_multiply

scipy.sparse.linalg.**expm_multiply**(*A*, *B*, *start=None*, *stop=None*, *num=None*, *endpoint=None*)

Compute the action of the matrix exponential of A on B.

Parameters

A	[transposable linear operator] The operator whose exponential is of interest.
B	[ndarray] The matrix or vector to be multiplied by the matrix exponential of A.
start	[scalar, optional] The starting time point of the sequence.
stop	[scalar, optional] The end time point of the sequence, unless *endpoint* is set to False. In that case, the sequence consists of all but the last of `num + 1` evenly spaced time points, so that *stop* is excluded. Note that the step size changes when *endpoint* is False.
num	[int, optional] Number of time points to use.
endpoint	[bool, optional] If True, *stop* is the last time point. Otherwise, it is not included.

Returns

expm_A_B
: [ndarray] The result of the action $e^{t_k A} B$.

Notes

The optional arguments defining the sequence of evenly spaced time points are compatible with the arguments of `numpy.linspace`.

The output ndarray shape is somewhat complicated so I explain it here. The ndim of the output could be either 1, 2, or 3. It would be 1 if you are computing the expm action on a single vector at a single time point. It would be 2 if you are computing the expm action on a vector at multiple time points, or if you are computing the expm action on a matrix at a single time point. It would be 3 if you want the action on a matrix with multiple columns at multiple time points. If multiple time points are requested, expm_A_B[0] will always be the action of the expm at the first time point, regardless of whether the action is on a vector or a matrix.

References

[1], [2]

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import expm, expm_multiply
>>> A = csc_matrix([[1, 0], [0, 1]])
>>> A.todense()
matrix([[1, 0],
        [0, 1]], dtype=int64)
>>> B = np.array([np.exp(-1.), np.exp(-2.)])
>>> B
array([ 0.36787944,  0.13533528])
>>> expm_multiply(A, B, start=1, stop=2, num=3, endpoint=True)
array([[ 1.        ,  0.36787944],
       [ 1.64872127,  0.60653066],
       [ 2.71828183,  1.        ]])
>>> expm(A).dot(B)                  # Verify 1st timestep
```

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```
array([ 1.        ,  0.36787944])
>>> expm(1.5*A).dot(B)               # Verify 2nd timestep
array([ 1.64872127,  0.60653066])
>>> expm(2*A).dot(B)                 # Verify 3rd timestep
array([ 2.71828183,  1.        ])
```

Matrix norms

norm(x[, ord, axis])	Norm of a sparse matrix
onenormest(A[, t, itmax, compute_v, compute_w])	Compute a lower bound of the 1-norm of a sparse matrix.

scipy.sparse.linalg.norm

scipy.sparse.linalg.**norm**(*x*, *ord=None*, *axis=None*)

Norm of a sparse matrix

This function is able to return one of seven different matrix norms, depending on the value of the ord parameter.

Parameters

x [a sparse matrix] Input sparse matrix.

ord [{non-zero int, inf, -inf, 'fro'}, optional] Order of the norm (see table under Notes). inf means numpy's *inf* object.

axis [{int, 2-tuple of ints, None}, optional] If *axis* is an integer, it specifies the axis of *x* along which to compute the vector norms. If *axis* is a 2-tuple, it specifies the axes that hold 2-D matrices, and the matrix norms of these matrices are computed. If *axis* is None then either a vector norm (when *x* is 1-D) or a matrix norm (when *x* is 2-D) is returned.

Returns

n [float or ndarray]

Notes

Some of the ord are not implemented because some associated functions like, _multi_svd_norm, are not yet available for sparse matrix.

This docstring is modified based on numpy.linalg.norm. https://github.com/numpy/numpy/blob/master/numpy/linalg/linalg.py

The following norms can be calculated:

ord	norm for sparse matrices
None	Frobenius norm
'fro'	Frobenius norm
inf	max(sum(abs(x), axis=1))
-inf	min(sum(abs(x), axis=1))
0	abs(x).sum(axis=axis)
1	max(sum(abs(x), axis=0))
-1	min(sum(abs(x), axis=0))
2	Not implemented
-2	Not implemented
other	Not implemented

The Frobenius norm is given by [1]:

$$||A||_F = [\sum_{i,j} abs(a_{i,j})^2]^{1/2}$$

References

[1]

Examples

```
>>> from scipy.sparse import *
>>> import numpy as np
>>> from scipy.sparse.linalg import norm
>>> a = np.arange(9) - 4
>>> a
array([-4, -3, -2, -1, 0, 1, 2, 3, 4])
>>> b = a.reshape((3, 3))
>>> b
array([[-4, -3, -2],
       [-1, 0, 1],
       [ 2, 3, 4]])
```

```
>>> b = csr_matrix(b)
>>> norm(b)
7.745966692414834
>>> norm(b, 'fro')
7.745966692414834
>>> norm(b, np.inf)
9
>>> norm(b, -np.inf)
2
>>> norm(b, 1)
7
>>> norm(b, -1)
6
```

scipy.sparse.linalg.onenormest

scipy.sparse.linalg.**onenormest**(*A*, *t=2*, *itmax=5*, *compute_v=False*, *compute_w=False*)

Compute a lower bound of the 1-norm of a sparse matrix.

Parameters

A [ndarray or other linear operator] A linear operator that can be transposed and that can produce matrix products.

t [int, optional] A positive parameter controlling the tradeoff between accuracy versus time and memory usage. Larger values take longer and use more memory but give more accurate output.

itmax [int, optional] Use at most this many iterations.

compute_v [bool, optional] Request a norm-maximizing linear operator input vector if True.

compute_w [bool, optional] Request a norm-maximizing linear operator output vector if True.

Returns

est	[float] An underestimate of the 1-norm of the sparse matrix.
v	[ndarray, optional] The vector such that ||Av||_1 == est*||v||_1. It can be thought of as an input to the linear operator that gives an output with particularly large norm.
w	[ndarray, optional] The vector Av which has relatively large 1-norm. It can be thought of as an output of the linear operator that is relatively large in norm compared to the input.

Notes

This is algorithm 2.4 of [1].

In [2] it is described as follows. "This algorithm typically requires the evaluation of about 4t matrix-vector products and almost invariably produces a norm estimate (which is, in fact, a lower bound on the norm) correct to within a factor 3."

New in version 0.13.0.

References

[1], [2]

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import onenormest
>>> A = csc_matrix([[1., 0., 0.], [5., 8., 2.], [0., -1., 0.]],␣
↪dtype=float)
>>> A.todense()
matrix([[ 1.,  0.,  0.],
        [ 5.,  8.,  2.],
        [ 0., -1.,  0.]])
>>> onenormest(A)
9.0
>>> np.linalg.norm(A.todense(), ord=1)
9.0
```

Solving linear problems

Direct methods for linear equation systems:

spsolve(A, b[, permc_spec, use_umfpack])	Solve the sparse linear system Ax=b, where b may be a vector or a matrix.
spsolve_triangular(A, b[, lower, …])	Solve the equation `A x = b` for *x*, assuming A is a triangular matrix.
factorized(A)	Return a function for solving a sparse linear system, with A pre-factorized.
MatrixRankWarning	
use_solver(**kwargs)	Select default sparse direct solver to be used.

scipy.sparse.linalg.spsolve

scipy.sparse.linalg.**spsolve**(*A*, *b*, *permc_spec=None*, *use_umfpack=True*)

Solve the sparse linear system Ax=b, where b may be a vector or a matrix.

Parameters

A [ndarray or sparse matrix] The square matrix A will be converted into CSC or CSR form

b [ndarray or sparse matrix] The matrix or vector representing the right hand side of the equation. If a vector, b.shape must be (n,) or (n, 1).

permc_spec [str, optional] How to permute the columns of the matrix for sparsity preservation. (default: 'COLAMD')

- NATURAL: natural ordering.
- MMD_ATA: minimum degree ordering on the structure of A^T A.
- MMD_AT_PLUS_A: minimum degree ordering on the structure of A^T+A.
- COLAMD: approximate minimum degree column ordering

use_umfpack [bool, optional] if True (default) then use umfpack for the solution. This is only referenced if b is a vector and scikit-umfpack is installed.

Returns

x [ndarray or sparse matrix] the solution of the sparse linear equation. If b is a vector, then x is a vector of size A.shape[1] If b is a matrix, then x is a matrix of size (A.shape[1], b.shape[1])

Notes

For solving the matrix expression AX = B, this solver assumes the resulting matrix X is sparse, as is often the case for very sparse inputs. If the resulting X is dense, the construction of this sparse result will be relatively expensive. In that case, consider converting A to a dense matrix and using scipy.linalg.solve or its variants.

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import spsolve
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> B = csc_matrix([[2, 0], [-1, 0], [2, 0]], dtype=float)
>>> x = spsolve(A, B)
>>> np.allclose(A.dot(x).todense(), B.todense())
True
```

scipy.sparse.linalg.spsolve_triangular

scipy.sparse.linalg.**spsolve_triangular**(*A*, *b*, *lower=True*, *overwrite_A=False*, *overwrite_b=False*, *unit_diagonal=False*)

Solve the equation `A x = b` for *x*, assuming A is a triangular matrix.

Parameters

A [(M, M) sparse matrix] A sparse square triangular matrix. Should be in CSR format.

b [(M,) or (M, N) array_like] Right-hand side matrix in `A x = b`

lower [bool, optional] Whether *A* is a lower or upper triangular matrix. Default is lower triangular matrix.

overwrite_A
: [bool, optional] Allow changing *A*. The indices of *A* are going to be sorted and zero entries are going to be removed. Enabling gives a performance gain. Default is False.

overwrite_b
: [bool, optional] Allow overwriting data in *b*. Enabling gives a performance gain. Default is False. If *overwrite_b* is True, it should be ensured that *b* has an appropriate dtype to be able to store the result.

unit_diagonal
: [bool, optional] If True, diagonal elements of *a* are assumed to be 1 and will not be referenced.
New in version 1.4.0.

Returns

x
: [(M,) or (M, N) ndarray] Solution to the system `A x = b`. Shape of return matches shape of *b*.

Raises

LinAlgError
: If *A* is singular or not triangular.

ValueError
: If shape of *A* or shape of *b* do not match the requirements.

Notes

New in version 0.19.0.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.linalg import spsolve_triangular
>>> A = csr_matrix([[3, 0, 0], [1, -1, 0], [2, 0, 1]], dtype=float)
>>> B = np.array([[2, 0], [-1, 0], [2, 0]], dtype=float)
>>> x = spsolve_triangular(A, B)
>>> np.allclose(A.dot(x), B)
True
```

scipy.sparse.linalg.factorized

scipy.sparse.linalg.**factorized**(*A*)
Return a function for solving a sparse linear system, with A pre-factorized.

Parameters

A
: [(N, N) array_like] Input.

Returns

solve
: [callable] To solve the linear system of equations given in *A*, the *solve* callable should be passed an ndarray of shape (N,).

Examples

```
>>> from scipy.sparse.linalg import factorized
>>> A = np.array([[ 3. ,  2. , -1. ],
...               [ 2. , -2. ,  4. ],
...               [-1. ,  0.5, -1. ]])
>>> solve = factorized(A) # Makes LU decomposition.
>>> rhs1 = np.array([1, -2, 0])
>>> solve(rhs1) # Uses the LU factors.
array([ 1., -2., -2.])
```

scipy.sparse.linalg.MatrixRankWarning

exception scipy.sparse.linalg.**MatrixRankWarning**

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.sparse.linalg.use_solver

scipy.sparse.linalg.**use_solver**(***kwargs*)
Select default sparse direct solver to be used.

Parameters

useUmfpack
[bool, optional] Use UMFPACK over SuperLU. Has effect only if scikits.umfpack is installed. Default: True

assumeSortedIndices
[bool, optional] Allow UMFPACK to skip the step of sorting indices for a CSR/CSC matrix. Has effect only if useUmfpack is True and scikits.umfpack is installed. Default: False

Notes

The default sparse solver is umfpack when available (scikits.umfpack is installed). This can be changed by passing useUmfpack = False, which then causes the always present SuperLU based solver to be used.

Umfpack requires a CSR/CSC matrix to have sorted column/row indices. If sure that the matrix fulfills this, pass `assumeSortedIndices=True` to gain some speed.

Iterative methods for linear equation systems:

bicg(A, b[, x0, tol, maxiter, M, callback, atol])	Use BIConjugate Gradient iteration to solve `Ax = b`.
bicgstab(A, b[, x0, tol, maxiter, M, …])	Use BIConjugate Gradient STABilized iteration to solve `Ax = b`.
cg(A, b[, x0, tol, maxiter, M, callback, atol])	Use Conjugate Gradient iteration to solve `Ax = b`.
cgs(A, b[, x0, tol, maxiter, M, callback, atol])	Use Conjugate Gradient Squared iteration to solve `Ax = b`.
gmres(A, b[, x0, tol, restart, maxiter, M, …])	Use Generalized Minimal RESidual iteration to solve `Ax = b`.
lgmres(A, b[, x0, tol, maxiter, M, …])	Solve a matrix equation using the LGMRES algorithm.
minres(A, b[, x0, shift, tol, maxiter, M, …])	Use MINimum RESidual iteration to solve Ax=b
qmr(A, b[, x0, tol, maxiter, M1, M2, …])	Use Quasi-Minimal Residual iteration to solve `Ax = b`.

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gcrotmk(A, b[, x0, tol, maxiter, M, …])	Solve a matrix equation using flexible GCROT(m,k) algorithm.

scipy.sparse.linalg.bicg

scipy.sparse.linalg.**bicg**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *M=None*, *callback=None*, *atol=None*)

Use BIConjugate Gradient iteration to solve `Ax = b`.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system. Alternatively, `A` can be a linear operator which can produce `Ax` and `A^T x` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x [{array, matrix}] The converged solution.

info [integer]
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, `norm(residual) <= max(tol*norm(b), atol)`. The default for `atol` is `'legacy'`, which emulates a different legacy behavior.

> **Warning:** The default value for *atol* will be changed in a future release. For future compatibility, specify *atol* explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import bicg
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = bicg(A, b)
>>> print(exitCode)            # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.bicgstab

scipy.sparse.linalg.**bicgstab**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *M=None*, *callback=None*, *atol=None*)

Use BIConjugate Gradient STABilized iteration to solve `Ax = b`.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system. Alternatively, `A` can be a linear operator which can produce `Ax` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x [{array, matrix}] The converged solution.

info [integer]
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, `norm(residual) <= max(tol*norm(b), atol)`. The default for `atol` is `'legacy'`, which emulates a different legacy behavior.

> **Warning:** The default value for *atol* will be changed in a future release. For future compatibility, specify *atol* explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.cg

scipy.sparse.linalg.**cg**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *M=None*, *callback=None*, *atol=None*)

Use Conjugate Gradient iteration to solve `Ax = b`.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system. `A` must represent a hermitian, positive definite matrix. Alternatively, `A` can be a linear operator which can produce `Ax` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x [{array, matrix}] The converged solution.

info [integer]

Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, `norm(residual) <= max(tol*norm(b), atol)`. The default for `atol` is `'legacy'`, which emulates a different legacy behavior.

> **Warning:** The default value for *atol* will be changed in a future release. For future compatibility, specify *atol* explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.cgs

`scipy.sparse.linalg.`**`cgs`**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *M=None*, *callback=None*, *atol=None*)

Use Conjugate Gradient Squared iteration to solve `Ax = b`.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real-valued N-by-N matrix of the linear system. Alternatively, `A` can be a linear operator which can produce `Ax` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x [{array, matrix}] The converged solution.

info [integer]
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, `norm(residual) <= max(tol*norm(b), atol)`. The default for `atol` is `'legacy'`, which emulates a different legacy behavior.

> **Warning:** The default value for *atol* will be changed in a future release. For future compatibility, specify *atol* explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

scipy.sparse.linalg.gmres

scipy.sparse.linalg.**gmres**(*A*, *b*, *x0=None*, *tol=1e-05*, *restart=None*, *maxiter=None*, *M=None*, *callback=None*, *restrt=None*, *atol=None*, *callback_type=None*)

Use Generalized Minimal RESidual iteration to solve `Ax = b`.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system. Alternatively, `A` can be a linear operator which can produce `Ax` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x [{array, matrix}] The converged solution.

info [int]
Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Other Parameters

x0 [{array, matrix}] Starting guess for the solution (a vector of zeros by default).

tol, atol [float, optional] Tolerances for convergence, `norm(residual) <= max(tol*norm(b), atol)`. The default for `atol` is `'legacy'`, which emulates a different legacy behavior.

> **Warning:** The default value for *atol* will be changed in a future release. For future compatibility, specify *atol* explicitly.

restart [int, optional] Number of iterations between restarts. Larger values increase iteration cost, but may be necessary for convergence. Default is 20.

maxiter [int, optional] Maximum number of iterations (restart cycles). Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Inverse of the preconditioner of A. M should approximate the inverse of A and be easy to solve for (see Notes). Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance. By default, no preconditioner is used.

callback [function] User-supplied function to call after each iteration. It is called as *callback(args)*, where *args* are selected by *callback_type*.

callback_type
[{'x', 'pr_norm', 'legacy'}, optional]
Callback function argument requested:

- `x`: current iterate (ndarray), called on every restart
- `pr_norm`: relative (preconditioned) residual norm (float), called on every inner iteration

- `legacy` (default): same as `pr_norm`, but also changes the meaning of 'maxiter' to count inner iterations instead of restart cycles.

restrt [int, optional] DEPRECATED - use *restart* instead.

See also:

`LinearOperator`

Notes

A preconditioner, P, is chosen such that P is close to A but easy to solve for. The preconditioner parameter required by this routine is `M = P^-1`. The inverse should preferably not be calculated explicitly. Rather, use the following template to produce M:

```
# Construct a linear operator that computes P^-1 * x.
import scipy.sparse.linalg as spla
M_x = lambda x: spla.spsolve(P, x)
M = spla.LinearOperator((n, n), M_x)
```

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import gmres
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = gmres(A, b)
>>> print(exitCode)            # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.lgmres

scipy.sparse.linalg.**lgmres**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=1000*, *M=None*, *callback=None*, *inner_m=30*, *outer_k=3*, *outer_v=None*, *store_outer_Av=True*, *prepend_outer_v=False*, *atol=None*)

Solve a matrix equation using the LGMRES algorithm.

The LGMRES algorithm [1] [2] is designed to avoid some problems in the convergence in restarted GMRES, and often converges in fewer iterations.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system. Alternatively, `A` can be a linear operator which can produce `Ax` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

x0 [{array, matrix}] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, `norm(residual) <= max(tol*norm(b), atol)`. The default for `atol` is *tol*.

> **Warning:** The default value for *atol* will be changed in a future release. For future compatibility, specify *atol* explicitly.

maxiter [int, optional] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}, optional] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function, optional] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

inner_m [int, optional] Number of inner GMRES iterations per each outer iteration.

outer_k [int, optional] Number of vectors to carry between inner GMRES iterations. According to [1], good values are in the range of 1…3. However, note that if you want to use the additional vectors to accelerate solving multiple similar problems, larger values may be beneficial.

outer_v [list of tuples, optional] List containing tuples `(v, Av)` of vectors and corresponding matrix-vector products, used to augment the Krylov subspace, and carried between inner GMRES iterations. The element `Av` can be *None* if the matrix-vector product should be re-evaluated. This parameter is modified in-place by `lgmres`, and can be used to pass "guess" vectors in and out of the algorithm when solving similar problems.

store_outer_Av [bool, optional] Whether LGMRES should store also A*v in addition to vectors *v* in the *outer_v* list. Default is True.

prepend_outer_v [bool, optional] Whether to put outer_v augmentation vectors before Krylov iterates. In standard LGMRES, prepend_outer_v=False.

Returns

x [array or matrix] The converged solution.

info [int] Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations
- <0 : illegal input or breakdown

Notes

The LGMRES algorithm [1] [2] is designed to avoid the slowing of convergence in restarted GMRES, due to alternating residual vectors. Typically, it often outperforms GMRES(m) of comparable memory requirements by some measure, or at least is not much worse.

Another advantage in this algorithm is that you can supply it with 'guess' vectors in the *outer_v* argument that augment the Krylov subspace. If the solution lies close to the span of these vectors, the algorithm converges faster. This can be useful if several very similar matrices need to be inverted one after another, such as in Newton-Krylov iteration where the Jacobian matrix often changes little in the nonlinear steps.

References

[1], [2]

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lgmres
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = lgmres(A, b)
>>> print(exitCode)            # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.minres

scipy.sparse.linalg.**minres**(*A*, *b*, *x0=None*, *shift=0.0*, *tol=1e-05*, *maxiter=None*, *M=None*, *callback=None*, *show=False*, *check=False*)

Use MINimum RESidual iteration to solve Ax=b

MINRES minimizes norm(A*x - b) for a real symmetric matrix A. Unlike the Conjugate Gradient method, A can be indefinite or singular.

If shift != 0 then the method solves (A - shift*I)x = b

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real symmetric N-by-N matrix of the linear system Alternatively, `A` can be a linear operator which can produce `Ax` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x [{array, matrix}] The converged solution.

info [integer]
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.

tol [float] Tolerance to achieve. The algorithm terminates when the relative residual is below *tol*.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}] Preconditioner for A. The preconditioner should approximate the inverse of A. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

References

Solution of sparse indefinite systems of linear equations,

C. C. Paige and M. A. Saunders (1975), SIAM J. Numer. Anal. 12(4), pp. 617-629. https://web.stanford.edu/group/SOL/software/minres/

This file is a translation of the following MATLAB implementation:

https://web.stanford.edu/group/SOL/software/minres/minres-matlab.zip

Examples

```
>>> import numpy as np
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import minres
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> A = A + A.T
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = minres(A, b)
>>> print(exitCode)            # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.qmr

scipy.sparse.linalg.**qmr**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=None*, *M1=None*, *M2=None*, *callback=None*, *atol=None*)

Use Quasi-Minimal Residual iteration to solve `Ax = b`.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real-valued N-by-N matrix of the linear system. Alternatively, `A` can be a linear operator which can produce `Ax` and `A^T x` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

Returns

x [{array, matrix}] The converged solution.

info [integer]
Provides convergence information:
0 : successful exit >0 : convergence to tolerance not achieved, number of iterations <0 : illegal input or breakdown

Other Parameters

x0 [{array, matrix}] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, `norm(residual) <= max(tol*norm(b), atol)`. The default for `atol` is `'legacy'`, which emulates a different legacy behavior.

> **Warning:** The default value for *atol* will be changed in a future release. For future compatibility, specify *atol* explicitly.

maxiter [integer] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M1 [{sparse matrix, dense matrix, LinearOperator}] Left preconditioner for A.

M2 [{sparse matrix, dense matrix, LinearOperator}] Right preconditioner for A. Used together with the left preconditioner M1. The matrix M1*A*M2 should have better conditioned than A alone.

callback [function] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

See also:

`LinearOperator`

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import qmr
>>> A = csc_matrix([[3, 2, 0], [1, -1, 0], [0, 5, 1]], dtype=float)
>>> b = np.array([2, 4, -1], dtype=float)
>>> x, exitCode = qmr(A, b)
>>> print(exitCode)            # 0 indicates successful convergence
0
>>> np.allclose(A.dot(x), b)
True
```

scipy.sparse.linalg.gcrotmk

scipy.sparse.linalg.**gcrotmk**(*A*, *b*, *x0=None*, *tol=1e-05*, *maxiter=1000*, *M=None*, *callback=None*, *m=20*, *k=None*, *CU=None*, *discard_C=False*, *truncate='oldest'*, *atol=None*)

Solve a matrix equation using flexible GCROT(m,k) algorithm.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The real or complex N-by-N matrix of the linear system. Alternatively, `A` can be a linear operator which can produce `Ax` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [{array, matrix}] Right hand side of the linear system. Has shape (N,) or (N,1).

x0 [{array, matrix}] Starting guess for the solution.

tol, atol [float, optional] Tolerances for convergence, `norm(residual) <= max(tol*norm(b), atol)`. The default for `atol` is *tol*.

> **Warning:** The default value for *atol* will be changed in a future release. For future compatibility, specify *atol* explicitly.

maxiter [int, optional] Maximum number of iterations. Iteration will stop after maxiter steps even if the specified tolerance has not been achieved.

M [{sparse matrix, dense matrix, LinearOperator}, optional] Preconditioner for A. The preconditioner should approximate the inverse of A. gcrotmk is a 'flexible' algorithm and the preconditioner can vary from iteration to iteration. Effective preconditioning dramatically improves the rate of convergence, which implies that fewer iterations are needed to reach a given error tolerance.

callback [function, optional] User-supplied function to call after each iteration. It is called as callback(xk), where xk is the current solution vector.

m [int, optional] Number of inner FGMRES iterations per each outer iteration. Default: 20

k [int, optional] Number of vectors to carry between inner FGMRES iterations. According to [2], good values are around m. Default: m

CU [list of tuples, optional] List of tuples `(c, u)` which contain the columns of the matrices C and U in the GCROT(m,k) algorithm. For details, see [2]. The list given and vectors contained in it are modified in-place. If not given, start from empty matrices. The `c` elements in the tuples can be `None`, in which case the vectors are recomputed via `c = A u` on start and orthogonalized as described in [3].

discard_C [bool, optional] Discard the C-vectors at the end. Useful if recycling Krylov subspaces for different linear systems.

truncate [{'oldest', 'smallest'}, optional] Truncation scheme to use. Drop: oldest vectors, or vectors with smallest singular values using the scheme discussed in [1,2]. See [2] for detailed comparison. Default: 'oldest'

Returns

x [array or matrix] The solution found.

info [int] Provides convergence information:

- 0 : successful exit
- >0 : convergence to tolerance not achieved, number of iterations

References

[1], [2], [3]

Iterative methods for least-squares problems:

lsqr(A, b[, damp, atol, btol, conlim, …])	Find the least-squares solution to a large, sparse, linear system of equations.
lsmr(A, b[, damp, atol, btol, conlim, …])	Iterative solver for least-squares problems.

scipy.sparse.linalg.lsqr

scipy.sparse.linalg.**lsqr**(*A*, *b*, *damp=0.0*, *atol=1e-08*, *btol=1e-08*, *conlim=100000000.0*, *iter_lim=None*, *show=False*, *calc_var=False*, *x0=None*)

Find the least-squares solution to a large, sparse, linear system of equations.

The function solves `Ax = b` or `min ||Ax - b||^2` or `min ||Ax - b||^2 + d^2 ||x||^2`.

The matrix A may be square or rectangular (over-determined or under-determined), and may have any rank.

```
1. Unsymmetric equations --    solve  A*x = b

2. Linear least squares  --    solve  A*x = b
                               in the least-squares sense

3. Damped least squares  --    solve  (   A    )*x = ( b )
                                      ( damp*I )     ( 0 )
                               in the least-squares sense
```

Parameters

A [{sparse matrix, ndarray, LinearOperator}] Representation of an m-by-n matrix. Alternatively, `A` can be a linear operator which can produce `Ax` and `A^T x` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [array_like, shape (m,)] Right-hand side vector `b`.

damp [float] Damping coefficient.

atol, btol [float, optional] Stopping tolerances. If both are 1.0e-9 (say), the final residual norm should be accurate to about 9 digits. (The final x will usually have fewer correct digits, depending on cond(A) and the size of damp.)

conlim [float, optional] Another stopping tolerance. lsqr terminates if an estimate of `cond(A)` exceeds *conlim*. For compatible systems `Ax = b`, *conlim* could be as large as 1.0e+12 (say). For least-squares problems, conlim should be less than 1.0e+8. Maximum precision can be obtained by setting `atol = btol = conlim = zero`, but the number of iterations may then be excessive.

iter_lim [int, optional] Explicit limitation on number of iterations (for safety).

show [bool, optional] Display an iteration log.

calc_var [bool, optional] Whether to estimate diagonals of `(A'A + damp^2*I)^{-1}`.

x0 [array_like, shape (n,), optional] Initial guess of x, if None zeros are used.
New in version 1.0.0.

Returns

x [ndarray of float] The final solution.

istop [int] Gives the reason for termination. 1 means x is an approximate solution to Ax = b. 2 means x approximately solves the least-squares problem.

itn [int] Iteration number upon termination.

r1norm [float] `norm(r)`, where `r = b - Ax`.

r2norm [float] `sqrt( norm(r)^2 + damp^2 * norm(x)^2 )`. Equal to *r1norm* if `damp == 0`.

anorm [float] Estimate of Frobenius norm of `Abar = [[A]; [damp*I]]`.

acond [float] Estimate of `cond(Abar)`.

arnorm [float] Estimate of `norm(A'*r - damp^2*x)`.

xnorm [float] `norm(x)`

var [ndarray of float] If `calc_var` is True, estimates all diagonals of `(A'A)^{-1}` (if `damp == 0`) or more generally `(A'A + damp^2*I)^{-1}`. This is well defined if A has full column rank or `damp > 0`. (Not sure what var means if `rank(A) < n` and `damp = 0`.)

Notes

LSQR uses an iterative method to approximate the solution. The number of iterations required to reach a certain accuracy depends strongly on the scaling of the problem. Poor scaling of the rows or columns of A should therefore be avoided where possible.

For example, in problem 1 the solution is unaltered by row-scaling. If a row of A is very small or large compared to the other rows of A, the corresponding row of (A b) should be scaled up or down.

In problems 1 and 2, the solution x is easily recovered following column-scaling. Unless better information is known, the nonzero columns of A should be scaled so that they all have the same Euclidean norm (e.g., 1.0).

In problem 3, there is no freedom to re-scale if damp is nonzero. However, the value of damp should be assigned only after attention has been paid to the scaling of A.

The parameter damp is intended to help regularize ill-conditioned systems, by preventing the true solution from being very large. Another aid to regularization is provided by the parameter acond, which may be used to terminate iterations before the computed solution becomes very large.

If some initial estimate `x0` is known and if `damp == 0`, one could proceed as follows:

1. Compute a residual vector `r0 = b - A*x0`.
2. Use LSQR to solve the system `A*dx = r0`.

3. Add the correction dx to obtain a final solution `x = x0 + dx`.

This requires that `x0` be available before and after the call to LSQR. To judge the benefits, suppose LSQR takes k1 iterations to solve A*x = b and k2 iterations to solve A*dx = r0. If x0 is "good", norm(r0) will be smaller than norm(b). If the same stopping tolerances atol and btol are used for each system, k1 and k2 will be similar, but the final solution x0 + dx should be more accurate. The only way to reduce the total work is to use a larger stopping tolerance for the second system. If some value btol is suitable for A*x = b, the larger value btol*norm(b)/norm(r0) should be suitable for A*dx = r0.

Preconditioning is another way to reduce the number of iterations. If it is possible to solve a related system `M*x = b` efficiently, where M approximates A in some helpful way (e.g. M - A has low rank or its elements are small relative to those of A), LSQR may converge more rapidly on the system `A*M(inverse)*z = b`, after which x can be recovered by solving M*x = z.

If A is symmetric, LSQR should not be used!

Alternatives are the symmetric conjugate-gradient method (cg) and/or SYMMLQ. SYMMLQ is an implementation of symmetric cg that applies to any symmetric A and will converge more rapidly than LSQR. If A is positive definite, there are other implementations of symmetric cg that require slightly less work per iteration than SYMMLQ (but will take the same number of iterations).

References

[1], [2], [3]

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lsqr
>>> A = csc_matrix([[1., 0.], [1., 1.], [0., 1.]], dtype=float)
```

The first example has the trivial solution *[0, 0]*

```
>>> b = np.array([0., 0., 0.], dtype=float)
>>> x, istop, itn, normr = lsqr(A, b)[:4]
>>> istop
0
>>> x
array([ 0.,  0.])
```

The stopping code *istop=0* returned indicates that a vector of zeros was found as a solution. The returned solution *x* indeed contains *[0., 0.]*. The next example has a non-trivial solution:

```
>>> b = np.array([1., 0., -1.], dtype=float)
>>> x, istop, itn, r1norm = lsqr(A, b)[:4]
>>> istop
1
>>> x
array([ 1., -1.])
>>> itn
1
>>> r1norm
4.440892098500627e-16
```

As indicated by *istop=1*, `lsqr` found a solution obeying the tolerance limits. The given solution *[1., -1.]* obviously solves the equation. The remaining return values include information about the number of iterations (*itn=1*) and the remaining difference of left and right side of the solved equation. The final example demonstrates the behavior in the case where there is no solution for the equation:

```
>>> b = np.array([1., 0.01, -1.], dtype=float)
>>> x, istop, itn, r1norm = lsqr(A, b)[:4]
>>> istop
2
>>> x
array([ 1.00333333, -0.99666667])
>>> A.dot(x)-b
array([ 0.00333333, -0.00333333,  0.00333333])
>>> r1norm
0.005773502691896255
```

istop indicates that the system is inconsistent and thus *x* is rather an approximate solution to the corresponding least-squares problem. *r1norm* contains the norm of the minimal residual that was found.

scipy.sparse.linalg.lsmr

scipy.sparse.linalg.**lsmr**(*A*, *b*, *damp=0.0*, *atol=1e-06*, *btol=1e-06*, *conlim=100000000.0*, *maxiter=None*, *show=False*, *x0=None*)

Iterative solver for least-squares problems.

lsmr solves the system of linear equations `Ax = b`. If the system is inconsistent, it solves the least-squares problem `min ||b - Ax||_2`. `A` is a rectangular matrix of dimension m-by-n, where all cases are allowed: m = n, m > n, or m < n. `b` is a vector of length m. The matrix A may be dense or sparse (usually sparse).

Parameters

A [{matrix, sparse matrix, ndarray, LinearOperator}] Matrix A in the linear system. Alternatively, `A` can be a linear operator which can produce `Ax` and `A^H x` using, e.g., `scipy.sparse.linalg.LinearOperator`.

b [array_like, shape (m,)] Vector `b` in the linear system.

damp [float] Damping factor for regularized least-squares. `lsmr` solves the regularized least-squares problem:

```
min ||(b) - (  A   )x||
    ||(0)   (damp*I) ||_2
```

where damp is a scalar. If damp is None or 0, the system is solved without regularization.

atol, btol [float, optional] Stopping tolerances. `lsmr` continues iterations until a certain backward error estimate is smaller than some quantity depending on atol and btol. Let `r = b - Ax` be the residual vector for the current approximate solution `x`. If `Ax = b` seems to be consistent, `lsmr` terminates when `norm(r) <= atol * norm(A) * norm(x) + btol * norm(b)`. Otherwise, lsmr terminates when `norm(A^H r) <= atol * norm(A) * norm(r)`. If both tolerances are 1.0e-6 (say), the final `norm(r)` should be accurate to about 6 digits. (The final `x` will usually have fewer correct digits, depending on `cond(A)` and the size of LAMBDA.) If *atol* or *btol* is None, a default value of 1.0e-6 will be used. Ideally, they should be estimates of the relative error in the entries of `A` and `b` respectively. For example, if the entries of `A` have 7 correct digits, set `atol = 1e-7`. This prevents the algorithm from doing unnecessary work beyond the uncertainty of the input data.

conlim [float, optional] `lsmr` terminates if an estimate of `cond(A)` exceeds *conlim*. For compatible systems `Ax = b`, conlim could be as large as 1.0e+12 (say). For least-squares problems, *conlim* should be less than 1.0e+8. If *conlim* is None, the default value is 1e+8. Maximum

precision can be obtained by setting `atol = btol = conlim = 0`, but the number of iterations may then be excessive.

maxiter [int, optional] *lsmr* terminates if the number of iterations reaches *maxiter*. The default is `maxiter = min(m, n)`. For ill-conditioned systems, a larger value of *maxiter* may be needed.

show [bool, optional] Print iterations logs if `show=True`.

x0 [array_like, shape (n,), optional] Initial guess of `x`, if None zeros are used.
New in version 1.0.0.

Returns

x [ndarray of float] Least-square solution returned.

istop [int] istop gives the reason for stopping:

```
istop   = 0 means x=0 is a solution.  If x0 was given, then x=x0 is a
            solution.
        = 1 means x is an approximate solution to A*x = B,
            according to atol and btol.
        = 2 means x approximately solves the least-squares problem
            according to atol.
        = 3 means COND(A) seems to be greater than CONLIM.
        = 4 is the same as 1 with atol = btol = eps (machine
            precision)
        = 5 is the same as 2 with atol = eps.
        = 6 is the same as 3 with CONLIM = 1/eps.
        = 7 means ITN reached maxiter before the other stopping
            conditions were satisfied.
```

itn [int] Number of iterations used.

normr [float] `norm(b-Ax)`

normar [float] `norm(A^H (b - Ax))`

norma [float] `norm(A)`

conda [float] Condition number of A.

normx [float] `norm(x)`

Notes

New in version 0.11.0.

References

[1], [2]

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import lsmr
>>> A = csc_matrix([[1., 0.], [1., 1.], [0., 1.]], dtype=float)
```

The first example has the trivial solution *[0, 0]*

```
>>> b = np.array([0., 0., 0.], dtype=float)
>>> x, istop, itn, normr = lsmr(A, b)[:4]
>>> istop
0
>>> x
array([ 0.,  0.])
```

The stopping code *istop=0* returned indicates that a vector of zeros was found as a solution. The returned solution *x* indeed contains *[0., 0.]*. The next example has a non-trivial solution:

```
>>> b = np.array([1., 0., -1.], dtype=float)
>>> x, istop, itn, normr = lsmr(A, b)[:4]
>>> istop
1
>>> x
array([ 1., -1.])
>>> itn
1
>>> normr
4.440892098500627e-16
```

As indicated by *istop=1*, `lsmr` found a solution obeying the tolerance limits. The given solution *[1., -1.]* obviously solves the equation. The remaining return values include information about the number of iterations (*itn=1*) and the remaining difference of left and right side of the solved equation. The final example demonstrates the behavior in the case where there is no solution for the equation:

```
>>> b = np.array([1., 0.01, -1.], dtype=float)
>>> x, istop, itn, normr = lsmr(A, b)[:4]
>>> istop
2
>>> x
array([ 1.00333333, -0.99666667])
>>> A.dot(x)-b
array([ 0.00333333, -0.00333333,  0.00333333])
>>> normr
0.005773502691896255
```

istop indicates that the system is inconsistent and thus *x* is rather an approximate solution to the corresponding least-squares problem. *normr* contains the minimal distance that was found.

Matrix factorizations

Eigenvalue problems:

eigs(A[, k, M, sigma, which, v0, ncv, …])	Find k eigenvalues and eigenvectors of the square matrix A.
eigsh(A[, k, M, sigma, which, v0, ncv, …])	Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex Hermitian matrix A.
lobpcg(A, X[, B, M, Y, tol, maxiter, …])	Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)

scipy.sparse.linalg.eigs

scipy.sparse.linalg.**eigs**(*A*, *k=6*, *M=None*, *sigma=None*, *which='LM'*, *v0=None*, *ncv=None*, *maxiter=None*, *tol=0*, *return_eigenvectors=True*, *Minv=None*, *OPinv=None*, *OPpart=None*)

Find k eigenvalues and eigenvectors of the square matrix A.

Solves `A * x[i] = w[i] * x[i]`, the standard eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i].

If M is specified, solves `A * x[i] = w[i] * M * x[i]`, the generalized eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i]

Parameters

A [ndarray, sparse matrix or LinearOperator] An array, sparse matrix, or LinearOperator representing the operation `A * x`, where A is a real or complex square matrix.

k [int, optional] The number of eigenvalues and eigenvectors desired. *k* must be smaller than N-1. It is not possible to compute all eigenvectors of a matrix.

M [ndarray, sparse matrix or LinearOperator, optional] An array, sparse matrix, or LinearOperator representing the operation M*x for the generalized eigenvalue problem

A * x = w * M * x.

M must represent a real symmetric matrix if A is real, and must represent a complex Hermitian matrix if A is complex. For best results, the data type of M should be the same as that of A. Additionally:

If *sigma* is None, M is positive definite

If sigma is specified, M is positive semi-definite

If sigma is None, eigs requires an operator to compute the solution of the linear equation `M * x = b`. This is done internally via a (sparse) LU decomposition for an explicit matrix M, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives `x = Minv * b = M^-1 * b`.

sigma [real or complex, optional] Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system `[A - sigma * M] * x = b`, where M is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices A & M, or via an iterative solver if either A or M is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives `x = OPinv * b = [A - sigma * M]^-1 * b`. For a real matrix A, shift-invert can either be done in imaginary mode or real mode, specified by the parameter OPpart ('r' or 'i'). Note that when sigma is specified, the keyword 'which' (below) refers to the shifted eigenvalues `w'[i]` where:

If A is real and OPpart == 'r' (default),

`w'[i] = 1/2 * [1/(w[i]-sigma) + 1/(w[i]-conj(sigma))].`

If A is real and OPpart == 'i',

`w'[i] = 1/2i * [1/(w[i]-sigma) - 1/(w[i]-conj(sigma))]`.

If A is complex, `w'[i] = 1/(w[i]-sigma)`.

v0 [ndarray, optional] Starting vector for iteration. Default: random

ncv [int, optional] The number of Lanczos vectors generated *ncv* must be greater than *k*; it is recommended that `ncv > 2*k`. Default: `min(n, max(2*k + 1, 20))`

which [str, ['LM' | 'SM' | 'LR' | 'SR' | 'LI' | 'SI'], optional] Which *k* eigenvectors and eigenvalues to find:

'LM' : largest magnitude
'SM' : smallest magnitude
'LR' : largest real part
'SR' : smallest real part
'LI' : largest imaginary part
'SI' : smallest imaginary part

When sigma != None, 'which' refers to the shifted eigenvalues w'[i] (see discussion in 'sigma', above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter [int, optional] Maximum number of Arnoldi update iterations allowed Default: `n*10`

tol [float, optional] Relative accuracy for eigenvalues (stopping criterion) The default value of 0 implies machine precision.

return_eigenvectors [bool, optional] Return eigenvectors (True) in addition to eigenvalues

Minv [ndarray, sparse matrix or LinearOperator, optional] See notes in M, above.

OPinv [ndarray, sparse matrix or LinearOperator, optional] See notes in sigma, above.

OPpart [{'r' or 'i'}, optional] See notes in sigma, above

Returns

w [ndarray] Array of k eigenvalues.

v [ndarray] An array of *k* eigenvectors. `v[:, i]` is the eigenvector corresponding to the eigenvalue w[i].

Raises

ArpackNoConvergence When the requested convergence is not obtained. The currently converged eigenvalues and eigenvectors can be found as `eigenvalues` and `eigenvectors` attributes of the exception object.

See also:

eigsh

eigenvalues and eigenvectors for symmetric matrix A

svds

singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [1] SNEUPD, DNEUPD, CNEUPD, ZNEUPD, functions which use the Implicitly Restarted Arnoldi Method to find the eigenvalues and eigenvectors [2].

References

[1], [2]

Examples

Find 6 eigenvectors of the identity matrix:

```
>>> from scipy.sparse.linalg import eigs
>>> id = np.eye(13)
>>> vals, vecs = eigs(id, k=6)
>>> vals
array([ 1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j,  1.+0.j])
>>> vecs.shape
(13, 6)
```

scipy.sparse.linalg.eigsh

scipy.sparse.linalg.**eigsh**(*A*, *k=6*, *M=None*, *sigma=None*, *which='LM'*, *v0=None*, *ncv=None*, *maxiter=None*, *tol=0*, *return_eigenvectors=True*, *Minv=None*, *OPinv=None*, *mode='normal'*)

Find k eigenvalues and eigenvectors of the real symmetric square matrix or complex Hermitian matrix A.

Solves `A * x[i] = w[i] * x[i]`, the standard eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i].

If M is specified, solves `A * x[i] = w[i] * M * x[i]`, the generalized eigenvalue problem for w[i] eigenvalues with corresponding eigenvectors x[i].

Note that there is no specialized routine for the case when A is a complex Hermitian matrix. In this case, `eigsh()` will call `eigs()` and return the real parts of the eigenvalues thus obtained.

Parameters

A [ndarray, sparse matrix or LinearOperator] A square operator representing the operation `A * x`, where `A` is real symmetric or complex Hermitian. For buckling mode (see below) `A` must additionally be positive-definite.

k [int, optional] The number of eigenvalues and eigenvectors desired. *k* must be smaller than N. It is not possible to compute all eigenvectors of a matrix.

Returns

w [array] Array of k eigenvalues.

v [array] An array representing the *k* eigenvectors. The column `v[:, i]` is the eigenvector corresponding to the eigenvalue `w[i]`.

Other Parameters

M [An N x N matrix, array, sparse matrix, or linear operator representing] the operation `M @ x` for the generalized eigenvalue problem

A @ x = w * M @ x.

M must represent a real symmetric matrix if A is real, and must represent a complex Hermitian matrix if A is complex. For best results, the data type of M should be the same as that of A. Additionally:

If sigma is None, M is symmetric positive definite.

If sigma is specified, M is symmetric positive semi-definite.

In buckling mode, M is symmetric indefinite.

If sigma is None, eigsh requires an operator to compute the solution of the linear equation `M @ x = b`. This is done internally via a (sparse) LU decomposition for an explicit matrix M, or via an iterative solver for a general linear operator. Alternatively, the user can supply the matrix or operator Minv, which gives `x = Minv @ b = M^-1 @ b`.

sigma [real] Find eigenvalues near sigma using shift-invert mode. This requires an operator to compute the solution of the linear system `[A - sigma * M] x = b`, where M is the identity matrix if unspecified. This is computed internally via a (sparse) LU decomposition for explicit matrices A & M, or via an iterative solver if either A or M is a general linear operator. Alternatively, the user can supply the matrix or operator OPinv, which gives `x = OPinv @ b = [A - sigma * M]^-1 @ b`. Note that when sigma is specified, the keyword 'which' refers to the shifted eigenvalues `w'[i]` where:

if mode == 'normal', `w'[i] = 1 / (w[i] - sigma)`.

if mode == 'cayley', `w'[i] = (w[i] + sigma) / (w[i] - sigma)`.

if mode == 'buckling', `w'[i] = w[i] / (w[i] - sigma)`.

(see further discussion in 'mode' below)

v0 [ndarray, optional] Starting vector for iteration. Default: random

ncv [int, optional] The number of Lanczos vectors generated ncv must be greater than k and smaller than n; it is recommended that `ncv > 2*k`. Default: `min(n, max(2*k + 1, 20))`

which [str ['LM' | 'SM' | 'LA' | 'SA' | 'BE']] If A is a complex Hermitian matrix, 'BE' is invalid. Which *k* eigenvectors and eigenvalues to find:

'LM' : Largest (in magnitude) eigenvalues.

'SM' : Smallest (in magnitude) eigenvalues.

'LA' : Largest (algebraic) eigenvalues.

'SA' : Smallest (algebraic) eigenvalues.

'BE' : Half (k/2) from each end of the spectrum.

When k is odd, return one more (k/2+1) from the high end. When sigma != None, 'which' refers to the shifted eigenvalues `w'[i]` (see discussion in 'sigma', above). ARPACK is generally better at finding large values than small values. If small eigenvalues are desired, consider using shift-invert mode for better performance.

maxiter [int, optional] Maximum number of Arnoldi update iterations allowed. Default: `n*10`

tol [float] Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

Minv [N x N matrix, array, sparse matrix, or LinearOperator] See notes in M, above.

OPinv [N x N matrix, array, sparse matrix, or LinearOperator] See notes in sigma, above.

return_eigenvectors

[bool] Return eigenvectors (True) in addition to eigenvalues. This value determines the order in which eigenvalues are sorted. The sort order is also dependent on the *which* variable.

For which = 'LM' or 'SA':

If *return_eigenvectors* is True, eigenvalues are sorted by algebraic value.

If *return_eigenvectors* is False, eigenvalues are sorted by absolute value.

For which = 'BE' or 'LA':

eigenvalues are always sorted by algebraic value.

For which = 'SM':

If *return_eigenvectors* is True, eigenvalues are sorted by algebraic value.

If *return_eigenvectors* is False, eigenvalues are sorted by decreasing absolute value.

mode [string ['normal' | 'buckling' | 'cayley']] Specify strategy to use for shift-invert mode. This argument applies only for real-valued A and sigma != None. For shift-invert mode, ARPACK internally solves the eigenvalue problem `OP * x'[i] = w'[i] * B * x'[i]` and transforms the resulting Ritz vectors x'[i] and Ritz values w'[i] into the desired eigenvectors and eigenvalues of the problem `A * x[i] = w[i] * M * x[i]`. The modes are as follows:

'normal' : OP = [A - sigma * M]^-1 @ M, B = M, w'[i] = 1 / (w[i] - sigma)

'buckling' : OP = [A - sigma * M]^-1 @ A, B = A, w'[i] = w[i] / (w[i] - sigma)

'cayley' : OP = [A - sigma * M]^-1 @ [A + sigma * M], B = M, w'[i] = (w[i] + sigma) / (w[i] - sigma)

The choice of mode will affect which eigenvalues are selected by the keyword 'which', and can also impact the stability of convergence (see [2] for a discussion).

Raises

ArpackNoConvergence
When the requested convergence is not obtained.
The currently converged eigenvalues and eigenvectors can be found as `eigenvalues` and `eigenvectors` attributes of the exception object.

See also:

eigs

eigenvalues and eigenvectors for a general (nonsymmetric) matrix A

svds

singular value decomposition for a matrix A

Notes

This function is a wrapper to the ARPACK [1] SSEUPD and DSEUPD functions which use the Implicitly Restarted Lanczos Method to find the eigenvalues and eigenvectors [2].

References

[1], [2]

Examples

```
>>> from scipy.sparse.linalg import eigsh
>>> identity = np.eye(13)
>>> eigenvalues, eigenvectors = eigsh(identity, k=6)
>>> eigenvalues
array([1., 1., 1., 1., 1., 1.])
>>> eigenvectors.shape
(13, 6)
```

scipy.sparse.linalg.lobpcg

scipy.sparse.linalg.**lobpcg**(*A*, *X*, *B=None*, *M=None*, *Y=None*, *tol=None*, *maxiter=None*, *largest=True*, *verbosityLevel=0*, *retLambdaHistory=False*, *retResidualNormsHistory=False*)

Locally Optimal Block Preconditioned Conjugate Gradient Method (LOBPCG)

LOBPCG is a preconditioned eigensolver for large symmetric positive definite (SPD) generalized eigenproblems.

Parameters

A [{sparse matrix, dense matrix, LinearOperator}] The symmetric linear operator of the problem, usually a sparse matrix. Often called the "stiffness matrix".

X [ndarray, float32 or float64] Initial approximation to the `k` eigenvectors (non-sparse). If *A* has `shape=(n,n)` then *X* should have shape `shape=(n,k)`.

B [{dense matrix, sparse matrix, LinearOperator}, optional] The right hand side operator in a generalized eigenproblem. By default, `B = Identity`. Often called the "mass matrix".

M [{dense matrix, sparse matrix, LinearOperator}, optional] Preconditioner to *A*; by default `M = Identity`. *M* should approximate the inverse of *A*.

Y [ndarray, float32 or float64, optional] n-by-sizeY matrix of constraints (non-sparse), sizeY < n The iterations will be performed in the B-orthogonal complement of the column-space of Y. Y must be full rank.

tol [scalar, optional] Solver tolerance (stopping criterion). The default is `tol=n*sqrt(eps)`.

maxiter [int, optional] Maximum number of iterations. The default is `maxiter = 20`.

largest [bool, optional] When True, solve for the largest eigenvalues, otherwise the smallest.

verbosityLevel [int, optional] Controls solver output. The default is `verbosityLevel=0`.

retLambdaHistory [bool, optional] Whether to return eigenvalue history. Default is False.

retResidualNormsHistory [bool, optional] Whether to return history of residual norms. Default is False.

Returns

w [ndarray] Array of `k` eigenvalues

v [ndarray] An array of `k` eigenvectors. *v* has the same shape as *X*.

lambdas [list of ndarray, optional] The eigenvalue history, if *retLambdaHistory* is True.

rnorms [list of ndarray, optional] The history of residual norms, if *retResidualNormsHistory* is True.

Notes

If both `retLambdaHistory` and `retResidualNormsHistory` are True, the return tuple has the following format `(lambda, V, lambda history, residual norms history)`.

In the following `n` denotes the matrix size and `m` the number of required eigenvalues (smallest or largest).

The LOBPCG code internally solves eigenproblems of the size `3m` on every iteration by calling the "standard" dense eigensolver, so if `m` is not small enough compared to `n`, it does not make sense to call the LOBPCG code, but rather one should use the "standard" eigensolver, e.g. numpy or scipy function in this case. If one calls the LOBPCG algorithm for `5m > n`, it will most likely break internally, so the code tries to call the standard function instead.

It is not that `n` should be large for the LOBPCG to work, but rather the ratio `n / m` should be large. It you call LOBPCG with `m=1` and `n=10`, it works though `n` is small. The method is intended for extremely large `n / m` [4].

The convergence speed depends basically on two factors:

1. How well relatively separated the seeking eigenvalues are from the rest of the eigenvalues. One can try to vary `m` to make this better.

2. How well conditioned the problem is. This can be changed by using proper preconditioning. For example, a rod vibration test problem (under tests directory) is ill-conditioned for large `n`, so convergence will be slow, unless efficient preconditioning is used. For this specific problem, a good simple preconditioner function would be a linear solve for *A*, which is easy to code since A is tridiagonal.

References

[1], [2], [3], [4]

Examples

Solve `A x = lambda x` with constraints and preconditioning.

```
>>> import numpy as np
>>> from scipy.sparse import spdiags, issparse
>>> from scipy.sparse.linalg import lobpcg, LinearOperator
>>> n = 100
>>> vals = np.arange(1, n + 1)
>>> A = spdiags(vals, 0, n, n)
>>> A.toarray()
array([[  1.,   0.,   0., ...,   0.,   0.,   0.],
       [  0.,   2.,   0., ...,   0.,   0.,   0.],
       [  0.,   0.,   3., ...,   0.,   0.,   0.],
       ...,
       [  0.,   0.,   0., ...,  98.,   0.,   0.],
       [  0.,   0.,   0., ...,   0.,  99.,   0.],
       [  0.,   0.,   0., ...,   0.,   0., 100.]])
```

Constraints:

```
>>> Y = np.eye(n, 3)
```

Initial guess for eigenvectors, should have linearly independent columns. Column dimension = number of requested eigenvalues.

```
>>> rng = np.random.default_rng()
>>> X = rng.random((n, 3))
```

Preconditioner in the inverse of A in this example:

```
>>> invA = spdiags([1./vals], 0, n, n)
```

The preconditiner must be defined by a function:

```
>>> def precond( x ):
...     return invA @ x
```

The argument x of the preconditioner function is a matrix inside *lobpcg*, thus the use of matrix-matrix product `@`.

The preconditioner function is passed to lobpcg as a *LinearOperator*:

```
>>> M = LinearOperator(matvec=precond, matmat=precond,
...                    shape=(n, n), dtype=float)
```

Let us now solve the eigenvalue problem for the matrix A:

```
>>> eigenvalues, _ = lobpcg(A, X, Y=Y, M=M, largest=False)
>>> eigenvalues
array([4., 5., 6.])
```

Note that the vectors passed in Y are the eigenvectors of the 3 smallest eigenvalues. The results returned are orthogonal to those.

Singular values problems:

svds(A[, k, ncv, tol, which, v0, maxiter, …])	Compute the largest or smallest k singular values/vectors for a sparse matrix.

scipy.sparse.linalg.svds

scipy.sparse.linalg.**svds**(*A*, *k=6*, *ncv=None*, *tol=0*, *which='LM'*, *v0=None*, *maxiter=None*, *return_singular_vectors=True*, *solver='arpack'*)

Compute the largest or smallest k singular values/vectors for a sparse matrix. The order of the singular values is not guaranteed.

Parameters

A [{sparse matrix, LinearOperator}] Array to compute the SVD on, of shape (M, N)

k [int, optional] Number of singular values and vectors to compute. Must be 1 <= k < min(A.shape).

ncv [int, optional] The number of Lanczos vectors generated ncv must be greater than k+1 and smaller than n; it is recommended that ncv > 2*k Default: `min(n, max(2*k + 1, 20))`

tol [float, optional] Tolerance for singular values. Zero (default) means machine precision.

which [str, [‘LM’ | ‘SM’], optional] Which *k* singular values to find:
- ‘LM’ : largest singular values
- ‘SM’ : smallest singular values

New in version 0.12.0.

v0 [ndarray, optional] Starting vector for iteration, of length min(A.shape). Should be an (approximate) left singular vector if N > M and a right singular vector otherwise. Default: random
New in version 0.12.0.

maxiter [int, optional] Maximum number of iterations.
New in version 0.12.0.

return_singular_vectors
[bool or str, optional]
- True: return singular vectors (True) in addition to singular values.

New in version 0.12.0.
- “u”: only return the u matrix, without computing vh (if N > M).
- “vh”: only return the vh matrix, without computing u (if N <= M).

New in version 0.16.0.

solver [str, optional] Eigenvalue solver to use. Should be ‘arpack’ or ‘lobpcg’. Default: ‘arpack’

Returns

u [ndarray, shape=(M, k)] Unitary matrix having left singular vectors as columns. If *return_singular_vectors* is “vh”, this variable is not computed, and None is returned instead.

s [ndarray, shape=(k,)] The singular values.

vt [ndarray, shape=(k, N)] Unitary matrix having right singular vectors as rows. If *return_singular_vectors* is “u”, this variable is not computed, and None is returned instead.

Notes

This is a naive implementation using ARPACK or LOBPCG as an eigensolver on A.H * A or A * A.H, depending on which one is more efficient.

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import svds, eigs
>>> A = csc_matrix([[1, 0, 0], [5, 0, 2], [0, -1, 0], [0, 0, 3]],␣
↪dtype=float)
>>> u, s, vt = svds(A, k=2)
>>> s
array([ 2.75193379,  5.6059665 ])
>>> np.sqrt(eigs(A.dot(A.T), k=2)[0]).real
array([ 5.6059665 ,  2.75193379])
```

Complete or incomplete LU factorizations

splu(A[, permc_spec, diag_pivot_thresh, …])	Compute the LU decomposition of a sparse, square matrix.
spilu(A[, drop_tol, fill_factor, drop_rule, …])	Compute an incomplete LU decomposition for a sparse, square matrix.
SuperLU()	LU factorization of a sparse matrix.

scipy.sparse.linalg.splu

scipy.sparse.linalg.**splu**(*A*, *permc_spec=None*, *diag_pivot_thresh=None*, *relax=None*, *panel_size=None*, *options={}*)

Compute the LU decomposition of a sparse, square matrix.

Parameters

A [sparse matrix] Sparse matrix to factorize. Should be in CSR or CSC format.

permc_spec [str, optional] How to permute the columns of the matrix for sparsity preservation. (default: 'COLAMD')

- `NATURAL`: natural ordering.
- `MMD_ATA`: minimum degree ordering on the structure of A^T A.
- `MMD_AT_PLUS_A`: minimum degree ordering on the structure of A^T+A.
- `COLAMD`: approximate minimum degree column ordering

diag_pivot_thresh [float, optional] Threshold used for a diagonal entry to be an acceptable pivot. See SuperLU user's guide for details [1]

relax [int, optional] Expert option for customizing the degree of relaxing supernodes. See SuperLU user's guide for details [1]

panel_size [int, optional] Expert option for customizing the panel size. See SuperLU user's guide for details [1]

options [dict, optional] Dictionary containing additional expert options to SuperLU. See SuperLU user guide [1] (section 2.4 on the 'Options' argument) for more details. For example, you can specify `options=dict(Equil=False, IterRefine='SINGLE'))` to turn equilibration off and perform a single iterative refinement.

Returns

invA [scipy.sparse.linalg.SuperLU] Object, which has a `solve` method.

See also:

spilu

incomplete LU decomposition

Notes

This function uses the SuperLU library.

References

[1]

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import splu
>>> A = csc_matrix([[1., 0., 0.], [5., 0., 2.], [0., -1., 0.]],␣
↪dtype=float)
>>> B = splu(A)
>>> x = np.array([1., 2., 3.], dtype=float)
>>> B.solve(x)
array([ 1. , -3. , -1.5])
>>> A.dot(B.solve(x))
array([ 1.,  2.,  3.])
>>> B.solve(A.dot(x))
array([ 1.,  2.,  3.])
```

scipy.sparse.linalg.spilu

scipy.sparse.linalg.**spilu**(*A*, *drop_tol=None*, *fill_factor=None*, *drop_rule=None*, *permc_spec=None*, *diag_pivot_thresh=None*, *relax=None*, *panel_size=None*, *options=None*)

Compute an incomplete LU decomposition for a sparse, square matrix.

The resulting object is an approximation to the inverse of *A*.

Parameters

A [(N, N) array_like] Sparse matrix to factorize

drop_tol [float, optional] Drop tolerance (0 <= tol <= 1) for an incomplete LU decomposition. (default: 1e-4)

fill_factor [float, optional] Specifies the fill ratio upper bound (>= 1.0) for ILU. (default: 10)

drop_rule [str, optional] Comma-separated string of drop rules to use. Available rules: `basic`, `prows`, `column`, `area`, `secondary`, `dynamic`, `interp`. (Default: `basic,area`) See SuperLU documentation for details.

Remaining other options

Same as for *splu*

Returns

invA_approx

[scipy.sparse.linalg.SuperLU] Object, which has a `solve` method.

See also:

splu

complete LU decomposition

Notes

To improve the better approximation to the inverse, you may need to increase *fill_factor* AND decrease *drop_tol*.

This function uses the SuperLU library.

Examples

```
>>> from scipy.sparse import csc_matrix
>>> from scipy.sparse.linalg import spilu
>>> A = csc_matrix([[1., 0., 0.], [5., 0., 2.], [0., -1., 0.]],␣
↪dtype=float)
>>> B = spilu(A)
>>> x = np.array([1., 2., 3.], dtype=float)
>>> B.solve(x)
array([ 1. , -3. , -1.5])
>>> A.dot(B.solve(x))
array([ 1.,  2.,  3.])
>>> B.solve(A.dot(x))
array([ 1.,  2.,  3.])
```

scipy.sparse.linalg.SuperLU

class scipy.sparse.linalg.**SuperLU**

LU factorization of a sparse matrix.

Factorization is represented as:

```
Pr * A * Pc = L * U
```

To construct these *SuperLU* objects, call the *splu* and *spilu* functions.

Notes

New in version 0.14.0.

Examples

The LU decomposition can be used to solve matrix equations. Consider:

```
>>> import numpy as np
>>> from scipy.sparse import csc_matrix, linalg as sla
>>> A = csc_matrix([[1,2,0,4],[1,0,0,1],[1,0,2,1],[2,2,1,0.]])
```

This can be solved for a given right-hand side:

```
>>> lu = sla.splu(A)
>>> b = np.array([1, 2, 3, 4])
>>> x = lu.solve(b)
>>> A.dot(x)
array([ 1.,  2.,  3.,  4.])
```

The `lu` object also contains an explicit representation of the decomposition. The permutations are represented as mappings of indices:

```
>>> lu.perm_r
array([0, 2, 1, 3], dtype=int32)
>>> lu.perm_c
array([2, 0, 1, 3], dtype=int32)
```

The L and U factors are sparse matrices in CSC format:

```
>>> lu.L.A
array([[ 1. ,  0. ,  0. ,  0. ],
       [ 0. ,  1. ,  0. ,  0. ],
       [ 0. ,  0. ,  1. ,  0. ],
       [ 1. ,  0.5,  0.5,  1. ]])
>>> lu.U.A
array([[ 2.,  0.,  1.,  4.],
       [ 0.,  2.,  1.,  1.],
       [ 0.,  0.,  1.,  1.],
       [ 0.,  0.,  0., -5.]])
```

The permutation matrices can be constructed:

```
>>> Pr = csc_matrix((np.ones(4), (lu.perm_r, np.arange(4))))
>>> Pc = csc_matrix((np.ones(4), (np.arange(4), lu.perm_c)))
```

We can reassemble the original matrix:

```
>>> (Pr.T * (lu.L * lu.U) * Pc.T).A
array([[ 1.,  2.,  0.,  4.],
       [ 1.,  0.,  0.,  1.],
       [ 1.,  0.,  2.,  1.],
       [ 2.,  2.,  1.,  0.]])
```

Attributes

shape	Shape of the original matrix as a tuple of ints.
nnz	Number of nonzero elements in the matrix.
perm_c	Permutation Pc represented as an array of indices.
perm_r	Permutation Pr represented as an array of indices.
L	Lower triangular factor with unit diagonal as a *scipy.sparse.csc_matrix*.
U	Upper triangular factor as a *scipy.sparse.csc_matrix*.

Methods

solve(rhs[, trans])	Solves linear system of equations with one or several right-hand sides.

scipy.sparse.linalg.SuperLU.solve

SuperLU.**solve**(*rhs*[, *trans*])

Solves linear system of equations with one or several right-hand sides.

Parameters

rhs [ndarray, shape (n,) or (n, k)] Right hand side(s) of equation

trans [{'N', 'T', 'H'}, optional] Type of system to solve:

```
'N':   A   * x == rhs  (default)
'T':   A^T * x == rhs
'H':   A^H * x == rhs
```

i.e., normal, transposed, and hermitian conjugate.

Returns

x [ndarray, shape `rhs.shape`] Solution vector(s)

Exceptions

ArpackNoConvergence(msg, eigenvalues, ...)	ARPACK iteration did not converge
ArpackError(info[, infodict])	ARPACK error

scipy.sparse.linalg.ArpackNoConvergence

exception scipy.sparse.linalg.**ArpackNoConvergence**(*msg*, *eigenvalues*, *eigenvectors*)

ARPACK iteration did not converge

Attributes

eigenvalues
: [ndarray] Partial result. Converged eigenvalues.

eigenvectors
: [ndarray] Partial result. Converged eigenvectors.

with_traceback()

Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.sparse.linalg.ArpackError

exception scipy.sparse.linalg.**ArpackError**(*info*, *infodict={'c': {- 9999: 'Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.', - 13: "NEV and WHICH = 'BE' are incompatible.", - 12: 'IPARAM(1) must be equal to 0 or 1.', - 11: "IPARAM(7) = 1 and BMAT = 'G' are incompatible.", - 10: 'IPARAM(7) must be 1,2,3.', - 9: 'Starting vector is zero.', - 8: 'Error return from LAPACK eigenvalue calculation;', - 7: 'Length of private work array WORKL is not sufficient.', - 6: "BMAT must be one of 'I' or 'G'.", - 5: " WHICH must be one of 'LM', 'SM', 'LR', 'SR', 'LI', 'SI'", - 4: 'The maximum number of Arnoldi update iterations allowed must be greater than zero.', - 3: 'NCV-NEV >= 2 and less than or equal to N.', - 2: 'NEV must be positive.', - 1: 'N must be positive.', 0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. Deprecated starting with release 2 of ARPACK.', 3: 'No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. '}, 'd': {- 9999: 'Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.', - 13: "NEV and WHICH = 'BE' are incompatible.", - 12: 'IPARAM(1) must be equal to 0 or 1.', - 11: "IPARAM(7) = 1 and BMAT = 'G' are incompatible.", - 10: 'IPARAM(7) must be 1,2,3,4.', - 9: 'Starting vector is zero.', - 8: 'Error return from LAPACK eigenvalue calculation;', - 7: 'Length of private work array WORKL is not sufficient.', - 6: "BMAT must be one of 'I' or 'G'.", - 5: " WHICH must be one of 'LM', 'SM', 'LR', 'SR', 'LI', 'SI'", - 4: 'The maximum number of Arnoldi update iterations allowed must be greater than zero.', - 3: 'NCV-NEV >= 2 and less than or equal to N.', - 2: 'NEV must be positive.', - 1: 'N must be positive.', 0: 'Normal exit.', 1: 'Maximum number of iterations taken. All possible eigenvalues of OP has been found. IPARAM(5) returns the number of wanted converged Ritz values.', 2: 'No longer an informational error. Deprecated starting with release 2 of ARPACK.', 3: 'No shifts could be applied during a cycle of the Implicitly restarted Arnoldi iteration. One possibility is to increase the size of NCV relative to NEV. '}, 's': {- 9999: 'Could not build an Arnoldi factorization. IPARAM(5) returns the size of the current Arnoldi factorization. The user is advised to check that enough workspace and array storage has been allocated.', - 13: "NEV and WHICH = 'BE' are incompatible.", - 12: 'IPARAM(1) must be equal to 0 or 1.', - 11: "IPARAM(7) = 1 and BMAT = 'G' are incompat-*)

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

3.3.25 Compressed sparse graph routines (scipy.sparse.csgraph)

Fast graph algorithms based on sparse matrix representations.

Contents

connected_components(csgraph[, directed, …])	Analyze the connected components of a sparse graph
laplacian(csgraph[, normed, return_diag, …])	Return the Laplacian matrix of a directed graph.
shortest_path(csgraph[, method, directed, …])	Perform a shortest-path graph search on a positive directed or undirected graph.
dijkstra(csgraph[, directed, indices, …])	Dijkstra algorithm using Fibonacci Heaps
floyd_warshall(csgraph[, directed, …])	Compute the shortest path lengths using the Floyd-Warshall algorithm
bellman_ford(csgraph[, directed, indices, …])	Compute the shortest path lengths using the Bellman-Ford algorithm.
johnson(csgraph[, directed, indices, …])	Compute the shortest path lengths using Johnson's algorithm.
breadth_first_order(csgraph, i_start[, …])	Return a breadth-first ordering starting with specified node.
depth_first_order(csgraph, i_start[, …])	Return a depth-first ordering starting with specified node.
breadth_first_tree(csgraph, i_start[, directed])	Return the tree generated by a breadth-first search
depth_first_tree(csgraph, i_start[, directed])	Return a tree generated by a depth-first search.
minimum_spanning_tree(csgraph[, overwrite])	Return a minimum spanning tree of an undirected graph
reverse_cuthill_mckee(graph[, symmetric_mode])	Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.
maximum_flow(csgraph, source, sink)	Maximize the flow between two vertices in a graph.
maximum_bipartite_matching(graph[, perm_type])	Returns a matching of a bipartite graph whose cardinality is as least that of any given matching of the graph.
min_weight_full_bipartite_matching(…[, …])	Returns the minimum weight full matching of a bipartite graph.
structural_rank(graph)	Compute the structural rank of a graph (matrix) with a given sparsity pattern.
NegativeCycleError([message])	

scipy.sparse.csgraph.connected_components

scipy.sparse.csgraph.**connected_components**(*csgraph*, *directed=True*, *connection='weak'*, *return_labels=True*)

Analyze the connected components of a sparse graph

New in version 0.11.0.

Parameters

csgraph [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

connection
: [str, optional] ['weak'|'strong']. For directed graphs, the type of connection to use. Nodes i and j are strongly connected if a path exists both from i to j and from j to i. A directed graph is weakly connected if replacing all of its directed edges with undirected edges produces a connected (undirected) graph. If directed == False, this keyword is not referenced.

return_labels
: [bool, optional] If True (default), then return the labels for each of the connected components.

Returns

n_components: int
: The number of connected components.

labels: ndarray
: The length-N array of labels of the connected components.

References

[1]

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import connected_components
```

```
>>> graph = [
... [ 0, 1 , 1, 0 , 0 ],
... [ 0, 0 , 1 , 0 ,0 ],
... [ 0, 0, 0, 0, 0],
... [0, 0 , 0, 0, 1],
... [0, 0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    1
  (1, 2)    1
  (3, 4)    1
```

```
>>> n_components, labels = connected_components(csgraph=graph,␣
↪directed=False, return_labels=True)
>>> n_components
2
>>> labels
array([0, 0, 0, 1, 1], dtype=int32)
```

scipy.sparse.csgraph.laplacian

scipy.sparse.csgraph.**laplacian**(*csgraph*, *normed=False*, *return_diag=False*, *use_out_degree=False*)

Return the Laplacian matrix of a directed graph.

Parameters

csgraph [array_like or sparse matrix, 2 dimensions] compressed-sparse graph, with shape (N, N).

normed [bool, optional] If True, then compute symmetric normalized Laplacian.

return_diag [bool, optional] If True, then also return an array related to vertex degrees.

use_out_degree [bool, optional] If True, then use out-degree instead of in-degree. This distinction matters only if the graph is asymmetric. Default: False.

Returns

lap [ndarray or sparse matrix] The N x N laplacian matrix of csgraph. It will be a NumPy array (dense) if the input was dense, or a sparse matrix otherwise.

diag [ndarray, optional] The length-N diagonal of the Laplacian matrix. For the normalized Laplacian, this is the array of square roots of vertex degrees or 1 if the degree is zero.

Notes

The Laplacian matrix of a graph is sometimes referred to as the "Kirchoff matrix" or the "admittance matrix", and is useful in many parts of spectral graph theory. In particular, the eigen-decomposition of the laplacian matrix can give insight into many properties of the graph.

Examples

```
>>> from scipy.sparse import csgraph
>>> G = np.arange(5) * np.arange(5)[:, np.newaxis]
>>> G
array([[ 0,  0,  0,  0,  0],
       [ 0,  1,  2,  3,  4],
       [ 0,  2,  4,  6,  8],
       [ 0,  3,  6,  9, 12],
       [ 0,  4,  8, 12, 16]])
>>> csgraph.laplacian(G, normed=False)
array([[  0,   0,   0,   0,   0],
       [  0,   9,  -2,  -3,  -4],
       [  0,  -2,  16,  -6,  -8],
       [  0,  -3,  -6,  21, -12],
       [  0,  -4,  -8, -12,  24]])
```

scipy.sparse.csgraph.shortest_path

scipy.sparse.csgraph.**shortest_path**(*csgraph*, *method='auto'*, *directed=True*, *return_predecessors=False*, *unweighted=False*, *overwrite=False*, *indices=None*)

Perform a shortest-path graph search on a positive directed or undirected graph.

New in version 0.11.0.

Parameters

csgraph [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.

method [string ['auto'|'FW'|'D'], optional] Algorithm to use for shortest paths. Options are:

'auto' – (default) select the best among 'FW', 'D', 'BF', or 'J'
based on the input data.

'FW' – Floyd-Warshall algorithm. Computational cost is
approximately `O[N^3]`. The input csgraph will be converted to a dense representation.

'D' – Dijkstra's algorithm with Fibonacci heaps. Computational
cost is approximately `O[N(N*k + N*log(N))]`, where `k` is the average number of connected edges per node. The input csgraph will be converted to a csr representation.

'BF' – Bellman-Ford algorithm. This algorithm can be used when
weights are negative. If a negative cycle is encountered, an error will be raised. Computational cost is approximately `O[N(N^2 k)]`, where `k` is the average number of connected edges per node. The input csgraph will be converted to a csr representation.

'J' – Johnson's algorithm. Like the Bellman-Ford algorithm,
Johnson's algorithm is designed for use when the weights are negative. It combines the Bellman-Ford algorithm with Dijkstra's algorithm for faster computation.

directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

return_predecessors
[bool, optional] If True, return the size (N, N) predecesor matrix

unweighted
[bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

overwrite [bool, optional] If True, overwrite csgraph with the result. This applies only if method == 'FW' and csgraph is a dense, c-ordered array with dtype=float64.

indices [array_like or int, optional] If specified, only compute the paths from the points at the given indices. Incompatible with method == 'FW'.

Returns

dist_matrix
[ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors
[ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index

of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError:
if there are negative cycles in the graph

Notes

As currently implemented, Dijkstra's algorithm and Johnson's algorithm do not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are non-equal edges, method='D' may yield an incorrect result.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import shortest_path
```

```
>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 0)    2
  (2, 3)    3
```

```
>>> dist_matrix, predecessors = shortest_path(csgraph=graph,␣
↪directed=False, indices=0, return_predecessors=True)
>>> dist_matrix
array([ 0.,  1.,  2.,  2.])
>>> predecessors
array([-9999,     0,     0,     1], dtype=int32)
```

scipy.sparse.csgraph.dijkstra

scipy.sparse.csgraph.**dijkstra**(*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*, *limit=np.inf*, *min_only=False*)

Dijkstra algorithm using Fibonacci Heaps

New in version 0.11.0.

Parameters

csgraph [array, matrix, or sparse matrix, 2 dimensions] The N x N array of non-negative distances representing the input graph.

directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j] and from point j to i along paths csgraph[j, i]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j or j to i along either csgraph[i, j] or csgraph[j, i].

indices [array_like or int, optional] if specified, only compute the paths from the points at the given indices.

return_predecessors
[bool, optional] If True, return the size (N, N) predecesor matrix

unweighted
[bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

limit [float, optional] The maximum distance to calculate, must be >= 0. Using a smaller limit will decrease computation time by aborting calculations between pairs that are separated by a distance > limit. For such pairs, the distance will be equal to np.inf (i.e., not connected).
New in version 0.14.0.

min_only [bool, optional] If False (default), for every node in the graph, find the shortest path from every node in indices. If True, for every node in the graph, find the shortest path from any of the nodes in indices (which can be substantially faster).
New in version 1.3.0.

Returns

dist_matrix
[ndarray, shape ([n_indices,]n_nodes,)] The matrix of distances between graph nodes. If min_only=False, dist_matrix has shape (n_indices, n_nodes) and dist_matrix[i, j] gives the shortest distance from point i to point j along the graph. If min_only=True, dist_matrix has shape (n_nodes,) and contains for a given node the shortest path to that node from any of the nodes in indices.

predecessors
[ndarray, shape ([n_indices,]n_nodes,)] If min_only=False, this has shape (n_indices, n_nodes), otherwise it has shape (n_nodes,). Returned only if return_predecessors == True. The matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

sources [ndarray, shape (n_nodes,)] Returned only if min_only=True and return_predecessors=True. Contains the index of the source which had the shortest path to each target. If no path exists within the limit, this will contain -9999. The value at the indices passed will be equal to that index (i.e. the fastest way to reach node i, is to start on node i).

Notes

As currently implemented, Dijkstra's algorithm does not work for graphs with direction-dependent distances when directed == False. i.e., if csgraph[i,j] and csgraph[j,i] are not equal and both are nonzero, setting directed=False will not yield the correct result.

Also, this routine does not work for graphs with negative distances. Negative distances can lead to infinite cycles that must be handled by specialized algorithms such as Bellman-Ford's algorithm or Johnson's algorithm.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import dijkstra
```

```
>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 3)    3
```

```
>>> dist_matrix, predecessors = dijkstra(csgraph=graph, directed=False,␣
↪indices=0, return_predecessors=True)
>>> dist_matrix
array([ 0.,  1.,  2.,  2.])
>>> predecessors
array([-9999,     0,     0,     1], dtype=int32)
```

scipy.sparse.csgraph.floyd_warshall

scipy.sparse.csgraph.**floyd_warshall**(*csgraph*, *directed=True*, *return_predecessors=False*, *unweighted=False*, *overwrite=False*)

Compute the shortest path lengths using the Floyd-Warshall algorithm

New in version 0.11.0.

Parameters

csgraph [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.

directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

return_predecessors
[bool, optional] If True, return the size (N, N) predecesor matrix

unweighted
[bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

overwrite [bool, optional] If True, overwrite csgraph with the result. This applies only if csgraph is a dense, c-ordered array with dtype=float64.

Returns

dist_matrix
[ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors
: [ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError:
: if there are negative cycles in the graph

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import floyd_warshall
```

```
>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 0)    2
  (2, 3)    3
```

```
>>> dist_matrix, predecessors = floyd_warshall(csgraph=graph,␣
↪directed=False, return_predecessors=True)
>>> dist_matrix
array([[ 0.,  1.,  2.,  2.],
       [ 1.,  0.,  3.,  1.],
       [ 2.,  3.,  0.,  3.],
       [ 2.,  1.,  3.,  0.]])
>>> predecessors
array([[-9999,     0,     0,     1],
       [    1, -9999,     0,     1],
       [    2,     0, -9999,     2],
       [    1,     3,     3, -9999]], dtype=int32)
```

scipy.sparse.csgraph.bellman_ford

scipy.sparse.csgraph.**bellman_ford**(*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*)

Compute the shortest path lengths using the Bellman-Ford algorithm.

The Bellman-Ford algorithm can robustly deal with graphs with negative weights. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, Dijkstra's algorithm may be faster.

New in version 0.11.0.

Parameters

csgraph [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.

directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

indices [array_like or int, optional] if specified, only compute the paths from the points at the given indices.

return_predecessors
[bool, optional] If True, return the size (N, N) predecesor matrix

unweighted
[bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns

dist_matrix
[ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors
[ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError:
if there are negative cycles in the graph

Notes

This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra's algorithm is a better choice.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import bellman_ford
```

```
>>> graph = [
... [0, 1 ,2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 0)    2
  (2, 3)    3
```

```
>>> dist_matrix, predecessors = bellman_ford(csgraph=graph,␣
↪directed=False, indices=0, return_predecessors=True)
>>> dist_matrix
array([ 0.,  1.,  2.,  2.])
>>> predecessors
array([-9999,     0,     0,     1], dtype=int32)
```

scipy.sparse.csgraph.johnson

scipy.sparse.csgraph.**johnson**(*csgraph*, *directed=True*, *indices=None*, *return_predecessors=False*, *unweighted=False*)

Compute the shortest path lengths using Johnson's algorithm.

Johnson's algorithm combines the Bellman-Ford algorithm and Dijkstra's algorithm to quickly find shortest paths in a way that is robust to the presence of negative cycles. If a negative cycle is detected, an error is raised. For graphs without negative edge weights, dijkstra may be faster.

New in version 0.11.0.

Parameters

csgraph [array, matrix, or sparse matrix, 2 dimensions] The N x N array of distances representing the input graph.

directed [bool, optional] If True (default), then find the shortest path on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i]

indices [array_like or int, optional] if specified, only compute the paths from the points at the given indices.

return_predecessors
[bool, optional] If True, return the size (N, N) predecesor matrix

unweighted
[bool, optional] If True, then find unweighted distances. That is, rather than finding the path between each point such that the sum of weights is minimized, find the path such that the number of edges is minimized.

Returns

dist_matrix
: [ndarray] The N x N matrix of distances between graph nodes. dist_matrix[i,j] gives the shortest distance from point i to point j along the graph.

predecessors
: [ndarray] Returned only if return_predecessors == True. The N x N matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Raises

NegativeCycleError:
: if there are negative cycles in the graph

Notes

This routine is specially designed for graphs with negative edge weights. If all edge weights are positive, then Dijkstra's algorithm is a better choice.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import johnson
```

```
>>> graph = [
... [0, 1, 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 0)    2
  (2, 3)    3
```

```
>>> dist_matrix, predecessors = johnson(csgraph=graph, directed=False,␣
↪indices=0, return_predecessors=True)
>>> dist_matrix
array([ 0.,  1.,  2.,  2.])
>>> predecessors
array([-9999,     0,     0,     1], dtype=int32)
```

scipy.sparse.csgraph.breadth_first_order

scipy.sparse.csgraph.**breadth_first_order**(*csgraph*, *i_start*, *directed=True*, *return_predecessors=True*)

Return a breadth-first ordering starting with specified node.

Note that a breadth-first order is not unique, but the tree which it generates is unique.

New in version 0.11.0.

Parameters

csgraph [array_like or sparse matrix] The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start [int] The index of starting node.

directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

return_predecessors [bool, optional] If True (default), then return the predecesor array (see below).

Returns

node_array [ndarray, one dimension] The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.

predecessors [ndarray, one dimension] Returned only if return_predecessors is True. The length-N list of predecessors of each node in a breadth-first tree. If node i is in the tree, then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import breadth_first_order
```

```
>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 0)    2
  (2, 3)    3
```

```
>>> breadth_first_order(graph,0)
(array([0, 1, 2, 3], dtype=int32), array([-9999,     0,     0,     1],␣
↪dtype=int32))
```

scipy.sparse.csgraph.depth_first_order

scipy.sparse.csgraph.**depth_first_order**(*csgraph*, *i_start*, *directed=True*, *return_predecessors=True*)

Return a depth-first ordering starting with specified node.

Note that a depth-first order is not unique. Furthermore, for graphs with cycles, the tree generated by a depth-first search is not unique either.

New in version 0.11.0.

Parameters

csgraph [array_like or sparse matrix] The N x N compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start [int] The index of starting node.

directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

return_predecessors [bool, optional] If True (default), then return the predecesor array (see below).

Returns

node_array [ndarray, one dimension] The depth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.

predecessors [ndarray, one dimension] Returned only if return_predecessors is True. The length-N list of predecessors of each node in a depth-first tree. If node i is in the tree, then its parent is given by predecessors[i]. If node i is not in the tree (and for the parent node) then predecessors[i] = -9999.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import depth_first_order
```

```
>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 0)    2
  (2, 3)    3
```

```
>>> depth_first_order(graph,0)
(array([0, 1, 3, 2], dtype=int32), array([-9999,     0,     0,     1],␣
↪dtype=int32))
```

scipy.sparse.csgraph.breadth_first_tree

scipy.sparse.csgraph.**breadth_first_tree**(*csgraph*, *i_start*, *directed=True*)

Return the tree generated by a breadth-first search

Note that a breadth-first tree from a specified node is unique.

New in version 0.11.0.

Parameters

csgraph [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start [int] The index of starting node.

directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns

cstree [csr matrix] The N x N directed compressed-sparse representation of the breadth- first tree drawn from csgraph, starting at the specified node.

Examples

The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

```
 input graph           breadth first tree from (0)

     (0)                         (0)
    /   \                       /   \
   3     8                     3     8
  /       \                   /       \
(3)---5---(1)               (3)         (1)
  \       /                               /
   6     2                               2
    \   /                               /
     (2)                             (2)
```

In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import breadth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = breadth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 3],
       [0, 0, 2, 0],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. A breadth-first tree from a given node is unique.

scipy.sparse.csgraph.depth_first_tree

scipy.sparse.csgraph.**depth_first_tree**(*csgraph*, *i_start*, *directed=True*)

Return a tree generated by a depth-first search.

Note that a tree generated by a depth-first search is not unique: it depends on the order that the children of each node are searched.

New in version 0.11.0.

Parameters

csgraph [array_like or sparse matrix] The N x N matrix representing the compressed sparse graph. The input csgraph will be converted to csr format for the calculation.

i_start [int] The index of starting node.

directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then find the shortest path on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns

cstree [csr matrix] The N x N directed compressed-sparse representation of the depth- first tree drawn from csgraph, starting at the specified node.

Examples

The following example shows the computation of a depth-first tree over a simple four-component graph, starting at node 0:

```
 input graph            depth first tree from (0)

     (0)                                (0)
    /   \                                \
   3     8                                8
  /       \                                \
(3)---5---(1)                      (3)       (1)
  \       /                          \       /
   6     2                            6     2
    \   /                              \   /
     (2)                                (2)
```

In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import depth_first_tree
>>> X = csr_matrix([[0, 8, 0, 3],
...                 [0, 0, 2, 5],
...                 [0, 0, 0, 6],
...                 [0, 0, 0, 0]])
>>> Tcsr = depth_first_tree(X, 0, directed=False)
>>> Tcsr.toarray().astype(int)
array([[0, 8, 0, 0],
       [0, 0, 2, 0],
       [0, 0, 0, 6],
       [0, 0, 0, 0]])
```

Note that the resulting graph is a Directed Acyclic Graph which spans the graph. Unlike a breadth-first tree, a depth-first tree of a given graph is not unique if the graph contains cycles. If the above solution had begun with the edge connecting nodes 0 and 3, the result would have been different.

scipy.sparse.csgraph.minimum_spanning_tree

scipy.sparse.csgraph.**minimum_spanning_tree**(*csgraph*, *overwrite=False*)

Return a minimum spanning tree of an undirected graph

A minimum spanning tree is a graph consisting of the subset of edges which together connect all connected nodes, while minimizing the total sum of weights on the edges. This is computed using the Kruskal algorithm.

New in version 0.11.0.

Parameters

csgraph [array_like or sparse matrix, 2 dimensions] The N x N matrix representing an undirected graph over N nodes (see notes below).

overwrite [bool, optional] if true, then parts of the input graph will be overwritten for efficiency.

Returns

span_tree [csr matrix] The N x N compressed-sparse representation of the undirected minimum spanning tree over the input (see notes below).

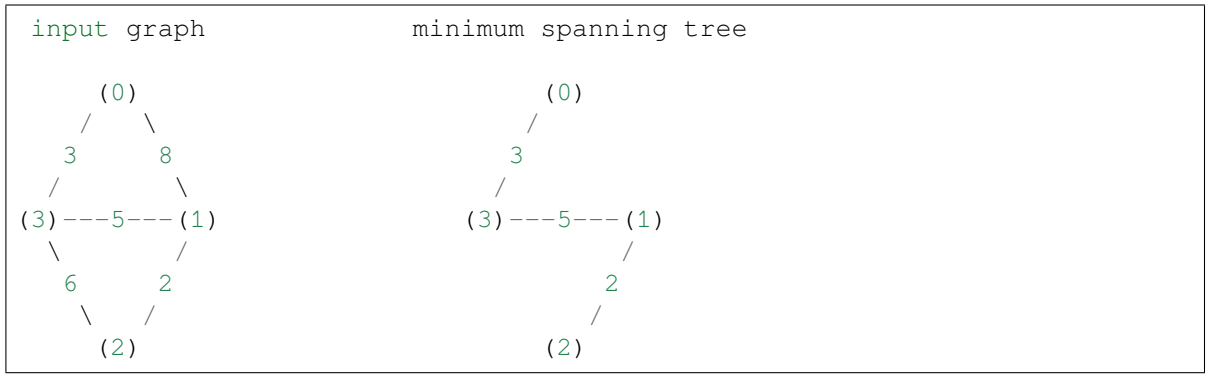
Notes

This routine uses undirected graphs as input and output. That is, if graph[i, j] and graph[j, i] are both zero, then nodes i and j do not have an edge connecting them. If either is nonzero, then the two are connected by the minimum nonzero value of the two.

This routine loses precision when users input a dense matrix. Small elements < 1E-8 of the dense matrix are rounded to zero. All users should input sparse matrices if possible to avoid it.

Examples

The following example shows the computation of a minimum spanning tree over a simple four-component graph:



It is easy to see from inspection that the minimum spanning tree involves removing the edges with weights 8 and 6. In compressed sparse representation, the solution looks like this:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import minimum_spanning_tree
>>> X = csr_matrix([[0, 8, 0, 3],
```

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```
...                   [0, 0, 2, 5],
...                   [0, 0, 0, 6],
...                   [0, 0, 0, 0]])
>>> Tcsr = minimum_spanning_tree(X)
>>> Tcsr.toarray().astype(int)
array([[0, 0, 0, 3],
       [0, 0, 2, 5],
       [0, 0, 0, 0],
       [0, 0, 0, 0]])
```

scipy.sparse.csgraph.reverse_cuthill_mckee

scipy.sparse.csgraph.**reverse_cuthill_mckee**(*graph*, *symmetric_mode=False*)

Returns the permutation array that orders a sparse CSR or CSC matrix in Reverse-Cuthill McKee ordering.

It is assumed by default, `symmetric_mode=False`, that the input matrix is not symmetric and works on the matrix `A+A.T`. If you are guaranteed that the matrix is symmetric in structure (values of matrix elements do not matter) then set `symmetric_mode=True`.

Parameters

graph [sparse matrix] Input sparse in CSC or CSR sparse matrix format.

symmetric_mode
[bool, optional] Is input matrix guaranteed to be symmetric.

Returns

perm [ndarray] Array of permuted row and column indices.

Notes

New in version 0.15.0.

References

E. Cuthill and J. McKee, “Reducing the Bandwidth of Sparse Symmetric Matrices”, ACM ‘69 Proceedings of the 1969 24th national conference, (1969).

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import reverse_cuthill_mckee
```

```
>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
```

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```
  (0, 2)    2
  (1, 3)    1
  (2, 0)    2
  (2, 3)    3
```

```
>>> reverse_cuthill_mckee(graph)
array([3, 2, 1, 0], dtype=int32)
```

scipy.sparse.csgraph.maximum_flow

scipy.sparse.csgraph.**maximum_flow**(*csgraph*, *source*, *sink*)

Maximize the flow between two vertices in a graph.

New in version 1.4.0.

Parameters

csgraph [csr_matrix] The square matrix representing a directed graph whose (i, j)'th entry is an integer representing the capacity of the edge between vertices i and j.

source [int] The source vertex from which the flow flows.

sink [int] The sink vertex to which the flow flows.

Returns

res [MaximumFlowResult] A maximum flow represented by a `MaximumFlowResult` which includes the value of the flow in `flow_value`, and the residual graph in `residual`.

Raises

TypeError:
if the input graph is not in CSR format.

ValueError:
if the capacity values are not integers, or the source or sink are out of bounds.

Notes

This solves the maximum flow problem on a given directed weighted graph: A flow associates to every edge a value, also called a flow, less than the capacity of the edge, so that for every vertex (apart from the source and the sink vertices), the total incoming flow is equal to the total outgoing flow. The value of a flow is the sum of the flow of all edges leaving the source vertex, and the maximum flow problem consists of finding a flow whose value is maximal.

By the max-flow min-cut theorem, the maximal value of the flow is also the total weight of the edges in a minimum cut.

To solve the problem, we use the Edmonds–Karp algorithm. [1] This particular implementation strives to exploit sparsity. Its time complexity is $O(VE^2)$ and its space complexity is $O(E)$.

The maximum flow problem is usually defined with real valued capacities, but we require that all capacities are integral to ensure convergence. When dealing with rational capacities, or capacities belonging to $x\mathbb{Q}$ for some fixed $x \in \mathbb{R}$, it is possible to reduce the problem to the integral case by scaling all capacities accordingly.

Solving a maximum-flow problem can be used for example for graph cuts optimization in computer vision [3].

References

[1], [2], [3]

Examples

Perhaps the simplest flow problem is that of a graph of only two vertices with an edge from source (0) to sink (1):

```
(0) --5--> (1)
```

Here, the maximum flow is simply the capacity of the edge:

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import maximum_flow
>>> graph = csr_matrix([[0, 5], [0, 0]])
>>> maximum_flow(graph, 0, 1).flow_value
5
```

If, on the other hand, there is a bottleneck between source and sink, that can reduce the maximum flow:

```
(0) --5--> (1) --3--> (2)
```

```
>>> graph = csr_matrix([[0, 5, 0], [0, 0, 3], [0, 0, 0]])
>>> maximum_flow(graph, 0, 2).flow_value
3
```

A less trivial example is given in [2], Chapter 26.1:

```
>>> graph = csr_matrix([[0, 16, 13,  0,  0,  0],
...                     [0, 10,  0, 12,  0,  0],
...                     [0,  4,  0,  0, 14,  0],
...                     [0,  0,  9,  0,  0, 20],
...                     [0,  0,  0,  7,  0,  4],
...                     [0,  0,  0,  0,  0,  0]])
>>> maximum_flow(graph, 0, 5).flow_value
23
```

It is possible to reduce the problem of finding a maximum matching in a bipartite graph to a maximum flow problem: Let $G = ((U, V), E)$ be a bipartite graph. Then, add to the graph a source vertex with edges to every vertex in U and a sink vertex with edges from every vertex in V. Finally, give every edge in the resulting graph a capacity of 1. Then, a maximum flow in the new graph gives a maximum matching in the original graph consisting of the edges in E whose flow is positive.

Assume that the edges are represented by a $|U| \times |V|$ matrix in CSR format whose (i, j)'th entry is 1 if there is an edge from $i \in U$ to $j \in V$ and 0 otherwise; that is, the input is of the form required by *maximum_bipartite_matching*. Then the CSR representation of the graph constructed above contains this matrix as a block. Here's an example:

```
>>> graph = csr_matrix([[0, 1, 0, 1], [1, 0, 1, 0], [0, 1, 1, 0]])
>>> print(graph.toarray())
[[0 1 0 1]
 [1 0 1 0]
 [0 1 1 0]]
```

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```
>>> i, j = graph.shape
>>> n = graph.nnz
>>> indptr = np.concatenate([[0],
...                          graph.indptr + i,
...                          np.arange(n + i + 1, n + i + j + 1),
...                          [n + i + j]])
>>> indices = np.concatenate([np.arange(1, i + 1),
...                           graph.indices + i + 1,
...                           np.repeat(i + j + 1, j)])
>>> data = np.ones(n + i + j, dtype=int)
>>>
>>> graph_flow = csr_matrix((data, indices, indptr))
>>> print(graph_flow.toarray())
[[0 1 1 1 0 0 0 0 0]
 [0 0 0 0 0 1 0 1 0]
 [0 0 0 0 1 0 1 0 0]
 [0 0 0 0 0 1 1 0 0]
 [0 0 0 0 0 0 0 0 1]
 [0 0 0 0 0 0 0 0 1]
 [0 0 0 0 0 0 0 0 1]
 [0 0 0 0 0 0 0 0 1]
 [0 0 0 0 0 0 0 0 0]]
```

At this point, we can find the maximum flow between the added sink and the added source and the desired matching can be obtained by restricting the residual graph to the block corresponding to the original graph:

```
>>> flow = maximum_flow(graph_flow, 0, i+j+1)
>>> matching = flow.residual[1:i+1, i+1:i+j+1]
>>> print(matching.toarray())
[[0 1 0 0]
 [1 0 0 0]
 [0 0 1 0]]
```

This tells us that the first, second, and third vertex in U are matched with the second, first, and third vertex in V respectively.

While this solves the maximum bipartite matching problem in general, note that algorithms specialized to that problem, such as *maximum_bipartite_matching*, will generally perform better.

This approach can also be used to solve various common generalizations of the maximum bipartite matching problem. If, for instance, some vertices can be matched with more than one other vertex, this may be handled by modifying the capacities of the new graph appropriately.

scipy.sparse.csgraph.maximum_bipartite_matching

scipy.sparse.csgraph.**maximum_bipartite_matching**(*graph*, *perm_type='row'*)

Returns a matching of a bipartite graph whose cardinality is as least that of any given matching of the graph.

Parameters

graph [sparse matrix] Input sparse in CSR format whose rows represent one partition of the graph and whose columns represent the other partition. An edge between two vertices is indicated by the corresponding entry in the matrix existing in its sparse representation.

perm_type [str, {'row', 'column'}] Which partition to return the matching in terms of: If `'row'`, the function produces an array whose length is the number of columns in the input, and whose

j'th element is the row matched to the j'th column. Conversely, if `perm_type` is `'column'`, this returns the columns matched to each row.

Returns

perm [ndarray] A matching of the vertices in one of the two partitions. Unmatched vertices are represented by a `-1` in the result.

Notes

This function implements the Hopcroft–Karp algorithm [1]. Its time complexity is $O(|E|\sqrt{|V|})$, and its space complexity is linear in the number of rows. In practice, this asymmetry between rows and columns means that it can be more efficient to transpose the input if it contains more columns than rows.

By Konig's theorem, the cardinality of the matching is also the number of vertices appearing in a minimum vertex cover of the graph.

Note that if the sparse representation contains explicit zeros, these are still counted as edges.

The implementation was changed in SciPy 1.4.0 to allow matching of general bipartite graphs, where previous versions would assume that a perfect matching existed. As such, code written against 1.4.0 will not necessarily work on older versions.

References

[1]

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import maximum_bipartite_matching
```

As a simple example, consider a bipartite graph in which the partitions contain 2 and 3 elements respectively. Suppose that one partition contains vertices labelled 0 and 1, and that the other partition contains vertices labelled A, B, and C. Suppose that there are edges connecting 0 and C, 1 and A, and 1 and B. This graph would then be represented by the following sparse matrix:

```
>>> graph = csr_matrix([[0, 0, 1], [1, 1, 0]])
```

Here, the 1s could be anything, as long as they end up being stored as elements in the sparse matrix. We can now calculate maximum matchings as follows:

```
>>> print(maximum_bipartite_matching(graph, perm_type='column'))
[2 0]
>>> print(maximum_bipartite_matching(graph, perm_type='row'))
[ 1 -1  0]
```

The first output tells us that 1 and 2 are matched with C and A respectively, and the second output tells us that A, B, and C are matched with 1, nothing, and 0 respectively.

Note that explicit zeros are still converted to edges. This means that a different way to represent the above graph is by using the CSR structure directly as follows:

```
>>> data = [0, 0, 0]
>>> indices = [2, 0, 1]
>>> indptr = [0, 1, 3]
>>> graph = csr_matrix((data, indices, indptr))
>>> print(maximum_bipartite_matching(graph, perm_type='column'))
[2 0]
>>> print(maximum_bipartite_matching(graph, perm_type='row'))
[ 1 -1  0]
```

When one or both of the partitions are empty, the matching is empty as well:

```
>>> graph = csr_matrix((2, 0))
>>> print(maximum_bipartite_matching(graph, perm_type='column'))
[-1 -1]
>>> print(maximum_bipartite_matching(graph, perm_type='row'))
[]
```

When the input matrix is square, and the graph is known to admit a perfect matching, i.e. a matching with the property that every vertex in the graph belongs to some edge in the matching, then one can view the output as the permutation of rows (or columns) turning the input matrix into one with the property that all diagonal elements are non-empty:

```
>>> a = [[0, 1, 2, 0], [1, 0, 0, 1], [2, 0, 0, 3], [0, 1, 3, 0]]
>>> graph = csr_matrix(a)
>>> perm = maximum_bipartite_matching(graph, perm_type='row')
>>> print(graph[perm].toarray())
[[1 0 0 1]
 [0 1 2 0]
 [0 1 3 0]
 [2 0 0 3]]
```

scipy.sparse.csgraph.min_weight_full_bipartite_matching

scipy.sparse.csgraph.**min_weight_full_bipartite_matching**(*biadjacency_matrix*, *maximize=False*)

Returns the minimum weight full matching of a bipartite graph.

New in version 1.6.0.

Parameters

biadjacency_matrix
: [sparse matrix] Biadjacency matrix of the bipartite graph: A sparse matrix in CSR, CSC, or COO format whose rows represent one partition of the graph and whose columns represent the other partition. An edge between two vertices is indicated by the corresponding entry in the matrix, and the weight of the edge is given by the value of that entry. This should not be confused with the full adjacency matrix of the graph, as we only need the submatrix defining the bipartite structure.

maximize
: [bool (default: False)] Calculates a maximum weight matching if true.

Returns

row_ind, col_ind
: [array] An array of row indices and one of corresponding column indices giving the optimal matching. The total weight of the matching can be computed as `graph[row_ind, col_ind].sum()`. The row indices will be sorted; in the case of a square matrix they will be equal to `numpy.arange(graph.shape[0])`.

Notes

Let $G = ((U, V), E)$ be a weighted bipartite graph with non-zero weights $w : E \to \mathbb{R} \setminus \{0\}$. This function then produces a matching $M \subseteq E$ with cardinality

$$|M| = \min(|U|, |V|),$$

which minimizes the sum of the weights of the edges included in the matching, $\sum_{e \in M} w(e)$, or raises an error if no such matching exists.

When $|U| = |V|$, this is commonly referred to as a perfect matching; here, since we allow $|U|$ and $|V|$ to differ, we follow Karp [1] and refer to the matching as *full*.

This function implements the LAPJVsp algorithm [2], short for "Linear assignment problem, Jonker–Volgenant, sparse".

The problem it solves is equivalent to the rectangular linear assignment problem. [3] As such, this function can be used to solve the same problems as *scipy.optimize.linear_sum_assignment*. That function may perform better when the input is dense, or for certain particular types of inputs, such as those for which the (i, j)'th entry is the distance between two points in Euclidean space.

If no full matching exists, this function raises a `ValueError`. For determining the size of the largest matching in the graph, see *maximum_bipartite_matching*.

We require that weights are non-zero only to avoid issues with the handling of explicit zeros when converting between different sparse representations. Zero weights can be handled by adding a constant to all weights, so that the resulting matrix contains no zeros.

References

[1], [2], [3]

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import min_weight_full_bipartite_matching
```

Let us first consider an example in which all weights are equal:

```
>>> biadjacency_matrix = csr_matrix([[1, 1, 1], [1, 0, 0], [0, 1, 0]])
```

Here, all we get is a perfect matching of the graph:

```
>>> print(min_weight_full_bipartite_matching(biadjacency_matrix)[1])
[2 0 1]
```

That is, the first, second, and third rows are matched with the third, first, and second column respectively. Note that in this example, the 0 in the input matrix does *not* correspond to an edge with weight 0, but rather a pair of vertices not paired by an edge.

Note also that in this case, the output matches the result of applying *maximum_bipartite_matching*:

```
>>> from scipy.sparse.csgraph import maximum_bipartite_matching
>>> biadjacency = csr_matrix([[1, 1, 1], [1, 0, 0], [0, 1, 0]])
>>> print(maximum_bipartite_matching(biadjacency, perm_type='column'))
[2 0 1]
```

When multiple edges are available, the ones with lowest weights are preferred:

```
>>> biadjacency = csr_matrix([[3, 3, 6], [4, 3, 5], [10, 1, 8]])
>>> row_ind, col_ind = min_weight_full_bipartite_matching(biadjacency)
>>> print(col_ind)
[0 2 1]
```

The total weight in this case is $3 + 5 + 1 = 9$:

```
>>> print(biadjacency[row_ind, col_ind].sum())
9
```

When the matrix is not square, i.e. when the two partitions have different cardinalities, the matching is as large as the smaller of the two partitions:

```
>>> biadjacency = csr_matrix([[0, 1, 1], [0, 2, 3]])
>>> row_ind, col_ind = min_weight_full_bipartite_matching(biadjacency)
>>> print(row_ind, col_ind)
[0 1] [2 1]
>>> biadjacency = csr_matrix([[0, 1], [3, 1], [1, 4]])
>>> row_ind, col_ind = min_weight_full_bipartite_matching(biadjacency)
>>> print(row_ind, col_ind)
[0 2] [1 0]
```

When one or both of the partitions are empty, the matching is empty as well:

```
>>> biadjacency = csr_matrix((2, 0))
>>> row_ind, col_ind = min_weight_full_bipartite_matching(biadjacency)
>>> print(row_ind, col_ind)
[] []
```

In general, we will always reach the same sum of weights as if we had used *scipy.optimize.linear_sum_assignment* but note that for that one, missing edges are represented by a matrix entry of `float('inf')`. Let us generate a random sparse matrix with integer entries between 1 and 10:

```
>>> import numpy as np
>>> from scipy.sparse import random
>>> from scipy.optimize import linear_sum_assignment
>>> sparse = random(10, 10, random_state=42, density=.5, format='coo') *␣
↪10
>>> sparse.data = np.ceil(sparse.data)
>>> dense = sparse.toarray()
>>> dense = np.full(sparse.shape, np.inf)
>>> dense[sparse.row, sparse.col] = sparse.data
>>> sparse = sparse.tocsr()
>>> row_ind, col_ind = linear_sum_assignment(dense)
>>> print(dense[row_ind, col_ind].sum())
28.0
>>> row_ind, col_ind = min_weight_full_bipartite_matching(sparse)
>>> print(sparse[row_ind, col_ind].sum())
28.0
```

scipy.sparse.csgraph.structural_rank

scipy.sparse.csgraph.**structural_rank**(*graph*)

Compute the structural rank of a graph (matrix) with a given sparsity pattern.

The structural rank of a matrix is the number of entries in the maximum transversal of the corresponding bipartite graph, and is an upper bound on the numerical rank of the matrix. A graph has full structural rank if it is possible to permute the elements to make the diagonal zero-free.

New in version 0.19.0.

Parameters

graph [sparse matrix] Input sparse matrix.

Returns

rank [int] The structural rank of the sparse graph.

References

[1], [2]

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import structural_rank
```

```
>>> graph = [
... [0, 1, 2, 0],
... [1, 0, 0, 1],
... [2, 0, 0, 3],
... [0, 1, 3, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 0)    1
  (1, 3)    1
  (2, 0)    2
  (2, 3)    3
  (3, 1)    1
  (3, 2)    3
```

```
>>> structural_rank(graph)
4
```

scipy.sparse.csgraph.NegativeCycleError

exception scipy.sparse.csgraph.**NegativeCycleError**(*message=''*)

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

construct_dist_matrix(graph, predecessors[, …])	Construct distance matrix from a predecessor matrix
csgraph_from_dense(graph[, null_value, …])	Construct a CSR-format sparse graph from a dense matrix.
csgraph_from_masked(graph)	Construct a CSR-format graph from a masked array.
csgraph_masked_from_dense(graph[, …])	Construct a masked array graph representation from a dense matrix.
csgraph_to_dense(csgraph[, null_value])	Convert a sparse graph representation to a dense representation
csgraph_to_masked(csgraph)	Convert a sparse graph representation to a masked array representation
reconstruct_path(csgraph, predecessors[, …])	Construct a tree from a graph and a predecessor list.

scipy.sparse.csgraph.construct_dist_matrix

scipy.sparse.csgraph.**construct_dist_matrix**(*graph*, *predecessors*, *directed=True*, *null_value=np.inf*)

Construct distance matrix from a predecessor matrix

New in version 0.11.0.

Parameters

graph [array_like or sparse] The N x N matrix representation of a directed or undirected graph. If dense, then non-edges are indicated by zeros or infinities.

predecessors [array_like] The N x N matrix of predecessors of each node (see Notes below).

directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then operate on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

null_value [bool, optional] value to use for distances between unconnected nodes. Default is np.inf

Returns

dist_matrix [ndarray] The N x N matrix of distances between nodes along the path specified by the predecessor matrix. If no path exists, the distance is zero.

Notes

The predecessor matrix is of the form returned by *shortest_path*. Row i of the predecessor matrix contains information on the shortest paths from point i: each entry predecessors[i, j] gives the index of the previous node in the path from point i to point j. If no path exists between point i and j, then predecessors[i, j] = -9999

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import construct_dist_matrix
```

```
>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 3)    3
```

```
>>> pred = np.array([[-9999, 0, 0, 2],
... [1, -9999, 0, 1],
... [2, 0, -9999, 2],
... [1, 3, 3, -9999]], dtype=np.int32)
```

```
>>> construct_dist_matrix(graph=graph, predecessors=pred, directed=False)
array([[ 0.,  1.,  2.,  5.],
       [ 1.,  0.,  3.,  1.],
       [ 2.,  3.,  0.,  3.],
       [ 2.,  1.,  3.,  0.]])
```

scipy.sparse.csgraph.csgraph_from_dense

scipy.sparse.csgraph.**csgraph_from_dense**(*graph*, *null_value=0*, *nan_null=True*, *infinity_null=True*)

Construct a CSR-format sparse graph from a dense matrix.

New in version 0.11.0.

Parameters

graph [array_like] Input graph. Shape should be (n_nodes, n_nodes).

null_value [float or None (optional)] Value that denotes non-edges in the graph. Default is zero.

infinity_null [bool] If True (default), then infinite entries (both positive and negative) are treated as null edges.

nan_null [bool] If True (default), then NaN entries are treated as non-edges

Returns

csgraph [csr_matrix] Compressed sparse representation of graph,

Examples

```
>>> from scipy.sparse.csgraph import csgraph_from_dense
```

```
>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
```

```
>>> csgraph_from_dense(graph)
<4x4 sparse matrix of type '<class 'numpy.float64'>'
    with 4 stored elements in Compressed Sparse Row format>
```

scipy.sparse.csgraph.csgraph_from_masked

scipy.sparse.csgraph.**csgraph_from_masked**(*graph*)

Construct a CSR-format graph from a masked array.

New in version 0.11.0.

Parameters

graph [MaskedArray] Input graph. Shape should be (n_nodes, n_nodes).

Returns

csgraph [csr_matrix] Compressed sparse representation of graph,

Examples

```
>>> import numpy as np
>>> from scipy.sparse.csgraph import csgraph_from_masked
```

```
>>> graph_masked = np.ma.masked_array(data =[
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
...  ],
... mask=[[ True, False, False , True],
... [ True,  True , True, False],
... [ True , True,  True ,False],
... [ True ,True , True , True]],
... fill_value = 0)
```

```
>>> csgraph_from_masked(graph_masked)
<4x4 sparse matrix of type '<class 'numpy.float64'>'
    with 4 stored elements in Compressed Sparse Row format>
```

scipy.sparse.csgraph.csgraph_masked_from_dense

scipy.sparse.csgraph.**csgraph_masked_from_dense**(*graph*, *null_value=0*, *nan_null=True*, *infinity_null=True*, *copy=True*)

Construct a masked array graph representation from a dense matrix.

New in version 0.11.0.

Parameters

graph [array_like] Input graph. Shape should be (n_nodes, n_nodes).
null_value [float or None (optional)] Value that denotes non-edges in the graph. Default is zero.
infinity_null [bool] If True (default), then infinite entries (both positive and negative) are treated as null edges.
nan_null [bool] If True (default), then NaN entries are treated as non-edges

Returns

csgraph [MaskedArray] masked array representation of graph

Examples

```
>>> from scipy.sparse.csgraph import csgraph_masked_from_dense
```

```
>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
```

```
>>> csgraph_masked_from_dense(graph)
masked_array(
  data=[[--, 1, 2, --],
        [--, --, --, 1],
        [--, --, --, 3],
        [--, --, --, --]],
  mask=[[ True, False, False,  True],
        [ True,  True,  True, False],
        [ True,  True,  True, False],
        [ True,  True,  True,  True]],
  fill_value=0)
```

scipy.sparse.csgraph.csgraph_to_dense

scipy.sparse.csgraph.**csgraph_to_dense**(*csgraph*, *null_value=0*)

Convert a sparse graph representation to a dense representation

New in version 0.11.0.

Parameters

csgraph [csr_matrix, csc_matrix, or lil_matrix] Sparse representation of a graph.
null_value [float, optional] The value used to indicate null edges in the dense representation. Default is 0.

Returns

graph [ndarray] The dense representation of the sparse graph.

Notes

For normal sparse graph representations, calling csgraph_to_dense with null_value=0 produces an equivalent result to using dense format conversions in the main sparse package. When the sparse representations have repeated values, however, the results will differ. The tools in scipy.sparse will add repeating values to obtain a final value. This function will select the minimum among repeating values to obtain a final value. For example, here we'll create a two-node directed sparse graph with multiple edges from node 0 to node 1, of weights 2 and 3. This illustrates the difference in behavior:

```
>>> from scipy.sparse import csr_matrix, csgraph
>>> data = np.array([2, 3])
>>> indices = np.array([1, 1])
>>> indptr = np.array([0, 2, 2])
>>> M = csr_matrix((data, indices, indptr), shape=(2, 2))
>>> M.toarray()
array([[0, 5],
       [0, 0]])
>>> csgraph.csgraph_to_dense(M)
array([[0., 2.],
       [0., 0.]])
```

The reason for this difference is to allow a compressed sparse graph to represent multiple edges between any two nodes. As most sparse graph algorithms are concerned with the single lowest-cost edge between any two nodes, the default scipy.sparse behavior of summming multiple weights does not make sense in this context.

The other reason for using this routine is to allow for graphs with zero-weight edges. Let's look at the example of a two-node directed graph, connected by an edge of weight zero:

```
>>> from scipy.sparse import csr_matrix, csgraph
>>> data = np.array([0.0])
>>> indices = np.array([1])
>>> indptr = np.array([0, 1, 1])
>>> M = csr_matrix((data, indices, indptr), shape=(2, 2))
>>> M.toarray()
array([[0, 0],
       [0, 0]])
>>> csgraph.csgraph_to_dense(M, np.inf)
array([[ inf,   0.],
       [ inf,  inf]])
```

In the first case, the zero-weight edge gets lost in the dense representation. In the second case, we can choose a different null value and see the true form of the graph.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import csgraph_to_dense
```

```
>>> graph = csr_matrix( [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ])
>>> graph
<4x4 sparse matrix of type '<class 'numpy.int64'>'
    with 4 stored elements in Compressed Sparse Row format>
```

```
>>> csgraph_to_dense(graph)
array([[ 0.,  1.,  2.,  0.],
       [ 0.,  0.,  0.,  1.],
       [ 0.,  0.,  0.,  3.],
       [ 0.,  0.,  0.,  0.]])
```

scipy.sparse.csgraph.csgraph_to_masked

scipy.sparse.csgraph.**csgraph_to_masked**(*csgraph*)

Convert a sparse graph representation to a masked array representation

New in version 0.11.0.

Parameters

csgraph [csr_matrix, csc_matrix, or lil_matrix] Sparse representation of a graph.

Returns

graph [MaskedArray] The masked dense representation of the sparse graph.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import csgraph_to_masked
```

```
>>> graph = csr_matrix( [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ])
>>> graph
<4x4 sparse matrix of type '<class 'numpy.int64'>'
    with 4 stored elements in Compressed Sparse Row format>
```

```
>>> csgraph_to_masked(graph)
masked_array(
```

(continues on next page)

(continued from previous page)

```
  data=[[--, 1.0, 2.0, --],
        [--, --, --, 1.0],
        [--, --, --, 3.0],
        [--, --, --, --]],
  mask=[[ True, False, False,  True],
        [ True,  True,  True, False],
        [ True,  True,  True, False],
        [ True,  True,  True,  True]],
  fill_value=1e+20)
```

scipy.sparse.csgraph.reconstruct_path

scipy.sparse.csgraph.**reconstruct_path**(*csgraph*, *predecessors*, *directed=True*)

Construct a tree from a graph and a predecessor list.

New in version 0.11.0.

Parameters

csgraph [array_like or sparse matrix] The N x N matrix representing the directed or undirected graph from which the predecessors are drawn.

predecessors [array_like, one dimension] The length-N array of indices of predecessors for the tree. The index of the parent of node i is given by predecessors[i].

directed [bool, optional] If True (default), then operate on a directed graph: only move from point i to point j along paths csgraph[i, j]. If False, then operate on an undirected graph: the algorithm can progress from point i to j along csgraph[i, j] or csgraph[j, i].

Returns

cstree [csr matrix] The N x N directed compressed-sparse representation of the tree drawn from csgraph which is encoded by the predecessor list.

Examples

```
>>> from scipy.sparse import csr_matrix
>>> from scipy.sparse.csgraph import reconstruct_path
```

```
>>> graph = [
... [0, 1 , 2, 0],
... [0, 0, 0, 1],
... [0, 0, 0, 3],
... [0, 0, 0, 0]
... ]
>>> graph = csr_matrix(graph)
>>> print(graph)
  (0, 1)    1
  (0, 2)    2
  (1, 3)    1
  (2, 3)    3
```

```
>>> pred = np.array([-9999, 0, 0, 1], dtype=np.int32)
```

```
>>> cstree = reconstruct_path(csgraph=graph, predecessors=pred,␣
 ↪directed=False)
>>> cstree.todense()
matrix([[ 0.,  1.,  2.,  0.],
        [ 0.,  0.,  0.,  1.],
        [ 0.,  0.,  0.,  0.],
        [ 0.,  0.,  0.,  0.]])
```

Graph Representations

This module uses graphs which are stored in a matrix format. A graph with N nodes can be represented by an (N x N) adjacency matrix G. If there is a connection from node i to node j, then G[i, j] = w, where w is the weight of the connection. For nodes i and j which are not connected, the value depends on the representation:

- for dense array representations, non-edges are represented by G[i, j] = 0, infinity, or NaN.
- for dense masked representations (of type np.ma.MaskedArray), non-edges are represented by masked values. This can be useful when graphs with zero-weight edges are desired.
- for sparse array representations, non-edges are represented by non-entries in the matrix. This sort of sparse representation also allows for edges with zero weights.

As a concrete example, imagine that you would like to represent the following undirected graph:

```
      G

     (0)
    /   \
   1     2
  /       \
(2)       (1)
```

This graph has three nodes, where node 0 and 1 are connected by an edge of weight 2, and nodes 0 and 2 are connected by an edge of weight 1. We can construct the dense, masked, and sparse representations as follows, keeping in mind that an undirected graph is represented by a symmetric matrix:

```
>>> G_dense = np.array([[0, 2, 1],
...                     [2, 0, 0],
...                     [1, 0, 0]])
>>> G_masked = np.ma.masked_values(G_dense, 0)
>>> from scipy.sparse import csr_matrix
>>> G_sparse = csr_matrix(G_dense)
```

This becomes more difficult when zero edges are significant. For example, consider the situation when we slightly modify the above graph:

```
     G2

     (0)
    /   \
   0     2
  /       \
(2)       (1)
```

This is identical to the previous graph, except nodes 0 and 2 are connected by an edge of zero weight. In this case, the dense representation above leads to ambiguities: how can non-edges be represented if zero is a meaningful value? In this case, either a masked or sparse representation must be used to eliminate the ambiguity:

```
>>> G2_data = np.array([[np.inf, 2,      0     ],
...                     [2,      np.inf, np.inf],
...                     [0,      np.inf, np.inf]])
>>> G2_masked = np.ma.masked_invalid(G2_data)
>>> from scipy.sparse.csgraph import csgraph_from_dense
>>> # G2_sparse = csr_matrix(G2_data) would give the wrong result
>>> G2_sparse = csgraph_from_dense(G2_data, null_value=np.inf)
>>> G2_sparse.data
array([ 2.,  0.,  2.,  0.])
```

Here we have used a utility routine from the csgraph submodule in order to convert the dense representation to a sparse representation which can be understood by the algorithms in submodule. By viewing the data array, we can see that the zero values are explicitly encoded in the graph.

Directed vs. undirected

Matrices may represent either directed or undirected graphs. This is specified throughout the csgraph module by a boolean keyword. Graphs are assumed to be directed by default. In a directed graph, traversal from node i to node j can be accomplished over the edge G[i, j], but not the edge G[j, i]. Consider the following dense graph:

```
>>> G_dense = np.array([[0, 1, 0],
...                     [2, 0, 3],
...                     [0, 4, 0]])
```

When `directed=True` we get the graph:

```
  ---1--> ---3-->
(0)     (1)     (2)
  <--2--- <--4---
```

In a non-directed graph, traversal from node i to node j can be accomplished over either G[i, j] or G[j, i]. If both edges are not null, and the two have unequal weights, then the smaller of the two is used.

So for the same graph, when `directed=False` we get the graph:

```
(0)--1--(1)--2--(2)
```

Note that a symmetric matrix will represent an undirected graph, regardless of whether the 'directed' keyword is set to True or False. In this case, using `directed=True` generally leads to more efficient computation.

The routines in this module accept as input either scipy.sparse representations (csr, csc, or lil format), masked representations, or dense representations with non-edges indicated by zeros, infinities, and NaN entries.

3.3.26 Spatial algorithms and data structures (`scipy.spatial`)

Spatial transformations

These are contained in the `scipy.spatial.transform` submodule.

Nearest-neighbor queries

KDTree(data[, leafsize, compact_nodes, …])	kd-tree for quick nearest-neighbor lookup.
cKDTree(data[, leafsize, compact_nodes, …])	kd-tree for quick nearest-neighbor lookup
Rectangle(maxes, mins)	Hyperrectangle class.

scipy.spatial.KDTree

class scipy.spatial.**KDTree**(*data*, *leafsize=10*, *compact_nodes=True*, *copy_data=False*, *balanced_tree=True*, *boxsize=None*)

kd-tree for quick nearest-neighbor lookup.

This class provides an index into a set of k-dimensional points which can be used to rapidly look up the nearest neighbors of any point.

Parameters

data [array_like, shape (n,m)] The n data points of dimension m to be indexed. This array is not copied unless this is necessary to produce a contiguous array of doubles, and so modifying this data will result in bogus results. The data are also copied if the kd-tree is built with copy_data=True.

leafsize [positive int, optional] The number of points at which the algorithm switches over to brute-force. Default: 10.

compact_nodes
[bool, optional] If True, the kd-tree is built to shrink the hyperrectangles to the actual data range. This usually gives a more compact tree that is robust against degenerated input data and gives faster queries at the expense of longer build time. Default: True.

copy_data [bool, optional] If True the data is always copied to protect the kd-tree against data corruption. Default: False.

balanced_tree
[bool, optional] If True, the median is used to split the hyperrectangles instead of the midpoint. This usually gives a more compact tree and faster queries at the expense of longer build time. Default: True.

boxsize [array_like or scalar, optional] Apply a m-d toroidal topology to the KDTree.. The topology is generated by $x_i + n_i L_i$ where n_i are integers and L_i is the boxsize along i-th dimension. The input data shall be wrapped into $[0, L_i)$. A ValueError is raised if any of the data is outside of this bound.

Notes

The algorithm used is described in Maneewongvatana and Mount 1999. The general idea is that the kd-tree is a binary tree, each of whose nodes represents an axis-aligned hyperrectangle. Each node specifies an axis and splits the set of points based on whether their coordinate along that axis is greater than or less than a particular value.

During construction, the axis and splitting point are chosen by the "sliding midpoint" rule, which ensures that the cells do not all become long and thin.

The tree can be queried for the r closest neighbors of any given point (optionally returning only those within some maximum distance of the point). It can also be queried, with a substantial gain in efficiency, for the r approximate closest neighbors.

For large dimensions (20 is already large) do not expect this to run significantly faster than brute force. High-dimensional nearest-neighbor queries are a substantial open problem in computer science.

Attributes

data	[ndarray, shape (n,m)] The n data points of dimension m to be indexed. This array is not copied unless this is necessary to produce a contiguous array of doubles. The data are also copied if the kd-tree is built with *copy_data=True*.
leafsize	[positive int] The number of points at which the algorithm switches over to brute-force.
m	[int] The dimension of a single data-point.
n	[int] The number of data points.
maxes	[ndarray, shape (m,)] The maximum value in each dimension of the n data points.
mins	[ndarray, shape (m,)] The minimum value in each dimension of the n data points.
size	[int] The number of nodes in the tree.

Methods

count_neighbors(other, r[, p, weights, …])	Count how many nearby pairs can be formed.
query(x[, k, eps, p, distance_upper_bound, …])	Query the kd-tree for nearest neighbors.
query_ball_point(x, r[, p, eps, workers, …])	Find all points within distance r of point(s) x.
query_ball_tree(other, r[, p, eps])	Find all pairs of points between *self* and *other* whose distance is at most r.
query_pairs(r[, p, eps, output_type])	Find all pairs of points in *self* whose distance is at most r.
sparse_distance_matrix(other, max_distance)	Compute a sparse distance matrix.

scipy.spatial.KDTree.count_neighbors

KDTree.**count_neighbors**(*other*, *r*, *p=2.0*, *weights=None*, *cumulative=True*)

Count how many nearby pairs can be formed.

Count the number of pairs `(x1,x2)` can be formed, with `x1` drawn from `self` and `x2` drawn from `other`, and where `distance(x1, x2, p) <= r`.

Data points on `self` and `other` are optionally weighted by the `weights` argument. (See below)

This is adapted from the "two-point correlation" algorithm described by Gray and Moore [1]. See notes for further discussion.

Parameters

other	[KDTree] The other tree to draw points from, can be the same tree as self.

r [float or one-dimensional array of floats] The radius to produce a count for. Multiple radii are searched with a single tree traversal. If the count is non-cumulative(`cumulative=False`), `r` defines the edges of the bins, and must be non-decreasing.

p [float, optional] 1<=p<=infinity. Which Minkowski p-norm to use. Default 2.0. A finite large p may cause a ValueError if overflow can occur.

weights [tuple, array_like, or None, optional] If None, the pair-counting is unweighted. If given as a tuple, weights[0] is the weights of points in `self`, and weights[1] is the weights of points in `other`; either can be None to indicate the points are unweighted. If given as an array_like, weights is the weights of points in `self` and `other`. For this to make sense, `self` and `other` must be the same tree. If `self` and `other` are two different trees, a `ValueError` is raised. Default: None
New in version 1.6.0.

cumulative [bool, optional] Whether the returned counts are cumulative. When cumulative is set to `False` the algorithm is optimized to work with a large number of bins (>10) specified by `r`. When `cumulative` is set to True, the algorithm is optimized to work with a small number of `r`. Default: True
New in version 1.6.0.

Returns

result [scalar or 1-D array] The number of pairs. For unweighted counts, the result is integer. For weighted counts, the result is float. If cumulative is False, `result[i]` contains the counts with `(-inf if i == 0 else r[i-1]) < R <= r[i]`

Notes

Pair-counting is the basic operation used to calculate the two point correlation functions from a data set composed of position of objects.

Two point correlation function measures the clustering of objects and is widely used in cosmology to quantify the large scale structure in our Universe, but it may be useful for data analysis in other fields where self-similar assembly of objects also occur.

The Landy-Szalay estimator for the two point correlation function of `D` measures the clustering signal in `D`. [2]

For example, given the position of two sets of objects,

- objects `D` (data) contains the clustering signal, and
- objects `R` (random) that contains no signal,

$$\xi(r) = \frac{< D, D > -2f < D, R > +f^2 < R, R >}{f^2 < R, R >},$$

where the brackets represents counting pairs between two data sets in a finite bin around `r` (distance), corresponding to setting *cumulative=False*, and `f = float(len(D)) / float(len(R))` is the ratio between number of objects from data and random.

The algorithm implemented here is loosely based on the dual-tree algorithm described in [1]. We switch between two different pair-cumulation scheme depending on the setting of `cumulative`. The computing time of the method we use when for `cumulative == False` does not scale with the total number of bins. The algorithm for `cumulative == True` scales linearly with the number of bins, though it is slightly faster when only 1 or 2 bins are used. [5].

As an extension to the naive pair-counting, weighted pair-counting counts the product of weights instead of number of pairs. Weighted pair-counting is used to estimate marked correlation functions ([3], section 2.2), or to properly calculate the average of data per distance bin (e.g. [4], section 2.1 on redshift).

Examples

You can count neighbors number between two kd-trees within a distance:

```
>>> import numpy as np
>>> from scipy.spatial import KDTree
>>> rng = np.random.default_rng()
>>> points1 = rng.random((5, 2))
>>> points2 = rng.random((5, 2))
>>> kd_tree1 = KDTree(points1)
>>> kd_tree2 = KDTree(points2)
>>> kd_tree1.count_neighbors(kd_tree2, 0.2)
1
```

This number is same as the total pair number calculated by *query_ball_tree*:

```
>>> indexes = kd_tree1.query_ball_tree(kd_tree2, r=0.2)
>>> sum([len(i) for i in indexes])
1
```

scipy.spatial.KDTree.query

KDTree.**query**(*x*, *k=1*, *eps=0*, *p=2*, *distance_upper_bound=inf*, *workers=1*)

Query the kd-tree for nearest neighbors.

Parameters

x [array_like, last dimension self.m] An array of points to query.

k [int or Sequence[int], optional] Either the number of nearest neighbors to return, or a list of the k-th nearest neighbors to return, starting from 1.

eps [nonnegative float, optional] Return approximate nearest neighbors; the kth returned value is guaranteed to be no further than (1+eps) times the distance to the real kth nearest neighbor.

p [float, 1<=p<=infinity, optional] Which Minkowski p-norm to use. 1 is the sum-of-absolute-values distance ("Manhattan" distance). 2 is the usual Euclidean distance. infinity is the maximum-coordinate-difference distance. A large, finite p may cause a ValueError if overflow can occur.

distance_upper_bound

[nonnegative float, optional] Return only neighbors within this distance. This is used to prune tree searches, so if you are doing a series of nearest-neighbor queries, it may help to supply the distance to the nearest neighbor of the most recent point.

workers [int, optional] Number of workers to use for parallel processing. If -1 is given all CPU threads are used. Default: 1.
New in version 1.6.0.

Returns

d [float or array of floats] The distances to the nearest neighbors. If `x` has shape `tuple+(self.m,)`, then `d` has shape `tuple+(k,)`. When k == 1, the last dimen-

sion of the output is squeezed. Missing neighbors are indicated with infinite distances. Hits are sorted by distance (nearest first).
Deprecated since version 1.6.0: If `k=None`, then `d` is an object array of shape `tuple`, containing lists of distances. This behavior is deprecated and will be removed in SciPy 1.8.0, use `query_ball_point` instead.

i [integer or array of integers] The index of each neighbor in `self.data`. `i` is the same shape as d. Missing neighbors are indicated with `self.n`.

Examples

```
>>> import numpy as np
>>> from scipy.spatial import KDTree
>>> x, y = np.mgrid[0:5, 2:8]
>>> tree = KDTree(np.c_[x.ravel(), y.ravel()])
```

To query the nearest neighbours and return squeezed result, use

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=1)
>>> print(dd, ii)
[2.         0.14142136] [ 0 13]
```

To query the nearest neighbours and return unsqueezed result, use

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=[1])
>>> print(dd, ii)
[[2.        ]
 [0.14142136]] [[ 0]
 [13]]
```

To query the second nearest neighbours and return unsqueezed result, use

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=[2])
>>> print(dd, ii)
[[2.23606798]
 [0.90553851]] [[ 6]
 [12]]
```

To query the first and second nearest neighbours, use

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=2)
>>> print(dd, ii)
[[2.         2.23606798]
 [0.14142136 0.90553851]] [[ 0  6]
 [13 12]]
```

or, be more specific

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=[1, 2])
>>> print(dd, ii)
[[2.         2.23606798]
 [0.14142136 0.90553851]] [[ 0  6]
 [13 12]]
```

scipy.spatial.KDTree.query_ball_point

KDTree.**query_ball_point**(*x*, *r*, *p=2.0*, *eps=0*, *workers=1*, *return_sorted=None*, *return_length=False*)

Find all points within distance r of point(s) x.

Parameters

x [array_like, shape tuple + (self.m,)] The point or points to search for neighbors of.

r [array_like, float] The radius of points to return, must broadcast to the length of x.

p [float, optional] Which Minkowski p-norm to use. Should be in the range [1, inf]. A finite large p may cause a ValueError if overflow can occur.

eps [nonnegative float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than `r / (1 + eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1 + eps)`.

workers [int, optional] Number of jobs to schedule for parallel processing. If -1 is given all processors are used. Default: 1.
New in version 1.6.0.

return_sorted
[bool, optional] Sorts returned indicies if True and does not sort them if False. If None, does not sort single point queries, but does sort multi-point queries which was the behavior before this option was added.
New in version 1.6.0.

return_length: bool, optional
Return the number of points inside the radius instead of a list of the indices.
New in version 1.6.0.

Returns

results [list or array of lists] If *x* is a single point, returns a list of the indices of the neighbors of *x*. If *x* is an array of points, returns an object array of shape tuple containing lists of neighbors.

Notes

If you have many points whose neighbors you want to find, you may save substantial amounts of time by putting them in a KDTree and using query_ball_tree.

Examples

```
>>> from scipy import spatial
>>> x, y = np.mgrid[0:5, 0:5]
>>> points = np.c_[x.ravel(), y.ravel()]
>>> tree = spatial.KDTree(points)
>>> sorted(tree.query_ball_point([2, 0], 1))
[5, 10, 11, 15]
```

Query multiple points and plot the results:

```
>>> import matplotlib.pyplot as plt
>>> points = np.asarray(points)
>>> plt.plot(points[:,0], points[:,1], '.')
>>> for results in tree.query_ball_point(([2, 0], [3, 3]), 1):
```

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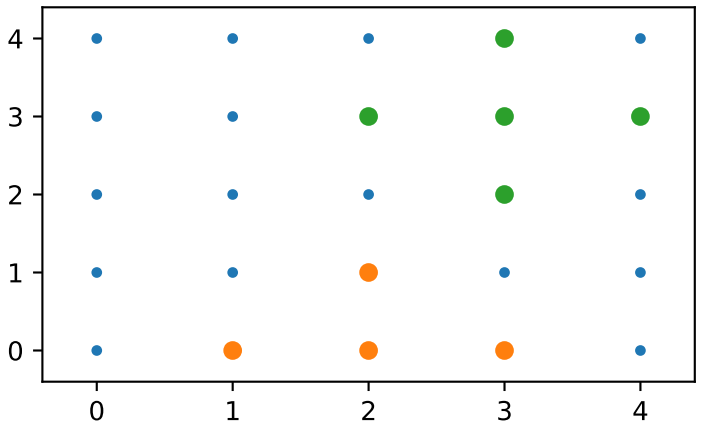
```
...     nearby_points = points[results]
...     plt.plot(nearby_points[:,0], nearby_points[:,1], 'o')
>>> plt.margins(0.1, 0.1)
>>> plt.show()
```



scipy.spatial.KDTree.query_ball_tree

KDTree.**query_ball_tree**(*other*, *r*, *p=2.0*, *eps=0*)

Find all pairs of points between *self* and *other* whose distance is at most r.

Parameters

other [KDTree instance] The tree containing points to search against.

r [float] The maximum distance, has to be positive.

p [float, optional] Which Minkowski norm to use. *p* has to meet the condition `1 <= p <= infinity`.

eps [float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than `r/(1+eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1+eps)`. *eps* has to be non-negative.

Returns

results [list of lists] For each element `self.data[i]` of this tree, `results[i]` is a list of the indices of its neighbors in `other.data`.

Examples

You can search all pairs of points between two kd-trees within a distance:

```
>>> import matplotlib.pyplot as plt
>>> import numpy as np
>>> from scipy.spatial import KDTree
>>> rng = np.random.default_rng()
>>> points1 = rng.random((15, 2))
>>> points2 = rng.random((15, 2))
>>> plt.figure(figsize=(6, 6))
>>> plt.plot(points1[:, 0], points1[:, 1], "xk", markersize=14)
>>> plt.plot(points2[:, 0], points2[:, 1], "og", markersize=14)
>>> kd_tree1 = KDTree(points1)
>>> kd_tree2 = KDTree(points2)
>>> indexes = kd_tree1.query_ball_tree(kd_tree2, r=0.2)
>>> for i in range(len(indexes)):
...     for j in indexes[i]:
...         plt.plot([points1[i, 0], points2[j, 0]],
...             [points1[i, 1], points2[j, 1]], "-r")
>>> plt.show()
```

scipy.spatial.KDTree.query_pairs

KDTree.**query_pairs**(*r*, *p=2.0*, *eps=0*, *output_type='set'*)

Find all pairs of points in *self* whose distance is at most r.

Parameters

r [positive float] The maximum distance.

p [float, optional] Which Minkowski norm to use. *p* has to meet the condition `1 <= p <= infinity`.

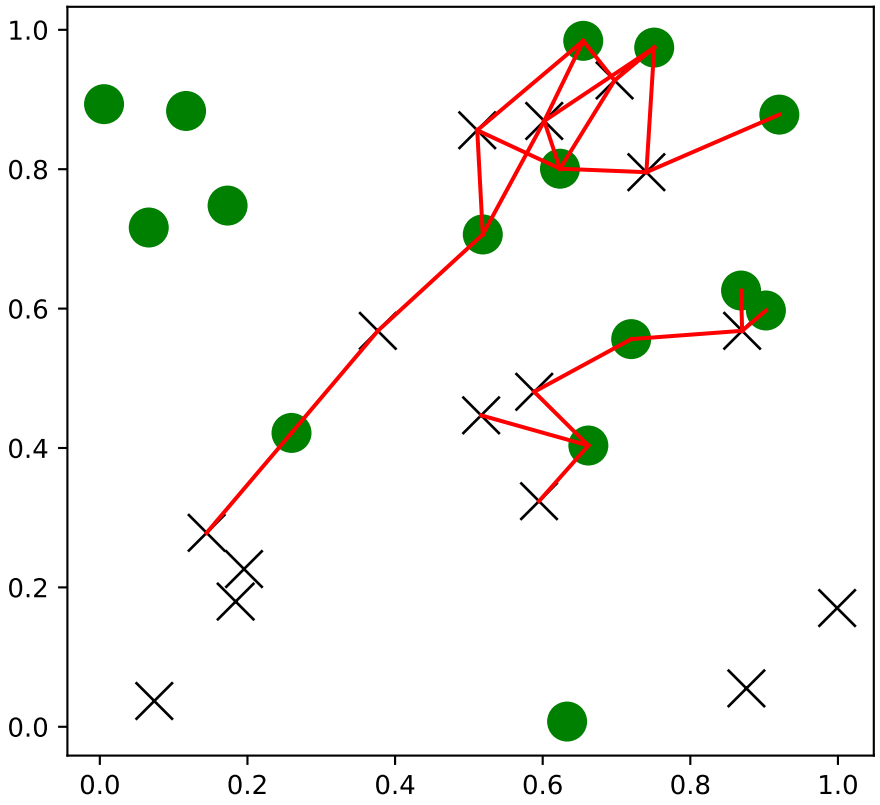
eps [float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than `r/(1+eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1+eps)`. *eps* has to be non-negative.

output_type

[string, optional] Choose the output container, 'set' or 'ndarray'. Default: 'set'
New in version 1.6.0.

Returns

results [set or ndarray] Set of pairs `(i,j)`, with `i < j`, for which the corresponding positions are close. If output_type is 'ndarray', an ndarry is returned instead of a set.


1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0

Examples

You can search all pairs of points in a kd-tree within a distance:

```
>>> import matplotlib.pyplot as plt
>>> import numpy as np
>>> from scipy.spatial import KDTree
>>> rng = np.random.default_rng()
>>> points = rng.random((20, 2))
>>> plt.figure(figsize=(6, 6))
>>> plt.plot(points[:, 0], points[:, 1], "xk", markersize=14)
>>> kd_tree = KDTree(points)
>>> pairs = kd_tree.query_pairs(r=0.2)
>>> for (i, j) in pairs:
...     plt.plot([points[i, 0], points[j, 0]],
...              [points[i, 1], points[j, 1]], "-r")
>>> plt.show()
```

scipy.spatial.KDTree.sparse_distance_matrix

KDTree.**sparse_distance_matrix**(*other*, *max_distance*, *p=2.0*, *output_type='dok_matrix'*)

Compute a sparse distance matrix.

Computes a distance matrix between two KDTrees, leaving as zero any distance greater than max_distance.

Parameters

other [KDTree]

max_distance
[positive float]

p [float, 1<=p<=infinity] Which Minkowski p-norm to use. A finite large p may cause a ValueError if overflow can occur.

output_type
[string, optional] Which container to use for output data. Options: 'dok_matrix', 'coo_matrix', 'dict', or 'ndarray'. Default: 'dok_matrix'.
New in version 1.6.0.

Returns

result [dok_matrix, coo_matrix, dict or ndarray] Sparse matrix representing the results in "dictionary of keys" format. If a dict is returned the keys are (i,j) tuples of indices. If output_type is 'ndarray' a record array with fields 'i', 'j', and 'v' is returned,

Examples

You can compute a sparse distance matrix between two kd-trees:

```
>>> import numpy as np
>>> from scipy.spatial import KDTree
>>> rng = np.random.default_rng()
>>> points1 = rng.random((5, 2))
>>> points2 = rng.random((5, 2))
>>> kd_tree1 = KDTree(points1)
>>> kd_tree2 = KDTree(points2)
```

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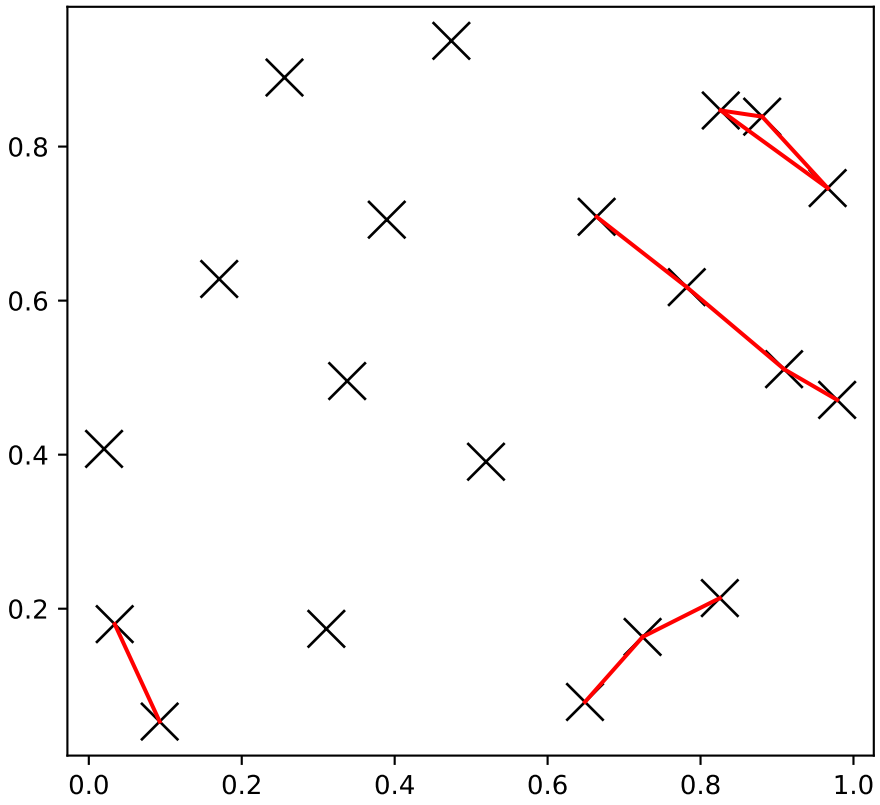
0.8
0.6
0.4
0.2
0.0
0.2
0.4
0.6
0.8
1.0

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```
>>> sdm = kd_tree1.sparse_distance_matrix(kd_tree2, 0.3)
>>> sdm.toarray()
array([[0.        , 0.        , 0.12295571, 0.        , 0.        ],
   [0.        , 0.        , 0.        , 0.        , 0.        ],
   [0.28942611, 0.        , 0.        , 0.2333084 , 0.        ],
   [0.        , 0.        , 0.        , 0.        , 0.        ],
   [0.24617575, 0.29571802, 0.26836782, 0.        , 0.        ]])
```

You can check distances above the *max_distance* are zeros:

```
>>> from scipy.spatial import distance_matrix
>>> distance_matrix(points1, points2)
array([[0.56906522, 0.39923701, 0.12295571, 0.8658745 , 0.79428925],
   [0.37327919, 0.7225693 , 0.87665969, 0.32580855, 0.75679479],
   [0.28942611, 0.30088013, 0.6395831 , 0.2333084 , 0.33630734],
   [0.31994999, 0.72658602, 0.71124834, 0.55396483, 0.90785663],
   [0.24617575, 0.29571802, 0.26836782, 0.57714465, 0.6473269 ]])
```

innernode	
leafnode	
node	

scipy.spatial.cKDTree

class scipy.spatial.**cKDTree**(*data*, *leafsize=16*, *compact_nodes=True*, *copy_data=False*, *balanced_tree=True*, *boxsize=None*)

kd-tree for quick nearest-neighbor lookup

This class provides an index into a set of k-dimensional points which can be used to rapidly look up the nearest neighbors of any point.

Note: *cKDTree* is functionally identical to *KDTree*. Prior to SciPy v1.6.0, *cKDTree* had better performance and slightly different functionality but now the two names exist only for backward-compatibility reasons. If compatibility with SciPy < 1.6 is not a concern, prefer *KDTree*.

Parameters

data [array_like, shape (n,m)] The n data points of dimension m to be indexed. This array is not copied unless this is necessary to produce a contiguous array of doubles, and so modifying this data will result in bogus results. The data are also copied if the kd-tree is built with copy_data=True.

leafsize [positive int, optional] The number of points at which the algorithm switches over to brute-force. Default: 16.

compact_nodes
[bool, optional] If True, the kd-tree is built to shrink the hyperrectangles to the actual data range. This usually gives a more compact tree that is robust against degenerated input data and gives faster queries at the expense of longer build time. Default: True.

copy_data [bool, optional] If True the data is always copied to protect the kd-tree against data corruption. Default: False.

balanced_tree

[bool, optional] If True, the median is used to split the hyperrectangles instead of the midpoint. This usually gives a more compact tree and faster queries at the expense of longer build time. Default: True.

boxsize [array_like or scalar, optional] Apply a m-d toroidal topology to the KDTree.. The topology is generated by $x_i + n_i L_i$ where n_i are integers and L_i is the boxsize along i-th dimension. The input data shall be wrapped into $[0, L_i)$. A ValueError is raised if any of the data is outside of this bound.

Notes

The algorithm used is described in Maneewongvatana and Mount 1999. The general idea is that the kd-tree is a binary tree, each of whose nodes represents an axis-aligned hyperrectangle. Each node specifies an axis and splits the set of points based on whether their coordinate along that axis is greater than or less than a particular value.

During construction, the axis and splitting point are chosen by the "sliding midpoint" rule, which ensures that the cells do not all become long and thin.

The tree can be queried for the r closest neighbors of any given point (optionally returning only those within some maximum distance of the point). It can also be queried, with a substantial gain in efficiency, for the r approximate closest neighbors.

For large dimensions (20 is already large) do not expect this to run significantly faster than brute force. High-dimensional nearest-neighbor queries are a substantial open problem in computer science.

Attributes

data [ndarray, shape (n,m)] The n data points of dimension m to be indexed. This array is not copied unless this is necessary to produce a contiguous array of doubles. The data are also copied if the kd-tree is built with *copy_data=True*.

leafsize [positive int] The number of points at which the algorithm switches over to brute-force.

m [int] The dimension of a single data-point.

n [int] The number of data points.

maxes [ndarray, shape (m,)] The maximum value in each dimension of the n data points.

mins [ndarray, shape (m,)] The minimum value in each dimension of the n data points.

tree [object, class cKDTreeNode] This attribute exposes a Python view of the root node in the cKDTree object. A full Python view of the kd-tree is created dynamically on the first access. This attribute allows you to create your own query functions in Python.

size [int] The number of nodes in the tree.

Methods

count_neighbors(self, other, r[, p, …])	Count how many nearby pairs can be formed.
query(self, x[, k, eps, p, …])	Query the kd-tree for nearest neighbors
query_ball_point(self, x, r[, p, eps, …])	Find all points within distance r of point(s) x.
query_ball_tree(self, other, r[, p, eps])	Find all pairs of points between *self* and *other* whose distance is at most r
query_pairs(self, r[, p, eps])	Find all pairs of points in *self* whose distance is at most r.
sparse_distance_matrix(self, other, max_distance)	Compute a sparse distance matrix

scipy.spatial.cKDTree.count_neighbors

cKDTree.**count_neighbors**(*self*, *other*, *r*, *p=2.*, *weights=None*, *cumulative=True*)

Count how many nearby pairs can be formed.

Count the number of pairs `(x1,x2)` can be formed, with `x1` drawn from `self` and `x2` drawn from `other`, and where `distance(x1, x2, p) <= r`.

Data points on `self` and `other` are optionally weighted by the `weights` argument. (See below)

This is adapted from the "two-point correlation" algorithm described by Gray and Moore [1]. See notes for further discussion.

Parameters

other [cKDTree instance] The other tree to draw points from, can be the same tree as self.

r [float or one-dimensional array of floats] The radius to produce a count for. Multiple radii are searched with a single tree traversal. If the count is non-cumulative(`cumulative=False`), `r` defines the edges of the bins, and must be non-decreasing.

p [float, optional] 1<=p<=infinity. Which Minkowski p-norm to use. Default 2.0. A finite large p may cause a ValueError if overflow can occur.

weights [tuple, array_like, or None, optional] If None, the pair-counting is unweighted. If given as a tuple, weights[0] is the weights of points in `self`, and weights[1] is the weights of points in `other`; either can be None to indicate the points are unweighted. If given as an array_like, weights is the weights of points in `self` and `other`. For this to make sense, `self` and `other` must be the same tree. If `self` and `other` are two different trees, a `ValueError` is raised. Default: None

cumulative [bool, optional] Whether the returned counts are cumulative. When cumulative is set to `False` the algorithm is optimized to work with a large number of bins (>10) specified by `r`. When `cumulative` is set to True, the algorithm is optimized to work with a small number of `r`. Default: True

Returns

result [scalar or 1-D array] The number of pairs. For unweighted counts, the result is integer. For weighted counts, the result is float. If cumulative is False, `result[i]` contains the counts with `(-inf if i == 0 else r[i-1]) < R <= r[i]`

Notes

Pair-counting is the basic operation used to calculate the two point correlation functions from a data set composed of position of objects.

Two point correlation function measures the clustering of objects and is widely used in cosmology to quantify the large scale structure in our Universe, but it may be useful for data analysis in other fields where self-similar assembly of objects also occur.

The Landy-Szalay estimator for the two point correlation function of `D` measures the clustering signal in `D`. [2]

For example, given the position of two sets of objects,

- objects `D` (data) contains the clustering signal, and
- objects `R` (random) that contains no signal,

$$\xi(r) = \frac{< D, D > -2f < D, R > +f^2 < R, R >}{f^2 < R, R >},$$

where the brackets represents counting pairs between two data sets in a finite bin around `r` (distance), corresponding to setting *cumulative=False*, and `f = float(len(D)) / float(len(R))` is the ratio between number of objects from data and random.

The algorithm implemented here is loosely based on the dual-tree algorithm described in [1]. We switch between two different pair-cumulation scheme depending on the setting of `cumulative`. The computing time of the method we use when for `cumulative == False` does not scale with the total number of bins. The algorithm for `cumulative == True` scales linearly with the number of bins, though it is slightly faster when only 1 or 2 bins are used. [5].

As an extension to the naive pair-counting, weighted pair-counting counts the product of weights instead of number of pairs. Weighted pair-counting is used to estimate marked correlation functions ([3], section 2.2), or to properly calculate the average of data per distance bin (e.g. [4], section 2.1 on redshift).

Examples

You can count neighbors number between two kd-trees within a distance:

```
>>> import numpy as np
>>> from scipy.spatial import cKDTree
>>> rng = np.random.default_rng()
>>> points1 = rng.random((5, 2))
>>> points2 = rng.random((5, 2))
>>> kd_tree1 = cKDTree(points1)
>>> kd_tree2 = cKDTree(points2)
>>> kd_tree1.count_neighbors(kd_tree2, 0.2)
1
```

This number is same as the total pair number calculated by *query_ball_tree*:

```
>>> indexes = kd_tree1.query_ball_tree(kd_tree2, r=0.2)
>>> sum([len(i) for i in indexes])
1
```

scipy.spatial.cKDTree.query

`cKDTree.`**`query`**(*self*, *x*, *k=1*, *eps=0*, *p=2*, *distance_upper_bound=np.inf*, *workers=1*)

Query the kd-tree for nearest neighbors

Parameters

x : [array_like, last dimension self.m] An array of points to query.

k : [list of integer or integer] The list of k-th nearest neighbors to return. If k is an integer it is treated as a list of [1, … k] (range(1, k+1)). Note that the counting starts from 1.

eps : [non-negative float] Return approximate nearest neighbors; the k-th returned value is guaranteed to be no further than (1+eps) times the distance to the real k-th nearest neighbor.

p : [float, 1<=p<=infinity] Which Minkowski p-norm to use. 1 is the sum-of-absolute-values “Manhattan” distance 2 is the usual Euclidean distance infinity is the maximum-coordinate-difference distance A finite large p may cause a ValueError if overflow can occur.

distance_upper_bound
: [nonnegative float] Return only neighbors within this distance. This is used to prune tree searches, so if you are doing a series of nearest-neighbor queries, it may help to supply the distance to the nearest neighbor of the most recent point.

workers
: [int, optional] Number of workers to use for parallel processing. If -1 is given all CPU threads are used. Default: 1.
Changed in version 1.6.0: The "n_jobs" argument was renamed "workers". The old name "n_jobs" is deprecated and will stop working in SciPy 1.8.0.

Returns

d
: [array of floats] The distances to the nearest neighbors. If `x` has shape `tuple+(self.m,)`, then `d` has shape `tuple+(k,)`. When k == 1, the last dimension of the output is squeezed. Missing neighbors are indicated with infinite distances.

i
: [ndarray of ints] The index of each neighbor in `self.data`. If `x` has shape `tuple+(self.m,)`, then `i` has shape `tuple+(k,)`. When k == 1, the last dimension of the output is squeezed. Missing neighbors are indicated with `self.n`.

Notes

If the KD-Tree is periodic, the position `x` is wrapped into the box.

When the input k is a list, a query for arange(max(k)) is performed, but only columns that store the requested values of k are preserved. This is implemented in a manner that reduces memory usage.

Examples

```
>>> import numpy as np
>>> from scipy.spatial import cKDTree
>>> x, y = np.mgrid[0:5, 2:8]
>>> tree = cKDTree(np.c_[x.ravel(), y.ravel()])
```

To query the nearest neighbours and return squeezed result, use

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=1)
>>> print(dd, ii)
[2.         0.14142136] [ 0 13]
```

To query the nearest neighbours and return unsqueezed result, use

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=[1])
>>> print(dd, ii)
[[2.        ]
 [0.14142136]] [[ 0]
 [13]]
```

To query the second nearest neighbours and return unsqueezed result, use

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=[2])
>>> print(dd, ii)
[[2.23606798]
 [0.90553851]] [[ 6]
 [12]]
```

To query the first and second nearest neighbours, use

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=2)
>>> print(dd, ii)
[[2.         2.23606798]
 [0.14142136 0.90553851]] [[ 0  6]
 [13 12]]
```

or, be more specific

```
>>> dd, ii = tree.query([[0, 0], [2.1, 2.9]], k=[1, 2])
>>> print(dd, ii)
[[2.         2.23606798]
 [0.14142136 0.90553851]] [[ 0  6]
 [13 12]]
```

scipy.spatial.cKDTree.query_ball_point

cKDTree.**query_ball_point**(*self*, *x*, *r*, *p=2.*, *eps=0*, *workers=1*, *return_sorted=None*, *return_length=False*)

Find all points within distance r of point(s) x.

Parameters

x [array_like, shape tuple + (self.m,)] The point or points to search for neighbors of.

r [array_like, float] The radius of points to return, shall broadcast to the length of x.

p [float, optional] Which Minkowski p-norm to use. Should be in the range [1, inf]. A finite large p may cause a ValueError if overflow can occur.

eps [nonnegative float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than `r / (1 + eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1 + eps)`.

workers [int, optional] Number of jobs to schedule for parallel processing. If -1 is given all processors are used. Default: 1.
Changed in version 1.6.0: The “n_jobs” argument was renamed “workers”. The old name “n_jobs” is deprecated and will stop working in SciPy 1.8.0.

return_sorted
[bool, optional] Sorts returned indicies if True and does not sort them if False. If None, does not sort single point queries, but does sort multi-point queries which was the behavior before this option was added.
New in version 1.2.0.

return_length: bool, optional
Return the number of points inside the radius instead of a list of the indices. .. versionadded:: 1.3.0

Returns

results [list or array of lists] If *x* is a single point, returns a list of the indices of the neighbors of *x*. If *x* is an array of points, returns an object array of shape tuple containing lists of neighbors.

Notes

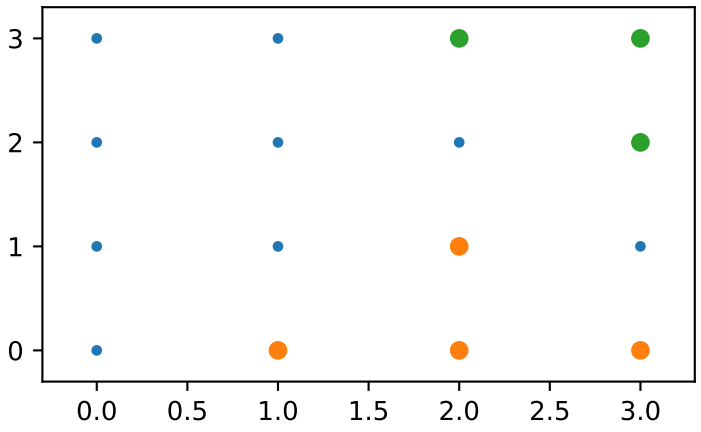
If you have many points whose neighbors you want to find, you may save substantial amounts of time by putting them in a cKDTree and using query_ball_tree.

Examples

```
>>> from scipy import spatial
>>> x, y = np.mgrid[0:4, 0:4]
>>> points = np.c_[x.ravel(), y.ravel()]
>>> tree = spatial.cKDTree(points)
>>> tree.query_ball_point([2, 0], 1)
[4, 8, 9, 12]
```

Query multiple points and plot the results:

```
>>> import matplotlib.pyplot as plt
>>> points = np.asarray(points)
>>> plt.plot(points[:,0], points[:,1], '.')
>>> for results in tree.query_ball_point(([2, 0], [3, 3]), 1):
...     nearby_points = points[results]
...     plt.plot(nearby_points[:,0], nearby_points[:,1], 'o')
>>> plt.margins(0.1, 0.1)
>>> plt.show()
```



scipy.spatial.cKDTree.query_ball_tree

cKDTree.**query_ball_tree**(*self*, *other*, *r*, *p=2.*, *eps=0*)

Find all pairs of points between *self* and *other* whose distance is at most r

Parameters

other [cKDTree instance] The tree containing points to search against.

r [float] The maximum distance, has to be positive.

p [float, optional] Which Minkowski norm to use. *p* has to meet the condition `1 <= p <= infinity`. A finite large p may cause a ValueError if overflow can occur.

eps [float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than `r/(1+eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1+eps)`. *eps* has to be non-negative.

Returns

results [list of lists] For each element `self.data[i]` of this tree, `results[i]` is a list of the indices of its neighbors in `other.data`.

Examples

You can search all pairs of points between two kd-trees within a distance:

```
>>> import matplotlib.pyplot as plt
>>> import numpy as np
>>> from scipy.spatial import cKDTree
>>> rng = np.random.default_rng()
>>> points1 = rng.random((15, 2))
>>> points2 = rng.random((15, 2))
>>> plt.figure(figsize=(6, 6))
>>> plt.plot(points1[:, 0], points1[:, 1], "xk", markersize=14)
>>> plt.plot(points2[:, 0], points2[:, 1], "og", markersize=14)
>>> kd_tree1 = cKDTree(points1)
>>> kd_tree2 = cKDTree(points2)
>>> indexes = kd_tree1.query_ball_tree(kd_tree2, r=0.2)
>>> for i in range(len(indexes)):
...     for j in indexes[i]:
...         plt.plot([points1[i, 0], points2[j, 0]],
...             [points1[i, 1], points2[j, 1]], "-r")
>>> plt.show()
```

scipy.spatial.cKDTree.query_pairs

cKDTree.**query_pairs**(*self*, *r*, *p=2.*, *eps=0*)

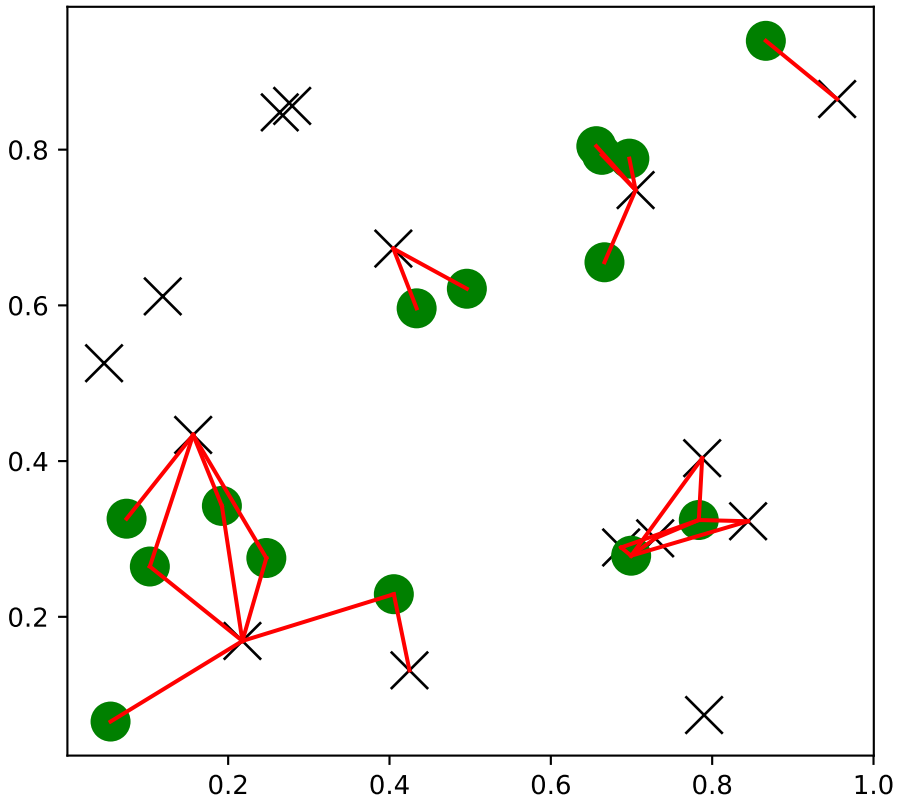
Find all pairs of points in *self* whose distance is at most r.

Parameters

r [positive float] The maximum distance.

p [float, optional] Which Minkowski norm to use. `p` has to meet the condition `1 <= p <= infinity`. A finite large p may cause a ValueError if overflow can occur.

eps [float, optional] Approximate search. Branches of the tree are not explored if their nearest points are further than `r/(1+eps)`, and branches are added in bulk if their furthest points are nearer than `r * (1+eps)`. *eps* has to be non-negative.


0.8
0.6
0.4
0.2
0.2
0.4
0.6
0.8
1.0

output_type
[string, optional] Choose the output container, 'set' or 'ndarray'. Default: 'set'

Returns

results [set or ndarray] Set of pairs `(i,j)`, with `i < j`, for which the corresponding positions are close. If output_type is 'ndarray', an ndarry is returned instead of a set.

Examples

You can search all pairs of points in a kd-tree within a distance:

```
>>> import matplotlib.pyplot as plt
>>> import numpy as np
>>> from scipy.spatial import cKDTree
>>> rng = np.random.default_rng()
>>> points = rng.random((20, 2))
>>> plt.figure(figsize=(6, 6))
>>> plt.plot(points[:, 0], points[:, 1], "xk", markersize=14)
>>> kd_tree = cKDTree(points)
>>> pairs = kd_tree.query_pairs(r=0.2)
>>> for (i, j) in pairs:
...     plt.plot([points[i, 0], points[j, 0]],
...              [points[i, 1], points[j, 1]], "-r")
>>> plt.show()
```

scipy.spatial.cKDTree.sparse_distance_matrix

cKDTree.**sparse_distance_matrix**(*self*, *other*, *max_distance*, *p=2.*)
Compute a sparse distance matrix

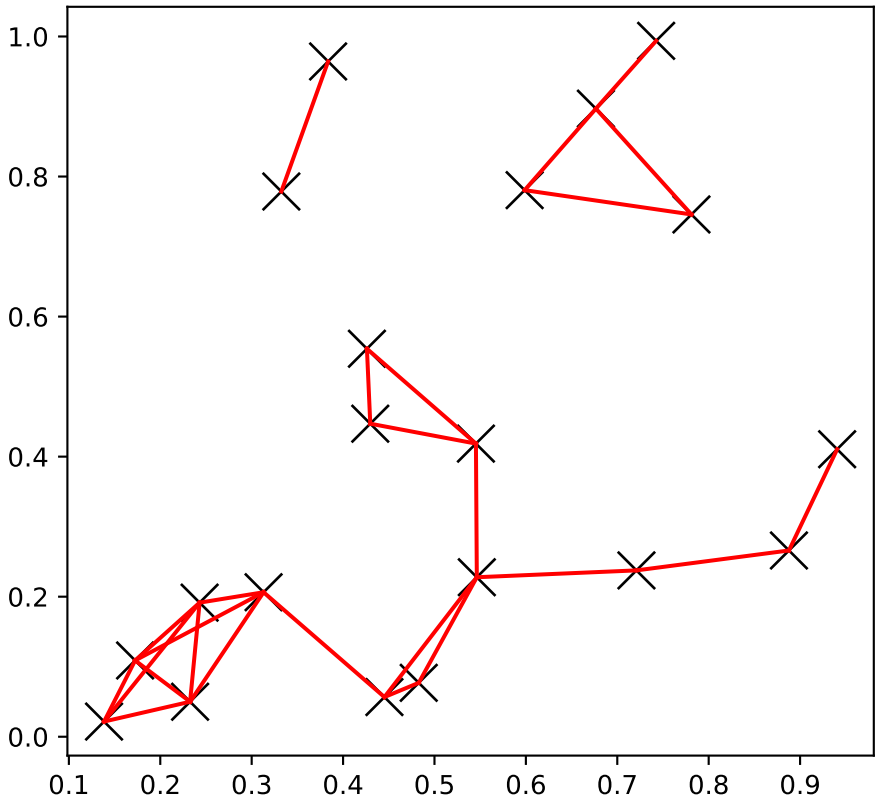
Computes a distance matrix between two cKDTrees, leaving as zero any distance greater than max_distance.

Parameters

other [cKDTree]
max_distance
[positive float]
p [float, 1<=p<=infinity] Which Minkowski p-norm to use. A finite large p may cause a ValueError if overflow can occur.
output_type
[string, optional] Which container to use for output data. Options: 'dok_matrix', 'coo_matrix', 'dict', or 'ndarray'. Default: 'dok_matrix'.

Returns

result [dok_matrix, coo_matrix, dict or ndarray] Sparse matrix representing the results in "dictionary of keys" format. If a dict is returned the keys are (i,j) tuples of indices. If output_type is 'ndarray' a record array with fields 'i', 'j', and 'v' is returned,


1.0
0.8
0.6
0.4
0.2
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9

Examples

You can compute a sparse distance matrix between two kd-trees:

```
>>> import numpy as np
>>> from scipy.spatial import cKDTree
>>> rng = np.random.default_rng()
>>> points1 = rng.random((5, 2))
>>> points2 = rng.random((5, 2))
>>> kd_tree1 = cKDTree(points1)
>>> kd_tree2 = cKDTree(points2)
>>> sdm = kd_tree1.sparse_distance_matrix(kd_tree2, 0.3)
>>> sdm.toarray()
array([[0.        , 0.        , 0.12295571, 0.        , 0.        ],
   [0.        , 0.        , 0.        , 0.        , 0.        ],
   [0.28942611, 0.        , 0.        , 0.2333084 , 0.        ],
   [0.        , 0.        , 0.        , 0.        , 0.        ],
   [0.24617575, 0.29571802, 0.26836782, 0.        , 0.        ]])
```

You can check distances above the *max_distance* are zeros:

```
>>> from scipy.spatial import distance_matrix
>>> distance_matrix(points1, points2)
array([[0.56906522, 0.39923701, 0.12295571, 0.8658745 , 0.79428925],
   [0.37327919, 0.7225693 , 0.87665969, 0.32580855, 0.75679479],
   [0.28942611, 0.30088013, 0.6395831 , 0.2333084 , 0.33630734],
   [0.31994999, 0.72658602, 0.71124834, 0.55396483, 0.90785663],
   [0.24617575, 0.29571802, 0.26836782, 0.57714465, 0.6473269 ]])
```

scipy.spatial.Rectangle

class scipy.spatial.**Rectangle**(*maxes*, *mins*)

Hyperrectangle class.

Represents a Cartesian product of intervals.

Methods

max_distance_point(x[, p])	Return the maximum distance between input and points in the hyperrectangle.
max_distance_rectangle(other[, p])	Compute the maximum distance between points in the two hyperrectangles.
min_distance_point(x[, p])	Return the minimum distance between input and points in the hyperrectangle.
min_distance_rectangle(other[, p])	Compute the minimum distance between points in the two hyperrectangles.
split(d, split)	Produce two hyperrectangles by splitting.
volume()	Total volume.

scipy.spatial.Rectangle.max_distance_point

Rectangle.**max_distance_point**(*x*, *p=2.0*)

Return the maximum distance between input and points in the hyperrectangle.

Parameters

x	[array_like] Input array.
p	[float, optional] Input.

scipy.spatial.Rectangle.max_distance_rectangle

Rectangle.**max_distance_rectangle**(*other*, *p=2.0*)

Compute the maximum distance between points in the two hyperrectangles.

Parameters

other	[hyperrectangle] Input.
p	[float, optional] Input.

scipy.spatial.Rectangle.min_distance_point

Rectangle.**min_distance_point**(*x*, *p=2.0*)

Return the minimum distance between input and points in the hyperrectangle.

Parameters

x	[array_like] Input.
p	[float, optional] Input.

scipy.spatial.Rectangle.min_distance_rectangle

Rectangle.**min_distance_rectangle**(*other*, *p=2.0*)

Compute the minimum distance between points in the two hyperrectangles.

Parameters

other	[hyperrectangle] Input.
p	[float] Input.

scipy.spatial.Rectangle.split

Rectangle.**split**(*d*, *split*)

Produce two hyperrectangles by splitting.

In general, if you need to compute maximum and minimum distances to the children, it can be done more efficiently by updating the maximum and minimum distances to the parent.

Parameters

d	[int] Axis to split hyperrectangle along.
split	[float] Position along axis *d* to split at.

scipy.spatial.Rectangle.volume

Rectangle.**volume**()
Total volume.

Distance metrics are contained in the *scipy.spatial.distance* submodule.

Delaunay triangulation, convex hulls, and Voronoi diagrams

Delaunay(points[, furthest_site, …])	Delaunay tessellation in N dimensions.
ConvexHull(points[, incremental, qhull_options])	Convex hulls in N dimensions.
Voronoi(points[, furthest_site, …])	Voronoi diagrams in N dimensions.
SphericalVoronoi(points[, radius, center, …])	Voronoi diagrams on the surface of a sphere.
HalfspaceIntersection(halfspaces, interior_point)	Halfspace intersections in N dimensions.

scipy.spatial.Delaunay

class scipy.spatial.**Delaunay**(*points*, *furthest_site=False*, *incremental=False*, *qhull_options=None*)
Delaunay tessellation in N dimensions.

New in version 0.9.

Parameters

points [ndarray of floats, shape (npoints, ndim)] Coordinates of points to triangulate

furthest_site
[bool, optional] Whether to compute a furthest-site Delaunay triangulation. Default: False
New in version 0.12.0.

incremental
[bool, optional] Allow adding new points incrementally. This takes up some additional resources.

qhull_options
[str, optional] Additional options to pass to Qhull. See Qhull manual for details. Option "Qt" is always enabled. Default:"Qbb Qc Qz Qx Q12" for ndim > 4 and "Qbb Qc Qz Q12" otherwise. Incremental mode omits "Qz".
New in version 0.12.0.

Raises

QhullError
Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

ValueError
Raised if an incompatible array is given as input.

Notes

The tessellation is computed using the Qhull library Qhull library.

Note: Unless you pass in the Qhull option "QJ", Qhull does not guarantee that each input point appears as a vertex in the Delaunay triangulation. Omitted points are listed in the *coplanar* attribute.

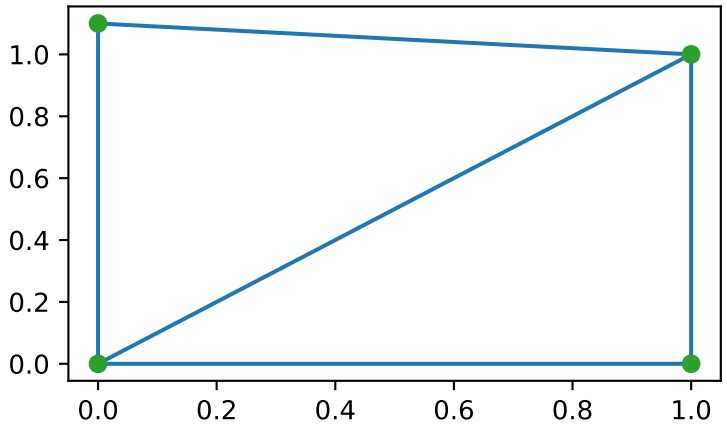
Examples

Triangulation of a set of points:

```
>>> points = np.array([[0, 0], [0, 1.1], [1, 0], [1, 1]])
>>> from scipy.spatial import Delaunay
>>> tri = Delaunay(points)
```

We can plot it:

```
>>> import matplotlib.pyplot as plt
>>> plt.triplot(points[:,0], points[:,1], tri.simplices)
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> plt.show()
```



Point indices and coordinates for the two triangles forming the triangulation:

```
>>> tri.simplices
array([[2, 3, 0],                  # may vary
       [3, 1, 0]], dtype=int32)
```

Note that depending on how rounding errors go, the simplices may be in a different order than above.

```
>>> points[tri.simplices]
array([[[ 1. ,  0. ],             # may vary
```

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```
        [ 1. ,  1. ],
        [ 0. ,  0. ]],
       [[ 1. ,  1. ],
        [ 0. ,  1.1],
        [ 0. ,  0. ]]])
```

Triangle 0 is the only neighbor of triangle 1, and it's opposite to vertex 1 of triangle 1:

```
>>> tri.neighbors[1]
array([-1,  0, -1], dtype=int32)
>>> points[tri.simplices[1,1]]
array([ 0. ,  1.1])
```

We can find out which triangle points are in:

```
>>> p = np.array([(0.1, 0.2), (1.5, 0.5), (0.5, 1.05)])
>>> tri.find_simplex(p)
array([ 1, -1, 1], dtype=int32)
```

The returned integers in the array are the indices of the simplex the corresponding point is in. If -1 is returned, the point is in no simplex. Be aware that the shortcut in the following example only works corretcly for valid points as invalid points result in -1 which is itself a valid index for the last simplex in the list.

```
>>> p_valids = np.array([(0.1, 0.2), (0.5, 1.05)])
>>> tri.simplices[tri.find_simplex(p_valids)]
array([[3, 1, 0],                   # may vary
       [3, 1, 0]], dtype=int32)
```

We can also compute barycentric coordinates in triangle 1 for these points:

```
>>> b = tri.transform[1,:2].dot(np.transpose(p - tri.transform[1,2]))
>>> np.c_[np.transpose(b), 1 - b.sum(axis=0)]
array([[ 0.1       ,  0.09090909,  0.80909091],
       [ 1.5       , -0.90909091,  0.40909091],
       [ 0.5       ,  0.5       ,  0.        ]])
```

The coordinates for the first point are all positive, meaning it is indeed inside the triangle. The third point is on a vertex, hence its null third coordinate.

Attributes

points [ndarray of double, shape (npoints, ndim)] Coordinates of input points.

simplices [ndarray of ints, shape (nsimplex, ndim+1)] Indices of the points forming the simplices in the triangulation. For 2-D, the points are oriented counterclockwise.

neighbors [ndarray of ints, shape (nsimplex, ndim+1)] Indices of neighbor simplices for each simplex. The kth neighbor is opposite to the kth vertex. For simplices at the boundary, -1 denotes no neighbor.

equations [ndarray of double, shape (nsimplex, ndim+2)] [normal, offset] forming the hyperplane equation of the facet on the paraboloid (see Qhull documentation for more).

paraboloid_scale, paraboloid_shift
[float] Scale and shift for the extra paraboloid dimension (see Qhull documentation for more).

`transform`
[ndarray of double, shape (nsimplex, ndim+1, ndim)] Affine transform from `x` to the barycentric coordinates `c`.

vertex_to_simplex
: [ndarray of int, shape (npoints,)] Lookup array, from a vertex, to some simplex which it is a part of.

convex_hull
: [ndarray of int, shape (nfaces, ndim)] Vertices of facets forming the convex hull of the point set.

coplanar
: [ndarray of int, shape (ncoplanar, 3)] Indices of coplanar points and the corresponding indices of the nearest facet and the nearest vertex. Coplanar points are input points which were *not* included in the triangulation due to numerical precision issues.
If option "Qc" is not specified, this list is not computed.
New in version 0.12.0.

vertices
: Same as *simplices*, but deprecated.

vertex_neighbor_vertices
: [tuple of two ndarrays of int; (indptr, indices)] Neighboring vertices of vertices.

furthest_site
: True if this was a furthest site triangulation and False if not.
New in version 1.4.0.

Methods

add_points(points[, restart])	Process a set of additional new points.
close()	Finish incremental processing.
find_simplex(self, xi[, bruteforce, tol])	Find the simplices containing the given points.
lift_points(self, x)	Lift points to the Qhull paraboloid.
plane_distance(self, xi)	Compute hyperplane distances to the point *xi* from all simplices.

scipy.spatial.Delaunay.add_points

Delaunay.**add_points**(*points*, *restart=False*)

Process a set of additional new points.

Parameters

points
: [ndarray] New points to add. The dimensionality should match that of the initial points.

restart
: [bool, optional] Whether to restart processing from scratch, rather than adding points incrementally.

Raises

QhullError
: Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:

close

Notes

You need to specify `incremental=True` when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after *close* has been called.

scipy.spatial.Delaunay.close

`Delaunay.`**`close`**`()`

Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

scipy.spatial.Delaunay.find_simplex

`Delaunay.`**`find_simplex`**(*self*, *xi*, *bruteforce=False*, *tol=None*)

Find the simplices containing the given points.

Parameters

tri	[DelaunayInfo] Delaunay triangulation
xi	[ndarray of double, shape (…, ndim)] Points to locate
bruteforce	[bool, optional] Whether to only perform a brute-force search
tol	[float, optional] Tolerance allowed in the inside-triangle check. Default is `100*eps`.

Returns

i	[ndarray of int, same shape as *xi*] Indices of simplices containing each point. Points outside the triangulation get the value -1.

Notes

This uses an algorithm adapted from Qhull's `qh_findbestfacet`, which makes use of the connection between a convex hull and a Delaunay triangulation. After finding the simplex closest to the point in N+1 dimensions, the algorithm falls back to directed search in N dimensions.

scipy.spatial.Delaunay.lift_points

`Delaunay.`**`lift_points`**(*self*, *x*)

Lift points to the Qhull paraboloid.

scipy.spatial.Delaunay.plane_distance

`Delaunay.`**`plane_distance`**(*self*, *xi*)

Compute hyperplane distances to the point *xi* from all simplices.

scipy.spatial.ConvexHull

class scipy.spatial.**ConvexHull**(*points*, *incremental=False*, *qhull_options=None*)

Convex hulls in N dimensions.

New in version 0.12.0.

Parameters

points [ndarray of floats, shape (npoints, ndim)] Coordinates of points to construct a convex hull from

incremental [bool, optional] Allow adding new points incrementally. This takes up some additional resources.

qhull_options [str, optional] Additional options to pass to Qhull. See Qhull manual for details. (Default: "Qx" for ndim > 4 and "" otherwise) Option "Qt" is always enabled.

Raises

QhullError Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

ValueError Raised if an incompatible array is given as input.

Notes

The convex hull is computed using the Qhull library.

References

[Qhull]

Examples

Convex hull of a random set of points:

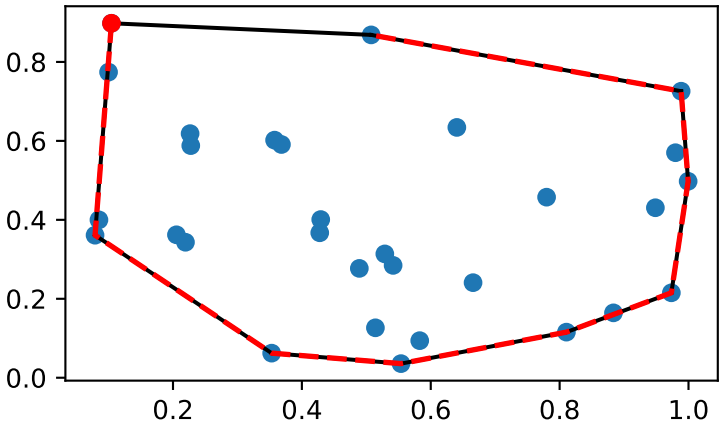
```
>>> from scipy.spatial import ConvexHull, convex_hull_plot_2d
>>> rng = np.random.default_rng()
>>> points = rng.random((30, 2))   # 30 random points in 2-D
>>> hull = ConvexHull(points)
```

Plot it:

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(points[:,0], points[:,1], 'o')
>>> for simplex in hull.simplices:
...     plt.plot(points[simplex, 0], points[simplex, 1], 'k-')
```

We could also have directly used the vertices of the hull, which for 2-D are guaranteed to be in counterclockwise order:

```
>>> plt.plot(points[hull.vertices,0], points[hull.vertices,1], 'r--',␣
↪lw=2)
>>> plt.plot(points[hull.vertices[0],0], points[hull.vertices[0],1], 'ro')
>>> plt.show()
```



Facets visible from a point:

Create a square and add a point above the square.

```
>>> generators = np.array([[0.2, 0.2],
...                        [0.2, 0.4],
...                        [0.4, 0.4],
...                        [0.4, 0.2],
...                        [0.3, 0.6]])
```

Call ConvexHull with the QG option. QG4 means compute the portions of the hull not including point 4, indicating the facets that are visible from point 4.

```
>>> hull = ConvexHull(points=generators,
...                   qhull_options='QG4')
```

The “good” array indicates which facets are visible from point 4.

```
>>> print(hull.simplices)
    [[1 0]
     [1 2]
     [3 0]
     [3 2]]
>>> print(hull.good)
    [False  True False False]
```

Now plot it, highlighting the visible facets.

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(1,1,1)
```

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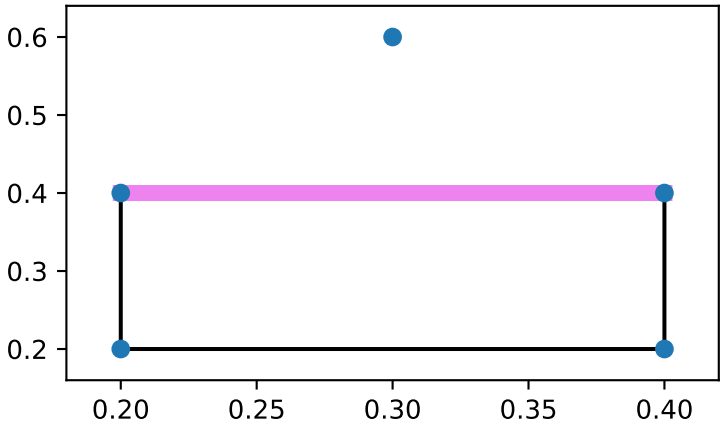
```
>>> for visible_facet in hull.simplices[hull.good]:
...     ax.plot(hull.points[visible_facet, 0],
...             hull.points[visible_facet, 1],
...             color='violet',
...             lw=6)
>>> convex_hull_plot_2d(hull, ax=ax)
    <Figure size 640x480 with 1 Axes> # may vary
>>> plt.show()
```



Attributes

points [ndarray of double, shape (npoints, ndim)] Coordinates of input points.

vertices [ndarray of ints, shape (nvertices,)] Indices of points forming the vertices of the convex hull. For 2-D convex hulls, the vertices are in counterclockwise order. For other dimensions, they are in input order.

simplices [ndarray of ints, shape (nfacet, ndim)] Indices of points forming the simplical facets of the convex hull.

neighbors [ndarray of ints, shape (nfacet, ndim)] Indices of neighbor facets for each facet. The kth neighbor is opposite to the kth vertex. -1 denotes no neighbor.

equations [ndarray of double, shape (nfacet, ndim+1)] [normal, offset] forming the hyperplane equation of the facet (see Qhull documentation for more).

coplanar [ndarray of int, shape (ncoplanar, 3)] Indices of coplanar points and the corresponding indices of the nearest facets and nearest vertex indices. Coplanar points are input points which were *not* included in the triangulation due to numerical precision issues.
If option "Qc" is not specified, this list is not computed.

good [ndarray of bool or None] A one-dimensional Boolean array indicating which facets are good. Used with options that compute good facets, e.g. QGn and QG-n. Good facets are defined as those that are visible (n) or invisible (-n) from point n, where n is the nth point in 'points'. The 'good' attribute may be used as an index into 'simplices' to return the good (visible) facets: simplices[good]. A facet is visible from the outside of the hull only, and neither coplanarity nor degeneracy count as cases of visibility.
If a "QGn" or "QG-n" option is not specified, None is returned.
New in version 1.3.0.

area [float] Surface area of the convex hull when input dimension > 2. When input `points` are 2-dimensional, this is the perimeter of the convex hull.
New in version 0.17.0.

volume [float] Volume of the convex hull when input dimension > 2. When input `points` are 2-dimensional, this is the area of the convex hull.
New in version 0.17.0.

Methods

add_points(points[, restart])	Process a set of additional new points.
close()	Finish incremental processing.

scipy.spatial.ConvexHull.add_points

ConvexHull.**add_points**(*points*, *restart=False*)

Process a set of additional new points.

Parameters

points [ndarray] New points to add. The dimensionality should match that of the initial points.

restart [bool, optional] Whether to restart processing from scratch, rather than adding points incrementally.

Raises

QhullError

Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:

close

Notes

You need to specify `incremental=True` when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after *close* has been called.

scipy.spatial.ConvexHull.close

ConvexHull.**close**()

Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

scipy.spatial.Voronoi

class scipy.spatial.**Voronoi**(*points*, *furthest_site=False*, *incremental=False*, *qhull_options=None*)

Voronoi diagrams in N dimensions.

New in version 0.12.0.

Parameters

points [ndarray of floats, shape (npoints, ndim)] Coordinates of points to construct a Voronoi diagram from

furthest_site
[bool, optional] Whether to compute a furthest-site Voronoi diagram. Default: False

incremental
[bool, optional] Allow adding new points incrementally. This takes up some additional resources.

qhull_options
[str, optional] Additional options to pass to Qhull. See Qhull manual for details. (Default: "Qbb Qc Qz Qx" for ndim > 4 and "Qbb Qc Qz" otherwise. Incremental mode omits "Qz".)

Raises

QhullError
Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

ValueError
Raised if an incompatible array is given as input.

Notes

The Voronoi diagram is computed using the Qhull library.

Examples

Voronoi diagram for a set of point:

```
>>> points = np.array([[0, 0], [0, 1], [0, 2], [1, 0], [1, 1], [1, 2],
...                    [2, 0], [2, 1], [2, 2]])
>>> from scipy.spatial import Voronoi, voronoi_plot_2d
>>> vor = Voronoi(points)
```

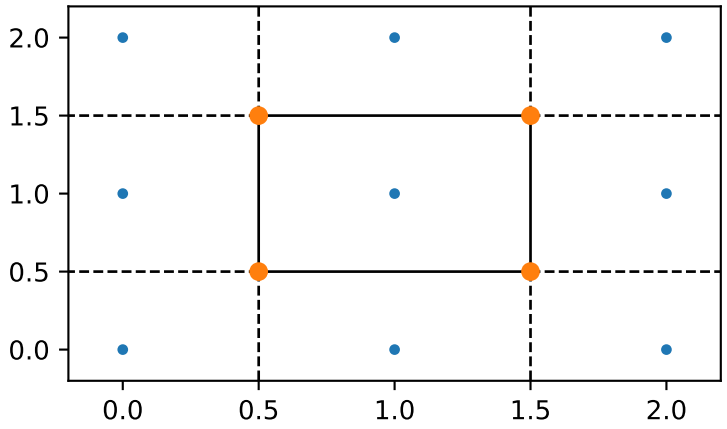
Plot it:

```
>>> import matplotlib.pyplot as plt
>>> fig = voronoi_plot_2d(vor)
>>> plt.show()
```

The Voronoi vertices:

```
>>> vor.vertices
array([[0.5, 0.5],
       [0.5, 1.5],
       [1.5, 0.5],
       [1.5, 1.5]])
```

There is a single finite Voronoi region, and four finite Voronoi ridges:




```
>>> vor.regions
[[], [-1, 0], [-1, 1], [1, -1, 0], [3, -1, 2], [-1, 3], [-1, 2], [0, 1, 3,
 ↪ 2], [2, -1, 0], [3, -1, 1]]
>>> vor.ridge_vertices
[[-1, 0], [-1, 0], [-1, 1], [-1, 1], [0, 1], [-1, 3], [-1, 2], [2, 3], [-
↪1, 3], [-1, 2], [1, 3], [0, 2]]
```

The ridges are perpendicular between lines drawn between the following input points:

```
>>> vor.ridge_points
array([[0, 3],
       [0, 1],
       [2, 5],
       [2, 1],
       [1, 4],
       [7, 8],
       [7, 6],
       [7, 4],
       [8, 5],
       [6, 3],
       [4, 5],
       [4, 3]], dtype=int32)
```

Attributes

points [ndarray of double, shape (npoints, ndim)] Coordinates of input points.
vertices [ndarray of double, shape (nvertices, ndim)] Coordinates of the Voronoi vertices.
ridge_points
[ndarray of ints, shape `(nridges, 2)`] Indices of the points between which each Voronoi ridge lies.
ridge_vertices
[list of list of ints, shape `(nridges, *)`] Indices of the Voronoi vertices forming each Voronoi ridge.

regions [list of list of ints, shape `(nregions, *)`] Indices of the Voronoi vertices forming each Voronoi region. -1 indicates vertex outside the Voronoi diagram.

point_region
[list of ints, shape (npoints)] Index of the Voronoi region for each input point. If qhull option "Qc" was not specified, the list will contain -1 for points that are not associated with a Voronoi region.

furthest_site
True if this was a furthest site triangulation and False if not.
New in version 1.4.0.

Methods

add_points(points[, restart])	Process a set of additional new points.
close()	Finish incremental processing.

scipy.spatial.Voronoi.add_points

Voronoi.**add_points**(*points*, *restart=False*)

Process a set of additional new points.

Parameters

points [ndarray] New points to add. The dimensionality should match that of the initial points.

restart [bool, optional] Whether to restart processing from scratch, rather than adding points incrementally.

Raises

QhullError
Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:

close

Notes

You need to specify `incremental=True` when constructing the object to be able to add points incrementally. Incremental addition of points is also not possible after *close* has been called.

scipy.spatial.Voronoi.close

Voronoi.**close**()

Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

scipy.spatial.SphericalVoronoi

class scipy.spatial.**SphericalVoronoi**(*points*, *radius=1*, *center=None*, *threshold=1e-06*)

Voronoi diagrams on the surface of a sphere.

New in version 0.18.0.

Parameters

points [ndarray of floats, shape (npoints, ndim)] Coordinates of points from which to construct a spherical Voronoi diagram.

radius [float, optional] Radius of the sphere (Default: 1)

center [ndarray of floats, shape (ndim,)] Center of sphere (Default: origin)

threshold [float] Threshold for detecting duplicate points and mismatches between points and sphere parameters. (Default: 1e-06)

Raises

ValueError
If there are duplicates in *points*. If the provided *radius* is not consistent with *points*.

See also:

`Voronoi`

Conventional Voronoi diagrams in N dimensions.

Notes

The spherical Voronoi diagram algorithm proceeds as follows. The Convex Hull of the input points (generators) is calculated, and is equivalent to their Delaunay triangulation on the surface of the sphere [Caroli]. The Convex Hull neighbour information is then used to order the Voronoi region vertices around each generator. The latter approach is substantially less sensitive to floating point issues than angle-based methods of Voronoi region vertex sorting.

Empirical assessment of spherical Voronoi algorithm performance suggests quadratic time complexity (loglinear is optimal, but algorithms are more challenging to implement).

References

[Caroli], [VanOosterom]

Examples

Do some imports and take some points on a cube:

```
>>> import matplotlib.pyplot as plt
>>> from scipy.spatial import SphericalVoronoi, geometric_slerp
>>> from mpl_toolkits.mplot3d import proj3d
>>> # set input data
>>> points = np.array([[0, 0, 1], [0, 0, -1], [1, 0, 0],
...                    [0, 1, 0], [0, -1, 0], [-1, 0, 0], ])
```

Calculate the spherical Voronoi diagram:

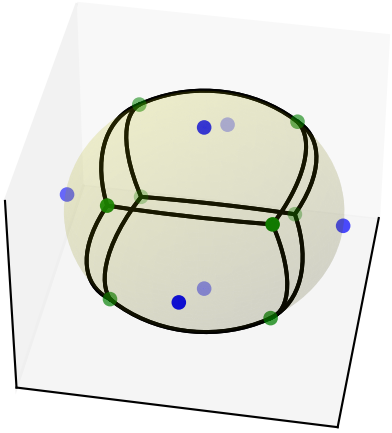
```
>>> radius = 1
>>> center = np.array([0, 0, 0])
>>> sv = SphericalVoronoi(points, radius, center)
```

Generate plot:

```
>>> # sort vertices (optional, helpful for plotting)
>>> sv.sort_vertices_of_regions()
>>> t_vals = np.linspace(0, 1, 2000)
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111, projection='3d')
>>> # plot the unit sphere for reference (optional)
>>> u = np.linspace(0, 2 * np.pi, 100)
>>> v = np.linspace(0, np.pi, 100)
>>> x = np.outer(np.cos(u), np.sin(v))
>>> y = np.outer(np.sin(u), np.sin(v))
>>> z = np.outer(np.ones(np.size(u)), np.cos(v))
>>> ax.plot_surface(x, y, z, color='y', alpha=0.1)
>>> # plot generator points
>>> ax.scatter(points[:, 0], points[:, 1], points[:, 2], c='b')
>>> # plot Voronoi vertices
>>> ax.scatter(sv.vertices[:, 0], sv.vertices[:, 1], sv.vertices[:, 2],
...                    c='g')
>>> # indicate Voronoi regions (as Euclidean polygons)
>>> for region in sv.regions:
...    n = len(region)
...    for i in range(n):
...        start = sv.vertices[region][i]
...        end = sv.vertices[region][(i + 1) % n]
...        result = geometric_slerp(start, end, t_vals)
...        ax.plot(result[..., 0],
...                result[..., 1],
...                result[..., 2],
...                c='k')
>>> ax.azim = 10
>>> ax.elev = 40
>>> _ = ax.set_xticks([])
>>> _ = ax.set_yticks([])
>>> _ = ax.set_zticks([])
>>> fig.set_size_inches(4, 4)
>>> plt.show()
```

Attributes

points	[double array of shape (npoints, ndim)] the points in *ndim* dimensions to generate the Voronoi diagram from
radius	[double] radius of the sphere
center	[double array of shape (ndim,)] center of the sphere
vertices	[double array of shape (nvertices, ndim)] Voronoi vertices corresponding to points
regions	[list of list of integers of shape (npoints, _)] the n-th entry is a list consisting of the indices of the vertices belonging to the n-th point in points



Methods

calculate_areas()	Calculates the areas of the Voronoi regions.

scipy.spatial.SphericalVoronoi.calculate_areas

SphericalVoronoi.**calculate_areas**()

Calculates the areas of the Voronoi regions.

For 2D point sets, the regions are circular arcs. The sum of the areas is *2 * pi * radius*.

For 3D point sets, the regions are spherical polygons. The sum of the areas is *4 * pi * radius**2*.

New in version 1.5.0.

Returns

areas [double array of shape (npoints,)] The areas of the Voronoi regions.

scipy.spatial.HalfspaceIntersection

class scipy.spatial.**HalfspaceIntersection**(*halfspaces*, *interior_point*, *incremental=False*, *qhull_options=None*)

Halfspace intersections in N dimensions.

New in version 0.19.0.

Parameters

halfspaces [ndarray of floats, shape (nineq, ndim+1)] Stacked Inequalities of the form Ax + b <= 0 in format [A; b]

interior_point [ndarray of floats, shape (ndim,)] Point clearly inside the region defined by halfspaces. Also called a feasible point, it can be obtained by linear programming.

incremental [bool, optional] Allow adding new halfspaces incrementally. This takes up some additional resources.

Notes

The intersections are computed using the Qhull library. This reproduces the "qhalf" functionality of Qhull.

References

[Qhull], [1]

Examples

Halfspace intersection of planes forming some polygon

```
>>> from scipy.spatial import HalfspaceIntersection
>>> halfspaces = np.array([[-1, 0., 0.],
...                        [0., -1., 0.],
...                        [2., 1., -4.],
...                        [-0.5, 1., -2.]])
>>> feasible_point = np.array([0.5, 0.5])
>>> hs = HalfspaceIntersection(halfspaces, feasible_point)
```

Plot halfspaces as filled regions and intersection points:

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax = fig.add_subplot(1, 1, 1, aspect='equal')
>>> xlim, ylim = (-1, 3), (-1, 3)
>>> ax.set_xlim(xlim)
>>> ax.set_ylim(ylim)
>>> x = np.linspace(-1, 3, 100)
>>> symbols = ['-', '+', 'x', '*']
>>> signs = [0, 0, -1, -1]
>>> fmt = {"color": None, "edgecolor": "b", "alpha": 0.5}
>>> for h, sym, sign in zip(halfspaces, symbols, signs):
...     hlist = h.tolist()
...     fmt["hatch"] = sym
...     if h[1]== 0:
...         ax.axvline(-h[2]/h[0], label='{}x+{}y+{}=0'.format(*hlist))
...         xi = np.linspace(xlim[sign], -h[2]/h[0], 100)
...         ax.fill_between(xi, ylim[0], ylim[1], **fmt)
...     else:
...         ax.plot(x, (-h[2]-h[0]*x)/h[1], label='{}x+{}y+{}=0'.
↪format(*hlist))
...         ax.fill_between(x, (-h[2]-h[0]*x)/h[1], ylim[sign], **fmt)
>>> x, y = zip(*hs.intersections)
>>> ax.plot(x, y, 'o', markersize=8)
```

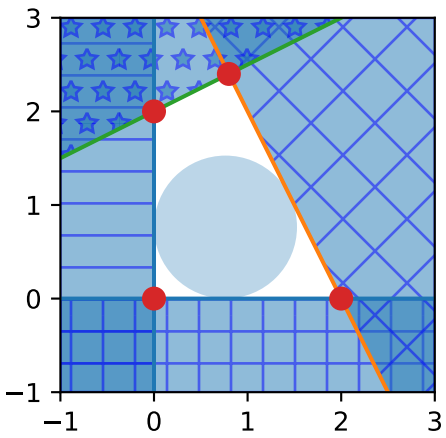
By default, qhull does not provide with a way to compute an interior point. This can easily be computed using linear programming. Considering halfspaces of the form $Ax + b \leq 0$, solving the linear program:

$$max\ y$$
$$s.t. Ax + y||A_i|| \leq -b$$

With A_i being the rows of A, i.e. the normals to each plane.

Will yield a point x that is furthest inside the convex polyhedron. To be precise, it is the center of the largest hypersphere of radius y inscribed in the polyhedron. This point is called the Chebyshev center of the polyhedron (see [1] 4.3.1, pp148-149). The equations outputted by Qhull are always normalized.

```
>>> from scipy.optimize import linprog
>>> from matplotlib.patches import Circle
>>> norm_vector = np.reshape(np.linalg.norm(halfspaces[:, :-1], axis=1),
...     (halfspaces.shape[0], 1))
>>> c = np.zeros((halfspaces.shape[1],))
>>> c[-1] = -1
>>> A = np.hstack((halfspaces[:, :-1], norm_vector))
>>> b = - halfspaces[:, -1:]
>>> res = linprog(c, A_ub=A, b_ub=b, bounds=(None, None))
>>> x = res.x[:-1]
>>> y = res.x[-1]
>>> circle = Circle(x, radius=y, alpha=0.3)
>>> ax.add_patch(circle)
>>> plt.legend(bbox_to_anchor=(1.6, 1.0))
>>> plt.show()
```



Attributes

halfspaces [ndarray of double, shape (nineq, ndim+1)] Input halfspaces.

interior_point :ndarray of floats, shape (ndim,)
Input interior point.

intersections
[ndarray of double, shape (ninter, ndim)] Intersections of all halfspaces.

dual_points
[ndarray of double, shape (nineq, ndim)] Dual points of the input halfspaces.

dual_facets
[list of lists of ints] Indices of points forming the (non necessarily simplicial) facets of the dual convex hull.

dual_vertices

[ndarray of ints, shape (nvertices,)] Indices of halfspaces forming the vertices of the dual convex hull. For 2-D convex hulls, the vertices are in counterclockwise order. For other dimensions, they are in input order.

dual_equations
[ndarray of double, shape (nfacet, ndim+1)] [normal, offset] forming the hyperplane equation of the dual facet (see Qhull documentation for more).

dual_area [float] Area of the dual convex hull

dual_volume
[float] Volume of the dual convex hull

Methods

add_halfspaces(halfspaces[, restart])	Process a set of additional new halfspaces.
close()	Finish incremental processing.

scipy.spatial.HalfspaceIntersection.add_halfspaces

HalfspaceIntersection.**add_halfspaces**(*halfspaces*, *restart=False*)

Process a set of additional new halfspaces.

Parameters

halfspaces [ndarray] New halfspaces to add. The dimensionality should match that of the initial halfspaces.

restart [bool, optional] Whether to restart processing from scratch, rather than adding halfspaces incrementally.

Raises

QhullError
Raised when Qhull encounters an error condition, such as geometrical degeneracy when options to resolve are not enabled.

See also:

close

Notes

You need to specify `incremental=True` when constructing the object to be able to add halfspaces incrementally. Incremental addition of halfspaces is also not possible after *close* has been called.

scipy.spatial.HalfspaceIntersection.close

HalfspaceIntersection.**close**()

Finish incremental processing.

Call this to free resources taken up by Qhull, when using the incremental mode. After calling this, adding more points is no longer possible.

Plotting helpers

delaunay_plot_2d(tri[, ax])	Plot the given Delaunay triangulation in 2-D
convex_hull_plot_2d(hull[, ax])	Plot the given convex hull diagram in 2-D
voronoi_plot_2d(vor[, ax])	Plot the given Voronoi diagram in 2-D

scipy.spatial.delaunay_plot_2d

scipy.spatial.**delaunay_plot_2d**(*tri*, *ax=None*)

Plot the given Delaunay triangulation in 2-D

Parameters

tri [scipy.spatial.Delaunay instance] Triangulation to plot

ax [matplotlib.axes.Axes instance, optional] Axes to plot on

Returns

fig [matplotlib.figure.Figure instance] Figure for the plot

See also:

Delaunay

matplotlib.pyplot.triplot

Notes

Requires Matplotlib.

Examples

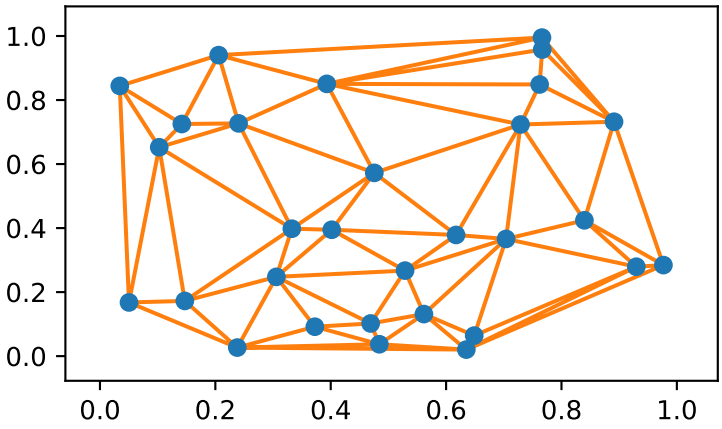
```
>>> import matplotlib.pyplot as plt
>>> from scipy.spatial import Delaunay, delaunay_plot_2d
```

The Delaunay triangulation of a set of random points:

```
>>> rng = np.random.default_rng()
>>> points = rng.random((30, 2))
>>> tri = Delaunay(points)
```

Plot it:

```
>>> _ = delaunay_plot_2d(tri)
>>> plt.show()
```



scipy.spatial.convex_hull_plot_2d

scipy.spatial.**convex_hull_plot_2d**(*hull*, *ax=None*)

Plot the given convex hull diagram in 2-D

Parameters

hull	[scipy.spatial.ConvexHull instance] Convex hull to plot
ax	[matplotlib.axes.Axes instance, optional] Axes to plot on

Returns

fig	[matplotlib.figure.Figure instance] Figure for the plot

See also:

`ConvexHull`

Notes

Requires Matplotlib.

Examples

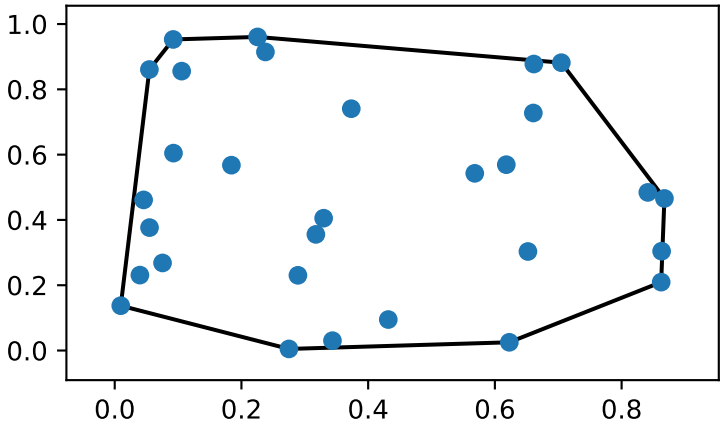
```
>>> import matplotlib.pyplot as plt
>>> from scipy.spatial import ConvexHull, convex_hull_plot_2d
```

The convex hull of a random set of points:

```
>>> rng = np.random.default_rng()
>>> points = rng.random((30, 2))
>>> hull = ConvexHull(points)
```

Plot it:

```
>>> _ = convex_hull_plot_2d(hull)
>>> plt.show()
```



scipy.spatial.voronoi_plot_2d

scipy.spatial.**voronoi_plot_2d**(*vor*, *ax=None*, ***kw*)

Plot the given Voronoi diagram in 2-D

Parameters

vor [scipy.spatial.Voronoi instance] Diagram to plot

ax [matplotlib.axes.Axes instance, optional] Axes to plot on

show_points: bool, optional
Add the Voronoi points to the plot.

show_vertices
[bool, optional] Add the Voronoi vertices to the plot.

line_colors
[string, optional] Specifies the line color for polygon boundaries

line_width [float, optional] Specifies the line width for polygon boundaries

line_alpha: float, optional
Specifies the line alpha for polygon boundaries

point_size: float, optional
Specifies the size of points

Returns

fig [matplotlib.figure.Figure instance] Figure for the plot

See also:

Voronoi

Notes

Requires Matplotlib.

Examples

Set of point:

```
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> points = rng.random((10,2))
```

Voronoi diagram of the points:

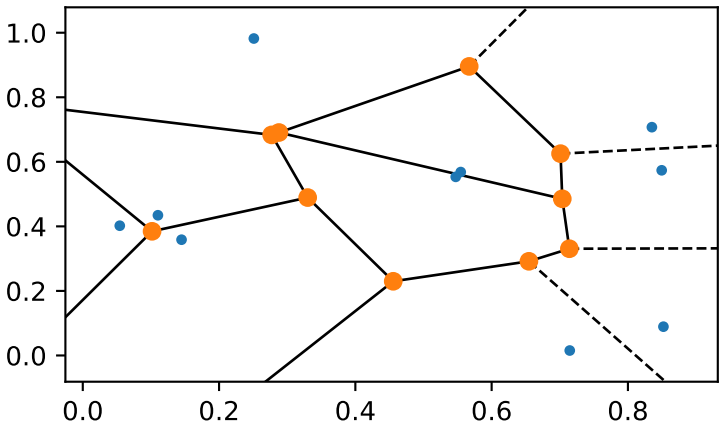
```
>>> from scipy.spatial import Voronoi, voronoi_plot_2d
>>> vor = Voronoi(points)
```

using *voronoi_plot_2d* for visualisation:

```
>>> fig = voronoi_plot_2d(vor)
```

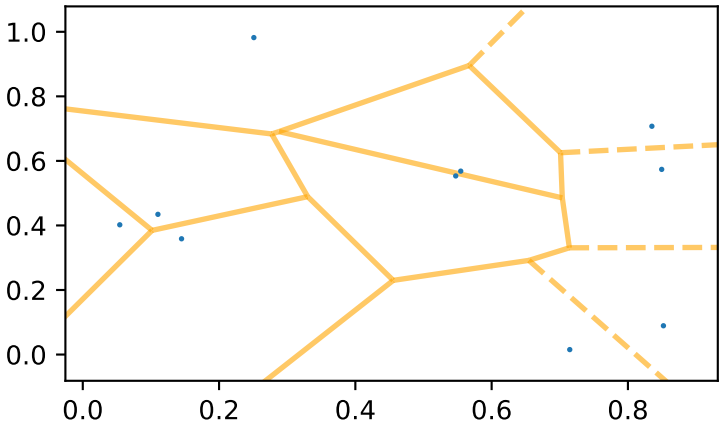
using *voronoi_plot_2d* for visualisation with enhancements:

```
>>> fig = voronoi_plot_2d(vor, show_vertices=False, line_colors='orange',
...                       line_width=2, line_alpha=0.6, point_size=2)
>>> plt.show()
```



See also:

Tutorial



Simplex representation

The simplices (triangles, tetrahedra, etc.) appearing in the Delaunay tessellation (N-D simplices), convex hull facets, and Voronoi ridges (N-1-D simplices) are represented in the following scheme:

```
tess = Delaunay(points)
hull = ConvexHull(points)
voro = Voronoi(points)

# coordinates of the jth vertex of the ith simplex
tess.points[tess.simplices[i, j], :]        # tessellation element
hull.points[hull.simplices[i, j], :]        # convex hull facet
voro.vertices[voro.ridge_vertices[i, j], :] # ridge between Voronoi cells
```

For Delaunay triangulations and convex hulls, the neighborhood structure of the simplices satisfies the condition: `tess.neighbors[i,j]` is the neighboring simplex of the ith simplex, opposite to the `j`-vertex. It is -1 in case of no neighbor.

Convex hull facets also define a hyperplane equation:

```
(hull.equations[i,:-1] * coord).sum() + hull.equations[i,-1] == 0
```

Similar hyperplane equations for the Delaunay triangulation correspond to the convex hull facets on the corresponding N+1-D paraboloid.

The Delaunay triangulation objects offer a method for locating the simplex containing a given point, and barycentric coordinate computations.

Functions

tsearch(tri, xi)	Find simplices containing the given points.
distance_matrix(x, y[, p, threshold])	Compute the distance matrix.
minkowski_distance(x, y[, p])	Compute the L**p distance between two arrays.
minkowski_distance_p(x, y[, p])	Compute the pth power of the L**p distance between two arrays.
procrustes(data1, data2)	Procrustes analysis, a similarity test for two data sets.
geometric_slerp(start, end, t[, tol])	Geometric spherical linear interpolation.

scipy.spatial.tsearch

scipy.spatial.**tsearch**(*tri*, *xi*)

Find simplices containing the given points. This function does the same thing as *Delaunay.find_simplex*.

New in version 0.9.

See also:

Delaunay.find_simplex

Examples

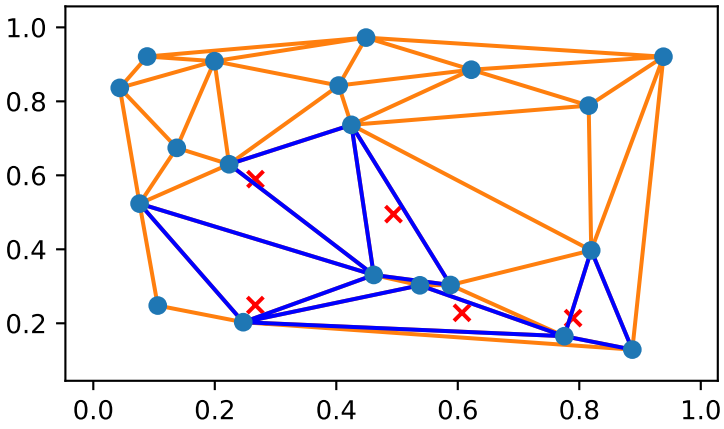
```
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy.spatial import Delaunay, delaunay_plot_2d, tsearch
>>> rng = np.random.default_rng()
```

The Delaunay triangulation of a set of random points:

```
>>> pts = rng.random((20, 2))
>>> tri = Delaunay(pts)
>>> _ = delaunay_plot_2d(tri)
```

Find the simplices containing a given set of points:

```
>>> loc = rng.uniform(0.2, 0.8, (5, 2))
>>> s = tsearch(tri, loc)
>>> plt.triplot(pts[:, 0], pts[:, 1], tri.simplices[s], 'b-', mask=s==-1)
>>> plt.scatter(loc[:, 0], loc[:, 1], c='r', marker='x')
>>> plt.show()
```



scipy.spatial.distance_matrix

scipy.spatial.**distance_matrix**(*x*, *y*, *p=2*, *threshold=1000000*)

Compute the distance matrix.

Returns the matrix of all pair-wise distances.

Parameters

x	[(M, K) array_like] Matrix of M vectors in K dimensions.
y	[(N, K) array_like] Matrix of N vectors in K dimensions.
p	[float, 1 <= p <= infinity] Which Minkowski p-norm to use.
threshold	[positive int] If `M * N * K` > *threshold*, algorithm uses a Python loop instead of large temporary arrays.

Returns

result	[(M, N) ndarray] Matrix containing the distance from every vector in *x* to every vector in *y*.

Examples

```
>>> from scipy.spatial import distance_matrix
>>> distance_matrix([[0,0],[0,1]], [[1,0],[1,1]])
array([[ 1.        ,  1.41421356],
       [ 1.41421356,  1.        ]])
```

scipy.spatial.minkowski_distance

scipy.spatial.**minkowski_distance**(*x*, *y*, *p=2*)

Compute the L**p distance between two arrays.

Parameters

x	[(M, K) array_like] Input array.
y	[(N, K) array_like] Input array.
p	[float, 1 <= p <= infinity] Which Minkowski p-norm to use.

Examples

```
>>> from scipy.spatial import minkowski_distance
>>> minkowski_distance([[0,0],[0,0]], [[1,1],[0,1]])
array([ 1.41421356,  1.        ])
```

scipy.spatial.minkowski_distance_p

scipy.spatial.**minkowski_distance_p**(*x*, *y*, *p=2*)

Compute the pth power of the L**p distance between two arrays.

For efficiency, this function computes the L**p distance but does not extract the pth root. If *p* is 1 or infinity, this is equal to the actual L**p distance.

Parameters

x	[(M, K) array_like] Input array.
y	[(N, K) array_like] Input array.
p	[float, 1 <= p <= infinity] Which Minkowski p-norm to use.

Examples

```
>>> from scipy.spatial import minkowski_distance_p
>>> minkowski_distance_p([[0,0],[0,0]], [[1,1],[0,1]])
array([2, 1])
```

scipy.spatial.procrustes

scipy.spatial.**procrustes**(*data1*, *data2*)

Procrustes analysis, a similarity test for two data sets.

Each input matrix is a set of points or vectors (the rows of the matrix). The dimension of the space is the number of columns of each matrix. Given two identically sized matrices, procrustes standardizes both such that:

- $tr(AA^T) = 1$.
- Both sets of points are centered around the origin.

Procrustes ([1], [2]) then applies the optimal transform to the second matrix (including scaling/dilation, rotations, and reflections) to minimize $M^2 = \sum(data1 - data2)^2$, or the sum of the squares of the pointwise differences between the two input datasets.

This function was not designed to handle datasets with different numbers of datapoints (rows). If two data sets have different dimensionality (different number of columns), simply add columns of zeros to the smaller of the two.

Parameters

data1 [array_like] Matrix, n rows represent points in k (columns) space *data1* is the reference data, after it is standardised, the data from *data2* will be transformed to fit the pattern in *data1* (must have >1 unique points).

data2 [array_like] n rows of data in k space to be fit to *data1*. Must be the same shape `(numrows, numcols)` as data1 (must have >1 unique points).

Returns

mtx1 [array_like] A standardized version of *data1*.

mtx2 [array_like] The orientation of *data2* that best fits *data1*. Centered, but not necessarily $tr(AA^T) = 1$.

disparity [float] M^2 as defined above.

Raises

ValueError If the input arrays are not two-dimensional. If the shape of the input arrays is different. If the input arrays have zero columns or zero rows.

See also:

`scipy.linalg.orthogonal_procrustes`

`scipy.spatial.distance.directed_hausdorff`

Another similarity test for two data sets

Notes

- The disparity should not depend on the order of the input matrices, but the output matrices will, as only the first output matrix is guaranteed to be scaled such that $tr(AA^T) = 1$.
- Duplicate data points are generally ok, duplicating a data point will increase its effect on the procrustes fit.
- The disparity scales as the number of points per input matrix.

References

[1], [2]

Examples

```
>>> from scipy.spatial import procrustes
```

The matrix `b` is a rotated, shifted, scaled and mirrored version of `a` here:

```
>>> a = np.array([[1, 3], [1, 2], [1, 1], [2, 1]], 'd')
>>> b = np.array([[4, -2], [4, -4], [4, -6], [2, -6]], 'd')
>>> mtx1, mtx2, disparity = procrustes(a, b)
>>> round(disparity)
0.0
```

scipy.spatial.geometric_slerp

scipy.spatial.**geometric_slerp**(*start*, *end*, *t*, *tol=1e-07*)

Geometric spherical linear interpolation.

The interpolation occurs along a unit-radius great circle arc in arbitrary dimensional space.

Parameters

start [(n_dimensions,) array-like] Single n-dimensional input coordinate in a 1-D array-like object. *n* must be greater than 1.

end [(n_dimensions,) array-like] Single n-dimensional input coordinate in a 1-D array-like object. *n* must be greater than 1.

t: float or (n_points,) array-like
A float or array-like of doubles representing interpolation parameters, with values required in the inclusive interval between 0 and 1. A common approach is to generate the array with `np.linspace(0, 1, n_pts)` for linearly spaced points. Ascending, descending, and scrambled orders are permitted.

tol: float The absolute tolerance for determining if the start and end coordinates are antipodes.

Returns

result [(t.size, D)] An array of doubles containing the interpolated spherical path and including start and end when 0 and 1 t are used. The interpolated values should correspond to the same sort order provided in the t array. The result may be 1-dimensional if `t` is a float.

Raises

ValueError
If `start` and `end` are antipodes, not on the unit n-sphere, or for a variety of degenerate conditions.

See also:

scipy.spatial.transform.Slerp

3-D Slerp that works with quaternions

Notes

The implementation is based on the mathematical formula provided in [1], and the first known presentation of this algorithm, derived from study of 4-D geometry, is credited to Glenn Davis in a footnote of the original quaternion Slerp publication by Ken Shoemake [2].

New in version 1.5.0.

References

[1], [2]

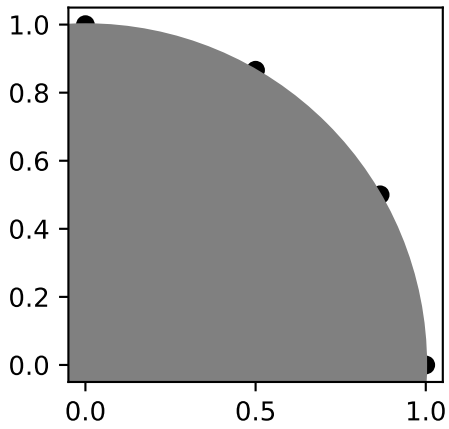
Examples

Interpolate four linearly-spaced values on the circumference of a circle spanning 90 degrees:

```
>>> from scipy.spatial import geometric_slerp
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> start = np.array([1, 0])
>>> end = np.array([0, 1])
>>> t_vals = np.linspace(0, 1, 4)
>>> result = geometric_slerp(start,
...                          end,
...                          t_vals)
```

The interpolated results should be at 30 degree intervals recognizable on the unit circle:

```
>>> ax.scatter(result[...,0], result[...,1], c='k')
>>> circle = plt.Circle((0, 0), 1, color='grey')
>>> ax.add_artist(circle)
>>> ax.set_aspect('equal')
>>> plt.show()
```



Attempting to interpolate between antipodes on a circle is ambiguous because there are two possible paths, and on a sphere there are infinite possible paths on the geodesic surface. Nonetheless, one of the ambiguous paths is returned along with a warning:

```
>>> opposite_pole = np.array([-1, 0])
>>> with np.testing.suppress_warnings() as sup:
...     sup.filter(UserWarning)
...     geometric_slerp(start,
...                     opposite_pole,
...                     t_vals)
array([[ 1.00000000e+00,  0.00000000e+00],
```

(continues on next page)

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```
       [ 5.00000000e-01,  8.66025404e-01],
       [-5.00000000e-01,  8.66025404e-01],
       [-1.00000000e+00,  1.22464680e-16]])
```

Extend the original example to a sphere and plot interpolation points in 3D:

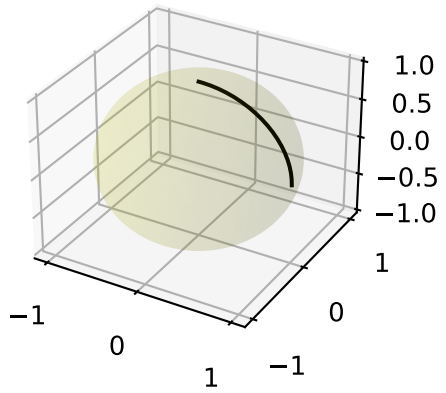
```
>>> from mpl_toolkits.mplot3d import proj3d
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111, projection='3d')
```

Plot the unit sphere for reference (optional):

```
>>> u = np.linspace(0, 2 * np.pi, 100)
>>> v = np.linspace(0, np.pi, 100)
>>> x = np.outer(np.cos(u), np.sin(v))
>>> y = np.outer(np.sin(u), np.sin(v))
>>> z = np.outer(np.ones(np.size(u)), np.cos(v))
>>> ax.plot_surface(x, y, z, color='y', alpha=0.1)
```

Interpolating over a larger number of points may provide the appearance of a smooth curve on the surface of the sphere, which is also useful for discretized integration calculations on a sphere surface:

```
>>> start = np.array([1, 0, 0])
>>> end = np.array([0, 0, 1])
>>> t_vals = np.linspace(0, 1, 200)
>>> result = geometric_slerp(start,
...                          end,
...                          t_vals)
>>> ax.plot(result[...,0],
...         result[...,1],
...         result[...,2],
...         c='k')
>>> plt.show()
```



3.3.27 Distance computations (scipy.spatial.distance)

Function reference

Distance matrix computation from a collection of raw observation vectors stored in a rectangular array.

pdist(X[, metric, out])	Pairwise distances between observations in n-dimensional space.
cdist(XA, XB[, metric, out])	Compute distance between each pair of the two collections of inputs.
squareform(X[, force, checks])	Convert a vector-form distance vector to a square-form distance matrix, and vice-versa.
directed_hausdorff(u, v[, seed])	Compute the directed Hausdorff distance between two N-D arrays.

scipy.spatial.distance.pdist

scipy.spatial.distance.**pdist**(*X*, *metric='euclidean'*, ***, *out=None*, ***kwargs*)

Pairwise distances between observations in n-dimensional space.

See Notes for common calling conventions.

Parameters

X [array_like] An m by n array of m original observations in an n-dimensional space.

metric [str or function, optional] The distance metric to use. The distance function can be 'braycurtis', 'canberra', 'chebyshev', 'cityblock', 'correlation', 'cosine', 'dice', 'euclidean', 'hamming', 'jaccard', 'jensenshannon', 'kulsinski', 'mahalanobis', 'matching', 'minkowski', 'rogerstanimoto', 'russellrao', 'seuclidean', 'sokalmichener', 'sokalsneath', 'sqeuclidean', 'yule'.

****kwargs** [dict, optional] Extra arguments to *metric*: refer to each metric documentation for a list of all possible arguments.
Some possible arguments:
p : scalar The p-norm to apply for Minkowski, weighted and unweighted. Default: 2.
w : ndarray The weight vector for metrics that support weights (e.g., Minkowski).
V : ndarray The variance vector for standardized Euclidean. Default: var(X, axis=0, ddof=1)
VI : ndarray The inverse of the covariance matrix for Mahalanobis. Default: inv(cov(X.T)).T
out : ndarray. The output array If not None, condensed distance matrix Y is stored in this array.

Returns

Y [ndarray] Returns a condensed distance matrix Y. For each i and j (where $i < j < m$),where m is the number of original observations. The metric `dist(u=X[i], v=X[j])` is computed and stored in entry `m * i + j - ((i + 2) * (i + 1)) // 2`.

See also:

squareform

converts between condensed distance matrices and square distance matrices.

Notes

See `squareform` for information on how to calculate the index of this entry or to convert the condensed distance matrix to a redundant square matrix.

The following are common calling conventions.

1. `Y = pdist(X, 'euclidean')`

   Computes the distance between m points using Euclidean distance (2-norm) as the distance metric between the points. The points are arranged as m n-dimensional row vectors in the matrix X.

2. `Y = pdist(X, 'minkowski', p=2.)`

   Computes the distances using the Minkowski distance $||u-v||_p$ (p-norm) where $p \geq 1$.

3. `Y = pdist(X, 'cityblock')`

   Computes the city block or Manhattan distance between the points.

4. `Y = pdist(X, 'seuclidean', V=None)`

   Computes the standardized Euclidean distance. The standardized Euclidean distance between two n-vectors `u` and `v` is

   $$\sqrt{\sum (u_i - v_i)^2 / V[x_i]}$$

   V is the variance vector; V[i] is the variance computed over all the i'th components of the points. If not passed, it is automatically computed.

5. `Y = pdist(X, 'sqeuclidean')`

   Computes the squared Euclidean distance $||u-v||_2^2$ between the vectors.

6. `Y = pdist(X, 'cosine')`

   Computes the cosine distance between vectors u and v,

   $$1 - \frac{u \cdot v}{||u||_2 ||v||_2}$$

   where $||*||_2$ is the 2-norm of its argument `*`, and $u \cdot v$ is the dot product of `u` and `v`.

7. `Y = pdist(X, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

   $$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{||(u - \bar{u})||_2 ||(v - \bar{v})||_2}$$

   where $\bar{v}$ is the mean of the elements of vector v, and $x \cdot y$ is the dot product of x and y.

8. `Y = pdist(X, 'hamming')`

   Computes the normalized Hamming distance, or the proportion of those vector elements between two n-vectors `u` and `v` which disagree. To save memory, the matrix `X` can be of type boolean.

9. `Y = pdist(X, 'jaccard')`

   Computes the Jaccard distance between the points. Given two vectors, `u` and `v`, the Jaccard distance is the proportion of those elements `u[i]` and `v[i]` that disagree.

10. `Y = pdist(X, 'jensenshannon')`

Computes the Jensen-Shannon distance between two probability arrays. Given two probability vectors, p and q, the Jensen-Shannon distance is

$$\sqrt{\frac{D(p \parallel m) + D(q \parallel m)}{2}}$$

where m is the pointwise mean of p and q and D is the Kullback-Leibler divergence.

11. `Y = pdist(X, 'chebyshev')`

    Computes the Chebyshev distance between the points. The Chebyshev distance between two n-vectors `u` and `v` is the maximum norm-1 distance between their respective elements. More precisely, the distance is given by

    $$d(u, v) = \max_i |u_i - v_i|$$

12. `Y = pdist(X, 'canberra')`

    Computes the Canberra distance between the points. The Canberra distance between two points `u` and `v` is

    $$d(u, v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}$$

13. `Y = pdist(X, 'braycurtis')`

    Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points `u` and `v` is

    $$d(u, v) = \frac{\sum_i |u_i - v_i|}{\sum_i |u_i + v_i|}$$

14. `Y = pdist(X, 'mahalanobis', VI=None)`

    Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points `u` and `v` is $\sqrt{(u - v)(1/V)(u - v)^T}$ where $(1/V)$ (the `VI` variable) is the inverse covariance. If `VI` is not None, `VI` will be used as the inverse covariance matrix.

15. `Y = pdist(X, 'yule')`

    Computes the Yule distance between each pair of boolean vectors. (see yule function documentation)

16. `Y = pdist(X, 'matching')`

    Synonym for 'hamming'.

17. `Y = pdist(X, 'dice')`

    Computes the Dice distance between each pair of boolean vectors. (see dice function documentation)

18. `Y = pdist(X, 'kulsinski')`

    Computes the Kulsinski distance between each pair of boolean vectors. (see kulsinski function documentation)

19. `Y = pdist(X, 'rogerstanimoto')`

    Computes the Rogers-Tanimoto distance between each pair of boolean vectors. (see rogerstanimoto function documentation)

20. `Y = pdist(X, 'russellrao')`

    Computes the Russell-Rao distance between each pair of boolean vectors. (see russellrao function documentation)

21. `Y = pdist(X, 'sokalmichener')`

    Computes the Sokal-Michener distance between each pair of boolean vectors. (see sokalmichener function documentation)

22. `Y = pdist(X, 'sokalsneath')`

    Computes the Sokal-Sneath distance between each pair of boolean vectors. (see sokalsneath function documentation)

23. `Y = pdist(X, 'wminkowski', p=2, w=w)`

    Computes the weighted Minkowski distance between each pair of vectors. (see wminkowski function documentation)

    'wminkowski' is deprecated and will be removed in SciPy 1.8.0. Use 'minkowski' instead.

24. `Y = pdist(X, f)`

    Computes the distance between all pairs of vectors in X using the user supplied 2-arity function f. For example, Euclidean distance between the vectors could be computed as follows:

    ```
    dm = pdist(X, lambda u, v: np.sqrt(((u-v)**2).sum()))
    ```

    Note that you should avoid passing a reference to one of the distance functions defined in this library. For example,:

    ```
    dm = pdist(X, sokalsneath)
    ```

    would calculate the pair-wise distances between the vectors in X using the Python function sokalsneath. This would result in sokalsneath being called $\binom{n}{2}$ times, which is inefficient. Instead, the optimized C version is more efficient, and we call it using the following syntax.:

    ```
    dm = pdist(X, 'sokalsneath')
    ```

scipy.spatial.distance.cdist

scipy.spatial.distance.**cdist**(*XA*, *XB*, *metric='euclidean'*, ***, *out=None*, ***kwargs*)

Compute distance between each pair of the two collections of inputs.

See Notes for common calling conventions.

Parameters

XA [array_like] An m_A by n array of m_A original observations in an n-dimensional space. Inputs are converted to float type.

XB [array_like] An m_B by n array of m_B original observations in an n-dimensional space. Inputs are converted to float type.

metric [str or callable, optional] The distance metric to use. If a string, the distance function can be 'braycurtis', 'canberra', 'chebyshev', 'cityblock', 'correlation', 'cosine', 'dice', 'euclidean', 'hamming', 'jaccard', 'jensenshannon', 'kulsinski', 'mahalanobis', 'matching', 'minkowski', 'rogerstanimoto', 'russellrao', 'seuclidean', 'sokalmichener', 'sokalsneath', 'sqeuclidean', 'wminkowski', 'yule'.

****kwargs** [dict, optional] Extra arguments to *metric*: refer to each metric documentation for a list of all possible arguments.
Some possible arguments:
p : scalar The p-norm to apply for Minkowski, weighted and unweighted. Default: 2.
w : array_like The weight vector for metrics that support weights (e.g., Minkowski).
V : array_like The variance vector for standardized Euclidean. Default: var(vstack([XA, XB]), axis=0, ddof=1)

VI : array_like The inverse of the covariance matrix for Mahalanobis. Default: inv(cov(vstack([XA, XB].T))).T
out : ndarray The output array If not None, the distance matrix Y is stored in this array.

Returns

Y [ndarray] A m_A by m_B distance matrix is returned. For each i and j, the metric `dist(u=XA[i], v=XB[j])` is computed and stored in the ij th entry.

Raises

ValueError
An exception is thrown if *XA* and *XB* do not have the same number of columns.

Notes

The following are common calling conventions:

1. `Y = cdist(XA, XB, 'euclidean')`

   Computes the distance between m points using Euclidean distance (2-norm) as the distance metric between the points. The points are arranged as m n-dimensional row vectors in the matrix X.

2. `Y = cdist(XA, XB, 'minkowski', p=2.)`

   Computes the distances using the Minkowski distance $||u-v||_p$ (p-norm) where $p \geq 1$.

3. `Y = cdist(XA, XB, 'cityblock')`

   Computes the city block or Manhattan distance between the points.

4. `Y = cdist(XA, XB, 'seuclidean', V=None)`

   Computes the standardized Euclidean distance. The standardized Euclidean distance between two n-vectors `u` and `v` is

   $$\sqrt{\sum (u_i - v_i)^2 / V[x_i]}.$$

   V is the variance vector; V[i] is the variance computed over all the i'th components of the points. If not passed, it is automatically computed.

5. `Y = cdist(XA, XB, 'sqeuclidean')`

   Computes the squared Euclidean distance $||u-v||_2^2$ between the vectors.

6. `Y = cdist(XA, XB, 'cosine')`

   Computes the cosine distance between vectors u and v,

   $$1 - \frac{u \cdot v}{||u||_2 ||v||_2}$$

   where $||*||_2$ is the 2-norm of its argument `*`, and $u \cdot v$ is the dot product of u and v.

7. `Y = cdist(XA, XB, 'correlation')`

   Computes the correlation distance between vectors u and v. This is

   $$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{||(u - \bar{u})||_2 ||(v - \bar{v})||_2}$$

   where $\bar{v}$ is the mean of the elements of vector v, and $x \cdot y$ is the dot product of x and y.

8. `Y = cdist(XA, XB, 'hamming')`

   Computes the normalized Hamming distance, or the proportion of those vector elements between two n-vectors `u` and `v` which disagree. To save memory, the matrix `X` can be of type boolean.

9. `Y = cdist(XA, XB, 'jaccard')`

   Computes the Jaccard distance between the points. Given two vectors, `u` and `v`, the Jaccard distance is the proportion of those elements `u[i]` and `v[i]` that disagree where at least one of them is non-zero.

10. `Y = cdist(XA, XB, 'jensenshannon')`

    Computes the Jensen-Shannon distance between two probability arrays. Given two probability vectors, p and q, the Jensen-Shannon distance is

    $$\sqrt{\frac{D(p \parallel m) + D(q \parallel m)}{2}}$$

    where m is the pointwise mean of p and q and D is the Kullback-Leibler divergence.

11. `Y = cdist(XA, XB, 'chebyshev')`

    Computes the Chebyshev distance between the points. The Chebyshev distance between two n-vectors `u` and `v` is the maximum norm-1 distance between their respective elements. More precisely, the distance is given by

    $$d(u, v) = \max_i |u_i - v_i|.$$

12. `Y = cdist(XA, XB, 'canberra')`

    Computes the Canberra distance between the points. The Canberra distance between two points `u` and `v` is

    $$d(u, v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}.$$

13. `Y = cdist(XA, XB, 'braycurtis')`

    Computes the Bray-Curtis distance between the points. The Bray-Curtis distance between two points `u` and `v` is

    $$d(u, v) = \frac{\sum_i (|u_i - v_i|)}{\sum_i (|u_i + v_i|)}$$

14. `Y = cdist(XA, XB, 'mahalanobis', VI=None)`

    Computes the Mahalanobis distance between the points. The Mahalanobis distance between two points `u` and `v` is $\sqrt{(u - v)(1/V)(u - v)^T}$ where $(1/V)$ (the `VI` variable) is the inverse covariance. If `VI` is not None, `VI` will be used as the inverse covariance matrix.

15. `Y = cdist(XA, XB, 'yule')`

    Computes the Yule distance between the boolean vectors. (see *yule* function documentation)

16. `Y = cdist(XA, XB, 'matching')`

    Synonym for 'hamming'.

17. `Y = cdist(XA, XB, 'dice')`

    Computes the Dice distance between the boolean vectors. (see *dice* function documentation)

18. `Y = cdist(XA, XB, 'kulsinski')`

    Computes the Kulsinski distance between the boolean vectors. (see *kulsinski* function documentation)

19. `Y = cdist(XA, XB, 'rogerstanimoto')`

    Computes the Rogers-Tanimoto distance between the boolean vectors. (see *rogerstanimoto* function documentation)

20. `Y = cdist(XA, XB, 'russellrao')`

    Computes the Russell-Rao distance between the boolean vectors. (see *russellrao* function documentation)

21. `Y = cdist(XA, XB, 'sokalmichener')`

    Computes the Sokal-Michener distance between the boolean vectors. (see *sokalmichener* function documentation)

22. `Y = cdist(XA, XB, 'sokalsneath')`

    Computes the Sokal-Sneath distance between the vectors. (see *sokalsneath* function documentation)

23. `Y = cdist(XA, XB, 'wminkowski', p=2., w=w)`

    Computes the weighted Minkowski distance between the vectors. (see *wminkowski* function documentation)

    'wminkowski' is deprecated and will be removed in SciPy 1.8.0. Use 'minkowski' instead.

24. `Y = cdist(XA, XB, f)`

    Computes the distance between all pairs of vectors in X using the user supplied 2-arity function f. For example, Euclidean distance between the vectors could be computed as follows:

    ```
    dm = cdist(XA, XB, lambda u, v: np.sqrt(((u-v)**2).sum()))
    ```

    Note that you should avoid passing a reference to one of the distance functions defined in this library. For example,:

    ```
    dm = cdist(XA, XB, sokalsneath)
    ```

    would calculate the pair-wise distances between the vectors in X using the Python function *sokalsneath*. This would result in sokalsneath being called $\binom{n}{2}$ times, which is inefficient. Instead, the optimized C version is more efficient, and we call it using the following syntax:

    ```
    dm = cdist(XA, XB, 'sokalsneath')
    ```

Examples

Find the Euclidean distances between four 2-D coordinates:

```
>>> from scipy.spatial import distance
>>> coords = [(35.0456, -85.2672),
...           (35.1174, -89.9711),
...           (35.9728, -83.9422),
...           (36.1667, -86.7833)]
>>> distance.cdist(coords, coords, 'euclidean')
array([[ 0.    ,  4.7044,  1.6172,  1.8856],
       [ 4.7044,  0.    ,  6.0893,  3.3561],
       [ 1.6172,  6.0893,  0.    ,  2.8477],
       [ 1.8856,  3.3561,  2.8477,  0.    ]])
```

Find the Manhattan distance from a 3-D point to the corners of the unit cube:

```
>>> a = np.array([[0, 0, 0],
...               [0, 0, 1],
...               [0, 1, 0],
...               [0, 1, 1],
...               [1, 0, 0],
...               [1, 0, 1],
...               [1, 1, 0],
...               [1, 1, 1]])
>>> b = np.array([[ 0.1,  0.2,  0.4]])
>>> distance.cdist(a, b, 'cityblock')
array([[ 0.7],
       [ 0.9],
       [ 1.3],
       [ 1.5],
       [ 1.5],
       [ 1.7],
       [ 2.1],
       [ 2.3]])
```

scipy.spatial.distance.squareform

scipy.spatial.distance.**squareform**(*X*, *force='no'*, *checks=True*)

Convert a vector-form distance vector to a square-form distance matrix, and vice-versa.

Parameters

X [array_like] Either a condensed or redundant distance matrix.

force [str, optional] As with MATLAB(TM), if force is equal to `'tovector'` or `'tomatrix'`, the input will be treated as a distance matrix or distance vector respectively.

checks [bool, optional] If set to False, no checks will be made for matrix symmetry nor zero diagonals. This is useful if it is known that `X - X.T1` is small and `diag(X)` is close to zero. These values are ignored any way so they do not disrupt the squareform transformation.

Returns

Y [ndarray] If a condensed distance matrix is passed, a redundant one is returned, or if a redundant one is passed, a condensed distance matrix is returned.

Notes

1. `v = squareform(X)`

   Given a square n-by-n symmetric distance matrix `X`, `v = squareform(X)` returns a `n * (n-1) / 2` (i.e. binomial coefficient n choose 2) sized vector *v* where $v[\binom{n}{2} - \binom{n-i}{2} + (j - i - 1)]$ is the distance between distinct points `i` and `j`. If `X` is non-square or asymmetric, an error is raised.

2. `X = squareform(v)`

   Given a `n * (n-1) / 2` sized vector `v` for some integer `n >= 1` encoding distances as described, `X = squareform(v)` returns a n-by-n distance matrix `X`. The `X[i, j]` and `X[j, i]` values are set to $v[\binom{n}{2} - \binom{n-i}{2} + (j - i - 1)]$ and all diagonal elements are zero.

In SciPy 0.19.0, `squareform` stopped casting all input types to float64, and started returning arrays of the same dtype as the input.

scipy.spatial.distance.directed_hausdorff

scipy.spatial.distance.**directed_hausdorff**(*u*, *v*, *seed=0*)

Compute the directed Hausdorff distance between two N-D arrays.

Distances between pairs are calculated using a Euclidean metric.

Parameters

u	[(M,N) array_like] Input array.
v	[(O,N) array_like] Input array.
seed	[int or None] Local `numpy.random.RandomState` seed. Default is 0, a random shuffling of u and v that guarantees reproducibility.

Returns

d	[double] The directed Hausdorff distance between arrays *u* and *v*,
index_1	[int] index of point contributing to Hausdorff pair in *u*
index_2	[int] index of point contributing to Hausdorff pair in *v*

Raises

ValueError
An exception is thrown if *u* and *v* do not have the same number of columns.

See also:

scipy.spatial.procrustes

Another similarity test for two data sets

Notes

Uses the early break technique and the random sampling approach described by [1]. Although worst-case performance is `O(m * o)` (as with the brute force algorithm), this is unlikely in practice as the input data would have to require the algorithm to explore every single point interaction, and after the algorithm shuffles the input points at that. The best case performance is O(m), which is satisfied by selecting an inner loop distance that is less than cmax and leads to an early break as often as possible. The authors have formally shown that the average runtime is closer to O(m).

New in version 0.19.0.

References

[1]

Examples

Find the directed Hausdorff distance between two 2-D arrays of coordinates:

```
>>> from scipy.spatial.distance import directed_hausdorff
>>> u = np.array([(1.0, 0.0),
...               (0.0, 1.0),
...               (-1.0, 0.0),
...               (0.0, -1.0)])
>>> v = np.array([(2.0, 0.0),
```

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```
...                 (0.0, 2.0),
...                 (-2.0, 0.0),
...                 (0.0, -4.0)])
```

```
>>> directed_hausdorff(u, v)[0]
2.23606797749979
>>> directed_hausdorff(v, u)[0]
3.0
```

Find the general (symmetric) Hausdorff distance between two 2-D arrays of coordinates:

```
>>> max(directed_hausdorff(u, v)[0], directed_hausdorff(v, u)[0])
3.0
```

Find the indices of the points that generate the Hausdorff distance (the Hausdorff pair):

```
>>> directed_hausdorff(v, u)[1:]
(3, 3)
```

Predicates for checking the validity of distance matrices, both condensed and redundant. Also contained in this module are functions for computing the number of observations in a distance matrix.

is_valid_dm(D[, tol, throw, name, warning])	Return True if input array is a valid distance matrix.
is_valid_y(y[, warning, throw, name])	Return True if the input array is a valid condensed distance matrix.
num_obs_dm(d)	Return the number of original observations that correspond to a square, redundant distance matrix.
num_obs_y(Y)	Return the number of original observations that correspond to a condensed distance matrix.

scipy.spatial.distance.is_valid_dm

scipy.spatial.distance.**is_valid_dm**(*D*, *tol=0.0*, *throw=False*, *name='D'*, *warning=False*)

Return True if input array is a valid distance matrix.

Distance matrices must be 2-dimensional numpy arrays. They must have a zero-diagonal, and they must be symmetric.

Parameters

D	[array_like] The candidate object to test for validity.
tol	[float, optional] The distance matrix should be symmetric. *tol* is the maximum difference between entries `ij` and `ji` for the distance metric to be considered symmetric.
throw	[bool, optional] An exception is thrown if the distance matrix passed is not valid.
name	[str, optional] The name of the variable to checked. This is useful if throw is set to True so the offending variable can be identified in the exception message when an exception is thrown.
warning	[bool, optional] Instead of throwing an exception, a warning message is raised.

Returns

valid	[bool] True if the variable *D* passed is a valid distance matrix.

Notes

Small numerical differences in *D* and *D.T* and non-zeroness of the diagonal are ignored if they are within the tolerance specified by *tol*.

scipy.spatial.distance.is_valid_y

scipy.spatial.distance.**is_valid_y**(*y*, *warning=False*, *throw=False*, *name=None*)

Return True if the input array is a valid condensed distance matrix.

Condensed distance matrices must be 1-dimensional numpy arrays. Their length must be a binomial coefficient $\binom{n}{2}$ for some positive integer n.

Parameters

y [array_like] The condensed distance matrix.

warning [bool, optional] Invokes a warning if the variable passed is not a valid condensed distance matrix. The warning message explains why the distance matrix is not valid. *name* is used when referencing the offending variable.

throw [bool, optional] Throws an exception if the variable passed is not a valid condensed distance matrix.

name [bool, optional] Used when referencing the offending variable in the warning or exception message.

scipy.spatial.distance.num_obs_dm

scipy.spatial.distance.**num_obs_dm**(*d*)

Return the number of original observations that correspond to a square, redundant distance matrix.

Parameters

d [array_like] The target distance matrix.

Returns

num_obs_dm

[int] The number of observations in the redundant distance matrix.

scipy.spatial.distance.num_obs_y

scipy.spatial.distance.**num_obs_y**(*Y*)

Return the number of original observations that correspond to a condensed distance matrix.

Parameters

Y [array_like] Condensed distance matrix.

Returns

n [int] The number of observations in the condensed distance matrix *Y*.

Distance functions between two numeric vectors `u` and `v`. Computing distances over a large collection of vectors is inefficient for these functions. Use `pdist` for this purpose.

braycurtis(u, v[, w])	Compute the Bray-Curtis distance between two 1-D arrays.
canberra(u, v[, w])	Compute the Canberra distance between two 1-D arrays.
chebyshev(u, v[, w])	Compute the Chebyshev distance.
cityblock(u, v[, w])	Compute the City Block (Manhattan) distance.

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correlation(u, v[, w, centered])	Compute the correlation distance between two 1-D arrays.
cosine(u, v[, w])	Compute the Cosine distance between 1-D arrays.
euclidean(u, v[, w])	Computes the Euclidean distance between two 1-D arrays.
jensenshannon(p, q[, base, axis, keepdims])	Compute the Jensen-Shannon distance (metric) between two probability arrays.
mahalanobis(u, v, VI)	Compute the Mahalanobis distance between two 1-D arrays.
minkowski(u, v[, p, w])	Compute the Minkowski distance between two 1-D arrays.
seuclidean(u, v, V)	Return the standardized Euclidean distance between two 1-D arrays.
sqeuclidean(u, v[, w])	Compute the squared Euclidean distance between two 1-D arrays.
wminkowski(u, v, p, w)	Compute the weighted Minkowski distance between two 1-D arrays.

scipy.spatial.distance.braycurtis

scipy.spatial.distance.**braycurtis**(*u*, *v*, *w=None*)

Compute the Bray-Curtis distance between two 1-D arrays.

Bray-Curtis distance is defined as

$$\sum |u_i - v_i| / \sum |u_i + v_i|$$

The Bray-Curtis distance is in the range [0, 1] if all coordinates are positive, and is undefined if the inputs are of length zero.

Parameters

u [(N,) array_like] Input array.

v [(N,) array_like] Input array.

w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

braycurtis [double] The Bray-Curtis distance between 1-D arrays *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.braycurtis([1, 0, 0], [0, 1, 0])
1.0
>>> distance.braycurtis([1, 1, 0], [0, 1, 0])
0.33333333333333331
```

scipy.spatial.distance.canberra

scipy.spatial.distance.**canberra**(*u*, *v*, *w=None*)

Compute the Canberra distance between two 1-D arrays.

The Canberra distance is defined as

$$d(u,v) = \sum_i \frac{|u_i - v_i|}{|u_i| + |v_i|}.$$

Parameters

u	[(N,) array_like] Input array.
v	[(N,) array_like] Input array.
w	[(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

canberra	[double] The Canberra distance between vectors *u* and *v*.

Notes

When *u[i]* and *v[i]* are 0 for given i, then the fraction 0/0 = 0 is used in the calculation.

Examples

```
>>> from scipy.spatial import distance
>>> distance.canberra([1, 0, 0], [0, 1, 0])
2.0
>>> distance.canberra([1, 1, 0], [0, 1, 0])
1.0
```

scipy.spatial.distance.chebyshev

scipy.spatial.distance.**chebyshev**(*u*, *v*, *w=None*)

Compute the Chebyshev distance.

Computes the Chebyshev distance between two 1-D arrays *u* and *v*, which is defined as

$$\max_i |u_i - v_i|.$$

Parameters

u	[(N,) array_like] Input vector.
v	[(N,) array_like] Input vector.
w	[(N,) array_like, optional] Unused, as 'max' is a weightless operation. Here for API consistency.

Returns

chebyshev	[double] The Chebyshev distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.chebyshev([1, 0, 0], [0, 1, 0])
1
>>> distance.chebyshev([1, 1, 0], [0, 1, 0])
1
```

scipy.spatial.distance.cityblock

scipy.spatial.distance.**cityblock**(*u*, *v*, *w=None*)

Compute the City Block (Manhattan) distance.

Computes the Manhattan distance between two 1-D arrays *u* and *v*, which is defined as

$$\sum_i |u_i - v_i|.$$

Parameters

u [(N,) array_like] Input array.

v [(N,) array_like] Input array.

w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

cityblock [double] The City Block (Manhattan) distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.cityblock([1, 0, 0], [0, 1, 0])
2
>>> distance.cityblock([1, 0, 0], [0, 2, 0])
3
>>> distance.cityblock([1, 0, 0], [1, 1, 0])
1
```

scipy.spatial.distance.correlation

scipy.spatial.distance.**correlation**(*u*, *v*, *w=None*, *centered=True*)

Compute the correlation distance between two 1-D arrays.

The correlation distance between *u* and *v*, is defined as

$$1 - \frac{(u - \bar{u}) \cdot (v - \bar{v})}{||(u - \bar{u})||_2 ||(v - \bar{v})||_2}$$

where $\bar{u}$ is the mean of the elements of *u* and $x \cdot y$ is the dot product of x and y.

Parameters

u [(N,) array_like] Input array.

v [(N,) array_like] Input array.

w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

centered [bool, optional] If True, *u* and *v* will be centered. Default is True.

Returns

correlation
[double] The correlation distance between 1-D array *u* and *v*.

scipy.spatial.distance.cosine

scipy.spatial.distance.**cosine**(*u*, *v*, *w=None*)
Compute the Cosine distance between 1-D arrays.

The Cosine distance between *u* and *v*, is defined as

$$1 - \frac{u \cdot v}{||u||_2||v||_2}.$$

where $u \cdot v$ is the dot product of u and v.

Parameters

u [(N,) array_like] Input array.
v [(N,) array_like] Input array.
w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

cosine [double] The Cosine distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.cosine([1, 0, 0], [0, 1, 0])
1.0
>>> distance.cosine([100, 0, 0], [0, 1, 0])
1.0
>>> distance.cosine([1, 1, 0], [0, 1, 0])
0.29289321881345254
```

scipy.spatial.distance.euclidean

scipy.spatial.distance.**euclidean**(*u*, *v*, *w=None*)
Computes the Euclidean distance between two 1-D arrays.

The Euclidean distance between 1-D arrays *u* and *v*, is defined as

$$\frac{||u - v||_2}{\left(\sum (w_i|(u_i - v_i)|^2)\right)^{1/2}}$$

Parameters

u [(N,) array_like] Input array.
v [(N,) array_like] Input array.
w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

euclidean [double] The Euclidean distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.euclidean([1, 0, 0], [0, 1, 0])
1.4142135623730951
>>> distance.euclidean([1, 1, 0], [0, 1, 0])
1.0
```

scipy.spatial.distance.jensenshannon

scipy.spatial.distance.**jensenshannon**(*p*, *q*, *base=None*, ***, *axis=0*, *keepdims=False*)

Compute the Jensen-Shannon distance (metric) between two probability arrays. This is the square root of the Jensen-Shannon divergence.

The Jensen-Shannon distance between two probability vectors p and q is defined as,

$$\sqrt{\frac{D(p \parallel m) + D(q \parallel m)}{2}}$$

where m is the pointwise mean of p and q and D is the Kullback-Leibler divergence.

This routine will normalize p and q if they don't sum to 1.0.

Parameters

p [(N,) array_like] left probability vector

q [(N,) array_like] right probability vector

base [double, optional] the base of the logarithm used to compute the output if not given, then the routine uses the default base of scipy.stats.entropy.

axis [int, optional] Axis along which the Jensen-Shannon distances are computed. The default is 0.
New in version 1.7.0.

keepdims [bool, optional] If this is set to *True*, the reduced axes are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array. Default is False.
New in version 1.7.0.

Returns

js [double or ndarray] The Jensen-Shannon distances between p and q along the *axis*.

Notes

New in version 1.2.0.

Examples

```
>>> from scipy.spatial import distance
>>> distance.jensenshannon([1.0, 0.0, 0.0], [0.0, 1.0, 0.0], 2.0)
1.0
>>> distance.jensenshannon([1.0, 0.0], [0.5, 0.5])
0.46450140402245893
>>> distance.jensenshannon([1.0, 0.0, 0.0], [1.0, 0.0, 0.0])
0.0
>>> a = np.array([[1, 2, 3, 4],
```

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```
...                [5, 6, 7, 8],
...                [9, 10, 11, 12]])
>>> b = np.array([[13, 14, 15, 16],
...                [17, 18, 19, 20],
...                [21, 22, 23, 24]])
>>> distance.jensenshannon(a, b, axis=0)
array([0.1954288, 0.1447697, 0.1138377, 0.0927636])
>>> distance.jensenshannon(a, b, axis=1)
array([0.1402339, 0.0399106, 0.0201815])
```

scipy.spatial.distance.mahalanobis

scipy.spatial.distance.**mahalanobis**(*u*, *v*, *VI*)

Compute the Mahalanobis distance between two 1-D arrays.

The Mahalanobis distance between 1-D arrays *u* and *v*, is defined as

$$\sqrt{(u-v)V^{-1}(u-v)^T}$$

where V is the covariance matrix. Note that the argument *VI* is the inverse of V.

Parameters

u	[(N,) array_like] Input array.
v	[(N,) array_like] Input array.
VI	[array_like] The inverse of the covariance matrix.

Returns

mahalanobis
: [double] The Mahalanobis distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> iv = [[1, 0.5, 0.5], [0.5, 1, 0.5], [0.5, 0.5, 1]]
>>> distance.mahalanobis([1, 0, 0], [0, 1, 0], iv)
1.0
>>> distance.mahalanobis([0, 2, 0], [0, 1, 0], iv)
1.0
>>> distance.mahalanobis([2, 0, 0], [0, 1, 0], iv)
1.7320508075688772
```

scipy.spatial.distance.minkowski

scipy.spatial.distance.**minkowski**(*u*, *v*, *p=2*, *w=None*)

Compute the Minkowski distance between two 1-D arrays.

The Minkowski distance between 1-D arrays *u* and *v*, is defined as

$$||u-v||_p = (\sum |u_i - v_i|^p)^{1/p}.$$
$$\left(\sum w_i(|(u_i - v_i)|^p)\right)^{1/p}.$$

Parameters

u [(N,) array_like] Input array.
v [(N,) array_like] Input array.
p [scalar] The order of the norm of the difference $||u - v||_p$.
w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

minkowski
[double] The Minkowski distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.minkowski([1, 0, 0], [0, 1, 0], 1)
2.0
>>> distance.minkowski([1, 0, 0], [0, 1, 0], 2)
1.4142135623730951
>>> distance.minkowski([1, 0, 0], [0, 1, 0], 3)
1.2599210498948732
>>> distance.minkowski([1, 1, 0], [0, 1, 0], 1)
1.0
>>> distance.minkowski([1, 1, 0], [0, 1, 0], 2)
1.0
>>> distance.minkowski([1, 1, 0], [0, 1, 0], 3)
1.0
```

scipy.spatial.distance.seuclidean

scipy.spatial.distance.**seuclidean**(*u*, *v*, *V*)
Return the standardized Euclidean distance between two 1-D arrays.

The standardized Euclidean distance between *u* and *v*.

Parameters

u [(N,) array_like] Input array.
v [(N,) array_like] Input array.
V [(N,) array_like] *V* is an 1-D array of component variances. It is usually computed among a larger collection vectors.

Returns

seuclidean [double] The standardized Euclidean distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.seuclidean([1, 0, 0], [0, 1, 0], [0.1, 0.1, 0.1])
4.4721359549995796
>>> distance.seuclidean([1, 0, 0], [0, 1, 0], [1, 0.1, 0.1])
3.3166247903553998
>>> distance.seuclidean([1, 0, 0], [0, 1, 0], [10, 0.1, 0.1])
3.1780497164141406
```

scipy.spatial.distance.sqeuclidean

scipy.spatial.distance.**sqeuclidean**(*u*, *v*, *w=None*)

Compute the squared Euclidean distance between two 1-D arrays.

The squared Euclidean distance between *u* and *v* is defined as

$$||u - v||_2^2$$
$$\left(\sum (w_i|(u_i - v_i)|^2)\right)$$

Parameters

u [(N,) array_like] Input array.
v [(N,) array_like] Input array.
w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

sqeuclidean
[double] The squared Euclidean distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.sqeuclidean([1, 0, 0], [0, 1, 0])
2.0
>>> distance.sqeuclidean([1, 1, 0], [0, 1, 0])
1.0
```

scipy.spatial.distance.wminkowski

scipy.spatial.distance.**wminkowski**(*u*, *v*, *p*, *w*)

Compute the weighted Minkowski distance between two 1-D arrays.

The weighted Minkowski distance between *u* and *v*, defined as

$$\left(\sum (|w_i(u_i - v_i)|^p)\right)^{1/p}.$$

Parameters

u [(N,) array_like] Input array.
v [(N,) array_like] Input array.
p [scalar] The order of the norm of the difference $||u - v||_p$.
w [(N,) array_like] The weight vector.

Returns

wminkowski
[double] The weighted Minkowski distance between vectors *u* and *v*.

Notes

wminkowski is deprecated and will be removed in SciPy 1.8.0. Use *minkowski* with the w argument instead.

Examples

```
>>> from scipy.spatial import distance
>>> distance.wminkowski([1, 0, 0], [0, 1, 0], 1, np.ones(3))
2.0
>>> distance.wminkowski([1, 0, 0], [0, 1, 0], 2, np.ones(3))
1.4142135623730951
>>> distance.wminkowski([1, 0, 0], [0, 1, 0], 3, np.ones(3))
1.2599210498948732
>>> distance.wminkowski([1, 1, 0], [0, 1, 0], 1, np.ones(3))
1.0
>>> distance.wminkowski([1, 1, 0], [0, 1, 0], 2, np.ones(3))
1.0
>>> distance.wminkowski([1, 1, 0], [0, 1, 0], 3, np.ones(3))
1.0
```

Distance functions between two boolean vectors (representing sets) u and v. As in the case of numerical vectors, pdist is more efficient for computing the distances between all pairs.

dice(u, v[, w])	Compute the Dice dissimilarity between two boolean 1-D arrays.
hamming(u, v[, w])	Compute the Hamming distance between two 1-D arrays.
jaccard(u, v[, w])	Compute the Jaccard-Needham dissimilarity between two boolean 1-D arrays.
kulsinski(u, v[, w])	Compute the Kulsinski dissimilarity between two boolean 1-D arrays.
rogerstanimoto(u, v[, w])	Compute the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.
russellrao(u, v[, w])	Compute the Russell-Rao dissimilarity between two boolean 1-D arrays.
sokalmichener(u, v[, w])	Compute the Sokal-Michener dissimilarity between two boolean 1-D arrays.
sokalsneath(u, v[, w])	Compute the Sokal-Sneath dissimilarity between two boolean 1-D arrays.
yule(u, v[, w])	Compute the Yule dissimilarity between two boolean 1-D arrays.

scipy.spatial.distance.dice

scipy.spatial.distance.**dice**(*u*, *v*, *w=None*)

Compute the Dice dissimilarity between two boolean 1-D arrays.

The Dice dissimilarity between *u* and *v*, is

$$\frac{c_{TF} + c_{FT}}{2c_{TT} + c_{FT} + c_{TF}}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u [(N,) array_like, bool] Input 1-D array.
v [(N,) array_like, bool] Input 1-D array.
w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

dice [double] The Dice dissimilarity between 1-D arrays *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.dice([1, 0, 0], [0, 1, 0])
1.0
>>> distance.dice([1, 0, 0], [1, 1, 0])
0.3333333333333333
>>> distance.dice([1, 0, 0], [2, 0, 0])
-0.3333333333333333
```

scipy.spatial.distance.hamming

scipy.spatial.distance.**hamming**(*u*, *v*, *w=None*)
Compute the Hamming distance between two 1-D arrays.

The Hamming distance between 1-D arrays *u* and *v*, is simply the proportion of disagreeing components in *u* and *v*. If *u* and *v* are boolean vectors, the Hamming distance is

$$\frac{c_{01} + c_{10}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u [(N,) array_like] Input array.
v [(N,) array_like] Input array.
w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

hamming [double] The Hamming distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.hamming([1, 0, 0], [0, 1, 0])
0.66666666666666663
>>> distance.hamming([1, 0, 0], [1, 1, 0])
0.33333333333333331
>>> distance.hamming([1, 0, 0], [2, 0, 0])
0.33333333333333331
>>> distance.hamming([1, 0, 0], [3, 0, 0])
0.33333333333333331
```

scipy.spatial.distance.jaccard

scipy.spatial.distance.**jaccard**(*u*, *v*, *w=None*)

Compute the Jaccard-Needham dissimilarity between two boolean 1-D arrays.

The Jaccard-Needham dissimilarity between 1-D boolean arrays *u* and *v*, is defined as

$$\frac{c_{TF} + c_{FT}}{c_{TT} + c_{FT} + c_{TF}}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u	[(N,) array_like, bool] Input array.
v	[(N,) array_like, bool] Input array.
w	[(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

jaccard	[double] The Jaccard distance between vectors *u* and *v*.

Notes

When both *u* and *v* lead to a *0/0* division i.e. there is no overlap between the items in the vectors the returned distance is 0. See the Wikipedia page on the Jaccard index [1], and this paper [2].

Changed in version 1.2.0: Previously, when *u* and *v* lead to a *0/0* division, the function would return NaN. This was changed to return 0 instead.

References

[1], [2]

Examples

```
>>> from scipy.spatial import distance
>>> distance.jaccard([1, 0, 0], [0, 1, 0])
1.0
>>> distance.jaccard([1, 0, 0], [1, 1, 0])
0.5
>>> distance.jaccard([1, 0, 0], [1, 2, 0])
0.5
>>> distance.jaccard([1, 0, 0], [1, 1, 1])
0.6666666666666663
```

scipy.spatial.distance.kulsinski

scipy.spatial.distance.**kulsinski**(*u*, *v*, *w=None*)

Compute the Kulsinski dissimilarity between two boolean 1-D arrays.

The Kulsinski dissimilarity between two boolean 1-D arrays *u* and *v*, is defined as

$$\frac{c_{TF} + c_{FT} - c_{TT} + n}{c_{FT} + c_{TF} + n}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u [(N,) array_like, bool] Input array.

v [(N,) array_like, bool] Input array.

w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

kulsinski [double] The Kulsinski distance between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.kulsinski([1, 0, 0], [0, 1, 0])
1.0
>>> distance.kulsinski([1, 0, 0], [1, 1, 0])
0.75
>>> distance.kulsinski([1, 0, 0], [2, 1, 0])
0.3333333333333331
>>> distance.kulsinski([1, 0, 0], [3, 1, 0])
-0.5
```

scipy.spatial.distance.rogerstanimoto

scipy.spatial.distance.**rogerstanimoto**(*u*, *v*, *w=None*)

Compute the Rogers-Tanimoto dissimilarity between two boolean 1-D arrays.

The Rogers-Tanimoto dissimilarity between two boolean 1-D arrays *u* and *v*, is defined as

$$\frac{R}{c_{TT} + c_{FF} + R}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

Parameters

u [(N,) array_like, bool] Input array.

v [(N,) array_like, bool] Input array.

w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

rogerstanimoto
[double] The Rogers-Tanimoto dissimilarity between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.rogerstanimoto([1, 0, 0], [0, 1, 0])
0.8
>>> distance.rogerstanimoto([1, 0, 0], [1, 1, 0])
0.5
>>> distance.rogerstanimoto([1, 0, 0], [2, 0, 0])
-1.0
```

scipy.spatial.distance.russellrao

scipy.spatial.distance.**russellrao**(*u*, *v*, *w=None*)

Compute the Russell-Rao dissimilarity between two boolean 1-D arrays.

The Russell-Rao dissimilarity between two boolean 1-D arrays, *u* and *v*, is defined as

$$\frac{n - c_{TT}}{n}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$.

Parameters

u	[(N,) array_like, bool] Input array.
v	[(N,) array_like, bool] Input array.
w	[(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

russellrao	[double] The Russell-Rao dissimilarity between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.russellrao([1, 0, 0], [0, 1, 0])
1.0
>>> distance.russellrao([1, 0, 0], [1, 1, 0])
0.6666666666666666
>>> distance.russellrao([1, 0, 0], [2, 0, 0])
0.3333333333333333
```

scipy.spatial.distance.sokalmichener

scipy.spatial.distance.**sokalmichener**(*u*, *v*, *w=None*)

Compute the Sokal-Michener dissimilarity between two boolean 1-D arrays.

The Sokal-Michener dissimilarity between boolean 1-D arrays *u* and *v*, is defined as

$$\frac{R}{S + R}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$, $R = 2 * (c_{TF} + c_{FT})$ and $S = c_{FF} + c_{TT}$.

Parameters

u [(N,) array_like, bool] Input array.
v [(N,) array_like, bool] Input array.
w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

sokalmichener
[double] The Sokal-Michener dissimilarity between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.sokalmichener([1, 0, 0], [0, 1, 0])
0.8
>>> distance.sokalmichener([1, 0, 0], [1, 1, 0])
0.5
>>> distance.sokalmichener([1, 0, 0], [2, 0, 0])
-1.0
```

scipy.spatial.distance.sokalsneath

scipy.spatial.distance.**sokalsneath**(*u*, *v*, *w=None*)
Compute the Sokal-Sneath dissimilarity between two boolean 1-D arrays.

The Sokal-Sneath dissimilarity between *u* and *v*,

$$\frac{R}{c_{TT} + R}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$ and $R = 2(c_{TF} + c_{FT})$.

Parameters

u [(N,) array_like, bool] Input array.
v [(N,) array_like, bool] Input array.
w [(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

sokalsneath
[double] The Sokal-Sneath dissimilarity between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.sokalsneath([1, 0, 0], [0, 1, 0])
1.0
>>> distance.sokalsneath([1, 0, 0], [1, 1, 0])
0.66666666666666663
>>> distance.sokalsneath([1, 0, 0], [2, 1, 0])
0.0
>>> distance.sokalsneath([1, 0, 0], [3, 1, 0])
-2.0
```

scipy.spatial.distance.yule

scipy.spatial.distance.**yule**(*u*, *v*, *w=None*)

Compute the Yule dissimilarity between two boolean 1-D arrays.

The Yule dissimilarity is defined as

$$\frac{R}{c_{TT} * c_{FF} + \frac{R}{2}}$$

where c_{ij} is the number of occurrences of $\mathtt{u}[\mathtt{k}] = i$ and $\mathtt{v}[\mathtt{k}] = j$ for $k < n$ and $R = 2.0 * c_{TF} * c_{FT}$.

Parameters

u	[(N,) array_like, bool] Input array.
v	[(N,) array_like, bool] Input array.
w	[(N,) array_like, optional] The weights for each value in *u* and *v*. Default is None, which gives each value a weight of 1.0

Returns

yule	[double] The Yule dissimilarity between vectors *u* and *v*.

Examples

```
>>> from scipy.spatial import distance
>>> distance.yule([1, 0, 0], [0, 1, 0])
2.0
>>> distance.yule([1, 1, 0], [0, 1, 0])
0.0
```

hamming also operates over discrete numerical vectors.

3.3.28 Special functions (scipy.special)

Nearly all of the functions below are universal functions and follow broadcasting and automatic array-looping rules.

See also:

scipy.special.cython_special – Typed Cython versions of special functions

Error handling

Errors are handled by returning NaNs or other appropriate values. Some of the special function routines can emit warnings or raise exceptions when an error occurs. By default this is disabled; to query and control the current error handling state the following functions are provided.

geterr	Get the current way of handling special-function errors.
seterr	Set how special-function errors are handled.
errstate(**kwargs)	Context manager for special-function error handling.
SpecialFunctionWarning	Warning that can be emitted by special functions.
SpecialFunctionError	Exception that can be raised by special functions.

scipy.special.geterr

scipy.special.**geterr**()

Get the current way of handling special-function errors.

Returns

err : [dict] A dictionary with keys "singular", "underflow", "overflow", "slow", "loss", "no_result", "domain", "arg", and "other", whose values are from the strings "ignore", "warn", and "raise". The keys represent possible special-function errors, and the values define how these errors are handled.

See also:

seterr

set how special-function errors are handled

errstate

context manager for special-function error handling

numpy.geterr

similar numpy function for floating-point errors

Notes

For complete documentation of the types of special-function errors and treatment options, see *seterr*.

Examples

By default all errors are ignored.

```
>>> import scipy.special as sc
>>> for key, value in sorted(sc.geterr().items()):
...     print("{}: {}".format(key, value))
...
arg: ignore
domain: ignore
loss: ignore
no_result: ignore
other: ignore
overflow: ignore
singular: ignore
slow: ignore
underflow: ignore
```

scipy.special.seterr

scipy.special.**seterr**()

Set how special-function errors are handled.

Parameters

all	[{'ignore', 'warn' 'raise'}, optional] Set treatment for all type of special-function errors at once. The options are: • 'ignore' Take no action when the error occurs • 'warn' Print a *SpecialFunctionWarning* when the error occurs (via the Python warnings module) • 'raise' Raise a *SpecialFunctionError* when the error occurs. The default is to not change the current behavior. If behaviors for additional categories of special-function errors are specified, then all is applied first, followed by the additional categories.
singular	[{'ignore', 'warn', 'raise'}, optional] Treatment for singularities.
underflow	[{'ignore', 'warn', 'raise'}, optional] Treatment for underflow.
overflow	[{'ignore', 'warn', 'raise'}, optional] Treatment for overflow.
slow	[{'ignore', 'warn', 'raise'}, optional] Treatment for slow convergence.
loss	[{'ignore', 'warn', 'raise'}, optional] Treatment for loss of accuracy.
no_result	[{'ignore', 'warn', 'raise'}, optional] Treatment for failing to find a result.
domain	[{'ignore', 'warn', 'raise'}, optional] Treatment for an invalid argument to a function.
arg	[{'ignore', 'warn', 'raise'}, optional] Treatment for an invalid parameter to a function.
other	[{'ignore', 'warn', 'raise'}, optional] Treatment for an unknown error.

Returns

olderr	[dict] Dictionary containing the old settings.

See also:

geterr

get the current way of handling special-function errors

errstate

context manager for special-function error handling

numpy.seterr

similar numpy function for floating-point errors

Examples

```
>>> import scipy.special as sc
>>> from pytest import raises
>>> sc.gammaln(0)
inf
>>> olderr = sc.seterr(singular='raise')
>>> with raises(sc.SpecialFunctionError):
...     sc.gammaln(0)
...
>>> _ = sc.seterr(**olderr)
```

We can also raise for every category except one.

```
>>> olderr = sc.seterr(all='raise', singular='ignore')
>>> sc.gammaln(0)
inf
>>> with raises(sc.SpecialFunctionError):
...     sc.spence(-1)
...
>>> _ = sc.seterr(**olderr)
```

scipy.special.errstate

class scipy.special.**errstate**(***kwargs*)

Context manager for special-function error handling.

Using an instance of *errstate* as a context manager allows statements in that context to execute with a known error handling behavior. Upon entering the context the error handling is set with *seterr*, and upon exiting it is restored to what it was before.

Parameters

kwargs [{all, singular, underflow, overflow, slow, loss, no_result, domain, arg, other}] Keyword arguments. The valid keywords are possible special-function errors. Each keyword should have a string value that defines the treatement for the particular type of error. Values must be 'ignore', 'warn', or 'other'. See *seterr* for details.

See also:

geterr

get the current way of handling special-function errors

seterr

set how special-function errors are handled

numpy.errstate

similar numpy function for floating-point errors

Examples

```
>>> import scipy.special as sc
>>> from pytest import raises
>>> sc.gammaln(0)
inf
>>> with sc.errstate(singular='raise'):
...     with raises(sc.SpecialFunctionError):
...         sc.gammaln(0)
...
>>> sc.gammaln(0)
inf
```

We can also raise on every category except one.

```
>>> with sc.errstate(all='raise', singular='ignore'):
...     sc.gammaln(0)
...     with raises(sc.SpecialFunctionError):
```

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```
...          sc.spence(-1)
...
inf
```

scipy.special.SpecialFunctionWarning

exception scipy.special.**SpecialFunctionWarning**
Warning that can be emitted by special functions.

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.special.SpecialFunctionError

exception scipy.special.**SpecialFunctionError**
Exception that can be raised by special functions.

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

Available functions

Airy functions

airy(z)	Airy functions and their derivatives.
airye(z)	Exponentially scaled Airy functions and their derivatives.
ai_zeros(nt)	Compute *nt* zeros and values of the Airy function Ai and its derivative.
bi_zeros(nt)	Compute *nt* zeros and values of the Airy function Bi and its derivative.
itairy(x)	Integrals of Airy functions

scipy.special.airy

scipy.special.**airy**(*z*) **= <ufunc 'airy'>**
Airy functions and their derivatives.

Parameters

z [array_like] Real or complex argument.

Returns

Ai, Aip, Bi, Bip
[ndarrays] Airy functions Ai and Bi, and their derivatives Aip and Bip.

See also:

airye

exponentially scaled Airy functions.

Notes

The Airy functions Ai and Bi are two independent solutions of

$$y''(x) = xy(x).$$

For real z in [-10, 10], the computation is carried out by calling the Cephes [1] *airy* routine, which uses power series summation for small z and rational minimax approximations for large z.

Outside this range, the AMOS [2] *zairy* and *zbiry* routines are employed. They are computed using power series for $|z| < 1$ and the following relations to modified Bessel functions for larger z (where $t \equiv 2z^{3/2}/3$):

$$Ai(z) = \frac{1}{\pi\sqrt{3}} K_{1/3}(t)$$

$$Ai'(z) = -\frac{z}{\pi\sqrt{3}} K_{2/3}(t)$$

$$Bi(z) = \sqrt{\frac{z}{3}} \left(I_{-1/3}(t) + I_{1/3}(t)\right)$$

$$Bi'(z) = \frac{z}{\sqrt{3}} \left(I_{-2/3}(t) + I_{2/3}(t)\right)$$

References

[1], [2]

Examples

Compute the Airy functions on the interval [-15, 5].

```
>>> from scipy import special
>>> x = np.linspace(-15, 5, 201)
>>> ai, aip, bi, bip = special.airy(x)
```

Plot Ai(x) and Bi(x).

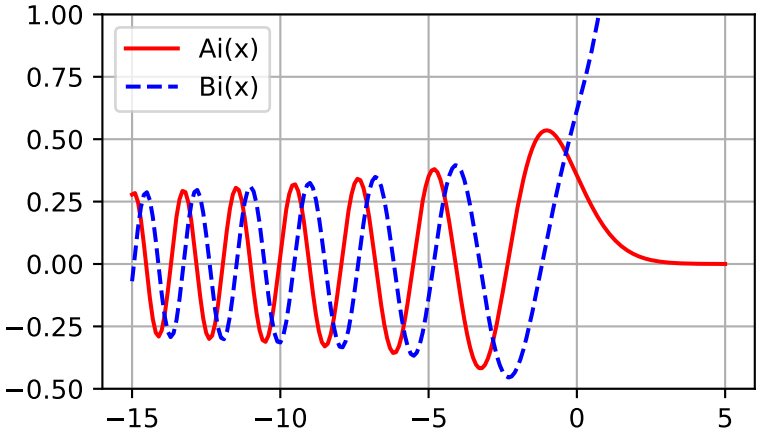
```
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, ai, 'r', label='Ai(x)')
>>> plt.plot(x, bi, 'b--', label='Bi(x)')
>>> plt.ylim(-0.5, 1.0)
>>> plt.grid()
>>> plt.legend(loc='upper left')
>>> plt.show()
```

scipy.special.airye

scipy.special.**airye**(*z*) **= <ufunc 'airye'>**

Exponentially scaled Airy functions and their derivatives.

Scaling:




```
eAi  = Ai  * exp(2.0/3.0*z*sqrt(z))
eAip = Aip * exp(2.0/3.0*z*sqrt(z))
eBi  = Bi  * exp(-abs(2.0/3.0*(z*sqrt(z)).real))
eBip = Bip * exp(-abs(2.0/3.0*(z*sqrt(z)).real))
```

Parameters

z [array_like] Real or complex argument.

Returns

eAi, eAip, eBi, eBip
[array_like] Exponentially scaled Airy functions eAi and eBi, and their derivatives eAip and eBip

See also:

`airy`

Notes

Wrapper for the AMOS [1] routines *zairy* and *zbiry*.

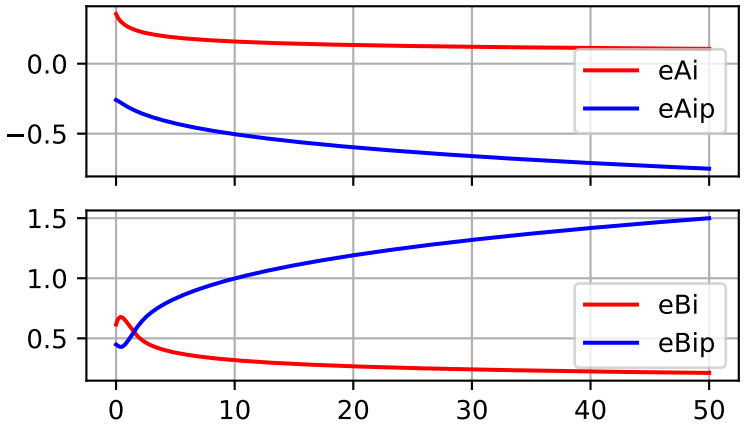
References

[1]

Examples

We can compute exponentially scaled Airy functions and their derivatives:

```
>>> from scipy.special import airye
>>> import matplotlib.pyplot as plt
>>> z = np.linspace(0, 50, 500)
>>> eAi, eAip, eBi, eBip = airye(z)
>>> f, ax = plt.subplots(2, 1, sharex=True)
>>> for ind, data in enumerate([[eAi, eAip, ["eAi", "eAip"]],
...                             [eBi, eBip, ["eBi", "eBip"]]]):
...     ax[ind].plot(z, data[0], "-r", z, data[1], "-b")
...     ax[ind].legend(data[2])
...     ax[ind].grid(True)
>>> plt.show()
```



We can compute these using usual non-scaled Airy functions by:

```
>>> from scipy.special import airy
>>> Ai, Aip, Bi, Bip = airy(z)
>>> np.allclose(eAi, Ai * np.exp(2.0 / 3.0 * z * np.sqrt(z)))
True
>>> np.allclose(eAip, Aip * np.exp(2.0 / 3.0 * z * np.sqrt(z)))
True
>>> np.allclose(eBi, Bi * np.exp(-abs(np.real(2.0 / 3.0 * z * np.
↪sqrt(z)))))
True
>>> np.allclose(eBip, Bip * np.exp(-abs(np.real(2.0 / 3.0 * z * np.
↪sqrt(z)))))
True
```

Comparing non-scaled and exponentially scaled ones, the usual non-scaled function quickly underflows for large values, whereas the exponentially scaled function does not.

```
>>> airy(200)
(0.0, 0.0, nan, nan)
>>> airye(200)
(0.07501041684381093, -1.0609012305109042, 0.15003188417418148, 2.
↪1215836725571093)
```

scipy.special.ai_zeros

scipy.special.**ai_zeros**(*nt*)

Compute *nt* zeros and values of the Airy function Ai and its derivative.

Computes the first *nt* zeros, *a*, of the Airy function Ai(x); first *nt* zeros, *ap*, of the derivative of the Airy function Ai'(x); the corresponding values Ai(a'); and the corresponding values Ai'(a).

Parameters

nt	[int] Number of zeros to compute

Returns

a	[ndarray] First *nt* zeros of Ai(x)
ap	[ndarray] First *nt* zeros of Ai'(x)
ai	[ndarray] Values of Ai(x) evaluated at first *nt* zeros of Ai'(x)
aip	[ndarray] Values of Ai'(x) evaluated at first *nt* zeros of Ai(x)

References

[1]

Examples

```
>>> from scipy import special
>>> a, ap, ai, aip = special.ai_zeros(3)
>>> a
array([-2.33810741, -4.08794944, -5.52055983])
>>> ap
array([-1.01879297, -3.24819758, -4.82009921])
>>> ai
array([ 0.53565666, -0.41901548,  0.38040647])
>>> aip
array([ 0.70121082, -0.80311137,  0.86520403])
```

scipy.special.bi_zeros

scipy.special.**bi_zeros**(*nt*)

Compute *nt* zeros and values of the Airy function Bi and its derivative.

Computes the first *nt* zeros, b, of the Airy function Bi(x); first *nt* zeros, b', of the derivative of the Airy function Bi'(x); the corresponding values Bi(b'); and the corresponding values Bi'(b).

Parameters

nt [int] Number of zeros to compute

Returns

b [ndarray] First *nt* zeros of Bi(x)
bp [ndarray] First *nt* zeros of Bi'(x)
bi [ndarray] Values of Bi(x) evaluated at first *nt* zeros of Bi'(x)
bip [ndarray] Values of Bi'(x) evaluated at first *nt* zeros of Bi(x)

References

[1]

Examples

```
>>> from scipy import special
>>> b, bp, bi, bip = special.bi_zeros(3)
>>> b
array([-1.17371322, -3.2710933 , -4.83073784])
>>> bp
array([-2.29443968, -4.07315509, -5.51239573])
>>> bi
array([-0.45494438,  0.39652284, -0.36796916])
>>> bip
array([ 0.60195789, -0.76031014,  0.83699101])
```

scipy.special.itairy

scipy.special.**itairy**(*x*) **= <ufunc 'itairy'>**

Integrals of Airy functions

Calculates the integrals of Airy functions from 0 to *x*.

Parameters

x: array_like
Upper limit of integration (float).

Returns

Apt Integral of Ai(t) from 0 to x.
Bpt Integral of Bi(t) from 0 to x.
Ant Integral of Ai(-t) from 0 to x.
Bnt Integral of Bi(-t) from 0 to x.

Notes

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

References

[1]

Elliptic functions and integrals

ellipj(u, m)	Jacobian elliptic functions
ellipk(m)	Complete elliptic integral of the first kind.
ellipkm1(p)	Complete elliptic integral of the first kind around $m = 1$
ellipkinc(phi, m)	Incomplete elliptic integral of the first kind
ellipe(m)	Complete elliptic integral of the second kind
ellipeinc(phi, m)	Incomplete elliptic integral of the second kind

scipy.special.ellipj

scipy.special.**ellipj**(*u*, *m*) **= <ufunc 'ellipj'>**

Jacobian elliptic functions

Calculates the Jacobian elliptic functions of parameter *m* between 0 and 1, and real argument *u*.

Parameters

m [array_like] Parameter.
u [array_like] Argument.

Returns

sn, cn, dn, ph
[ndarrays] The returned functions:

```
sn(u|m), cn(u|m), dn(u|m)
```

The value *ph* is such that if $u = ellipkinc(ph, m)$, then $sn(u|m) = sin(ph)$ and $cn(u|m) = cos(ph)$.

See also:

ellipk

Complete elliptic integral of the first kind

ellipkinc

Incomplete elliptic integral of the first kind

Notes

Wrapper for the Cephes [1] routine *ellpj*.

These functions are periodic, with quarter-period on the real axis equal to the complete elliptic integral *ellipk(m)*.

Relation to incomplete elliptic integral: If *u* = *ellipkinc(phi,m)*, then *sn(u|m)* = *sin(phi)*, and *cn(u|m)* = *cos(phi)*. The *phi* is called the amplitude of *u*.

Computation is by means of the arithmetic-geometric mean algorithm, except when *m* is within 1e-9 of 0 or 1. In the latter case with *m* close to 1, the approximation applies only for *phi* < *pi/2*.

References

[1]

scipy.special.ellipk

scipy.special.**ellipk**(*m*) **= <ufunc 'ellipk'>**

Complete elliptic integral of the first kind.

This function is defined as

$$K(m) = \int_0^{\pi/2} [1 - m \sin(t)^2]^{-1/2} dt$$

Parameters

m [array_like] The parameter of the elliptic integral.

Returns

K [array_like] Value of the elliptic integral.

See also:

ellipkm1

Complete elliptic integral of the first kind around m = 1

ellipkinc

Incomplete elliptic integral of the first kind

ellipe

Complete elliptic integral of the second kind

ellipeinc

Incomplete elliptic integral of the second kind

Notes

For more precision around point m = 1, use `ellipkm1`, which this function calls.

The parameterization in terms of m follows that of section 17.2 in [1]. Other parameterizations in terms of the complementary parameter $1 - m$, modular angle $\sin^2(\alpha) = m$, or modulus $k^2 = m$ are also used, so be careful that you choose the correct parameter.

References

[1]

scipy.special.ellipkm1

scipy.special.**ellipkm1**(*p*) **= <ufunc 'ellipkm1'>**

Complete elliptic integral of the first kind around *m* = 1

This function is defined as

$$K(p) = \int_0^{\pi/2} [1 - m \sin(t)^2]^{-1/2} dt$$

where *m = 1 - p*.

Parameters

p [array_like] Defines the parameter of the elliptic integral as *m = 1 - p*.

Returns

K [ndarray] Value of the elliptic integral.

See also:

ellipk

Complete elliptic integral of the first kind

ellipkinc

Incomplete elliptic integral of the first kind

ellipe

Complete elliptic integral of the second kind

ellipeinc

Incomplete elliptic integral of the second kind

Notes

Wrapper for the Cephes [1] routine *ellpk*.

For *p* <= *1*, computation uses the approximation,

$$K(p) \approx P(p) - \log(p)Q(p),$$

where P and Q are tenth-order polynomials. The argument *p* is used internally rather than *m* so that the logarithmic singularity at *m* = *1* will be shifted to the origin; this preserves maximum accuracy. For *p* > *1*, the identity

$$K(p) = K(1/p)/\sqrt{(}p)$$

is used.

References

[1]

scipy.special.ellipkinc

scipy.special.**ellipkinc**(*phi*, *m*) **= <ufunc 'ellipkinc'>**

Incomplete elliptic integral of the first kind

This function is defined as

$$K(\phi, m) = \int_0^{\phi} [1 - m \sin(t)^2]^{-1/2} dt$$

This function is also called *F(phi, m)*.

Parameters

phi	[array_like] amplitude of the elliptic integral
m	[array_like] parameter of the elliptic integral

Returns

K	[ndarray] Value of the elliptic integral

See also:

ellipkm1

Complete elliptic integral of the first kind, near *m* = 1

ellipk

Complete elliptic integral of the first kind

ellipe

Complete elliptic integral of the second kind

ellipeinc

Incomplete elliptic integral of the second kind

Notes

Wrapper for the Cephes [1] routine *ellik*. The computation is carried out using the arithmetic-geometric mean algorithm.

The parameterization in terms of m follows that of section 17.2 in [2]. Other parameterizations in terms of the complementary parameter $1 - m$, modular angle $\sin^2(\alpha) = m$, or modulus $k^2 = m$ are also used, so be careful that you choose the correct parameter.

References

[1], [2]

scipy.special.ellipe

scipy.special.**ellipe**(*m*) **= <ufunc 'ellipe'>**

Complete elliptic integral of the second kind

This function is defined as

$$E(m) = \int_0^{\pi/2} [1 - m \sin(t)^2]^{1/2} dt$$

Parameters

m [array_like] Defines the parameter of the elliptic integral.

Returns

E [ndarray] Value of the elliptic integral.

See also:

ellipkm1

Complete elliptic integral of the first kind, near *m* = 1

ellipk

Complete elliptic integral of the first kind

ellipkinc

Incomplete elliptic integral of the first kind

ellipeinc

Incomplete elliptic integral of the second kind

Notes

Wrapper for the Cephes [1] routine *ellpe*.

For *m > 0* the computation uses the approximation,

$$E(m) \approx P(1 - m) - (1 - m) \log(1 - m) Q(1 - m),$$

where P and Q are tenth-order polynomials. For *m < 0*, the relation

$$E(m) = E(m/(m - 1)) \sqrt{(1 - m)}$$

is used.

The parameterization in terms of m follows that of section 17.2 in [2]. Other parameterizations in terms of the complementary parameter $1 - m$, modular angle $\sin^2(\alpha) = m$, or modulus $k^2 = m$ are also used, so be careful that you choose the correct parameter.

References

[1], [2]

Examples

This function is used in finding the circumference of an ellipse with semi-major axis *a* and semi-minor axis *b*.

```
>>> from scipy import special
```

```
>>> a = 3.5
>>> b = 2.1
>>> e_sq = 1.0 - b**2/a**2  # eccentricity squared
```

Then the circumference is found using the following:

```
>>> C = 4*a*special.ellipe(e_sq)  # circumference formula
>>> C
17.868899204378693
```

When *a* and *b* are the same (meaning eccentricity is 0), this reduces to the circumference of a circle.

```
>>> 4*a*special.ellipe(0.0)  # formula for ellipse with a = b
21.991148575128552
>>> 2*np.pi*a  # formula for circle of radius a
21.991148575128552
```

scipy.special.ellipeinc

scipy.special.**ellipeinc**(*phi*, *m*) **= <ufunc 'ellipeinc'>**

Incomplete elliptic integral of the second kind

This function is defined as

$$E(\phi, m) = \int_0^{\phi} [1 - m \sin(t)^2]^{1/2} dt$$

Parameters

phi	[array_like] amplitude of the elliptic integral.
m	[array_like] parameter of the elliptic integral.

Returns

E	[ndarray] Value of the elliptic integral.

See also:

ellipkm1

Complete elliptic integral of the first kind, near $m = 1$

ellipk

Complete elliptic integral of the first kind

ellipkinc

Incomplete elliptic integral of the first kind

ellipe

Complete elliptic integral of the second kind

Notes

Wrapper for the Cephes [1] routine *ellie*.

Computation uses arithmetic-geometric means algorithm.

The parameterization in terms of m follows that of section 17.2 in [2]. Other parameterizations in terms of the complementary parameter $1 - m$, modular angle $\sin^2(\alpha) = m$, or modulus $k^2 = m$ are also used, so be careful that you choose the correct parameter.

References

[1], [2]

Bessel functions

jv(v, z)	Bessel function of the first kind of real order and complex argument.
jve(v, z)	Exponentially scaled Bessel function of order *v*.
yn(n, x)	Bessel function of the second kind of integer order and real argument.
yv(v, z)	Bessel function of the second kind of real order and complex argument.
yve(v, z)	Exponentially scaled Bessel function of the second kind of real order.
kn(n, x)	Modified Bessel function of the second kind of integer order *n*
kv(v, z)	Modified Bessel function of the second kind of real order *v*
kve(v, z)	Exponentially scaled modified Bessel function of the second kind.
iv(v, z)	Modified Bessel function of the first kind of real order.
ive(v, z)	Exponentially scaled modified Bessel function of the first kind
hankel1(v, z)	Hankel function of the first kind
hankel1e(v, z)	Exponentially scaled Hankel function of the first kind
hankel2(v, z)	Hankel function of the second kind
hankel2e(v, z)	Exponentially scaled Hankel function of the second kind
wright_bessel(a, b, x)	Wright's generalized Bessel function.

scipy.special.jv

scipy.special.**jv**(*v*, *z*) **= <ufunc 'jv'>**

Bessel function of the first kind of real order and complex argument.

Parameters

v	[array_like] Order (float).
z	[array_like] Argument (float or complex).

Returns

J	[ndarray] Value of the Bessel function, $J_v(z)$.

See also:

jve

J_v with leading exponential behavior stripped off.

spherical_jn

spherical Bessel functions.

Notes

For positive *v* values, the computation is carried out using the AMOS [1] *zbesj* routine, which exploits the connection to the modified Bessel function I_v,

$$J_v(z) = \exp(v\pi\imath/2) I_v(-\imath z) \qquad (\Im z > 0)$$
$$J_v(z) = \exp(-v\pi\imath/2) I_v(\imath z) \qquad (\Im z < 0)$$

For negative *v* values the formula,

$$J_{-v}(z) = J_v(z)\cos(\pi v) - Y_v(z)\sin(\pi v)$$

is used, where $Y_v(z)$ is the Bessel function of the second kind, computed using the AMOS routine *zbesy*. Note that the second term is exactly zero for integer *v*; to improve accuracy the second term is explicitly omitted for *v* values such that *v = floor(v)*.

Not to be confused with the spherical Bessel functions (see *spherical_jn*).

References

[1]

scipy.special.jve

scipy.special.**jve**(*v*, *z*) **= <ufunc 'jve'>**

Exponentially scaled Bessel function of order *v*.

Defined as:

```
jve(v, z) = jv(v, z) * exp(-abs(z.imag))
```

Parameters

v [array_like] Order (float).
z [array_like] Argument (float or complex).

Returns

J [ndarray] Value of the exponentially scaled Bessel function.

Notes

For positive *v* values, the computation is carried out using the AMOS [1] *zbesj* routine, which exploits the connection to the modified Bessel function I_v,

$$J_v(z) = \exp(v\pi\imath/2) I_v(-\imath z) \qquad (\Im z > 0)$$
$$J_v(z) = \exp(-v\pi\imath/2) I_v(\imath z) \qquad (\Im z < 0)$$

For negative *v* values the formula,

$$J_{-v}(z) = J_v(z)\cos(\pi v) - Y_v(z)\sin(\pi v)$$

is used, where $Y_v(z)$ is the Bessel function of the second kind, computed using the AMOS routine *zbesy*. Note that the second term is exactly zero for integer *v*; to improve accuracy the second term is explicitly omitted for *v* values such that *v = floor(v)*.

References

[1]

scipy.special.yn

`scipy.special.`**`yn`**`(n, x) = <ufunc 'yn'>`

Bessel function of the second kind of integer order and real argument.

Parameters

n [array_like] Order (integer).
z [array_like] Argument (float).

Returns

Y [ndarray] Value of the Bessel function, $Y_n(x)$.

See also:

`yv`

For real order and real or complex argument.

Notes

Wrapper for the Cephes [1] routine *yn*.

The function is evaluated by forward recurrence on *n*, starting with values computed by the Cephes routines *y0* and *y1*. If *n* = *0* or 1, the routine for *y0* or *y1* is called directly.

References

[1]

scipy.special.yv

scipy.special.**yv**(*v*, *z*) **= <ufunc 'yv'>**

Bessel function of the second kind of real order and complex argument.

Parameters

v	[array_like] Order (float).
z	[array_like] Argument (float or complex).

Returns

Y	[ndarray] Value of the Bessel function of the second kind, $Y_v(x)$.

See also:

yve

Y_v with leading exponential behavior stripped off.

Notes

For positive *v* values, the computation is carried out using the AMOS [1] *zbesy* routine, which exploits the connection to the Hankel Bessel functions $H_v^{(1)}$ and $H_v^{(2)}$,

$$Y_v(z) = \frac{1}{2\imath}(H_v^{(1)} - H_v^{(2)}).$$

For negative *v* values the formula,

$$Y_{-v}(z) = Y_v(z)\cos(\pi v) + J_v(z)\sin(\pi v)$$

is used, where $J_v(z)$ is the Bessel function of the first kind, computed using the AMOS routine *zbesj*. Note that the second term is exactly zero for integer *v*; to improve accuracy the second term is explicitly omitted for *v* values such that *v* = *floor(v)*.

References

[1]

scipy.special.yve

scipy.special.**yve**(*v*, *z*) **= <ufunc 'yve'>**

Exponentially scaled Bessel function of the second kind of real order.

Returns the exponentially scaled Bessel function of the second kind of real order *v* at complex *z*:

```
yve(v, z) = yv(v, z) * exp(-abs(z.imag))
```

Parameters

v	[array_like] Order (float).
z	[array_like] Argument (float or complex).

Returns

Y	[ndarray] Value of the exponentially scaled Bessel function.

Notes

For positive *v* values, the computation is carried out using the AMOS [1] *zbesy* routine, which exploits the connection to the Hankel Bessel functions $H_v^{(1)}$ and $H_v^{(2)}$,

$$Y_v(z) = \frac{1}{2\imath}(H_v^{(1)} - H_v^{(2)}).$$

For negative *v* values the formula,

$$Y_{-v}(z) = Y_v(z)\cos(\pi v) + J_v(z)\sin(\pi v)$$

is used, where $J_v(z)$ is the Bessel function of the first kind, computed using the AMOS routine *zbesj*. Note that the second term is exactly zero for integer *v*; to improve accuracy the second term is explicitly omitted for *v* values such that *v = floor(v)*.

References

[1]

scipy.special.kn

scipy.special.**kn**(*n*, *x*) **= <ufunc 'kn'>**

Modified Bessel function of the second kind of integer order *n*

Returns the modified Bessel function of the second kind for integer order *n* at real *z*.

These are also sometimes called functions of the third kind, Basset functions, or Macdonald functions.

Parameters

n	[array_like of int] Order of Bessel functions (floats will truncate with a warning)
z	[array_like of float] Argument at which to evaluate the Bessel functions

Returns

out [ndarray] The results

See also:

kv

Same function, but accepts real order and complex argument

kvp

Derivative of this function

Notes

Wrapper for AMOS [1] routine *zbesk*. For a discussion of the algorithm used, see [2] and the references therein.

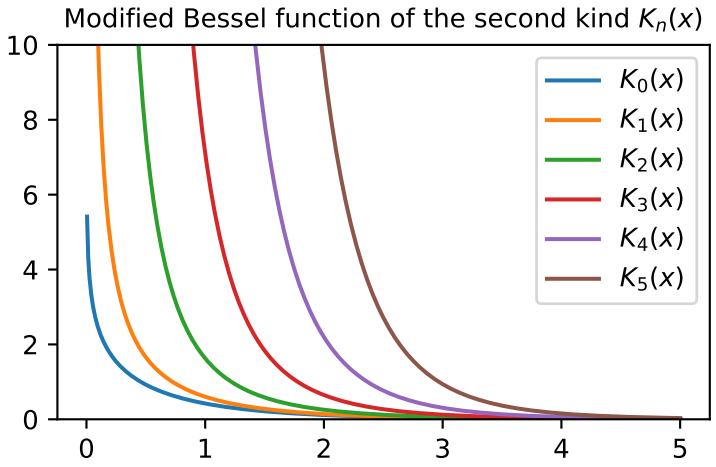
References

[1], [2]

Examples

Plot the function of several orders for real input:

```
>>> from scipy.special import kn
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(0, 5, 1000)
>>> for N in range(6):
...     plt.plot(x, kn(N, x), label='$K_{}(x)$'.format(N))
>>> plt.ylim(0, 10)
>>> plt.legend()
>>> plt.title(r'Modified Bessel function of the second kind $K_n(x)$')
>>> plt.show()
```



Calculate for a single value at multiple orders:

```
>>> kn([4, 5, 6], 1)
array([   44.23241585,   360.9605896 ,  3653.83831186])
```

scipy.special.kv

scipy.special.**kv**(*v*, *z*) **= <ufunc 'kv'>**

Modified Bessel function of the second kind of real order *v*

Returns the modified Bessel function of the second kind for real order *v* at complex *z*.

These are also sometimes called functions of the third kind, Basset functions, or Macdonald functions. They are defined as those solutions of the modified Bessel equation for which,

$$K_v(x) \sim \sqrt{\pi/(2x)}\exp(-x)$$

as $x \to \infty$ [3].

Parameters

v	[array_like of float] Order of Bessel functions
z	[array_like of complex] Argument at which to evaluate the Bessel functions

Returns

out	[ndarray] The results. Note that input must be of complex type to get complex output, e.g. `kv(3, -2+0j)` instead of `kv(3, -2)`.

See also:

kve

This function with leading exponential behavior stripped off.

kvp

Derivative of this function

Notes

Wrapper for AMOS [1] routine *zbesk*. For a discussion of the algorithm used, see [2] and the references therein.

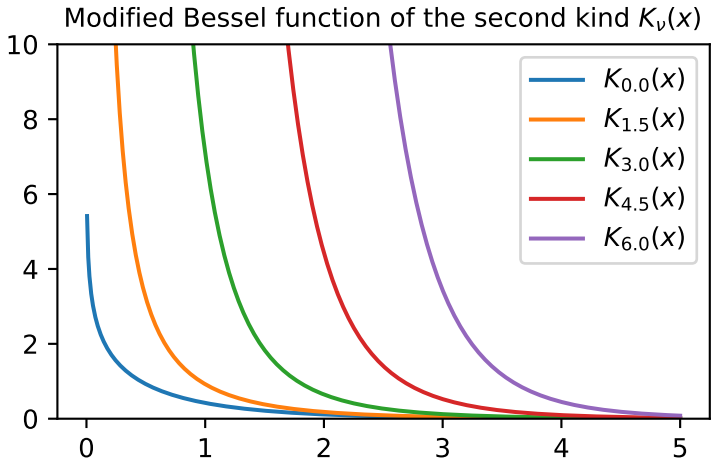
References

[1], [2], [3]

Examples

Plot the function of several orders for real input:

```
>>> from scipy.special import kv
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(0, 5, 1000)
>>> for N in np.linspace(0, 6, 5):
...     plt.plot(x, kv(N, x), label='$K_{{{}}}(x)$'.format(N))
>>> plt.ylim(0, 10)
>>> plt.legend()
>>> plt.title(r'Modified Bessel function of the second kind $K_\nu(x)$')
>>> plt.show()
```



Calculate for a single value at multiple orders:

```
>>> kv([4, 4.5, 5], 1+2j)
array([ 0.1992+2.3892j,  2.3493+3.6j    ,  7.2827+3.8104j])
```

scipy.special.kve

scipy.special.**kve**(*v*, *z*) **= <ufunc 'kve'>**

Exponentially scaled modified Bessel function of the second kind.

Returns the exponentially scaled, modified Bessel function of the second kind (sometimes called the third kind) for real order *v* at complex *z*:

```
kve(v, z) = kv(v, z) * exp(z)
```

Parameters

v	[array_like of float] Order of Bessel functions
z	[array_like of complex] Argument at which to evaluate the Bessel functions

Returns

out [ndarray] The exponentially scaled modified Bessel function of the second kind.

Notes

Wrapper for AMOS [1] routine *zbesk*. For a discussion of the algorithm used, see [2] and the references therein.

References

[1], [2]

scipy.special.iv

scipy.special.**iv**(*v*, *z*) **= <ufunc 'iv'>**

Modified Bessel function of the first kind of real order.

Parameters

v [array_like] Order. If *z* is of real type and negative, *v* must be integer valued.
z [array_like of float or complex] Argument.

Returns

out [ndarray] Values of the modified Bessel function.

See also:

kve

This function with leading exponential behavior stripped off.

Notes

For real z and $v \in [-50, 50]$, the evaluation is carried out using Temme's method [1]. For larger orders, uniform asymptotic expansions are applied.

For complex *z* and positive *v*, the AMOS [2] *zbesi* routine is called. It uses a power series for small *z*, the asymptotic expansion for large *abs(z)*, the Miller algorithm normalized by the Wronskian and a Neumann series for intermediate magnitudes, and the uniform asymptotic expansions for $I_v(z)$ and $J_v(z)$ for large orders. Backward recurrence is used to generate sequences or reduce orders when necessary.

The calculations above are done in the right half plane and continued into the left half plane by the formula,

$$I_v(z \exp(\pm \imath\pi)) = \exp(\pm \pi v) I_v(z)$$

(valid when the real part of *z* is positive). For negative *v*, the formula

$$I_{-v}(z) = I_v(z) + \frac{2}{\pi} \sin(\pi v) K_v(z)$$

is used, where $K_v(z)$ is the modified Bessel function of the second kind, evaluated using the AMOS routine *zbesk*.

References

[1], [2]

scipy.special.ive

scipy.special.**ive**(*v*, *z*) **= <ufunc 'ive'>**
Exponentially scaled modified Bessel function of the first kind

Defined as:

```
ive(v, z) = iv(v, z) * exp(-abs(z.real))
```

Parameters

v [array_like of float] Order.
z [array_like of float or complex] Argument.

Returns

out [ndarray] Values of the exponentially scaled modified Bessel function.

Notes

For positive *v*, the AMOS [1] *zbesi* routine is called. It uses a power series for small *z*, the asymptotic expansion for large *abs(z)*, the Miller algorithm normalized by the Wronskian and a Neumann series for intermediate magnitudes, and the uniform asymptotic expansions for $I_v(z)$ and $J_v(z)$ for large orders. Backward recurrence is used to generate sequences or reduce orders when necessary.

The calculations above are done in the right half plane and continued into the left half plane by the formula,

$$I_v(z \exp(\pm \imath\pi)) = \exp(\pm \pi v) I_v(z)$$

(valid when the real part of z is positive). For negative *v*, the formula

$$I_{-v}(z) = I_v(z) + \frac{2}{\pi} \sin(\pi v) K_v(z)$$

is used, where $K_v(z)$ is the modified Bessel function of the second kind, evaluated using the AMOS routine *zbesk*.

References

[1]

scipy.special.hankel1

scipy.special.**hankel1**(*v*, *z*) **= <ufunc 'hankel1'>**
Hankel function of the first kind

Parameters

v [array_like] Order (float).
z [array_like] Argument (float or complex).

Returns

out [Values of the Hankel function of the first kind.]

See also:

hankel1e

this function with leading exponential behavior stripped off.

Notes

A wrapper for the AMOS [1] routine *zbesh*, which carries out the computation using the relation,

$$H_v^{(1)}(z) = \frac{2}{\imath\pi}\exp(-\imath\pi v/2)K_v(z\exp(-\imath\pi/2))$$

where K_v is the modified Bessel function of the second kind. For negative orders, the relation

$$H_{-v}^{(1)}(z) = H_v^{(1)}(z)\exp(\imath\pi v)$$

is used.

References

[1]

scipy.special.hankel1e

scipy.special.**hankel1e**(*v*, *z*) **= <ufunc 'hankel1e'>**

Exponentially scaled Hankel function of the first kind

Defined as:

```
hankel1e(v, z) = hankel1(v, z) * exp(-1j * z)
```

Parameters

v [array_like] Order (float).
z [array_like] Argument (float or complex).

Returns

out [Values of the exponentially scaled Hankel function.]

Notes

A wrapper for the AMOS [1] routine *zbesh*, which carries out the computation using the relation,

$$H_v^{(1)}(z) = \frac{2}{\imath\pi}\exp(-\imath\pi v/2)K_v(z\exp(-\imath\pi/2))$$

where K_v is the modified Bessel function of the second kind. For negative orders, the relation

$$H_{-v}^{(1)}(z) = H_v^{(1)}(z)\exp(\imath\pi v)$$

is used.

References

[1]

scipy.special.hankel2

scipy.special.**hankel2**(*v*, *z*) **= <ufunc 'hankel2'>**

Hankel function of the second kind

Parameters

v	[array_like] Order (float).
z	[array_like] Argument (float or complex).

Returns

out	[Values of the Hankel function of the second kind.]

See also:

hankel2e

this function with leading exponential behavior stripped off.

Notes

A wrapper for the AMOS [1] routine *zbesh*, which carries out the computation using the relation,

$$H_v^{(2)}(z) = -\frac{2}{\imath\pi}\exp(\imath\pi v/2)K_v(z\exp(\imath\pi/2))$$

where K_v is the modified Bessel function of the second kind. For negative orders, the relation

$$H_{-v}^{(2)}(z) = H_v^{(2)}(z)\exp(-\imath\pi v)$$

is used.

References

[1]

scipy.special.hankel2e

scipy.special.**hankel2e**(*v*, *z*) **= <ufunc 'hankel2e'>**

Exponentially scaled Hankel function of the second kind

Defined as:

```
hankel2e(v, z) = hankel2(v, z) * exp(1j * z)
```

Parameters

v	[array_like] Order (float).
z	[array_like] Argument (float or complex).

Returns

out	[Values of the exponentially scaled Hankel function of the second kind.]

Notes

A wrapper for the AMOS [1] routine *zbesh*, which carries out the computation using the relation,

$$H_v^{(2)}(z) = -\frac{2}{\imath\pi}\exp(\frac{\imath\pi v}{2})K_v(zexp(\frac{\imath\pi}{2}))$$

where K_v is the modified Bessel function of the second kind. For negative orders, the relation

$$H_{-v}^{(2)}(z) = H_v^{(2)}(z)\exp(-\imath\pi v)$$

is used.

References

[1]

scipy.special.wright_bessel

scipy.special.**wright_bessel**(a, b, x) **= <ufunc 'wright_bessel'>**

Wright's generalized Bessel function.

Wright's generalized Bessel function is an entire function and defined as

$$\Phi(a, b; x) = \sum_{k=0}^{\infty} \frac{x^k}{k!\Gamma(ak+b)}$$

See also [1].

Parameters

a	[array_like of float] a >= 0
b	[array_like of float] b >= 0
x	[array_like of float] x >= 0

Notes

Due to the compexity of the function with its three parameters, only non-negative arguments are implemented.

References

[1]

Examples

```
>>> from scipy.special import wright_bessel
>>> a, b, x = 1.5, 1.1, 2.5
>>> wright_bessel(a, b-1, x)
4.5314465939443025
```

Now, let us verify the relation

$$\Phi(a, b-1; x) = ax\Phi(a, b+a; x) + (b-1)\Phi(a, b; x)$$

```
>>> a * x * wright_bessel(a, b+a, x) + (b-1) * wright_bessel(a, b, x)
4.5314465939443025
```

The following is not a universal function:

lmbda(v, x)	Jahnke-Emden Lambda function, Lambdav(x).

scipy.special.lmbda

scipy.special.**lmbda**(*v*, *x*)

Jahnke-Emden Lambda function, Lambdav(x).

This function is defined as [2],

$$\Lambda_v(x) = \Gamma(v+1)\frac{J_v(x)}{(x/2)^v},$$

where Γ is the gamma function and J_v is the Bessel function of the first kind.

Parameters

v	[float] Order of the Lambda function
x	[float] Value at which to evaluate the function and derivatives

Returns

vl	[ndarray] Values of Lambda_vi(x), for vi=v-int(v), vi=1+v-int(v), …, vi=v.
dl	[ndarray] Derivatives Lambda_vi'(x), for vi=v-int(v), vi=1+v-int(v), …, vi=v.

References

[1], [2]

Zeros of Bessel functions

These are not universal functions:

jnjnp_zeros(nt)	Compute zeros of integer-order Bessel functions Jn and Jn'.
jnyn_zeros(n, nt)	Compute nt zeros of Bessel functions Jn(x), Jn'(x), Yn(x), and Yn'(x).
jn_zeros(n, nt)	Compute zeros of integer-order Bessel functions Jn.
jnp_zeros(n, nt)	Compute zeros of integer-order Bessel function derivatives Jn'.
yn_zeros(n, nt)	Compute zeros of integer-order Bessel function Yn(x).
ynp_zeros(n, nt)	Compute zeros of integer-order Bessel function derivatives Yn'(x).

continues on next page

Table 224 – continued from previous page

y0_zeros(nt[, complex])	Compute nt zeros of Bessel function Y0(z), and derivative at each zero.
y1_zeros(nt[, complex])	Compute nt zeros of Bessel function Y1(z), and derivative at each zero.
y1p_zeros(nt[, complex])	Compute nt zeros of Bessel derivative Y1'(z), and value at each zero.

scipy.special.jnjnp_zeros

scipy.special.**jnjnp_zeros**(*nt*)

Compute zeros of integer-order Bessel functions Jn and Jn'.

Results are arranged in order of the magnitudes of the zeros.

Parameters

nt [int] Number (<=1200) of zeros to compute

Returns

zo[l-1] [ndarray] Value of the lth zero of Jn(x) and Jn'(x). Of length *nt*.
n[l-1] [ndarray] Order of the Jn(x) or Jn'(x) associated with lth zero. Of length *nt*.
m[l-1] [ndarray] Serial number of the zeros of Jn(x) or Jn'(x) associated with lth zero. Of length *nt*.
t[l-1] [ndarray] 0 if lth zero in zo is zero of Jn(x), 1 if it is a zero of Jn'(x). Of length *nt*.

See also:

jn_zeros, **jnp_zeros**

to get separated arrays of zeros.

References

[1]

scipy.special.jnyn_zeros

scipy.special.**jnyn_zeros**(*n*, *nt*)

Compute nt zeros of Bessel functions Jn(x), Jn'(x), Yn(x), and Yn'(x).

Returns 4 arrays of length *nt*, corresponding to the first *nt* zeros of Jn(x), Jn'(x), Yn(x), and Yn'(x), respectively. The zeros are returned in ascending order.

Parameters

n [int] Order of the Bessel functions
nt [int] Number (<=1200) of zeros to compute

Returns

Jn [ndarray] First *nt* zeros of Jn
Jnp [ndarray] First *nt* zeros of Jn'
Yn [ndarray] First *nt* zeros of Yn
Ynp [ndarray] First *nt* zeros of Yn'

See also:

jn_zeros, **jnp_zeros**, **yn_zeros**, **ynp_zeros**

References

[1]

scipy.special.jn_zeros

scipy.special.**jn_zeros**(*n*, *nt*)

Compute zeros of integer-order Bessel functions Jn.

Compute *nt* zeros of the Bessel functions $J_n(x)$ on the interval $(0, \infty)$. The zeros are returned in ascending order. Note that this interval excludes the zero at $x = 0$ that exists for $n > 0$.

Parameters

n	[int] Order of Bessel function
nt	[int] Number of zeros to return

Returns

ndarray	First *n* zeros of the Bessel function.

See also:

jv

References

[1]

Examples

```
>>> import scipy.special as sc
```

We can check that we are getting approximations of the zeros by evaluating them with *jv*.

```
>>> n = 1
>>> x = sc.jn_zeros(n, 3)
>>> x
array([ 3.83170597,  7.01558667, 10.17346814])
>>> sc.jv(n, x)
array([-0.00000000e+00,  1.72975330e-16,  2.89157291e-16])
```

Note that the zero at `x = 0` for `n > 0` is not included.

```
>>> sc.jv(1, 0)
0.0
```

scipy.special.jnp_zeros

scipy.special.**jnp_zeros**(*n*, *nt*)

Compute zeros of integer-order Bessel function derivatives Jn'.

Compute *nt* zeros of the functions $J_n'(x)$ on the interval $(0, \infty)$. The zeros are returned in ascending order. Note that this interval excludes the zero at $x = 0$ that exists for $n > 1$.

Parameters

n	[int] Order of Bessel function
nt	[int] Number of zeros to return

Returns

ndarray	First *n* zeros of the Bessel function.

See also:

jvp, **jv**

References

[1]

Examples

```
>>> import scipy.special as sc
```

We can check that we are getting approximations of the zeros by evaluating them with *jvp*.

```
>>> n = 2
>>> x = sc.jnp_zeros(n, 3)
>>> x
array([3.05423693, 6.70613319, 9.96946782])
>>> sc.jvp(n, x)
array([ 2.77555756e-17,  2.08166817e-16, -3.01841885e-16])
```

Note that the zero at `x = 0` for `n > 1` is not included.

```
>>> sc.jvp(n, 0)
0.0
```

scipy.special.yn_zeros

scipy.special.**yn_zeros**(*n*, *nt*)

Compute zeros of integer-order Bessel function Yn(x).

Compute *nt* zeros of the functions $Y_n(x)$ on the interval $(0, \infty)$. The zeros are returned in ascending order.

Parameters

n	[int] Order of Bessel function
nt	[int] Number of zeros to return

Returns

ndarray First *n* zeros of the Bessel function.

See also:

yn, **yv**

References

[1]

Examples

```
>>> import scipy.special as sc
```

We can check that we are getting approximations of the zeros by evaluating them with *yn*.

```
>>> n = 2
>>> x = sc.yn_zeros(n, 3)
>>> x
array([ 3.38424177,  6.79380751, 10.02347798])
>>> sc.yn(n, x)
array([-1.94289029e-16,  8.32667268e-17, -1.52655666e-16])
```

scipy.special.ynp_zeros

scipy.special.**ynp_zeros**(*n*, *nt*)

Compute zeros of integer-order Bessel function derivatives Yn'(x).

Compute *nt* zeros of the functions $Y_n'(x)$ on the interval $(0, \infty)$. The zeros are returned in ascending order.

Parameters

n [int] Order of Bessel function
nt [int] Number of zeros to return

See also:

yvp

References

[1]

Examples

```
>>> import scipy.special as sc
```

We can check that we are getting approximations of the zeros by evaluating them with *yvp*.

```
>>> n = 2
>>> x = sc.ynp_zeros(n, 3)
>>> x
array([ 5.00258293,  8.3507247 , 11.57419547])
>>> sc.yvp(n, x)
array([ 2.22044605e-16, -3.33066907e-16,  2.94902991e-16])
```

scipy.special.y0_zeros

scipy.special.**y0_zeros**(*nt*, *complex=False*)

Compute nt zeros of Bessel function Y0(z), and derivative at each zero.

The derivatives are given by Y0'(z0) = -Y1(z0) at each zero z0.

Parameters

nt	[int] Number of zeros to return
complex	[bool, default False] Set to False to return only the real zeros; set to True to return only the complex zeros with negative real part and positive imaginary part. Note that the complex conjugates of the latter are also zeros of the function, but are not returned by this routine.

Returns

z0n	[ndarray] Location of nth zero of Y0(z)
y0pz0n	[ndarray] Value of derivative Y0'(z0) for nth zero

References

[1]

scipy.special.y1_zeros

scipy.special.**y1_zeros**(*nt*, *complex=False*)

Compute nt zeros of Bessel function Y1(z), and derivative at each zero.

The derivatives are given by Y1'(z1) = Y0(z1) at each zero z1.

Parameters

nt	[int] Number of zeros to return
complex	[bool, default False] Set to False to return only the real zeros; set to True to return only the complex zeros with negative real part and positive imaginary part. Note that the complex conjugates of the latter are also zeros of the function, but are not returned by this routine.

Returns

z1n	[ndarray] Location of nth zero of Y1(z)
y1pz1n	[ndarray] Value of derivative Y1'(z1) for nth zero

References

[1]

scipy.special.y1p_zeros

scipy.special.**y1p_zeros**(*nt*, *complex=False*)

Compute nt zeros of Bessel derivative Y1'(z), and value at each zero.

The values are given by Y1(z1) at each z1 where Y1'(z1)=0.

Parameters

nt [int] Number of zeros to return

complex [bool, default False] Set to False to return only the real zeros; set to True to return only the complex zeros with negative real part and positive imaginary part. Note that the complex conjugates of the latter are also zeros of the function, but are not returned by this routine.

Returns

z1pn [ndarray] Location of nth zero of Y1'(z)

y1z1pn [ndarray] Value of derivative Y1(z1) for nth zero

References

[1]

Faster versions of common Bessel functions

j0(x)	Bessel function of the first kind of order 0.
j1(x)	Bessel function of the first kind of order 1.
y0(x)	Bessel function of the second kind of order 0.
y1(x)	Bessel function of the second kind of order 1.
i0(x)	Modified Bessel function of order 0.
i0e(x)	Exponentially scaled modified Bessel function of order 0.
i1(x)	Modified Bessel function of order 1.
i1e(x)	Exponentially scaled modified Bessel function of order 1.
k0(x)	Modified Bessel function of the second kind of order 0, K_0.
k0e(x)	Exponentially scaled modified Bessel function K of order 0
k1(x)	Modified Bessel function of the second kind of order 1, $K_1(x)$.
k1e(x)	Exponentially scaled modified Bessel function K of order 1

scipy.special.j0

scipy.special.**j0**(*x*) **= <ufunc 'j0'>**

Bessel function of the first kind of order 0.

Parameters

x [array_like] Argument (float).

Returns

J [ndarray] Value of the Bessel function of the first kind of order 0 at *x*.

See also:

jv

Bessel function of real order and complex argument.

spherical_jn

spherical Bessel functions.

Notes

The domain is divided into the intervals [0, 5] and (5, infinity). In the first interval the following rational approximation is used:

$$J_0(x) \approx (w - r_1^2)(w - r_2^2)\frac{P_3(w)}{Q_8(w)},$$

where $w = x^2$ and r_1, r_2 are the zeros of J_0, and P_3 and Q_8 are polynomials of degrees 3 and 8, respectively.

In the second interval, the Hankel asymptotic expansion is employed with two rational functions of degree 6/6 and 7/7.

This function is a wrapper for the Cephes [1] routine *j0*. It should not be confused with the spherical Bessel functions (see *spherical_jn*).

References

[1]

scipy.special.j1

scipy.special.**j1**(*x*) **= <ufunc 'j1'>**

Bessel function of the first kind of order 1.

Parameters

x [array_like] Argument (float).

Returns

J [ndarray] Value of the Bessel function of the first kind of order 1 at *x*.

See also:

jv

spherical_jn

spherical Bessel functions.

Notes

The domain is divided into the intervals [0, 8] and (8, infinity). In the first interval a 24 term Chebyshev expansion is used. In the second, the asymptotic trigonometric representation is employed using two rational functions of degree 5/5.

This function is a wrapper for the Cephes [1] routine *j1*. It should not be confused with the spherical Bessel functions (see *spherical_jn*).

References

[1]

scipy.special.y0

scipy.special.**y0**(*x*) **= <ufunc 'y0'>**

Bessel function of the second kind of order 0.

Parameters

x [array_like] Argument (float).

Returns

Y [ndarray] Value of the Bessel function of the second kind of order 0 at *x*.

See also:

j0

yv

Notes

The domain is divided into the intervals [0, 5] and (5, infinity). In the first interval a rational approximation $R(x)$ is employed to compute,

$$Y_0(x) = R(x) + \frac{2\log(x)J_0(x)}{\pi},$$

where J_0 is the Bessel function of the first kind of order 0.

In the second interval, the Hankel asymptotic expansion is employed with two rational functions of degree 6/6 and 7/7.

This function is a wrapper for the Cephes [1] routine *y0*.

References

[1]

scipy.special.y1

scipy.special.**y1**(*x*) **= <ufunc 'y1'>**

Bessel function of the second kind of order 1.

Parameters

x [array_like] Argument (float).

Returns

Y [ndarray] Value of the Bessel function of the second kind of order 1 at *x*.

See also:

j1

yn

yv

Notes

The domain is divided into the intervals [0, 8] and (8, infinity). In the first interval a 25 term Chebyshev expansion is used, and computing J_1 (the Bessel function of the first kind) is required. In the second, the asymptotic trigonometric representation is employed using two rational functions of degree 5/5.

This function is a wrapper for the Cephes [1] routine *y1*.

References

[1]

scipy.special.i0

scipy.special.**i0**(*x*) **= <ufunc 'i0'>**

Modified Bessel function of order 0.

Defined as,

$$I_0(x) = \sum_{k=0}^{\infty} \frac{(x^2/4)^k}{(k!)^2} = J_0(\imath x),$$

where J_0 is the Bessel function of the first kind of order 0.

Parameters

x [array_like] Argument (float)

Returns

I [ndarray] Value of the modified Bessel function of order 0 at *x*.

See also:

iv

i0e

Notes

The range is partitioned into the two intervals [0, 8] and (8, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine *i0*.

References

[1]

scipy.special.i0e

scipy.special.**i0e**(*x*) **= <ufunc 'i0e'>**

Exponentially scaled modified Bessel function of order 0.

Defined as:

```
i0e(x) = exp(-abs(x)) * i0(x).
```

Parameters

x [array_like] Argument (float)

Returns

I [ndarray] Value of the exponentially scaled modified Bessel function of order 0 at *x*.

See also:

iv

i0

Notes

The range is partitioned into the two intervals [0, 8] and (8, infinity). Chebyshev polynomial expansions are employed in each interval. The polynomial expansions used are the same as those in *i0*, but they are not multiplied by the dominant exponential factor.

This function is a wrapper for the Cephes [1] routine *i0e*.

References

[1]

scipy.special.i1

scipy.special.**i1**(*x*) **= <ufunc 'i1'>**

Modified Bessel function of order 1.

Defined as,

$$I_1(x) = \frac{1}{2}x\sum_{k=0}^{\infty}\frac{(x^2/4)^k}{k!(k+1)!} = -\imath J_1(\imath x),$$

where J_1 is the Bessel function of the first kind of order 1.

Parameters

x [array_like] Argument (float)

Returns

I [ndarray] Value of the modified Bessel function of order 1 at *x*.

See also:

iv

i1e

Notes

The range is partitioned into the two intervals [0, 8] and (8, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine *i1*.

References

[1]

scipy.special.i1e

scipy.special.**i1e**(*x*) **= <ufunc 'i1e'>**

Exponentially scaled modified Bessel function of order 1.

Defined as:

```
i1e(x) = exp(-abs(x)) * i1(x)
```

Parameters

x [array_like] Argument (float)

Returns

I [ndarray] Value of the exponentially scaled modified Bessel function of order 1 at *x*.

See also:

iv

i1

Notes

The range is partitioned into the two intervals [0, 8] and (8, infinity). Chebyshev polynomial expansions are employed in each interval. The polynomial expansions used are the same as those in *i1*, but they are not multiplied by the dominant exponential factor.

This function is a wrapper for the Cephes [1] routine *i1e*.

References

[1]

scipy.special.k0

scipy.special.**k0**(*x*) **= <ufunc 'k0'>**

Modified Bessel function of the second kind of order 0, K_0.

This function is also sometimes referred to as the modified Bessel function of the third kind of order 0.

Parameters

x [array_like] Argument (float).

Returns

K [ndarray] Value of the modified Bessel function K_0 at *x*.

See also:

kv

k0e

Notes

The range is partitioned into the two intervals [0, 2] and (2, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine *k0*.

References

[1]

scipy.special.k0e

scipy.special.**k0e**(*x*) **= <ufunc 'k0e'>**

Exponentially scaled modified Bessel function K of order 0

Defined as:

```
k0e(x) = exp(x) * k0(x).
```

Parameters

x [array_like] Argument (float)

Returns

K [ndarray] Value of the exponentially scaled modified Bessel function K of order 0 at *x*.

See also:

kv

k0

Notes

The range is partitioned into the two intervals [0, 2] and (2, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine *k0e*.

References

[1]

scipy.special.k1

scipy.special.**k1**(*x*) **= <ufunc 'k1'>**

Modified Bessel function of the second kind of order 1, $K_1(x)$.

Parameters

x [array_like] Argument (float)

Returns

K [ndarray] Value of the modified Bessel function K of order 1 at *x*.

See also:

kv

k1e

Notes

The range is partitioned into the two intervals [0, 2] and (2, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine *k1*.

References

[1]

scipy.special.k1e

scipy.special.**k1e**(*x*) **= <ufunc 'k1e'>**

Exponentially scaled modified Bessel function K of order 1

Defined as:

```
k1e(x) = exp(x) * k1(x)
```

Parameters

x [array_like] Argument (float)

Returns

K [ndarray] Value of the exponentially scaled modified Bessel function K of order 1 at *x*.

See also:

kv

k1

Notes

The range is partitioned into the two intervals [0, 2] and (2, infinity). Chebyshev polynomial expansions are employed in each interval.

This function is a wrapper for the Cephes [1] routine *k1e*.

References

[1]

Integrals of Bessel functions

itj0y0(x[, out])	Integrals of Bessel functions of the first kind of order 0.
it2j0y0(x[, out])	Integrals related to Bessel functions of the first kind of order 0.
iti0k0(x[, out])	Integrals of modified Bessel functions of order 0.
it2i0k0(x[, out])	Integrals related to modified Bessel functions of order 0.
besselpoly(a, lmb, nu[, out])	Weighted integral of the Bessel function of the first kind.

scipy.special.itj0y0

scipy.special.**itj0y0**(*x*, *out=None*) **= <ufunc 'itj0y0'>**

Integrals of Bessel functions of the first kind of order 0.

Computes the integrals

$$\int_0^x J_0(t)dt$$
$$\int_0^x Y_0(t)dt.$$

For more on J_0 and Y_0 see j0 and y0.

Parameters

x [array_like] Values at which to evaluate the integrals.
out [tuple of ndarrays, optional] Optional output arrays for the function results.

Returns

ij0 [scalar or ndarray] The integral of j0
iy0 [scalar or ndarray] The integral of y0

scipy.special.it2j0y0

scipy.special.**it2j0y0**(*x*, *out=None*) **= <ufunc 'it2j0y0'>**

Integrals related to Bessel functions of the first kind of order 0.

Computes the integrals

$$\int_0^x \frac{1 - J_0(t)}{t} dt$$
$$\int_x^\infty \frac{Y_0(t)}{t} dt.$$

For more on J_0 and Y_0 see j0 and y0.

Parameters

x [array_like] Values at which to evaluate the integrals.
out [tuple of ndarrays, optional] Optional output arrays for the function results.

Returns

ij0 [scalar or ndarray] The integral for j0
iy0 [scalar or ndarray] The integral for y0

scipy.special.iti0k0

scipy.special.**iti0k0**(*x*, *out=None*) **= <ufunc 'iti0k0'>**

Integrals of modified Bessel functions of order 0.

Computes the integrals

$$\int_0^x I_0(t)dt$$
$$\int_0^x K_0(t)dt.$$

For more on I_0 and K_0 see *i0* and *k0*.

Parameters

x	[array_like] Values at which to evaluate the integrals.
out	[tuple of ndarrays, optional] Optional output arrays for the function results.

Returns

ii0	[scalar or ndarray] The integral for *i0*
ik0	[scalar or ndarray] The integral for *k0*

scipy.special.it2i0k0

scipy.special.**it2i0k0**(*x*, *out=None*) **= <ufunc 'it2i0k0'>**

Integrals related to modified Bessel functions of order 0.

Computes the integrals

$$\int_0^x \frac{I_0(t)-1}{t}dt$$
$$\int_x^\infty \frac{K_0(t)}{t}dt.$$

Parameters

x	[array_like] Values at which to evaluate the integrals.
out	[tuple of ndarrays, optional] Optional output arrays for the function results.

Returns

ii0	[scalar or ndarray] The integral for *i0*
ik0	[scalar or ndarray] The integral for *k0*

scipy.special.besselpoly

scipy.special.**besselpoly**(*a*, *lmb*, *nu*, *out=None*) **= <ufunc 'besselpoly'>**

Weighted integral of the Bessel function of the first kind.

Computes

$$\int_0^1 x^\lambda J_\nu(2ax)\,dx$$

where J_ν is a Bessel function and $\lambda = lmb$, $\nu = nu$.

Parameters

a [array_like] Scale factor inside the Bessel function.
lmb [array_like] Power of x
nu [array_like] Order of the Bessel function.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Value of the integral.

Derivatives of Bessel functions

jvp(v, z[, n])	Compute derivatives of Bessel functions of the first kind.
yvp(v, z[, n])	Compute derivatives of Bessel functions of the second kind.
kvp(v, z[, n])	Compute nth derivative of real-order modified Bessel function Kv(z)
ivp(v, z[, n])	Compute derivatives of modified Bessel functions of the first kind.
h1vp(v, z[, n])	Compute nth derivative of Hankel function H1v(z) with respect to z.
h2vp(v, z[, n])	Compute nth derivative of Hankel function H2v(z) with respect to z.

scipy.special.jvp

scipy.special.**jvp**(*v*, *z*, *n=1*)
Compute derivatives of Bessel functions of the first kind.

Compute the nth derivative of the Bessel function Jv with respect to z.

Parameters

v [float] Order of Bessel function
z [complex] Argument at which to evaluate the derivative; can be real or complex.
n [int, default 1] Order of derivative

Returns

scalar or ndarray
Values of the derivative of the Bessel function.

Notes

The derivative is computed using the relation DLFM 10.6.7 [2].

References

[1], [2]

scipy.special.yvp

scipy.special.**yvp**(*v*, *z*, *n=1*)

Compute derivatives of Bessel functions of the second kind.

Compute the nth derivative of the Bessel function *Yv* with respect to *z*.

Parameters

v	[float] Order of Bessel function
z	[complex] Argument at which to evaluate the derivative
n	[int, default 1] Order of derivative

Returns

scalar or ndarray
nth derivative of the Bessel function.

Notes

The derivative is computed using the relation DLFM 10.6.7 [2].

References

[1], [2]

scipy.special.kvp

scipy.special.**kvp**(*v*, *z*, *n=1*)

Compute nth derivative of real-order modified Bessel function Kv(z)

Kv(z) is the modified Bessel function of the second kind. Derivative is calculated with respect to *z*.

Parameters

v	[array_like of float] Order of Bessel function
z	[array_like of complex] Argument at which to evaluate the derivative
n	[int] Order of derivative. Default is first derivative.

Returns

out	[ndarray] The results

Notes

The derivative is computed using the relation DLFM 10.29.5 [2].

References

[1], [2]

Examples

Calculate multiple values at order 5:

```
>>> from scipy.special import kvp
>>> kvp(5, (1, 2, 3+5j))
array([-1.84903536e+03+0.j        , -2.57735387e+01+0.j        ,
       -3.06627741e-02+0.08750845j])
```

Calculate for a single value at multiple orders:

```
>>> kvp((4, 4.5, 5), 1)
array([ -184.0309,  -568.9585, -1849.0354])
```

scipy.special.ivp

scipy.special.**ivp**(*v*, *z*, *n=1*)

Compute derivatives of modified Bessel functions of the first kind.

Compute the nth derivative of the modified Bessel function *Iv* with respect to *z*.

Parameters

v [array_like] Order of Bessel function
z [array_like] Argument at which to evaluate the derivative; can be real or complex.
n [int, default 1] Order of derivative

Returns

scalar or ndarray
nth derivative of the modified Bessel function.

See also:

iv

Notes

The derivative is computed using the relation DLFM 10.29.5 [2].

References

[1], [2]

scipy.special.h1vp

scipy.special.**h1vp**(*v*, *z*, *n=1*)

Compute nth derivative of Hankel function H1v(z) with respect to *z*.

Parameters

v	[array_like] Order of Hankel function
z	[array_like] Argument at which to evaluate the derivative. Can be real or complex.
n	[int, default 1] Order of derivative

Returns

scalar or ndarray
Values of the derivative of the Hankel function.

Notes

The derivative is computed using the relation DLFM 10.6.7 [2].

References

[1], [2]

scipy.special.h2vp

scipy.special.**h2vp**(*v*, *z*, *n=1*)

Compute nth derivative of Hankel function H2v(z) with respect to *z*.

Parameters

v	[array_like] Order of Hankel function
z	[array_like] Argument at which to evaluate the derivative. Can be real or complex.
n	[int, default 1] Order of derivative

Returns

scalar or ndarray
Values of the derivative of the Hankel function.

Notes

The derivative is computed using the relation DLFM 10.6.7 [2].

References

[1], [2]

Spherical Bessel functions

spherical_jn(n, z[, derivative])	Spherical Bessel function of the first kind or its derivative.
spherical_yn(n, z[, derivative])	Spherical Bessel function of the second kind or its derivative.
spherical_in(n, z[, derivative])	Modified spherical Bessel function of the first kind or its derivative.
spherical_kn(n, z[, derivative])	Modified spherical Bessel function of the second kind or its derivative.

scipy.special.spherical_jn

scipy.special.**spherical_jn**(*n*, *z*, *derivative=False*)

Spherical Bessel function of the first kind or its derivative.

Defined as [1],

$$j_n(z) = \sqrt{\frac{\pi}{2z}} J_{n+1/2}(z),$$

where J_n is the Bessel function of the first kind.

Parameters

n	[int, array_like] Order of the Bessel function (n >= 0).
z	[complex or float, array_like] Argument of the Bessel function.
derivative	[bool, optional] If True, the value of the derivative (rather than the function itself) is returned.

Returns

jn	[ndarray]

Notes

For real arguments greater than the order, the function is computed using the ascending recurrence [2]. For small real or complex arguments, the definitional relation to the cylindrical Bessel function of the first kind is used.

The derivative is computed using the relations [3],

$$j_n'(z) = j_{n-1}(z) - \frac{n+1}{z} j_n(z).$$
$$j_0'(z) = -j_1(z)$$

New in version 0.18.0.

References

[1], [2], [3]

scipy.special.spherical_yn

scipy.special.**spherical_yn**(*n*, *z*, *derivative=False*)

Spherical Bessel function of the second kind or its derivative.

Defined as [1],

$$y_n(z) = \sqrt{\frac{\pi}{2z}} Y_{n+1/2}(z),$$

where Y_n is the Bessel function of the second kind.

Parameters

n	[int, array_like] Order of the Bessel function (n >= 0).
z	[complex or float, array_like] Argument of the Bessel function.
derivative	[bool, optional] If True, the value of the derivative (rather than the function itself) is returned.

Returns

yn	[ndarray]

Notes

For real arguments, the function is computed using the ascending recurrence [2]. For complex arguments, the definitional relation to the cylindrical Bessel function of the second kind is used.

The derivative is computed using the relations [3],

$$y_n' = y_{n-1} - \frac{n+1}{z} y_n.$$
$$y_0' = -y_1$$

New in version 0.18.0.

References

[1], [2], [3]

scipy.special.spherical_in

scipy.special.**spherical_in**(*n*, *z*, *derivative=False*)

Modified spherical Bessel function of the first kind or its derivative.

Defined as [1],

$$i_n(z) = \sqrt{\frac{\pi}{2z}} I_{n+1/2}(z),$$

where I_n is the modified Bessel function of the first kind.

Parameters

n [int, array_like] Order of the Bessel function (n >= 0).
z [complex or float, array_like] Argument of the Bessel function.
derivative [bool, optional] If True, the value of the derivative (rather than the function itself) is returned.

Returns

in [ndarray]

Notes

The function is computed using its definitional relation to the modified cylindrical Bessel function of the first kind.

The derivative is computed using the relations [2],

$$i'_n = i_{n-1} - \frac{n+1}{z} i_n.$$
$$i'_1 = i_0$$

New in version 0.18.0.

References

[1], [2]

scipy.special.spherical_kn

scipy.special.**spherical_kn**(*n*, *z*, *derivative=False*)
Modified spherical Bessel function of the second kind or its derivative.

Defined as [1],

$$k_n(z) = \sqrt{\frac{\pi}{2z}} K_{n+1/2}(z),$$

where K_n is the modified Bessel function of the second kind.

Parameters

n [int, array_like] Order of the Bessel function (n >= 0).
z [complex or float, array_like] Argument of the Bessel function.
derivative [bool, optional] If True, the value of the derivative (rather than the function itself) is returned.

Returns

kn [ndarray]

Notes

The function is computed using its definitional relation to the modified cylindrical Bessel function of the second kind.

The derivative is computed using the relations [2],

$$k'_n = -k_{n-1} - \frac{n+1}{z} k_n.$$
$$k'_0 = -k_1$$

New in version 0.18.0.

References

[1], [2]

Riccati-Bessel functions

These are not universal functions:

riccati_jn(n, x)	Compute Ricatti-Bessel function of the first kind and its derivative.
riccati_yn(n, x)	Compute Ricatti-Bessel function of the second kind and its derivative.

scipy.special.riccati_jn

scipy.special.**riccati_jn**(*n*, *x*)

Compute Ricatti-Bessel function of the first kind and its derivative.

The Ricatti-Bessel function of the first kind is defined as $xj_n(x)$, where j_n is the spherical Bessel function of the first kind of order n.

This function computes the value and first derivative of the Ricatti-Bessel function for all orders up to and including *n*.

Parameters

n	[int] Maximum order of function to compute
x	[float] Argument at which to evaluate

Returns

jn	[ndarray] Value of j0(x), …, jn(x)
jnp	[ndarray] First derivative j0’(x), …, jn’(x)

Notes

The computation is carried out via backward recurrence, using the relation DLMF 10.51.1 [2].

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

References

[1], [2]

scipy.special.riccati_yn

scipy.special.**riccati_yn**(*n*, *x*)

Compute Ricatti-Bessel function of the second kind and its derivative.

The Ricatti-Bessel function of the second kind is defined as $xy_n(x)$, where y_n is the spherical Bessel function of the second kind of order n.

This function computes the value and first derivative of the function for all orders up to and including *n*.

Parameters

n	[int] Maximum order of function to compute
x	[float] Argument at which to evaluate

Returns

yn	[ndarray] Value of y0(x), …, yn(x)
ynp	[ndarray] First derivative y0'(x), …, yn'(x)

Notes

The computation is carried out via ascending recurrence, using the relation DLMF 10.51.1 [2].

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

References

[1], [2]

Struve functions

struve(v, x)	Struve function.
modstruve(v, x)	Modified Struve function.
itstruve0(x)	Integral of the Struve function of order 0.
it2struve0(x)	Integral related to the Struve function of order 0.
itmodstruve0(x)	Integral of the modified Struve function of order 0.

scipy.special.struve

scipy.special.**struve**(*v*, *x*) **= <ufunc 'struve'>**

Struve function.

Return the value of the Struve function of order *v* at *x*. The Struve function is defined as,

$$H_v(x) = (z/2)^{v+1} \sum_{n=0}^{\infty} \frac{(-1)^n (z/2)^{2n}}{\Gamma(n+\frac{3}{2})\Gamma(n+v+\frac{3}{2})},$$

where Γ is the gamma function.

Parameters

v	[array_like] Order of the Struve function (float).
x	[array_like] Argument of the Struve function (float; must be positive unless *v* is an integer).

Returns

H [ndarray] Value of the Struve function of order *v* at *x*.

See also:

`modstruve`

Notes

Three methods discussed in [1] are used to evaluate the Struve function:

- power series
- expansion in Bessel functions (if $|z| < |v| + 20$)
- asymptotic large-z expansion (if $z \geq 0.7v + 12$)

Rounding errors are estimated based on the largest terms in the sums, and the result associated with the smallest error is returned.

References

[1]

scipy.special.modstruve

scipy.special.**modstruve**(*v*, *x*) **= <ufunc 'modstruve'>**

Modified Struve function.

Return the value of the modified Struve function of order *v* at *x*. The modified Struve function is defined as,

$$L_v(x) = -\imath \exp(-\pi\imath v/2) H_v(\imath x),$$

where H_v is the Struve function.

Parameters

v [array_like] Order of the modified Struve function (float).
x [array_like] Argument of the Struve function (float; must be positive unless *v* is an integer).

Returns

L [ndarray] Value of the modified Struve function of order *v* at *x*.

See also:

`struve`

Notes

Three methods discussed in [1] are used to evaluate the function:

- power series
- expansion in Bessel functions (if $|x| < |v| + 20$)
- asymptotic large-x expansion (if $x \geq 0.7v + 12$)

Rounding errors are estimated based on the largest terms in the sums, and the result associated with the smallest error is returned.

References

[1]

scipy.special.itstruve0

scipy.special.**itstruve0**(*x*) **= <ufunc 'itstruve0'>**

Integral of the Struve function of order 0.

$$I = \int_0^x H_0(t)\,dt$$

Parameters

x [array_like] Upper limit of integration (float).

Returns

I [ndarray] The integral of H_0 from 0 to x.

See also:

struve

Notes

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

References

[1]

scipy.special.it2struve0

scipy.special.**it2struve0**(*x*) **= <ufunc 'it2struve0'>**

Integral related to the Struve function of order 0.

Returns the integral,

$$\int_x^\infty \frac{H_0(t)}{t}\,dt$$

where H_0 is the Struve function of order 0.

Parameters

x [array_like] Lower limit of integration.

Returns

I [ndarray] The value of the integral.

See also:

struve

Notes

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

References

[1]

scipy.special.itmodstruve0

scipy.special.**itmodstruve0**(*x*) **= <ufunc 'itmodstruve0'>**

Integral of the modified Struve function of order 0.

$$I = \int_0^x L_0(t)\,dt$$

Parameters

x [array_like] Upper limit of integration (float).

Returns

I [ndarray] The integral of L_0 from 0 to x.

Notes

Wrapper for a Fortran routine created by Shanjie Zhang and Jianming Jin [1].

References

[1]

Raw statistical functions

See also:

scipy.stats: Friendly versions of these functions.

bdtr(k, n, p)	Binomial distribution cumulative distribution function.
bdtrc(k, n, p)	Binomial distribution survival function.
bdtri(k, n, y)	Inverse function to *bdtr* with respect to *p*.
bdtrik(y, n, p)	Inverse function to *bdtr* with respect to *k*.
bdtrin(k, y, p)	Inverse function to *bdtr* with respect to *n*.
btdtr(a, b, x)	Cumulative distribution function of the beta distribution.
btdtri(a, b, p)	The *p*-th quantile of the beta distribution.
btdtria(p, b, x)	Inverse of *btdtr* with respect to *a*.
btdtrib(a, p, x)	Inverse of *btdtr* with respect to *b*.
fdtr(dfn, dfd, x)	F cumulative distribution function.
fdtrc(dfn, dfd, x)	F survival function.
fdtri(dfn, dfd, p)	The *p*-th quantile of the F-distribution.
fdtridfd(dfn, p, x)	Inverse to *fdtr* vs dfd
gdtr(a, b, x)	Gamma distribution cumulative distribution function.

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gdtrc(a, b, x)	Gamma distribution survival function.
gdtria(p, b, x[, out])	Inverse of gdtr vs a.
gdtrib(a, p, x[, out])	Inverse of gdtr vs b.
gdtrix(a, b, p[, out])	Inverse of gdtr vs x.
nbdtr(k, n, p)	Negative binomial cumulative distribution function.
nbdtrc(k, n, p)	Negative binomial survival function.
nbdtri(k, n, y)	Inverse of nbdtr vs *p*.
nbdtrik(y, n, p)	Inverse of nbdtr vs *k*.
nbdtrin(k, y, p)	Inverse of nbdtr vs *n*.
ncfdtr(dfn, dfd, nc, f)	Cumulative distribution function of the non-central F distribution.
ncfdtridfd(dfn, p, nc, f)	Calculate degrees of freedom (denominator) for the non-central F-distribution.
ncfdtridfn(p, dfd, nc, f)	Calculate degrees of freedom (numerator) for the noncentral F-distribution.
ncfdtri(dfn, dfd, nc, p)	Inverse with respect to *f* of the CDF of the non-central F distribution.
ncfdtrinc(dfn, dfd, p, f)	Calculate non-centrality parameter for non-central F distribution.
nctdtr(df, nc, t)	Cumulative distribution function of the non-central *t* distribution.
nctdtridf(p, nc, t)	Calculate degrees of freedom for non-central t distribution.
nctdtrit(df, nc, p)	Inverse cumulative distribution function of the non-central t distribution.
nctdtrinc(df, p, t)	Calculate non-centrality parameter for non-central t distribution.
nrdtrimn(p, x, std)	Calculate mean of normal distribution given other params.
nrdtrisd(p, x, mn)	Calculate standard deviation of normal distribution given other params.
pdtr(k, m[, out])	Poisson cumulative distribution function.
pdtrc(k, m)	Poisson survival function
pdtri(k, y)	Inverse to pdtr vs m
pdtrik(p, m)	Inverse to pdtr vs k
stdtr(df, t)	Student t distribution cumulative distribution function
stdtridf(p, t)	Inverse of stdtr vs df
stdtrit(df, p)	Inverse of stdtr vs *t*
chdtr(v, x[, out])	Chi square cumulative distribution function.
chdtrc(v, x[, out])	Chi square survival function.
chdtri(v, p[, out])	Inverse to chdtrc with respect to *x*.
chdtriv(p, x[, out])	Inverse to chdtr with respect to *v*.
ndtr(x)	Gaussian cumulative distribution function.
log_ndtr(x)	Logarithm of Gaussian cumulative distribution function.
ndtri(y)	Inverse of ndtr vs x
ndtri_exp(y)	Inverse of log_ndtr vs x.
chndtr(x, df, nc)	Non-central chi square cumulative distribution function
chndtridf(x, p, nc)	Inverse to chndtr vs *df*
chndtrinc(x, df, p)	Inverse to chndtr vs *nc*
chndtrix(p, df, nc)	Inverse to chndtr vs *x*

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smirnov(n, d)	Kolmogorov-Smirnov complementary cumulative distribution function
smirnovi(n, p)	Inverse to *smirnov*
kolmogorov(y)	Complementary cumulative distribution (Survival Function) function of Kolmogorov distribution.
kolmogi(p)	Inverse Survival Function of Kolmogorov distribution
tklmbda(x, lmbda)	Tukey-Lambda cumulative distribution function
logit(x)	Logit ufunc for ndarrays.
expit(x)	Expit (a.k.a.
boxcox(x, lmbda)	Compute the Box-Cox transformation.
boxcox1p(x, lmbda)	Compute the Box-Cox transformation of 1 + *x*.
inv_boxcox(y, lmbda)	Compute the inverse of the Box-Cox transformation.
inv_boxcox1p(y, lmbda)	Compute the inverse of the Box-Cox transformation.
owens_t(h, a)	Owen's T Function.

scipy.special.bdtr

scipy.special.**bdtr**(*k*, *n*, *p*) **= <ufunc 'bdtr'>**

Binomial distribution cumulative distribution function.

Sum of the terms 0 through *floor(k)* of the Binomial probability density.

$$\mathrm{bdtr}(k, n, p) = \sum_{j=0}^{\lfloor k \rfloor} \binom{n}{j} p^j (1-p)^{n-j}$$

Parameters

k [array_like] Number of successes (double), rounded down to the nearest integer.
n [array_like] Number of events (int).
p [array_like] Probability of success in a single event (float).

Returns

y [ndarray] Probability of *floor(k)* or fewer successes in *n* independent events with success probabilities of *p*.

Notes

The terms are not summed directly; instead the regularized incomplete beta function is employed, according to the formula,

$$\mathrm{bdtr}(k, n, p) = I_{1-p}(n - \lfloor k \rfloor, \lfloor k \rfloor + 1).$$

Wrapper for the Cephes [1] routine *bdtr*.

References

[1]

scipy.special.bdtrc

scipy.special.**bdtrc**(*k*, *n*, *p*) **= <ufunc 'bdtrc'>**

Binomial distribution survival function.

Sum of the terms *floor(k) + 1* through *n* of the binomial probability density,

$$\mathrm{bdtrc}(k, n, p) = \sum_{j=\lfloor k \rfloor + 1}^{n} \binom{n}{j} p^j (1-p)^{n-j}$$

Parameters

k	[array_like] Number of successes (double), rounded down to nearest integer.
n	[array_like] Number of events (int)
p	[array_like] Probability of success in a single event.

Returns

y	[ndarray] Probability of *floor(k) + 1* or more successes in *n* independent events with success probabilities of *p*.

See also:

bdtr

betainc

Notes

The terms are not summed directly; instead the regularized incomplete beta function is employed, according to the formula,

$$\mathrm{bdtrc}(k, n, p) = I_p(\lfloor k \rfloor + 1, n - \lfloor k \rfloor).$$

Wrapper for the Cephes [1] routine *bdtrc*.

References

[1]

scipy.special.bdtri

scipy.special.**bdtri**(*k*, *n*, *y*) **= <ufunc 'bdtri'>**

Inverse function to *bdtr* with respect to *p*.

Finds the event probability *p* such that the sum of the terms 0 through *k* of the binomial probability density is equal to the given cumulative probability *y*.

Parameters

k	[array_like] Number of successes (float), rounded down to the nearest integer.

n [array_like] Number of events (float)
y [array_like] Cumulative probability (probability of *k* or fewer successes in *n* events).

Returns

p [ndarray] The event probability such that *bdtr(lfloor k rfloor, n, p) = y*.

See also:

bdtr

betaincinv

Notes

The computation is carried out using the inverse beta integral function and the relation,:

```
1 - p = betaincinv(n - k, k + 1, y).
```

Wrapper for the Cephes [1] routine *bdtri*.

References

[1]

scipy.special.bdtrik

scipy.special.**bdtrik**(*y*, *n*, *p*) **= <ufunc 'bdtrik'>**
Inverse function to *bdtr* with respect to *k*.

Finds the number of successes *k* such that the sum of the terms 0 through *k* of the Binomial probability density for *n* events with probability *p* is equal to the given cumulative probability *y*.

Parameters

y [array_like] Cumulative probability (probability of *k* or fewer successes in *n* events).
n [array_like] Number of events (float).
p [array_like] Success probability (float).

Returns

k [ndarray] The number of successes *k* such that *bdtr(k, n, p) = y*.

See also:

bdtr

Notes

Formula 26.5.24 of [1] is used to reduce the binomial distribution to the cumulative incomplete beta distribution.

Computation of *k* involves a search for a value that produces the desired value of *y*. The search relies on the monotonicity of *y* with *k*.

Wrapper for the CDFLIB [2] Fortran routine *cdfbin*.

References

[1], [2]

scipy.special.bdtrin

scipy.special.**bdtrin**(*k*, *y*, *p*) **= <ufunc 'bdtrin'>**

Inverse function to *bdtr* with respect to *n*.

Finds the number of events *n* such that the sum of the terms 0 through *k* of the Binomial probability density for events with probability *p* is equal to the given cumulative probability *y*.

Parameters

k	[array_like] Number of successes (float).
y	[array_like] Cumulative probability (probability of *k* or fewer successes in *n* events).
p	[array_like] Success probability (float).

Returns

n	[ndarray] The number of events *n* such that *bdtr(k, n, p) = y*.

See also:

bdtr

Notes

Formula 26.5.24 of [1] is used to reduce the binomial distribution to the cumulative incomplete beta distribution.

Computation of *n* involves a search for a value that produces the desired value of *y*. The search relies on the monotonicity of *y* with *n*.

Wrapper for the CDFLIB [2] Fortran routine *cdfbin*.

References

[1], [2]

scipy.special.btdtr

scipy.special.**btdtr**(*a*, *b*, *x*) **= <ufunc 'btdtr'>**

Cumulative distribution function of the beta distribution.

Returns the integral from zero to *x* of the beta probability density function,

$$I = \int_0^x \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} t^{a-1}(1-t)^{b-1}\,dt$$

where Γ is the gamma function.

Parameters

a	[array_like] Shape parameter (a > 0).
b	[array_like] Shape parameter (b > 0).
x	[array_like] Upper limit of integration, in [0, 1].

Returns

I	[ndarray] Cumulative distribution function of the beta distribution with parameters *a* and *b* at *x*.

See also:

`betainc`

Notes

This function is identical to the incomplete beta integral function `betainc`.

Wrapper for the Cephes [1] routine `btdtr`.

References

[1]

scipy.special.btdtri

scipy.special.**btdtri**(*a*, *b*, *p*) **= <ufunc 'btdtri'>**

The *p*-th quantile of the beta distribution.

This function is the inverse of the beta cumulative distribution function, `btdtr`, returning the value of *x* for which *btdtr(a, b, x)* = *p*, or

$$p = \int_0^x \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} t^{a-1}(1-t)^{b-1}\,dt$$

Parameters

a	[array_like] Shape parameter ($a > 0$).
b	[array_like] Shape parameter ($b > 0$).
p	[array_like] Cumulative probability, in [0, 1].

Returns

x	[ndarray] The quantile corresponding to *p*.

See also:

betaincinv

btdtr

Notes

The value of *x* is found by interval halving or Newton iterations.

Wrapper for the Cephes [1] routine *incbi*, which solves the equivalent problem of finding the inverse of the incomplete beta integral.

References

[1]

scipy.special.btdtria

scipy.special.**btdtria**(*p*, *b*, *x*) **= <ufunc 'btdtria'>**

Inverse of *btdtr* with respect to *a*.

This is the inverse of the beta cumulative distribution function, *btdtr*, considered as a function of *a*, returning the value of *a* for which *btdtr(a, b, x)* = *p*, or

$$p = \int_0^x \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} t^{a-1}(1-t)^{b-1}\,dt$$

Parameters

p	[array_like] Cumulative probability, in [0, 1].
b	[array_like] Shape parameter ($b > 0$).
x	[array_like] The quantile, in [0, 1].

Returns

a	[ndarray] The value of the shape parameter *a* such that *btdtr(a, b, x)* = *p*.

See also:

btdtr

Cumulative distribution function of the beta distribution.

btdtri

Inverse with respect to *x*.

btdtrib

Inverse with respect to *b*.

Notes

Wrapper for the CDFLIB [1] Fortran routine *cdfbet*.

The cumulative distribution function *p* is computed using a routine by DiDinato and Morris [2]. Computation of *a* involves a search for a value that produces the desired value of *p*. The search relies on the monotonicity of *p* with *a*.

References

[1], [2]

scipy.special.btdtrib

scipy.special.**btdtrib**(*a*, *p*, *x*) **= <ufunc 'btdtrib'>**

Inverse of `btdtr` with respect to *b*.

This is the inverse of the beta cumulative distribution function, `btdtr`, considered as a function of *b*, returning the value of *b* for which *btdtr(a, b, x)* = *p*, or

$$p = \int_0^x \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} t^{a-1}(1-t)^{b-1}\,dt$$

Parameters

a	[array_like] Shape parameter ($a > 0$).
p	[array_like] Cumulative probability, in [0, 1].
x	[array_like] The quantile, in [0, 1].

Returns

b	[ndarray] The value of the shape parameter *b* such that *btdtr(a, b, x)* = *p*.

See also:

btdtr

Cumulative distribution function of the beta distribution.

btdtri

Inverse with respect to *x*.

btdtria

Inverse with respect to *a*.

Notes

Wrapper for the CDFLIB [1] Fortran routine *cdfbet*.

The cumulative distribution function *p* is computed using a routine by DiDinato and Morris [2]. Computation of *b* involves a search for a value that produces the desired value of *p*. The search relies on the monotonicity of *p* with *b*.

References

[1], [2]

scipy.special.fdtr

scipy.special.**fdtr**(*dfn*, *dfd*, *x*) **= <ufunc 'fdtr'>**

F cumulative distribution function.

Returns the value of the cumulative distribution function of the F-distribution, also known as Snedecor's F-distribution or the Fisher-Snedecor distribution.

The F-distribution with parameters d_n and d_d is the distribution of the random variable,

$$X = \frac{U_n/d_n}{U_d/d_d},$$

where U_n and U_d are random variables distributed χ^2, with d_n and d_d degrees of freedom, respectively.

Parameters

dfn	[array_like] First parameter (positive float).
dfd	[array_like] Second parameter (positive float).
x	[array_like] Argument (nonnegative float).

Returns

y	[ndarray] The CDF of the F-distribution with parameters *dfn* and *dfd* at *x*.

Notes

The regularized incomplete beta function is used, according to the formula,

$$F(d_n, d_d; x) = I_{xd_n/(d_d+xd_n)}(d_n/2, d_d/2).$$

Wrapper for the Cephes [1] routine `fdtr`.

References

[1]

scipy.special.fdtrc

scipy.special.**fdtrc**(*dfn*, *dfd*, *x*) **= <ufunc 'fdtrc'>**

F survival function.

Returns the complemented F-distribution function (the integral of the density from *x* to infinity).

Parameters

dfn	[array_like] First parameter (positive float).
dfd	[array_like] Second parameter (positive float).
x	[array_like] Argument (nonnegative float).

Returns

y [ndarray] The complemented F-distribution function with parameters *dfn* and *dfd* at *x*.

See also:

`fdtr`

Notes

The regularized incomplete beta function is used, according to the formula,

$$F(d_n, d_d; x) = I_{d_d/(d_d+xd_n)}(d_d/2, d_n/2).$$

Wrapper for the Cephes [1] routine `fdtrc`.

References

[1]

scipy.special.fdtri

scipy.special.**fdtri**(*dfn*, *dfd*, *p*) **= <ufunc 'fdtri'>**

The *p*-th quantile of the F-distribution.

This function is the inverse of the F-distribution CDF, `fdtr`, returning the *x* such that *fdtr(dfn, dfd, x) = p*.

Parameters

dfn [array_like] First parameter (positive float).
dfd [array_like] Second parameter (positive float).
p [array_like] Cumulative probability, in [0, 1].

Returns

x [ndarray] The quantile corresponding to *p*.

Notes

The computation is carried out using the relation to the inverse regularized beta function, $I_x^{-1}(a, b)$. Let $z = I_p^{-1}(d_d/2, d_n/2)$. Then,

$$x = \frac{d_d(1-z)}{d_n z}.$$

If *p* is such that $x < 0.5$, the following relation is used instead for improved stability: let $z' = I_{1-p}^{-1}(d_n/2, d_d/2)$. Then,

$$x = \frac{d_d z'}{d_n(1-z')}.$$

Wrapper for the Cephes [1] routine `fdtri`.

References

[1]

scipy.special.fdtridfd

scipy.special.**fdtridfd**(*dfn*, *p*, *x*) **= <ufunc 'fdtridfd'>**
Inverse to *fdtr* vs dfd

Finds the F density argument dfd such that `fdtr(dfn, dfd, x) == p`.

scipy.special.gdtr

scipy.special.**gdtr**(*a*, *b*, *x*) **= <ufunc 'gdtr'>**
Gamma distribution cumulative distribution function.

Returns the integral from zero to *x* of the gamma probability density function,

$$F = \int_0^x \frac{a^b}{\Gamma(b)} t^{b-1} e^{-at}\,dt,$$

where Γ is the gamma function.

Parameters

a	[array_like] The rate parameter of the gamma distribution, sometimes denoted β (float). It is also the reciprocal of the scale parameter θ.
b	[array_like] The shape parameter of the gamma distribution, sometimes denoted α (float).
x	[array_like] The quantile (upper limit of integration; float).

Returns

F	[ndarray] The CDF of the gamma distribution with parameters *a* and *b* evaluated at *x*.

See also:

gdtrc

1 - CDF of the gamma distribution.

Notes

The evaluation is carried out using the relation to the incomplete gamma integral (regularized gamma function).

Wrapper for the Cephes [1] routine *gdtr*.

References

[1]

scipy.special.gdtrc

scipy.special.**gdtrc**(*a*, *b*, *x*) **= <ufunc 'gdtrc'>**

Gamma distribution survival function.

Integral from *x* to infinity of the gamma probability density function,

$$F = \int_x^\infty \frac{a^b}{\Gamma(b)} t^{b-1} e^{-at}\,dt,$$

where Γ is the gamma function.

Parameters

a	[array_like] The rate parameter of the gamma distribution, sometimes denoted β (float). It is also the reciprocal of the scale parameter θ.
b	[array_like] The shape parameter of the gamma distribution, sometimes denoted α (float).
x	[array_like] The quantile (lower limit of integration; float).

Returns

F	[ndarray] The survival function of the gamma distribution with parameters *a* and *b* evaluated at *x*.

See also:

gdtr, **gdtrix**

Notes

The evaluation is carried out using the relation to the incomplete gamma integral (regularized gamma function).

Wrapper for the Cephes [1] routine *gdtrc*.

References

[1]

scipy.special.gdtria

scipy.special.**gdtria**(*p*, *b*, *x*, *out=None*) **= <ufunc 'gdtria'>**

Inverse of *gdtr* vs a.

Returns the inverse with respect to the parameter *a* of `p = gdtr(a, b, x)`, the cumulative distribution function of the gamma distribution.

Parameters

p	[array_like] Probability values.
b	[array_like] *b* parameter values of *gdtr(a, b, x)*. *b* is the "shape" parameter of the gamma distribution.
x	[array_like] Nonnegative real values, from the domain of the gamma distribution.
out	[ndarray, optional] If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of *a*, *b* and *x*. *out* is then the array returned by the function.

Returns

a [ndarray] Values of the *a* parameter such that *p = gdtr(a, b, x)*. *1/a* is the "scale" parameter of the gamma distribution.

See also:

gdtr

CDF of the gamma distribution.

gdtrib

Inverse with respect to *b* of *gdtr(a, b, x)*.

gdtrix

Inverse with respect to *x* of *gdtr(a, b, x)*.

Notes

Wrapper for the CDFLIB [1] Fortran routine *cdfgam*.

The cumulative distribution function *p* is computed using a routine by DiDinato and Morris [2]. Computation of *a* involves a search for a value that produces the desired value of *p*. The search relies on the monotonicity of *p* with *a*.

References

[1], [2]

Examples

First evaluate *gdtr*.

```
>>> from scipy.special import gdtr, gdtria
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```

Verify the inverse.

```
>>> gdtria(p, 3.4, 5.6)
1.2
```

scipy.special.gdtrib

scipy.special.**gdtrib**(*a*, *p*, *x*, *out=None*) **= <ufunc 'gdtrib'>**

Inverse of *gdtr* vs b.

Returns the inverse with respect to the parameter *b* of `p = gdtr(a, b, x)`, the cumulative distribution function of the gamma distribution.

Parameters

a [array_like] *a* parameter values of *gdtr(a, b, x)*. *1/a* is the "scale" parameter of the gamma distribution.

p	[array_like] Probability values.
x	[array_like] Nonnegative real values, from the domain of the gamma distribution.
out	[ndarray, optional] If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of *a*, *b* and *x*. *out* is then the array returned by the function.

Returns

b	[ndarray] Values of the *b* parameter such that *p = gdtr(a, b, x)*. *b* is the "shape" parameter of the gamma distribution.

See also:

gdtr

CDF of the gamma distribution.

gdtria

Inverse with respect to *a* of *gdtr(a, b, x)*.

gdtrix

Inverse with respect to *x* of *gdtr(a, b, x)*.

Notes

Wrapper for the CDFLIB [1] Fortran routine *cdfgam*.

The cumulative distribution function *p* is computed using a routine by DiDinato and Morris [2]. Computation of *b* involves a search for a value that produces the desired value of *p*. The search relies on the monotonicity of *p* with *b*.

References

[1], [2]

Examples

First evaluate *gdtr*.

```
>>> from scipy.special import gdtr, gdtrib
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```

Verify the inverse.

```
>>> gdtrib(1.2, p, 5.6)
3.3999999999723882
```

scipy.special.gdtrix

scipy.special.**gdtrix**(*a*, *b*, *p*, *out=None*) **= <ufunc 'gdtrix'>**

Inverse of *gdtr* vs x.

Returns the inverse with respect to the parameter *x* of `p = gdtr(a, b, x)`, the cumulative distribution function of the gamma distribution. This is also known as the pth quantile of the distribution.

Parameters

a	[array_like] *a* parameter values of *gdtr(a, b, x)*. *1/a* is the "scale" parameter of the gamma distribution.
b	[array_like] *b* parameter values of *gdtr(a, b, x)*. *b* is the "shape" parameter of the gamma distribution.
p	[array_like] Probability values.
out	[ndarray, optional] If a fourth argument is given, it must be a numpy.ndarray whose size matches the broadcast result of *a*, *b* and *x*. *out* is then the array returned by the function.

Returns

x	[ndarray] Values of the *x* parameter such that *p* = *gdtr(a, b, x)*.

See also:

gdtr

CDF of the gamma distribution.

gdtria

Inverse with respect to *a* of *gdtr(a, b, x)*.

gdtrib

Inverse with respect to *b* of *gdtr(a, b, x)*.

Notes

Wrapper for the CDFLIB [1] Fortran routine *cdfgam*.

The cumulative distribution function *p* is computed using a routine by DiDinato and Morris [2]. Computation of *x* involves a search for a value that produces the desired value of *p*. The search relies on the monotonicity of *p* with *x*.

References

[1], [2]

Examples

First evaluate *gdtr*.

```
>>> from scipy.special import gdtr, gdtrix
>>> p = gdtr(1.2, 3.4, 5.6)
>>> print(p)
0.94378087442
```

Verify the inverse.

```
>>> gdtrix(1.2, 3.4, p)
5.5999999999999996
```

scipy.special.nbdtr

scipy.special.**nbdtr**(*k*, *n*, *p*) **= <ufunc 'nbdtr'>**

Negative binomial cumulative distribution function.

Returns the sum of the terms 0 through *k* of the negative binomial distribution probability mass function,

$$F = \sum_{j=0}^{k} \binom{n+j-1}{j} p^n (1-p)^j.$$

In a sequence of Bernoulli trials with individual success probabilities *p*, this is the probability that *k* or fewer failures precede the nth success.

Parameters

k	[array_like] The maximum number of allowed failures (nonnegative int).
n	[array_like] The target number of successes (positive int).
p	[array_like] Probability of success in a single event (float).

Returns

F	[ndarray] The probability of *k* or fewer failures before *n* successes in a sequence of events with individual success probability *p*.

See also:

nbdtrc

Notes

If floating point values are passed for *k* or *n*, they will be truncated to integers.

The terms are not summed directly; instead the regularized incomplete beta function is employed, according to the formula,

$$\mathrm{nbdtr}(k, n, p) = I_p(n, k+1).$$

Wrapper for the Cephes [1] routine *nbdtr*.

References

[1]

scipy.special.nbdtrc

scipy.special.**nbdtrc**(*k*, *n*, *p*) **= <ufunc 'nbdtrc'>**

Negative binomial survival function.

Returns the sum of the terms *k + 1* to infinity of the negative binomial distribution probability mass function,

$$F = \sum_{j=k+1}^{\infty} \binom{n+j-1}{j} p^n (1-p)^j.$$

In a sequence of Bernoulli trials with individual success probabilities *p*, this is the probability that more than *k* failures precede the nth success.

Parameters

k [array_like] The maximum number of allowed failures (nonnegative int).
n [array_like] The target number of successes (positive int).
p [array_like] Probability of success in a single event (float).

Returns

F [ndarray] The probability of *k + 1* or more failures before *n* successes in a sequence of events with individual success probability *p*.

Notes

If floating point values are passed for *k* or *n*, they will be truncated to integers.

The terms are not summed directly; instead the regularized incomplete beta function is employed, according to the formula,

$$\mathrm{nbdtrc}(k, n, p) = I_{1-p}(k+1, n).$$

Wrapper for the Cephes [1] routine *nbdtrc*.

References

[1]

scipy.special.nbdtri

scipy.special.**nbdtri**(*k*, *n*, *y*) **= <ufunc 'nbdtri'>**

Inverse of *nbdtr* vs *p*.

Returns the inverse with respect to the parameter *p* of *y = nbdtr(k, n, p)*, the negative binomial cumulative distribution function.

Parameters

k [array_like] The maximum number of allowed failures (nonnegative int).
n [array_like] The target number of successes (positive int).

y [array_like] The probability of *k* or fewer failures before *n* successes (float).

Returns

p [ndarray] Probability of success in a single event (float) such that *nbdtr(k, n, p) = y*.

See also:

nbdtr

Cumulative distribution function of the negative binomial.

nbdtrik

Inverse with respect to *k* of *nbdtr(k, n, p)*.

nbdtrin

Inverse with respect to *n* of *nbdtr(k, n, p)*.

Notes

Wrapper for the Cephes [1] routine *nbdtri*.

References

[1]

scipy.special.nbdtrik

scipy.special.**nbdtrik**(*y*, *n*, *p*) **= <ufunc 'nbdtrik'>**

Inverse of *nbdtr* vs *k*.

Returns the inverse with respect to the parameter *k* of *y = nbdtr(k, n, p)*, the negative binomial cumulative distribution function.

Parameters

y [array_like] The probability of *k* or fewer failures before *n* successes (float).
n [array_like] The target number of successes (positive int).
p [array_like] Probability of success in a single event (float).

Returns

k [ndarray] The maximum number of allowed failures such that *nbdtr(k, n, p) = y*.

See also:

nbdtr

Cumulative distribution function of the negative binomial.

nbdtri

Inverse with respect to *p* of *nbdtr(k, n, p)*.

nbdtrin

Inverse with respect to *n* of *nbdtr(k, n, p)*.

Notes

Wrapper for the CDFLIB [1] Fortran routine *cdfnbn*.

Formula 26.5.26 of [2],

$$\sum_{j=k+1}^{\infty} \binom{n+j-1}{j} p^n (1-p)^j = I_{1-p}(k+1, n),$$

is used to reduce calculation of the cumulative distribution function to that of a regularized incomplete beta I.

Computation of k involves a search for a value that produces the desired value of y. The search relies on the monotonicity of y with k.

References

[1], [2]

scipy.special.nbdtrin

scipy.special.**nbdtrin**(*k*, *y*, *p*) **= <ufunc 'nbdtrin'>**

Inverse of *nbdtr* vs *n*.

Returns the inverse with respect to the parameter *n* of *y = nbdtr(k, n, p)*, the negative binomial cumulative distribution function.

Parameters

k	[array_like] The maximum number of allowed failures (nonnegative int).
y	[array_like] The probability of *k* or fewer failures before *n* successes (float).
p	[array_like] Probability of success in a single event (float).

Returns

n	[ndarray] The number of successes *n* such that *nbdtr(k, n, p) = y*.

See also:

nbdtr

Cumulative distribution function of the negative binomial.

nbdtri

Inverse with respect to *p* of *nbdtr(k, n, p)*.

nbdtrik

Inverse with respect to *k* of *nbdtr(k, n, p)*.

Notes

Wrapper for the CDFLIB [1] Fortran routine *cdfnbn*.

Formula 26.5.26 of [2],

$$\sum_{j=k+1}^{\infty} \binom{n+j-1}{j} p^n (1-p)^j = I_{1-p}(k+1, n),$$

is used to reduce calculation of the cumulative distribution function to that of a regularized incomplete beta I.

Computation of *n* involves a search for a value that produces the desired value of *y*. The search relies on the monotonicity of *y* with *n*.

References

[1], [2]

scipy.special.ncfdtr

scipy.special.**ncfdtr**(*dfn*, *dfd*, *nc*, *f*) **= <ufunc 'ncfdtr'>**

Cumulative distribution function of the non-central F distribution.

The non-central F describes the distribution of,

$$Z = \frac{X/d_n}{Y/d_d}$$

where X and Y are independently distributed, with X distributed non-central χ^2 with noncentrality parameter *nc* and d_n degrees of freedom, and Y distributed χ^2 with d_d degrees of freedom.

Parameters

dfn	[array_like] Degrees of freedom of the numerator sum of squares. Range (0, inf).
dfd	[array_like] Degrees of freedom of the denominator sum of squares. Range (0, inf).
nc	[array_like] Noncentrality parameter. Should be in range (0, 1e4).
f	[array_like] Quantiles, i.e. the upper limit of integration.

Returns

cdf	[float or ndarray] The calculated CDF. If all inputs are scalar, the return will be a float. Otherwise it will be an array.

See also:

ncfdtri

Quantile function; inverse of *ncfdtr* with respect to *f*.

ncfdtridfd

Inverse of *ncfdtr* with respect to *dfd*.

ncfdtridfn

Inverse of *ncfdtr* with respect to *dfn*.

ncfdtrinc

Inverse of *ncfdtr* with respect to *nc*.

Notes

Wrapper for the CDFLIB [1] Fortran routine *cdffnc*.

The cumulative distribution function is computed using Formula 26.6.20 of [2]:

$$F(d_n, d_d, n_c, f) = \sum_{j=0}^{\infty} e^{-n_c/2} \frac{(n_c/2)^j}{j!} I_x(\frac{d_n}{2} + j, \frac{d_d}{2}),$$

where I is the regularized incomplete beta function, and $x = f d_n/(f d_n + d_d)$.

The computation time required for this routine is proportional to the noncentrality parameter *nc*. Very large values of this parameter can consume immense computer resources. This is why the search range is bounded by 10,000.

References

[1], [2]

Examples

```
>>> from scipy import special
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

Plot the CDF of the non-central F distribution, for nc=0. Compare with the F-distribution from scipy.stats:

```
>>> x = np.linspace(-1, 8, num=500)
>>> dfn = 3
>>> dfd = 2
>>> ncf_stats = stats.f.cdf(x, dfn, dfd)
>>> ncf_special = special.ncfdtr(dfn, dfd, 0, x)
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, ncf_stats, 'b-', lw=3)
>>> ax.plot(x, ncf_special, 'r-')
>>> plt.show()
```

scipy.special.ncfdtridfd

scipy.special.**ncfdtridfd**(*dfn*, *p*, *nc*, *f*) **= <ufunc 'ncfdtridfd'>**

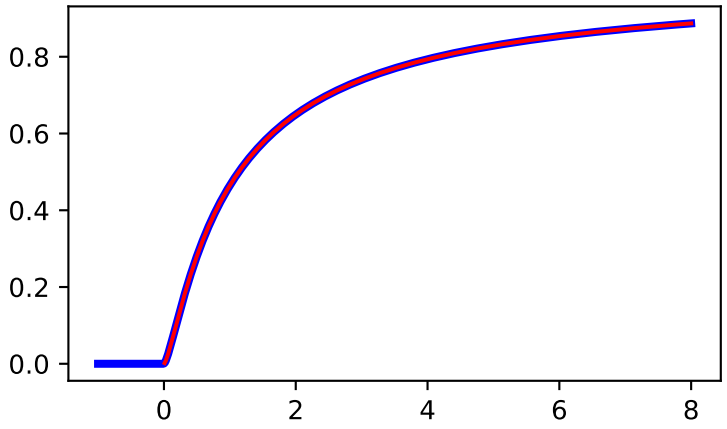
Calculate degrees of freedom (denominator) for the noncentral F-distribution.

This is the inverse with respect to *dfd* of *ncfdtr*. See *ncfdtr* for more details.

Parameters

dfn	[array_like] Degrees of freedom of the numerator sum of squares. Range (0, inf).
p	[array_like] Value of the cumulative distribution function. Must be in the range [0, 1].
nc	[array_like] Noncentrality parameter. Should be in range (0, 1e4).
f	[array_like] Quantiles, i.e., the upper limit of integration.

Returns



dfd [float] Degrees of freedom of the denominator sum of squares.

See also:

ncfdtr

CDF of the non-central F distribution.

ncfdtri

Quantile function; inverse of *ncfdtr* with respect to *f*.

ncfdtridfn

Inverse of *ncfdtr* with respect to *dfn*.

ncfdtrinc

Inverse of *ncfdtr* with respect to *nc*.

Notes

The value of the cumulative noncentral F distribution is not necessarily monotone in either degrees of freedom. There thus may be two values that provide a given CDF value. This routine assumes monotonicity and will find an arbitrary one of the two values.

Examples

```
>>> from scipy.special import ncfdtr, ncfdtridfd
```

Compute the CDF for several values of *dfd*:

```
>>> dfd = [1, 2, 3]
>>> p = ncfdtr(2, dfd, 0.25, 15)
>>> p
array([ 0.8097138 ,  0.93020416,  0.96787852])
```

Compute the inverse. We recover the values of *dfd*, as expected:

```
>>> ncfdtridfd(2, p, 0.25, 15)
array([ 1.,  2.,  3.])
```

scipy.special.ncfdtridfn

scipy.special.**ncfdtridfn**(*p*, *dfd*, *nc*, *f*) **= <ufunc 'ncfdtridfn'>**

Calculate degrees of freedom (numerator) for the noncentral F-distribution.

This is the inverse with respect to *dfn* of *ncfdtr*. See *ncfdtr* for more details.

Parameters

p	[array_like] Value of the cumulative distribution function. Must be in the range [0, 1].
dfd	[array_like] Degrees of freedom of the denominator sum of squares. Range (0, inf).
nc	[array_like] Noncentrality parameter. Should be in range (0, 1e4).
f	[float] Quantiles, i.e., the upper limit of integration.

Returns

dfn	[float] Degrees of freedom of the numerator sum of squares.

See also:

ncfdtr

CDF of the non-central F distribution.

ncfdtri

Quantile function; inverse of *ncfdtr* with respect to *f*.

ncfdtridfd

Inverse of *ncfdtr* with respect to *dfd*.

ncfdtrinc

Inverse of *ncfdtr* with respect to *nc*.

Notes

The value of the cumulative noncentral F distribution is not necessarily monotone in either degrees of freedom. There thus may be two values that provide a given CDF value. This routine assumes monotonicity and will find an arbitrary one of the two values.

Examples

```
>>> from scipy.special import ncfdtr, ncfdtridfn
```

Compute the CDF for several values of *dfn*:

```
>>> dfn = [1, 2, 3]
>>> p = ncfdtr(dfn, 2, 0.25, 15)
>>> p
array([ 0.92562363,  0.93020416,  0.93188394])
```

Compute the inverse. We recover the values of *dfn*, as expected:

```
>>> ncfdtridfn(p, 2, 0.25, 15)
array([ 1.,  2.,  3.])
```

scipy.special.ncfdtri

scipy.special.**ncfdtri**(*dfn*, *dfd*, *nc*, *p*) **= <ufunc 'ncfdtri'>**

Inverse with respect to *f* of the CDF of the non-central F distribution.

See *ncfdtr* for more details.

Parameters

dfn	[array_like] Degrees of freedom of the numerator sum of squares. Range (0, inf).
dfd	[array_like] Degrees of freedom of the denominator sum of squares. Range (0, inf).
nc	[array_like] Noncentrality parameter. Should be in range (0, 1e4).
p	[array_like] Value of the cumulative distribution function. Must be in the range [0, 1].

Returns

f	[float] Quantiles, i.e., the upper limit of integration.

See also:

ncfdtr

CDF of the non-central F distribution.

ncfdtridfd

Inverse of *ncfdtr* with respect to *dfd*.

ncfdtridfn

Inverse of *ncfdtr* with respect to *dfn*.

ncfdtrinc

Inverse of *ncfdtr* with respect to *nc*.

Examples

```
>>> from scipy.special import ncfdtr, ncfdtri
```

Compute the CDF for several values of *f*:

```
>>> f = [0.5, 1, 1.5]
>>> p = ncfdtr(2, 3, 1.5, f)
>>> p
array([ 0.20782291,  0.36107392,  0.47345752])
```

Compute the inverse. We recover the values of *f*, as expected:

```
>>> ncfdtri(2, 3, 1.5, p)
array([ 0.5,  1. ,  1.5])
```

scipy.special.ncfdtrinc

scipy.special.**ncfdtrinc**(*dfn*, *dfd*, *p*, *f*) **= <ufunc 'ncfdtrinc'>**

Calculate non-centrality parameter for non-central F distribution.

This is the inverse with respect to *nc* of `ncfdtr`. See `ncfdtr` for more details.

Parameters

dfn	[array_like] Degrees of freedom of the numerator sum of squares. Range (0, inf).
dfd	[array_like] Degrees of freedom of the denominator sum of squares. Range (0, inf).
p	[array_like] Value of the cumulative distribution function. Must be in the range [0, 1].
f	[array_like] Quantiles, i.e., the upper limit of integration.

Returns

nc	[float] Noncentrality parameter.

See also:

ncfdtr

CDF of the non-central F distribution.

ncfdtri

Quantile function; inverse of `ncfdtr` with respect to *f*.

ncfdtridfd

Inverse of `ncfdtr` with respect to *dfd*.

ncfdtridfn

Inverse of `ncfdtr` with respect to *dfn*.

Examples

```
>>> from scipy.special import ncfdtr, ncfdtrinc
```

Compute the CDF for several values of *nc*:

```
>>> nc = [0.5, 1.5, 2.0]
>>> p = ncfdtr(2, 3, nc, 15)
>>> p
array([ 0.96309246,  0.94327955,  0.93304098])
```

Compute the inverse. We recover the values of *nc*, as expected:

```
>>> ncfdtrinc(2, 3, p, 15)
array([ 0.5,  1.5,  2. ])
```

scipy.special.nctdtr

scipy.special.**nctdtr**(*df*, *nc*, *t*) **= <ufunc 'nctdtr'>**

Cumulative distribution function of the non-central *t* distribution.

Parameters

df	[array_like] Degrees of freedom of the distribution. Should be in range (0, inf).
nc	[array_like] Noncentrality parameter. Should be in range (-1e6, 1e6).
t	[array_like] Quantiles, i.e., the upper limit of integration.

Returns

cdf	[float or ndarray] The calculated CDF. If all inputs are scalar, the return will be a float. Otherwise, it will be an array.

See also:

nctdtrit

Inverse CDF (iCDF) of the non-central t distribution.

nctdtridf

Calculate degrees of freedom, given CDF and iCDF values.

nctdtrinc

Calculate non-centrality parameter, given CDF iCDF values.

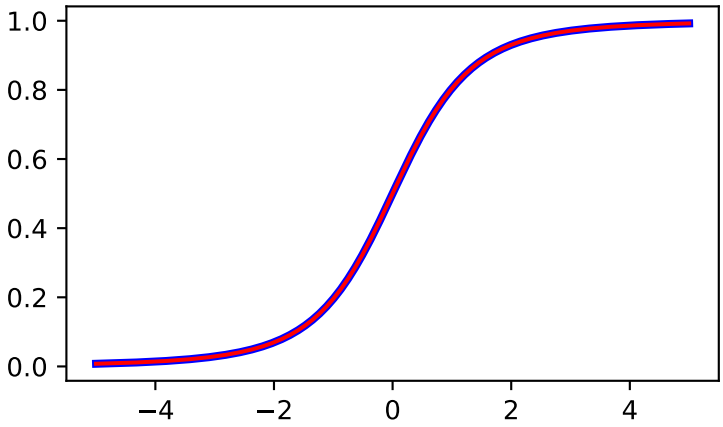
Examples

```
>>> from scipy import special
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

Plot the CDF of the non-central t distribution, for nc=0. Compare with the t-distribution from scipy.stats:

```
>>> x = np.linspace(-5, 5, num=500)
>>> df = 3
>>> nct_stats = stats.t.cdf(x, df)
>>> nct_special = special.nctdtr(df, 0, x)
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, nct_stats, 'b-', lw=3)
>>> ax.plot(x, nct_special, 'r-')
>>> plt.show()
```



scipy.special.nctdtridf

scipy.special.**nctdtridf**(*p*, *nc*, *t*) **= <ufunc 'nctdtridf'>**

Calculate degrees of freedom for non-central t distribution.

See *nctdtr* for more details.

Parameters

p	[array_like] CDF values, in range (0, 1].
nc	[array_like] Noncentrality parameter. Should be in range (-1e6, 1e6).
t	[array_like] Quantiles, i.e., the upper limit of integration.

scipy.special.nctdtrit

scipy.special.**nctdtrit**(*df*, *nc*, *p*) **= <ufunc 'nctdtrit'>**

Inverse cumulative distribution function of the non-central t distribution.

See *nctdtr* for more details.

Parameters

df	[array_like] Degrees of freedom of the distribution. Should be in range (0, inf).
nc	[array_like] Noncentrality parameter. Should be in range (-1e6, 1e6).
p	[array_like] CDF values, in range (0, 1].

scipy.special.nctdtrinc

scipy.special.**nctdtrinc**(*df*, *p*, *t*) **= <ufunc 'nctdtrinc'>**

Calculate non-centrality parameter for non-central t distribution.

See *nctdtr* for more details.

Parameters

df	[array_like] Degrees of freedom of the distribution. Should be in range (0, inf).
p	[array_like] CDF values, in range (0, 1].
t	[array_like] Quantiles, i.e., the upper limit of integration.

scipy.special.nrdtrimn

scipy.special.**nrdtrimn**(*p*, *x*, *std*) **= <ufunc 'nrdtrimn'>**

Calculate mean of normal distribution given other params.

Parameters

p	[array_like] CDF values, in range (0, 1].
x	[array_like] Quantiles, i.e. the upper limit of integration.
std	[array_like] Standard deviation.

Returns

mn	[float or ndarray] The mean of the normal distribution.

See also:

nrdtrimn, **ndtr**

scipy.special.nrdtrisd

scipy.special.**nrdtrisd**(*p*, *x*, *mn*) **= <ufunc 'nrdtrisd'>**

Calculate standard deviation of normal distribution given other params.

Parameters

p	[array_like] CDF values, in range (0, 1].
x	[array_like] Quantiles, i.e. the upper limit of integration.
mn	[float or ndarray] The mean of the normal distribution.

Returns

std	[array_like] Standard deviation.

See also:

ndtr

scipy.special.pdtr

scipy.special.**pdtr**(*k*, *m*, *out=None*) **= <ufunc 'pdtr'>**

Poisson cumulative distribution function.

Defined as the probability that a Poisson-distributed random variable with event rate m is less than or equal to k. More concretely, this works out to be [1]

$$\exp(-m) \sum_{j=0}^{\lfloor k \rfloor} \frac{m^j}{m!}.$$

Parameters

k	[array_like] Nonnegative real argument
m	[array_like] Nonnegative real shape parameter
out	[ndarray] Optional output array for the function results

Returns

scalar or ndarray
Values of the Poisson cumulative distribution function

See also:

pdtrc

Poisson survival function

pdtrik

inverse of *pdtr* with respect to *k*

pdtri

inverse of *pdtr* with respect to *m*

References

[1]

Examples

```
>>> import scipy.special as sc
```

It is a cumulative distribution function, so it converges to 1 monotonically as *k* goes to infinity.

```
>>> sc.pdtr([1, 10, 100, np.inf], 1)
array([0.73575888, 0.99999999, 1.        , 1.        ])
```

It is discontinuous at integers and constant between integers.

```
>>> sc.pdtr([1, 1.5, 1.9, 2], 1)
array([0.73575888, 0.73575888, 0.73575888, 0.9196986 ])
```

scipy.special.pdtrc

scipy.special.**pdtrc**(*k*, *m*) **= <ufunc 'pdtrc'>**
Poisson survival function

Returns the sum of the terms from k+1 to infinity of the Poisson distribution: sum(exp(-m) * m**j / j!, j=k+1..inf) = gammainc(k+1, m). Arguments must both be non-negative doubles.

scipy.special.pdtri

scipy.special.**pdtri**(*k*, *y*) **= <ufunc 'pdtri'>**
Inverse to *pdtr* vs m

Returns the Poisson variable *m* such that the sum from 0 to *k* of the Poisson density is equal to the given probability *y*: calculated by gammaincinv(k+1, y). *k* must be a nonnegative integer and *y* between 0 and 1.

scipy.special.pdtrik

scipy.special.**pdtrik**(*p*, *m*) **= <ufunc 'pdtrik'>**
Inverse to *pdtr* vs k

Returns the quantile k such that `pdtr(k, m) = p`

scipy.special.stdtr

scipy.special.**stdtr**(*df*, *t*) **= <ufunc 'stdtr'>**
Student t distribution cumulative distribution function

Returns the integral from minus infinity to t of the Student t distribution with df > 0 degrees of freedom:

```
gamma((df+1)/2)/(sqrt(df*pi)*gamma(df/2)) *
integral((1+x**2/df)**(-df/2-1/2), x=-inf..t)
```

scipy.special.stdtridf

scipy.special.**stdtridf**(*p*, *t*) **= <ufunc 'stdtridf'>**
Inverse of *stdtr* vs df

Returns the argument df such that stdtr(df, t) is equal to *p*.

scipy.special.stdtrit

scipy.special.**stdtrit**(*df*, *p*) **= <ufunc 'stdtrit'>**
Inverse of *stdtr* vs *t*

Returns the argument *t* such that stdtr(df, t) is equal to *p*.

scipy.special.chdtr

scipy.special.**chdtr**(*v*, *x*, *out=None*) **= <ufunc 'chdtr'>**

Chi square cumulative distribution function.

Returns the area under the left tail (from 0 to *x*) of the Chi square probability density function with *v* degrees of freedom:

$$\frac{1}{2^{v/2}\Gamma(v/2)} \int_0^x t^{v/2-1} e^{-t/2} dt$$

Here Γ is the Gamma function; see *gamma*. This integral can be expressed in terms of the regularized lower incomplete gamma function *gammainc* as `gammainc(v / 2, x / 2)`. [1]

Parameters

v	[array_like] Degrees of freedom.
x	[array_like] Upper bound of the integral.
out	[ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of the cumulative distribution function.

See also:

chdtrc, **chdtri**, **chdtriv**, **gammainc**

References

[1]

Examples

```
>>> import scipy.special as sc
```

It can be expressed in terms of the regularized lower incomplete gamma function.

```
>>> v = 1
>>> x = np.arange(4)
>>> sc.chdtr(v, x)
array([0.        , 0.68268949, 0.84270079, 0.91673548])
>>> sc.gammainc(v / 2, x / 2)
array([0.        , 0.68268949, 0.84270079, 0.91673548])
```

scipy.special.chdtrc

scipy.special.**chdtrc**(*v*, *x*, *out=None*) **= <ufunc 'chdtrc'>**

Chi square survival function.

Returns the area under the right hand tail (from *x* to infinity) of the Chi square probability density function with *v* degrees of freedom:

$$\frac{1}{2^{v/2}\Gamma(v/2)} \int_x^\infty t^{v/2-1} e^{-t/2} dt$$

Here Γ is the Gamma function; see *gamma*. This integral can be expressed in terms of the regularized upper incomplete gamma function *gammaincc* as `gammaincc(v / 2, x / 2)`. [1]

Parameters

v	[array_like] Degrees of freedom.
x	[array_like] Lower bound of the integral.
out	[ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of the survival function.

See also:

chdtr, **chdtri**, **chdtriv**, **gammaincc**

References

[1]

Examples

```
>>> import scipy.special as sc
```

It can be expressed in terms of the regularized upper incomplete gamma function.

```
>>> v = 1
>>> x = np.arange(4)
>>> sc.chdtrc(v, x)
array([1.        , 0.31731051, 0.15729921, 0.08326452])
>>> sc.gammaincc(v / 2, x / 2)
array([1.        , 0.31731051, 0.15729921, 0.08326452])
```

scipy.special.chdtri

scipy.special.**chdtri**(*v*, *p*, *out=None*) **= <ufunc 'chdtri'>**

Inverse to *chdtrc* with respect to *x*.

Returns *x* such that `chdtrc(v, x) == p`.

Parameters

v	[array_like] Degrees of freedom.
p	[array_like] Probability.
out	[ndarray, optional] Optional output array for the function results.

Returns

x	[scalar or ndarray] Value so that the probability a Chi square random variable with *v* degrees of freedom is greater than *x* equals *p*.

See also:

chdtrc, **chdtr**, **chdtriv**

References

[1]

Examples

```
>>> import scipy.special as sc
```

It inverts *chdtrc*.

```
>>> v, p = 1, 0.3
>>> sc.chdtrc(v, sc.chdtri(v, p))
0.3
>>> x = 1
>>> sc.chdtri(v, sc.chdtrc(v, x))
1.0
```

scipy.special.chdtriv

scipy.special.**chdtriv**(*p*, *x*, *out=None*) **= <ufunc 'chdtriv'>**

Inverse to *chdtr* with respect to *v*.

Returns *v* such that `chdtr(v, x) == p`.

Parameters

p	[array_like] Probability that the Chi square random variable is less than or equal to *x*.
x	[array_like] Nonnegative input.
out	[ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray	Degrees of freedom.

See also:

chdtr, **chdtrc**, **chdtri**

References

[1]

Examples

```
>>> import scipy.special as sc
```

It inverts *chdtr*.

```
>>> p, x = 0.5, 1
>>> sc.chdtr(sc.chdtriv(p, x), x)
0.5000000000202172
>>> v = 1
>>> sc.chdtriv(sc.chdtr(v, x), v)
1.0000000000000013
```

scipy.special.ndtr

scipy.special.**ndtr**(*x*) **= <ufunc 'ndtr'>**

Gaussian cumulative distribution function.

Returns the area under the standard Gaussian probability density function, integrated from minus infinity to *x*

$$\frac{1}{\sqrt{2\pi}} \int_{-\infty}^{x} \exp(-t^2/2) dt$$

Parameters

x [array_like, real or complex] Argument

Returns

ndarray The value of the normal CDF evaluated at *x*

See also:

erf

erfc

scipy.stats.norm

log_ndtr

scipy.special.log_ndtr

scipy.special.**log_ndtr**(*x*) **= <ufunc 'log_ndtr'>**

Logarithm of Gaussian cumulative distribution function.

Returns the log of the area under the standard Gaussian probability density function, integrated from minus infinity to *x*:

```
log(1/sqrt(2*pi) * integral(exp(-t**2 / 2), t=-inf..x))
```

Parameters

x [array_like, real or complex] Argument

Returns

ndarray The value of the log of the normal CDF evaluated at *x*

See also:

erf

erfc

scipy.stats.norm

ndtr

scipy.special.ndtri

scipy.special.**ndtri**(*y*) **= <ufunc 'ndtri'>**

Inverse of *ndtr* vs x

Returns the argument x for which the area under the Gaussian probability density function (integrated from minus infinity to *x*) is equal to y.

scipy.special.ndtri_exp

scipy.special.**ndtri_exp**(*y*) **= <ufunc 'ndtri_exp'>**

Inverse of *log_ndtr* vs x. Allows for greater precision than *ndtri* composed with numpy.exp for very small values of y and for y close to 0.

Parameters

y [array_like of float]

Returns

scalar or ndarray
Inverse of the log CDF of the standard normal distribution, evaluated at y.

See also:

log_ndtr, **ndtri**, **ndtr**

Examples

```
>>> import scipy.special as sc
```

ndtri_exp agrees with the naive implementation when the latter does not suffer from underflow.

```
>>> sc.ndtri_exp(-1)
-0.33747496376420244
>>> sc.ndtri(np.exp(-1))
-0.33747496376420244
```

For extreme values of y, the naive approach fails

```
>>> sc.ndtri(np.exp(-800))
-inf
>>> sc.ndtri(np.exp(-1e-20))
inf
```

whereas *ndtri_exp* is still able to compute the result to high precision.

```
>>> sc.ndtri_exp(-800)
-39.88469483825668
>>> sc.ndtri_exp(-1e-20)
9.262340089798409
```

scipy.special.chndtr

scipy.special.**chndtr**(*x*, *df*, *nc*) **= <ufunc 'chndtr'>**
Non-central chi square cumulative distribution function

scipy.special.chndtridf

scipy.special.**chndtridf**(*x*, *p*, *nc*) **= <ufunc 'chndtridf'>**
Inverse to *chndtr* vs *df*

scipy.special.chndtrinc

scipy.special.**chndtrinc**(*x*, *df*, *p*) **= <ufunc 'chndtrinc'>**
Inverse to *chndtr* vs *nc*

scipy.special.chndtrix

scipy.special.**chndtrix**(*p*, *df*, *nc*) **= <ufunc 'chndtrix'>**
Inverse to *chndtr* vs *x*

scipy.special.smirnov

scipy.special.**smirnov**(*n*, *d*) **= <ufunc 'smirnov'>**

Kolmogorov-Smirnov complementary cumulative distribution function

Returns the exact Kolmogorov-Smirnov complementary cumulative distribution function,(aka the Survival Function) of Dn+ (or Dn-) for a one-sided test of equality between an empirical and a theoretical distribution. It is equal to the probability that the maximum difference between a theoretical distribution and an empirical one based on *n* samples is greater than d.

Parameters

n	[int] Number of samples
d	[float array_like] Deviation between the Empirical CDF (ECDF) and the target CDF.

Returns

float	The value(s) of smirnov(n, d), Prob(Dn+ >= d) (Also Prob(Dn- >= d))

See also:

smirnovi

The Inverse Survival Function for the distribution

scipy.stats.ksone

Provides the functionality as a continuous distribution

kolmogorov, **kolmogi**

Functions for the two-sided distribution

Notes

smirnov is used by *stats.kstest* in the application of the Kolmogorov-Smirnov Goodness of Fit test. For historial reasons this function is exposed in *scpy.special*, but the recommended way to achieve the most accurate CDF/SF/PDF/PPF/ISF computations is to use the *stats.ksone* distribution.

Examples

```
>>> from scipy.special import smirnov
```

Show the probability of a gap at least as big as 0, 0.5 and 1.0 for a sample of size 5

```
>>> smirnov(5, [0, 0.5, 1.0])
array([ 1.   ,  0.056,  0.   ])
```

Compare a sample of size 5 drawn from a source N(0.5, 1) distribution against a target N(0, 1) CDF.

```
>>> from scipy.stats import norm
>>> rng = np.random.default_rng()
>>> n = 5
>>> gendist = norm(0.5, 1)        # Normal distribution, mean 0.5, stddev 1
>>> x = np.sort(gendist.rvs(size=n, random_state=rng))
>>> x
array([-1.3922078 , -0.13526532,  0.1371477 ,  0.18981686,  1.81948167])
```

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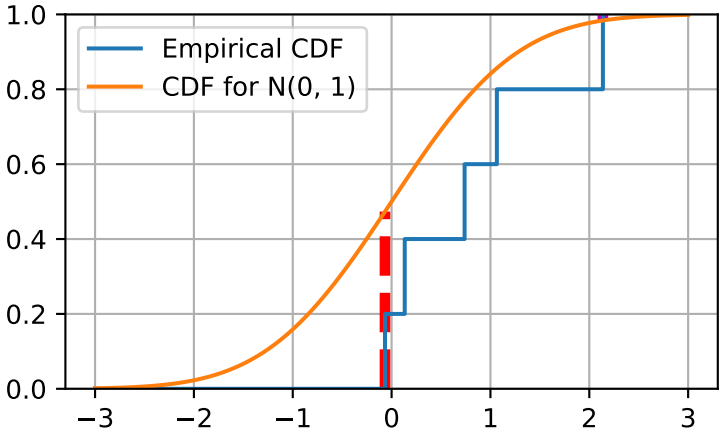
```
>>> target = norm(0, 1)
>>> cdfs = target.cdf(x)
>>> cdfs
array([0.08192974, 0.44620105, 0.55454297, 0.57527368, 0.96558101])
# Construct the Empirical CDF and the K-S statistics (Dn+, Dn-, Dn)
>>> ecdfs = np.arange(n+1, dtype=float)/n
>>> cols = np.column_stack([x, ecdfs[1:], cdfs, cdfs - ecdfs[:n],␣
↪ecdfs[1:] - cdfs])
>>> np.set_printoptions(precision=3)
>>> cols
array([[-1.392,  0.2  ,  0.082,  0.082,  0.118],
       [-0.135,  0.4  ,  0.446,  0.246, -0.046],
       [ 0.137,  0.6  ,  0.555,  0.155,  0.045],
       [ 0.19 ,  0.8  ,  0.575, -0.025,  0.225],
       [ 1.819,  1.   ,  0.966,  0.166,  0.034]])
>>> gaps = cols[:, -2:]
>>> Dnpm = np.max(gaps, axis=0)
>>> print('Dn-=%f, Dn+=%f' % (Dnpm[0], Dnpm[1]))
Dn-=0.246201, Dn+=0.224726
>>> probs = smirnov(n, Dnpm)
>>> print(chr(10).join(['For a sample of size %d drawn from a N(0, 1)␣
↪distribution:' % n,
...       ' Smirnov n=%d: Prob(Dn- >= %f) = %.4f' % (n, Dnpm[0],␣
↪probs[0]),
...       ' Smirnov n=%d: Prob(Dn+ >= %f) = %.4f' % (n, Dnpm[1],␣
↪probs[1])]))
For a sample of size 5 drawn from a N(0, 1) distribution:
 Smirnov n=5: Prob(Dn- >= 0.246201) = 0.4713
 Smirnov n=5: Prob(Dn+ >= 0.224726) = 0.5243
```

Plot the Empirical CDF against the target N(0, 1) CDF

```
>>> import matplotlib.pyplot as plt
>>> plt.step(np.concatenate([[-3], x]), ecdfs, where='post', label=
↪'Empirical CDF')
>>> x3 = np.linspace(-3, 3, 100)
>>> plt.plot(x3, target.cdf(x3), label='CDF for N(0, 1)')
>>> plt.ylim([0, 1]); plt.grid(True); plt.legend();
# Add vertical lines marking Dn+ and Dn-
>>> iminus, iplus = np.argmax(gaps, axis=0)
>>> plt.vlines([x[iminus]], ecdfs[iminus], cdfs[iminus], color='r',␣
↪linestyle='dashed', lw=4)
>>> plt.vlines([x[iplus]], cdfs[iplus], ecdfs[iplus+1], color='m',␣
↪linestyle='dashed', lw=4)
>>> plt.show()
```



scipy.special.smirnovi

scipy.special.**smirnovi**(*n*, *p*) **= <ufunc 'smirnovi'>**

Inverse to *smirnov*

Returns *d* such that `smirnov(n, d) == p`, the critical value corresponding to *p*.

Parameters

n	[int] Number of samples
p	[float array_like] Probability

Returns

float	The value(s) of smirnovi(n, p), the critical values.

See also:

smirnov

The Survival Function (SF) for the distribution

scipy.stats.ksone

Provides the functionality as a continuous distribution

kolmogorov, **kolmogi**, **scipy.stats.kstwobign**

Functions for the two-sided distribution

Notes

smirnov is used by *stats.kstest* in the application of the Kolmogorov-Smirnov Goodness of Fit test. For historial reasons this function is exposed in *scpy.special*, but the recommended way to achieve the most accurate CDF/SF/PDF/PPF/ISF computations is to use the *stats.ksone* distribution.

scipy.special.kolmogorov

scipy.special.**kolmogorov**(*y*) **= <ufunc 'kolmogorov'>**

Complementary cumulative distribution (Survival Function) function of Kolmogorov distribution.

Returns the complementary cumulative distribution function of Kolmogorov's limiting distribution (`D_n*\ sqrt(n)` as n goes to infinity) of a two-sided test for equality between an empirical and a theoretical distribution. It is equal to the (limit as n->infinity of the) probability that `sqrt(n) * max absolute deviation > y`.

Parameters

y [float array_like] Absolute deviation between the Empirical CDF (ECDF) and the target CDF, multiplied by sqrt(n).

Returns

float The value(s) of kolmogorov(y)

See also:

kolmogi

The Inverse Survival Function for the distribution

scipy.stats.kstwobign

Provides the functionality as a continuous distribution

smirnov, **smirnovi**

Functions for the one-sided distribution

Notes

kolmogorov is used by *stats.kstest* in the application of the Kolmogorov-Smirnov Goodness of Fit test. For historial reasons this function is exposed in *scpy.special*, but the recommended way to achieve the most accurate CDF/SF/PDF/PPF/ISF computations is to use the *stats.kstwobign* distribution.

Examples

Show the probability of a gap at least as big as 0, 0.5 and 1.0.

```
>>> from scipy.special import kolmogorov
>>> from scipy.stats import kstwobign
>>> kolmogorov([0, 0.5, 1.0])
array([ 1.        ,  0.96394524,  0.26999967])
```

Compare a sample of size 1000 drawn from a Laplace(0, 1) distribution against the target distribution, a Normal(0, 1) distribution.

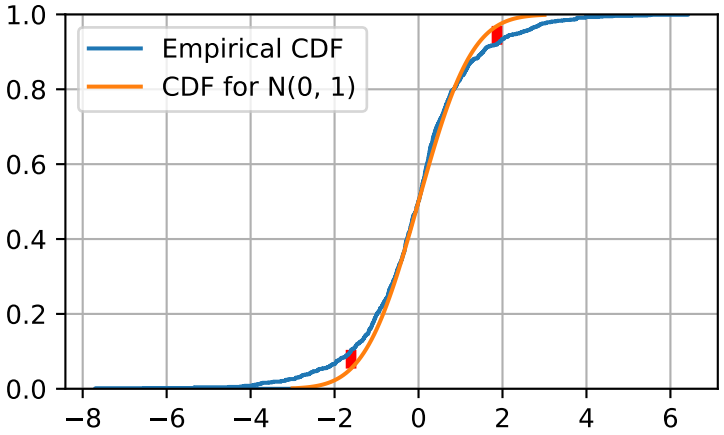
```
>>> from scipy.stats import norm, laplace
>>> rng = np.random.default_rng()
>>> n = 1000
>>> lap01 = laplace(0, 1)
>>> x = np.sort(lap01.rvs(n, random_state=rng))
>>> np.mean(x), np.std(x)
(-0.05841730131499543, 1.3968109101997568)
```

Construct the Empirical CDF and the K-S statistic Dn.

```
>>> target = norm(0,1)  # Normal mean 0, stddev 1
>>> cdfs = target.cdf(x)
>>> ecdfs = np.arange(n+1, dtype=float)/n
>>> gaps = np.column_stack([cdfs - ecdfs[:n], ecdfs[1:] - cdfs])
>>> Dn = np.max(gaps)
>>> Kn = np.sqrt(n) * Dn
>>> print('Dn=%f, sqrt(n)*Dn=%f' % (Dn, Kn))
Dn=0.043363, sqrt(n)*Dn=1.371265
>>> print(chr(10).join(['For a sample of size n drawn from a N(0, 1)␣
↪distribution:',
...   ' the approximate Kolmogorov probability that sqrt(n)*Dn>=%f is %f
↪' %  (Kn, kolmogorov(Kn)),
...   ' the approximate Kolmogorov probability that sqrt(n)*Dn<=%f is %f
↪' %  (Kn, kstwobign.cdf(Kn))]))
For a sample of size n drawn from a N(0, 1) distribution:
 the approximate Kolmogorov probability that sqrt(n)*Dn>=1.371265 is 0.
↪046533
 the approximate Kolmogorov probability that sqrt(n)*Dn<=1.371265 is 0.
↪953467
```

Plot the Empirical CDF against the target N(0, 1) CDF.

```
>>> import matplotlib.pyplot as plt
>>> plt.step(np.concatenate([[-3], x]), ecdfs, where='post', label=
↪'Empirical CDF')
>>> x3 = np.linspace(-3, 3, 100)
>>> plt.plot(x3, target.cdf(x3), label='CDF for N(0, 1)')
>>> plt.ylim([0, 1]); plt.grid(True); plt.legend();
>>> # Add vertical lines marking Dn+ and Dn-
>>> iminus, iplus = np.argmax(gaps, axis=0)
>>> plt.vlines([x[iminus]], ecdfs[iminus], cdfs[iminus], color='r',␣
↪linestyle='dashed', lw=4)
>>> plt.vlines([x[iplus]], cdfs[iplus], ecdfs[iplus+1], color='r',␣
↪linestyle='dashed', lw=4)
>>> plt.show()
```



scipy.special.kolmogi

scipy.special.**kolmogi**(*p*) **= <ufunc 'kolmogi'>**

Inverse Survival Function of Kolmogorov distribution

It is the inverse function to *kolmogorov*. Returns y such that `kolmogorov(y) == p`.

Parameters

p [float array_like] Probability

Returns

float The value(s) of kolmogi(p)

See also:

kolmogorov

The Survival Function for the distribution

scipy.stats.kstwobign

Provides the functionality as a continuous distribution

smirnov, **smirnovi**

Functions for the one-sided distribution

Notes

kolmogorov is used by *stats.kstest* in the application of the Kolmogorov-Smirnov Goodness of Fit test. For historial reasons this function is exposed in *scpy.special*, but the recommended way to achieve the most accurate CDF/SF/PDF/PPF/ISF computations is to use the *stats.kstwobign* distribution.

Examples

```
>>> from scipy.special import kolmogi
>>> kolmogi([0, 0.1, 0.25, 0.5, 0.75, 0.9, 1.0])
array([        inf,  1.22384787,  1.01918472,  0.82757356,  0.67644769,
        0.57117327,  0.        ])
```

scipy.special.tklmbda

scipy.special.**tklmbda**(*x*, *lmbda*) **= <ufunc 'tklmbda'>**

Tukey-Lambda cumulative distribution function

scipy.special.logit

scipy.special.**logit**(*x*) **= <ufunc 'logit'>**

Logit ufunc for ndarrays.

The logit function is defined as logit(p) = log(p/(1-p)). Note that logit(0) = -inf, logit(1) = inf, and logit(p) for p<0 or p>1 yields nan.

Parameters

x [ndarray] The ndarray to apply logit to element-wise.

Returns

out [ndarray] An ndarray of the same shape as x. Its entries are logit of the corresponding entry of x.

See also:

expit

Notes

As a ufunc logit takes a number of optional keyword arguments. For more information see ufuncs

New in version 0.10.0.

Examples

```
>>> from scipy.special import logit, expit
```

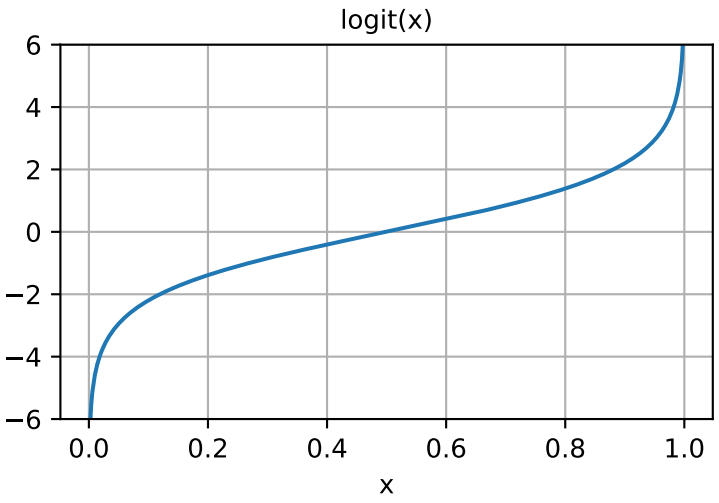
```
>>> logit([0, 0.25, 0.5, 0.75, 1])
array([       -inf, -1.09861229,  0.        ,  1.09861229,         inf])
```

expit is the inverse of *logit*:

```
>>> expit(logit([0.1, 0.75, 0.999]))
array([ 0.1  ,  0.75 ,  0.999])
```

Plot logit(x) for x in [0, 1]:

```
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(0, 1, 501)
>>> y = logit(x)
>>> plt.plot(x, y)
>>> plt.grid()
>>> plt.ylim(-6, 6)
>>> plt.xlabel('x')
>>> plt.title('logit(x)')
>>> plt.show()
```



scipy.special.expit

scipy.special.**expit**(*x*) **= <ufunc 'expit'>**

Expit (a.k.a. logistic sigmoid) ufunc for ndarrays.

The expit function, also known as the logistic sigmoid function, is defined as `expit(x) = 1/(1+exp(-x))`. It is the inverse of the logit function.

Parameters

x [ndarray] The ndarray to apply expit to element-wise.

Returns

out [ndarray] An ndarray of the same shape as x. Its entries are *expit* of the corresponding entry of x.

See also:

logit

Notes

As a ufunc expit takes a number of optional keyword arguments. For more information see ufuncs

New in version 0.10.0.

Examples

```
>>> from scipy.special import expit, logit
```

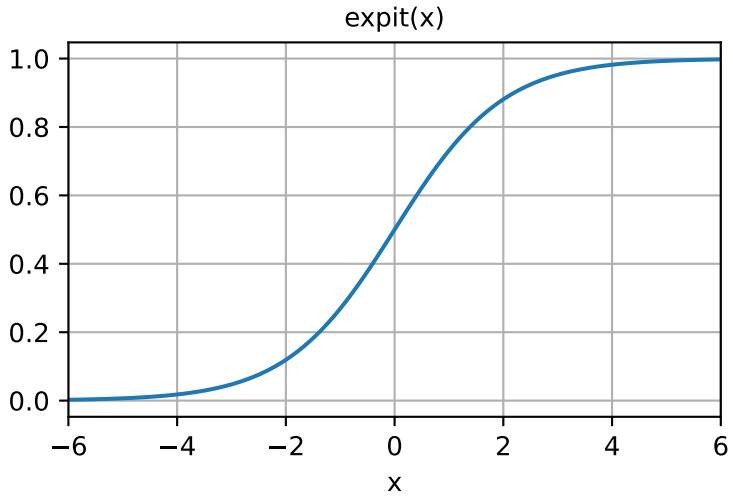
```
>>> expit([-np.inf, -1.5, 0, 1.5, np.inf])
array([ 0.        ,  0.18242552,  0.5       ,  0.81757448,  1.        ])
```

logit is the inverse of *expit*:

```
>>> logit(expit([-2.5, 0, 3.1, 5.0]))
array([-2.5,  0. ,  3.1,  5. ])
```

Plot expit(x) for x in [-6, 6]:

```
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-6, 6, 121)
>>> y = expit(x)
>>> plt.plot(x, y)
>>> plt.grid()
>>> plt.xlim(-6, 6)
>>> plt.xlabel('x')
>>> plt.title('expit(x)')
>>> plt.show()
```



scipy.special.boxcox

`scipy.special.`**boxcox**(*x*, *lmbda*) **= <ufunc 'boxcox'>**

Compute the Box-Cox transformation.

The Box-Cox transformation is:

```
y = (x**lmbda - 1) / lmbda  if lmbda != 0
    log(x)                  if lmbda == 0
```

Returns *nan* if `x < 0`. Returns *-inf* if `x == 0` and `lmbda < 0`.

Parameters

x	[array_like] Data to be transformed.
lmbda	[array_like] Power parameter of the Box-Cox transform.

Returns

y	[array] Transformed data.

Notes

New in version 0.14.0.

Examples

```
>>> from scipy.special import boxcox
>>> boxcox([1, 4, 10], 2.5)
array([   0.        ,   12.4       ,  126.09110641])
>>> boxcox(2, [0, 1, 2])
array([ 0.69314718,  1.        ,  1.5       ])
```

scipy.special.boxcox1p

scipy.special.**boxcox1p**(*x*, *lmbda*) **= <ufunc 'boxcox1p'>**

Compute the Box-Cox transformation of 1 + *x*.

The Box-Cox transformation computed by *boxcox1p* is:

```
y = ((1+x)**lmbda - 1) / lmbda  if lmbda != 0
    log(1+x)                    if lmbda == 0
```

Returns *nan* if `x < -1`. Returns *-inf* if `x == -1` and `lmbda < 0`.

Parameters

x [array_like] Data to be transformed.
lmbda [array_like] Power parameter of the Box-Cox transform.

Returns

y [array] Transformed data.

Notes

New in version 0.14.0.

Examples

```
>>> from scipy.special import boxcox1p
>>> boxcox1p(1e-4, [0, 0.5, 1])
array([  9.99950003e-05,   9.99975001e-05,   1.00000000e-04])
>>> boxcox1p([0.01, 0.1], 0.25)
array([ 0.00996272,  0.09645476])
```

scipy.special.inv_boxcox

scipy.special.**inv_boxcox**(*y*, *lmbda*) **= <ufunc 'inv_boxcox'>**

Compute the inverse of the Box-Cox transformation.

Find `x` such that:

```
y = (x**lmbda - 1) / lmbda  if lmbda != 0
    log(x)                  if lmbda == 0
```

Parameters

y [array_like] Data to be transformed.
lmbda [array_like] Power parameter of the Box-Cox transform.

Returns

x [array] Transformed data.

Notes

New in version 0.16.0.

Examples

```
>>> from scipy.special import boxcox, inv_boxcox
>>> y = boxcox([1, 4, 10], 2.5)
>>> inv_boxcox(y, 2.5)
array([1., 4., 10.])
```

scipy.special.inv_boxcox1p

scipy.special.**inv_boxcox1p**(*y*, *lmbda*) **= <ufunc 'inv_boxcox1p'>**

Compute the inverse of the Box-Cox transformation.

Find x such that:

```
y = ((1+x)**lmbda - 1) / lmbda  if lmbda != 0
    log(1+x)                    if lmbda == 0
```

Parameters

y [array_like] Data to be transformed.

lmbda [array_like] Power parameter of the Box-Cox transform.

Returns

x [array] Transformed data.

Notes

New in version 0.16.0.

Examples

```
>>> from scipy.special import boxcox1p, inv_boxcox1p
>>> y = boxcox1p([1, 4, 10], 2.5)
>>> inv_boxcox1p(y, 2.5)
array([1., 4., 10.])
```

scipy.special.owens_t

scipy.special.**owens_t**(*h*, *a*) **= <ufunc 'owens_t'>**

Owen's T Function.

The function T(h, a) gives the probability of the event (X > h and 0 < Y < a * X) where X and Y are independent standard normal random variables.

Parameters

h: array_like
Input value.

a: array_like
Input value.

Returns

t: scalar or ndarray
Probability of the event (X > h and 0 < Y < a * X), where X and Y are independent standard normal random variables.

References

[1]

Examples

```
>>> from scipy import special
>>> a = 3.5
>>> h = 0.78
>>> special.owens_t(h, a)
0.10877216734852274
```

Information Theory functions

entr(x)	Elementwise function for computing entropy.
rel_entr(x, y[, out])	Elementwise function for computing relative entropy.
kl_div(x, y[, out])	Elementwise function for computing Kullback-Leibler divergence.
huber(delta, r)	Huber loss function.
pseudo_huber(delta, r)	Pseudo-Huber loss function.

scipy.special.entr

scipy.special.**entr**(*x*) **= <ufunc 'entr'>**

Elementwise function for computing entropy.

$$\mathrm{entr}(x) = \begin{cases} -x\log(x) & x > 0 \\ 0 & x = 0 \\ -\infty & \text{otherwise} \end{cases}$$

Parameters

x [ndarray] Input array.

Returns

res [ndarray] The value of the elementwise entropy function at the given points *x*.

See also:

kl_div, **rel_entr**

Notes

This function is concave.

New in version 0.15.0.

scipy.special.rel_entr

scipy.special.**rel_entr**(*x*, *y*, *out=None*) **= <ufunc 'rel_entr'>**

Elementwise function for computing relative entropy.

$$\mathrm{rel_entr}(x, y) = \begin{cases} x \log(x/y) & x > 0, y > 0 \\ 0 & x = 0, y \geq 0 \\ \infty & \text{otherwise} \end{cases}$$

Parameters

x, y [array_like] Input arrays
out [ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
Relative entropy of the inputs

See also:

entr, **kl_div**

Notes

New in version 0.15.0.

This function is jointly convex in x and y.

The origin of this function is in convex programming; see [1]. Given two discrete probability distributions $p_1, \ldots, p_n$ and $q_1, \ldots, q_n$, to get the relative entropy of statistics compute the sum

$$\sum_{i=1}^{n} \mathrm{rel_entr}(p_i, q_i).$$

See [2] for details.

References

[1], [2]

scipy.special.kl_div

scipy.special.**kl_div**(*x*, *y*, *out=None*) **= <ufunc 'kl_div'>**

Elementwise function for computing Kullback-Leibler divergence.

$$\mathrm{kl_div}(x, y) = \begin{cases} x \log(x/y) - x + y & x > 0, y > 0 \\ y & x = 0, y \geq 0 \\ \infty & \text{otherwise} \end{cases}$$

Parameters

x, y [array_like] Real arguments
out [ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
Values of the Kullback-Liebler divergence.

See also:

entr, **rel_entr**

Notes

New in version 0.15.0.

This function is non-negative and is jointly convex in *x* and *y*.

The origin of this function is in convex programming; see [1] for details. This is why the the function contains the extra $-x + y$ terms over what might be expected from the Kullback-Leibler divergence. For a version of the function without the extra terms, see *rel_entr*.

References

[1]

scipy.special.huber

scipy.special.**huber**(*delta*, *r*) **= <ufunc 'huber'>**

Huber loss function.

$$\mathrm{huber}(\delta, r) = \begin{cases} \infty & \delta < 0 \\ \frac{1}{2} r^2 & 0 \leq \delta, |r| \leq \delta \\ \delta(|r| - \frac{1}{2}\delta) & \text{otherwise} \end{cases}$$

Parameters

delta [ndarray] Input array, indicating the quadratic vs. linear loss changepoint.
r [ndarray] Input array, possibly representing residuals.

Returns

res [ndarray] The computed Huber loss function values.

Notes

This function is convex in r.

New in version 0.15.0.

scipy.special.pseudo_huber

scipy.special.**pseudo_huber**(*delta*, *r*) **= <ufunc 'pseudo_huber'>**

Pseudo-Huber loss function.

$$\mathrm{pseudo_huber}(\delta, r) = \delta^2 \left(\sqrt{1 + \left(\frac{r}{\delta} \right)^2} - 1 \right)$$

Parameters

delta [ndarray] Input array, indicating the soft quadratic vs. linear loss changepoint.

r [ndarray] Input array, possibly representing residuals.

Returns

res [ndarray] The computed Pseudo-Huber loss function values.

Notes

This function is convex in r.

New in version 0.15.0.

Gamma and related functions

gamma(z)	gamma function.
gammaln(x[, out])	Logarithm of the absolute value of the gamma function.
loggamma(z[, out])	Principal branch of the logarithm of the gamma function.
gammasgn(x)	Sign of the gamma function.
gammainc(a, x)	Regularized lower incomplete gamma function.
gammaincinv(a, y)	Inverse to the lower incomplete gamma function with respect to x.
gammaincc(a, x)	Regularized upper incomplete gamma function.
gammainccinv(a, y)	Inverse of the upper incomplete gamma function with respect to x
beta(a, b[, out])	Beta function.
betaln(a, b)	Natural logarithm of absolute value of beta function.
betainc(a, b, x[, out])	Incomplete beta function.
betaincinv(a, b, y[, out])	Inverse of the incomplete beta function.
psi(z[, out])	The digamma function.
rgamma(z[, out])	Reciprocal of the gamma function.
polygamma(n, x)	Polygamma functions.

continues on next page

Table 233 – continued from previous page

multigammaln(a, d)	Returns the log of multivariate gamma, also sometimes called the generalized gamma.
digamma(z[, out])	The digamma function.
poch(z, m)	Pochhammer symbol.

scipy.special.gamma

scipy.special.**gamma**(*z*) **= <ufunc 'gamma'>**

gamma function.

The gamma function is defined as

$$\Gamma(z) = \int_0^\infty t^{z-1} e^{-t} dt$$

for $\Re(z) > 0$ and is extended to the rest of the complex plane by analytic continuation. See [dlmf] for more details.

Parameters

z [array_like] Real or complex valued argument

Returns

scalar or ndarray
Values of the gamma function

Notes

The gamma function is often referred to as the generalized factorial since $\Gamma(n+1) = n!$ for natural numbers n. More generally it satisfies the recurrence relation $\Gamma(z+1) = z \cdot \Gamma(z)$ for complex z, which, combined with the fact that $\Gamma(1) = 1$, implies the above identity for $z = n$.

References

[dlmf]

Examples

```
>>> from scipy.special import gamma, factorial
```

```
>>> gamma([0, 0.5, 1, 5])
array([         inf,   1.77245385,   1.        ,  24.        ])
```

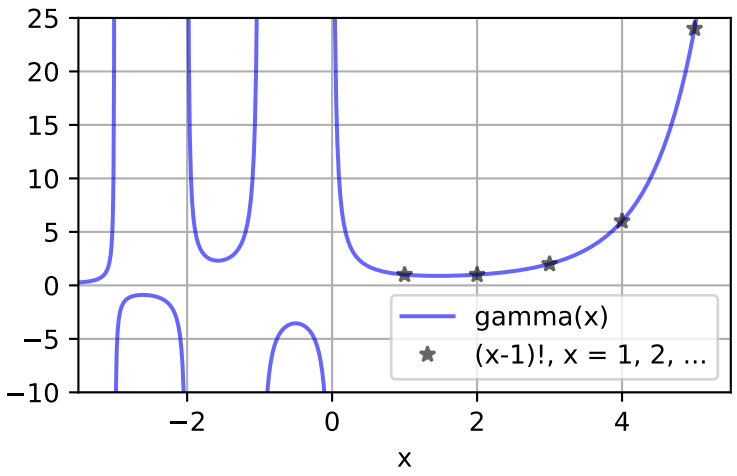
```
>>> z = 2.5 + 1j
>>> gamma(z)
(0.77476210455108352+0.70763120437959293j)
>>> gamma(z+1), z*gamma(z)  # Recurrence property
((1.2292740569981171+2.5438401155000685j),
 (1.2292740569981158+2.5438401155000658j))
```

```
>>> gamma(0.5)**2  # gamma(0.5) = sqrt(pi)
3.1415926535897927
```

Plot gamma(x) for real x

```
>>> x = np.linspace(-3.5, 5.5, 2251)
>>> y = gamma(x)
```

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(x, y, 'b', alpha=0.6, label='gamma(x)')
>>> k = np.arange(1, 7)
>>> plt.plot(k, factorial(k-1), 'k*', alpha=0.6,
...          label='(x-1)!, x = 1, 2, ...')
>>> plt.xlim(-3.5, 5.5)
>>> plt.ylim(-10, 25)
>>> plt.grid()
>>> plt.xlabel('x')
>>> plt.legend(loc='lower right')
>>> plt.show()
```



scipy.special.gammaln

scipy.special.**gammaln**(*x*, *out=None*) **= <ufunc 'gammaln'>**

Logarithm of the absolute value of the gamma function.

Defined as

$$\ln(|\Gamma(x)|)$$

where Γ is the gamma function. For more details on the gamma function, see [dlmf].

Parameters

x [array_like] Real argument

out [ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
Values of the log of the absolute value of gamma

See also:

gammasgn

sign of the gamma function

loggamma

principal branch of the logarithm of the gamma function

Notes

It is the same function as the Python standard library function `math.lgamma`.

When used in conjunction with *gammasgn*, this function is useful for working in logspace on the real axis without having to deal with complex numbers via the relation `exp(gammaln(x)) = gammasgn(x) * gamma(x)`.

For complex-valued log-gamma, use *loggamma* instead of *gammaln*.

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

It has two positive zeros.

```
>>> sc.gammaln([1, 2])
array([0., 0.])
```

It has poles at nonpositive integers.

```
>>> sc.gammaln([0, -1, -2, -3, -4])
array([inf, inf, inf, inf, inf])
```

It asymptotically approaches `x * log(x)` (Stirling's formula).

```
>>> x = np.array([1e10, 1e20, 1e40, 1e80])
>>> sc.gammaln(x)
array([2.20258509e+11, 4.50517019e+21, 9.11034037e+41, 1.83206807e+82])
>>> x * np.log(x)
array([2.30258509e+11, 4.60517019e+21, 9.21034037e+41, 1.84206807e+82])
```

scipy.special.loggamma

scipy.special.**loggamma**(*z*, *out=None*) **= <ufunc 'loggamma'>**

Principal branch of the logarithm of the gamma function.

Defined to be $\log(\Gamma(x))$ for $x > 0$ and extended to the complex plane by analytic continuation. The function has a single branch cut on the negative real axis.

New in version 0.18.0.

Parameters

z	[array-like] Values in the complex plain at which to compute `loggamma`
out	[ndarray, optional] Output array for computed values of `loggamma`

Returns

loggamma	[ndarray] Values of `loggamma` at z.

See also:

gammaln

logarithm of the absolute value of the gamma function

gammasgn

sign of the gamma function

Notes

It is not generally true that $\log\Gamma(z) = \log(\Gamma(z))$, though the real parts of the functions do agree. The benefit of not defining *loggamma* as $\log(\Gamma(z))$ is that the latter function has a complicated branch cut structure whereas *loggamma* is analytic except for on the negative real axis.

The identities

$$\exp(\log\Gamma(z)) = \Gamma(z)$$
$$\log\Gamma(z+1) = \log(z) + \log\Gamma(z)$$

make *loggamma* useful for working in complex logspace.

On the real line *loggamma* is related to *gammaln* via `exp(loggamma(x + 0j)) = gammasgn(x)*exp(gammaln(x))`, up to rounding error.

The implementation here is based on [hare1997].

References

[hare1997]

scipy.special.gammasgn

scipy.special.**gammasgn**(*x*) = <ufunc 'gammasgn'>

Sign of the gamma function.

It is defined as

$$\text{gammasgn}(x) = \begin{cases} +1 & \Gamma(x) > 0 \\ -1 & \Gamma(x) < 0 \end{cases}$$

where Γ is the gamma function; see *gamma*. This definition is complete since the gamma function is never zero; see the discussion after [dlmf].

Parameters

x [array_like] Real argument

Returns

scalar or ndarray
Sign of the gamma function

See also:

gamma

the gamma function

gammaln

log of the absolute value of the gamma function

loggamma

analytic continuation of the log of the gamma function

Notes

The gamma function can be computed as `gammasgn(x) * np.exp(gammaln(x))`.

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

It is 1 for $x > 0$.

```
>>> sc.gammasgn([1, 2, 3, 4])
array([1., 1., 1., 1.])
```

It alternates between -1 and 1 for negative integers.

```
>>> sc.gammasgn([-0.5, -1.5, -2.5, -3.5])
array([-1.,  1., -1.,  1.])
```

It can be used to compute the gamma function.

```
>>> x = [1.5, 0.5, -0.5, -1.5]
>>> sc.gammasgn(x) * np.exp(sc.gammaln(x))
array([ 0.88622693,  1.77245385, -3.5449077 ,  2.3632718 ])
>>> sc.gamma(x)
array([ 0.88622693,  1.77245385, -3.5449077 ,  2.3632718 ])
```

scipy.special.gammainc

scipy.special.**gammainc**(a, x) **= <ufunc 'gammainc'>**

Regularized lower incomplete gamma function.

It is defined as

$$P(a,x) = \frac{1}{\Gamma(a)} \int_0^x t^{a-1} e^{-t} dt$$

for $a > 0$ and $x \geq 0$. See [dlmf] for details.

Parameters

a [array_like] Positive parameter
x [array_like] Nonnegative argument

Returns

scalar or ndarray
Values of the lower incomplete gamma function

See also:

gammaincc

regularized upper incomplete gamma function

gammaincinv

inverse of the regularized lower incomplete gamma function with respect to x

gammainccinv

inverse of the regularized upper incomplete gamma function with respect to x

Notes

The function satisfies the relation `gammainc(a, x) + gammaincc(a, x) = 1` where *gammaincc* is the regularized upper incomplete gamma function.

The implementation largely follows that of [boost].

References

[dlmf], [boost]

Examples

```
>>> import scipy.special as sc
```

It is the CDF of the gamma distribution, so it starts at 0 and monotonically increases to 1.

```
>>> sc.gammainc(0.5, [0, 1, 10, 100])
array([0.        , 0.84270079, 0.99999226, 1.        ])
```

It is equal to one minus the upper incomplete gamma function.

```
>>> a, x = 0.5, 0.4
>>> sc.gammainc(a, x)
0.6289066304773024
>>> 1 - sc.gammaincc(a, x)
0.6289066304773024
```

scipy.special.gammaincinv

scipy.special.**gammaincinv**(*a*, *y*) **= <ufunc 'gammaincinv'>**

Inverse to the lower incomplete gamma function with respect to *x*.

Given an input y between 0 and 1, returns x such that $y = P(a, x)$. Here P is the regularized lower incomplete gamma function; see *gammainc*. This is well-defined because the lower incomplete gamma function is monotonic as can be seen from its definition in [dlmf].

Parameters

a [array_like] Positive parameter
y [array_like] Parameter between 0 and 1, inclusive

Returns

scalar or ndarray
Values of the inverse of the lower incomplete gamma function

See also:

gammainc

regularized lower incomplete gamma function

gammaincc

regularized upper incomplete gamma function

gammainccinv

inverse of the regualizred upper incomplete gamma function with respect to *x*

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

It starts at 0 and monotonically increases to infinity.

```
>>> sc.gammaincinv(0.5, [0, 0.1 ,0.5, 1])
array([0.        , 0.00789539, 0.22746821,        inf])
```

It inverts the lower incomplete gamma function.

```
>>> a, x = 0.5, [0, 0.1, 0.5, 1]
>>> sc.gammainc(a, sc.gammaincinv(a, x))
array([0. , 0.1, 0.5, 1. ])
```

```
>>> a, x = 0.5, [0, 10, 25]
>>> sc.gammaincinv(a, sc.gammainc(a, x))
array([ 0.        , 10.        , 25.00001465])
```

scipy.special.gammaincc

scipy.special.**gammaincc**(a, x) **= <ufunc 'gammaincc'>**

Regularized upper incomplete gamma function.

It is defined as

$$Q(a, x) = \frac{1}{\Gamma(a)} \int_x^\infty t^{a-1} e^{-t} dt$$

for $a > 0$ and $x \geq 0$. See [dlmf] for details.

Parameters

a [array_like] Positive parameter
x [array_like] Nonnegative argument

Returns

scalar or ndarray
Values of the upper incomplete gamma function

See also:

gammainc

regularized lower incomplete gamma function

gammaincinv

inverse of the regularized lower incomplete gamma function with respect to x

gammainccinv

inverse to of the regularized upper incomplete gamma function with respect to x

Notes

The function satisfies the relation `gammainc(a, x) + gammaincc(a, x) = 1` where *gammainc* is the regularized lower incomplete gamma function.

The implementation largely follows that of [boost].

References

[dlmf], [boost]

Examples

```
>>> import scipy.special as sc
```

It is the survival function of the gamma distribution, so it starts at 1 and monotonically decreases to 0.

```
>>> sc.gammaincc(0.5, [0, 1, 10, 100, 1000])
array([1.00000000e+00, 1.57299207e-01, 7.74421643e-06, 2.08848758e-45,
       0.00000000e+00])
```

It is equal to one minus the lower incomplete gamma function.

```
>>> a, x = 0.5, 0.4
>>> sc.gammaincc(a, x)
0.37109336952269756
>>> 1 - sc.gammainc(a, x)
0.37109336952269756
```

scipy.special.gammainccinv

scipy.special.**gammainccinv**(*a*, *y*) **= <ufunc 'gammainccinv'>**

Inverse of the upper incomplete gamma function with respect to x

Given an input y between 0 and 1, returns x such that $y = Q(a, x)$. Here Q is the upper incomplete gamma function; see *gammaincc*. This is well-defined because the upper incomplete gamma function is monotonic as can be seen from its definition in [dlmf].

Parameters

a [array_like] Positive parameter
y [array_like] Argument between 0 and 1, inclusive

Returns

scalar or ndarray
Values of the inverse of the upper incomplete gamma function

See also:

gammaincc

regularized upper incomplete gamma function

gammainc

regularized lower incomplete gamma function

gammaincinv

inverse of the regularized lower incomplete gamma function with respect to x

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

It starts at infinity and monotonically decreases to 0.

```
>>> sc.gammainccinv(0.5, [0, 0.1, 0.5, 1])
array([       inf, 1.35277173, 0.22746821, 0.        ])
```

It inverts the upper incomplete gamma function.

```
>>> a, x = 0.5, [0, 0.1, 0.5, 1]
>>> sc.gammaincc(a, sc.gammainccinv(a, x))
array([0. , 0.1, 0.5, 1. ])
```

```
>>> a, x = 0.5, [0, 10, 50]
>>> sc.gammainccinv(a, sc.gammaincc(a, x))
array([ 0., 10., 50.])
```

scipy.special.beta

scipy.special.**beta**(*a*, *b*, *out=None*) **= <ufunc 'beta'>**

Beta function.

This function is defined in [1] as

$$B(a, b) = \int_0^1 t^{a-1}(1-t)^{b-1}dt = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)},$$

where Γ is the gamma function.

Parameters

a, b [array-like] Real-valued arguments
out [ndarray, optional] Optional output array for the function result

Returns

scalar or ndarray
Value of the beta function

See also:

gamma

the gamma function

betainc

the incomplete beta function

betaln

the natural logarithm of the absolute value of the beta function

References

[1]

Examples

```
>>> import scipy.special as sc
```

The beta function relates to the gamma function by the definition given above:

```
>>> sc.beta(2, 3)
0.08333333333333333
>>> sc.gamma(2)*sc.gamma(3)/sc.gamma(2 + 3)
0.08333333333333333
```

As this relationship demonstrates, the beta function is symmetric:

```
>>> sc.beta(1.7, 2.4)
0.16567527689031739
>>> sc.beta(2.4, 1.7)
0.16567527689031739
```

This function satisfies $B(1, b) = 1/b$:

```
>>> sc.beta(1, 4)
0.25
```

scipy.special.betaln

scipy.special.**betaln**(*a*, *b*) **= <ufunc 'betaln'>**

Natural logarithm of absolute value of beta function.

Computes `ln(abs(beta(a, b)))`.

scipy.special.betainc

scipy.special.**betainc**(*a*, *b*, *x*, *out=None*) **= <ufunc 'betainc'>**

Incomplete beta function.

Computes the incomplete beta function, defined as [1]:

$$I_x(a,b) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \int_0^x t^{a-1}(1-t)^{b-1}dt,$$

for $0 \leq x \leq 1$.

Parameters

a, b	[array-like] Positive, real-valued parameters
x	[array-like] Real-valued such that $0 \leq x \leq 1$, the upper limit of integration
out	[ndarray, optional] Optional output array for the function values

Returns

array-like	Value of the incomplete beta function

See also:

beta

beta function

betaincinv

inverse of the incomplete beta function

Notes

The incomplete beta function is also sometimes defined without the *gamma* terms, in which case the above definition is the so-called regularized incomplete beta function. Under this definition, you can get the incomplete beta function by multiplying the result of the SciPy function by *beta*.

References

[1]

Examples

Let $B(a,b)$ be the *beta* function.

```
>>> import scipy.special as sc
```

The coefficient in terms of *gamma* is equal to $1/B(a,b)$. Also, when $x = 1$ the integral is equal to $B(a,b)$. Therefore, $I_{x=1}(a,b) = 1$ for any a,b.

```
>>> sc.betainc(0.2, 3.5, 1.0)
1.0
```

It satisfies $I_x(a,b) = x^a F(a, 1-b, a+1, x)/(aB(a,b))$, where F is the hypergeometric function *hyp2f1*:

```
>>> a, b, x = 1.4, 3.1, 0.5
>>> x**a * sc.hyp2f1(a, 1 - b, a + 1, x)/(a * sc.beta(a, b))
0.8148904036225295
>>> sc.betainc(a, b, x)
0.8148904036225296
```

This functions satisfies the relationship $I_x(a,b) = 1 - I_{1-x}(b,a)$:

```
>>> sc.betainc(2.2, 3.1, 0.4)
0.49339638807619446
>>> 1 - sc.betainc(3.1, 2.2, 1 - 0.4)
0.49339638807619446
```

scipy.special.betaincinv

scipy.special.**betaincinv**(*a*, *b*, *y*, *out=None*) **= <ufunc 'betaincinv'>**

Inverse of the incomplete beta function.

Computes x such that:

$$y = I_x(a,b) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} \int_0^x t^{a-1}(1-t)^{b-1}dt,$$

where I_x is the normalized incomplete beta function *betainc* and Γ is the *gamma* function [1].

Parameters

a, b	[array-like] Positive, real-valued parameters
y	[array-like] Real-valued input
out	[ndarray, optional] Optional output array for function values

Returns

array-like	Value of the inverse of the incomplete beta function

See also:

betainc

incomplete beta function

gamma

gamma function

References

[1]

Examples

```
>>> import scipy.special as sc
```

This function is the inverse of *betainc* for fixed values of a and b.

```
>>> a, b = 1.2, 3.1
>>> y = sc.betainc(a, b, 0.2)
>>> sc.betaincinv(a, b, y)
0.2
>>>
>>> a, b = 7.5, 0.4
>>> x = sc.betaincinv(a, b, 0.5)
>>> sc.betainc(a, b, x)
0.5
```

scipy.special.psi

scipy.special.**psi**(*z*, *out=None*) **= <ufunc 'psi'>**

The digamma function.

The logarithmic derivative of the gamma function evaluated at `z`.

Parameters

z	[array_like] Real or complex argument.
out	[ndarray, optional] Array for the computed values of `psi`.

Returns

digamma	[ndarray] Computed values of `psi`.

Notes

For large values not close to the negative real axis, `psi` is computed using the asymptotic series (5.11.2) from [1]. For small arguments not close to the negative real axis, the recurrence relation (5.5.2) from [1] is used until the argument is large enough to use the asymptotic series. For values close to the negative real axis, the reflection formula (5.5.4) from [1] is used first. Note that `psi` has a family of zeros on the negative real axis which occur between the poles at nonpositive integers. Around the zeros the reflection formula suffers from cancellation and the implementation loses precision. The sole positive zero and the first negative zero, however, are handled separately by precomputing series expansions using [2], so the function should maintain full accuracy around the origin.

References

[1], [2]

Examples

```
>>> from scipy.special import psi
>>> z = 3 + 4j
>>> psi(z)
(1.55035981733341+1.0105022091860445j)
```

Verify psi(z) = psi(z + 1) - 1/z:

```
>>> psi(z + 1) - 1/z
(1.55035981733341+1.0105022091860445j)
```

scipy.special.rgamma

scipy.special.**rgamma**(*z*, *out=None*) **= <ufunc 'rgamma'>**

Reciprocal of the gamma function.

Defined as $1/\Gamma(z)$, where Γ is the gamma function. For more on the gamma function see *gamma*.

Parameters

z	[array_like] Real or complex valued input
out	[ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
Function results

See also:

gamma, **gammaln**, **loggamma**

Notes

The gamma function has no zeros and has simple poles at nonpositive integers, so *rgamma* is an entire function with zeros at the nonpositive integers. See the discussion in [dlmf] for more details.

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

It is the reciprocal of the gamma function.

```
>>> sc.rgamma([1, 2, 3, 4])
array([1.        , 1.        , 0.5       , 0.16666667])
>>> 1 / sc.gamma([1, 2, 3, 4])
array([1.        , 1.        , 0.5       , 0.16666667])
```

It is zero at nonpositive integers.

```
>>> sc.rgamma([0, -1, -2, -3])
array([0., 0., 0., 0.])
```

It rapidly underflows to zero along the positive real axis.

```
>>> sc.rgamma([10, 100, 179])
array([2.75573192e-006, 1.07151029e-156, 0.00000000e+000])
```

scipy.special.polygamma

scipy.special.**polygamma**(*n*, *x*)

Polygamma functions.

Defined as $\psi^{(n)}(x)$ where ψ is the *digamma* function. See [dlmf] for details.

Parameters

n	[array_like] The order of the derivative of the digamma function; must be integral
x	[array_like] Real valued input

Returns

ndarray	Function results

See also:

digamma

References

[dlmf]

Examples

```
>>> from scipy import special
>>> x = [2, 3, 25.5]
>>> special.polygamma(1, x)
array([ 0.64493407,  0.39493407,  0.03999467])
>>> special.polygamma(0, x) == special.psi(x)
array([ True,  True,  True], dtype=bool)
```

scipy.special.multigammaln

scipy.special.**multigammaln**(*a*, *d*)

Returns the log of multivariate gamma, also sometimes called the generalized gamma.

Parameters

a	[ndarray] The multivariate gamma is computed for each item of a.
d	[int] The dimension of the space of integration.

Returns

res [ndarray] The values of the log multivariate gamma at the given points a.

Notes

The formal definition of the multivariate gamma of dimension d for a real a is

$$\Gamma_d(a) = \int_{A>0} e^{-tr(A)} |A|^{a-(d+1)/2} dA$$

with the condition $a > (d-1)/2$, and $A > 0$ being the set of all the positive definite matrices of dimension d. Note that a is a scalar: the integrand only is multivariate, the argument is not (the function is defined over a subset of the real set).

This can be proven to be equal to the much friendlier equation

$$\Gamma_d(a) = \pi^{d(d-1)/4} \prod_{i=1}^{d} \Gamma(a - (i-1)/2).$$

References

R. J. Muirhead, Aspects of multivariate statistical theory (Wiley Series in probability and mathematical statistics).

scipy.special.digamma

scipy.special.**digamma**(*z*, *out=None*) **= <ufunc 'psi'>**

The digamma function.

The logarithmic derivative of the gamma function evaluated at `z`.

Parameters

z [array_like] Real or complex argument.
out [ndarray, optional] Array for the computed values of `psi`.

Returns

digamma [ndarray] Computed values of `psi`.

Notes

For large values not close to the negative real axis, `psi` is computed using the asymptotic series (5.11.2) from [1]. For small arguments not close to the negative real axis, the recurrence relation (5.5.2) from [1] is used until the argument is large enough to use the asymptotic series. For values close to the negative real axis, the reflection formula (5.5.4) from [1] is used first. Note that `psi` has a family of zeros on the negative real axis which occur between the poles at nonpositive integers. Around the zeros the reflection formula suffers from cancellation and the implementation loses precision. The sole positive zero and the first negative zero, however, are handled separately by precomputing series expansions using [2], so the function should maintain full accuracy around the origin.

References

[1], [2]

Examples

```
>>> from scipy.special import psi
>>> z = 3 + 4j
>>> psi(z)
(1.55035981733341+1.0105022091860445j)
```

Verify psi(z) = psi(z + 1) - 1/z:

```
>>> psi(z + 1) - 1/z
(1.55035981733341+1.0105022091860445j)
```

scipy.special.poch

scipy.special.**poch**(*z*, *m*) **= <ufunc 'poch'>**

Pochhammer symbol.

The Pochhammer symbol (rising factorial) is defined as

$$(z)_m = \frac{\Gamma(z+m)}{\Gamma(z)}$$

For positive integer *m* it reads

$$(z)_m = z(z+1)...(z+m-1)$$

See [dlmf] for more details.

Parameters

z, m [array_like] Real-valued arguments.

Returns

scalar or ndarray
The value of the function.

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

It is 1 when m is 0.

```
>>> sc.poch([1, 2, 3, 4], 0)
array([1., 1., 1., 1.])
```

For z equal to 1 it reduces to the factorial function.

```
>>> sc.poch(1, 5)
120.0
>>> 1 * 2 * 3 * 4 * 5
120
```

It can be expressed in terms of the gamma function.

```
>>> z, m = 3.7, 2.1
>>> sc.poch(z, m)
20.529581933776953
>>> sc.gamma(z + m) / sc.gamma(z)
20.52958193377696
```

Error function and Fresnel integrals

erf(z)	Returns the error function of complex argument.
erfc(x[, out])	Complementary error function, `1 - erf(x)`.
erfcx(x[, out])	Scaled complementary error function, `exp(x**2) * erfc(x)`.
erfi(z[, out])	Imaginary error function, `-i erf(i z)`.
erfinv(x, /[, out, where, casting, order, …])	Inverse of the error function.
erfcinv(x, /[, out, where, casting, order, …])	Inverse of the complementary error function.
wofz(z)	Faddeeva function
dawsn(x)	Dawson's integral.
fresnel(z[, out])	Fresnel integrals.
fresnel_zeros(nt)	Compute nt complex zeros of sine and cosine Fresnel integrals S(z) and C(z).
modfresnelp(x)	Modified Fresnel positive integrals
modfresnelm(x)	Modified Fresnel negative integrals
voigt_profile(x, sigma, gamma[, out])	Voigt profile.

scipy.special.erf

scipy.special.**erf**(*z*) **= <ufunc 'erf'>**

Returns the error function of complex argument.

It is defined as `2/sqrt(pi)*integral(exp(-t**2), t=0..z)`.

Parameters

x [ndarray] Input array.

Returns

res [ndarray] The values of the error function at the given points *x*.

See also:

erfc, **erfinv**, **erfcinv**, **wofz**, **erfcx**, **erfi**

Notes

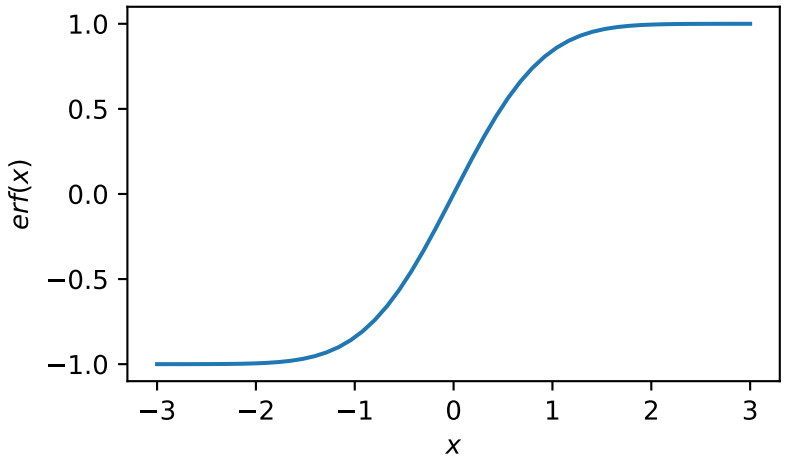
The cumulative of the unit normal distribution is given by `Phi(z) = 1/2[1 + erf(z/sqrt(2))]`.

References

[1], [2], [3]

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-3, 3)
>>> plt.plot(x, special.erf(x))
>>> plt.xlabel('$x$')
>>> plt.ylabel('$erf(x)$')
>>> plt.show()
```



scipy.special.erfc

`scipy.special.`**`erfc`**(*x*, *out=None*) **`= <ufunc 'erfc'>`**

Complementary error function, `1 - erf(x)`.

Parameters

x [array_like] Real or complex valued argument
out [ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
Values of the complementary error function

See also:

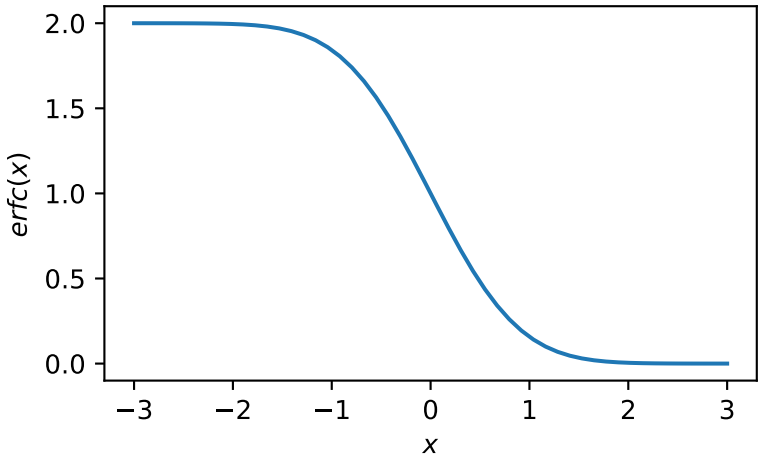
erf, **erfi**, **erfcx**, **dawsn**, **wofz**

References

[1]

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-3, 3)
>>> plt.plot(x, special.erfc(x))
>>> plt.xlabel('$x$')
>>> plt.ylabel('$erfc(x)$')
>>> plt.show()
```



scipy.special.erfcx

scipy.special.**erfcx**(*x*, *out=None*) **= <ufunc 'erfcx'>**

Scaled complementary error function, `exp(x**2) * erfc(x)`.

Parameters

x [array_like] Real or complex valued argument
out [ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
Values of the scaled complementary error function

See also:

erf, **erfc**, **erfi**, **dawsn**, **wofz**

Notes

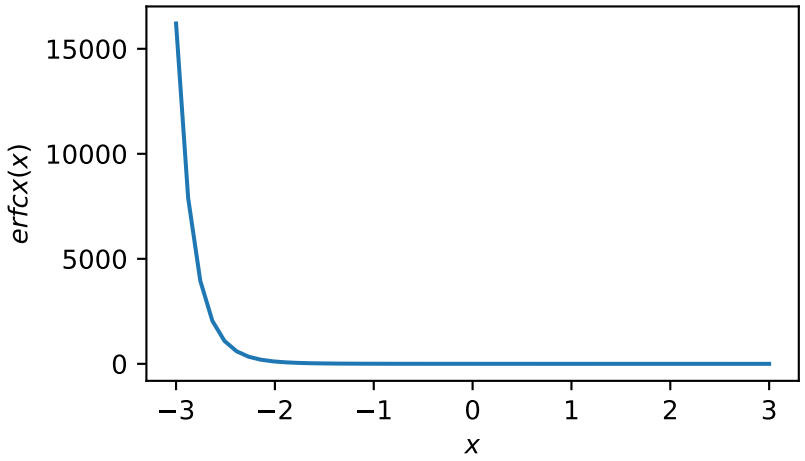
New in version 0.12.0.

References

[1]

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-3, 3)
>>> plt.plot(x, special.erfcx(x))
>>> plt.xlabel('$x$')
>>> plt.ylabel('$erfcx(x)$')
>>> plt.show()
```



scipy.special.erfi

scipy.special.**erfi**(*z*, *out=None*) **= <ufunc 'erfi'>**

Imaginary error function, `-i erf(i z)`.

Parameters

z	[array_like] Real or complex valued argument
out	[ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
Values of the imaginary error function

See also:

erf, **erfc**, **erfcx**, **dawsn**, **wofz**

Notes

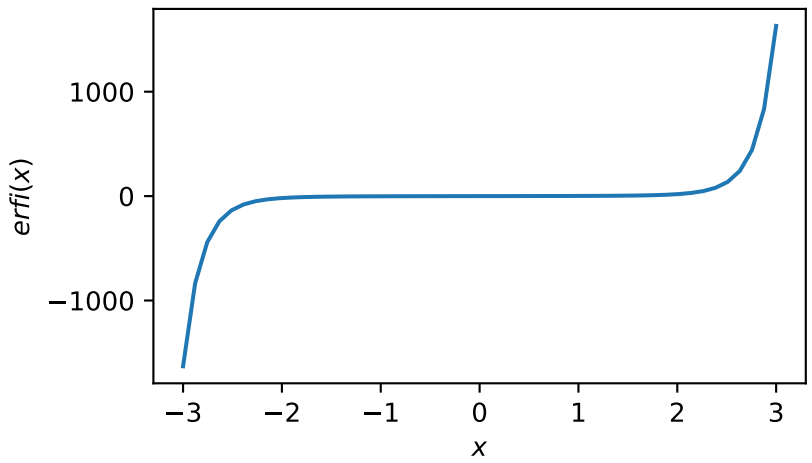
New in version 0.12.0.

References

[1]

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-3, 3)
>>> plt.plot(x, special.erfi(x))
>>> plt.xlabel('$x$')
>>> plt.ylabel('$erfi(x)$')
>>> plt.show()
```



scipy.special.erfinv

scipy.special.**erfinv**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*]) **= <ufunc 'erfinv'>**

Inverse of the error function.

Computes the inverse of the error function.
In the complex domain, there is no unique complex number w satisfying erf(w)=z. This indicates a true inverse function would have multi-value. When the domain restricts to the real, -1 < x < 1, there is a unique real number satisfying erf(erfinv(x)) = x.

Parameters

y [ndarray] Argument at which to evaluate. Domain: [-1, 1]

Returns

erfinv [ndarray] The inverse of erf of y, element-wise)

See also:

erf

Error function of a complex argument

erfc

Complementary error function, `1 - erf(x)`

erfcinv

Inverse of the complementary error function

Examples

1) evaluating a float number

```
>>> from scipy import special
>>> special.erfinv(0.5)
0.4769362762044698
```

2) evaluating an ndarray

```
>>> from scipy import special
>>> y = np.linspace(-1.0, 1.0, num=10)
>>> special.erfinv(y)
array([       -inf, -0.86312307, -0.5407314 , -0.30457019, -0.0987901 ,
        0.0987901 ,  0.30457019,  0.5407314 ,  0.86312307,         inf])
```

scipy.special.erfcinv

scipy.special.**erfcinv**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*]) **= <ufunc 'erfcinv'>**

Inverse of the complementary error function.

Computes the inverse of the complementary error function.
In the complex domain, there is no unique complex number w satisfying erfc(w)=z. This indicates a true inverse function would have multi-value. When the domain restricts to the real, 0 < x < 2, there is a unique real number satisfying erfc(erfcinv(x)) = erfcinv(erfc(x)).
It is related to inverse of the error function by erfcinv(1-x) = erfinv(x)

Parameters

y [ndarray] Argument at which to evaluate. Domain: [0, 2]

Returns

erfcinv [ndarray] The inverse of erfc of y, element-wise

See also:

erf

Error function of a complex argument

erfc

Complementary error function, `1 - erf(x)`

erfinv

Inverse of the error function

Examples

1) evaluating a float number

```
>>> from scipy import special
>>> special.erfcinv(0.5)
0.4769362762044698
```

2) evaluating an ndarray

```
>>> from scipy import special
>>> y = np.linspace(0.0, 2.0, num=11)
>>> special.erfcinv(y)
array([        inf,  0.9061938 ,  0.59511608,  0.37080716,  0.17914345,
       -0.        , -0.17914345, -0.37080716, -0.59511608, -0.9061938 ,
              -inf])
```

scipy.special.wofz

scipy.special.**wofz**(*z*) = <ufunc 'wofz'>

Faddeeva function

Returns the value of the Faddeeva function for complex argument:

```
exp(-z**2) * erfc(-i*z)
```

See also:

dawsn, **erf**, **erfc**, **erfcx**, **erfi**

References

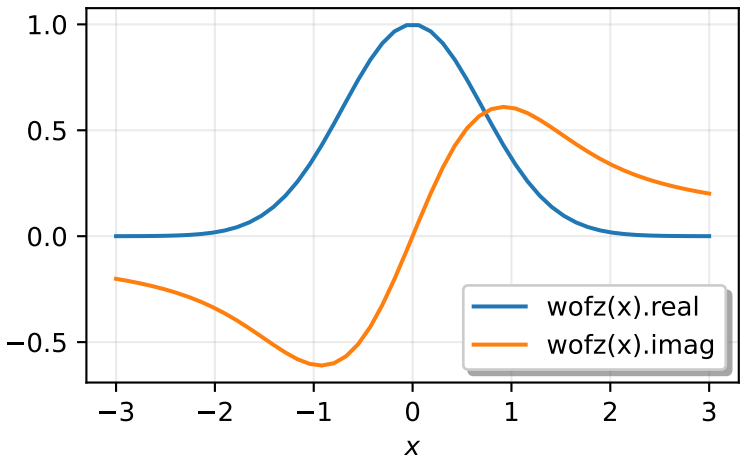
[1]

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
```

```
>>> x = np.linspace(-3, 3)
>>> z = special.wofz(x)
```

```
>>> plt.plot(x, z.real, label='wofz(x).real')
>>> plt.plot(x, z.imag, label='wofz(x).imag')
>>> plt.xlabel('$x$')
>>> plt.legend(framealpha=1, shadow=True)
>>> plt.grid(alpha=0.25)
>>> plt.show()
```



scipy.special.dawsn

scipy.special.**dawsn**(*x*) **= <ufunc 'dawsn'>**

Dawson's integral.

Computes:

```
exp(-x**2) * integral(exp(t**2), t=0..x).
```

See also:

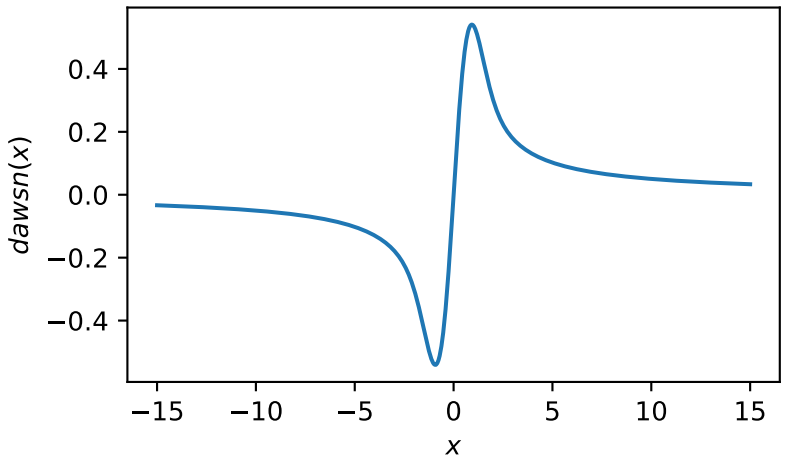
wofz, **erf**, **erfc**, **erfcx**, **erfi**

References

[1]

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-15, 15, num=1000)
>>> plt.plot(x, special.dawsn(x))
>>> plt.xlabel('$x$')
>>> plt.ylabel('$dawsn(x)$')
>>> plt.show()
```



scipy.special.fresnel

scipy.special.**fresnel**(*z*, *out=None*) **= <ufunc 'fresnel'>**

Fresnel integrals.

The Fresnel integrals are defined as

$$S(z) = \int_0^z \sin(\pi t^2/2)dt$$
$$C(z) = \int_0^z \cos(\pi t^2/2)dt.$$

See [dlmf] for details.

Parameters

z	[array_like] Real or complex valued argument
out	[2-tuple of ndarrays, optional] Optional output arrays for the function results

Returns

S, C	[2-tuple of scalar or ndarray] Values of the Fresnel integrals

See also:

fresnel_zeros

zeros of the Fresnel integrals

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

As z goes to infinity along the real axis, S and C converge to 0.5.

```
>>> S, C = sc.fresnel([0.1, 1, 10, 100, np.inf])
>>> S
array([0.00052359, 0.43825915, 0.46816998, 0.4968169 , 0.5       ])
>>> C
array([0.09999753, 0.7798934 , 0.49989869, 0.4999999 , 0.5       ])
```

They are related to the error function *erf*.

```
>>> z = np.array([1, 2, 3, 4])
>>> zeta = 0.5 * np.sqrt(np.pi) * (1 - 1j) * z
>>> S, C = sc.fresnel(z)
>>> C + 1j*S
array([0.7798934 +0.43825915j, 0.48825341+0.34341568j,
       0.60572079+0.496313j  , 0.49842603+0.42051575j])
>>> 0.5 * (1 + 1j) * sc.erf(zeta)
array([0.7798934 +0.43825915j, 0.48825341+0.34341568j,
       0.60572079+0.496313j  , 0.49842603+0.42051575j])
```

scipy.special.fresnel_zeros

scipy.special.**fresnel_zeros**(*nt*)
Compute nt complex zeros of sine and cosine Fresnel integrals S(z) and C(z).

References

[1]

scipy.special.modfresnelp

scipy.special.**modfresnelp**(*x*) **= <ufunc 'modfresnelp'>**
Modified Fresnel positive integrals

Returns

fp	Integral `F_+(x): integral(exp(1j*t*t), t=x..inf)`
kp	Integral `K_+(x): 1/sqrt(pi)*exp(-1j*(x*x+pi/4))*fp`

scipy.special.modfresnelm

scipy.special.**modfresnelm**(*x*) **= <ufunc 'modfresnelm'>**
Modified Fresnel negative integrals

Returns

fm	Integral `F_-(x): integral(exp(-1j*t*t), t=x..inf)`
km	Integral `K_-(x): 1/sqrt(pi)*exp(1j*(x*x+pi/4))*fp`

scipy.special.voigt_profile

scipy.special.**voigt_profile**(*x*, *sigma*, *gamma*, *out=None*) **= <ufunc 'voigt_profile'>**
Voigt profile.

The Voigt profile is a convolution of a 1-D Normal distribution with standard deviation `sigma` and a 1-D Cauchy distribution with half-width at half-maximum `gamma`.

If `sigma = 0`, PDF of Cauchy distribution is returned. Conversely, if `gamma = 0`, PDF of Normal distribution is returned. If `sigma = gamma = 0`, the return value is `Inf` for `x = 0`, and `0` for all other `x`.

Parameters

x	[array_like] Real argument
sigma	[array_like] The standard deviation of the Normal distribution part
gamma	[array_like] The half-width at half-maximum of the Cauchy distribution part
out	[ndarray, optional] Optional output array for the function values

Returns

scalar or ndarray
The Voigt profile at the given arguments

See also:

wofz

Faddeeva function

Notes

It can be expressed in terms of Faddeeva function

$$V(x;\sigma,\gamma) = \frac{Re[w(z)]}{\sigma\sqrt{2\pi}},$$

$$z = \frac{x+i\gamma}{\sqrt{2}\sigma}$$

where $w(z)$ is the Faddeeva function.

References

[1]

These are not universal functions:

erf_zeros(nt)	Compute the first nt zero in the first quadrant, ordered by absolute value.
fresnelc_zeros(nt)	Compute nt complex zeros of cosine Fresnel integral C(z).
fresnels_zeros(nt)	Compute nt complex zeros of sine Fresnel integral S(z).

scipy.special.erf_zeros

scipy.special.**erf_zeros**(*nt*)

Compute the first nt zero in the first quadrant, ordered by absolute value.

Zeros in the other quadrants can be obtained by using the symmetries erf(-z) = erf(z) and erf(conj(z)) = conj(erf(z)).

Parameters

nt [int] The number of zeros to compute

Returns

The locations of the zeros of erf
[ndarray (complex)] Complex values at which zeros of erf(z)

References

[1]

Examples

```
>>> from scipy import special
>>> special.erf_zeros(1)
array([1.45061616+1.880943j])
```

Check that erf is (close to) zero for the value returned by erf_zeros

```
>>> special.erf(special.erf_zeros(1))
array([4.95159469e-14-1.16407394e-16j])
```

scipy.special.fresnelc_zeros

scipy.special.**fresnelc_zeros**(*nt*)
Compute nt complex zeros of cosine Fresnel integral C(z).

References

[1]

scipy.special.fresnels_zeros

scipy.special.**fresnels_zeros**(*nt*)
Compute nt complex zeros of sine Fresnel integral S(z).

References

[1]

Legendre functions

lpmv(m, v, x)	Associated Legendre function of integer order and real degree.
sph_harm(m, n, theta, phi)	Compute spherical harmonics.

scipy.special.lpmv

scipy.special.**lpmv**(*m*, *v*, *x*) **= <ufunc 'lpmv'>**
Associated Legendre function of integer order and real degree.

Defined as

$$P_v^m = (-1)^m (1 - x^2)^{m/2} \frac{d^m}{dx^m} P_v(x)$$

where

$$P_v = \sum_{k=0}^{\infty} \frac{(-v)_k (v+1)_k}{(k!)^2} \left(\frac{1-x}{2}\right)^k$$

is the Legendre function of the first kind. Here $(\cdot)_k$ is the Pochhammer symbol; see *poch*.

Parameters

m [array_like] Order (int or float). If passed a float not equal to an integer the function returns NaN.
v [array_like] Degree (float).
x [array_like] Argument (float). Must have `|x| <= 1`.

Returns

pmv [ndarray] Value of the associated Legendre function.

See also:

lpmn

Compute the associated Legendre function for all orders `0, ..., m` and degrees `0, ..., n`.

clpmn

Compute the associated Legendre function at complex arguments.

Notes

Note that this implementation includes the Condon-Shortley phase.

References

[1]

scipy.special.sph_harm

scipy.special.**sph_harm**(*m*, *n*, *theta*, *phi*) **= <ufunc 'sph_harm'>**

Compute spherical harmonics.

The spherical harmonics are defined as

$$Y_n^m(\theta,\phi) = \sqrt{\frac{2n+1}{4\pi}\frac{(n-m)!}{(n+m)!}}e^{im\theta}P_n^m(\cos(\phi))$$

where P_n^m are the associated Legendre functions; see *lpmv*.

Parameters

m [array_like] Order of the harmonic (int); must have `|m| <= n`.
n [array_like] Degree of the harmonic (int); must have `n >= 0`. This is often denoted by `l` (lower case L) in descriptions of spherical harmonics.
theta [array_like] Azimuthal (longitudinal) coordinate; must be in `[0, 2*pi]`.
phi [array_like] Polar (colatitudinal) coordinate; must be in `[0, pi]`.

Returns

y_mn [complex float] The harmonic Y_n^m sampled at `theta` and `phi`.

Notes

There are different conventions for the meanings of the input arguments `theta` and `phi`. In SciPy `theta` is the azimuthal angle and `phi` is the polar angle. It is common to see the opposite convention, that is, `theta` as the polar angle and `phi` as the azimuthal angle.

Note that SciPy's spherical harmonics include the Condon-Shortley phase [2] because it is part of *lpmv*.

With SciPy's conventions, the first several spherical harmonics are

$$Y_0^0(\theta, \phi) = \frac{1}{2}\sqrt{\frac{1}{\pi}}$$
$$Y_1^{-1}(\theta, \phi) = \frac{1}{2}\sqrt{\frac{3}{2\pi}}e^{-i\theta}\sin(\phi)$$
$$Y_1^0(\theta, \phi) = \frac{1}{2}\sqrt{\frac{3}{\pi}}\cos(\phi)$$
$$Y_1^1(\theta, \phi) = -\frac{1}{2}\sqrt{\frac{3}{2\pi}}e^{i\theta}\sin(\phi).$$

References

[1], [2]

These are not universal functions:

clpmn(m, n, z[, type])	Associated Legendre function of the first kind for complex arguments.
lpn(n, z)	Legendre function of the first kind.
lqn(n, z)	Legendre function of the second kind.
lpmn(m, n, z)	Sequence of associated Legendre functions of the first kind.
lqmn(m, n, z)	Sequence of associated Legendre functions of the second kind.

scipy.special.clpmn

scipy.special.**clpmn**(*m*, *n*, *z*, *type=3*)

Associated Legendre function of the first kind for complex arguments.

Computes the associated Legendre function of the first kind of order m and degree n, `Pmn(z)` = $P_n^m(z)$, and its derivative, `Pmn'(z)`. Returns two arrays of size `(m+1, n+1)` containing `Pmn(z)` and `Pmn'(z)` for all orders from `0..m` and degrees from `0..n`.

Parameters

m	[int] `|m| <= n`; the order of the Legendre function.
n	[int] where `n >= 0`; the degree of the Legendre function. Often called `l` (lower case L) in descriptions of the associated Legendre function
z	[float or complex] Input value.
type	[int, optional] takes values 2 or 3 2: cut on the real axis `|x| > 1` 3: cut on the real axis `-1 < x < 1` (default)

Returns

Pmn_z [(m+1, n+1) array] Values for all orders `0..m` and degrees `0..n`
Pmn_d_z [(m+1, n+1) array] Derivatives for all orders `0..m` and degrees `0..n`

See also:

`lpmn`

associated Legendre functions of the first kind for real z

Notes

By default, i.e. for `type=3`, phase conventions are chosen according to [1] such that the function is analytic. The cut lies on the interval (-1, 1). Approaching the cut from above or below in general yields a phase factor with respect to Ferrer's function of the first kind (cf. *lpmn*).

For `type=2` a cut at `|x| > 1` is chosen. Approaching the real values on the interval (-1, 1) in the complex plane yields Ferrer's function of the first kind.

References

[1], [2]

scipy.special.lpn

`scipy.special.`**`lpn`**(*n*, *z*)
Legendre function of the first kind.

Compute sequence of Legendre functions of the first kind (polynomials), Pn(z) and derivatives for all degrees from 0 to n (inclusive).

See also special.legendre for polynomial class.

References

[1]

scipy.special.lqn

`scipy.special.`**`lqn`**(*n*, *z*)
Legendre function of the second kind.

Compute sequence of Legendre functions of the second kind, Qn(z) and derivatives for all degrees from 0 to n (inclusive).

References

[1]

scipy.special.lpmn

scipy.special.**lpmn**(*m*, *n*, *z*)

Sequence of associated Legendre functions of the first kind.

Computes the associated Legendre function of the first kind of order m and degree n, `Pmn(z)` = $P_n^m(z)$, and its derivative, `Pmn'(z)`. Returns two arrays of size `(m+1, n+1)` containing `Pmn(z)` and `Pmn'(z)` for all orders from `0..m` and degrees from `0..n`.

This function takes a real argument `z`. For complex arguments `z` use clpmn instead.

Parameters

m	[int] `|m| <= n`; the order of the Legendre function.
n	[int] where `n >= 0`; the degree of the Legendre function. Often called `l` (lower case L) in descriptions of the associated Legendre function
z	[float] Input value.

Returns

Pmn_z	[(m+1, n+1) array] Values for all orders 0..m and degrees 0..n
Pmn_d_z	[(m+1, n+1) array] Derivatives for all orders 0..m and degrees 0..n

See also:

clpmn

associated Legendre functions of the first kind for complex z

Notes

In the interval (-1, 1), Ferrer's function of the first kind is returned. The phase convention used for the intervals (1, inf) and (-inf, -1) is such that the result is always real.

References

[1], [2]

scipy.special.lqmn

scipy.special.**lqmn**(*m*, *n*, *z*)

Sequence of associated Legendre functions of the second kind.

Computes the associated Legendre function of the second kind of order m and degree n, `Qmn(z)` = $Q_n^m(z)$, and its derivative, `Qmn'(z)`. Returns two arrays of size `(m+1, n+1)` containing `Qmn(z)` and `Qmn'(z)` for all orders from `0..m` and degrees from `0..n`.

Parameters

m	[int] `|m| <= n`; the order of the Legendre function.
n	[int] where `n >= 0`; the degree of the Legendre function. Often called `l` (lower case L) in descriptions of the associated Legendre function

z [complex] Input value.

Returns

Qmn_z [(m+1, n+1) array] Values for all orders 0..m and degrees 0..n
Qmn_d_z [(m+1, n+1) array] Derivatives for all orders 0..m and degrees 0..n

References

[1]

Ellipsoidal harmonics

ellip_harm(h2, k2, n, p, s[, signm, signn])	Ellipsoidal harmonic functions E^p_n(l)
ellip_harm_2(h2, k2, n, p, s)	Ellipsoidal harmonic functions F^p_n(l)
ellip_normal(h2, k2, n, p)	Ellipsoidal harmonic normalization constants gamma^p_n

scipy.special.ellip_harm

scipy.special.**ellip_harm**(*h2*, *k2*, *n*, *p*, *s*, *signm=1*, *signn=1*)

Ellipsoidal harmonic functions E^p_n(l)

These are also known as Lame functions of the first kind, and are solutions to the Lame equation:

$$(s^2 - h^2)(s^2 - k^2)E''(s) + s(2s^2 - h^2 - k^2)E'(s) + (a - qs^2)E(s) = 0$$

where $q = (n+1)n$ and a is the eigenvalue (not returned) corresponding to the solutions.

Parameters

h2 [float] `h**2`
k2 [float] `k**2`; should be larger than `h**2`
n [int] Degree
s [float] Coordinate
p [int] Order, can range between [1,2n+1]
signm [{1, -1}, optional] Sign of prefactor of functions. Can be +/-1. See Notes.
signn [{1, -1}, optional] Sign of prefactor of functions. Can be +/-1. See Notes.

Returns

E [float] the harmonic $E^p_n(s)$

See also:

ellip_harm_2, **ellip_normal**

Notes

The geometric interpretation of the ellipsoidal functions is explained in [2], [3], [4]. The *signm* and *signn* arguments control the sign of prefactors for functions according to their type:

```
K : +1
L : signm
M : signn
N : signm*signn
```

New in version 0.15.0.

References

[1], [2], [3], [4]

Examples

```
>>> from scipy.special import ellip_harm
>>> w = ellip_harm(5,8,1,1,2.5)
>>> w
2.5
```

Check that the functions indeed are solutions to the Lame equation:

```
>>> from scipy.interpolate import UnivariateSpline
>>> def eigenvalue(f, df, ddf):
...     r = ((s**2 - h**2)*(s**2 - k**2)*ddf + s*(2*s**2 - h**2 -␣
↪k**2)*df - n*(n+1)*s**2*f)/f
...     return -r.mean(), r.std()
>>> s = np.linspace(0.1, 10, 200)
>>> k, h, n, p = 8.0, 2.2, 3, 2
>>> E = ellip_harm(h**2, k**2, n, p, s)
>>> E_spl = UnivariateSpline(s, E)
>>> a, a_err = eigenvalue(E_spl(s), E_spl(s,1), E_spl(s,2))
>>> a, a_err
(583.44366156701483, 6.4580890640310646e-11)
```

scipy.special.ellip_harm_2

scipy.special.**ellip_harm_2**(*h2*, *k2*, *n*, *p*, *s*)

Ellipsoidal harmonic functions F^p_n(l)

These are also known as Lame functions of the second kind, and are solutions to the Lame equation:

$$(s^2 - h^2)(s^2 - k^2)F''(s) + s(2s^2 - h^2 - k^2)F'(s) + (a - qs^2)F(s) = 0$$

where $q = (n + 1)n$ and a is the eigenvalue (not returned) corresponding to the solutions.

Parameters

h2 [float] `h**2`

k2 [float] `k**2`; should be larger than `h**2`

n	[int] Degree.
p	[int] Order, can range between [1,2n+1].
s	[float] Coordinate

Returns

F	[float] The harmonic $F_n^p(s)$

See also:

ellip_harm, **ellip_normal**

Notes

Lame functions of the second kind are related to the functions of the first kind:

$$F_n^p(s) = (2n+1)E_n^p(s)\int_0^{1/s} \frac{du}{(E_n^p(1/u))^2\sqrt{(1-u^2k^2)(1-u^2h^2)}}$$

New in version 0.15.0.

Examples

```
>>> from scipy.special import ellip_harm_2
>>> w = ellip_harm_2(5,8,2,1,10)
>>> w
0.00108056853382
```

scipy.special.ellip_normal

scipy.special.**ellip_normal**(*h2*, *k2*, *n*, *p*)

Ellipsoidal harmonic normalization constants gamma^p_n

The normalization constant is defined as

$$\gamma_n^p = 8\int_0^h dx \int_h^k dy \frac{(y^2-x^2)(E_n^p(y)E_n^p(x))^2}{\sqrt((k^2-y^2)(y^2-h^2)(h^2-x^2)(k^2-x^2)}$$

Parameters

h2	[float] `h**2`
k2	[float] `k**2`; should be larger than `h**2`
n	[int] Degree.
p	[int] Order, can range between [1,2n+1].

Returns

gamma	[float] The normalization constant γ_n^p

See also:

ellip_harm, **ellip_harm_2**

Notes

New in version 0.15.0.

Examples

```
>>> from scipy.special import ellip_normal
>>> w = ellip_normal(5,8,3,7)
>>> w
1723.38796997
```

Orthogonal polynomials

The following functions evaluate values of orthogonal polynomials:

assoc_laguerre(x, n[, k])	Compute the generalized (associated) Laguerre polynomial of degree n and order k.
eval_legendre(n, x[, out])	Evaluate Legendre polynomial at a point.
eval_chebyt(n, x[, out])	Evaluate Chebyshev polynomial of the first kind at a point.
eval_chebyu(n, x[, out])	Evaluate Chebyshev polynomial of the second kind at a point.
eval_chebyc(n, x[, out])	Evaluate Chebyshev polynomial of the first kind on [-2, 2] at a point.
eval_chebys(n, x[, out])	Evaluate Chebyshev polynomial of the second kind on [-2, 2] at a point.
eval_jacobi(n, alpha, beta, x[, out])	Evaluate Jacobi polynomial at a point.
eval_laguerre(n, x[, out])	Evaluate Laguerre polynomial at a point.
eval_genlaguerre(n, alpha, x[, out])	Evaluate generalized Laguerre polynomial at a point.
eval_hermite(n, x[, out])	Evaluate physicist's Hermite polynomial at a point.
eval_hermitenorm(n, x[, out])	Evaluate probabilist's (normalized) Hermite polynomial at a point.
eval_gegenbauer(n, alpha, x[, out])	Evaluate Gegenbauer polynomial at a point.
eval_sh_legendre(n, x[, out])	Evaluate shifted Legendre polynomial at a point.
eval_sh_chebyt(n, x[, out])	Evaluate shifted Chebyshev polynomial of the first kind at a point.
eval_sh_chebyu(n, x[, out])	Evaluate shifted Chebyshev polynomial of the second kind at a point.
eval_sh_jacobi(n, p, q, x[, out])	Evaluate shifted Jacobi polynomial at a point.

scipy.special.assoc_laguerre

scipy.special.**assoc_laguerre**(*x*, *n*, *k=0.0*)

Compute the generalized (associated) Laguerre polynomial of degree n and order k.

The polynomial $L_n^{(k)}(x)$ is orthogonal over `[0, inf)`, with weighting function `exp(-x) * x**k` with `k > -1`.

Notes

assoc_laguerre is a simple wrapper around *eval_genlaguerre*, with reversed argument order `(x, n, k=0.0) --> (n, k, x)`.

scipy.special.eval_legendre

scipy.special.**eval_legendre**(*n*, *x*, *out=None*) **= <ufunc 'eval_legendre'>**

Evaluate Legendre polynomial at a point.

The Legendre polynomials can be defined via the Gauss hypergeometric function ${}_2F_1$ as

$$P_n(x) = {}_2F_1(-n, n+1; 1; (1-x)/2).$$

When n is an integer the result is a polynomial of degree n. See 22.5.49 in [AS] for details.

Parameters

n	[array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the Gauss hypergeometric function.
x	[array_like] Points at which to evaluate the Legendre polynomial

Returns

P	[ndarray] Values of the Legendre polynomial

See also:

roots_legendre

roots and quadrature weights of Legendre polynomials

legendre

Legendre polynomial object

hyp2f1

Gauss hypergeometric function

numpy.polynomial.legendre.Legendre

Legendre series

References

[AS]

Examples

```
>>> from scipy.special import eval_legendre
```

Evaluate the zero-order Legendre polynomial at x = 0

```
>>> eval_legendre(0, 0)
1.0
```

Evaluate the first-order Legendre polynomial between -1 and 1

```
>>> X = np.linspace(-1, 1, 5)  # Domain of Legendre polynomials
>>> eval_legendre(1, X)
array([-1. , -0.5,  0. ,  0.5,  1. ])
```

Evaluate Legendre polynomials of order 0 through 4 at x = 0

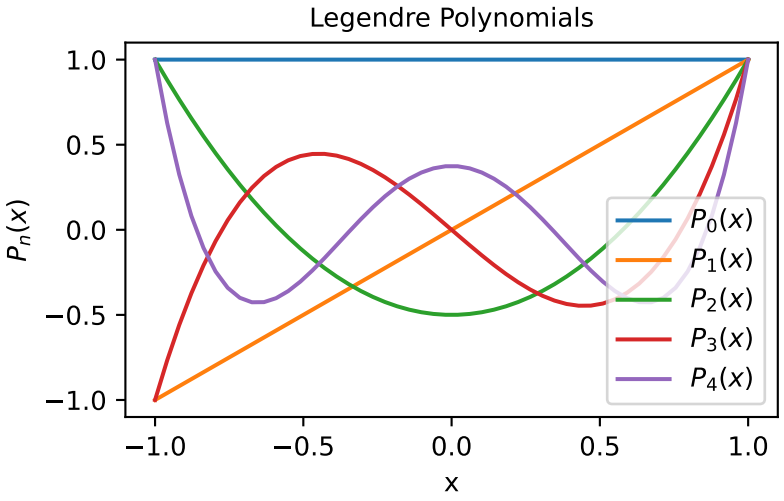
```
>>> N = range(0, 5)
>>> eval_legendre(N, 0)
array([ 1.   ,  0.   , -0.5  ,  0.   ,  0.375])
```

Plot Legendre polynomials of order 0 through 4

```
>>> X = np.linspace(-1, 1)
```

```
>>> import matplotlib.pyplot as plt
>>> for n in range(0, 5):
...     y = eval_legendre(n, X)
...     plt.plot(X, y, label=r'$P_{}(x)$'.format(n))
```

```
>>> plt.title("Legendre Polynomials")
>>> plt.xlabel("x")
>>> plt.ylabel(r'$P_n(x)$')
>>> plt.legend(loc='lower right')
>>> plt.show()
```



scipy.special.eval_chebyt

scipy.special.**eval_chebyt**(*n*, *x*, *out=None*) **= <ufunc 'eval_chebyt'>**

Evaluate Chebyshev polynomial of the first kind at a point.

The Chebyshev polynomials of the first kind can be defined via the Gauss hypergeometric function ${}_2F_1$ as

$$T_n(x) = {}_2F_1(n, -n; 1/2; (1-x)/2).$$

When n is an integer the result is a polynomial of degree n. See 22.5.47 in [AS] for details.

Parameters

n	[array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the Gauss hypergeometric function.
x	[array_like] Points at which to evaluate the Chebyshev polynomial

Returns

T	[ndarray] Values of the Chebyshev polynomial

See also:

roots_chebyt

roots and quadrature weights of Chebyshev polynomials of the first kind

chebyu

Chebychev polynomial object

eval_chebyu

evaluate Chebyshev polynomials of the second kind

hyp2f1

Gauss hypergeometric function

numpy.polynomial.chebyshev.Chebyshev

Chebyshev series

Notes

This routine is numerically stable for *x* in `[-1, 1]` at least up to order `10000`.

References

[AS]

scipy.special.eval_chebyu

scipy.special.**eval_chebyu**(*n*, *x*, *out=None*) **= <ufunc 'eval_chebyu'>**

Evaluate Chebyshev polynomial of the second kind at a point.

The Chebyshev polynomials of the second kind can be defined via the Gauss hypergeometric function ${}_2F_1$ as

$$U_n(x) = (n+1){}_2F_1(-n, n+2; 3/2; (1-x)/2).$$

When n is an integer the result is a polynomial of degree n. See 22.5.48 in [AS] for details.

Parameters

n [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the Gauss hypergeometric function.

x [array_like] Points at which to evaluate the Chebyshev polynomial

Returns

U [ndarray] Values of the Chebyshev polynomial

See also:

roots_chebyu

roots and quadrature weights of Chebyshev polynomials of the second kind

chebyu

Chebyshev polynomial object

eval_chebyt

evaluate Chebyshev polynomials of the first kind

hyp2f1

Gauss hypergeometric function

References

[AS]

scipy.special.eval_chebyc

scipy.special.**eval_chebyc**(*n*, *x*, *out=None*) **= <ufunc 'eval_chebyc'>**

Evaluate Chebyshev polynomial of the first kind on [-2, 2] at a point.

These polynomials are defined as

$$C_n(x) = 2T_n(x/2)$$

where T_n is a Chebyshev polynomial of the first kind. See 22.5.11 in [AS] for details.

Parameters

n [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to *eval_chebyt*.

x [array_like] Points at which to evaluate the Chebyshev polynomial

Returns

C [ndarray] Values of the Chebyshev polynomial

See also:

`roots_chebyc`

roots and quadrature weights of Chebyshev polynomials of the first kind on [-2, 2]

`chebyc`

Chebyshev polynomial object

`numpy.polynomial.chebyshev.Chebyshev`

Chebyshev series

`eval_chebyt`

evaluate Chebycshev polynomials of the first kind

References

[AS]

Examples

```
>>> import scipy.special as sc
```

They are a scaled version of the Chebyshev polynomials of the first kind.

```
>>> x = np.linspace(-2, 2, 6)
>>> sc.eval_chebyc(3, x)
array([-2.   ,  1.872,  1.136, -1.136, -1.872,  2.   ])
>>> 2 * sc.eval_chebyt(3, x / 2)
array([-2.   ,  1.872,  1.136, -1.136, -1.872,  2.   ])
```

scipy.special.eval_chebys

scipy.special.**eval_chebys**(*n*, *x*, *out=None*) **= <ufunc 'eval_chebys'>**

Evaluate Chebyshev polynomial of the second kind on [-2, 2] at a point.

These polynomials are defined as

$$S_n(x) = U_n(x/2)$$

where U_n is a Chebyshev polynomial of the second kind. See 22.5.13 in [AS] for details.

Parameters

n [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to *`eval_chebyu`*.

x [array_like] Points at which to evaluate the Chebyshev polynomial

Returns

S [ndarray] Values of the Chebyshev polynomial

See also:

roots_chebys

roots and quadrature weights of Chebyshev polynomials of the second kind on [-2, 2]

chebys

Chebyshev polynomial object

eval_chebyu

evaluate Chebyshev polynomials of the second kind

References

[AS]

Examples

```
>>> import scipy.special as sc
```

They are a scaled version of the Chebyshev polynomials of the second kind.

```
>>> x = np.linspace(-2, 2, 6)
>>> sc.eval_chebys(3, x)
array([-4.   ,  0.672,  0.736, -0.736, -0.672,  4.   ])
>>> sc.eval_chebyu(3, x / 2)
array([-4.   ,  0.672,  0.736, -0.736, -0.672,  4.   ])
```

scipy.special.eval_jacobi

scipy.special.**eval_jacobi**(*n*, *alpha*, *beta*, *x*, *out=None*) **= <ufunc 'eval_jacobi'>**

Evaluate Jacobi polynomial at a point.

The Jacobi polynomials can be defined via the Gauss hypergeometric function ${}_2F_1$ as

$$P_n^{(\alpha,\beta)}(x) = \frac{(\alpha+1)_n}{\Gamma(n+1)} {}_2F_1(-n, 1+\alpha+\beta+n; \alpha+1; (1-z)/2)$$

where $(\cdot)_n$ is the Pochhammer symbol; see *poch*. When n is an integer the result is a polynomial of degree n. See 22.5.42 in [AS] for details.

Parameters

n	[array_like] Degree of the polynomial. If not an integer the result is determined via the relation to the Gauss hypergeometric function.
alpha	[array_like] Parameter
beta	[array_like] Parameter
x	[array_like] Points at which to evaluate the polynomial

Returns

P	[ndarray] Values of the Jacobi polynomial

See also:

roots_jacobi

roots and quadrature weights of Jacobi polynomials

jacobi

Jacobi polynomial object

hyp2f1

Gauss hypergeometric function

References

[AS]

scipy.special.eval_laguerre

scipy.special.**eval_laguerre**(*n*, *x*, *out=None*) **= <ufunc 'eval_laguerre'>**

Evaluate Laguerre polynomial at a point.

The Laguerre polynomials can be defined via the confluent hypergeometric function ${}_1F_1$ as

$$L_n(x) = {}_1F_1(-n, 1, x).$$

See 22.5.16 and 22.5.54 in [AS] for details. When n is an integer the result is a polynomial of degree n.

Parameters

n [array_like] Degree of the polynomial. If not an integer the result is determined via the relation to the confluent hypergeometric function.

x [array_like] Points at which to evaluate the Laguerre polynomial

Returns

L [ndarray] Values of the Laguerre polynomial

See also:

roots_laguerre

roots and quadrature weights of Laguerre polynomials

laguerre

Laguerre polynomial object

numpy.polynomial.laguerre.Laguerre

Laguerre series

eval_genlaguerre

evaluate generalized Laguerre polynomials

References

[AS]

scipy.special.eval_genlaguerre

scipy.special.**eval_genlaguerre**(*n*, *alpha*, *x*, *out=None*) **= <ufunc 'eval_genlaguerre'>**

Evaluate generalized Laguerre polynomial at a point.

The generalized Laguerre polynomials can be defined via the confluent hypergeometric function ${}_1F_1$ as

$$L_n^{(\alpha)}(x) = \binom{n+\alpha}{n} {}_1F_1(-n, \alpha+1, x).$$

When n is an integer the result is a polynomial of degree n. See 22.5.54 in [AS] for details. The Laguerre polynomials are the special case where $\alpha = 0$.

Parameters

n	[array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the confluent hypergeometric function.
alpha	[array_like] Parameter; must have `alpha > -1`
x	[array_like] Points at which to evaluate the generalized Laguerre polynomial

Returns

L	[ndarray] Values of the generalized Laguerre polynomial

See also:

roots_genlaguerre

roots and quadrature weights of generalized Laguerre polynomials

genlaguerre

generalized Laguerre polynomial object

hyp1f1

confluent hypergeometric function

eval_laguerre

evaluate Laguerre polynomials

References

[AS]

scipy.special.eval_hermite

scipy.special.**eval_hermite**(*n*, *x*, *out=None*) **= <ufunc 'eval_hermite'>**

Evaluate physicist's Hermite polynomial at a point.

Defined by

$$H_n(x) = (-1)^n e^{x^2} \frac{d^n}{dx^n} e^{-x^2};$$

H_n is a polynomial of degree n. See 22.11.7 in [AS] for details.

Parameters

n	[array_like] Degree of the polynomial
x	[array_like] Points at which to evaluate the Hermite polynomial

Returns

H	[ndarray] Values of the Hermite polynomial

See also:

roots_hermite

roots and quadrature weights of physicist's Hermite polynomials

hermite

physicist's Hermite polynomial object

numpy.polynomial.hermite.Hermite

Physicist's Hermite series

eval_hermitenorm

evaluate Probabilist's Hermite polynomials

References

[AS]

scipy.special.eval_hermitenorm

scipy.special.**eval_hermitenorm**(*n*, *x*, *out=None*) **= <ufunc 'eval_hermitenorm'>**

Evaluate probabilist's (normalized) Hermite polynomial at a point.

Defined by

$$He_n(x) = (-1)^n e^{x^2/2} \frac{d^n}{dx^n} e^{-x^2/2};$$

He_n is a polynomial of degree n. See 22.11.8 in [AS] for details.

Parameters

n	[array_like] Degree of the polynomial
x	[array_like] Points at which to evaluate the Hermite polynomial

Returns

He [ndarray] Values of the Hermite polynomial

See also:

roots_hermitenorm

roots and quadrature weights of probabilist's Hermite polynomials

hermitenorm

probabilist's Hermite polynomial object

numpy.polynomial.hermite_e.HermiteE

Probabilist's Hermite series

eval_hermite

evaluate physicist's Hermite polynomials

References

[AS]

scipy.special.eval_gegenbauer

scipy.special.**eval_gegenbauer**(*n*, *alpha*, *x*, *out=None*) **= <ufunc 'eval_gegenbauer'>**

Evaluate Gegenbauer polynomial at a point.

The Gegenbauer polynomials can be defined via the Gauss hypergeometric function ${}_2F_1$ as

$$C_n^{(\alpha)} = \frac{(2\alpha)_n}{\Gamma(n+1)} {}_2F_1(-n, 2\alpha+n; \alpha+1/2; (1-z)/2).$$

When n is an integer the result is a polynomial of degree n. See 22.5.46 in [AS] for details.

Parameters

n [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to the Gauss hypergeometric function.

alpha [array_like] Parameter

x [array_like] Points at which to evaluate the Gegenbauer polynomial

Returns

C [ndarray] Values of the Gegenbauer polynomial

See also:

roots_gegenbauer

roots and quadrature weights of Gegenbauer polynomials

gegenbauer

Gegenbauer polynomial object

hyp2f1

Gauss hypergeometric function

References

[AS]

scipy.special.eval_sh_legendre

scipy.special.**eval_sh_legendre**(*n*, *x*, *out=None*) **= <ufunc 'eval_sh_legendre'>**

Evaluate shifted Legendre polynomial at a point.

These polynomials are defined as

$$P_n^*(x) = P_n(2x - 1)$$

where P_n is a Legendre polynomial. See 2.2.11 in [AS] for details.

Parameters

n	[array_like] Degree of the polynomial. If not an integer, the value is determined via the relation to *eval_legendre*.
x	[array_like] Points at which to evaluate the shifted Legendre polynomial

Returns

P	[ndarray] Values of the shifted Legendre polynomial

See also:

roots_sh_legendre

roots and quadrature weights of shifted Legendre polynomials

sh_legendre

shifted Legendre polynomial object

eval_legendre

evaluate Legendre polynomials

numpy.polynomial.legendre.Legendre

Legendre series

References

[AS]

scipy.special.eval_sh_chebyt

scipy.special.**eval_sh_chebyt**(*n*, *x*, *out=None*) **= <ufunc 'eval_sh_chebyt'>**

Evaluate shifted Chebyshev polynomial of the first kind at a point.

These polynomials are defined as

$$T_n^*(x) = T_n(2x - 1)$$

where T_n is a Chebyshev polynomial of the first kind. See 22.5.14 in [AS] for details.

Parameters

n [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to *eval_chebyt*.

x [array_like] Points at which to evaluate the shifted Chebyshev polynomial

Returns

T [ndarray] Values of the shifted Chebyshev polynomial

See also:

roots_sh_chebyt

roots and quadrature weights of shifted Chebyshev polynomials of the first kind

sh_chebyt

shifted Chebyshev polynomial object

eval_chebyt

evaluate Chebyshev polynomials of the first kind

numpy.polynomial.chebyshev.Chebyshev

Chebyshev series

References

[AS]

scipy.special.eval_sh_chebyu

scipy.special.**eval_sh_chebyu**(*n*, *x*, *out=None*) **= <ufunc 'eval_sh_chebyu'>**

Evaluate shifted Chebyshev polynomial of the second kind at a point.

These polynomials are defined as

$$U_n^*(x) = U_n(2x - 1)$$

where U_n is a Chebyshev polynomial of the first kind. See 22.5.15 in [AS] for details.

Parameters

n [array_like] Degree of the polynomial. If not an integer, the result is determined via the relation to *eval_chebyu*.

x [array_like] Points at which to evaluate the shifted Chebyshev polynomial

Returns

U [ndarray] Values of the shifted Chebyshev polynomial

See also:

roots_sh_chebyu

roots and quadrature weights of shifted Chebychev polynomials of the second kind

sh_chebyu

shifted Chebyshev polynomial object

eval_chebyu

evaluate Chebyshev polynomials of the second kind

References

[AS]

scipy.special.eval_sh_jacobi

scipy.special.**eval_sh_jacobi**(*n*, *p*, *q*, *x*, *out=None*) **= <ufunc 'eval_sh_jacobi'>**

Evaluate shifted Jacobi polynomial at a point.

Defined by

$$G_n^{(p,q)}(x) = \binom{2n+p-1}{n}^{-1} P_n^{(p-q,q-1)}(2x-1),$$

where $P_n^{(\cdot,\cdot)}$ is the n-th Jacobi polynomial. See 22.5.2 in [AS] for details.

Parameters

n	[int] Degree of the polynomial. If not an integer, the result is determined via the relation to *binom* and *eval_jacobi*.
p	[float] Parameter
q	[float] Parameter

Returns

G	[ndarray] Values of the shifted Jacobi polynomial.

See also:

roots_sh_jacobi

roots and quadrature weights of shifted Jacobi polynomials

sh_jacobi

shifted Jacobi polynomial object

eval_jacobi

evaluate Jacobi polynomials

References

[AS]

The following functions compute roots and quadrature weights for orthogonal polynomials:

roots_legendre(n[, mu])	Gauss-Legendre quadrature.
roots_chebyt(n[, mu])	Gauss-Chebyshev (first kind) quadrature.
roots_chebyu(n[, mu])	Gauss-Chebyshev (second kind) quadrature.
roots_chebyc(n[, mu])	Gauss-Chebyshev (first kind) quadrature.
roots_chebys(n[, mu])	Gauss-Chebyshev (second kind) quadrature.
roots_jacobi(n, alpha, beta[, mu])	Gauss-Jacobi quadrature.
roots_laguerre(n[, mu])	Gauss-Laguerre quadrature.
roots_genlaguerre(n, alpha[, mu])	Gauss-generalized Laguerre quadrature.
roots_hermite(n[, mu])	Gauss-Hermite (physicist's) quadrature.

continues on next page

Table 240 – continued from previous page

roots_hermitenorm(n[, mu])	Gauss-Hermite (statistician's) quadrature.
roots_gegenbauer(n, alpha[, mu])	Gauss-Gegenbauer quadrature.
roots_sh_legendre(n[, mu])	Gauss-Legendre (shifted) quadrature.
roots_sh_chebyt(n[, mu])	Gauss-Chebyshev (first kind, shifted) quadrature.
roots_sh_chebyu(n[, mu])	Gauss-Chebyshev (second kind, shifted) quadrature.
roots_sh_jacobi(n, p1, q1[, mu])	Gauss-Jacobi (shifted) quadrature.

scipy.special.roots_legendre

scipy.special.**roots_legendre**(*n*, *mu=False*)

Gauss-Legendre quadrature.

Compute the sample points and weights for Gauss-Legendre quadrature. The sample points are the roots of the nth degree Legendre polynomial $P_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-1, 1]$ with weight function $w(x) = 1.0$. See 2.2.10 in [AS] for more details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

numpy.polynomial.legendre.leggauss

References

[AS]

scipy.special.roots_chebyt

scipy.special.**roots_chebyt**(*n*, *mu=False*)

Gauss-Chebyshev (first kind) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the nth degree Chebyshev polynomial of the first kind, $T_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-1, 1]$ with weight function $w(x) = 1/\sqrt{1 - x^2}$. See 22.2.4 in [AS] for more details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

numpy.polynomial.chebyshev.chebgauss

References

[AS]

scipy.special.roots_chebyu

scipy.special.**roots_chebyu**(*n*, *mu=False*)

Gauss-Chebyshev (second kind) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the nth degree Chebyshev polynomial of the second kind, $U_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-1, 1]$ with weight function $w(x) = \sqrt{1 - x^2}$. See 22.2.5 in [AS] for details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_chebyc

scipy.special.**roots_chebyc**(*n*, *mu=False*)

Gauss-Chebyshev (first kind) quadrature.

Compute the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the nth degree Chebyshev polynomial of the first kind, $C_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-2, 2]$ with weight function $w(x) = 1/\sqrt{1 - (x/2)^2}$. See 22.2.6 in [AS] for more details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_chebys

scipy.special.**roots_chebys**(*n*, *mu=False*)

Gauss-Chebyshev (second kind) quadrature.

Compute the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the nth degree Chebyshev polynomial of the second kind, $S_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-2, 2]$ with weight function $w(x) = \sqrt{1 - (x/2)^2}$. See 22.2.7 in [AS] for more details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_jacobi

scipy.special.**roots_jacobi**(*n*, *alpha*, *beta*, *mu=False*)

Gauss-Jacobi quadrature.

Compute the sample points and weights for Gauss-Jacobi quadrature. The sample points are the roots of the nth degree Jacobi polynomial, $P_n^{\alpha,\beta}(x)$. These sample points and weights correctly integrate polynomials of degree $2n-1$ or less over the interval $[-1,1]$ with weight function $w(x) = (1-x)^\alpha(1+x)^\beta$. See 22.2.1 in [AS] for details.

Parameters

n	[int] quadrature order
alpha	[float] alpha must be > -1
beta	[float] beta must be > -1
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_laguerre

scipy.special.**roots_laguerre**(*n*, *mu=False*)

Gauss-Laguerre quadrature.

Compute the sample points and weights for Gauss-Laguerre quadrature. The sample points are the roots of the nth degree Laguerre polynomial, $L_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n-1$ or less over the interval $[0,\infty]$ with weight function $w(x) = e^{-x}$. See 22.2.13 in [AS] for details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

numpy.polynomial.laguerre.laggauss

References

[AS]

scipy.special.roots_genlaguerre

scipy.special.**roots_genlaguerre**(*n*, *alpha*, *mu=False*)

Gauss-generalized Laguerre quadrature.

Compute the sample points and weights for Gauss-generalized Laguerre quadrature. The sample points are the roots of the nth degree generalized Laguerre polynomial, $L_n^{\alpha}(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[0, \infty]$ with weight function $w(x) = x^{\alpha} e^{-x}$. See 22.3.9 in [AS] for details.

Parameters

n	[int] quadrature order
alpha	[float] alpha must be > -1
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_hermite

scipy.special.**roots_hermite**(*n*, *mu=False*)

Gauss-Hermite (physicist's) quadrature.

Compute the sample points and weights for Gauss-Hermite quadrature. The sample points are the roots of the nth degree Hermite polynomial, $H_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-\infty, \infty]$ with weight function $w(x) = e^{-x^2}$. See 22.2.14 in [AS] for details.

Parameters

n	[int] quadrature order

mu [bool, optional] If True, return the sum of the weights, optional.

Returns

x [ndarray] Sample points
w [ndarray] Weights
mu [float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

numpy.polynomial.hermite.hermgauss

roots_hermitenorm

Notes

For small n up to 150 a modified version of the Golub-Welsch algorithm is used. Nodes are computed from the eigenvalue problem and improved by one step of a Newton iteration. The weights are computed from the well-known analytical formula.

For n larger than 150 an optimal asymptotic algorithm is applied which computes nodes and weights in a numerically stable manner. The algorithm has linear runtime making computation for very large n (several thousand or more) feasible.

References

[townsend.trogdon.olver-2014], [townsend.trogdon.olver-2015], [AS]

scipy.special.roots_hermitenorm

scipy.special.**roots_hermitenorm**(*n*, *mu=False*)

Gauss-Hermite (statistician's) quadrature.

Compute the sample points and weights for Gauss-Hermite quadrature. The sample points are the roots of the nth degree Hermite polynomial, $He_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-\infty, \infty]$ with weight function $w(x) = e^{-x^2/2}$. See 22.2.15 in [AS] for more details.

Parameters

n [int] quadrature order
mu [bool, optional] If True, return the sum of the weights, optional.

Returns

x [ndarray] Sample points
w [ndarray] Weights
mu [float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

numpy.polynomial.hermite_e.hermegauss

Notes

For small n up to 150 a modified version of the Golub-Welsch algorithm is used. Nodes are computed from the eigenvalue problem and improved by one step of a Newton iteration. The weights are computed from the well-known analytical formula.

For n larger than 150 an optimal asymptotic algorithm is used which computes nodes and weights in a numerical stable manner. The algorithm has linear runtime making computation for very large n (several thousand or more) feasible.

References

[AS]

scipy.special.roots_gegenbauer

scipy.special.**roots_gegenbauer**(*n*, *alpha*, *mu=False*)

Gauss-Gegenbauer quadrature.

Compute the sample points and weights for Gauss-Gegenbauer quadrature. The sample points are the roots of the nth degree Gegenbauer polynomial, $C_n^{\alpha}(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[-1, 1]$ with weight function $w(x) = (1 - x^2)^{\alpha - 1/2}$. See 22.2.3 in [AS] for more details.

Parameters

n	[int] quadrature order
alpha	[float] alpha must be > -0.5
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_sh_legendre

scipy.special.**roots_sh_legendre**(*n*, *mu=False*)

Gauss-Legendre (shifted) quadrature.

Compute the sample points and weights for Gauss-Legendre quadrature. The sample points are the roots of the nth degree shifted Legendre polynomial $P_n^*(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[0, 1]$ with weight function $w(x) = 1.0$. See 2.2.11 in [AS] for details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_sh_chebyt

scipy.special.**roots_sh_chebyt**(*n*, *mu=False*)

Gauss-Chebyshev (first kind, shifted) quadrature.

Compute the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the nth degree shifted Chebyshev polynomial of the first kind, $T_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[0, 1]$ with weight function $w(x) = 1/\sqrt{x - x^2}$. See 22.2.8 in [AS] for more details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_sh_chebyu

scipy.special.**roots_sh_chebyu**(*n*, *mu=False*)

Gauss-Chebyshev (second kind, shifted) quadrature.

Computes the sample points and weights for Gauss-Chebyshev quadrature. The sample points are the roots of the nth degree shifted Chebyshev polynomial of the second kind, $U_n(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[0, 1]$ with weight function $w(x) = \sqrt{x - x^2}$. See 22.2.9 in [AS] for more details.

Parameters

n	[int] quadrature order
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

scipy.special.roots_sh_jacobi

scipy.special.**roots_sh_jacobi**(*n*, *p1*, *q1*, *mu=False*)

Gauss-Jacobi (shifted) quadrature.

Compute the sample points and weights for Gauss-Jacobi (shifted) quadrature. The sample points are the roots of the nth degree shifted Jacobi polynomial, $G_n^{p,q}(x)$. These sample points and weights correctly integrate polynomials of degree $2n - 1$ or less over the interval $[0, 1]$ with weight function $w(x) = (1 - x)^{p-q} x^{q-1}$. See 22.2.2 in [AS] for details.

Parameters

n	[int] quadrature order
p1	[float] (p1 - q1) must be > -1
q1	[float] q1 must be > 0
mu	[bool, optional] If True, return the sum of the weights, optional.

Returns

x	[ndarray] Sample points
w	[ndarray] Weights
mu	[float] Sum of the weights

See also:

scipy.integrate.quadrature

scipy.integrate.fixed_quad

References

[AS]

The functions below, in turn, return the polynomial coefficients in `orthopoly1d` objects, which function similarly as `numpy.poly1d`. The `orthopoly1d` class also has an attribute `weights`, which returns the roots, weights, and total weights for the appropriate form of Gaussian quadrature. These are returned in an `n x 3` array with roots in the first column, weights in the second column, and total weights in the final column. Note that `orthopoly1d` objects are converted to `poly1d` when doing arithmetic, and lose information of the original orthogonal polynomial.

legendre(n[, monic])	Legendre polynomial.
chebyt(n[, monic])	Chebyshev polynomial of the first kind.
chebyu(n[, monic])	Chebyshev polynomial of the second kind.
chebyc(n[, monic])	Chebyshev polynomial of the first kind on $[-2, 2]$.
chebys(n[, monic])	Chebyshev polynomial of the second kind on $[-2, 2]$.
jacobi(n, alpha, beta[, monic])	Jacobi polynomial.
laguerre(n[, monic])	Laguerre polynomial.
genlaguerre(n, alpha[, monic])	Generalized (associated) Laguerre polynomial.
hermite(n[, monic])	Physicist's Hermite polynomial.
hermitenorm(n[, monic])	Normalized (probabilist's) Hermite polynomial.
gegenbauer(n, alpha[, monic])	Gegenbauer (ultraspherical) polynomial.
sh_legendre(n[, monic])	Shifted Legendre polynomial.
sh_chebyt(n[, monic])	Shifted Chebyshev polynomial of the first kind.
sh_chebyu(n[, monic])	Shifted Chebyshev polynomial of the second kind.
sh_jacobi(n, p, q[, monic])	Shifted Jacobi polynomial.

scipy.special.legendre

scipy.special.**legendre**(*n*, *monic=False*)

Legendre polynomial.

Defined to be the solution of

$$\frac{d}{dx}\left[(1-x^2)\frac{d}{dx}P_n(x)\right] + n(n+1)P_n(x) = 0;$$

$P_n(x)$ is a polynomial of degree n.

Parameters

n	[int] Degree of the polynomial.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

P	[orthopoly1d] Legendre polynomial.

Notes

The polynomials P_n are orthogonal over $[-1, 1]$ with weight function 1.

Examples

Generate the 3rd-order Legendre polynomial 1/2*(5x^3 + 0x^2 - 3x + 0):

```
>>> from scipy.special import legendre
>>> legendre(3)
poly1d([ 2.5,  0. , -1.5,  0. ])
```

scipy.special.chebyt

scipy.special.**chebyt**(*n*, *monic=False*)

Chebyshev polynomial of the first kind.

Defined to be the solution of

$$(1 - x^2)\frac{d^2}{dx^2}T_n - x\frac{d}{dx}T_n + n^2 T_n = 0;$$

T_n is a polynomial of degree n.

Parameters

n	[int] Degree of the polynomial.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

T	[orthopoly1d] Chebyshev polynomial of the first kind.

See also:

chebyu

Chebyshev polynomial of the second kind.

Notes

The polynomials T_n are orthogonal over $[-1, 1]$ with weight function $(1 - x^2)^{-1/2}$.

scipy.special.chebyu

scipy.special.**chebyu**(*n*, *monic=False*)

Chebyshev polynomial of the second kind.

Defined to be the solution of

$$(1 - x^2)\frac{d^2}{dx^2}U_n - 3x\frac{d}{dx}U_n + n(n+2)U_n = 0;$$

U_n is a polynomial of degree n.

Parameters

n [int] Degree of the polynomial.
monic [bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

U [orthopoly1d] Chebyshev polynomial of the second kind.

See also:

`chebyt`

Chebyshev polynomial of the first kind.

Notes

The polynomials U_n are orthogonal over $[-1, 1]$ with weight function $(1 - x^2)^{1/2}$.

scipy.special.chebyc

`scipy.special.`**`chebyc`**(*n*, *monic=False*)

Chebyshev polynomial of the first kind on $[-2, 2]$.

Defined as $C_n(x) = 2T_n(x/2)$, where T_n is the nth Chebychev polynomial of the first kind.

Parameters

n [int] Degree of the polynomial.
monic [bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

C [orthopoly1d] Chebyshev polynomial of the first kind on $[-2, 2]$.

See also:

`chebyt`

Chebyshev polynomial of the first kind.

Notes

The polynomials $C_n(x)$ are orthogonal over $[-2, 2]$ with weight function $1/\sqrt{1 - (x/2)^2}$.

References

[1]

scipy.special.chebys

scipy.special.**chebys**(*n*, *monic=False*)

Chebyshev polynomial of the second kind on $[-2, 2]$.

Defined as $S_n(x) = U_n(x/2)$ where U_n is the nth Chebychev polynomial of the second kind.

Parameters

n	[int] Degree of the polynomial.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

S	[orthopoly1d] Chebyshev polynomial of the second kind on $[-2, 2]$.

See also:

chebyu

Chebyshev polynomial of the second kind

Notes

The polynomials $S_n(x)$ are orthogonal over $[-2, 2]$ with weight function $\sqrt{1 - (x/2)}^2$.

References

[1]

scipy.special.jacobi

scipy.special.**jacobi**(*n*, *alpha*, *beta*, *monic=False*)

Jacobi polynomial.

Defined to be the solution of

$$(1 - x^2)\frac{d^2}{dx^2}P_n^{(\alpha,\beta)} + (\beta - \alpha - (\alpha + \beta + 2)x)\frac{d}{dx}P_n^{(\alpha,\beta)} + n(n + \alpha + \beta + 1)P_n^{(\alpha,\beta)} = 0$$

for $\alpha, \beta > -1$; $P_n^{(\alpha,\beta)}$ is a polynomial of degree n.

Parameters

n	[int] Degree of the polynomial.
alpha	[float] Parameter, must be greater than -1.
beta	[float] Parameter, must be greater than -1.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

P	[orthopoly1d] Jacobi polynomial.

Notes

For fixed α, β, the polynomials $P_n^{(\alpha,\beta)}$ are orthogonal over $[-1, 1]$ with weight function $(1-x)^\alpha(1+x)^\beta$.

scipy.special.laguerre

`scipy.special.`**`laguerre`**(*n*, *monic=False*)

Laguerre polynomial.

Defined to be the solution of

$$x\frac{d^2}{dx^2}L_n + (1-x)\frac{d}{dx}L_n + nL_n = 0;$$

L_n is a polynomial of degree n.

Parameters

n	[int] Degree of the polynomial.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

L	[orthopoly1d] Laguerre Polynomial.

Notes

The polynomials L_n are orthogonal over $[0, \infty)$ with weight function e^{-x}.

scipy.special.genlaguerre

`scipy.special.`**`genlaguerre`**(*n*, *alpha*, *monic=False*)

Generalized (associated) Laguerre polynomial.

Defined to be the solution of

$$x\frac{d^2}{dx^2}L_n^{(\alpha)} + (\alpha+1-x)\frac{d}{dx}L_n^{(\alpha)} + nL_n^{(\alpha)} = 0,$$

where $\alpha > -1$; $L_n^{(\alpha)}$ is a polynomial of degree n.

Parameters

n	[int] Degree of the polynomial.
alpha	[float] Parameter, must be greater than -1.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

L	[orthopoly1d] Generalized Laguerre polynomial.

See also:

`laguerre`

Laguerre polynomial.

Notes

For fixed α, the polynomials $L_n^{(\alpha)}$ are orthogonal over $[0, \infty)$ with weight function $e^{-x}x^{\alpha}$.

The Laguerre polynomials are the special case where $\alpha = 0$.

scipy.special.hermite

scipy.special.**hermite**(*n*, *monic=False*)

Physicist's Hermite polynomial.

Defined by

$$H_n(x) = (-1)^n e^{x^2} \frac{d^n}{dx^n} e^{-x^2};$$

H_n is a polynomial of degree n.

Parameters

n	[int] Degree of the polynomial.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

H	[orthopoly1d] Hermite polynomial.

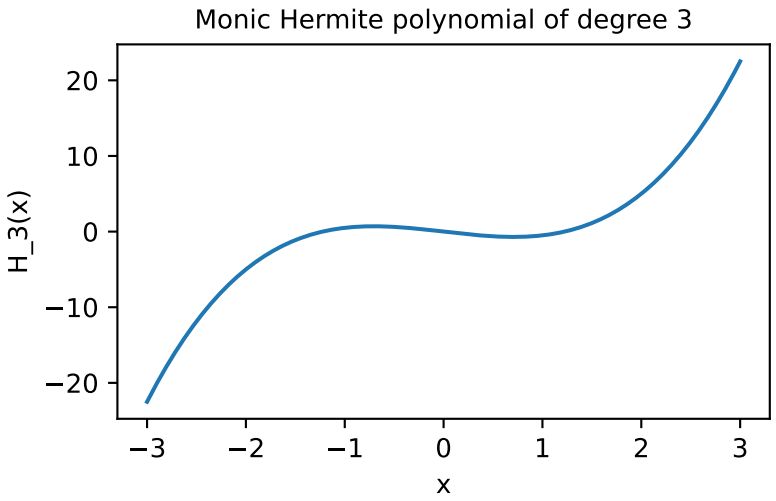
Notes

The polynomials H_n are orthogonal over $(-\infty, \infty)$ with weight function e^{-x^2}.

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
>>> import numpy as np
```

```
>>> p_monic = special.hermite(3, monic=True)
>>> p_monic
poly1d([ 1. ,  0. , -1.5,  0. ])
>>> p_monic(1)
-0.49999999999999983
>>> x = np.linspace(-3, 3, 400)
>>> y = p_monic(x)
>>> plt.plot(x, y)
>>> plt.title("Monic Hermite polynomial of degree 3")
>>> plt.xlabel("x")
>>> plt.ylabel("H_3(x)")
>>> plt.show()
```



scipy.special.hermitenorm

scipy.special.**hermitenorm**(*n*, *monic=False*)

Normalized (probabilist's) Hermite polynomial.

Defined by

$$He_n(x) = (-1)^n e^{x^2/2} \frac{d^n}{dx^n} e^{-x^2/2};$$

He_n is a polynomial of degree n.

Parameters

n	[int] Degree of the polynomial.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

He	[orthopoly1d] Hermite polynomial.

Notes

The polynomials He_n are orthogonal over $(-\infty, \infty)$ with weight function $e^{-x^2/2}$.

scipy.special.gegenbauer

scipy.special.**gegenbauer**(*n*, *alpha*, *monic=False*)

Gegenbauer (ultraspherical) polynomial.

Defined to be the solution of

$$(1-x^2)\frac{d^2}{dx^2}C_n^{(\alpha)} - (2\alpha+1)x\frac{d}{dx}C_n^{(\alpha)} + n(n+2\alpha)C_n^{(\alpha)} = 0$$

for $\alpha > -1/2$; $C_n^{(\alpha)}$ is a polynomial of degree n.

Parameters

n	[int] Degree of the polynomial.
alpha	[float] Parameter, must be greater than -0.5.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

C	[orthopoly1d] Gegenbauer polynomial.

Notes

The polynomials $C_n^{(\alpha)}$ are orthogonal over $[-1, 1]$ with weight function $(1 - x^2)^{(\alpha - 1/2)}$.

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
```

We can initialize a variable `p` as a Gegenbauer polynomial using the *`gegenbauer`* function and evaluate at a point `x = 1`.

```
>>> p = special.gegenbauer(3, 0.5, monic=False)
>>> p
poly1d([ 2.5,  0. , -1.5,  0. ])
>>> p(1)
1.0
```

To evaluate `p` at various points `x` in the interval `(-3, 3)`, simply pass an array `x` to `p` as follows:

```
>>> x = np.linspace(-3, 3, 400)
>>> y = p(x)
```

We can then visualize `x, y` using `matplotlib.pyplot`.

```
>>> fig, ax = plt.subplots()
>>> ax.plot(x, y)
>>> ax.set_title("Gegenbauer (ultraspherical) polynomial of degree 3")
>>> ax.set_xlabel("x")
>>> ax.set_ylabel("G_3(x)")
>>> plt.show()
```

scipy.special.sh_legendre

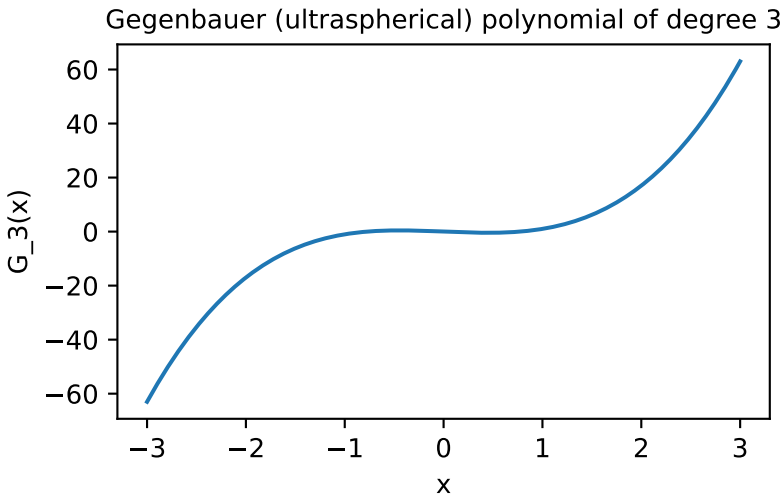
`scipy.special.`**`sh_legendre`**(*n*, *monic=False*)

Shifted Legendre polynomial.

Defined as $P_n^*(x) = P_n(2x - 1)$ for P_n the nth Legendre polynomial.

Parameters

n	[int] Degree of the polynomial.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.



Returns

P [orthopoly1d] Shifted Legendre polynomial.

Notes

The polynomials P_n^* are orthogonal over $[0, 1]$ with weight function 1.

scipy.special.sh_chebyt

`scipy.special.`**`sh_chebyt`**(*n*, *monic=False*)

Shifted Chebyshev polynomial of the first kind.

Defined as $T_n^*(x) = T_n(2x - 1)$ for T_n the nth Chebyshev polynomial of the first kind.

Parameters

n [int] Degree of the polynomial.

monic [bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

T [orthopoly1d] Shifted Chebyshev polynomial of the first kind.

Notes

The polynomials T_n^* are orthogonal over $[0, 1]$ with weight function $(x - x^2)^{-1/2}$.

scipy.special.sh_chebyu

scipy.special.**sh_chebyu**(*n*, *monic=False*)

Shifted Chebyshev polynomial of the second kind.

Defined as $U_n^*(x) = U_n(2x-1)$ for U_n the nth Chebyshev polynomial of the second kind.

Parameters

n	[int] Degree of the polynomial.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

U	[orthopoly1d] Shifted Chebyshev polynomial of the second kind.

Notes

The polynomials U_n^* are orthogonal over $[0, 1]$ with weight function $(x - x^2)^{1/2}$.

scipy.special.sh_jacobi

scipy.special.**sh_jacobi**(*n*, *p*, *q*, *monic=False*)

Shifted Jacobi polynomial.

Defined by

$$G_n^{(p,q)}(x) = \binom{2n+p-1}{n}^{-1} P_n^{(p-q,q-1)}(2x-1),$$

where $P_n^{(\cdot,\cdot)}$ is the nth Jacobi polynomial.

Parameters

n	[int] Degree of the polynomial.
p	[float] Parameter, must have $p > q - 1$.
q	[float] Parameter, must be greater than 0.
monic	[bool, optional] If *True*, scale the leading coefficient to be 1. Default is *False*.

Returns

G	[orthopoly1d] Shifted Jacobi polynomial.

Notes

For fixed p, q, the polynomials $G_n^{(p,q)}$ are orthogonal over $[0, 1]$ with weight function $(1-x)^{p-q}x^{q-1}$.

Warning: Computing values of high-order polynomials (around `order > 20`) using polynomial coefficients is numerically unstable. To evaluate polynomial values, the `eval_*` functions should be used instead.

Hypergeometric functions

hyp2f1(a, b, c, z)	Gauss hypergeometric function 2F1(a, b; c; z)
hyp1f1(a, b, x[, out])	Confluent hypergeometric function 1F1.
hyperu(a, b, x[, out])	Confluent hypergeometric function U
hyp0f1(v, z[, out])	Confluent hypergeometric limit function 0F1.

scipy.special.hyp2f1

scipy.special.**hyp2f1**(*a*, *b*, *c*, *z*) **= <ufunc 'hyp2f1'>**

Gauss hypergeometric function 2F1(a, b; c; z)

Parameters

a, b, c [array_like] Arguments, should be real-valued.
z [array_like] Argument, real or complex.

Returns

hyp2f1 [scalar or ndarray] The values of the gaussian hypergeometric function.

See also:

hyp0f1

confluent hypergeometric limit function.

hyp1f1

Kummer's (confluent hypergeometric) function.

Notes

This function is defined for $|z| < 1$ as

$$\mathrm{hyp2f1}(a, b, c, z) = \sum_{n=0}^{\infty} \frac{(a)_n (b)_n}{(c)_n} \frac{z^n}{n!},$$

and defined on the rest of the complex z-plane by analytic continuation [1]. Here $(\cdot)_n$ is the Pochhammer symbol; see *poch*. When n is an integer the result is a polynomial of degree n.

The implementation for complex values of z is described in [2].

References

[1], [2], [3]

Examples

```
>>> import scipy.special as sc
```

It has poles when *c* is a negative integer.

```
>>> sc.hyp2f1(1, 1, -2, 1)
inf
```

It is a polynomial when *a* or *b* is a negative integer.

```
>>> a, b, c = -1, 1, 1.5
>>> z = np.linspace(0, 1, 5)
>>> sc.hyp2f1(a, b, c, z)
array([1.        , 0.83333333, 0.66666667, 0.5       , 0.33333333])
>>> 1 + a * b * z / c
array([1.        , 0.83333333, 0.66666667, 0.5       , 0.33333333])
```

It is symmetric in *a* and *b*.

```
>>> a = np.linspace(0, 1, 5)
>>> b = np.linspace(0, 1, 5)
>>> sc.hyp2f1(a, b, 1, 0.5)
array([1.        , 1.03997334, 1.1803406 , 1.47074441, 2.        ])
>>> sc.hyp2f1(b, a, 1, 0.5)
array([1.        , 1.03997334, 1.1803406 , 1.47074441, 2.        ])
```

It contains many other functions as special cases.

```
>>> z = 0.5
>>> sc.hyp2f1(1, 1, 2, z)
1.3862943611198901
>>> -np.log(1 - z) / z
1.3862943611198906
```

```
>>> sc.hyp2f1(0.5, 1, 1.5, z**2)
1.098612288668109
>>> np.log((1 + z) / (1 - z)) / (2 * z)
1.0986122886681098
```

```
>>> sc.hyp2f1(0.5, 1, 1.5, -z**2)
0.9272952180016117
>>> np.arctan(z) / z
0.9272952180016123
```

scipy.special.hyp1f1

scipy.special.**hyp1f1**(*a*, *b*, *x*, *out=None*) **= <ufunc 'hyp1f1'>**

Confluent hypergeometric function 1F1.

The confluent hypergeometric function is defined by the series

$$ {}_1F_1(a; b; x) = \sum_{k=0}^{\infty} \frac{(a)_k}{(b)_k k!} x^k. $$

See [dlmf] for more details. Here $(\cdot)_k$ is the Pochhammer symbol; see *poch*.

Parameters

a, b	[array_like] Real parameters
x	[array_like] Real or complex argument
out	[ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
Values of the confluent hypergeometric function

See also:

hyperu

another confluent hypergeometric function

hyp0f1

confluent hypergeometric limit function

hyp2f1

Gaussian hypergeometric function

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

It is one when *x* is zero:

```
>>> sc.hyp1f1(0.5, 0.5, 0)
1.0
```

It is singular when *b* is a nonpositive integer.

```
>>> sc.hyp1f1(0.5, -1, 0)
inf
```

It is a polynomial when *a* is a nonpositive integer.

```
>>> a, b, x = -1, 0.5, np.array([1.0, 2.0, 3.0, 4.0])
>>> sc.hyp1f1(a, b, x)
array([-1., -3., -5., -7.])
>>> 1 + (a / b) * x
array([-1., -3., -5., -7.])
```

It reduces to the exponential function when $a = b$.

```
>>> sc.hyp1f1(2, 2, [1, 2, 3, 4])
array([ 2.71828183,  7.3890561 , 20.08553692, 54.59815003])
>>> np.exp([1, 2, 3, 4])
array([ 2.71828183,  7.3890561 , 20.08553692, 54.59815003])
```

scipy.special.hyperu

scipy.special.**hyperu**(*a*, *b*, *x*, *out=None*) **= <ufunc 'hyperu'>**

Confluent hypergeometric function U

It is defined as the solution to the equation

$$x\frac{d^2w}{dx^2} + (b - x)\frac{dw}{dx} - aw = 0$$

which satisfies the property

$$U(a, b, x) \sim x^{-a}$$

as $x \to \infty$. See [dlmf] for more details.

Parameters

a, b	[array_like] Real-valued parameters
x	[array_like] Real-valued argument
out	[ndarray] Optional output array for the function values

Returns

scalar or ndarray
Values of U

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

It has a branch cut along the negative x axis.

```
>>> x = np.linspace(-0.1, -10, 5)
>>> sc.hyperu(1, 1, x)
array([nan, nan, nan, nan, nan])
```

It approaches zero as x goes to infinity.

```
>>> x = np.array([1, 10, 100])
>>> sc.hyperu(1, 1, x)
array([0.59634736, 0.09156333, 0.00990194])
```

It satisfies Kummer's transformation.

```
>>> a, b, x = 2, 1, 1
>>> sc.hyperu(a, b, x)
0.1926947246463881
>>> x**(1 - b) * sc.hyperu(a - b + 1, 2 - b, x)
0.1926947246463881
```

scipy.special.hyp0f1

scipy.special.**hyp0f1**(*v*, *z*, *out=None*) **= <ufunc 'hyp0f1'>**

Confluent hypergeometric limit function 0F1.

Parameters

v	[array_like] Real-valued parameter
z	[array_like] Real- or complex-valued argument
out	[ndarray, optional] Optional output array for the function results

Returns

scalar or ndarray
The confluent hypergeometric limit function

Notes

This function is defined as:

$$ {}_0F_1(v, z) = \sum_{k=0}^{\infty} \frac{z^k}{(v)_k k!}. $$

It's also the limit as $q \to \infty$ of ${}_1F_1(q; v; z/q)$, and satisfies the differential equation $f''(z) + vf'(z) = f(z)$. See [1] for more information.

References

[1]

Examples

```
>>> import scipy.special as sc
```

It is one when z is zero.

```
>>> sc.hyp0f1(1, 0)
1.0
```

It is the limit of the confluent hypergeometric function as q goes to infinity.

```
>>> q = np.array([1, 10, 100, 1000])
>>> v = 1
>>> z = 1
>>> sc.hyp1f1(q, v, z / q)
array([2.71828183, 2.31481985, 2.28303778, 2.27992985])
>>> sc.hyp0f1(v, z)
2.2795853023360673
```

It is related to Bessel functions.

```
>>> n = 1
>>> x = np.linspace(0, 1, 5)
>>> sc.jv(n, x)
array([0.        , 0.12402598, 0.24226846, 0.3492436 , 0.44005059])
>>> (0.5 * x)**n / sc.factorial(n) * sc.hyp0f1(n + 1, -0.25 * x**2)
array([0.        , 0.12402598, 0.24226846, 0.3492436 , 0.44005059])
```

Parabolic cylinder functions

pbdv(v, x)	Parabolic cylinder function D
pbvv(v, x)	Parabolic cylinder function V
pbwa(a, x)	Parabolic cylinder function W.

scipy.special.pbdv

scipy.special.**pbdv**(*v*, *x*) **= <ufunc 'pbdv'>**

Parabolic cylinder function D

Returns (d, dp) the parabolic cylinder function Dv(x) in d and the derivative, Dv'(x) in dp.

Returns

d	Value of the function
dp	Value of the derivative vs x

scipy.special.pbvv

scipy.special.**pbvv**(*v*, *x*) **= <ufunc 'pbvv'>**
Parabolic cylinder function V

Returns the parabolic cylinder function Vv(x) in v and the derivative, Vv'(x) in vp.

Returns

v	Value of the function
vp	Value of the derivative vs x

scipy.special.pbwa

scipy.special.**pbwa**(*a*, *x*) **= <ufunc 'pbwa'>**
Parabolic cylinder function W.

The function is a particular solution to the differential equation

$$y'' + \left(\frac{1}{4}x^2 - a\right) y = 0,$$

for a full definition see section 12.14 in [1].

Parameters

a	[array_like] Real parameter
x	[array_like] Real argument

Returns

w	[scalar or ndarray] Value of the function
wp	[scalar or ndarray] Value of the derivative in x

Notes

The function is a wrapper for a Fortran routine by Zhang and Jin [2]. The implementation is accurate only for `|a|, |x| < 5` and returns NaN outside that range.

References

[1], [2]

These are not universal functions:

pbdv_seq(v, x)	Parabolic cylinder functions Dv(x) and derivatives.
pbvv_seq(v, x)	Parabolic cylinder functions Vv(x) and derivatives.
pbdn_seq(n, z)	Parabolic cylinder functions Dn(z) and derivatives.

scipy.special.pbdv_seq

scipy.special.**pbdv_seq**(*v*, *x*)
Parabolic cylinder functions Dv(x) and derivatives.

Parameters

v	[float] Order of the parabolic cylinder function
x	[float] Value at which to evaluate the function and derivatives

Returns

dv	[ndarray] Values of D_vi(x), for vi=v-int(v), vi=1+v-int(v), …, vi=v.
dp	[ndarray] Derivatives D_vi'(x), for vi=v-int(v), vi=1+v-int(v), …, vi=v.

References

[1]

scipy.special.pbvv_seq

scipy.special.**pbvv_seq**(*v*, *x*)
Parabolic cylinder functions Vv(x) and derivatives.

Parameters

v	[float] Order of the parabolic cylinder function
x	[float] Value at which to evaluate the function and derivatives

Returns

dv	[ndarray] Values of V_vi(x), for vi=v-int(v), vi=1+v-int(v), …, vi=v.
dp	[ndarray] Derivatives V_vi'(x), for vi=v-int(v), vi=1+v-int(v), …, vi=v.

References

[1]

scipy.special.pbdn_seq

scipy.special.**pbdn_seq**(*n*, *z*)
Parabolic cylinder functions Dn(z) and derivatives.

Parameters

n	[int] Order of the parabolic cylinder function
z	[complex] Value at which to evaluate the function and derivatives

Returns

dv	[ndarray] Values of D_i(z), for i=0, …, i=n.
dp	[ndarray] Derivatives D_i'(z), for i=0, …, i=n.

References

[1]

Mathieu and related functions

mathieu_a(m, q)	Characteristic value of even Mathieu functions
mathieu_b(m, q)	Characteristic value of odd Mathieu functions

scipy.special.mathieu_a

scipy.special.**mathieu_a**(*m*, *q*) **= <ufunc 'mathieu_a'>**
Characteristic value of even Mathieu functions

Returns the characteristic value for the even solution, `ce_m(z, q)`, of Mathieu's equation.

scipy.special.mathieu_b

scipy.special.**mathieu_b**(*m*, *q*) **= <ufunc 'mathieu_b'>**
Characteristic value of odd Mathieu functions

Returns the characteristic value for the odd solution, `se_m(z, q)`, of Mathieu's equation.

These are not universal functions:

mathieu_even_coef(m, q)	Fourier coefficients for even Mathieu and modified Mathieu functions.
mathieu_odd_coef(m, q)	Fourier coefficients for even Mathieu and modified Mathieu functions.

scipy.special.mathieu_even_coef

scipy.special.**mathieu_even_coef**(*m*, *q*)
Fourier coefficients for even Mathieu and modified Mathieu functions.

The Fourier series of the even solutions of the Mathieu differential equation are of the form

$$\mathrm{ce}_{2n}(z,q) = \sum_{k=0}^{\infty} A_{(2n)}^{(2k)} \cos 2kz$$

$$\mathrm{ce}_{2n+1}(z,q) = \sum_{k=0}^{\infty} A_{(2n+1)}^{(2k+1)} \cos(2k+1)z$$

This function returns the coefficients $A_{(2n)}^{(2k)}$ for even input m=2n, and the coefficients $A_{(2n+1)}^{(2k+1)}$ for odd input m=2n+1.

Parameters

m [int] Order of Mathieu functions. Must be non-negative.
q [float (>=0)] Parameter of Mathieu functions. Must be non-negative.

Returns

Ak [ndarray] Even or odd Fourier coefficients, corresponding to even or odd m.

References

[1], [2]

scipy.special.mathieu_odd_coef

scipy.special.**mathieu_odd_coef**(*m*, *q*)

Fourier coefficients for even Mathieu and modified Mathieu functions.

The Fourier series of the odd solutions of the Mathieu differential equation are of the form

$$\mathrm{se}_{2n+1}(z,q) = \sum_{k=0}^{\infty} B_{(2n+1)}^{(2k+1)} \sin(2k+1)z$$

$$\mathrm{se}_{2n+2}(z,q) = \sum_{k=0}^{\infty} B_{(2n+2)}^{(2k+2)} \sin(2k+2)z$$

This function returns the coefficients $B_{(2n+2)}^{(2k+2)}$ for even input m=2n+2, and the coefficients $B_{(2n+1)}^{(2k+1)}$ for odd input m=2n+1.

Parameters

m	[int] Order of Mathieu functions. Must be non-negative.
q	[float (>=0)] Parameter of Mathieu functions. Must be non-negative.

Returns

Bk	[ndarray] Even or odd Fourier coefficients, corresponding to even or odd m.

References

[1]

The following return both function and first derivative:

mathieu_cem(m, q, x)	Even Mathieu function and its derivative
mathieu_sem(m, q, x)	Odd Mathieu function and its derivative
mathieu_modcem1(m, q, x)	Even modified Mathieu function of the first kind and its derivative
mathieu_modcem2(m, q, x)	Even modified Mathieu function of the second kind and its derivative
mathieu_modsem1(m, q, x)	Odd modified Mathieu function of the first kind and its derivative
mathieu_modsem2(m, q, x)	Odd modified Mathieu function of the second kind and its derivative

scipy.special.mathieu_cem

scipy.special.**mathieu_cem**(*m*, *q*, *x*) **= <ufunc 'mathieu_cem'>**

Even Mathieu function and its derivative

Returns the even Mathieu function, `ce_m(x, q)`, of order *m* and parameter *q* evaluated at *x* (given in degrees). Also returns the derivative with respect to *x* of ce_m(x, q)

Parameters

m	Order of the function
q	Parameter of the function
x	Argument of the function, *given in degrees, not radians*

Returns

y	Value of the function
yp	Value of the derivative vs x

scipy.special.mathieu_sem

scipy.special.**mathieu_sem**(*m*, *q*, *x*) **= <ufunc 'mathieu_sem'>**

Odd Mathieu function and its derivative

Returns the odd Mathieu function, se_m(x, q), of order *m* and parameter *q* evaluated at *x* (given in degrees). Also returns the derivative with respect to *x* of se_m(x, q).

Parameters

m	Order of the function
q	Parameter of the function
x	Argument of the function, *given in degrees, not radians*.

Returns

y	Value of the function
yp	Value of the derivative vs x

scipy.special.mathieu_modcem1

scipy.special.**mathieu_modcem1**(*m*, *q*, *x*) **= <ufunc 'mathieu_modcem1'>**

Even modified Mathieu function of the first kind and its derivative

Evaluates the even modified Mathieu function of the first kind, `Mc1m(x, q)`, and its derivative at *x* for order *m* and parameter *q*.

Returns

y	Value of the function
yp	Value of the derivative vs x

scipy.special.mathieu_modcem2

scipy.special.**mathieu_modcem2**(*m*, *q*, *x*) **= <ufunc 'mathieu_modcem2'>**

Even modified Mathieu function of the second kind and its derivative

Evaluates the even modified Mathieu function of the second kind, Mc2m(x, q), and its derivative at *x* (given in degrees) for order *m* and parameter *q*.

Returns

y	Value of the function
yp	Value of the derivative vs x

scipy.special.mathieu_modsem1

scipy.special.**mathieu_modsem1**(*m*, *q*, *x*) **= <ufunc 'mathieu_modsem1'>**

Odd modified Mathieu function of the first kind and its derivative

Evaluates the odd modified Mathieu function of the first kind, Ms1m(x, q), and its derivative at *x* (given in degrees) for order *m* and parameter *q*.

Returns

y	Value of the function
yp	Value of the derivative vs x

scipy.special.mathieu_modsem2

scipy.special.**mathieu_modsem2**(*m*, *q*, *x*) **= <ufunc 'mathieu_modsem2'>**

Odd modified Mathieu function of the second kind and its derivative

Evaluates the odd modified Mathieu function of the second kind, Ms2m(x, q), and its derivative at *x* (given in degrees) for order *m* and parameter q.

Returns

y	Value of the function
yp	Value of the derivative vs x

Spheroidal wave functions

pro_ang1(m, n, c, x)	Prolate spheroidal angular function of the first kind and its derivative
pro_rad1(m, n, c, x)	Prolate spheroidal radial function of the first kind and its derivative
pro_rad2(m, n, c, x)	Prolate spheroidal radial function of the second kind and its derivative
obl_ang1(m, n, c, x)	Oblate spheroidal angular function of the first kind and its derivative
obl_rad1(m, n, c, x)	Oblate spheroidal radial function of the first kind and its derivative
obl_rad2(m, n, c, x)	Oblate spheroidal radial function of the second kind and its derivative.
pro_cv(m, n, c)	Characteristic value of prolate spheroidal function
obl_cv(m, n, c)	Characteristic value of oblate spheroidal function

continues on next page

Table 248 – continued from previous page

pro_cv_seq(m, n, c)	Characteristic values for prolate spheroidal wave functions.
obl_cv_seq(m, n, c)	Characteristic values for oblate spheroidal wave functions.

scipy.special.pro_ang1

scipy.special.**pro_ang1**(*m*, *n*, *c*, *x*) **= <ufunc 'pro_ang1'>**

Prolate spheroidal angular function of the first kind and its derivative

Computes the prolate spheroidal angular function of the first kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.pro_rad1

scipy.special.**pro_rad1**(*m*, *n*, *c*, *x*) **= <ufunc 'pro_rad1'>**

Prolate spheroidal radial function of the first kind and its derivative

Computes the prolate spheroidal radial function of the first kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.pro_rad2

scipy.special.**pro_rad2**(*m*, *n*, *c*, *x*) **= <ufunc 'pro_rad2'>**

Prolate spheroidal radial function of the second kind and its derivative

Computes the prolate spheroidal radial function of the second kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.obl_ang1

scipy.special.**obl_ang1**(*m*, *n*, *c*, *x*) **= <ufunc 'obl_ang1'>**

Oblate spheroidal angular function of the first kind and its derivative

Computes the oblate spheroidal angular function of the first kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.obl_rad1

scipy.special.**obl_rad1**(*m*, *n*, *c*, *x*) **= <ufunc 'obl_rad1'>**

Oblate spheroidal radial function of the first kind and its derivative

Computes the oblate spheroidal radial function of the first kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.obl_rad2

scipy.special.**obl_rad2**(*m*, *n*, *c*, *x*) **= <ufunc 'obl_rad2'>**

Oblate spheroidal radial function of the second kind and its derivative.

Computes the oblate spheroidal radial function of the second kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.pro_cv

scipy.special.**pro_cv**(*m*, *n*, *c*) **= <ufunc 'pro_cv'>**

Characteristic value of prolate spheroidal function

Computes the characteristic value of prolate spheroidal wave functions of order *m*, *n* (n>=m) and spheroidal parameter *c*.

scipy.special.obl_cv

scipy.special.**obl_cv**(*m*, *n*, *c*) **= <ufunc 'obl_cv'>**

Characteristic value of oblate spheroidal function

Computes the characteristic value of oblate spheroidal wave functions of order *m*, *n* (n>=m) and spheroidal parameter *c*.

scipy.special.pro_cv_seq

scipy.special.**pro_cv_seq**(*m*, *n*, *c*)

Characteristic values for prolate spheroidal wave functions.

Compute a sequence of characteristic values for the prolate spheroidal wave functions for mode m and n'=m..n and spheroidal parameter c.

References

[1]

scipy.special.obl_cv_seq

scipy.special.**obl_cv_seq**(*m*, *n*, *c*)
Characteristic values for oblate spheroidal wave functions.

Compute a sequence of characteristic values for the oblate spheroidal wave functions for mode m and n'=m..n and spheroidal parameter c.

References

[1]

The following functions require pre-computed characteristic value:

pro_ang1_cv(m, n, c, cv, x)	Prolate spheroidal angular function pro_ang1 for precomputed characteristic value
pro_rad1_cv(m, n, c, cv, x)	Prolate spheroidal radial function pro_rad1 for precomputed characteristic value
pro_rad2_cv(m, n, c, cv, x)	Prolate spheroidal radial function pro_rad2 for precomputed characteristic value
obl_ang1_cv(m, n, c, cv, x)	Oblate spheroidal angular function obl_ang1 for precomputed characteristic value
obl_rad1_cv(m, n, c, cv, x)	Oblate spheroidal radial function obl_rad1 for precomputed characteristic value
obl_rad2_cv(m, n, c, cv, x)	Oblate spheroidal radial function obl_rad2 for precomputed characteristic value

scipy.special.pro_ang1_cv

scipy.special.**pro_ang1_cv**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'pro_ang1_cv'>**
Prolate spheroidal angular function pro_ang1 for precomputed characteristic value

Computes the prolate spheroidal angular function of the first kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.pro_rad1_cv

scipy.special.**pro_rad1_cv**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'pro_rad1_cv'>**

Prolate spheroidal radial function pro_rad1 for precomputed characteristic value

Computes the prolate spheroidal radial function of the first kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.pro_rad2_cv

scipy.special.**pro_rad2_cv**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'pro_rad2_cv'>**

Prolate spheroidal radial function pro_rad2 for precomputed characteristic value

Computes the prolate spheroidal radial function of the second kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.obl_ang1_cv

scipy.special.**obl_ang1_cv**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'obl_ang1_cv'>**

Oblate spheroidal angular function obl_ang1 for precomputed characteristic value

Computes the oblate spheroidal angular function of the first kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.obl_rad1_cv

scipy.special.**obl_rad1_cv**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'obl_rad1_cv'>**

Oblate spheroidal radial function obl_rad1 for precomputed characteristic value

Computes the oblate spheroidal radial function of the first kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns

s	Value of the function
sp	Value of the derivative vs x

scipy.special.obl_rad2_cv

scipy.special.**obl_rad2_cv**(*m*, *n*, *c*, *cv*, *x*) **= <ufunc 'obl_rad2_cv'>**

Oblate spheroidal radial function obl_rad2 for precomputed characteristic value

Computes the oblate spheroidal radial function of the second kind and its derivative (with respect to *x*) for mode parameters m>=0 and n>=m, spheroidal parameter *c* and `|x| < 1.0`. Requires pre-computed characteristic value.

Returns

s	Value of the function
sp	Value of the derivative vs x

Kelvin functions

kelvin(x)	Kelvin functions as complex numbers
kelvin_zeros(nt)	Compute nt zeros of all Kelvin functions.
ber(x[, out])	Kelvin function ber.
bei(x[, out])	Kelvin function bei.
berp(x[, out])	Derivative of the Kelvin function ber.
beip(x[, out])	Derivative of the Kelvin function bei.
ker(x[, out])	Kelvin function ker.
kei(x[, out])	Kelvin function kei.
kerp(x[, out])	Derivative of the Kelvin function ker.
keip(x[, out])	Derivative of the Kelvin function kei.

scipy.special.kelvin

scipy.special.**kelvin**(*x*) **= <ufunc 'kelvin'>**

Kelvin functions as complex numbers

Returns

Be, Ke, Bep, Kep
: The tuple (Be, Ke, Bep, Kep) contains complex numbers representing the real and imaginary Kelvin functions and their derivatives evaluated at *x*. For example, kelvin(x)[0].real = ber x and kelvin(x)[0].imag = bei x with similar relationships for ker and kei.

scipy.special.kelvin_zeros

scipy.special.**kelvin_zeros**(*nt*)

Compute nt zeros of all Kelvin functions.

Returned in a length-8 tuple of arrays of length nt. The tuple contains the arrays of zeros of (ber, bei, ker, kei, ber', bei', ker', kei').

References

[1]

scipy.special.ber

scipy.special.**ber**(*x*, *out=None*) **= <ufunc 'ber'>**

Kelvin function ber.

Defined as

$$\mathrm{ber}(x) = \Re[J_0(xe^{3\pi i/4})]$$

where J_0 is the Bessel function of the first kind of order zero (see `jv`). See [dlmf] for more details.

Parameters

x [array_like] Real argument.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of the Kelvin function.

See also:

bei

the corresponding real part

berp

the derivative of bei

jv

Bessel function of the first kind

References

[dlmf]

Examples

It can be expressed using Bessel functions.

```
>>> import scipy.special as sc
>>> x = np.array([1.0, 2.0, 3.0, 4.0])
>>> sc.jv(0, x * np.exp(3 * np.pi * 1j / 4)).real
array([ 0.98438178,  0.75173418, -0.22138025, -2.56341656])
>>> sc.ber(x)
array([ 0.98438178,  0.75173418, -0.22138025, -2.56341656])
```

scipy.special.bei

scipy.special.**bei**(*x*, *out=None*) **= <ufunc 'bei'>**

Kelvin function bei.

Defined as

$$\mathrm{bei}(x) = \Im[J_0(xe^{3\pi i/4})]$$

where J_0 is the Bessel function of the first kind of order zero (see `jv`). See [dlmf] for more details.

Parameters

x	[array_like] Real argument.
out	[ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of the Kelvin function.

See also:

ber

the corresponding real part

beip

the derivative of bei

jv

Bessel function of the first kind

References

[dlmf]

Examples

It can be expressed using Bessel functions.

```
>>> import scipy.special as sc
>>> x = np.array([1.0, 2.0, 3.0, 4.0])
>>> sc.jv(0, x * np.exp(3 * np.pi * 1j / 4)).imag
array([0.24956604, 0.97229163, 1.93758679, 2.29269032])
>>> sc.bei(x)
array([0.24956604, 0.97229163, 1.93758679, 2.29269032])
```

scipy.special.berp

scipy.special.**berp**(*x*, *out=None*) **= <ufunc 'berp'>**

Derivative of the Kelvin function ber.

Parameters

x [array_like] Real argument.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
The values of the derivative of ber.

See also:

ber

References

[dlmf]

scipy.special.beip

scipy.special.**beip**(*x*, *out=None*) **= <ufunc 'beip'>**

Derivative of the Kelvin function bei.

Parameters

x [array_like] Real argument.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
The values of the derivative of bei.

See also:

bei

References

[dlmf]

scipy.special.ker

scipy.special.**ker**(*x*, *out=None*) **= <ufunc 'ker'>**

Kelvin function ker.

Defined as

$$\mathrm{ker}(x) = \Re[K_0(xe^{\pi i/4})]$$

Where K_0 is the modified Bessel function of the second kind (see `kv`). See [dlmf] for more details.

Parameters

x	[array_like] Real argument.
out	[ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of the Kelvin function.

See also:

kei

the corresponding imaginary part

kerp

the derivative of ker

kv

modified Bessel function of the second kind

References

[dlmf]

Examples

It can be expressed using the modified Bessel function of the second kind.

```
>>> import scipy.special as sc
>>> x = np.array([1.0, 2.0, 3.0, 4.0])
>>> sc.kv(0, x * np.exp(np.pi * 1j / 4)).real
array([ 0.28670621, -0.04166451, -0.06702923, -0.03617885])
>>> sc.ker(x)
array([ 0.28670621, -0.04166451, -0.06702923, -0.03617885])
```

scipy.special.kei

scipy.special.**kei**(*x*, *out=None*) **= <ufunc 'kei'>**

Kelvin function kei.

Defined as

$$\mathrm{kei}(x) = \Im[K_0(xe^{\pi i/4})]$$

where K_0 is the modified Bessel function of the second kind (see `kv`). See [dlmf] for more details.

Parameters

x	[array_like] Real argument.
out	[ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of the Kelvin function.

See also:

ker

the corresponding real part

keip

the derivative of kei

kv

modified Bessel function of the second kind

References

[dlmf]

Examples

It can be expressed using the modified Bessel function of the second kind.

```
>>> import scipy.special as sc
>>> x = np.array([1.0, 2.0, 3.0, 4.0])
>>> sc.kv(0, x * np.exp(np.pi * 1j / 4)).imag
array([-0.49499464, -0.20240007, -0.05112188,  0.0021984 ])
>>> sc.kei(x)
array([-0.49499464, -0.20240007, -0.05112188,  0.0021984 ])
```

scipy.special.kerp

scipy.special.**kerp**(*x*, *out=None*) **= <ufunc 'kerp'>**

Derivative of the Kelvin function ker.

Parameters

x [array_like] Real argument.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of the derivative of ker.

See also:

ker

References

[dlmf]

scipy.special.keip

scipy.special.**keip**(*x*, *out=None*) **= <ufunc 'keip'>**

Derivative of the Kelvin function kei.

Parameters

x [array_like] Real argument.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
The values of the derivative of kei.

See also:

kei

References

[dlmf]

These are not universal functions:

ber_zeros(nt)	Compute nt zeros of the Kelvin function ber.
bei_zeros(nt)	Compute nt zeros of the Kelvin function bei.
berp_zeros(nt)	Compute nt zeros of the derivative of the Kelvin function ber.
beip_zeros(nt)	Compute nt zeros of the derivative of the Kelvin function bei.
ker_zeros(nt)	Compute nt zeros of the Kelvin function ker.

continues on next page

Table 251 – continued from previous page

kei_zeros(nt)	Compute nt zeros of the Kelvin function kei.
kerp_zeros(nt)	Compute nt zeros of the derivative of the Kelvin function ker.
keip_zeros(nt)	Compute nt zeros of the derivative of the Kelvin function kei.

scipy.special.ber_zeros

scipy.special.**ber_zeros**(*nt*)

Compute nt zeros of the Kelvin function ber.

Parameters

nt [int] Number of zeros to compute. Must be positive.

Returns

ndarray First *nt* zeros of the Kelvin function.

See also:

ber

References

[1]

scipy.special.bei_zeros

scipy.special.**bei_zeros**(*nt*)

Compute nt zeros of the Kelvin function bei.

Parameters

nt [int] Number of zeros to compute. Must be positive.

Returns

ndarray First *nt* zeros of the Kelvin function.

See also:

bei

References

[1]

scipy.special.berp_zeros

scipy.special.**berp_zeros**(*nt*)

Compute nt zeros of the derivative of the Kelvin function ber.

Parameters

nt [int] Number of zeros to compute. Must be positive.

Returns

ndarray First *nt* zeros of the derivative of the Kelvin function.

See also:

ber, **berp**

References

[1]

scipy.special.beip_zeros

scipy.special.**beip_zeros**(*nt*)

Compute nt zeros of the derivative of the Kelvin function bei.

Parameters

nt [int] Number of zeros to compute. Must be positive.

Returns

ndarray First *nt* zeros of the derivative of the Kelvin function.

See also:

bei, **beip**

References

[1]

scipy.special.ker_zeros

scipy.special.**ker_zeros**(*nt*)

Compute nt zeros of the Kelvin function ker.

Parameters

nt [int] Number of zeros to compute. Must be positive.

Returns

ndarray First *nt* zeros of the Kelvin function.

See also:

ker

References

[1]

scipy.special.kei_zeros

scipy.special.**kei_zeros**(*nt*)
Compute nt zeros of the Kelvin function kei.

Parameters

nt [int] Number of zeros to compute. Must be positive.

Returns

ndarray First *nt* zeros of the Kelvin function.

See also:

kei

References

[1]

scipy.special.kerp_zeros

scipy.special.**kerp_zeros**(*nt*)
Compute nt zeros of the derivative of the Kelvin function ker.

Parameters

nt [int] Number of zeros to compute. Must be positive.

Returns

ndarray First *nt* zeros of the derivative of the Kelvin function.

See also:

ker, **kerp**

References

[1]

scipy.special.keip_zeros

scipy.special.**keip_zeros**(*nt*)

Compute nt zeros of the derivative of the Kelvin function kei.

Parameters

nt [int] Number of zeros to compute. Must be positive.

Returns

ndarray First *nt* zeros of the derivative of the Kelvin function.

See also:

kei, **keip**

References

[1]

Combinatorics

comb(N, k[, exact, repetition])	The number of combinations of N things taken k at a time.
perm(N, k[, exact])	Permutations of N things taken k at a time, i.e., k-permutations of N.

scipy.special.comb

scipy.special.**comb**(*N*, *k*, *exact=False*, *repetition=False*)

The number of combinations of N things taken k at a time.

This is often expressed as “N choose k”.

Parameters

N [int, ndarray] Number of things.

k [int, ndarray] Number of elements taken.

exact [bool, optional] If *exact* is False, then floating point precision is used, otherwise exact long integer is computed.

repetition [bool, optional] If *repetition* is True, then the number of combinations with repetition is computed.

Returns

val [int, float, ndarray] The total number of combinations.

See also:

binom

Binomial coefficient ufunc

Notes

- Array arguments accepted only for exact=False case.
- If N < 0, or k < 0, then 0 is returned.
- If k > N and repetition=False, then 0 is returned.

Examples

```
>>> from scipy.special import comb
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> comb(n, k, exact=False)
array([ 120.,  210.])
>>> comb(10, 3, exact=True)
120
>>> comb(10, 3, exact=True, repetition=True)
220
```

scipy.special.perm

scipy.special.**perm**(*N*, *k*, *exact=False*)

Permutations of N things taken k at a time, i.e., k-permutations of N.

It's also known as "partial permutations".

Parameters

N	[int, ndarray] Number of things.
k	[int, ndarray] Number of elements taken.
exact	[bool, optional] If *exact* is False, then floating point precision is used, otherwise exact long integer is computed.

Returns

val	[int, ndarray] The number of k-permutations of N.

Notes

- Array arguments accepted only for exact=False case.
- If k > N, N < 0, or k < 0, then a 0 is returned.

Examples

```
>>> from scipy.special import perm
>>> k = np.array([3, 4])
>>> n = np.array([10, 10])
>>> perm(n, k)
array([  720.,  5040.])
>>> perm(10, 3, exact=True)
720
```

Lambert W and related functions

lambertw(z[, k, tol])	Lambert W function.
wrightomega(z[, out])	Wright Omega function.

scipy.special.lambertw

scipy.special.**lambertw**(*z*, *k=0*, *tol=1e-8*)

Lambert W function.

The Lambert W function *W(z)* is defined as the inverse function of `w * exp(w)`. In other words, the value of `W(z)` is such that `z = W(z) * exp(W(z))` for any complex number `z`.

The Lambert W function is a multivalued function with infinitely many branches. Each branch gives a separate solution of the equation `z = w exp(w)`. Here, the branches are indexed by the integer *k*.

Parameters

z	[array_like] Input argument.
k	[int, optional] Branch index.
tol	[float, optional] Evaluation tolerance.

Returns

w	[array] *w* will have the same shape as *z*.

See also:

wrightomega

the Wright Omega function

Notes

All branches are supported by *lambertw*:

- `lambertw(z)` gives the principal solution (branch 0)
- `lambertw(z, k)` gives the solution on branch *k*

The Lambert W function has two partially real branches: the principal branch (*k = 0*) is real for real `z > -1/e`, and the `k = -1` branch is real for `-1/e < z < 0`. All branches except `k = 0` have a logarithmic singularity at `z = 0`.

Possible issues

The evaluation can become inaccurate very close to the branch point at `-1/e`. In some corner cases, *lambertw* might currently fail to converge, or can end up on the wrong branch.

Algorithm

Halley's iteration is used to invert `w * exp(w)`, using a first-order asymptotic approximation (O(log(w)) or *O(w)*) as the initial estimate.

The definition, implementation and choice of branches is based on [2].

References

[1], [2]

Examples

The Lambert W function is the inverse of `w exp(w)`:

```
>>> from scipy.special import lambertw
>>> w = lambertw(1)
>>> w
(0.56714329040978384+0j)
>>> w * np.exp(w)
(1.0+0j)
```

Any branch gives a valid inverse:

```
>>> w = lambertw(1, k=3)
>>> w
(-2.8535817554090377+17.113535539412148j)
>>> w*np.exp(w)
(1.0000000000000002+1.609823385706477e-15j)
```

Applications to equation-solving

The Lambert W function may be used to solve various kinds of equations, such as finding the value of the infinite power tower $z^{z^{z^{\cdots}}}$:

```
>>> def tower(z, n):
...     if n == 0:
...         return z
...     return z ** tower(z, n-1)
...
>>> tower(0.5, 100)
0.641185744504986
>>> -lambertw(-np.log(0.5)) / np.log(0.5)
(0.64118574450498589+0j)
```

scipy.special.wrightomega

scipy.special.**wrightomega**(*z*, *out=None*) **= <ufunc 'wrightomega'>**

Wright Omega function.

Defined as the solution to

$$\omega + \log(\omega) = z$$

where $\log$ is the principal branch of the complex logarithm.

Parameters

z [array_like] Points at which to evaluate the Wright Omega function

Returns

omega [ndarray] Values of the Wright Omega function

See also:

lambertw

The Lambert W function

Notes

New in version 0.19.0.

The function can also be defined as

$$\omega(z) = W_{K(z)}(e^z)$$

where $K(z) = \lceil (\Im(z) - \pi)/(2\pi) \rceil$ is the unwinding number and W is the Lambert W function.

The implementation here is taken from [1].

References

[1]

Other special functions

agm(a, b)	Compute the arithmetic-geometric mean of *a* and *b*.
bernoulli(n)	Bernoulli numbers B0..Bn (inclusive).
binom(n, k)	Binomial coefficient
diric(x, n)	Periodic sinc function, also called the Dirichlet function.
euler(n)	Euler numbers E(0), E(1), …, E(n).
expn(n, x[, out])	Generalized exponential integral En.
exp1(z[, out])	Exponential integral E1.
expi(x[, out])	Exponential integral Ei.
factorial(n[, exact])	The factorial of a number or array of numbers.
factorial2(n[, exact])	Double factorial.
factorialk(n, k[, exact])	Multifactorial of n of order k, n(!!…!).
shichi(x[, out])	Hyperbolic sine and cosine integrals.
sici(x[, out])	Sine and cosine integrals.
softmax(x[, axis])	Softmax function
log_softmax(x[, axis])	Logarithm of softmax function.
spence(z[, out])	Spence's function, also known as the dilogarithm.
zeta(x[, q, out])	Riemann or Hurwitz zeta function.
zetac(x)	Riemann zeta function minus 1.

scipy.special.agm

scipy.special.**agm**(*a*, *b*) **= <ufunc 'agm'>**

Compute the arithmetic-geometric mean of *a* and *b*.

Start with a_0 = a and b_0 = b and iteratively compute:

```
a_{n+1} = (a_n + b_n)/2
b_{n+1} = sqrt(a_n*b_n)
```

a_n and b_n converge to the same limit as n increases; their common limit is agm(a, b).

Parameters

a, b [array_like] Real values only. If the values are both negative, the result is negative. If one value is negative and the other is positive, *nan* is returned.

Returns

float The arithmetic-geometric mean of *a* and *b*.

Examples

```
>>> from scipy.special import agm
>>> a, b = 24.0, 6.0
>>> agm(a, b)
13.458171481725614
```

Compare that result to the iteration:

```
>>> while a != b:
...     a, b = (a + b)/2, np.sqrt(a*b)
...     print("a = %19.16f  b=%19.16f" % (a, b))
...
a = 15.0000000000000000  b=12.0000000000000000
a = 13.5000000000000000  b=13.4164078649987388
a = 13.4582039324993694  b=13.4581390309909850
a = 13.4581714817451772  b=13.4581714817060547
a = 13.4581714817256159  b=13.4581714817256159
```

When array-like arguments are given, broadcasting applies:

```
>>> a = np.array([[1.5], [3], [6]])  # a has shape (3, 1).
>>> b = np.array([6, 12, 24, 48])    # b has shape (4,).
>>> agm(a, b)
array([[  3.36454287,   5.42363427,   9.05798751,  15.53650756],
       [  4.37037309,   6.72908574,  10.84726853,  18.11597502],
       [  6.        ,   8.74074619,  13.45817148,  21.69453707]])
```

scipy.special.bernoulli

scipy.special.**bernoulli**(*n*)

Bernoulli numbers B0..Bn (inclusive).

Parameters

n [int] Indicated the number of terms in the Bernoulli series to generate.

Returns

ndarray The Bernoulli numbers `[B(0), B(1), ..., B(n)]`.

References

[1], [2]

Examples

```
>>> from scipy.special import bernoulli, zeta
>>> bernoulli(4)
array([ 1.        , -0.5       ,  0.16666667,  0.        , -0.03333333])
```

The Wikipedia article ([2]) points out the relationship between the Bernoulli numbers and the zeta function, `B_n^+ = -n * zeta(1 - n)` for `n > 0`:

```
>>> n = np.arange(1, 5)
>>> -n * zeta(1 - n)
array([ 0.5       ,  0.16666667, -0.        , -0.03333333])
```

Note that, in the notation used in the wikipedia article, *bernoulli* computes `B_n^-` (i.e. it used the convention that `B_1` is -1/2). The relation given above is for `B_n^+`, so the sign of 0.5 does not match the output of `bernoulli(4)`.

scipy.special.binom

scipy.special.**binom**(*n*, *k*) **= <ufunc 'binom'>**

Binomial coefficient

See also:

comb

The number of combinations of N things taken k at a time.

scipy.special.diric

scipy.special.**diric**(*x*, *n*)

Periodic sinc function, also called the Dirichlet function.

The Dirichlet function is defined as:

```
diric(x, n) = sin(x * n/2) / (n * sin(x / 2)),
```

where *n* is a positive integer.

Parameters

x	[array_like] Input data
n	[int] Integer defining the periodicity.

Returns

diric	[ndarray]

Examples

```
>>> from scipy import special
>>> import matplotlib.pyplot as plt
```

```
>>> x = np.linspace(-8*np.pi, 8*np.pi, num=201)
>>> plt.figure(figsize=(8, 8));
>>> for idx, n in enumerate([2, 3, 4, 9]):
...     plt.subplot(2, 2, idx+1)
...     plt.plot(x, special.diric(x, n))
...     plt.title('diric, n={}'.format(n))
>>> plt.show()
```

The following example demonstrates that *diric* gives the magnitudes (modulo the sign and scaling) of the Fourier coefficients of a rectangular pulse.

Suppress output of values that are effectively 0:

```
>>> np.set_printoptions(suppress=True)
```

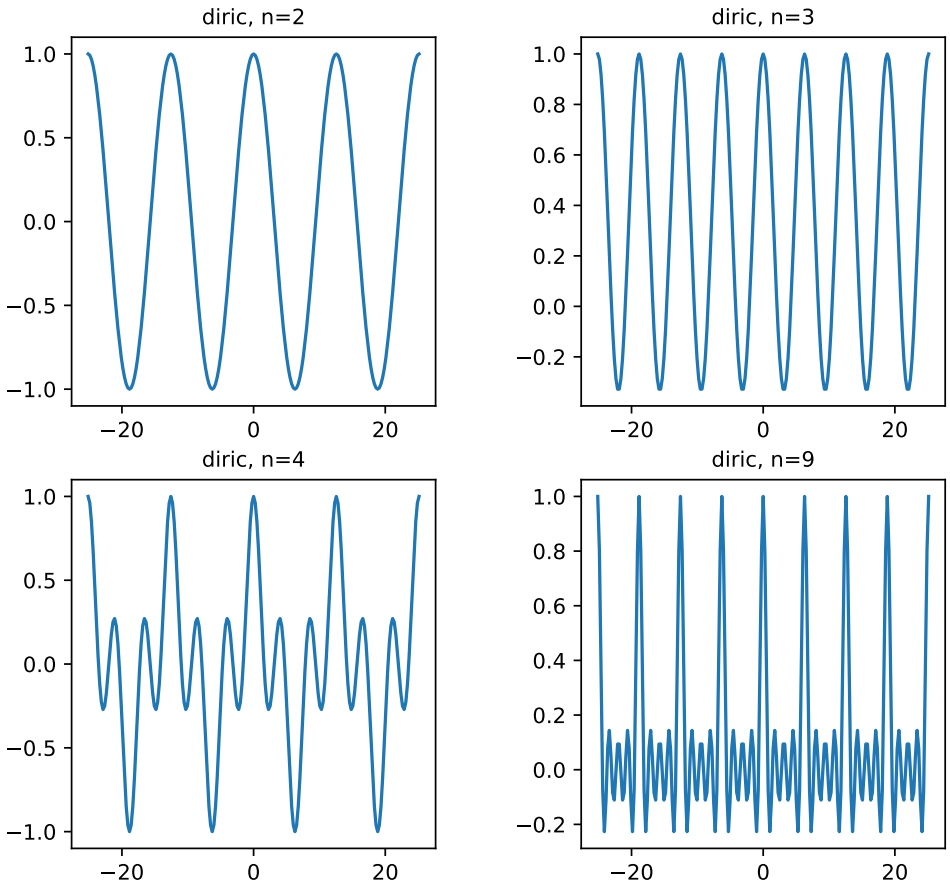
Create a signal *x* of length *m* with *k* ones:

```
>>> m = 8
>>> k = 3
>>> x = np.zeros(m)
>>> x[:k] = 1
```

Use the FFT to compute the Fourier transform of *x*, and inspect the magnitudes of the coefficients:

```
>>> np.abs(np.fft.fft(x))
array([ 3.        ,  2.41421356,  1.        ,  0.41421356,  1.        ,
        0.41421356,  1.        ,  2.41421356])
```

Now find the same values (up to sign) using *diric*. We multiply by *k* to account for the different scaling conventions of `numpy.fft.fft` and *diric*:


diric, n=2
diric, n=3
diric, n=4
diric, n=9
1.0
0.5
0.0
−0.5
−1.0
0.8
0.6
0.4
0.2
−0.2
−20
0
20

```
>>> theta = np.linspace(0, 2*np.pi, m, endpoint=False)
>>> k * special.diric(theta, k)
array([ 3.        ,  2.41421356,  1.        , -0.41421356, -1.        ,
       -0.41421356,  1.        ,  2.41421356])
```

scipy.special.euler

scipy.special.**euler**(*n*)

Euler numbers E(0), E(1), …, E(n).

The Euler numbers [1] are also known as the secant numbers.

Because `euler(n)` returns floating point values, it does not give exact values for large *n*. The first inexact value is E(22).

Parameters

n [int] The highest index of the Euler number to be returned.

Returns

ndarray The Euler numbers [E(0), E(1), …, E(n)]. The odd Euler numbers, which are all zero, are included.

References

[1], [2]

Examples

```
>>> from scipy.special import euler
>>> euler(6)
array([  1.,   0.,  -1.,   0.,   5.,   0., -61.])
```

```
>>> euler(13).astype(np.int64)
array([      1,       0,      -1,       0,       5,       0,     -61,
            0,    1385,       0,  -50521,       0, 2702765,       0])
```

```
>>> euler(22)[-1]  # Exact value of E(22) is -69348874393137901.
-69348874393137976.0
```

scipy.special.expn

scipy.special.**expn**(*n*, *x*, *out=None*) **= <ufunc 'expn'>**

Generalized exponential integral En.

For integer $n \geq 0$ and real $x \geq 0$ the generalized exponential integral is defined as [dlmf]

$$E_n(x) = x^{n-1} \int_x^\infty \frac{e^{-t}}{t^n} dt.$$

Parameters

n: array_like
Non-negative integers
x: array_like
Real argument
out: ndarray, optional
Optional output array for the function results

Returns

scalar or ndarray
Values of the generalized exponential integral

See also:

exp1

special case of E_n for $n = 1$

expi

related to E_n when $n = 1$

References

[dlmf]

Examples

```
>>> import scipy.special as sc
```

Its domain is nonnegative n and x.

```
>>> sc.expn(-1, 1.0), sc.expn(1, -1.0)
(nan, nan)
```

It has a pole at `x = 0` for `n = 1, 2`; for larger `n` it is equal to `1 / (n - 1)`.

```
>>> sc.expn([0, 1, 2, 3, 4], 0)
array([       inf,        inf, 1.        , 0.5       , 0.33333333])
```

For n equal to 0 it reduces to `exp(-x) / x`.

```
>>> x = np.array([1, 2, 3, 4])
>>> sc.expn(0, x)
array([0.36787944, 0.06766764, 0.01659569, 0.00457891])
>>> np.exp(-x) / x
array([0.36787944, 0.06766764, 0.01659569, 0.00457891])
```

For n equal to 1 it reduces to *exp1*.

```
>>> sc.expn(1, x)
array([0.21938393, 0.04890051, 0.01304838, 0.00377935])
>>> sc.exp1(x)
array([0.21938393, 0.04890051, 0.01304838, 0.00377935])
```

scipy.special.exp1

scipy.special.**exp1**(*z*, *out=None*) **= <ufunc 'exp1'>**

Exponential integral E1.

For complex $z \neq 0$ the exponential integral can be defined as [1]

$$E_1(z) = \int_z^\infty \frac{e^{-t}}{t} dt,$$

where the path of the integral does not cross the negative real axis or pass through the origin.

Parameters

z: array_like
Real or complex argument.

out: ndarray, optional
Optional output array for the function results

Returns

scalar or ndarray
Values of the exponential integral E1

See also:

expi

exponential integral Ei

expn

generalization of E_1

Notes

For $x > 0$ it is related to the exponential integral Ei (see *expi*) via the relation

$$E_1(x) = -Ei(-x).$$

References

[1]

Examples

```
>>> import scipy.special as sc
```

It has a pole at 0.

```
>>> sc.exp1(0)
inf
```

It has a branch cut on the negative real axis.

```
>>> sc.exp1(-1)
nan
>>> sc.exp1(complex(-1, 0))
(-1.8951178163559368-3.141592653589793j)
>>> sc.exp1(complex(-1, -0.0))
(-1.8951178163559368+3.141592653589793j)
```

It approaches 0 along the positive real axis.

```
>>> sc.exp1([1, 10, 100, 1000])
array([2.19383934e-01, 4.15696893e-06, 3.68359776e-46, 0.00000000e+00])
```

It is related to *expi*.

```
>>> x = np.array([1, 2, 3, 4])
>>> sc.exp1(x)
array([0.21938393, 0.04890051, 0.01304838, 0.00377935])
>>> -sc.expi(-x)
array([0.21938393, 0.04890051, 0.01304838, 0.00377935])
```

scipy.special.expi

scipy.special.**expi**(*x*, *out=None*) **= <ufunc 'expi'>**

Exponential integral Ei.

For real x, the exponential integral is defined as [1]

$$Ei(x) = \int_{-\infty}^{x} \frac{e^t}{t} dt.$$

For $x > 0$ the integral is understood as a Cauchy principle value.

It is extended to the complex plane by analytic continuation of the function on the interval $(0, \infty)$. The complex variant has a branch cut on the negative real axis.

Parameters

x: array_like
Real or complex valued argument

out: ndarray, optional
Optional output array for the function results

Returns

scalar or ndarray
Values of the exponential integral

See also:

exp1

Exponential integral E_1

expn

Generalized exponential integral E_n

Notes

The exponential integrals E_1 and Ei satisfy the relation

$$E_1(x) = -Ei(-x)$$

for $x > 0$.

References

[1]

Examples

```
>>> import scipy.special as sc
```

It is related to *exp1*.

```
>>> x = np.array([1, 2, 3, 4])
>>> -sc.expi(-x)
array([0.21938393, 0.04890051, 0.01304838, 0.00377935])
>>> sc.exp1(x)
array([0.21938393, 0.04890051, 0.01304838, 0.00377935])
```

The complex variant has a branch cut on the negative real axis.

```
>>> import scipy.special as sc
>>> sc.expi(-1 + 1e-12j)
(-0.21938393439552062+3.1415926535894254j)
>>> sc.expi(-1 - 1e-12j)
(-0.21938393439552062-3.1415926535894254j)
```

As the complex variant approaches the branch cut, the real parts approach the value of the real variant.

```
>>> sc.expi(-1)
-0.21938393439552062
```

The SciPy implementation returns the real variant for complex values on the branch cut.

```
>>> sc.expi(complex(-1, 0.0))
(-0.21938393439552062-0j)
>>> sc.expi(complex(-1, -0.0))
(-0.21938393439552062-0j)
```

scipy.special.factorial

scipy.special.**factorial**(*n*, *exact=False*)

The factorial of a number or array of numbers.

The factorial of non-negative integer *n* is the product of all positive integers less than or equal to *n*:

```
n! = n * (n - 1) * (n - 2) * ... * 1
```

Parameters

n : [int or array_like of ints] Input values. If `n < 0`, the return value is 0.

exact : [bool, optional] If True, calculate the answer exactly using long integer arithmetic. If False, result is approximated in floating point rapidly using the *gamma* function. Default is False.

Returns

nf : [float or int or ndarray] Factorial of *n*, as integer or float depending on *exact*.

Notes

For arrays with `exact=True`, the factorial is computed only once, for the largest input, with each other result computed in the process. The output dtype is increased to `int64` or `object` if necessary.

With `exact=False` the factorial is approximated using the gamma function:

$$n! = \Gamma(n+1)$$

Examples

```
>>> from scipy.special import factorial
>>> arr = np.array([3, 4, 5])
>>> factorial(arr, exact=False)
array([   6.,   24.,  120.])
>>> factorial(arr, exact=True)
array([  6,  24, 120])
>>> factorial(5, exact=True)
120
```

scipy.special.factorial2

scipy.special.**factorial2**(*n*, *exact=False*)

Double factorial.

This is the factorial with every second value skipped. E.g., `7!! = 7 * 5 * 3 * 1`. It can be approximated numerically as:

```
n!! = special.gamma(n/2+1)*2**((m+1)/2)/sqrt(pi)  n odd
    = 2**(n/2) * (n/2)!                           n even
```

Parameters

n [int or array_like] Calculate `n!!`. Arrays are only supported with *exact* set to False. If `n < 0`, the return value is 0.

exact [bool, optional] The result can be approximated rapidly using the gamma-formula above (default). If *exact* is set to True, calculate the answer exactly using integer arithmetic.

Returns

nff [float or int] Double factorial of *n*, as an int or a float depending on *exact*.

Examples

```
>>> from scipy.special import factorial2
>>> factorial2(7, exact=False)
array(105.00000000000001)
>>> factorial2(7, exact=True)
105
```

scipy.special.factorialk

scipy.special.**factorialk**(*n*, *k*, *exact=True*)

Multifactorial of n of order k, n(!!...!).

This is the multifactorial of n skipping k values. For example,

factorialk(17, 4) = 17!!!! = 17 * 13 * 9 * 5 * 1

In particular, for any integer `n`, we have

factorialk(n, 1) = factorial(n)
factorialk(n, 2) = factorial2(n)

Parameters

n [int] Calculate multifactorial. If *n* < 0, the return value is 0.

k [int] Order of multifactorial.

exact [bool, optional] If exact is set to True, calculate the answer exactly using integer arithmetic.

Returns

val [int] Multifactorial of *n*.

Raises

NotImplementedError
Raises when exact is False

Examples

```
>>> from scipy.special import factorialk
>>> factorialk(5, 1, exact=True)
120
>>> factorialk(5, 3, exact=True)
10
```

scipy.special.shichi

scipy.special.**shichi**(*x*, *out=None*) **= <ufunc 'shichi'>**

Hyperbolic sine and cosine integrals.

The hyperbolic sine integral is

$$\int_0^x \frac{\sinh t}{t} dt$$

and the hyperbolic cosine integral is

$$\gamma + \log(x) + \int_0^x \frac{\cosh t - 1}{t} dt$$

where γ is Euler's constant and $\log$ is the principle branch of the logarithm.

Parameters

x [array_like] Real or complex points at which to compute the hyperbolic sine and cosine integrals.

Returns

si [ndarray] Hyperbolic sine integral at `x`
ci [ndarray] Hyperbolic cosine integral at `x`

Notes

For real arguments with `x < 0`, `chi` is the real part of the hyperbolic cosine integral. For such points `chi(x)` and `chi(x + 0j)` differ by a factor of `1j*pi`.

For real arguments the function is computed by calling Cephes' [1] *shichi* routine. For complex arguments the algorithm is based on Mpmath's [2] *shi* and *chi* routines.

References

[1], [2]

scipy.special.sici

scipy.special.**sici**(*x*, *out=None*) **= <ufunc 'sici'>**

Sine and cosine integrals.

The sine integral is

$$\int_0^x \frac{\sin t}{t} dt$$

and the cosine integral is

$$\gamma + \log(x) + \int_0^x \frac{\cos t - 1}{t} dt$$

where γ is Euler's constant and $\log$ is the principle branch of the logarithm.

Parameters

x [array_like] Real or complex points at which to compute the sine and cosine integrals.

Returns

si [ndarray] Sine integral at `x`
ci [ndarray] Cosine integral at `x`

Notes

For real arguments with `x < 0`, `ci` is the real part of the cosine integral. For such points `ci(x)` and `ci(x + 0j)` differ by a factor of `1j*pi`.

For real arguments the function is computed by calling Cephes' [1] *sici* routine. For complex arguments the algorithm is based on Mpmath's [2] *si* and *ci* routines.

References

[1], [2]

scipy.special.softmax

`scipy.special.`**`softmax`**(*x*, *axis=None*)
Softmax function

The softmax function transforms each element of a collection by computing the exponential of each element divided by the sum of the exponentials of all the elements. That is, if *x* is a one-dimensional numpy array:

```
softmax(x) = np.exp(x)/sum(np.exp(x))
```

Parameters

x [array_like] Input array.
axis [int or tuple of ints, optional] Axis to compute values along. Default is None and softmax will be computed over the entire array *x*.

Returns

s [ndarray] An array the same shape as *x*. The result will sum to 1 along the specified axis.

Notes

The formula for the softmax function $\sigma(x)$ for a vector $x = \{x_0, x_1, ..., x_{n-1}\}$ is

$$\sigma(x)_j = \frac{e^{x_j}}{\sum_k e^{x_k}}$$

The *softmax* function is the gradient of *logsumexp*.

New in version 1.2.0.

Examples

```
>>> from scipy.special import softmax
>>> np.set_printoptions(precision=5)
```

```
>>> x = np.array([[1, 0.5, 0.2, 3],
...               [1,  -1,   7, 3],
...               [2,  12,  13, 3]])
...
```

Compute the softmax transformation over the entire array.

```
>>> m = softmax(x)
>>> m
array([[  4.48309e-06,   2.71913e-06,   2.01438e-06,   3.31258e-05],
       [  4.48309e-06,   6.06720e-07,   1.80861e-03,   3.31258e-05],
       [  1.21863e-05,   2.68421e-01,   7.29644e-01,   3.31258e-05]])
```

```
>>> m.sum()
1.0000000000000002
```

Compute the softmax transformation along the first axis (i.e., the columns).

```
>>> m = softmax(x, axis=0)
```

```
>>> m
array([[  2.11942e-01,   1.01300e-05,   2.75394e-06,   3.33333e-01],
       [  2.11942e-01,   2.26030e-06,   2.47262e-03,   3.33333e-01],
       [  5.76117e-01,   9.99988e-01,   9.97525e-01,   3.33333e-01]])
```

```
>>> m.sum(axis=0)
array([ 1.,  1.,  1.,  1.])
```

Compute the softmax transformation along the second axis (i.e., the rows).

```
>>> m = softmax(x, axis=1)
>>> m
array([[  1.05877e-01,   6.42177e-02,   4.75736e-02,   7.82332e-01],
       [  2.42746e-03,   3.28521e-04,   9.79307e-01,   1.79366e-02],
       [  1.22094e-05,   2.68929e-01,   7.31025e-01,   3.31885e-05]])
```

```
>>> m.sum(axis=1)
array([ 1.,  1.,  1.])
```

scipy.special.log_softmax

scipy.special.**log_softmax**(*x*, *axis=None*)

Logarithm of softmax function:

```
log_softmax(x) = log(softmax(x))
```

Parameters

x	[array_like] Input array.
axis	[int or tuple of ints, optional] Axis to compute values along. Default is None and softmax will be computed over the entire array *x*.

Returns

s	[ndarray or scalar] An array with the same shape as *x*. Exponential of the result will sum to 1 along the specified axis. If *x* is a scalar, a scalar is returned.

Notes

log_softmax is more accurate than `np.log(softmax(x))` with inputs that make *softmax* saturate (see examples below).

New in version 1.5.0.

Examples

```
>>> from scipy.special import log_softmax
>>> from scipy.special import softmax
>>> np.set_printoptions(precision=5)
```

```
>>> x = np.array([1000.0, 1.0])
```

```
>>> y = log_softmax(x)
>>> y
array([   0., -999.])
```

```
>>> with np.errstate(divide='ignore'):
...   y = np.log(softmax(x))
...
>>> y
array([  0., -inf])
```

scipy.special.spence

scipy.special.**spence**(*z*, *out=None*) **= <ufunc 'spence'>**

Spence's function, also known as the dilogarithm.

It is defined to be

$$\int_1^z \frac{\log(t)}{1-t}dt$$

for complex z, where the contour of integration is taken to avoid the branch cut of the logarithm. Spence's function is analytic everywhere except the negative real axis where it has a branch cut.

Parameters

z [array_like] Points at which to evaluate Spence's function

Returns

s [ndarray] Computed values of Spence's function

Notes

There is a different convention which defines Spence's function by the integral

$$-\int_0^z \frac{\log(1-t)}{t}dt;$$

this is our `spence(1 - z)`.

scipy.special.zeta

scipy.special.**zeta**(*x*, *q=None*, *out=None*)

Riemann or Hurwitz zeta function.

Parameters

x [array_like of float] Input data, must be real
q [array_like of float, optional] Input data, must be real. Defaults to Riemann zeta.
out [ndarray, optional] Output array for the computed values.

Returns

out [array_like] Values of zeta(x).

See also:

`zetac`

Notes

The two-argument version is the Hurwitz zeta function

$$\zeta(x, q) = \sum_{k=0}^{\infty} \frac{1}{(k+q)^x};$$

see [dlmf] for details. The Riemann zeta function corresponds to the case when `q = 1`.

References

[dlmf]

Examples

```
>>> from scipy.special import zeta, polygamma, factorial
```

Some specific values:

```
>>> zeta(2), np.pi**2/6
(1.6449340668482266, 1.6449340668482264)
```

```
>>> zeta(4), np.pi**4/90
(1.0823232337111381, 1.082323233711138)
```

Relation to the *polygamma* function:

```
>>> m = 3
>>> x = 1.25
>>> polygamma(m, x)
array(2.782144009188397)
>>> (-1)**(m+1) * factorial(m) * zeta(m+1, x)
2.7821440091883969
```

scipy.special.zetac

scipy.special.**zetac**(*x*) **= <ufunc 'zetac'>**

Riemann zeta function minus 1.

This function is defined as

$$\zeta(x) = \sum_{k=2}^{\infty} 1/k^x,$$

where `x > 1`. For `x < 1` the analytic continuation is computed. For more information on the Riemann zeta function, see [dlmf].

Parameters

x [array_like of float] Values at which to compute zeta(x) - 1 (must be real).

Returns

out [array_like] Values of zeta(x) - 1.

See also:

zeta

References

[dlmf]

Examples

```
>>> from scipy.special import zetac, zeta
```

Some special values:

```
>>> zetac(2), np.pi**2/6 - 1
(0.64493406684822641, 0.6449340668482264)
```

```
>>> zetac(-1), -1.0/12 - 1
(-1.0833333333333333, -1.0833333333333333)
```

Compare `zetac(x)` to `zeta(x) - 1` for large *x*:

```
>>> zetac(60), zeta(60) - 1
(8.673617380119933e-19, 0.0)
```

Convenience functions

cbrt(x)	Element-wise cube root of *x*.
exp10(x)	Compute `10**x` element-wise.
exp2(x)	Compute `2**x` element-wise.
radian(d, m, s[, out])	Convert from degrees to radians.
cosdg(x[, out])	Cosine of the angle *x* given in degrees.
sindg(x[, out])	Sine of the angle *x* given in degrees.
tandg(x[, out])	Tangent of angle *x* given in degrees.
cotdg(x[, out])	Cotangent of the angle *x* given in degrees.
log1p(x[, out])	Calculates log(1 + x) for use when *x* is near zero.
expm1(x)	Compute `exp(x) - 1`.
cosm1(x[, out])	cos(x) - 1 for use when *x* is near zero.
round(x[, out])	Round to the nearest integer.
xlogy(x, y)	Compute `x*log(y)` so that the result is 0 if `x = 0`.
xlog1py(x, y)	Compute `x*log1p(y)` so that the result is 0 if `x = 0`.
logsumexp(a[, axis, b, keepdims, return_sign])	Compute the log of the sum of exponentials of input elements.
exprel(x)	Relative error exponential, `(exp(x) - 1)/x`.
sinc(x)	Return the normalized sinc function.

scipy.special.cbrt

scipy.special.**cbrt**(*x*) = <ufunc 'cbrt'>

Element-wise cube root of *x*.

Parameters

x [array_like] *x* must contain real numbers.

Returns

float The cube root of each value in *x*.

Examples

```
>>> from scipy.special import cbrt
```

```
>>> cbrt(8)
2.0
>>> cbrt([-8, -3, 0.125, 1.331])
array([-2.        , -1.44224957,  0.5       ,  1.1       ])
```

scipy.special.exp10

scipy.special.**exp10**(*x*) = <ufunc 'exp10'>

Compute `10**x` element-wise.

Parameters

x [array_like] *x* must contain real numbers.

Returns

float `10**x`, computed element-wise.

Examples

```
>>> from scipy.special import exp10
```

```
>>> exp10(3)
1000.0
>>> x = np.array([[-1, -0.5, 0], [0.5, 1, 1.5]])
>>> exp10(x)
array([[  0.1       ,   0.31622777,   1.        ],
       [  3.16227766,  10.        ,  31.6227766 ]])
```

scipy.special.exp2

scipy.special.**exp2**(*x*) **= <ufunc 'exp2'>**

Compute `2**x` element-wise.

Parameters

x [array_like] *x* must contain real numbers.

Returns

float `2**x`, computed element-wise.

Examples

```
>>> from scipy.special import exp2
```

```
>>> exp2(3)
8.0
>>> x = np.array([[-1, -0.5, 0], [0.5, 1, 1.5]])
>>> exp2(x)
array([[ 0.5       ,  0.70710678,  1.        ],
       [ 1.41421356,  2.        ,  2.82842712]])
```

scipy.special.radian

scipy.special.**radian**(*d*, *m*, *s*, *out=None*) **= <ufunc 'radian'>**

Convert from degrees to radians.

Returns the angle given in (d)egrees, (m)inutes, and (s)econds in radians.

Parameters

d [array_like] Degrees, can be real-valued.
m [array_like] Minutes, can be real-valued.
s [array_like] Seconds, can be real-valued.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of the inputs in radians.

Examples

```
>>> import scipy.special as sc
```

There are many ways to specify an angle.

```
>>> sc.radian(90, 0, 0)
1.5707963267948966
>>> sc.radian(0, 60 * 90, 0)
1.5707963267948966
```

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```
>>> sc.radian(0, 0, 60**2 * 90)
1.5707963267948966
```

The inputs can be real-valued.

```
>>> sc.radian(1.5, 0, 0)
0.02617993877991494
>>> sc.radian(1, 30, 0)
0.02617993877991494
```

scipy.special.cosdg

scipy.special.**cosdg**(*x*, *out=None*) **= <ufunc 'cosdg'>**

Cosine of the angle *x* given in degrees.

Parameters

x	[array_like] Angle, given in degrees.
out	[ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Cosine of the input.

See also:

sindg, **tandg**, **cotdg**

Examples

```
>>> import scipy.special as sc
```

It is more accurate than using cosine directly.

```
>>> x = 90 + 180 * np.arange(3)
>>> sc.cosdg(x)
array([-0.,  0., -0.])
>>> np.cos(x * np.pi / 180)
array([ 6.1232340e-17, -1.8369702e-16,  3.0616170e-16])
```

scipy.special.sindg

scipy.special.**sindg**(*x*, *out=None*) **= <ufunc 'sindg'>**

Sine of the angle *x* given in degrees.

Parameters

x	[array_like] Angle, given in degrees.
out	[ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Sine at the input.

See also:

cosdg, **tandg**, **cotdg**

Examples

```
>>> import scipy.special as sc
```

It is more accurate than using sine directly.

```
>>> x = 180 * np.arange(3)
>>> sc.sindg(x)
array([ 0., -0.,  0.])
>>> np.sin(x * np.pi / 180)
array([ 0.0000000e+00,  1.2246468e-16, -2.4492936e-16])
```

scipy.special.tandg

scipy.special.**tandg**(*x*, *out=None*) **= <ufunc 'tandg'>**
Tangent of angle *x* given in degrees.

Parameters

x [array_like] Angle, given in degrees.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Tangent at the input.

See also:

sindg, **cosdg**, **cotdg**

Examples

```
>>> import scipy.special as sc
```

It is more accurate than using tangent directly.

```
>>> x = 180 * np.arange(3)
>>> sc.tandg(x)
array([0., 0., 0.])
>>> np.tan(x * np.pi / 180)
array([ 0.0000000e+00, -1.2246468e-16, -2.4492936e-16])
```

scipy.special.cotdg

scipy.special.**cotdg**(*x*, *out=None*) **= <ufunc 'cotdg'>**

Cotangent of the angle *x* given in degrees.

Parameters

x [array_like] Angle, given in degrees.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Cotangent at the input.

See also:

sindg, **cosdg**, **tandg**

Examples

```
>>> import scipy.special as sc
```

It is more accurate than using cotangent directly.

```
>>> x = 90 + 180 * np.arange(3)
>>> sc.cotdg(x)
array([0., 0., 0.])
>>> 1 / np.tan(x * np.pi / 180)
array([6.1232340e-17, 1.8369702e-16, 3.0616170e-16])
```

scipy.special.log1p

scipy.special.**log1p**(*x*, *out=None*) **= <ufunc 'log1p'>**

Calculates log(1 + x) for use when *x* is near zero.

Parameters

x [array_like] Real or complex valued input.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of `log(1 + x)`.

See also:

expm1, **cosm1**

Examples

```
>>> import scipy.special as sc
```

It is more accurate than using `log(1 + x)` directly for `x` near 0. Note that in the below example `1 + 1e-17 == 1` to double precision.

```
>>> sc.log1p(1e-17)
1e-17
>>> np.log(1 + 1e-17)
0.0
```

scipy.special.expm1

scipy.special.**expm1**(*x*) **= <ufunc 'expm1'>**

Compute `exp(x) - 1`.

When *x* is near zero, `exp(x)` is near 1, so the numerical calculation of `exp(x) - 1` can suffer from catastrophic loss of precision. `expm1(x)` is implemented to avoid the loss of precision that occurs when *x* is near zero.

Parameters

x [array_like] *x* must contain real numbers.

Returns

float `exp(x) - 1` computed element-wise.

Examples

```
>>> from scipy.special import expm1
```

```
>>> expm1(1.0)
1.7182818284590451
>>> expm1([-0.2, -0.1, 0, 0.1, 0.2])
array([-0.18126925, -0.09516258,  0.        ,  0.10517092,  0.22140276])
```

The exact value of `exp(7.5e-13) - 1` is:

```
7.50000000000281250000000070312500000001318...*10**-13.
```

Here is what `expm1(7.5e-13)` gives:

```
>>> expm1(7.5e-13)
7.5000000000028135e-13
```

Compare that to `exp(7.5e-13) - 1`, where the subtraction results in a "catastrophic" loss of precision:

```
>>> np.exp(7.5e-13) - 1
7.5006667543675576e-13
```

scipy.special.cosm1

scipy.special.**cosm1**(*x*, *out=None*) **= <ufunc 'cosm1'>**

cos(x) - 1 for use when *x* is near zero.

Parameters

x [array_like] Real valued argument.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
Values of `cos(x) - 1`.

See also:

expm1, **log1p**

Examples

```
>>> import scipy.special as sc
```

It is more accurate than computing `cos(x) - 1` directly for `x` around 0.

```
>>> x = 1e-30
>>> np.cos(x) - 1
0.0
>>> sc.cosm1(x)
-5.0000000000000005e-61
```

scipy.special.round

scipy.special.**round**(*x*, *out=None*) **= <ufunc 'round'>**

Round to the nearest integer.

Returns the nearest integer to *x*. If *x* ends in 0.5 exactly, the nearest even integer is chosen.

Parameters

x [array_like] Real valued input.
out [ndarray, optional] Optional output array for the function results.

Returns

scalar or ndarray
The nearest integers to the elements of *x*. The result is of floating type, not integer type.

Examples

```
>>> import scipy.special as sc
```

It rounds to even.

```
>>> sc.round([0.5, 1.5])
array([0., 2.])
```

scipy.special.xlogy

scipy.special.**xlogy**(*x*, *y*) **= <ufunc 'xlogy'>**

Compute `x*log(y)` so that the result is 0 if `x = 0`.

Parameters

x	[array_like] Multiplier
y	[array_like] Argument

Returns

z	[array_like] Computed x*log(y)

Notes

New in version 0.13.0.

scipy.special.xlog1py

scipy.special.**xlog1py**(*x*, *y*) **= <ufunc 'xlog1py'>**

Compute `x*log1p(y)` so that the result is 0 if `x = 0`.

Parameters

x	[array_like] Multiplier
y	[array_like] Argument

Returns

z	[array_like] Computed x*log1p(y)

Notes

New in version 0.13.0.

scipy.special.logsumexp

scipy.special.**logsumexp**(*a*, *axis=None*, *b=None*, *keepdims=False*, *return_sign=False*)

Compute the log of the sum of exponentials of input elements.

Parameters

a [array_like] Input array.

axis [None or int or tuple of ints, optional] Axis or axes over which the sum is taken. By default *axis* is None, and all elements are summed.
New in version 0.11.0.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original array.
New in version 0.15.0.

b [array-like, optional] Scaling factor for exp(a) must be of the same shape as a or broadcastable to a. These values may be negative in order to implement subtraction.
New in version 0.12.0.

return_sign [bool, optional] If this is set to True, the result will be a pair containing sign information; if False, results that are negative will be returned as NaN. Default is False (no sign information).
New in version 0.16.0.

Returns

res [ndarray] The result, `np.log(np.sum(np.exp(a)))` calculated in a numerically more stable way. If *b* is given then `np.log(np.sum(b*np.exp(a)))` is returned.

sgn [ndarray] If return_sign is True, this will be an array of floating-point numbers matching res and +1, 0, or -1 depending on the sign of the result. If False, only one result is returned.

See also:

numpy.logaddexp*, *numpy.logaddexp2

Notes

NumPy has a logaddexp function which is very similar to *logsumexp*, but only handles two arguments. *logaddexp.reduce* is similar to this function, but may be less stable.

Examples

```
>>> from scipy.special import logsumexp
>>> a = np.arange(10)
>>> np.log(np.sum(np.exp(a)))
9.4586297444267107
>>> logsumexp(a)
9.4586297444267107
```

With weights

```
>>> a = np.arange(10)
>>> b = np.arange(10, 0, -1)
>>> logsumexp(a, b=b)
9.9170178533034665
```

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```
>>> np.log(np.sum(b*np.exp(a)))
9.9170178533034647
```

Returning a sign flag

```
>>> logsumexp([1,2],b=[1,-1],return_sign=True)
(1.5413248546129181, -1.0)
```

Notice that *logsumexp* does not directly support masked arrays. To use it on a masked array, convert the mask into zero weights:

```
>>> a = np.ma.array([np.log(2), 2, np.log(3)],
...                 mask=[False, True, False])
>>> b = (~a.mask).astype(int)
>>> logsumexp(a.data, b=b), np.log(5)
1.6094379124341005, 1.6094379124341005
```

scipy.special.exprel

scipy.special.**exprel**(*x*) **= <ufunc 'exprel'>**

Relative error exponential, `(exp(x) - 1)/x`.

When *x* is near zero, `exp(x)` is near 1, so the numerical calculation of `exp(x) - 1` can suffer from catastrophic loss of precision. `exprel(x)` is implemented to avoid the loss of precision that occurs when *x* is near zero.

Parameters

x [ndarray] Input array. *x* must contain real numbers.

Returns

float `(exp(x) - 1)/x`, computed element-wise.

See also:

expm1

Notes

New in version 0.17.0.

Examples

```
>>> from scipy.special import exprel
```

```
>>> exprel(0.01)
1.0050167084168056
>>> exprel([-0.25, -0.1, 0, 0.1, 0.25])
array([ 0.88479687,  0.95162582,  1.        ,  1.05170918,  1.13610167])
```

Compare `exprel(5e-9)` to the naive calculation. The exact value is `1.0000000250000000416...`.

```
>>> exprel(5e-9)
1.0000000025
```

```
>>> (np.exp(5e-9) - 1)/5e-9
0.99999999392252903
```

scipy.special.sinc

scipy.special.**sinc**(x)

Return the normalized sinc function.

The sinc function is $\sin(\pi x)/(\pi x)$.

Note: Note the normalization factor of `pi` used in the definition. This is the most commonly used definition in signal processing. Use `sinc(x / np.pi)` to obtain the unnormalized sinc function $\sin(x)/(x)$ that is more common in mathematics.

Parameters

x [ndarray] Array (possibly multi-dimensional) of values for which to to calculate `sinc(x)`.

Returns

out [ndarray] `sinc(x)`, which has the same shape as the input.

Notes

`sinc(0)` is the limit value 1.

The name sinc is short for "sine cardinal" or "sinus cardinalis".

The sinc function is used in various signal processing applications, including in anti-aliasing, in the construction of a Lanczos resampling filter, and in interpolation.

For bandlimited interpolation of discrete-time signals, the ideal interpolation kernel is proportional to the sinc function.

References

[1], [2]

Examples

```
>>> import matplotlib.pyplot as plt
>>> x = np.linspace(-4, 4, 41)
>>> np.sinc(x)
 array([-3.89804309e-17,  -4.92362781e-02,  -8.40918587e-02, # may vary
        -8.90384387e-02,  -5.84680802e-02,   3.89804309e-17,
         6.68206631e-02,   1.16434881e-01,   1.26137788e-01,
         8.50444803e-02,  -3.89804309e-17,  -1.03943254e-01,
```

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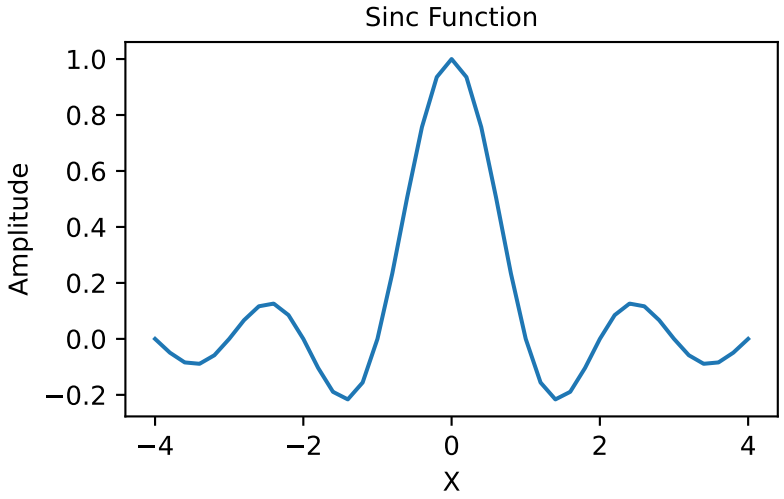
```
        -1.89206682e-01,  -2.16236208e-01,  -1.55914881e-01,
         3.89804309e-17,   2.33872321e-01,   5.04551152e-01,
         7.56826729e-01,   9.35489284e-01,   1.00000000e+00,
         9.35489284e-01,   7.56826729e-01,   5.04551152e-01,
         2.33872321e-01,   3.89804309e-17,  -1.55914881e-01,
        -2.16236208e-01,  -1.89206682e-01,  -1.03943254e-01,
        -3.89804309e-17,   8.50444803e-02,   1.26137788e-01,
         1.16434881e-01,   6.68206631e-02,   3.89804309e-17,
        -5.84680802e-02,  -8.90384387e-02,  -8.40918587e-02,
        -4.92362781e-02,  -3.89804309e-17])
```

```
>>> plt.plot(x, np.sinc(x))
[<matplotlib.lines.Line2D object at 0x...>]
>>> plt.title("Sinc Function")
Text(0.5, 1.0, 'Sinc Function')
>>> plt.ylabel("Amplitude")
Text(0, 0.5, 'Amplitude')
>>> plt.xlabel("X")
Text(0.5, 0, 'X')
>>> plt.show()
```



3.3.29 Statistical functions (`scipy.stats`)

This module contains a large number of probability distributions, summary and frequency statistics, correlation functions and statistical tests, masked statistics, kernel density estimation, quasi-Monte Carlo functionality, and more.

Statistics is a very large area, and there are topics that are out of scope for SciPy and are covered by other packages. Some of the most important ones are:

- statsmodels: regression, linear models, time series analysis, extensions to topics also covered by `scipy.stats`.
- Pandas: tabular data, time series functionality, interfaces to other statistical languages.
- PyMC3: Bayesian statistical modeling, probabilistic machine learning.

- scikit-learn: classification, regression, model selection.
- Seaborn: statistical data visualization.
- rpy2: Python to R bridge.

Probability distributions

Each univariate distribution is an instance of a subclass of *rv_continuous* (*rv_discrete* for discrete distributions):

rv_continuous([momtype, a, b, xtol, …])	A generic continuous random variable class meant for subclassing.
rv_discrete([a, b, name, badvalue, …])	A generic discrete random variable class meant for subclassing.
rv_histogram(histogram, *args, **kwargs)	Generates a distribution given by a histogram.

scipy.stats.rv_continuous

class scipy.stats.**rv_continuous**(*momtype=1*, *a=None*, *b=None*, *xtol=1e-14*, *badvalue=None*, *name=None*, *longname=None*, *shapes=None*, *extradoc=None*, *seed=None*)

A generic continuous random variable class meant for subclassing.

rv_continuous is a base class to construct specific distribution classes and instances for continuous random variables. It cannot be used directly as a distribution.

Parameters

momtype [int, optional] The type of generic moment calculation to use: 0 for pdf, 1 (default) for ppf.

a [float, optional] Lower bound of the support of the distribution, default is minus infinity.

b [float, optional] Upper bound of the support of the distribution, default is plus infinity.

xtol [float, optional] The tolerance for fixed point calculation for generic ppf.

badvalue [float, optional] The value in a result arrays that indicates a value that for which some argument restriction is violated, default is np.nan.

name [str, optional] The name of the instance. This string is used to construct the default example for distributions.

longname [str, optional] This string is used as part of the first line of the docstring returned when a subclass has no docstring of its own. Note: *longname* exists for backwards compatibility, do not use for new subclasses.

shapes [str, optional] The shape of the distribution. For example `"m, n"` for a distribution that takes two integers as the two shape arguments for all its methods. If not provided, shape parameters will be inferred from the signature of the private methods, `_pdf` and `_cdf` of the instance.

extradoc [str, optional, deprecated] This string is used as the last part of the docstring returned when a subclass has no docstring of its own. Note: *extradoc* exists for backwards compatibility, do not use for new subclasses.

seed [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Notes

Public methods of an instance of a distribution class (e.g., pdf, cdf) check their arguments and pass valid arguments to private, computational methods (_pdf, _cdf). For pdf(x), x is valid if it is within the support of the distribution. Whether a shape parameter is valid is decided by an _argcheck method (which defaults to checking that its arguments are strictly positive.)

Subclassing

New random variables can be defined by subclassing the *rv_continuous* class and re-defining at least the _pdf or the _cdf method (normalized to location 0 and scale 1).

If positive argument checking is not correct for your RV then you will also need to re-define the _argcheck method.

For most of the scipy.stats distributions, the support interval doesn't depend on the shape parameters. x being in the support interval is equivalent to self.a <= x <= self.b. If either of the endpoints of the support do depend on the shape parameters, then i) the distribution must implement the _get_support method; and ii) those dependent endpoints must be omitted from the distribution's call to the rv_continuous initializer.

Correct, but potentially slow defaults exist for the remaining methods but for speed and/or accuracy you can override:

```
_logpdf, _cdf, _logcdf, _ppf, _rvs, _isf, _sf, _logsf
```

The default method _rvs relies on the inverse of the cdf, _ppf, applied to a uniform random variate. In order to generate random variates efficiently, either the default _ppf needs to be overwritten (e.g. if the inverse cdf can expressed in an explicit form) or a sampling method needs to be implemented in a custom _rvs method.

If possible, you should override _isf, _sf or _logsf. The main reason would be to improve numerical accuracy: for example, the survival function _sf is computed as 1 - _cdf which can result in loss of precision if _cdf(x) is close to one.

Methods that can be overwritten by subclasses

```
_rvs
_pdf
_cdf
_sf
_ppf
_isf
_stats
_munp
_entropy
_argcheck
_get_support
```

There are additional (internal and private) generic methods that can be useful for cross-checking and for debugging, but might work in all cases when directly called.

A note on shapes: subclasses need not specify them explicitly. In this case, *shapes* will be automatically deduced from the signatures of the overridden methods (*pdf*, *cdf* etc). If, for some reason, you prefer to avoid relying on introspection, you can specify shapes explicitly as an argument to the instance constructor.

Frozen Distributions

Normally, you must provide shape parameters (and, optionally, location and scale parameters to each call of a method of a distribution.

Alternatively, the object may be called (as a function) to fix the shape, location, and scale parameters returning a "frozen" continuous RV object:

rv = generic(<shape(s)>, loc=0, scale=1)

rv_frozen object with the same methods but holding the given shape, location, and scale fixed

Statistics

Statistics are computed using numerical integration by default. For speed you can redefine this using `_stats`:

- take shape parameters and return mu, mu2, g1, g2
- If you can't compute one of these, return it as None
- Can also be defined with a keyword argument `moments`, which is a string composed of "m", "v", "s", and/or "k". Only the components appearing in string should be computed and returned in the order "m", "v", "s", or "k" with missing values returned as None.

Alternatively, you can override `_munp`, which takes `n` and shape parameters and returns the n-th non-central moment of the distribution.

Examples

To create a new Gaussian distribution, we would do the following:

```
>>> from scipy.stats import rv_continuous
>>> class gaussian_gen(rv_continuous):
...     "Gaussian distribution"
...     def _pdf(self, x):
...         return np.exp(-x**2 / 2.) / np.sqrt(2.0 * np.pi)
>>> gaussian = gaussian_gen(name='gaussian')
```

`scipy.stats` distributions are *instances*, so here we subclass *rv_continuous* and create an instance. With this, we now have a fully functional distribution with all relevant methods automagically generated by the framework.

Note that above we defined a standard normal distribution, with zero mean and unit variance. Shifting and scaling of the distribution can be done by using `loc` and `scale` parameters: `gaussian.pdf(x, loc, scale)` essentially computes `y = (x - loc) / scale` and `gaussian._pdf(y) / scale`.

Attributes

random_state
: Get or set the generator object for generating random variates.

Methods

rvs(*args, **kwds)	Random variates of given type.
pdf(x, *args, **kwds)	Probability density function at x of the given RV.
logpdf(x, *args, **kwds)	Log of the probability density function at x of the given RV.
cdf(x, *args, **kwds)	Cumulative distribution function of the given RV.
logcdf(x, *args, **kwds)	Log of the cumulative distribution function at x of the given RV.
sf(x, *args, **kwds)	Survival function (1 - *cdf*) at x of the given RV.
logsf(x, *args, **kwds)	Log of the survival function of the given RV.

continues on next page

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ppf(q, *args, **kwds)	Percent point function (inverse of *cdf*) at q of the given RV.
isf(q, *args, **kwds)	Inverse survival function (inverse of *sf*) at q of the given RV.
moment(n, *args, **kwds)	n-th order non-central moment of distribution.
stats(*args, **kwds)	Some statistics of the given RV.
entropy(*args, **kwds)	Differential entropy of the RV.
expect([func, args, loc, scale, lb, ub, …])	Calculate expected value of a function with respect to the distribution by numerical integration.
median(*args, **kwds)	Median of the distribution.
mean(*args, **kwds)	Mean of the distribution.
std(*args, **kwds)	Standard deviation of the distribution.
var(*args, **kwds)	Variance of the distribution.
interval(alpha, *args, **kwds)	Confidence interval with equal areas around the median.
__call__(*args, **kwds)	Freeze the distribution for the given arguments.
fit(data, *args, **kwds)	Return estimates of shape (if applicable), location, and scale parameters from data.
fit_loc_scale(data, *args)	Estimate loc and scale parameters from data using 1st and 2nd moments.
nnlf(theta, x)	Negative loglikelihood function.
support(*args, **kwargs)	Support of the distribution.

scipy.stats.rv_continuous.rvs

rv_continuous.**rvs**(**args*, ***kwds*)

Random variates of given type.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc
: [array_like, optional] Location parameter (default=0).

scale
: [array_like, optional] Scale parameter (default=1).

size
: [int or tuple of ints, optional] Defining number of random variates (default is 1).

random_state
: [{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Returns

rvs
: [ndarray or scalar] Random variates of given *size*.

scipy.stats.rv_continuous.pdf

rv_continuous.**pdf**(*x*, **args*, ***kwds*)
Probability density function at x of the given RV.

Parameters

x [array_like] quantiles
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

pdf [ndarray] Probability density function evaluated at x

scipy.stats.rv_continuous.logpdf

rv_continuous.**logpdf**(*x*, **args*, ***kwds*)
Log of the probability density function at x of the given RV.

This uses a more numerically accurate calculation if available.

Parameters

x [array_like] quantiles
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

logpdf [array_like] Log of the probability density function evaluated at x

scipy.stats.rv_continuous.cdf

rv_continuous.**cdf**(*x*, **args*, ***kwds*)
Cumulative distribution function of the given RV.

Parameters

x [array_like] quantiles
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

cdf [ndarray] Cumulative distribution function evaluated at *x*

scipy.stats.rv_continuous.logcdf

rv_continuous.**logcdf**(*x*, **args*, ***kwds*)

Log of the cumulative distribution function at x of the given RV.

Parameters

x [array_like] quantiles

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

logcdf [array_like] Log of the cumulative distribution function evaluated at x

scipy.stats.rv_continuous.sf

rv_continuous.**sf**(*x*, **args*, ***kwds*)

Survival function (1 - *cdf*) at x of the given RV.

Parameters

x [array_like] quantiles

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

sf [array_like] Survival function evaluated at x

scipy.stats.rv_continuous.logsf

rv_continuous.**logsf**(*x*, **args*, ***kwds*)

Log of the survival function of the given RV.

Returns the log of the "survival function," defined as (1 - *cdf*), evaluated at *x*.

Parameters

x [array_like] quantiles

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

logsf [ndarray] Log of the survival function evaluated at *x*.

scipy.stats.rv_continuous.ppf

rv_continuous.**ppf**(*q*, **args*, ***kwds*)
Percent point function (inverse of *cdf*) at q of the given RV.

Parameters

q [array_like] lower tail probability
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

x [array_like] quantile corresponding to the lower tail probability q.

scipy.stats.rv_continuous.isf

rv_continuous.**isf**(*q*, **args*, ***kwds*)
Inverse survival function (inverse of *sf*) at q of the given RV.

Parameters

q [array_like] upper tail probability
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

x [ndarray or scalar] Quantile corresponding to the upper tail probability q.

scipy.stats.rv_continuous.moment

rv_continuous.**moment**(*n*, **args*, ***kwds*)
n-th order non-central moment of distribution.

Parameters

n [int, n >= 1] Order of moment.
arg1, arg2, arg3,… [float] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

scipy.stats.rv_continuous.stats

rv_continuous.**stats**(**args*, ***kwds*)

Some statistics of the given RV.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc
: [array_like, optional] location parameter (default=0)

scale
: [array_like, optional (continuous RVs only)] scale parameter (default=1)

moments
: [str, optional] composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default is 'mv')

Returns

stats
: [sequence] of requested moments.

scipy.stats.rv_continuous.entropy

rv_continuous.**entropy**(**args*, ***kwds*)

Differential entropy of the RV.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc
: [array_like, optional] Location parameter (default=0).

scale
: [array_like, optional (continuous distributions only).] Scale parameter (default=1).

Notes

Entropy is defined base *e*:

```
>>> drv = rv_discrete(values=((0, 1), (0.5, 0.5)))
>>> np.allclose(drv.entropy(), np.log(2.0))
True
```

scipy.stats.rv_continuous.expect

rv_continuous.**expect**(*func=None*, *args=()*, *loc=0*, *scale=1*, *lb=None*, *ub=None*, *conditional=False*, ***kwds*)

Calculate expected value of a function with respect to the distribution by numerical integration.

The expected value of a function `f(x)` with respect to a distribution `dist` is defined as:

```
        ub
E[f(x)] = Integral(f(x) * dist.pdf(x)),
        lb
```

where `ub` and `lb` are arguments and `x` has the `dist.pdf(x)` distribution. If the bounds `lb` and `ub` correspond to the support of the distribution, e.g. `[-inf, inf]` in the default case, then the integral is the unrestricted expectation of `f(x)`. Also, the function `f(x)` may be defined such that `f(x)` is `0` outside a finite interval in which case the expectation is calculated within the finite range `[lb, ub]`.

Parameters

func [callable, optional] Function for which integral is calculated. Takes only one argument. The default is the identity mapping f(x) = x.

args [tuple, optional] Shape parameters of the distribution.

loc [float, optional] Location parameter (default=0).

scale [float, optional] Scale parameter (default=1).

lb, ub [scalar, optional] Lower and upper bound for integration. Default is set to the support of the distribution.

conditional [bool, optional] If True, the integral is corrected by the conditional probability of the integration interval. The return value is the expectation of the function, conditional on being in the given interval. Default is False.

Additional keyword arguments are passed to the integration routine.

Returns

expect [float] The calculated expected value.

Notes

The integration behavior of this function is inherited from *scipy.integrate.quad*. Neither this function nor *scipy.integrate.quad* can verify whether the integral exists or is finite. For example `cauchy(0).mean()` returns `np.nan` and `cauchy(0).expect()` returns `0.0`.

The function is not vectorized.

Examples

To understand the effect of the bounds of integration consider

```
>>> from scipy.stats import expon
>>> expon(1).expect(lambda x: 1, lb=0.0, ub=2.0)
0.6321205588285578
```

This is close to

```
>>> expon(1).cdf(2.0) - expon(1).cdf(0.0)
0.6321205588285577
```

If `conditional=True`

```
>>> expon(1).expect(lambda x: 1, lb=0.0, ub=2.0, conditional=True)
1.0000000000000002
```

The slight deviation from 1 is due to numerical integration.

scipy.stats.rv_continuous.median

rv_continuous.**median**(**args*, ***kwds*)

Median of the distribution.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc
: [array_like, optional] Location parameter, Default is 0.

scale
: [array_like, optional] Scale parameter, Default is 1.

Returns

median
: [float] The median of the distribution.

See also:

rv_discrete.ppf
: Inverse of the CDF

scipy.stats.rv_continuous.mean

rv_continuous.**mean**(**args*, ***kwds*)

Mean of the distribution.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc
: [array_like, optional] location parameter (default=0)

scale
: [array_like, optional] scale parameter (default=1)

Returns

mean
: [float] the mean of the distribution

scipy.stats.rv_continuous.std

rv_continuous.**std**(**args*, ***kwds*)

Standard deviation of the distribution.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc
: [array_like, optional] location parameter (default=0)

scale
: [array_like, optional] scale parameter (default=1)

Returns

std
: [float] standard deviation of the distribution

scipy.stats.rv_continuous.var

rv_continuous.**var**(**args*, ***kwds*)
Variance of the distribution.

Parameters

arg1, arg2, arg3,…
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

var [float] the variance of the distribution

scipy.stats.rv_continuous.interval

rv_continuous.**interval**(*alpha*, **args*, ***kwds*)
Confidence interval with equal areas around the median.

Parameters

alpha [array_like of float] Probability that an rv will be drawn from the returned range. Each value should be in the range [0, 1].
arg1, arg2, …
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] location parameter, Default is 0.
scale [array_like, optional] scale parameter, Default is 1.

Returns

a, b [ndarray of float] end-points of range that contain `100 * alpha %` of the rv's possible values.

scipy.stats.rv_continuous.__call__

rv_continuous.**__call__**(**args*, ***kwds*)
Freeze the distribution for the given arguments.

Parameters

arg1, arg2, arg3,…
[array_like] The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

Returns

rv_frozen [rv_frozen instance] The frozen distribution.

scipy.stats.rv_continuous.fit

rv_continuous.**fit**(*data*, **args*, ***kwds*)

Return estimates of shape (if applicable), location, and scale parameters from data. The default estimation method is Maximum Likelihood Estimation (MLE), but Method of Moments (MM) is also available.

Starting estimates for the fit are given by input arguments; for any arguments not provided with starting estimates, `self._fitstart(data)` is called to generate such.

One can hold some parameters fixed to specific values by passing in keyword arguments `f0`, `f1`, …, `fn` (for shape parameters) and `floc` and `fscale` (for location and scale parameters, respectively).

Parameters

data [array_like] Data to use in estimating the distribution parameters.

arg1, arg2, arg3,…
[floats, optional] Starting value(s) for any shape-characterizing arguments (those not provided will be determined by a call to `_fitstart(data)`). No default value.

kwds [floats, optional]
- *loc*: initial guess of the distribution's location parameter.
- *scale*: initial guess of the distribution's scale parameter.

Special keyword arguments are recognized as holding certain parameters fixed:
- f0…fn : hold respective shape parameters fixed. Alternatively, shape parameters to fix can be specified by name. For example, if `self.shapes == "a, b"`, `fa` and `fix_a` are equivalent to `f0`, and `fb` and `fix_b` are equivalent to `f1`.
- floc : hold location parameter fixed to specified value.
- fscale : hold scale parameter fixed to specified value.
- optimizer : The optimizer to use. The optimizer must take `func`, and starting position as the first two arguments, plus `args` (for extra arguments to pass to the function to be optimized) and `disp=0` to suppress output as keyword arguments.
- method : The method to use. The default is "MLE" (Maximum Likelihood Estimate); "MM" (Method of Moments) is also available.

Returns

parameter_tuple
[tuple of floats] Estimates for any shape parameters (if applicable), followed by those for location and scale. For most random variables, shape statistics will be returned, but there are exceptions (e.g. `norm`).

Notes

With `method="MLE"` (default), the fit is computed by minimizing the negative log-likelihood function. A large, finite penalty (rather than infinite negative log-likelihood) is applied for observations beyond the support of the distribution.

With `method="MM"`, the fit is computed by minimizing the L2 norm of the relative errors between the first *k* raw (about zero) data moments and the corresponding distribution moments, where *k* is the number of non-fixed parameters. More precisely, the objective function is:

```
(((data_moments - dist_moments)
  / np.maximum(np.abs(data_moments), 1e-8))**2).sum()
```

where the constant `1e-8` avoids division by zero in case of vanishing data moments. Typically, this error norm can be reduced to zero. Note that the standard method of moments can produce parameters for which some data are outside the support of the fitted distribution; this implementation does nothing to prevent this.

For either method, the returned answer is not guaranteed to be globally optimal; it may only be locally optimal, or the optimization may fail altogether. If the data contain any of `np.nan`, `np.inf`, or `-np.inf`, the *fit* method will raise a `RuntimeError`.

Examples

Generate some data to fit: draw random variates from the *beta* distribution

```
>>> from scipy.stats import beta
>>> a, b = 1., 2.
>>> x = beta.rvs(a, b, size=1000)
```

Now we can fit all four parameters (`a`, `b`, `loc` and `scale`):

```
>>> a1, b1, loc1, scale1 = beta.fit(x)
```

We can also use some prior knowledge about the dataset: let's keep `loc` and `scale` fixed:

```
>>> a1, b1, loc1, scale1 = beta.fit(x, floc=0, fscale=1)
>>> loc1, scale1
(0, 1)
```

We can also keep shape parameters fixed by using `f`-keywords. To keep the zero-th shape parameter `a` equal 1, use `f0=1` or, equivalently, `fa=1`:

```
>>> a1, b1, loc1, scale1 = beta.fit(x, fa=1, floc=0, fscale=1)
>>> a1
1
```

Not all distributions return estimates for the shape parameters. `norm` for example just returns estimates for location and scale:

```
>>> from scipy.stats import norm
>>> x = norm.rvs(a, b, size=1000, random_state=123)
>>> loc1, scale1 = norm.fit(x)
>>> loc1, scale1
(0.92087172783841631, 2.0015750750324668)
```

scipy.stats.rv_continuous.fit_loc_scale

`rv_continuous.`**`fit_loc_scale`**(*data*, **args*)

Estimate loc and scale parameters from data using 1st and 2nd moments.

Parameters

data [array_like] Data to fit.

arg1, arg2, arg3,... [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

Returns

Lhat [float] Estimated location parameter for the data.

Shat [float] Estimated scale parameter for the data.

scipy.stats.rv_continuous.nnlf

rv_continuous.**nnlf**(*theta*, *x*)
Negative loglikelihood function.

Notes

This is `-sum(log pdf(x, theta), axis=0)` where *theta* are the parameters (including loc and scale).

scipy.stats.rv_continuous.support

rv_continuous.**support**(**args*, ***kwargs*)
Support of the distribution.

Parameters

arg1, arg2, …
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] location parameter, Default is 0.
scale [array_like, optional] scale parameter, Default is 1.

Returns

a, b [array_like] end-points of the distribution's support.

scipy.stats.rv_discrete

class scipy.stats.**rv_discrete**(*a=0*, *b=inf*, *name=None*, *badvalue=None*, *moment_tol=1e-08*, *values=None*, *inc=1*, *longname=None*, *shapes=None*, *extradoc=None*, *seed=None*)
A generic discrete random variable class meant for subclassing.

rv_discrete is a base class to construct specific distribution classes and instances for discrete random variables. It can also be used to construct an arbitrary distribution defined by a list of support points and corresponding probabilities.

Parameters

a [float, optional] Lower bound of the support of the distribution, default: 0
b [float, optional] Upper bound of the support of the distribution, default: plus infinity
moment_tol
[float, optional] The tolerance for the generic calculation of moments.
values [tuple of two array_like, optional] `(xk, pk)` where `xk` are integers and `pk` are the non-zero probabilities between 0 and 1 with `sum(pk) = 1`. `xk` and `pk` must have the same shape.
inc [integer, optional] Increment for the support of the distribution. Default is 1. (other values have not been tested)
badvalue [float, optional] The value in a result arrays that indicates a value that for which some argument restriction is violated, default is np.nan.
name [str, optional] The name of the instance. This string is used to construct the default example for distributions.
longname [str, optional] This string is used as part of the first line of the docstring returned when a subclass has no docstring of its own. Note: *longname* exists for backwards compatibility, do not use for new subclasses.

shapes [str, optional] The shape of the distribution. For example "m, n" for a distribution that takes two integers as the two shape arguments for all its methods If not provided, shape parameters will be inferred from the signatures of the private methods, `_pmf` and `_cdf` of the instance.

extradoc [str, optional] This string is used as the last part of the docstring returned when a subclass has no docstring of its own. Note: *extradoc* exists for backwards compatibility, do not use for new subclasses.

seed [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Notes

This class is similar to *rv_continuous*. Whether a shape parameter is valid is decided by an `_argcheck` method (which defaults to checking that its arguments are strictly positive.) The main differences are:

- the support of the distribution is a set of integers
- instead of the probability density function, `pdf` (and the corresponding private `_pdf`), this class defines the *probability mass function*, *pmf* (and the corresponding private `_pmf`.)
- scale parameter is not defined.

To create a new discrete distribution, we would do the following:

```
>>> from scipy.stats import rv_discrete
>>> class poisson_gen(rv_discrete):
...     "Poisson distribution"
...     def _pmf(self, k, mu):
...         return exp(-mu) * mu**k / factorial(k)
```

and create an instance:

```
>>> poisson = poisson_gen(name="poisson")
```

Note that above we defined the Poisson distribution in the standard form. Shifting the distribution can be done by providing the `loc` parameter to the methods of the instance. For example, `poisson.pmf(x, mu, loc)` delegates the work to `poisson._pmf(x-loc, mu)`.

Discrete distributions from a list of probabilities

Alternatively, you can construct an arbitrary discrete rv defined on a finite set of values `xk` with `Prob{X=xk} = pk` by using the `values` keyword argument to the *rv_discrete* constructor.

Examples

Custom made discrete distribution:

```
>>> from scipy import stats
>>> xk = np.arange(7)
>>> pk = (0.1, 0.2, 0.3, 0.1, 0.1, 0.0, 0.2)
>>> custm = stats.rv_discrete(name='custm', values=(xk, pk))
>>>
>>> import matplotlib.pyplot as plt
```

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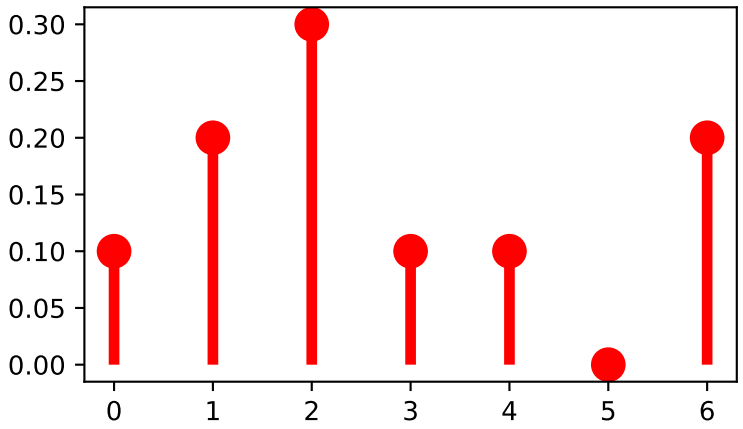
```
>>> fig, ax = plt.subplots(1, 1)
>>> ax.plot(xk, custm.pmf(xk), 'ro', ms=12, mec='r')
>>> ax.vlines(xk, 0, custm.pmf(xk), colors='r', lw=4)
>>> plt.show()
```



Random number generation:

```
>>> R = custm.rvs(size=100)
```

Attributes

random_state
Get or set the generator object for generating random variates.

Methods

rvs(*args, **kwargs)	Random variates of given type.
pmf(k, *args, **kwds)	Probability mass function at k of the given RV.
logpmf(k, *args, **kwds)	Log of the probability mass function at k of the given RV.
cdf(k, *args, **kwds)	Cumulative distribution function of the given RV.
logcdf(k, *args, **kwds)	Log of the cumulative distribution function at k of the given RV.
sf(k, *args, **kwds)	Survival function (1 - *cdf*) at k of the given RV.
logsf(k, *args, **kwds)	Log of the survival function of the given RV.
ppf(q, *args, **kwds)	Percent point function (inverse of *cdf*) at q of the given RV.
isf(q, *args, **kwds)	Inverse survival function (inverse of *sf*) at q of the given RV.
moment(n, *args, **kwds)	n-th order non-central moment of distribution.
stats(*args, **kwds)	Some statistics of the given RV.

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Table 258 – continued from previous page

entropy(*args, **kwds)	Differential entropy of the RV.
expect([func, args, loc, lb, ub, …])	Calculate expected value of a function with respect to the distribution for discrete distribution by numerical summation.
median(*args, **kwds)	Median of the distribution.
mean(*args, **kwds)	Mean of the distribution.
std(*args, **kwds)	Standard deviation of the distribution.
var(*args, **kwds)	Variance of the distribution.
interval(alpha, *args, **kwds)	Confidence interval with equal areas around the median.
__call__(*args, **kwds)	Freeze the distribution for the given arguments.
support(*args, **kwargs)	Support of the distribution.

scipy.stats.rv_discrete.rvs

rv_discrete.**rvs**(**args*, ***kwargs*)

Random variates of given type.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc
: [array_like, optional] Location parameter (default=0).

size
: [int or tuple of ints, optional] Defining number of random variates (Default is 1). Note that *size* has to be given as keyword, not as positional argument.

random_state
: [{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Returns

rvs
: [ndarray or scalar] Random variates of given *size*.

scipy.stats.rv_discrete.pmf

rv_discrete.**pmf**(*k*, **args*, ***kwds*)

Probability mass function at k of the given RV.

Parameters

k
: [array_like] Quantiles.

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc
: [array_like, optional] Location parameter (default=0).

Returns

pmf
: [array_like] Probability mass function evaluated at k

scipy.stats.rv_discrete.logpmf

rv_discrete.**logpmf**(*k*, **args*, ***kwds*)

Log of the probability mass function at k of the given RV.

Parameters

k [array_like] Quantiles.

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc [array_like, optional] Location parameter. Default is 0.

Returns

logpmf [array_like] Log of the probability mass function evaluated at k.

scipy.stats.rv_discrete.cdf

rv_discrete.**cdf**(*k*, **args*, ***kwds*)

Cumulative distribution function of the given RV.

Parameters

k [array_like, int] Quantiles.

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc [array_like, optional] Location parameter (default=0).

Returns

cdf [ndarray] Cumulative distribution function evaluated at *k*.

scipy.stats.rv_discrete.logcdf

rv_discrete.**logcdf**(*k*, **args*, ***kwds*)

Log of the cumulative distribution function at k of the given RV.

Parameters

k [array_like, int] Quantiles.

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc [array_like, optional] Location parameter (default=0).

Returns

logcdf [array_like] Log of the cumulative distribution function evaluated at k.

scipy.stats.rv_discrete.sf

rv_discrete.**sf**(*k*, **args*, ***kwds*)
Survival function (1 - *cdf*) at k of the given RV.

Parameters

k [array_like] Quantiles.
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).

Returns

sf [array_like] Survival function evaluated at k.

scipy.stats.rv_discrete.logsf

rv_discrete.**logsf**(*k*, **args*, ***kwds*)
Log of the survival function of the given RV.

Returns the log of the "survival function," defined as 1 - *cdf*, evaluated at *k*.

Parameters

k [array_like] Quantiles.
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).

Returns

logsf [ndarray] Log of the survival function evaluated at *k*.

scipy.stats.rv_discrete.ppf

rv_discrete.**ppf**(*q*, **args*, ***kwds*)
Percent point function (inverse of *cdf*) at q of the given RV.

Parameters

q [array_like] Lower tail probability.
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).

Returns

k [array_like] Quantile corresponding to the lower tail probability, q.

scipy.stats.rv_discrete.isf

rv_discrete.**isf**(*q*, **args*, ***kwds*)

Inverse survival function (inverse of *sf*) at q of the given RV.

Parameters

q [array_like] Upper tail probability.

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc [array_like, optional] Location parameter (default=0).

Returns

k [ndarray or scalar] Quantile corresponding to the upper tail probability, q.

scipy.stats.rv_discrete.moment

rv_discrete.**moment**(*n*, **args*, ***kwds*)

n-th order non-central moment of distribution.

Parameters

n [int, n >= 1] Order of moment.

arg1, arg2, arg3,… [float] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

scipy.stats.rv_discrete.stats

rv_discrete.**stats**(**args*, ***kwds*)

Some statistics of the given RV.

Parameters

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional (continuous RVs only)] scale parameter (default=1)

moments [str, optional] composed of letters [‘mvsk’] defining which moments to compute: ‘m’ = mean, ‘v’ = variance, ‘s’ = (Fisher’s) skew, ‘k’ = (Fisher’s) kurtosis. (default is ‘mv’)

Returns

stats [sequence] of requested moments.

scipy.stats.rv_discrete.entropy

rv_discrete.**entropy**(**args*, ***kwds*)

Differential entropy of the RV.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc
: [array_like, optional] Location parameter (default=0).

scale
: [array_like, optional (continuous distributions only).] Scale parameter (default=1).

Notes

Entropy is defined base *e*:

```
>>> drv = rv_discrete(values=((0, 1), (0.5, 0.5)))
>>> np.allclose(drv.entropy(), np.log(2.0))
True
```

scipy.stats.rv_discrete.expect

rv_discrete.**expect**(*func=None*, *args=()*, *loc=0*, *lb=None*, *ub=None*, *conditional=False*, *maxcount=1000*, *tolerance=1e-10*, *chunksize=32*)

Calculate expected value of a function with respect to the distribution for discrete distribution by numerical summation.

Parameters

func
: [callable, optional] Function for which the expectation value is calculated. Takes only one argument. The default is the identity mapping f(k) = k.

args
: [tuple, optional] Shape parameters of the distribution.

loc
: [float, optional] Location parameter. Default is 0.

lb, ub
: [int, optional] Lower and upper bound for the summation, default is set to the support of the distribution, inclusive (`lb <= k <= ub`).

conditional
: [bool, optional] If true then the expectation is corrected by the conditional probability of the summation interval. The return value is the expectation of the function, *func*, conditional on being in the given interval (k such that `lb <= k <= ub`). Default is False.

maxcount
: [int, optional] Maximal number of terms to evaluate (to avoid an endless loop for an infinite sum). Default is 1000.

tolerance
: [float, optional] Absolute tolerance for the summation. Default is 1e-10.

chunksize
: [int, optional] Iterate over the support of a distributions in chunks of this size. Default is 32.

Returns

expect
: [float] Expected value.

Notes

For heavy-tailed distributions, the expected value may or may not exist, depending on the function, *func*. If it does exist, but the sum converges slowly, the accuracy of the result may be rather low. For instance, for `zipf(4)`, accuracy for mean, variance in example is only 1e-5. increasing *maxcount* and/or *chunksize* may improve the result, but may also make zipf very slow.

The function is not vectorized.

scipy.stats.rv_discrete.median

`rv_discrete.`**`median`**`(*args, **kwds)`

Median of the distribution.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc
: [array_like, optional] Location parameter, Default is 0.

scale
: [array_like, optional] Scale parameter, Default is 1.

Returns

median
: [float] The median of the distribution.

See also:

`rv_discrete.ppf`

Inverse of the CDF

scipy.stats.rv_discrete.mean

`rv_discrete.`**`mean`**`(*args, **kwds)`

Mean of the distribution.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc
: [array_like, optional] location parameter (default=0)

scale
: [array_like, optional] scale parameter (default=1)

Returns

mean
: [float] the mean of the distribution

scipy.stats.rv_discrete.std

rv_discrete.**std**(**args*, ***kwds*)
Standard deviation of the distribution.

Parameters

arg1, arg2, arg3,…
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

std [float] standard deviation of the distribution

scipy.stats.rv_discrete.var

rv_discrete.**var**(**args*, ***kwds*)
Variance of the distribution.

Parameters

arg1, arg2, arg3,…
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

var [float] the variance of the distribution

scipy.stats.rv_discrete.interval

rv_discrete.**interval**(*alpha*, **args*, ***kwds*)
Confidence interval with equal areas around the median.

Parameters

alpha [array_like of float] Probability that an rv will be drawn from the returned range. Each value should be in the range [0, 1].
arg1, arg2, …
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] location parameter, Default is 0.
scale [array_like, optional] scale parameter, Default is 1.

Returns

a, b [ndarray of float] end-points of range that contain `100 * alpha %` of the rv's possible values.

scipy.stats.rv_discrete.__call__

rv_discrete.**__call__**(**args*, ***kwds*)
Freeze the distribution for the given arguments.

Parameters

arg1, arg2, arg3,…
[array_like] The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

Returns

rv_frozen [rv_frozen instance] The frozen distribution.

scipy.stats.rv_discrete.support

rv_discrete.**support**(**args*, ***kwargs*)
Support of the distribution.

Parameters

arg1, arg2, …
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] location parameter, Default is 0.
scale [array_like, optional] scale parameter, Default is 1.

Returns

a, b [array_like] end-points of the distribution's support.

scipy.stats.rv_histogram

class scipy.stats.**rv_histogram**(*histogram*, **args*, ***kwargs*)
Generates a distribution given by a histogram. This is useful to generate a template distribution from a binned datasample.

As a subclass of the *rv_continuous* class, *rv_histogram* inherits from it a collection of generic methods (see *rv_continuous* for the full list), and implements them based on the properties of the provided binned datasample.

Parameters

histogram [tuple of array_like] Tuple containing two array_like objects The first containing the content of n bins The second containing the (n+1) bin boundaries In particular the return value np.histogram is accepted

Notes

There are no additional shape parameters except for the loc and scale. The pdf is defined as a stepwise function from the provided histogram The cdf is a linear interpolation of the pdf.

New in version 0.19.0.

Examples

Create a scipy.stats distribution from a numpy histogram

```
>>> import scipy.stats
>>> import numpy as np
>>> data = scipy.stats.norm.rvs(size=100000, loc=0, scale=1.5, random_
↪state=123)
>>> hist = np.histogram(data, bins=100)
>>> hist_dist = scipy.stats.rv_histogram(hist)
```

Behaves like an ordinary scipy rv_continuous distribution

```
>>> hist_dist.pdf(1.0)
0.20538577847618705
>>> hist_dist.cdf(2.0)
0.90818568543056499
```

PDF is zero above (below) the highest (lowest) bin of the histogram, defined by the max (min) of the original dataset

```
>>> hist_dist.pdf(np.max(data))
0.0
>>> hist_dist.cdf(np.max(data))
1.0
>>> hist_dist.pdf(np.min(data))
7.7591907244498314e-05
>>> hist_dist.cdf(np.min(data))
0.0
```

PDF and CDF follow the histogram

```
>>> import matplotlib.pyplot as plt
>>> X = np.linspace(-5.0, 5.0, 100)
>>> plt.title("PDF from Template")
>>> plt.hist(data, density=True, bins=100)
>>> plt.plot(X, hist_dist.pdf(X), label='PDF')
>>> plt.plot(X, hist_dist.cdf(X), label='CDF')
>>> plt.show()
```

Attributes

random_state
: Get or set the generator object for generating random variates.

Methods

__call__(*args, **kwds)	Freeze the distribution for the given arguments.
cdf(x, *args, **kwds)	Cumulative distribution function of the given RV.
entropy(*args, **kwds)	Differential entropy of the RV.
expect([func, args, loc, scale, lb, ub, …])	Calculate expected value of a function with respect to the distribution by numerical integration.

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fit(data, *args, **kwds)	Return estimates of shape (if applicable), location, and scale parameters from data.
fit_loc_scale(data, *args)	Estimate loc and scale parameters from data using 1st and 2nd moments.
freeze(*args, **kwds)	Freeze the distribution for the given arguments.
interval(alpha, *args, **kwds)	Confidence interval with equal areas around the median.
isf(q, *args, **kwds)	Inverse survival function (inverse of *sf*) at q of the given RV.
logcdf(x, *args, **kwds)	Log of the cumulative distribution function at x of the given RV.
logpdf(x, *args, **kwds)	Log of the probability density function at x of the given RV.
logsf(x, *args, **kwds)	Log of the survival function of the given RV.
mean(*args, **kwds)	Mean of the distribution.
median(*args, **kwds)	Median of the distribution.
moment(n, *args, **kwds)	n-th order non-central moment of distribution.
nnlf(theta, x)	Negative loglikelihood function.
pdf(x, *args, **kwds)	Probability density function at x of the given RV.
ppf(q, *args, **kwds)	Percent point function (inverse of *cdf*) at q of the given RV.
rvs(*args, **kwds)	Random variates of given type.
sf(x, *args, **kwds)	Survival function (1 - *cdf*) at x of the given RV.
stats(*args, **kwds)	Some statistics of the given RV.
std(*args, **kwds)	Standard deviation of the distribution.
support(*args, **kwargs)	Support of the distribution.
var(*args, **kwds)	Variance of the distribution.

scipy.stats.rv_histogram.__call__

rv_histogram.**__call__**(**args*, ***kwds*)

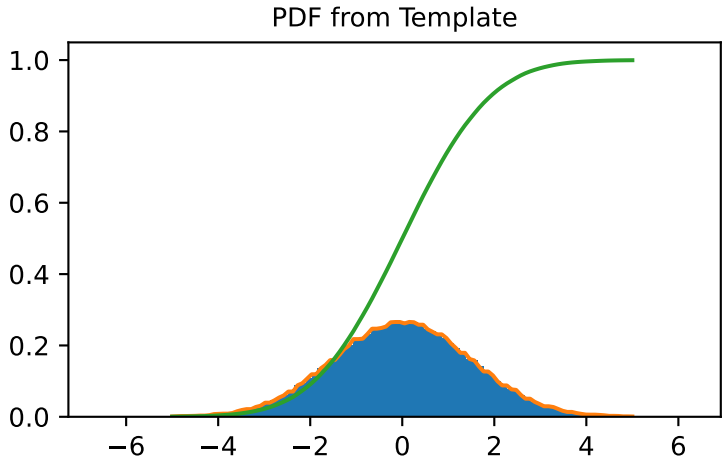
Freeze the distribution for the given arguments.

Parameters

arg1, arg2, arg3,…
: [array_like] The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

Returns

rv_frozen [rv_frozen instance] The frozen distribution.



scipy.stats.rv_histogram.cdf

rv_histogram.**cdf**(*x*, **args*, ***kwds*)
Cumulative distribution function of the given RV.

Parameters

x [array_like] quantiles
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

cdf [ndarray] Cumulative distribution function evaluated at *x*

scipy.stats.rv_histogram.entropy

rv_histogram.**entropy**(**args*, ***kwds*)
Differential entropy of the RV.

Parameters

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).
scale [array_like, optional (continuous distributions only).] Scale parameter (default=1).

Notes

Entropy is defined base *e*:

```
>>> drv = rv_discrete(values=((0, 1), (0.5, 0.5)))
>>> np.allclose(drv.entropy(), np.log(2.0))
True
```

scipy.stats.rv_histogram.expect

rv_histogram.**expect**(*func=None*, *args=()*, *loc=0*, *scale=1*, *lb=None*, *ub=None*, *conditional=False*, ***kwds*)

Calculate expected value of a function with respect to the distribution by numerical integration.

The expected value of a function `f(x)` with respect to a distribution `dist` is defined as:

```
        ub
E[f(x)] = Integral(f(x) * dist.pdf(x)),
        lb
```

where `ub` and `lb` are arguments and `x` has the `dist.pdf(x)` distribution. If the bounds `lb` and `ub` correspond to the support of the distribution, e.g. `[-inf, inf]` in the default case, then the integral is the unrestricted expectation of `f(x)`. Also, the function `f(x)` may be defined such that `f(x)` is `0` outside a finite interval in which case the expectation is calculated within the finite range `[lb, ub]`.

Parameters

func [callable, optional] Function for which integral is calculated. Takes only one argument. The default is the identity mapping f(x) = x.

args [tuple, optional] Shape parameters of the distribution.

loc [float, optional] Location parameter (default=0).

scale [float, optional] Scale parameter (default=1).

lb, ub [scalar, optional] Lower and upper bound for integration. Default is set to the support of the distribution.

conditional [bool, optional] If True, the integral is corrected by the conditional probability of the integration interval. The return value is the expectation of the function, conditional on being in the given interval. Default is False.

Additional keyword arguments are passed to the integration routine.

Returns

expect [float] The calculated expected value.

Notes

The integration behavior of this function is inherited from *scipy.integrate.quad*. Neither this function nor *scipy.integrate.quad* can verify whether the integral exists or is finite. For example `cauchy(0).mean()` returns `np.nan` and `cauchy(0).expect()` returns `0.0`.

The function is not vectorized.

Examples

To understand the effect of the bounds of integration consider

```
>>> from scipy.stats import expon
>>> expon(1).expect(lambda x: 1, lb=0.0, ub=2.0)
0.6321205588285578
```

This is close to

```
>>> expon(1).cdf(2.0) - expon(1).cdf(0.0)
0.6321205588285577
```

If `conditional=True`

```
>>> expon(1).expect(lambda x: 1, lb=0.0, ub=2.0, conditional=True)
1.0000000000000002
```

The slight deviation from 1 is due to numerical integration.

scipy.stats.rv_histogram.fit

`rv_histogram.`**`fit`**(*data*, **args*, ***kwds*)

Return estimates of shape (if applicable), location, and scale parameters from data. The default estimation method is Maximum Likelihood Estimation (MLE), but Method of Moments (MM) is also available.

Starting estimates for the fit are given by input arguments; for any arguments not provided with starting estimates, `self._fitstart(data)` is called to generate such.

One can hold some parameters fixed to specific values by passing in keyword arguments `f0`, `f1`, …, `fn` (for shape parameters) and `floc` and `fscale` (for location and scale parameters, respectively).

Parameters

data [array_like] Data to use in estimating the distribution parameters.

arg1, arg2, arg3,…
[floats, optional] Starting value(s) for any shape-characterizing arguments (those not provided will be determined by a call to `_fitstart(data)`). No default value.

kwds [floats, optional]

- *loc*: initial guess of the distribution's location parameter.
- *scale*: initial guess of the distribution's scale parameter.

Special keyword arguments are recognized as holding certain parameters fixed:

- f0…fn : hold respective shape parameters fixed. Alternatively, shape parameters to fix can be specified by name. For example, if `self.shapes == "a, b"`, `fa` and `fix_a` are equivalent to `f0`, and `fb` and `fix_b` are equivalent to `f1`.
- floc : hold location parameter fixed to specified value.
- fscale : hold scale parameter fixed to specified value.
- optimizer : The optimizer to use. The optimizer must take `func`, and starting position as the first two arguments, plus `args` (for extra arguments to pass to the function to be optimized) and `disp=0` to suppress output as keyword arguments.
- method : The method to use. The default is "MLE" (Maximum Likelihood Estimate); "MM" (Method of Moments) is also available.

Returns

parameter_tuple
: [tuple of floats] Estimates for any shape parameters (if applicable), followed by those for location and scale. For most random variables, shape statistics will be returned, but there are exceptions (e.g. `norm`).

Notes

With `method="MLE"` (default), the fit is computed by minimizing the negative log-likelihood function. A large, finite penalty (rather than infinite negative log-likelihood) is applied for observations beyond the support of the distribution.

With `method="MM"`, the fit is computed by minimizing the L2 norm of the relative errors between the first *k* raw (about zero) data moments and the corresponding distribution moments, where *k* is the number of non-fixed parameters. More precisely, the objective function is:

```
(((data_moments - dist_moments)
  / np.maximum(np.abs(data_moments), 1e-8))**2).sum()
```

where the constant `1e-8` avoids division by zero in case of vanishing data moments. Typically, this error norm can be reduced to zero. Note that the standard method of moments can produce parameters for which some data are outside the support of the fitted distribution; this implementation does nothing to prevent this.

For either method, the returned answer is not guaranteed to be globally optimal; it may only be locally optimal, or the optimization may fail altogether. If the data contain any of `np.nan`, `np.inf`, or `-np.inf`, the *fit* method will raise a `RuntimeError`.

Examples

Generate some data to fit: draw random variates from the *beta* distribution

```
>>> from scipy.stats import beta
>>> a, b = 1., 2.
>>> x = beta.rvs(a, b, size=1000)
```

Now we can fit all four parameters (`a`, `b`, `loc` and `scale`):

```
>>> a1, b1, loc1, scale1 = beta.fit(x)
```

We can also use some prior knowledge about the dataset: let's keep `loc` and `scale` fixed:

```
>>> a1, b1, loc1, scale1 = beta.fit(x, floc=0, fscale=1)
>>> loc1, scale1
(0, 1)
```

We can also keep shape parameters fixed by using `f`-keywords. To keep the zero-th shape parameter `a` equal 1, use `f0=1` or, equivalently, `fa=1`:

```
>>> a1, b1, loc1, scale1 = beta.fit(x, fa=1, floc=0, fscale=1)
>>> a1
1
```

Not all distributions return estimates for the shape parameters. `norm` for example just returns estimates for location and scale:

```
>>> from scipy.stats import norm
>>> x = norm.rvs(a, b, size=1000, random_state=123)
>>> loc1, scale1 = norm.fit(x)
>>> loc1, scale1
(0.92087172783841631, 2.0015750750324668)
```

scipy.stats.rv_histogram.fit_loc_scale

rv_histogram.**fit_loc_scale**(*data*, **args*)

Estimate loc and scale parameters from data using 1st and 2nd moments.

Parameters

data [array_like] Data to fit.

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

Returns

Lhat [float] Estimated location parameter for the data.

Shat [float] Estimated scale parameter for the data.

scipy.stats.rv_histogram.freeze

rv_histogram.**freeze**(**args*, ***kwds*)

Freeze the distribution for the given arguments.

Parameters

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution. Should include all the non-optional arguments, may include `loc` and `scale`.

Returns

rv_frozen [rv_frozen instance] The frozen distribution.

scipy.stats.rv_histogram.interval

rv_histogram.**interval**(*alpha*, **args*, ***kwds*)

Confidence interval with equal areas around the median.

Parameters

alpha [array_like of float] Probability that an rv will be drawn from the returned range. Each value should be in the range [0, 1].

arg1, arg2, … [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc [array_like, optional] location parameter, Default is 0.

scale [array_like, optional] scale parameter, Default is 1.

Returns

a, b [ndarray of float] end-points of range that contain `100 * alpha %` of the rv's possible values.

scipy.stats.rv_histogram.isf

`rv_histogram.`**`isf`**(*q*, **args*, ***kwds*)

Inverse survival function (inverse of *sf*) at q of the given RV.

Parameters

q [array_like] upper tail probability

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

x [ndarray or scalar] Quantile corresponding to the upper tail probability q.

scipy.stats.rv_histogram.logcdf

`rv_histogram.`**`logcdf`**(*x*, **args*, ***kwds*)

Log of the cumulative distribution function at x of the given RV.

Parameters

x [array_like] quantiles

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

logcdf [array_like] Log of the cumulative distribution function evaluated at x

scipy.stats.rv_histogram.logpdf

`rv_histogram.`**`logpdf`**(*x*, **args*, ***kwds*)

Log of the probability density function at x of the given RV.

This uses a more numerically accurate calculation if available.

Parameters

x [array_like] quantiles

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

logpdf [array_like] Log of the probability density function evaluated at x

scipy.stats.rv_histogram.logsf

rv_histogram.**logsf**(*x*, **args*, ***kwds*)

Log of the survival function of the given RV.

Returns the log of the "survival function," defined as (1 - `cdf`), evaluated at *x*.

Parameters

x [array_like] quantiles

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

logsf [ndarray] Log of the survival function evaluated at *x*.

scipy.stats.rv_histogram.mean

rv_histogram.**mean**(**args*, ***kwds*)

Mean of the distribution.

Parameters

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

mean [float] the mean of the distribution

scipy.stats.rv_histogram.median

rv_histogram.**median**(**args*, ***kwds*)

Median of the distribution.

Parameters

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] Location parameter, Default is 0.

scale [array_like, optional] Scale parameter, Default is 1.

Returns

median [float] The median of the distribution.

See also:

`rv_discrete.ppf`

Inverse of the CDF

scipy.stats.rv_histogram.moment

`rv_histogram.`**`moment`**(*n*, **args*, ***kwds*)

n-th order non-central moment of distribution.

Parameters

n [int, n >= 1] Order of moment.

arg1, arg2, arg3,… [float] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

scipy.stats.rv_histogram.nnlf

`rv_histogram.`**`nnlf`**(*theta*, *x*)

Negative loglikelihood function.

Notes

This is `-sum(log pdf(x, theta), axis=0)` where *theta* are the parameters (including loc and scale).

scipy.stats.rv_histogram.pdf

`rv_histogram.`**`pdf`**(*x*, **args*, ***kwds*)

Probability density function at x of the given RV.

Parameters

x [array_like] quantiles

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

pdf [ndarray] Probability density function evaluated at x

scipy.stats.rv_histogram.ppf

rv_histogram.**ppf**(*q*, **args*, ***kwds*)
Percent point function (inverse of *cdf*) at q of the given RV.

Parameters

q [array_like] lower tail probability
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

x [array_like] quantile corresponding to the lower tail probability q.

scipy.stats.rv_histogram.rvs

rv_histogram.**rvs**(**args*, ***kwds*)
Random variates of given type.

Parameters

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).
loc [array_like, optional] Location parameter (default=0).
scale [array_like, optional] Scale parameter (default=1).
size [int or tuple of ints, optional] Defining number of random variates (default is 1).
random_state [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Returns

rvs [ndarray or scalar] Random variates of given *size*.

scipy.stats.rv_histogram.sf

rv_histogram.**sf**(*x*, **args*, ***kwds*)
Survival function (1 - *cdf*) at x of the given RV.

Parameters

x [array_like] quantiles
arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)
loc [array_like, optional] location parameter (default=0)
scale [array_like, optional] scale parameter (default=1)

Returns

sf [array_like] Survival function evaluated at x

scipy.stats.rv_histogram.stats

rv_histogram.**stats**(**args*, ***kwds*)

Some statistics of the given RV.

Parameters

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional (continuous RVs only)] scale parameter (default=1)

moments [str, optional] composed of letters ['mvsk'] defining which moments to compute: 'm' = mean, 'v' = variance, 's' = (Fisher's) skew, 'k' = (Fisher's) kurtosis. (default is 'mv')

Returns

stats [sequence] of requested moments.

scipy.stats.rv_histogram.std

rv_histogram.**std**(**args*, ***kwds*)

Standard deviation of the distribution.

Parameters

arg1, arg2, arg3,… [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

std [float] standard deviation of the distribution

scipy.stats.rv_histogram.support

rv_histogram.**support**(**args*, ***kwargs*)

Support of the distribution.

Parameters

arg1, arg2, … [array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information).

loc [array_like, optional] location parameter, Default is 0.

scale [array_like, optional] scale parameter, Default is 1.

Returns

a, b [array_like] end-points of the distribution's support.

scipy.stats.rv_histogram.var

rv_histogram.**var**(**args*, ***kwds*)
Variance of the distribution.

Parameters

arg1, arg2, arg3,…
[array_like] The shape parameter(s) for the distribution (see docstring of the instance object for more information)

loc [array_like, optional] location parameter (default=0)

scale [array_like, optional] scale parameter (default=1)

Returns

var [float] the variance of the distribution

Continuous distributions

alpha	An alpha continuous random variable.
anglit	An anglit continuous random variable.
arcsine	An arcsine continuous random variable.
argus	Argus distribution
beta	A beta continuous random variable.
betaprime	A beta prime continuous random variable.
bradford	A Bradford continuous random variable.
burr	A Burr (Type III) continuous random variable.
burr12	A Burr (Type XII) continuous random variable.
cauchy	A Cauchy continuous random variable.
chi	A chi continuous random variable.
chi2	A chi-squared continuous random variable.
cosine	A cosine continuous random variable.
crystalball	Crystalball distribution
dgamma	A double gamma continuous random variable.
dweibull	A double Weibull continuous random variable.
erlang	An Erlang continuous random variable.
expon	An exponential continuous random variable.
exponnorm	An exponentially modified Normal continuous random variable.
exponweib	An exponentiated Weibull continuous random variable.
exponpow	An exponential power continuous random variable.
f	An F continuous random variable.
fatiguelife	A fatigue-life (Birnbaum-Saunders) continuous random variable.
fisk	A Fisk continuous random variable.
foldcauchy	A folded Cauchy continuous random variable.
foldnorm	A folded normal continuous random variable.
genlogistic	A generalized logistic continuous random variable.
gennorm	A generalized normal continuous random variable.
genpareto	A generalized Pareto continuous random variable.
genexpon	A generalized exponential continuous random variable.
genextreme	A generalized extreme value continuous random variable.
gausshyper	A Gauss hypergeometric continuous random variable.

continues on next page

Table 260 – continued from previous page

gamma	A gamma continuous random variable.
gengamma	A generalized gamma continuous random variable.
genhalflogistic	A generalized half-logistic continuous random variable.
genhyperbolic	A generalized hyperbolic continuous random variable.
geninvgauss	A Generalized Inverse Gaussian continuous random variable.
gilbrat	A Gilbrat continuous random variable.
gompertz	A Gompertz (or truncated Gumbel) continuous random variable.
gumbel_r	A right-skewed Gumbel continuous random variable.
gumbel_l	A left-skewed Gumbel continuous random variable.
halfcauchy	A Half-Cauchy continuous random variable.
halflogistic	A half-logistic continuous random variable.
halfnorm	A half-normal continuous random variable.
halfgennorm	The upper half of a generalized normal continuous random variable.
hypsecant	A hyperbolic secant continuous random variable.
invgamma	An inverted gamma continuous random variable.
invgauss	An inverse Gaussian continuous random variable.
invweibull	An inverted Weibull continuous random variable.
johnsonsb	A Johnson SB continuous random variable.
johnsonsu	A Johnson SU continuous random variable.
kappa4	Kappa 4 parameter distribution.
kappa3	Kappa 3 parameter distribution.
ksone	Kolmogorov-Smirnov one-sided test statistic distribution.
kstwo	Kolmogorov-Smirnov two-sided test statistic distribution.
kstwobign	Limiting distribution of scaled Kolmogorov-Smirnov two-sided test statistic.
laplace	A Laplace continuous random variable.
laplace_asymmetric	An asymmetric Laplace continuous random variable.
levy	A Levy continuous random variable.
levy_l	A left-skewed Levy continuous random variable.
levy_stable	A Levy-stable continuous random variable.
logistic	A logistic (or Sech-squared) continuous random variable.
loggamma	A log gamma continuous random variable.
loglaplace	A log-Laplace continuous random variable.
lognorm	A lognormal continuous random variable.
loguniform	A loguniform or reciprocal continuous random variable.
lomax	A Lomax (Pareto of the second kind) continuous random variable.
maxwell	A Maxwell continuous random variable.
mielke	A Mielke Beta-Kappa / Dagum continuous random variable.
moyal	A Moyal continuous random variable.
nakagami	A Nakagami continuous random variable.
ncx2	A non-central chi-squared continuous random variable.
ncf	A non-central F distribution continuous random variable.
nct	A non-central Student's t continuous random variable.
norm	A normal continuous random variable.
norminvgauss	A Normal Inverse Gaussian continuous random variable.

continues on next page

Table 260 – continued from previous page

pareto	A Pareto continuous random variable.
pearson3	A pearson type III continuous random variable.
powerlaw	A power-function continuous random variable.
powerlognorm	A power log-normal continuous random variable.
powernorm	A power normal continuous random variable.
rdist	An R-distributed (symmetric beta) continuous random variable.
rayleigh	A Rayleigh continuous random variable.
rice	A Rice continuous random variable.
recipinvgauss	A reciprocal inverse Gaussian continuous random variable.
semicircular	A semicircular continuous random variable.
skewcauchy	A skewed Cauchy random variable.
skewnorm	A skew-normal random variable.
studentized_range	A studentized range continuous random variable.
t	A Student's t continuous random variable.
trapezoid	A trapezoidal continuous random variable.
triang	A triangular continuous random variable.
truncexpon	A truncated exponential continuous random variable.
truncnorm	A truncated normal continuous random variable.
tukeylambda	A Tukey-Lamdba continuous random variable.
uniform	A uniform continuous random variable.
vonmises	A Von Mises continuous random variable.
vonmises_line	A Von Mises continuous random variable.
wald	A Wald continuous random variable.
weibull_min	Weibull minimum continuous random variable.
weibull_max	Weibull maximum continuous random variable.
wrapcauchy	A wrapped Cauchy continuous random variable.

scipy.stats.alpha

scipy.stats.**alpha = <scipy.stats._continuous_distns.alpha_gen object>**

An alpha continuous random variable.

As an instance of the *rv_continuous* class, *alpha* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *alpha* ([1], [2]) is:

$$f(x, a) = \frac{1}{x^2 \Phi(a) \sqrt{2\pi}} * \exp(-\frac{1}{2}(a - 1/x)^2)$$

where Φ is the normal CDF, $x > 0$, and $a > 0$.

alpha takes `a` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `alpha.pdf(x, a, loc, scale)` is identically equivalent to `alpha.pdf(y, a) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1], [2]

Examples

```
>>> from scipy.stats import alpha
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 3.57
>>> mean, var, skew, kurt = alpha.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(alpha.ppf(0.01, a),
...                 alpha.ppf(0.99, a), 100)
>>> ax.plot(x, alpha.pdf(x, a),
...         'r-', lw=5, alpha=0.6, label='alpha pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = alpha(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

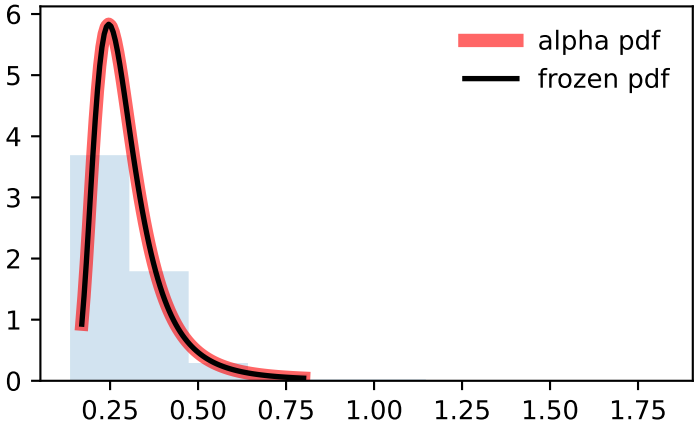
```
>>> vals = alpha.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], alpha.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = alpha.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.anglit

scipy.stats.**anglit = <scipy.stats._continuous_distns.anglit_gen object>**

An anglit continuous random variable.

As an instance of the *rv_continuous* class, *anglit* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *anglit* is:

$$f(x) = \sin(2x + \pi/2) = \cos(2x)$$

for $-\pi/4 \leq x \leq \pi/4$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `anglit.pdf(x, loc, scale)` is identically equivalent to `anglit.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import anglit
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = anglit.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(anglit.ppf(0.01),
...                 anglit.ppf(0.99), 100)
>>> ax.plot(x, anglit.pdf(x),
...         'r-', lw=5, alpha=0.6, label='anglit pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = anglit()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

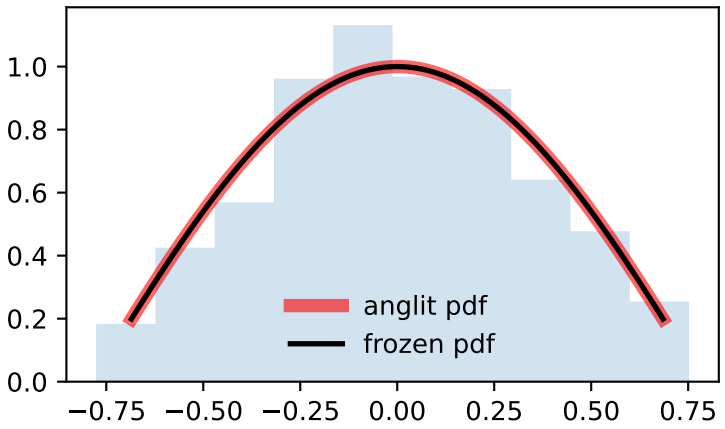
```
>>> vals = anglit.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], anglit.cdf(vals))
True
```

Generate random numbers:

```
>>> r = anglit.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.arcsine

scipy.stats.**arcsine = <scipy.stats._continuous_distns.arcsine_gen object>**

An arcsine continuous random variable.

As an instance of the *rv_continuous* class, *arcsine* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *arcsine* is:

$$f(x) = \frac{1}{\pi\sqrt{x(1-x)}}$$

for $0 < x < 1$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `arcsine.pdf(x, loc, scale)` is identically equivalent to `arcsine.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import arcsine
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = arcsine.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(arcsine.ppf(0.01),
...                 arcsine.ppf(0.99), 100)
>>> ax.plot(x, arcsine.pdf(x),
...         'r-', lw=5, alpha=0.6, label='arcsine pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = arcsine()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

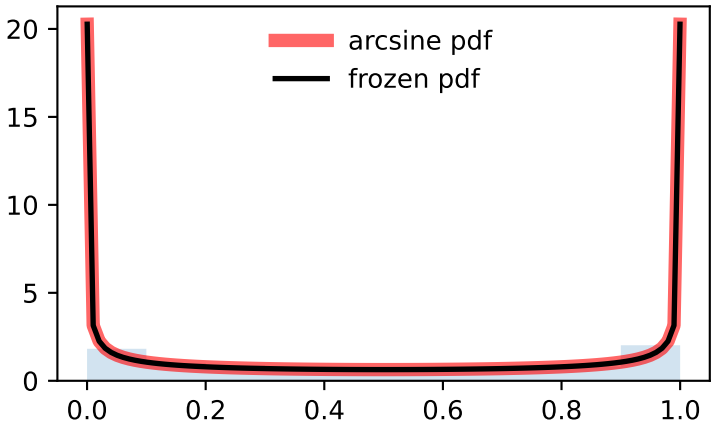
```
>>> vals = arcsine.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], arcsine.cdf(vals))
True
```

Generate random numbers:

```
>>> r = arcsine.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.argus

scipy.stats.**argus = <scipy.stats._continuous_distns.argus_gen object>**

Argus distribution

As an instance of the *rv_continuous* class, *argus* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *argus* is:

$$f(x, \chi) = \frac{\chi^3}{\sqrt{2\pi}\Psi(\chi)} x\sqrt{1-x^2}\exp(-\chi^2(1-x^2)/2)$$

for $0 < x < 1$ and $\chi > 0$, where

$$\Psi(\chi) = \Phi(\chi) - \chi\phi(\chi) - 1/2$$

with Φ and ϕ being the CDF and PDF of a standard normal distribution, respectively.

argus takes χ as shape a parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `argus.pdf(x, chi, loc, scale)` is identically equivalent to `argus.pdf(y, chi) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

New in version 0.19.0.

References

[1]

Examples

```
>>> from scipy.stats import argus
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> chi = 1
>>> mean, var, skew, kurt = argus.stats(chi, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(argus.ppf(0.01, chi),
...                 argus.ppf(0.99, chi), 100)
>>> ax.plot(x, argus.pdf(x, chi),
...         'r-', lw=5, alpha=0.6, label='argus pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = argus(chi)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

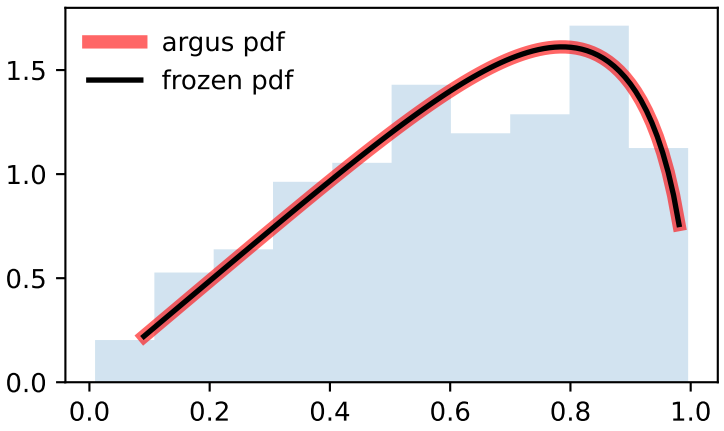
```
>>> vals = argus.ppf([0.001, 0.5, 0.999], chi)
>>> np.allclose([0.001, 0.5, 0.999], argus.cdf(vals, chi))
True
```

Generate random numbers:

```
>>> r = argus.rvs(chi, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(chi, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, chi, loc=0, scale=1)	Probability density function.
logpdf(x, chi, loc=0, scale=1)	Log of the probability density function.
cdf(x, chi, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, chi, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, chi, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, chi, loc=0, scale=1)	Log of the survival function.
ppf(q, chi, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, chi, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, chi, loc=0, scale=1)	Non-central moment of order n
stats(chi, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(chi, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(chi,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(chi, loc=0, scale=1)	Median of the distribution.
mean(chi, loc=0, scale=1)	Mean of the distribution.
var(chi, loc=0, scale=1)	Variance of the distribution.
std(chi, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, chi, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.beta

scipy.stats.**beta = <scipy.stats._continuous_distns.beta_gen object>**

A beta continuous random variable.

As an instance of the *rv_continuous* class, *beta* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *beta* is:

$$f(x, a, b) = \frac{\Gamma(a+b) x^{a-1} (1-x)^{b-1}}{\Gamma(a) \Gamma(b)}$$

for $0 <= x <= 1$, $a > 0$, $b > 0$, where Γ is the gamma function (*scipy.special.gamma*).

beta takes a and b as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `beta.pdf(x, a, b, loc, scale)` is identically equivalent to `beta.pdf(y, a, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import beta
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b = 2.31, 0.627
>>> mean, var, skew, kurt = beta.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(beta.ppf(0.01, a, b),
...                 beta.ppf(0.99, a, b), 100)
>>> ax.plot(x, beta.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='beta pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = beta(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

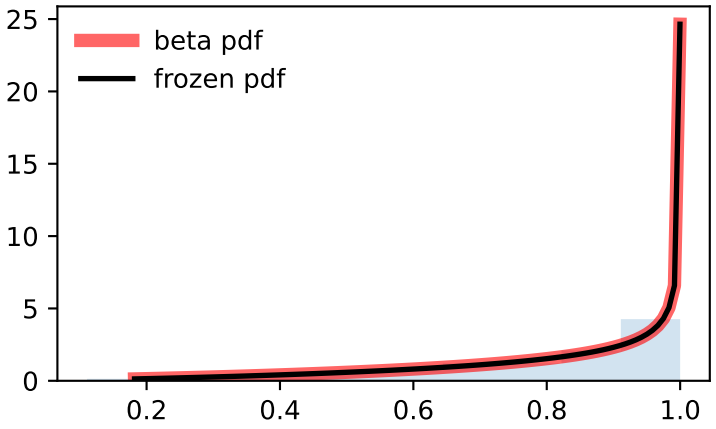
```
>>> vals = beta.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], beta.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = beta.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, loc=0, scale=1)	Non-central moment of order n
stats(a, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, loc=0, scale=1)	Median of the distribution.
mean(a, b, loc=0, scale=1)	Mean of the distribution.
var(a, b, loc=0, scale=1)	Variance of the distribution.
std(a, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.betaprime

scipy.stats.**betaprime = <scipy.stats._continuous_distns.betaprime_gen object>**

A beta prime continuous random variable.

As an instance of the *rv_continuous* class, *betaprime* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *betaprime* is:

$$f(x, a, b) = \frac{x^{a-1}(1+x)^{-a-b}}{\beta(a, b)}$$

for $x >= 0$, $a > 0$, $b > 0$, where $\beta(a, b)$ is the beta function (see *scipy.special.beta*).

betaprime takes `a` and `b` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `betaprime.pdf(x, a, b, loc, scale)` is identically equivalent to `betaprime.pdf(y, a, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import betaprime
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b = 5, 6
>>> mean, var, skew, kurt = betaprime.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(betaprime.ppf(0.01, a, b),
...                 betaprime.ppf(0.99, a, b), 100)
>>> ax.plot(x, betaprime.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='betaprime pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = betaprime(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

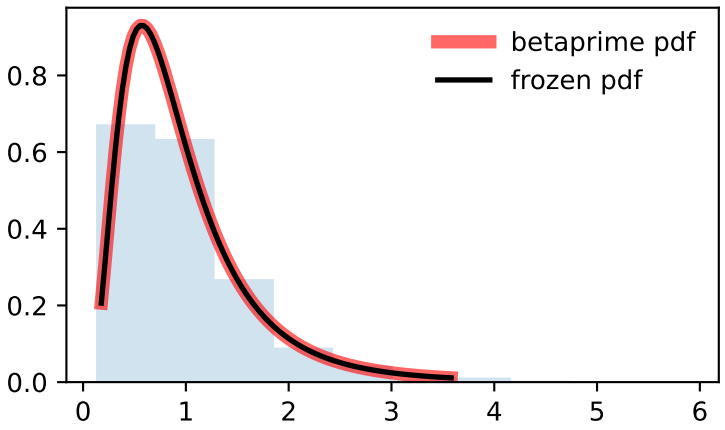
```
>>> vals = betaprime.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], betaprime.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = betaprime.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, loc=0, scale=1)	Non-central moment of order n
stats(a, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, loc=0, scale=1)	Median of the distribution.
mean(a, b, loc=0, scale=1)	Mean of the distribution.
var(a, b, loc=0, scale=1)	Variance of the distribution.
std(a, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.bradford

scipy.stats.**bradford = <scipy.stats._continuous_distns.bradford_gen object>**

A Bradford continuous random variable.

As an instance of the *rv_continuous* class, *bradford* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *bradford* is:

$$f(x, c) = \frac{c}{\log(1+c)(1+cx)}$$

for $0 <= x <= 1$ and $c > 0$.

bradford takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `bradford.pdf(x, c, loc, scale)` is identically equivalent to `bradford.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import bradford
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 0.299
>>> mean, var, skew, kurt = bradford.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(bradford.ppf(0.01, c),
...                 bradford.ppf(0.99, c), 100)
>>> ax.plot(x, bradford.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='bradford pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = bradford(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

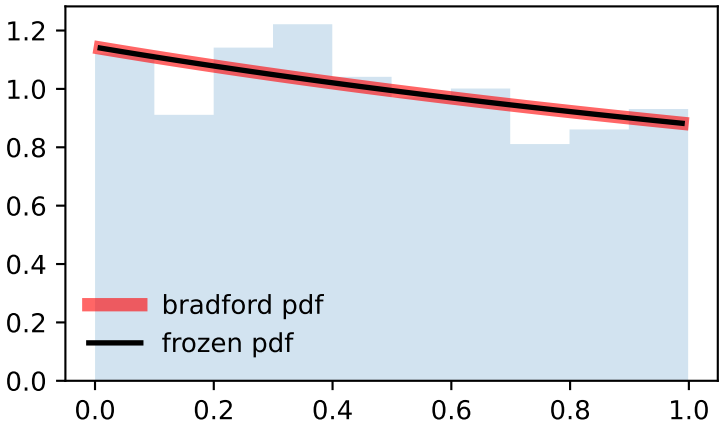
```
>>> vals = bradford.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], bradford.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = bradford.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.burr

scipy.stats.**burr = <scipy.stats._continuous_distns.burr_gen object>**

A Burr (Type III) continuous random variable.

As an instance of the *rv_continuous* class, *burr* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

fisk

a special case of either *burr* or *burr12* with d=1

burr12

Burr Type XII distribution

mielke

Mielke Beta-Kappa / Dagum distribution

Notes

The probability density function for *burr* is:

$$f(x, c, d) = cdx^{-c-1}/(1 + x^{-c})^{d+1}$$

for $x >= 0$ and $c, d > 0$.

burr takes c and d as shape parameters.

This is the PDF corresponding to the third CDF given in Burr's list; specifically, it is equation (11) in Burr's paper [1]. The distribution is also commonly referred to as the Dagum distribution [2]. If the parameter $c < 1$ then the mean of the distribution does not exist and if $c < 2$ the variance does not exist [2]. The PDF is finite at the left endpoint $x = 0$ if $c * d >= 1$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `burr.pdf(x, c, d, loc, scale)` is identically equivalent to `burr.pdf(y, c, d) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1], [2], [3]

Examples

```
>>> from scipy.stats import burr
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c, d = 10.5, 4.3
>>> mean, var, skew, kurt = burr.stats(c, d, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(burr.ppf(0.01, c, d),
...                 burr.ppf(0.99, c, d), 100)
>>> ax.plot(x, burr.pdf(x, c, d),
...         'r-', lw=5, alpha=0.6, label='burr pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = burr(c, d)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

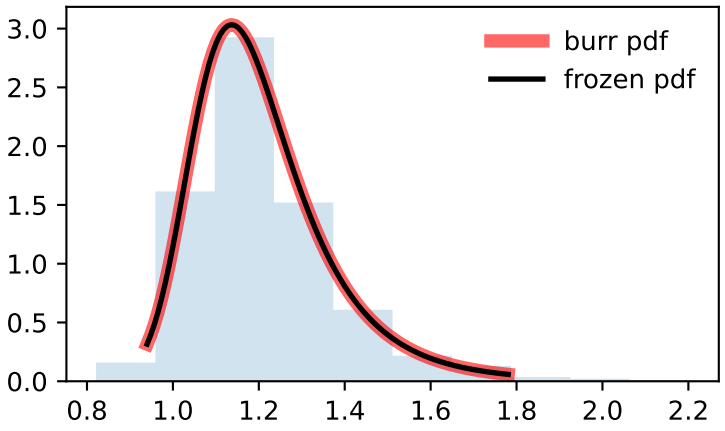
```
>>> vals = burr.ppf([0.001, 0.5, 0.999], c, d)
>>> np.allclose([0.001, 0.5, 0.999], burr.cdf(vals, c, d))
True
```

Generate random numbers:

```
>>> r = burr.rvs(c, d, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, d, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, d, loc=0, scale=1)	Probability density function.
logpdf(x, c, d, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, d, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, d, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, d, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, d, loc=0, scale=1)	Log of the survival function.
ppf(q, c, d, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, d, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, d, loc=0, scale=1)	Non-central moment of order n
stats(c, d, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, d, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c, d), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, d, loc=0, scale=1)	Median of the distribution.
mean(c, d, loc=0, scale=1)	Mean of the distribution.
var(c, d, loc=0, scale=1)	Variance of the distribution.
std(c, d, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, d, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.burr12

scipy.stats.**burr12 = <scipy.stats._continuous_distns.burr12_gen object>**

A Burr (Type XII) continuous random variable.

As an instance of the *rv_continuous* class, *burr12* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

fisk

a special case of either *burr* or *burr12* with `d=1`

burr

Burr Type III distribution

Notes

The probability density function for *burr* is:

$$f(x, c, d) = cdx^{c-1}/(1 + x^c)^{d+1}$$

for $x >= 0$ and $c, d > 0$.

burr12 takes `c` and `d` as shape parameters for c and d.

This is the PDF corresponding to the twelfth CDF given in Burr's list; specifically, it is equation (20) in Burr's paper [1].

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `burr12.pdf(x, c, d, loc, scale)` is identically equivalent to `burr12.pdf(y, c, d) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

The Burr type 12 distribution is also sometimes referred to as the Singh-Maddala distribution from NIST [2].

References

[1], [2], [3]

Examples

```
>>> from scipy.stats import burr12
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c, d = 10, 4
>>> mean, var, skew, kurt = burr12.stats(c, d, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(burr12.ppf(0.01, c, d),
...                 burr12.ppf(0.99, c, d), 100)
>>> ax.plot(x, burr12.pdf(x, c, d),
...         'r-', lw=5, alpha=0.6, label='burr12 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = burr12(c, d)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

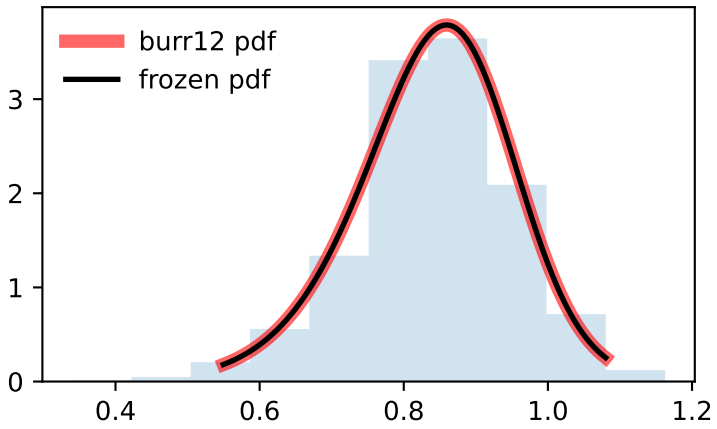
```
>>> vals = burr12.ppf([0.001, 0.5, 0.999], c, d)
>>> np.allclose([0.001, 0.5, 0.999], burr12.cdf(vals, c, d))
True
```

Generate random numbers:

```
>>> r = burr12.rvs(c, d, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, d, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, d, loc=0, scale=1)	Probability density function.
logpdf(x, c, d, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, d, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, d, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, d, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, d, loc=0, scale=1)	Log of the survival function.
ppf(q, c, d, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, d, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, d, loc=0, scale=1)	Non-central moment of order n
stats(c, d, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, d, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c, d), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, d, loc=0, scale=1)	Median of the distribution.
mean(c, d, loc=0, scale=1)	Mean of the distribution.
var(c, d, loc=0, scale=1)	Variance of the distribution.
std(c, d, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, d, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.cauchy

scipy.stats.**cauchy = <scipy.stats._continuous_distns.cauchy_gen object>**

A Cauchy continuous random variable.

As an instance of the *rv_continuous* class, *cauchy* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *cauchy* is

$$f(x) = \frac{1}{\pi(1+x^2)}$$

for a real number x.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `cauchy.pdf(x, loc, scale)` is identically equivalent to `cauchy.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import cauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = cauchy.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(cauchy.ppf(0.01),
...                 cauchy.ppf(0.99), 100)
>>> ax.plot(x, cauchy.pdf(x),
...         'r-', lw=5, alpha=0.6, label='cauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = cauchy()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

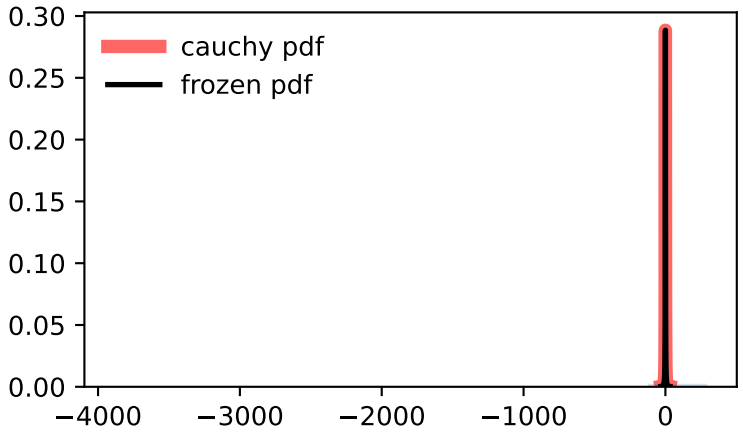
```
>>> vals = cauchy.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], cauchy.cdf(vals))
True
```

Generate random numbers:

```
>>> r = cauchy.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.chi

scipy.stats.**chi = <scipy.stats._continuous_distns.chi_gen object>**

A chi continuous random variable.

As an instance of the *rv_continuous* class, *chi* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *chi* is:

$$f(x, k) = \frac{1}{2^{k/2-1}\Gamma\left(k/2\right)} x^{k-1} \exp\left(-x^2/2\right)$$

for $x >= 0$ and $k > 0$ (degrees of freedom, denoted `df` in the implementation). Γ is the gamma function (*scipy.special.gamma*).

Special cases of *chi* are:

- `chi(1, loc, scale)` is equivalent to *halfnorm*
- `chi(2, 0, scale)` is equivalent to *rayleigh*
- `chi(3, 0, scale)` is equivalent to *maxwell*

chi takes `df` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `chi.pdf(x, df, loc, scale)` is identically equivalent to `chi.pdf(y, df) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import chi
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> df = 78
>>> mean, var, skew, kurt = chi.stats(df, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(chi.ppf(0.01, df),
...                 chi.ppf(0.99, df), 100)
>>> ax.plot(x, chi.pdf(x, df),
...         'r-', lw=5, alpha=0.6, label='chi pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = chi(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

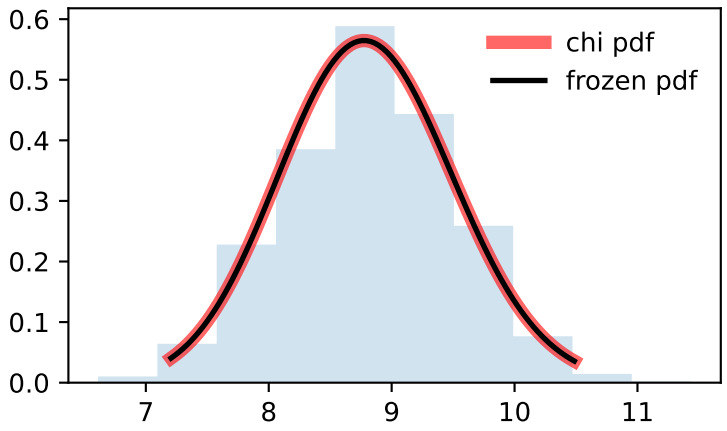
```
>>> vals = chi.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], chi.cdf(vals, df))
True
```

Generate random numbers:

```
>>> r = chi.rvs(df, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(df, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, df, loc=0, scale=1)	Probability density function.
logpdf(x, df, loc=0, scale=1)	Log of the probability density function.
cdf(x, df, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, df, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, df, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, df, loc=0, scale=1)	Log of the survival function.
ppf(q, df, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, df, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, df, loc=0, scale=1)	Non-central moment of order n
stats(df, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(df, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(df,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(df, loc=0, scale=1)	Median of the distribution.
mean(df, loc=0, scale=1)	Mean of the distribution.
var(df, loc=0, scale=1)	Variance of the distribution.
std(df, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, df, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.chi2

scipy.stats.**chi2 = <scipy.stats._continuous_distns.chi2_gen object>**

A chi-squared continuous random variable.

For the noncentral chi-square distribution, see *ncx2*.

As an instance of the *rv_continuous* class, *chi2* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

ncx2

Notes

The probability density function for *chi2* is:

$$f(x, k) = \frac{1}{2^{k/2}\Gamma\left(k/2\right)} x^{k/2-1} \exp\left(-x/2\right)$$

for $x > 0$ and $k > 0$ (degrees of freedom, denoted `df` in the implementation).

chi2 takes `df` as a shape parameter.

The chi-squared distribution is a special case of the gamma distribution, with gamma parameters `a = df/2`, `loc = 0` and `scale = 2`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `chi2.pdf(x, df, loc, scale)` is identically equivalent to `chi2.pdf(y, df) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import chi2
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> df = 55
>>> mean, var, skew, kurt = chi2.stats(df, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(chi2.ppf(0.01, df),
...                 chi2.ppf(0.99, df), 100)
>>> ax.plot(x, chi2.pdf(x, df),
...         'r-', lw=5, alpha=0.6, label='chi2 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = chi2(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

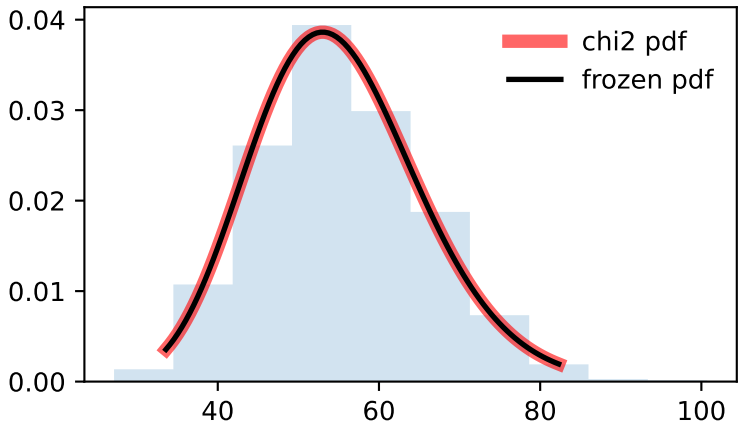
```
>>> vals = chi2.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], chi2.cdf(vals, df))
True
```

Generate random numbers:

```
>>> r = chi2.rvs(df, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(df, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, df, loc=0, scale=1)	Probability density function.
logpdf(x, df, loc=0, scale=1)	Log of the probability density function.
cdf(x, df, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, df, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, df, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, df, loc=0, scale=1)	Log of the survival function.
ppf(q, df, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, df, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, df, loc=0, scale=1)	Non-central moment of order n
stats(df, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(df, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(df,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(df, loc=0, scale=1)	Median of the distribution.
mean(df, loc=0, scale=1)	Mean of the distribution.
var(df, loc=0, scale=1)	Variance of the distribution.
std(df, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, df, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.cosine

scipy.stats.**cosine = <scipy.stats._continuous_distns.cosine_gen object>**

A cosine continuous random variable.

As an instance of the *rv_continuous* class, *cosine* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The cosine distribution is an approximation to the normal distribution. The probability density function for *cosine* is:

$$f(x) = \frac{1}{2\pi}(1+\cos(x))$$

for $-\pi \leq x \leq \pi$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `cosine.pdf(x, loc, scale)` is identically equivalent to `cosine.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import cosine
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = cosine.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(cosine.ppf(0.01),
...                 cosine.ppf(0.99), 100)
>>> ax.plot(x, cosine.pdf(x),
...         'r-', lw=5, alpha=0.6, label='cosine pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = cosine()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

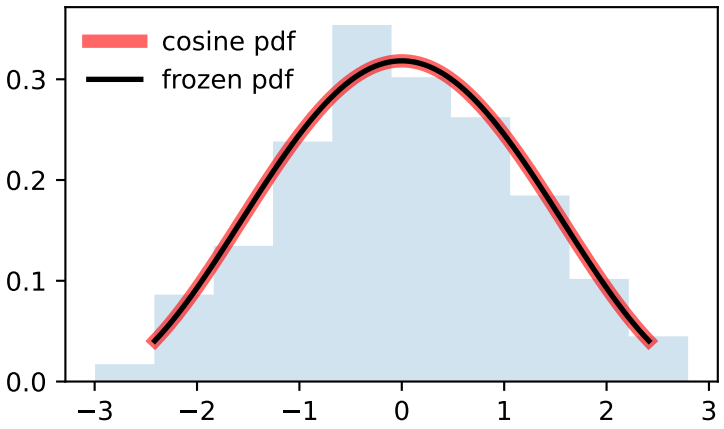
```
>>> vals = cosine.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], cosine.cdf(vals))
True
```

Generate random numbers:

```
>>> r = cosine.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.crystalball

scipy.stats.**crystalball = <scipy.stats._continuous_distns.crystalball_gen object>**

Crystalball distribution

As an instance of the *rv_continuous* class, *crystalball* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *crystalball* is:

$$f(x, \beta, m) = \begin{cases} N \exp(-x^2/2), & \text{for } x > -\beta \\ N A (B - x)^{-m} & \text{for } x \leq -\beta \end{cases}$$

where $A = (m/|\beta|)^m \exp(-\beta^2/2)$, $B = m/|\beta| - |\beta|$ and N is a normalisation constant.

crystalball takes $\beta > 0$ and $m > 1$ as shape parameters. β defines the point where the pdf changes from a power-law to a Gaussian distribution. m is the power of the power-law tail.

References

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `crystalball.pdf(x, beta, m, loc, scale)` is identically equivalent to `crystalball.pdf(y, beta, m) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

New in version 0.19.0.

[1]

Examples

```
>>> from scipy.stats import crystalball
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> beta, m = 2, 3
>>> mean, var, skew, kurt = crystalball.stats(beta, m, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(crystalball.ppf(0.01, beta, m),
...                 crystalball.ppf(0.99, beta, m), 100)
>>> ax.plot(x, crystalball.pdf(x, beta, m),
...         'r-', lw=5, alpha=0.6, label='crystalball pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = crystalball(beta, m)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

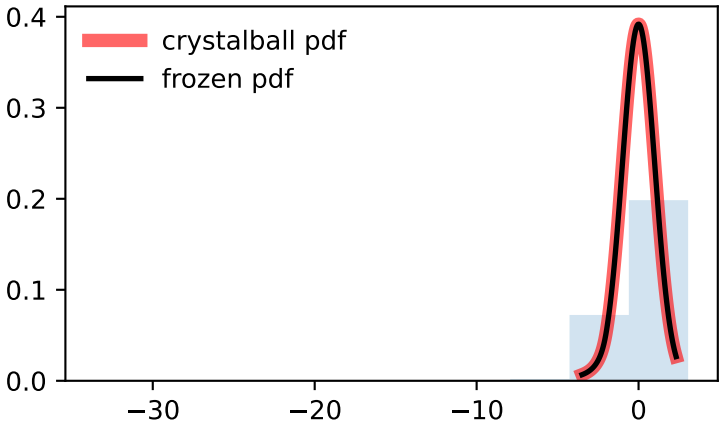
```
>>> vals = crystalball.ppf([0.001, 0.5, 0.999], beta, m)
>>> np.allclose([0.001, 0.5, 0.999], crystalball.cdf(vals, beta, m))
True
```

Generate random numbers:

```
>>> r = crystalball.rvs(beta, m, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(beta, m, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, beta, m, loc=0, scale=1)	Probability density function.
logpdf(x, beta, m, loc=0, scale=1)	Log of the probability density function.
cdf(x, beta, m, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, beta, m, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, beta, m, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, beta, m, loc=0, scale=1)	Log of the survival function.
ppf(q, beta, m, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, beta, m, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, beta, m, loc=0, scale=1)	Non-central moment of order n
stats(beta, m, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(beta, m, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(beta, m), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(beta, m, loc=0, scale=1)	Median of the distribution.
mean(beta, m, loc=0, scale=1)	Mean of the distribution.
var(beta, m, loc=0, scale=1)	Variance of the distribution.
std(beta, m, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, beta, m, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.dgamma

scipy.stats.**dgamma = <scipy.stats._continuous_distns.dgamma_gen object>**

A double gamma continuous random variable.

As an instance of the *rv_continuous* class, *dgamma* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *dgamma* is:

$$f(x, a) = \frac{1}{2\Gamma(a)}|x|^{a-1}\exp(-|x|)$$

for a real number x and $a > 0$. Γ is the gamma function (*scipy.special.gamma*).

dgamma takes `a` as a shape parameter for a.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `dgamma.pdf(x, a, loc, scale)` is identically equivalent to `dgamma.pdf(y, a) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import dgamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 1.1
>>> mean, var, skew, kurt = dgamma.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(dgamma.ppf(0.01, a),
...                 dgamma.ppf(0.99, a), 100)
>>> ax.plot(x, dgamma.pdf(x, a),
...         'r-', lw=5, alpha=0.6, label='dgamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = dgamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

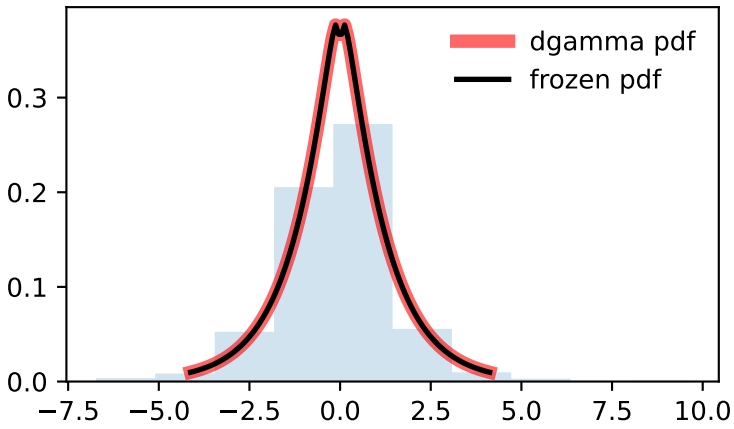
```
>>> vals = dgamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], dgamma.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = dgamma.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.dweibull

scipy.stats.**dweibull = <scipy.stats._continuous_distns.dweibull_gen object>**

A double Weibull continuous random variable.

As an instance of the *rv_continuous* class, *dweibull* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *dweibull* is given by

$$f(x, c) = c/2|x|^{c-1} \exp(-|x|^c)$$

for a real number x and $c > 0$.

dweibull takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `dweibull.pdf(x, c, loc, scale)` is identically equivalent to `dweibull.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import dweibull
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 2.07
>>> mean, var, skew, kurt = dweibull.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(dweibull.ppf(0.01, c),
...                 dweibull.ppf(0.99, c), 100)
>>> ax.plot(x, dweibull.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='dweibull pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = dweibull(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

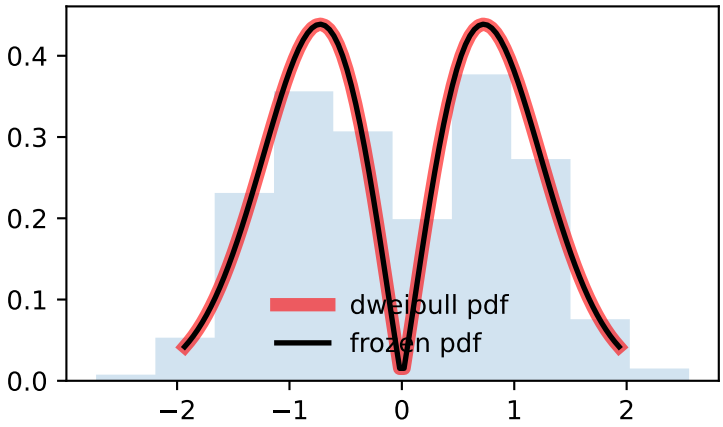
```
>>> vals = dweibull.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], dweibull.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = dweibull.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.erlang

scipy.stats.**erlang = <scipy.stats._continuous_distns.erlang_gen object>**

An Erlang continuous random variable.

As an instance of the *rv_continuous* class, *erlang* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

gamma

Notes

The Erlang distribution is a special case of the Gamma distribution, with the shape parameter a an integer. Note that this restriction is not enforced by *erlang*. It will, however, generate a warning the first time a non-integer value is used for the shape parameter.

Refer to *gamma* for examples.

Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.expon

scipy.stats.**expon = <scipy.stats._continuous_distns.expon_gen object>**

An exponential continuous random variable.

As an instance of the *rv_continuous* class, *expon* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *expon* is:

$$f(x) = \exp(-x)$$

for $x \geq 0$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `expon.pdf(x, loc, scale)` is identically equivalent to `expon.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

A common parameterization for *expon* is in terms of the rate parameter `lambda`, such that `pdf = lambda * exp(-lambda * x)`. This parameterization corresponds to using `scale = 1 / lambda`.

The exponential distribution is a special case of the gamma distributions, with gamma shape parameter `a = 1`.

Examples

```
>>> from scipy.stats import expon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = expon.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(expon.ppf(0.01),
...                 expon.ppf(0.99), 100)
>>> ax.plot(x, expon.pdf(x),
...         'r-', lw=5, alpha=0.6, label='expon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = expon()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

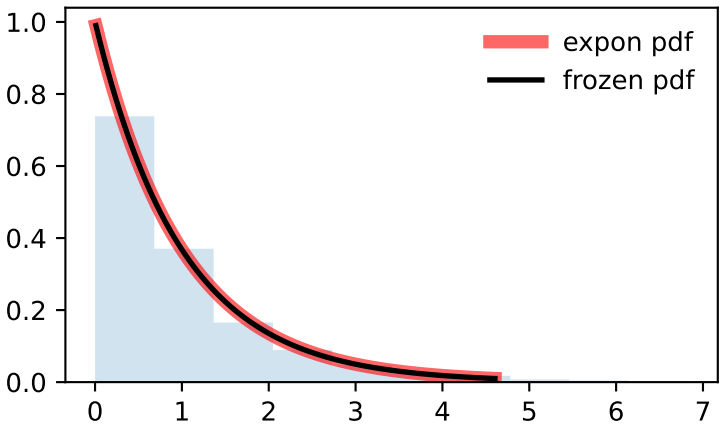
```
>>> vals = expon.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], expon.cdf(vals))
True
```

Generate random numbers:

```
>>> r = expon.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.exponnorm

scipy.stats.**exponnorm = <scipy.stats._continuous_distns.exponnorm_gen object>**

An exponentially modified Normal continuous random variable.

Also known as the exponentially modified Gaussian distribution [1].

As an instance of the *rv_continuous* class, *exponnorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *exponnorm* is:

$$f(x, K) = \frac{1}{2K} \exp\left(\frac{1}{2K^2} - x/K\right) \operatorname{erfc}\left(-\frac{x - 1/K}{\sqrt{2}}\right)$$

where x is a real number and $K > 0$.

It can be thought of as the sum of a standard normal random variable and an independent exponentially distributed random variable with rate `1/K`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `exponnorm.pdf(x, K, loc, scale)` is identically equivalent

to `exponnorm.pdf(y, K) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

An alternative parameterization of this distribution (for example, in the Wikpedia article [1]) involves three parameters, μ, λ and σ.

In the present parameterization this corresponds to having `loc` and `scale` equal to μ and σ, respectively, and shape parameter $K = 1/(\sigma\lambda)$.

New in version 0.16.0.

References

[1]

Examples

```
>>> from scipy.stats import exponnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> K = 1.5
>>> mean, var, skew, kurt = exponnorm.stats(K, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(exponnorm.ppf(0.01, K),
...                 exponnorm.ppf(0.99, K), 100)
>>> ax.plot(x, exponnorm.pdf(x, K),
...         'r-', lw=5, alpha=0.6, label='exponnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = exponnorm(K)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

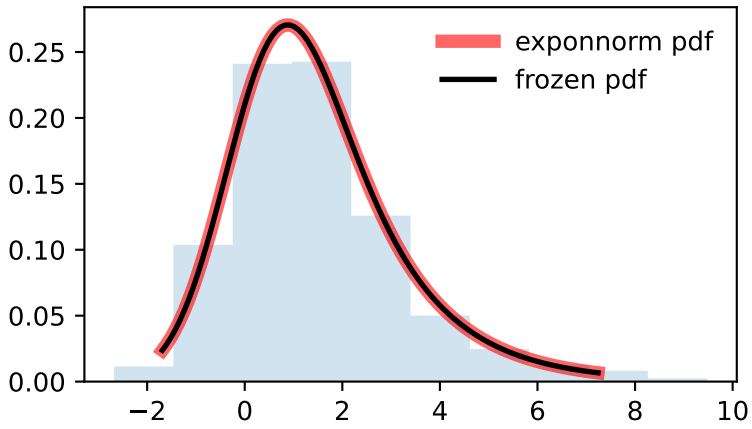
```
>>> vals = exponnorm.ppf([0.001, 0.5, 0.999], K)
>>> np.allclose([0.001, 0.5, 0.999], exponnorm.cdf(vals, K))
True
```

Generate random numbers:

```
>>> r = exponnorm.rvs(K, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(K, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, K, loc=0, scale=1)	Probability density function.
logpdf(x, K, loc=0, scale=1)	Log of the probability density function.
cdf(x, K, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, K, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, K, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, K, loc=0, scale=1)	Log of the survival function.
ppf(q, K, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, K, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, K, loc=0, scale=1)	Non-central moment of order n
stats(K, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(K, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(K,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(K, loc=0, scale=1)	Median of the distribution.
mean(K, loc=0, scale=1)	Mean of the distribution.
var(K, loc=0, scale=1)	Variance of the distribution.
std(K, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, K, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.exponweib

scipy.stats.**exponweib = <scipy.stats._continuous_distns.exponweib_gen object>**

An exponentiated Weibull continuous random variable.

As an instance of the *rv_continuous* class, *exponweib* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

weibull_min, ***numpy.random.Generator.weibull***

Notes

The probability density function for *exponweib* is:

$$f(x, a, c) = ac[1 - \exp(-x^c)]^{a-1} \exp(-x^c)x^{c-1}$$

and its cumulative distribution function is:

$$F(x, a, c) = [1 - \exp(-x^c)]^a$$

for $x > 0$, $a > 0$, $c > 0$.

exponweib takes a and c as shape parameters:

- a is the exponentiation parameter, with the special case $a = 1$ corresponding to the (non-exponentiated) Weibull distribution *weibull_min*.
- c is the shape parameter of the non-exponentiated Weibull law.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `exponweib.pdf(x, a, c, loc, scale)` is identically equivalent to `exponweib.pdf(y, a, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

https://en.wikipedia.org/wiki/Exponentiated_Weibull_distribution

Examples

```
>>> from scipy.stats import exponweib
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, c = 2.89, 1.95
>>> mean, var, skew, kurt = exponweib.stats(a, c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(exponweib.ppf(0.01, a, c),
...                 exponweib.ppf(0.99, a, c), 100)
>>> ax.plot(x, exponweib.pdf(x, a, c),
...         'r-', lw=5, alpha=0.6, label='exponweib pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = exponweib(a, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

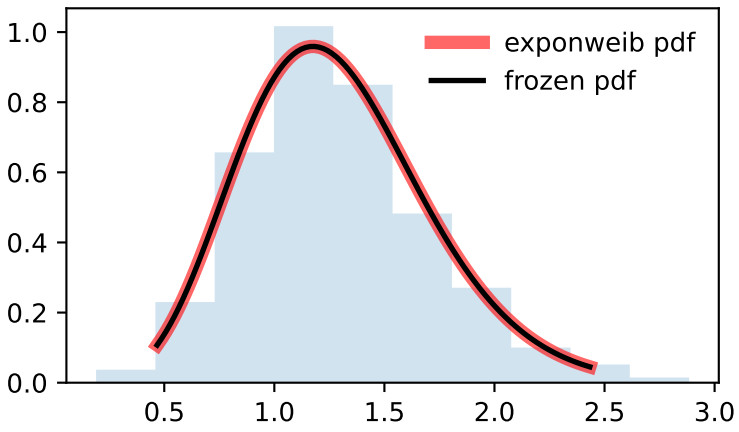
```
>>> vals = exponweib.ppf([0.001, 0.5, 0.999], a, c)
>>> np.allclose([0.001, 0.5, 0.999], exponweib.cdf(vals, a, c))
True
```

Generate random numbers:

```
>>> r = exponweib.rvs(a, c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, c, loc=0, scale=1)	Probability density function.
logpdf(x, a, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, c, loc=0, scale=1)	Log of the survival function.
ppf(q, a, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, c, loc=0, scale=1)	Non-central moment of order n
stats(a, c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, c), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, c, loc=0, scale=1)	Median of the distribution.
mean(a, c, loc=0, scale=1)	Mean of the distribution.
var(a, c, loc=0, scale=1)	Variance of the distribution.
std(a, c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.exponpow

scipy.stats.**exponpow = <scipy.stats._continuous_distns.exponpow_gen object>**

An exponential power continuous random variable.

As an instance of the *rv_continuous* class, *exponpow* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *exponpow* is:

$$f(x, b) = bx^{b-1} \exp(1 + x^b - \exp(x^b))$$

for $x \geq 0$, $b > 0$. Note that this is a different distribution from the exponential power distribution that is also known under the names "generalized normal" or "generalized Gaussian".

exponpow takes `b` as a shape parameter for b.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `exponpow.pdf(x, b, loc, scale)` is identically equivalent to `exponpow.pdf(y, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

http://www.math.wm.edu/~leemis/chart/UDR/PDFs/Exponentialpower.pdf

Examples

```
>>> from scipy.stats import exponpow
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> b = 2.7
>>> mean, var, skew, kurt = exponpow.stats(b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(exponpow.ppf(0.01, b),
...                 exponpow.ppf(0.99, b), 100)
>>> ax.plot(x, exponpow.pdf(x, b),
...         'r-', lw=5, alpha=0.6, label='exponpow pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = exponpow(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

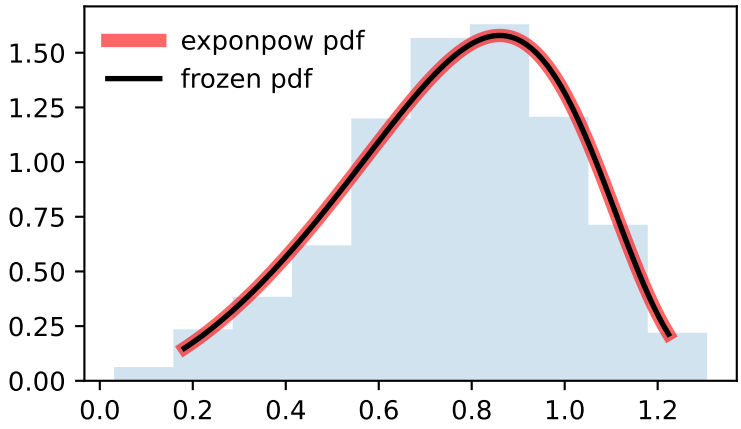
```
>>> vals = exponpow.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], exponpow.cdf(vals, b))
True
```

Generate random numbers:

```
>>> r = exponpow.rvs(b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, b, loc=0, scale=1)	Probability density function.
logpdf(x, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, b, loc=0, scale=1)	Log of the survival function.
ppf(q, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, b, loc=0, scale=1)	Non-central moment of order n
stats(b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(b,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(b, loc=0, scale=1)	Median of the distribution.
mean(b, loc=0, scale=1)	Mean of the distribution.
var(b, loc=0, scale=1)	Variance of the distribution.
std(b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.f

scipy.stats.**f = <scipy.stats._continuous_distns.f_gen object>**

An F continuous random variable.

For the noncentral F distribution, see *ncf*.

As an instance of the *rv_continuous* class, *f* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

ncf

Notes

The probability density function for *f* is:

$$f(x, df_1, df_2) = \frac{df_2^{df_2/2} df_1^{df_1/2} x^{df_1/2-1}}{(df_2 + df_1 x)^{(df_1+df_2)/2} B(df_1/2, df_2/2)}$$

for $x > 0$.

f takes `dfn` and `dfd` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `f.pdf(x, dfn, dfd, loc, scale)` is identically equivalent to `f.pdf(y, dfn, dfd) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import f
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> dfn, dfd = 29, 18
>>> mean, var, skew, kurt = f.stats(dfn, dfd, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(f.ppf(0.01, dfn, dfd),
...                 f.ppf(0.99, dfn, dfd), 100)
>>> ax.plot(x, f.pdf(x, dfn, dfd),
...         'r-', lw=5, alpha=0.6, label='f pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = f(dfn, dfd)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

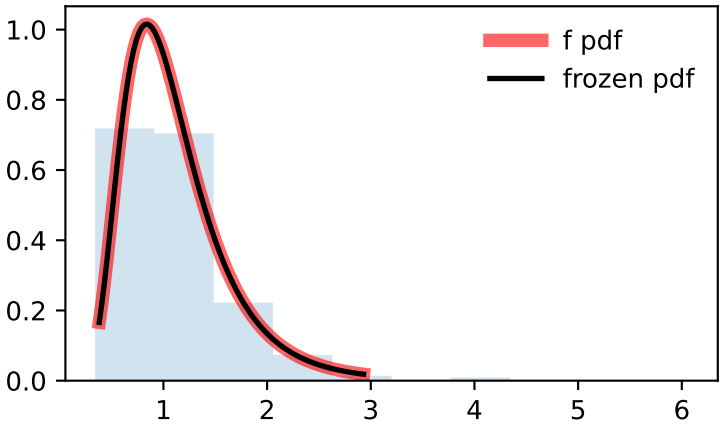
```
>>> vals = f.ppf([0.001, 0.5, 0.999], dfn, dfd)
>>> np.allclose([0.001, 0.5, 0.999], f.cdf(vals, dfn, dfd))
True
```

Generate random numbers:

```
>>> r = f.rvs(dfn, dfd, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(dfn, dfd, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, dfn, dfd, loc=0, scale=1)	Probability density function.
logpdf(x, dfn, dfd, loc=0, scale=1)	Log of the probability density function.
cdf(x, dfn, dfd, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, dfn, dfd, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, dfn, dfd, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, dfn, dfd, loc=0, scale=1)	Log of the survival function.
ppf(q, dfn, dfd, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, dfn, dfd, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, dfn, dfd, loc=0, scale=1)	Non-central moment of order n
stats(dfn, dfd, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(dfn, dfd, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(dfn, dfd), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(dfn, dfd, loc=0, scale=1)	Median of the distribution.
mean(dfn, dfd, loc=0, scale=1)	Mean of the distribution.
var(dfn, dfd, loc=0, scale=1)	Variance of the distribution.
std(dfn, dfd, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, dfn, dfd, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.fatiguelife

scipy.stats.**fatiguelife = <scipy.stats._continuous_distns.fatiguelife_gen object>**

A fatigue-life (Birnbaum-Saunders) continuous random variable.

As an instance of the *rv_continuous* class, *fatiguelife* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *fatiguelife* is:

$$f(x, c) = \frac{x+1}{2c\sqrt{2\pi x^3}} \exp(-\frac{(x-1)^2}{2xc^2})$$

for $x >= 0$ and $c > 0$.

fatiguelife takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `fatiguelife.pdf(x, c, loc, scale)` is identically equivalent to `fatiguelife.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that

shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import fatiguelife
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 29
>>> mean, var, skew, kurt = fatiguelife.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(fatiguelife.ppf(0.01, c),
...                 fatiguelife.ppf(0.99, c), 100)
>>> ax.plot(x, fatiguelife.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='fatiguelife pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = fatiguelife(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

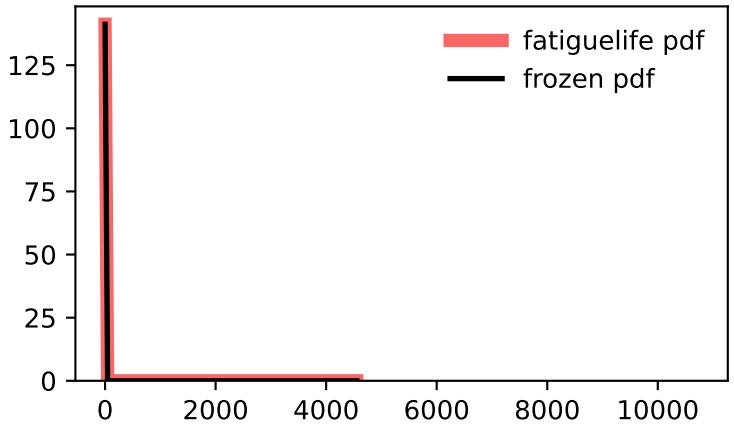
```
>>> vals = fatiguelife.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], fatiguelife.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = fatiguelife.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.fisk

scipy.stats.**fisk = <scipy.stats._continuous_distns.fisk_gen object>**

A Fisk continuous random variable.

The Fisk distribution is also known as the log-logistic distribution.

As an instance of the *rv_continuous* class, *fisk* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

burr

Notes

The probability density function for *fisk* is:

$$f(x, c) = cx^{-c-1}(1 + x^{-c})^{-2}$$

for $x >= 0$ and $c > 0$.

fisk takes `c` as a shape parameter for c.

fisk is a special case of *burr* or *burr12* with `d=1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `fisk.pdf(x, c, loc, scale)` is identically equivalent to `fisk.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import fisk
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 3.09
>>> mean, var, skew, kurt = fisk.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(fisk.ppf(0.01, c),
...                 fisk.ppf(0.99, c), 100)
>>> ax.plot(x, fisk.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='fisk pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = fisk(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

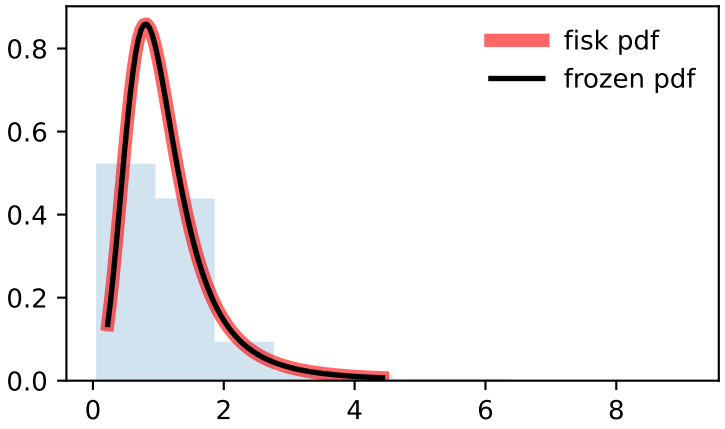
```
>>> vals = fisk.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], fisk.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = fisk.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.foldcauchy

scipy.stats.**foldcauchy = <scipy.stats._continuous_distns.foldcauchy_gen object>**

A folded Cauchy continuous random variable.

As an instance of the *rv_continuous* class, *foldcauchy* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *foldcauchy* is:

$$f(x, c) = \frac{1}{\pi(1 + (x - c)^2)} + \frac{1}{\pi(1 + (x + c)^2)}$$

for $x \geq 0$.

foldcauchy takes `c` as a shape parameter for c.

Examples

```
>>> from scipy.stats import foldcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 4.72
>>> mean, var, skew, kurt = foldcauchy.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(foldcauchy.ppf(0.01, c),
...                 foldcauchy.ppf(0.99, c), 100)
>>> ax.plot(x, foldcauchy.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='foldcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = foldcauchy(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

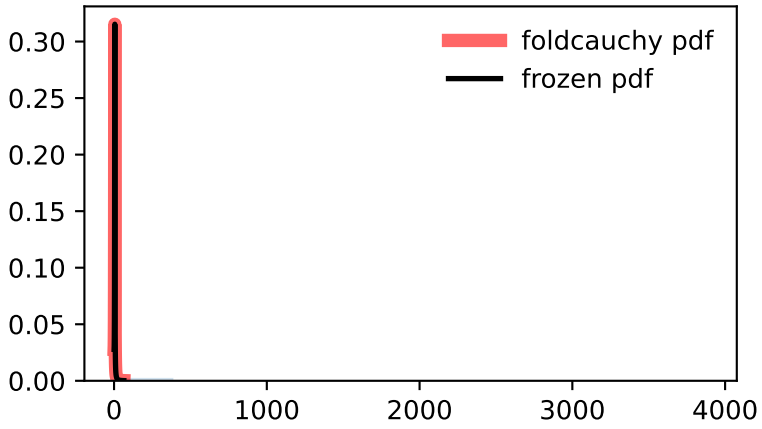
```
>>> vals = foldcauchy.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], foldcauchy.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = foldcauchy.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.foldnorm

scipy.stats.**foldnorm = <scipy.stats._continuous_distns.foldnorm_gen object>**

A folded normal continuous random variable.

As an instance of the *rv_continuous* class, *foldnorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *foldnorm* is:

$$f(x, c) = \sqrt{2/\pi} cosh(cx) \exp(-\frac{x^2+c^2}{2})$$

for $c \geq 0$.

foldnorm takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `foldnorm.pdf(x, c, loc, scale)` is identically equivalent to `foldnorm.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import foldnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 1.95
>>> mean, var, skew, kurt = foldnorm.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(foldnorm.ppf(0.01, c),
...                 foldnorm.ppf(0.99, c), 100)
>>> ax.plot(x, foldnorm.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='foldnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = foldnorm(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

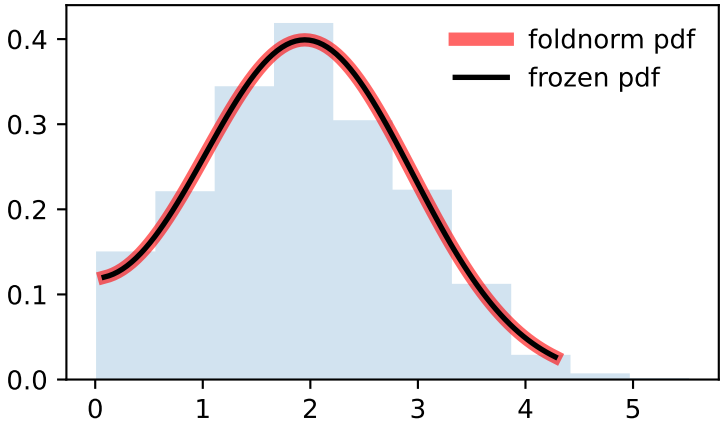
```
>>> vals = foldnorm.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], foldnorm.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = foldnorm.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.genlogistic

scipy.stats.**genlogistic = <scipy.stats._continuous_distns.genlogistic_gen object>**

A generalized logistic continuous random variable.

As an instance of the *rv_continuous* class, *genlogistic* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *genlogistic* is:

$$f(x, c) = c\frac{\exp(-x)}{(1+\exp(-x))^{c+1}}$$

for $x >= 0$, $c > 0$.

genlogistic takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genlogistic.pdf(x, c, loc, scale)` is identically equivalent to `genlogistic.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import genlogistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 0.412
>>> mean, var, skew, kurt = genlogistic.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genlogistic.ppf(0.01, c),
...                 genlogistic.ppf(0.99, c), 100)
>>> ax.plot(x, genlogistic.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='genlogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genlogistic(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

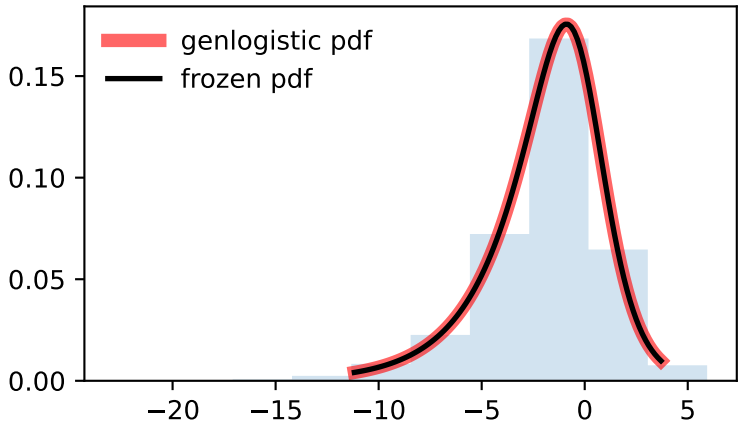
```
>>> vals = genlogistic.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genlogistic.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = genlogistic.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.gennorm

scipy.stats.**gennorm = <scipy.stats._continuous_distns.gennorm_gen object>**

A generalized normal continuous random variable.

As an instance of the *rv_continuous* class, *gennorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

laplace

Laplace distribution

norm

normal distribution

Notes

The probability density function for *gennorm* is [1]:

$$f(x, \beta) = \frac{\beta}{2\Gamma(1/\beta)} \exp(-|x|^\beta)$$

Γ is the gamma function (*scipy.special.gamma*).

gennorm takes `beta` as a shape parameter for β. For $\beta = 1$, it is identical to a Laplace distribution. For $\beta = 2$, it is identical to a normal distribution (with `scale=1/sqrt(2)`).

References

[1]

Examples

```
>>> from scipy.stats import gennorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> beta = 1.3
>>> mean, var, skew, kurt = gennorm.stats(beta, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gennorm.ppf(0.01, beta),
...                 gennorm.ppf(0.99, beta), 100)
>>> ax.plot(x, gennorm.pdf(x, beta),
...         'r-', lw=5, alpha=0.6, label='gennorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gennorm(beta)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

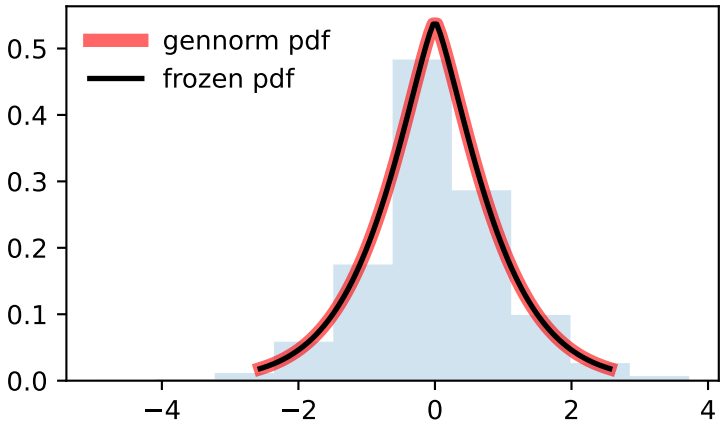
```
>>> vals = gennorm.ppf([0.001, 0.5, 0.999], beta)
>>> np.allclose([0.001, 0.5, 0.999], gennorm.cdf(vals, beta))
True
```

Generate random numbers:

```
>>> r = gennorm.rvs(beta, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(beta, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, beta, loc=0, scale=1)	Probability density function.
logpdf(x, beta, loc=0, scale=1)	Log of the probability density function.
cdf(x, beta, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, beta, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, beta, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, beta, loc=0, scale=1)	Log of the survival function.
ppf(q, beta, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, beta, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, beta, loc=0, scale=1)	Non-central moment of order n
stats(beta, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(beta, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(beta,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(beta, loc=0, scale=1)	Median of the distribution.
mean(beta, loc=0, scale=1)	Mean of the distribution.
var(beta, loc=0, scale=1)	Variance of the distribution.
std(beta, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, beta, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.genpareto

scipy.stats.**genpareto = <scipy.stats._continuous_distns.genpareto_gen object>**

A generalized Pareto continuous random variable.

As an instance of the *rv_continuous* class, *genpareto* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *genpareto* is:

$$f(x, c) = (1 + cx)^{-1-1/c}$$

defined for $x \geq 0$ if $c \geq 0$, and for $0 \leq x \leq -1/c$ if $c < 0$.

genpareto takes `c` as a shape parameter for c.

For $c = 0$, *genpareto* reduces to the exponential distribution, *expon*:

$$f(x, 0) = \exp(-x)$$

For $c = -1$, *genpareto* is uniform on `[0, 1]`:

$$f(x, -1) = 1$$

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genpareto.pdf(x, c, loc, scale)` is identically equivalent to `genpareto.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import genpareto
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 0.1
>>> mean, var, skew, kurt = genpareto.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genpareto.ppf(0.01, c),
...                 genpareto.ppf(0.99, c), 100)
>>> ax.plot(x, genpareto.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='genpareto pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genpareto(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

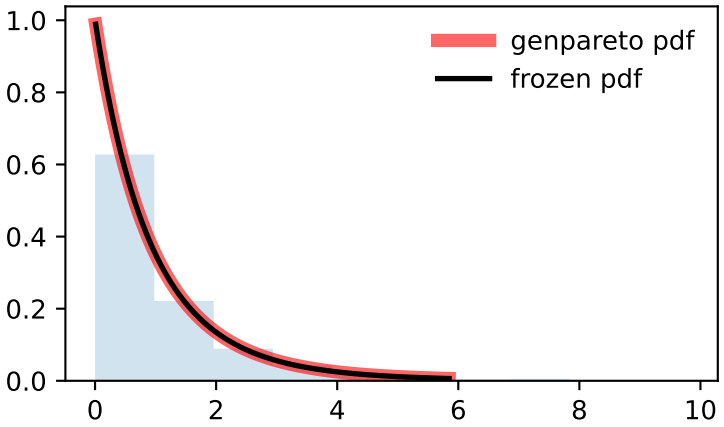
```
>>> vals = genpareto.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genpareto.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = genpareto.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.genexpon

scipy.stats.**genexpon = <scipy.stats._continuous_distns.genexpon_gen object>**

A generalized exponential continuous random variable.

As an instance of the *rv_continuous* class, *genexpon* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *genexpon* is:

$$f(x, a, b, c) = (a + b(1 - \exp(-cx))) \exp(-ax - bx + \frac{b}{c}(1 - \exp(-cx)))$$

for $x \geq 0$, $a, b, c > 0$.

genexpon takes a, b and c as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genexpon.pdf(x, a, b, c, loc, scale)` is identically equivalent to `genexpon.pdf(y, a, b, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

H.K. Ryu, "An Extension of Marshall and Olkin's Bivariate Exponential Distribution", Journal of the American Statistical Association, 1993.

N. Balakrishnan, "The Exponential Distribution: Theory, Methods and Applications", Asit P. Basu.

Examples

```
>>> from scipy.stats import genexpon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b, c = 9.13, 16.2, 3.28
>>> mean, var, skew, kurt = genexpon.stats(a, b, c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genexpon.ppf(0.01, a, b, c),
...                 genexpon.ppf(0.99, a, b, c), 100)
>>> ax.plot(x, genexpon.pdf(x, a, b, c),
...         'r-', lw=5, alpha=0.6, label='genexpon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genexpon(a, b, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

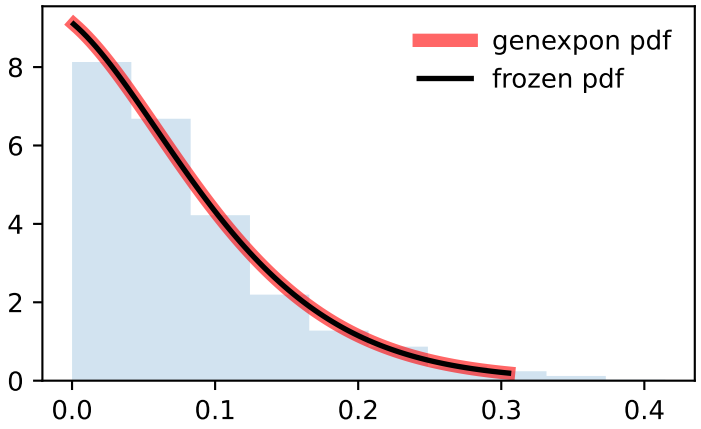
```
>>> vals = genexpon.ppf([0.001, 0.5, 0.999], a, b, c)
>>> np.allclose([0.001, 0.5, 0.999], genexpon.cdf(vals, a, b, c))
True
```

Generate random numbers:

```
>>> r = genexpon.rvs(a, b, c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, b, c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, c, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, c, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, c, loc=0, scale=1)	Non-central moment of order n
stats(a, b, c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b, c), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, c, loc=0, scale=1)	Median of the distribution.
mean(a, b, c, loc=0, scale=1)	Mean of the distribution.
var(a, b, c, loc=0, scale=1)	Variance of the distribution.
std(a, b, c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.genextreme

scipy.stats.**genextreme = <scipy.stats._continuous_distns.genextreme_gen object>**

A generalized extreme value continuous random variable.

As an instance of the *rv_continuous* class, *genextreme* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

gumbel_r

Notes

For $c = 0$, *genextreme* is equal to *gumbel_r*. The probability density function for *genextreme* is:

$$f(x, c) = \begin{cases} \exp(-\exp(-x))\exp(-x) & \text{for } c = 0 \\ \exp(-(1-cx)^{1/c})(1-cx)^{1/c-1} & \text{for } x \le 1/c, c > 0 \end{cases}$$

Note that several sources and software packages use the opposite convention for the sign of the shape parameter c.

genextreme takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genextreme.pdf(x, c, loc, scale)` is identically equivalent to `genextreme.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import genextreme
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = -0.1
>>> mean, var, skew, kurt = genextreme.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genextreme.ppf(0.01, c),
...                 genextreme.ppf(0.99, c), 100)
>>> ax.plot(x, genextreme.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='genextreme pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genextreme(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

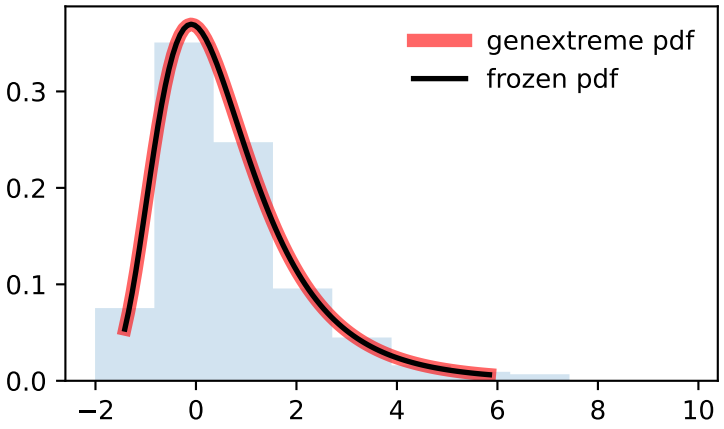
```
>>> vals = genextreme.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genextreme.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = genextreme.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.gausshyper

scipy.stats.**gausshyper = <scipy.stats._continuous_distns.gausshyper_gen object>**

A Gauss hypergeometric continuous random variable.

As an instance of the *rv_continuous* class, *gausshyper* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *gausshyper* is:

$$f(x, a, b, c, z) = Cx^{a-1}(1-x)^{b-1}(1+zx)^{-c}$$

for $0 \leq x \leq 1$, $a > 0$, $b > 0$, $z > -1$, and $C = \frac{1}{B(a,b)F[2,1](c,a;a+b;-z)}$. $F[2,1]$ is the Gauss hypergeometric function *scipy.special.hyp2f1*.

gausshyper takes a, b, c and z as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gausshyper.pdf(x, a, b, c, z, loc, scale)` is identically equivalent to `gausshyper.pdf(y, a, b, c, z) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import gausshyper
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b, c, z = 13.8, 3.12, 2.51, 5.18
>>> mean, var, skew, kurt = gausshyper.stats(a, b, c, z, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gausshyper.ppf(0.01, a, b, c, z),
...                 gausshyper.ppf(0.99, a, b, c, z), 100)
>>> ax.plot(x, gausshyper.pdf(x, a, b, c, z),
...         'r-', lw=5, alpha=0.6, label='gausshyper pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gausshyper(a, b, c, z)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

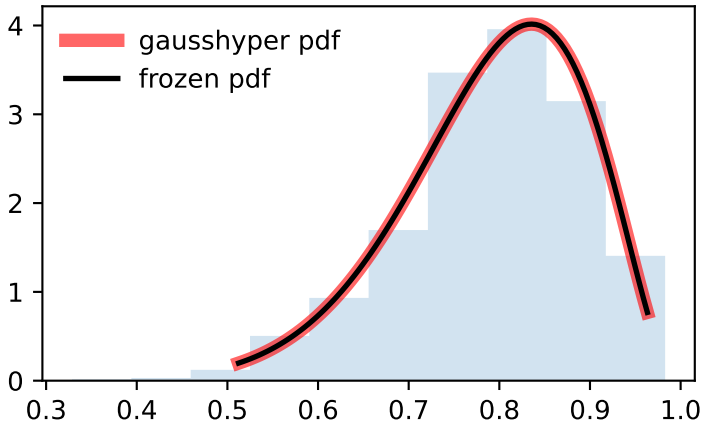
```
>>> vals = gausshyper.ppf([0.001, 0.5, 0.999], a, b, c, z)
>>> np.allclose([0.001, 0.5, 0.999], gausshyper.cdf(vals, a, b, c, z))
True
```

Generate random numbers:

```
>>> r = gausshyper.rvs(a, b, c, z, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, b, c, z, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, c, z, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, c, z, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, c, z, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, c, z, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, c, z, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, c, z, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, c, z, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, c, z, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, c, z, loc=0, scale=1)	Non-central moment of order n
stats(a, b, c, z, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, c, z, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b, c, z), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, c, z, loc=0, scale=1)	Median of the distribution.
mean(a, b, c, z, loc=0, scale=1)	Mean of the distribution.
var(a, b, c, z, loc=0, scale=1)	Variance of the distribution.
std(a, b, c, z, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, c, z, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.gamma

scipy.stats.**gamma = <scipy.stats._continuous_distns.gamma_gen object>**

A gamma continuous random variable.

As an instance of the *rv_continuous* class, *gamma* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

erlang, **expon**

Notes

The probability density function for *gamma* is:

$$f(x, a) = \frac{x^{a-1} e^{-x}}{\Gamma(a)}$$

for $x \geq 0$, $a > 0$. Here $\Gamma(a)$ refers to the gamma function.

gamma takes `a` as a shape parameter for a.

When a is an integer, *gamma* reduces to the Erlang distribution, and when $a = 1$ to the exponential distribution.

Gamma distributions are sometimes parameterized with two variables, with a probability density function of:

$$f(x, \alpha, \beta) = \frac{\beta^{\alpha} x^{\alpha-1} e^{-\beta x}}{\Gamma(\alpha)}$$

Note that this parameterization is equivalent to the above, with `scale = 1 / beta`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gamma.pdf(x, a, loc, scale)` is identically equivalent to `gamma.pdf(y, a) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import gamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 1.99
>>> mean, var, skew, kurt = gamma.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gamma.ppf(0.01, a),
...                 gamma.ppf(0.99, a), 100)
>>> ax.plot(x, gamma.pdf(x, a),
...         'r-', lw=5, alpha=0.6, label='gamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

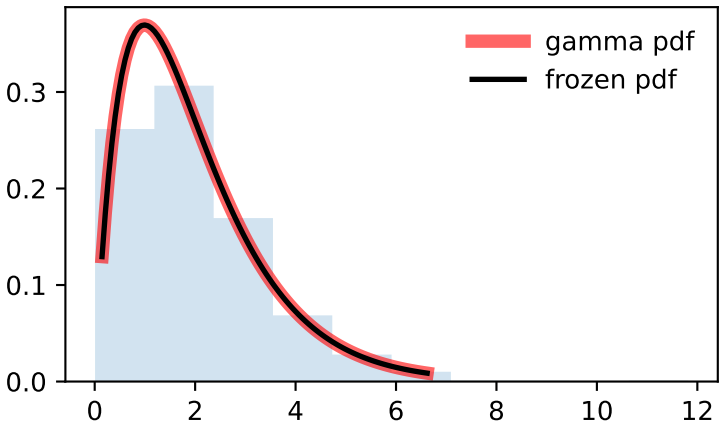
```
>>> vals = gamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], gamma.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = gamma.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.gengamma

scipy.stats.**gengamma = <scipy.stats._continuous_distns.gengamma_gen object>**

A generalized gamma continuous random variable.

As an instance of the *rv_continuous* class, *gengamma* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

gamma, **invgamma**, **weibull_min**

Notes

The probability density function for *gengamma* is ([1]):

$$f(x, a, c) = \frac{|c| x^{ca-1} \exp(-x^c)}{\Gamma(a)}$$

for $x \geq 0$, $a > 0$, and $c \neq 0$. Γ is the gamma function (*scipy.special.gamma*).

gengamma takes a and c as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gengamma.pdf(x, a, c, loc, scale)` is identically equivalent to `gengamma.pdf(y, a, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import gengamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, c = 4.42, -3.12
>>> mean, var, skew, kurt = gengamma.stats(a, c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gengamma.ppf(0.01, a, c),
...                 gengamma.ppf(0.99, a, c), 100)
>>> ax.plot(x, gengamma.pdf(x, a, c),
...         'r-', lw=5, alpha=0.6, label='gengamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gengamma(a, c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

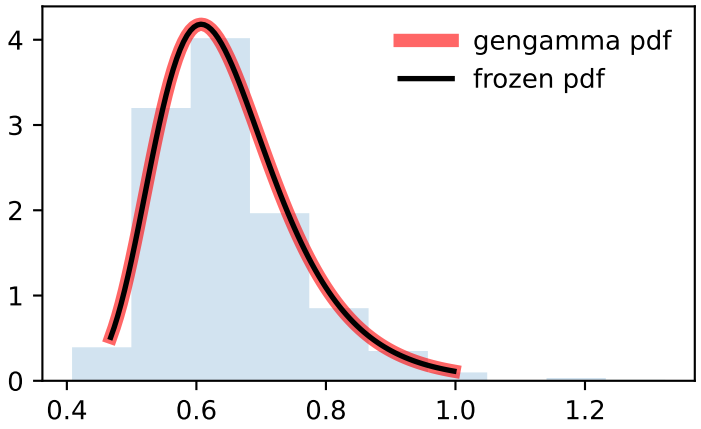
```
>>> vals = gengamma.ppf([0.001, 0.5, 0.999], a, c)
>>> np.allclose([0.001, 0.5, 0.999], gengamma.cdf(vals, a, c))
True
```

Generate random numbers:

```
>>> r = gengamma.rvs(a, c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, c, loc=0, scale=1)	Probability density function.
logpdf(x, a, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, c, loc=0, scale=1)	Log of the survival function.
ppf(q, a, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, c, loc=0, scale=1)	Non-central moment of order n
stats(a, c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, c), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, c, loc=0, scale=1)	Median of the distribution.
mean(a, c, loc=0, scale=1)	Mean of the distribution.
var(a, c, loc=0, scale=1)	Variance of the distribution.
std(a, c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.genhalflogistic

scipy.stats.**genhalflogistic = <scipy.stats._continuous_distns.genhalflogistic_gen object>**

A generalized half-logistic continuous random variable.

As an instance of the *rv_continuous* class, *genhalflogistic* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *genhalflogistic* is:

$$f(x, c) = \frac{2(1 - cx)^{1/(c-1)}}{[1 + (1 - cx)^{1/c}]^2}$$

for $0 \leq x \leq 1/c$, and $c > 0$.

genhalflogistic takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genhalflogistic.pdf(x, c, loc, scale)` is identically equivalent to `genhalflogistic.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import genhalflogistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 0.773
>>> mean, var, skew, kurt = genhalflogistic.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genhalflogistic.ppf(0.01, c),
...                 genhalflogistic.ppf(0.99, c), 100)
>>> ax.plot(x, genhalflogistic.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='genhalflogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genhalflogistic(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

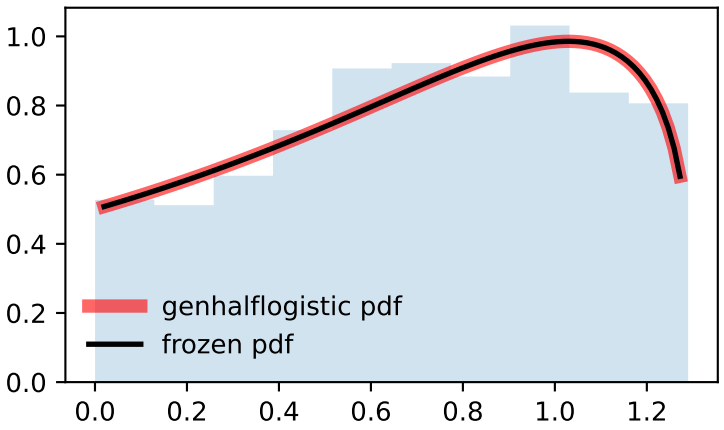
```
>>> vals = genhalflogistic.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], genhalflogistic.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = genhalflogistic.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.genhyperbolic

scipy.stats.**genhyperbolic = <scipy.stats._continuous_distns.genhyperbolic_gen object>**

A generalized hyperbolic continuous random variable.

As an instance of the *rv_continuous* class, *genhyperbolic* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

t, **norminvgauss**, **geninvgauss**, **laplace**, **cauchy**

Notes

The probability density function for *genhyperbolic* is:

$$f(x, p, a, b) = \frac{(a^2 - b^2)^{p/2}}{\sqrt{2\pi}a^{p-0.5}K_p\left(\sqrt{a^2 - b^2}\right)} e^{bx} \times \frac{K_{p-1/2}(a\sqrt{1+x^2})}{(\sqrt{1+x^2})^{1/2-p}}$$

for $x, p \in (-\infty; \infty)$, $|b| < a$ if $p \geq 0$, $|b| \leq a$ if $p < 0$. $K_p(.)$ denotes the modified Bessel function of the second kind and order p (*scipy.special.kn*)

genhyperbolic takes `p` as a tail parameter, `a` as a shape parameter, `b` as a skewness parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `genhyperbolic.pdf(x, p, a, b, loc, scale)` is identically equivalent to `genhyperbolic.pdf(y, p, a, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

The original parameterization of the Generalized Hyperbolic Distribution is found in [1] as follows

$$f(x, \lambda, \alpha, \beta, \delta, \mu) = \frac{(\gamma/\delta)^\lambda}{\sqrt{2\pi}K_\lambda(\delta\gamma)} e^{\beta(x-\mu)} \times \frac{K_{\lambda-1/2}(\alpha\sqrt{\delta^2+(x-\mu)^2})}{(\sqrt{\delta^2+(x-\mu)^2}/\alpha)^{1/2-\lambda}}$$

for $x \in (-\infty; \infty)$, $\gamma := \sqrt{\alpha^2 - \beta^2}$, $\lambda, \mu \in (-\infty; \infty)$, $\delta \geq 0, |\beta| < \alpha$ if $\lambda \geq 0$, $\delta > 0, |\beta| \leq \alpha$ if $\lambda < 0$.

The location-scale-based parameterization implemented in SciPy is based on [2], where $a = \alpha\delta$, $b = \beta\delta$, $p = \lambda$, $scale = \delta$ and $loc = \mu$

Moments are implemented based on [3] and [4].

For the distributions that are a special case such as Student's t, it is not recommended to rely on the implementation of genhyperbolic. To avoid potential numerical problems and for performance reasons, the methods of the specific distributions should be used.

References

[1], [2], [3], [4]

Examples

```
>>> from scipy.stats import genhyperbolic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> p, a, b = 0.5, 1.5, -0.5
>>> mean, var, skew, kurt = genhyperbolic.stats(p, a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(genhyperbolic.ppf(0.01, p, a, b),
...                 genhyperbolic.ppf(0.99, p, a, b), 100)
>>> ax.plot(x, genhyperbolic.pdf(x, p, a, b),
...         'r-', lw=5, alpha=0.6, label='genhyperbolic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = genhyperbolic(p, a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

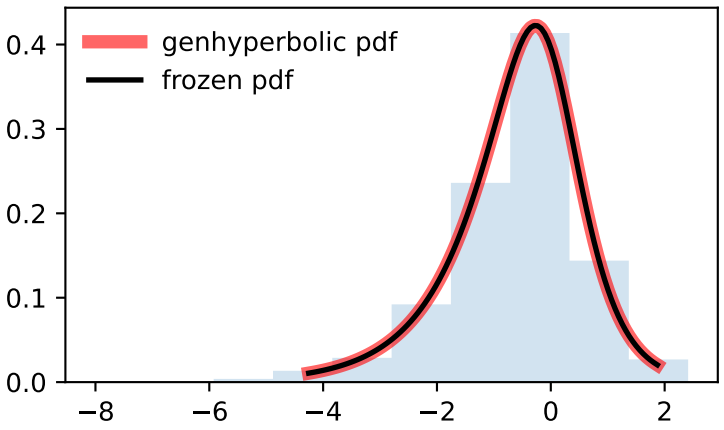
```
>>> vals = genhyperbolic.ppf([0.001, 0.5, 0.999], p, a, b)
>>> np.allclose([0.001, 0.5, 0.999], genhyperbolic.cdf(vals, p, a, b))
True
```

Generate random numbers:

```
>>> r = genhyperbolic.rvs(p, a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(p, a, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, p, a, b, loc=0, scale=1)	Probability density function.
logpdf(x, p, a, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, p, a, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, p, a, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, p, a, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, p, a, b, loc=0, scale=1)	Log of the survival function.
ppf(q, p, a, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, p, a, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, p, a, b, loc=0, scale=1)	Non-central moment of order n
stats(p, a, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(p, a, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(p, a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(p, a, b, loc=0, scale=1)	Median of the distribution.
mean(p, a, b, loc=0, scale=1)	Mean of the distribution.
var(p, a, b, loc=0, scale=1)	Variance of the distribution.
std(p, a, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, p, a, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.geninvgauss

scipy.stats.**geninvgauss = <scipy.stats._continuous_distns.geninvgauss_gen object>**

A Generalized Inverse Gaussian continuous random variable.

As an instance of the *rv_continuous* class, *geninvgauss* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *geninvgauss* is:

$$f(x, p, b) = x^{p-1} \exp(-b(x + 1/x)/2)/(2K_p(b))$$

where $x > 0$, and the parameters p, b satisfy $b > 0$ ([1]). K_p is the modified Bessel function of second kind of order p (*scipy.special.kv*).

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `geninvgauss.pdf(x, p, b, loc, scale)` is identically equivalent to `geninvgauss.pdf(y, p, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

The inverse Gaussian distribution *stats.invgauss(mu)* is a special case of `geninvgauss` with *p = -1/2*, *b = 1 / mu* and *scale = mu*.

Generating random variates is challenging for this distribution. The implementation is based on [2].

References

[1], [2]

Examples

```
>>> from scipy.stats import geninvgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> p, b = 2.3, 1.5
>>> mean, var, skew, kurt = geninvgauss.stats(p, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(geninvgauss.ppf(0.01, p, b),
...                 geninvgauss.ppf(0.99, p, b), 100)
>>> ax.plot(x, geninvgauss.pdf(x, p, b),
...         'r-', lw=5, alpha=0.6, label='geninvgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = geninvgauss(p, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

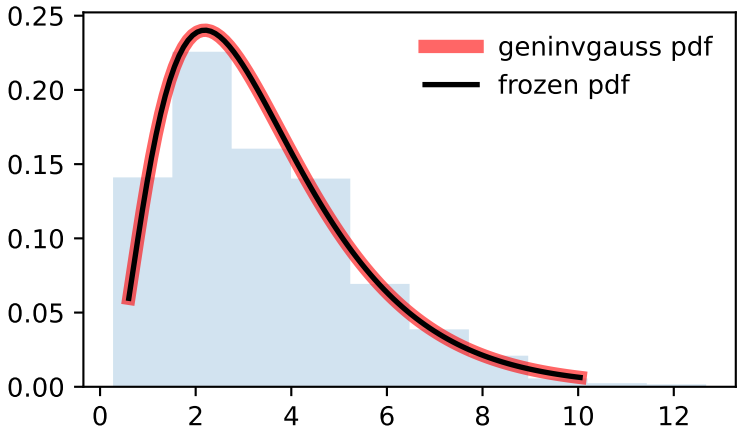
```
>>> vals = geninvgauss.ppf([0.001, 0.5, 0.999], p, b)
>>> np.allclose([0.001, 0.5, 0.999], geninvgauss.cdf(vals, p, b))
True
```

Generate random numbers:

```
>>> r = geninvgauss.rvs(p, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(p, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, p, b, loc=0, scale=1)	Probability density function.
logpdf(x, p, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, p, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, p, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, p, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, p, b, loc=0, scale=1)	Log of the survival function.
ppf(q, p, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, p, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, p, b, loc=0, scale=1)	Non-central moment of order n
stats(p, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(p, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(p, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(p, b, loc=0, scale=1)	Median of the distribution.
mean(p, b, loc=0, scale=1)	Mean of the distribution.
var(p, b, loc=0, scale=1)	Variance of the distribution.
std(p, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, p, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.gilbrat

scipy.stats.**gilbrat = <scipy.stats._continuous_distns.gilbrat_gen object>**

A Gilbrat continuous random variable.

As an instance of the *rv_continuous* class, *gilbrat* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *gilbrat* is:

$$f(x) = \frac{1}{x\sqrt{2\pi}} \exp(-\frac{1}{2}(\log(x))^2)$$

gilbrat is a special case of *lognorm* with `s=1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gilbrat.pdf(x, loc, scale)` is identically equivalent to `gilbrat.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import gilbrat
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = gilbrat.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gilbrat.ppf(0.01),
...                 gilbrat.ppf(0.99), 100)
>>> ax.plot(x, gilbrat.pdf(x),
...         'r-', lw=5, alpha=0.6, label='gilbrat pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gilbrat()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

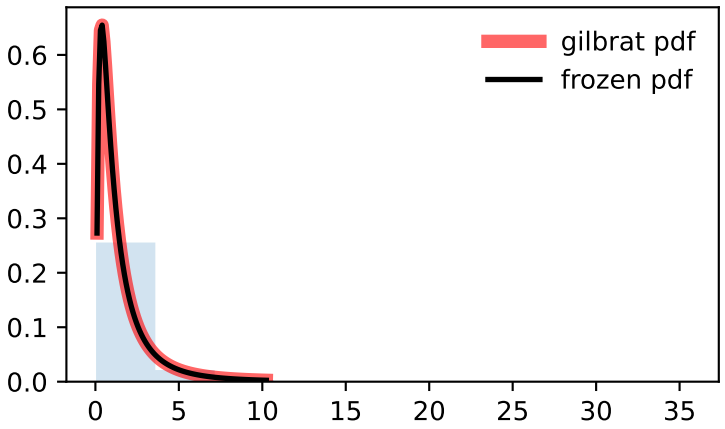
```
>>> vals = gilbrat.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gilbrat.cdf(vals))
True
```

Generate random numbers:

```
>>> r = gilbrat.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.gompertz

scipy.stats.**gompertz = <scipy.stats._continuous_distns.gompertz_gen object>**

A Gompertz (or truncated Gumbel) continuous random variable.

As an instance of the *rv_continuous* class, *gompertz* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *gompertz* is:

$$f(x, c) = c \exp(x) \exp(-c(e^x - 1))$$

for $x \geq 0$, $c > 0$.

gompertz takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gompertz.pdf(x, c, loc, scale)` is identically equivalent to `gompertz.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import gompertz
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 0.947
>>> mean, var, skew, kurt = gompertz.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gompertz.ppf(0.01, c),
...                 gompertz.ppf(0.99, c), 100)
>>> ax.plot(x, gompertz.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='gompertz pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gompertz(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

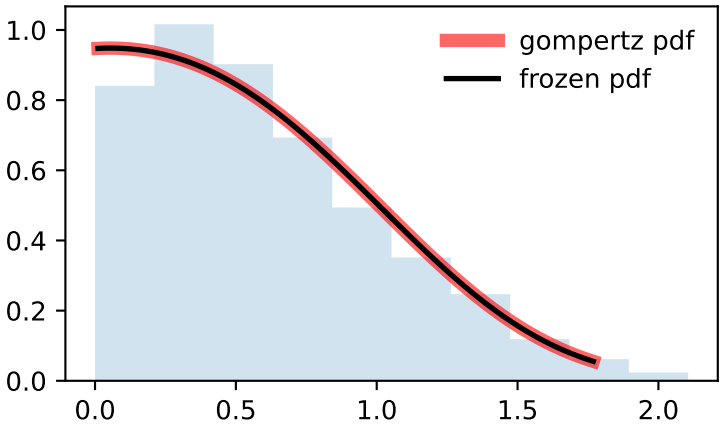
```
>>> vals = gompertz.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], gompertz.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = gompertz.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.gumbel_r

scipy.stats.**gumbel_r = <scipy.stats._continuous_distns.gumbel_r_gen object>**

A right-skewed Gumbel continuous random variable.

As an instance of the *rv_continuous* class, *gumbel_r* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

gumbel_l, **gompertz**, **genextreme**

Notes

The probability density function for *gumbel_r* is:

$$f(x) = \exp(-(x + e^{-x}))$$

The Gumbel distribution is sometimes referred to as a type I Fisher-Tippett distribution. It is also related to the extreme value distribution, log-Weibull and Gompertz distributions.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gumbel_r.pdf(x, loc, scale)` is identically equivalent to `gumbel_r.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import gumbel_r
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = gumbel_r.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gumbel_r.ppf(0.01),
...                 gumbel_r.ppf(0.99), 100)
>>> ax.plot(x, gumbel_r.pdf(x),
...         'r-', lw=5, alpha=0.6, label='gumbel_r pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gumbel_r()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

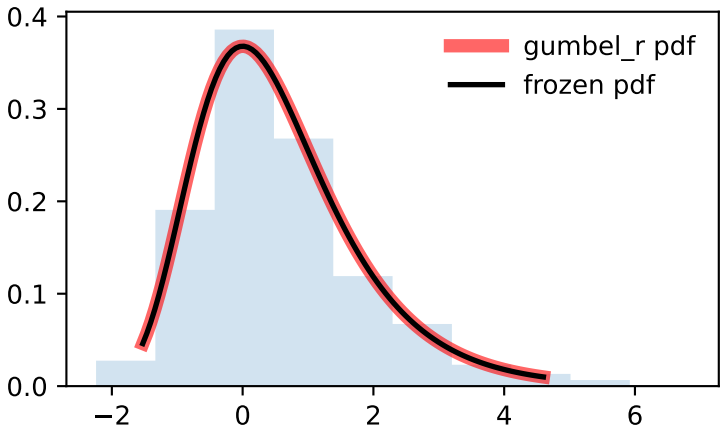
```
>>> vals = gumbel_r.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gumbel_r.cdf(vals))
True
```

Generate random numbers:

```
>>> r = gumbel_r.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.gumbel_l

scipy.stats.**gumbel_l = <scipy.stats._continuous_distns.gumbel_l_gen object>**

A left-skewed Gumbel continuous random variable.

As an instance of the *rv_continuous* class, *gumbel_l* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

gumbel_r, **gompertz**, **genextreme**

Notes

The probability density function for *gumbel_l* is:

$$f(x) = \exp(x - e^x)$$

The Gumbel distribution is sometimes referred to as a type I Fisher-Tippett distribution. It is also related to the extreme value distribution, log-Weibull and Gompertz distributions.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `gumbel_l.pdf(x, loc, scale)` is identically equivalent to

`gumbel_l.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import gumbel_l
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = gumbel_l.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(gumbel_l.ppf(0.01),
...                 gumbel_l.ppf(0.99), 100)
>>> ax.plot(x, gumbel_l.pdf(x),
...         'r-', lw=5, alpha=0.6, label='gumbel_l pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = gumbel_l()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

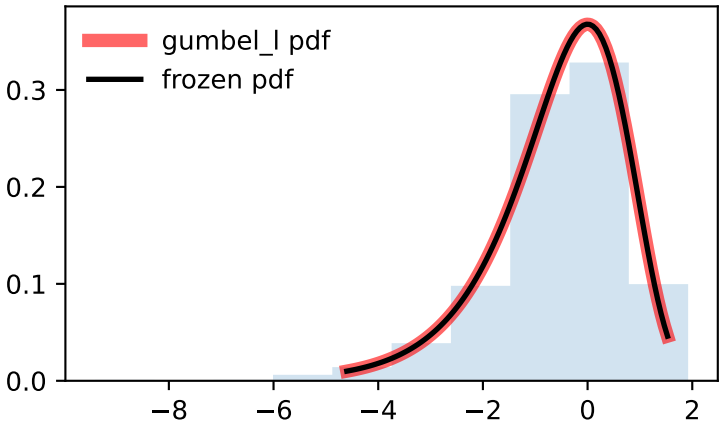
```
>>> vals = gumbel_l.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], gumbel_l.cdf(vals))
True
```

Generate random numbers:

```
>>> r = gumbel_l.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.halfcauchy

scipy.stats.**halfcauchy = <scipy.stats._continuous_distns.halfcauchy_gen object>**

A Half-Cauchy continuous random variable.

As an instance of the *rv_continuous* class, *halfcauchy* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *halfcauchy* is:

$$f(x) = \frac{2}{\pi(1+x^2)}$$

for $x \geq 0$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `halfcauchy.pdf(x, loc, scale)` is identically equivalent to `halfcauchy.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import halfcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = halfcauchy.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(halfcauchy.ppf(0.01),
...                 halfcauchy.ppf(0.99), 100)
>>> ax.plot(x, halfcauchy.pdf(x),
...         'r-', lw=5, alpha=0.6, label='halfcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = halfcauchy()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

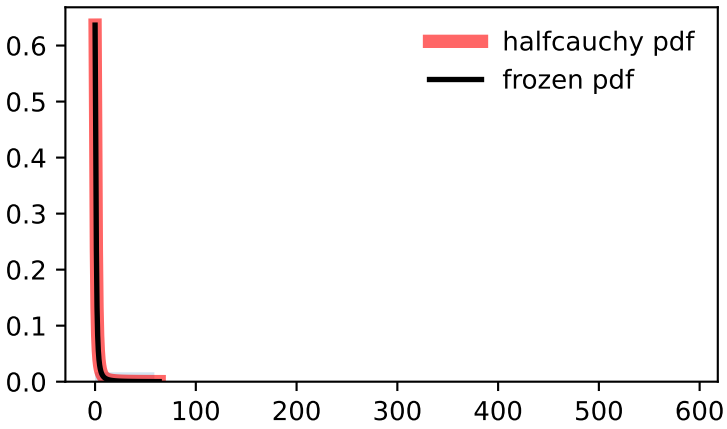
```
>>> vals = halfcauchy.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halfcauchy.cdf(vals))
True
```

Generate random numbers:

```
>>> r = halfcauchy.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.halflogistic

scipy.stats.**halflogistic = <scipy.stats._continuous_distns.halflogistic_gen object>**

A half-logistic continuous random variable.

As an instance of the *rv_continuous* class, *halflogistic* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *halflogistic* is:

$$f(x) = \frac{2e^{-x}}{(1+e^{-x})^2} = \frac{1}{2}\text{sech}(x/2)^2$$

for $x \geq 0$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `halflogistic.pdf(x, loc, scale)` is identically equivalent to `halflogistic.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import halflogistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = halflogistic.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(halflogistic.ppf(0.01),
...                 halflogistic.ppf(0.99), 100)
>>> ax.plot(x, halflogistic.pdf(x),
...         'r-', lw=5, alpha=0.6, label='halflogistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = halflogistic()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

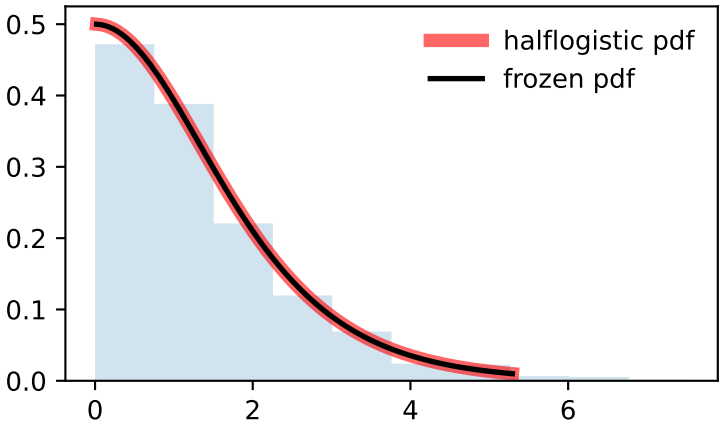
```
>>> vals = halflogistic.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halflogistic.cdf(vals))
True
```

Generate random numbers:

```
>>> r = halflogistic.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.halfnorm

scipy.stats.**halfnorm = <scipy.stats._continuous_distns.halfnorm_gen object>**

A half-normal continuous random variable.

As an instance of the *rv_continuous* class, *halfnorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *halfnorm* is:

$$f(x) = \sqrt{2/\pi}\exp(-x^2/2)$$

for $x >= 0$.

halfnorm is a special case of *chi* with `df=1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `halfnorm.pdf(x, loc, scale)` is identically equivalent to `halfnorm.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import halfnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = halfnorm.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(halfnorm.ppf(0.01),
...                 halfnorm.ppf(0.99), 100)
>>> ax.plot(x, halfnorm.pdf(x),
...         'r-', lw=5, alpha=0.6, label='halfnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = halfnorm()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

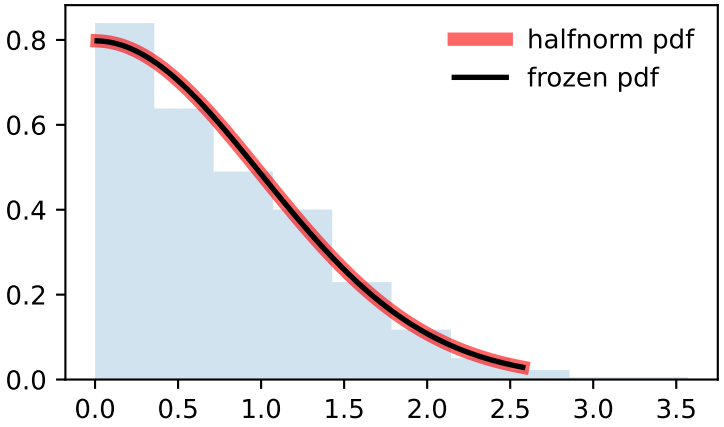
```
>>> vals = halfnorm.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], halfnorm.cdf(vals))
True
```

Generate random numbers:

```
>>> r = halfnorm.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.halfgennorm

scipy.stats.**halfgennorm = <scipy.stats._continuous_distns.halfgennorm_gen object>**

The upper half of a generalized normal continuous random variable.

As an instance of the *rv_continuous* class, *halfgennorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

gennorm

generalized normal distribution

expon

exponential distribution

halfnorm

half normal distribution

Notes

The probability density function for *halfgennorm* is:

$$f(x, \beta) = \frac{\beta}{\Gamma(1/\beta)} \exp(-|x|^\beta)$$

for $x > 0$. Γ is the gamma function (*scipy.special.gamma*).

gennorm takes `beta` as a shape parameter for β. For $\beta = 1$, it is identical to an exponential distribution. For $\beta = 2$, it is identical to a half normal distribution (with `scale=1/sqrt(2)`).

References

[1]

Examples

```
>>> from scipy.stats import halfgennorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> beta = 0.675
>>> mean, var, skew, kurt = halfgennorm.stats(beta, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(halfgennorm.ppf(0.01, beta),
...                 halfgennorm.ppf(0.99, beta), 100)
>>> ax.plot(x, halfgennorm.pdf(x, beta),
...         'r-', lw=5, alpha=0.6, label='halfgennorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = halfgennorm(beta)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

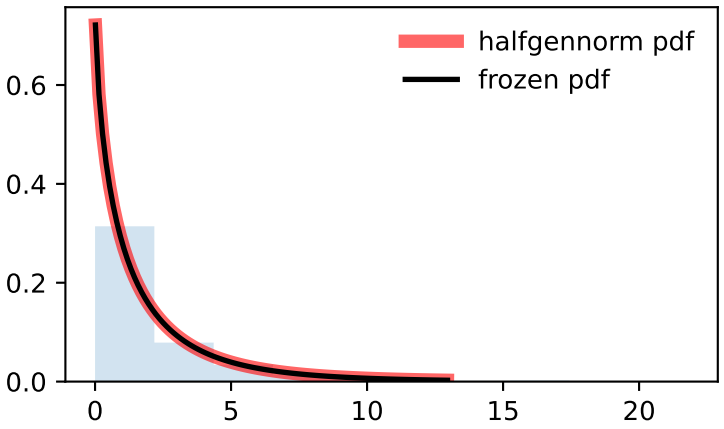
```
>>> vals = halfgennorm.ppf([0.001, 0.5, 0.999], beta)
>>> np.allclose([0.001, 0.5, 0.999], halfgennorm.cdf(vals, beta))
True
```

Generate random numbers:

```
>>> r = halfgennorm.rvs(beta, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(beta, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, beta, loc=0, scale=1)	Probability density function.
logpdf(x, beta, loc=0, scale=1)	Log of the probability density function.
cdf(x, beta, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, beta, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, beta, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, beta, loc=0, scale=1)	Log of the survival function.
ppf(q, beta, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, beta, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, beta, loc=0, scale=1)	Non-central moment of order n
stats(beta, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(beta, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(beta,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(beta, loc=0, scale=1)	Median of the distribution.
mean(beta, loc=0, scale=1)	Mean of the distribution.
var(beta, loc=0, scale=1)	Variance of the distribution.
std(beta, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, beta, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.hypsecant

scipy.stats.**hypsecant = <scipy.stats._continuous_distns.hypsecant_gen object>**

A hyperbolic secant continuous random variable.

As an instance of the *rv_continuous* class, *hypsecant* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *hypsecant* is:

$$f(x) = \frac{1}{\pi}\text{sech}(x)$$

for a real number x.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `hypsecant.pdf(x, loc, scale)` is identically equivalent to `hypsecant.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import hypsecant
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = hypsecant.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(hypsecant.ppf(0.01),
...                 hypsecant.ppf(0.99), 100)
>>> ax.plot(x, hypsecant.pdf(x),
...         'r-', lw=5, alpha=0.6, label='hypsecant pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = hypsecant()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

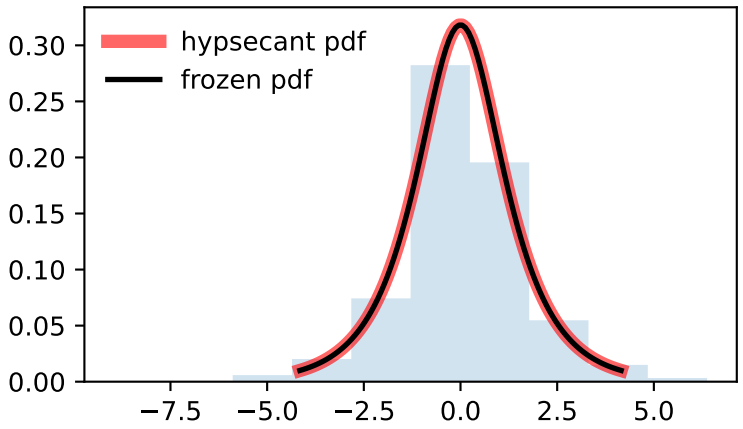
```
>>> vals = hypsecant.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], hypsecant.cdf(vals))
True
```

Generate random numbers:

```
>>> r = hypsecant.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.invgamma

scipy.stats.**invgamma = <scipy.stats._continuous_distns.invgamma_gen object>**

An inverted gamma continuous random variable.

As an instance of the *rv_continuous* class, *invgamma* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *invgamma* is:

$$f(x, a) = \frac{x^{-a-1}}{\Gamma(a)} \exp(-\frac{1}{x})$$

for $x >= 0$, $a > 0$. Γ is the gamma function (*scipy.special.gamma*).

invgamma takes `a` as a shape parameter for a.

invgamma is a special case of *gengamma* with `c=-1`, and it is a different parameterization of the scaled inverse chi-squared distribution. Specifically, if the scaled inverse chi-squared distribution is parameterized with degrees of freedom ν and scaling parameter τ^2, then it can be modeled using *invgamma* with `a=` $\nu/2$ and `scale=` $\nu\tau^2/2$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `invgamma.pdf(x, a, loc, scale)` is identically equivalent to `invgamma.pdf(y, a) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import invgamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 4.07
>>> mean, var, skew, kurt = invgamma.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(invgamma.ppf(0.01, a),
...                 invgamma.ppf(0.99, a), 100)
>>> ax.plot(x, invgamma.pdf(x, a),
...         'r-', lw=5, alpha=0.6, label='invgamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = invgamma(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

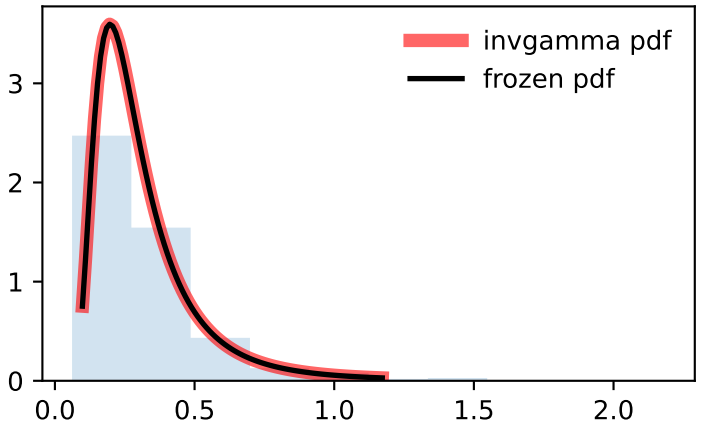
```
>>> vals = invgamma.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], invgamma.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = invgamma.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.invgauss

scipy.stats.**invgauss = <scipy.stats._continuous_distns.invgauss_gen object>**

An inverse Gaussian continuous random variable.

As an instance of the *rv_continuous* class, *invgauss* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *invgauss* is:

$$f(x, \mu) = \frac{1}{\sqrt{2\pi x^3}} \exp(-\frac{(x-\mu)^2}{2x\mu^2})$$

for $x >= 0$ and $\mu > 0$.

invgauss takes `mu` as a shape parameter for μ.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `invgauss.pdf(x, mu, loc, scale)` is identically equivalent to `invgauss.pdf(y, mu) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import invgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mu = 0.145
>>> mean, var, skew, kurt = invgauss.stats(mu, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(invgauss.ppf(0.01, mu),
...                 invgauss.ppf(0.99, mu), 100)
>>> ax.plot(x, invgauss.pdf(x, mu),
...         'r-', lw=5, alpha=0.6, label='invgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = invgauss(mu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

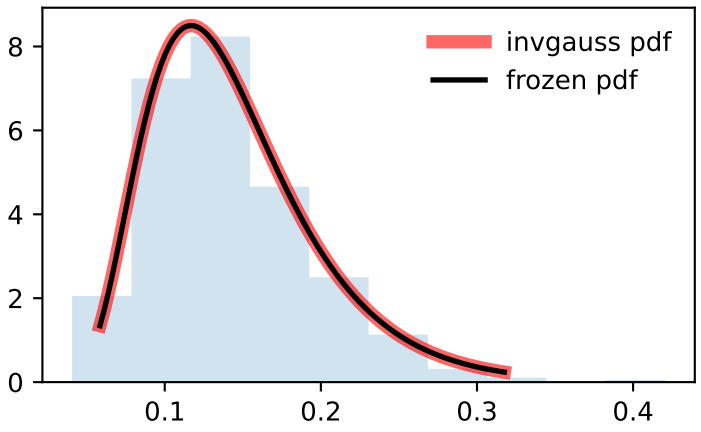
```
>>> vals = invgauss.ppf([0.001, 0.5, 0.999], mu)
>>> np.allclose([0.001, 0.5, 0.999], invgauss.cdf(vals, mu))
True
```

Generate random numbers:

```
>>> r = invgauss.rvs(mu, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(mu, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, mu, loc=0, scale=1)	Probability density function.
logpdf(x, mu, loc=0, scale=1)	Log of the probability density function.
cdf(x, mu, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, mu, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, mu, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, mu, loc=0, scale=1)	Log of the survival function.
ppf(q, mu, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, mu, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, mu, loc=0, scale=1)	Non-central moment of order n
stats(mu, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(mu, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(mu,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(mu, loc=0, scale=1)	Median of the distribution.
mean(mu, loc=0, scale=1)	Mean of the distribution.
var(mu, loc=0, scale=1)	Variance of the distribution.
std(mu, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, mu, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.invweibull

scipy.stats.**invweibull = <scipy.stats._continuous_distns.invweibull_gen object>**

An inverted Weibull continuous random variable.

This distribution is also known as the Fréchet distribution or the type II extreme value distribution.

As an instance of the *rv_continuous* class, *invweibull* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *invweibull* is:

$$f(x, c) = cx^{-c-1} \exp(-x^{-c})$$

for $x > 0$, $c > 0$.

invweibull takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `invweibull.pdf(x, c, loc, scale)` is identically equivalent to `invweibull.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location

of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

F.R.S. de Gusmao, E.M.M Ortega and G.M. Cordeiro, "The generalized inverse Weibull distribution", Stat. Papers, vol. 52, pp. 591-619, 2011.

Examples

```
>>> from scipy.stats import invweibull
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 10.6
>>> mean, var, skew, kurt = invweibull.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(invweibull.ppf(0.01, c),
...                 invweibull.ppf(0.99, c), 100)
>>> ax.plot(x, invweibull.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='invweibull pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = invweibull(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

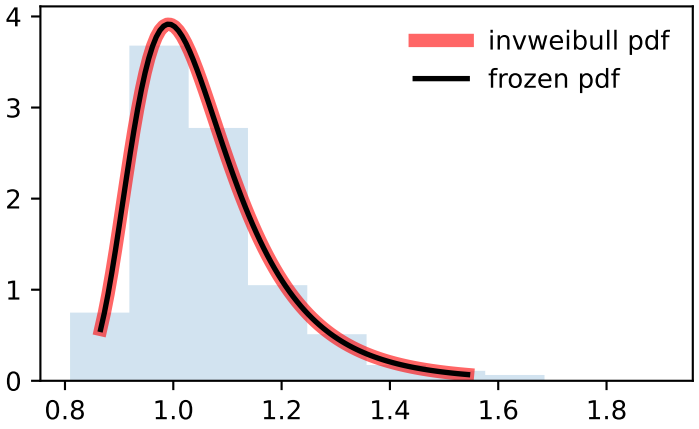
```
>>> vals = invweibull.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], invweibull.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = invweibull.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.johnsonsb

scipy.stats.**johnsonsb = <scipy.stats._continuous_distns.johnsonsb_gen object>**

A Johnson SB continuous random variable.

As an instance of the *rv_continuous* class, *johnsonsb* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

johnsonsu

Notes

The probability density function for *johnsonsb* is:

$$f(x, a, b) = \frac{b}{x(1-x)}\phi(a + b\log\frac{x}{1-x})$$

where x, a, and b are real scalars; $b > 0$ and $x \in [0, 1]$. ϕ is the pdf of the normal distribution.

johnsonsb takes a and b as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `johnsonsb.pdf(x, a, b, loc, scale)` is identically equivalent to `johnsonsb.pdf(y, a, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import johnsonsb
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b = 4.32, 3.18
>>> mean, var, skew, kurt = johnsonsb.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(johnsonsb.ppf(0.01, a, b),
...                 johnsonsb.ppf(0.99, a, b), 100)
>>> ax.plot(x, johnsonsb.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='johnsonsb pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = johnsonsb(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

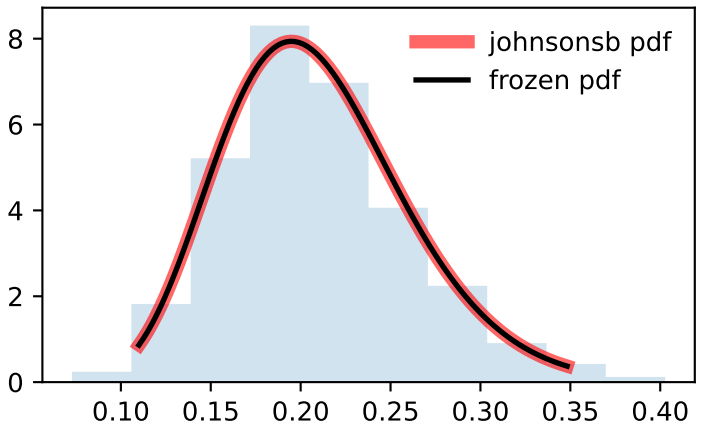
```
>>> vals = johnsonsb.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], johnsonsb.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = johnsonsb.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, loc=0, scale=1)	Non-central moment of order n
stats(a, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, loc=0, scale=1)	Median of the distribution.
mean(a, b, loc=0, scale=1)	Mean of the distribution.
var(a, b, loc=0, scale=1)	Variance of the distribution.
std(a, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.johnsonsu

scipy.stats.**johnsonsu = <scipy.stats._continuous_distns.johnsonsu_gen object>**

A Johnson SU continuous random variable.

As an instance of the *rv_continuous* class, *johnsonsu* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

johnsonsb

Notes

The probability density function for *johnsonsu* is:

$$f(x, a, b) = \frac{b}{\sqrt{x^2 + 1}} \phi(a + b \log(x + \sqrt{x^2 + 1}))$$

where x, a, and b are real scalars; $b > 0$. ϕ is the pdf of the normal distribution.

johnsonsu takes a and b as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `johnsonsu.pdf(x, a, b, loc, scale)` is identically equivalent to `johnsonsu.pdf(y, a, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import johnsonsu
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b = 2.55, 2.25
>>> mean, var, skew, kurt = johnsonsu.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(johnsonsu.ppf(0.01, a, b),
...                 johnsonsu.ppf(0.99, a, b), 100)
>>> ax.plot(x, johnsonsu.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='johnsonsu pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = johnsonsu(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

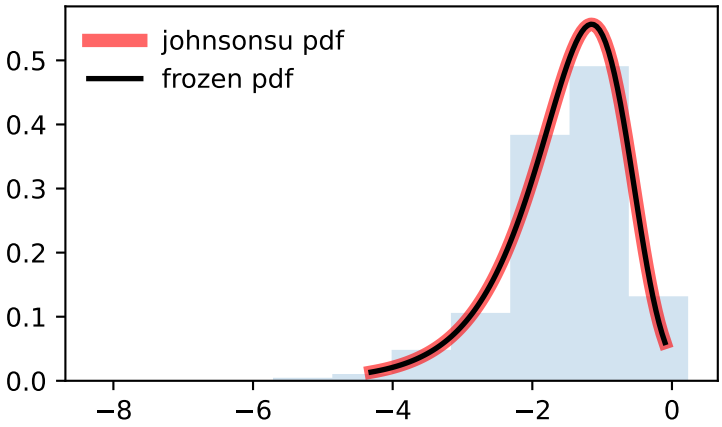
```
>>> vals = johnsonsu.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], johnsonsu.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = johnsonsu.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, loc=0, scale=1)	Non-central moment of order n
stats(a, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, loc=0, scale=1)	Median of the distribution.
mean(a, b, loc=0, scale=1)	Mean of the distribution.
var(a, b, loc=0, scale=1)	Variance of the distribution.
std(a, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.kappa4

scipy.stats.**kappa4 = <scipy.stats._continuous_distns.kappa4_gen object>**

Kappa 4 parameter distribution.

As an instance of the *rv_continuous* class, *kappa4* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for kappa4 is:

$$f(x, h, k) = (1 - kx)^{1/k-1}(1 - h(1 - kx)^{1/k})^{1/h-1}$$

if h and k are not equal to 0.

If h or k are zero then the pdf can be simplified:

h = 0 and k != 0:

```
kappa4.pdf(x, h, k) = (1.0 - k*x)**(1.0/k - 1.0)*
                      exp(-(1.0 - k*x)**(1.0/k))
```

h != 0 and k = 0:

```
kappa4.pdf(x, h, k) = exp(-x)*(1.0 - h*exp(-x))**(1.0/h - 1.0)
```

h = 0 and k = 0:

```
kappa4.pdf(x, h, k) = exp(-x)*exp(-exp(-x))
```

kappa4 takes h and k as shape parameters.

The kappa4 distribution returns other distributions when certain h and k values are used.

h	k=0.0	k=1.0	-inf<=k<=inf
-1.0	Logistic logistic(x)		Generalized Logistic(1)
0.0	Gumbel gumbel_r(x)	Reverse Exponential(2)	Generalized Extreme Value genextreme(x, k)
1.0	Exponential expon(x)	Uniform uniform(x)	Generalized Pareto genpareto(x, -k)

(1) There are at least five generalized logistic distributions. Four are described here: https://en.wikipedia.org/wiki/Generalized_logistic_distribution The "fifth" one is the one kappa4 should match which currently isn't implemented in scipy: https://en.wikipedia.org/wiki/Talk:Generalized_logistic_distribution https://www.mathwave.com/help/easyfit/html/analyses/distributions/gen_logistic.html

(2) This distribution is currently not in scipy.

References

J.C. Finney, “Optimization of a Skewed Logistic Distribution With Respect to the Kolmogorov-Smirnov Test”, A Dissertation Submitted to the Graduate Faculty of the Louisiana State University and Agricultural and Mechanical College, (August, 2004), https://digitalcommons.lsu.edu/gradschool_dissertations/3672

J.R.M. Hosking, “The four-parameter kappa distribution”. IBM J. Res. Develop. 38 (3), 25 1-258 (1994).

B. Kumphon, A. Kaew-Man, P. Seenoi, “A Rainfall Distribution for the Lampao Site in the Chi River Basin, Thailand”, Journal of Water Resource and Protection, vol. 4, 866-869, (2012). DOI:10.4236/jwarp.2012.410101

C. Winchester, “On Estimation of the Four-Parameter Kappa Distribution”, A Thesis Submitted to Dalhousie University, Halifax, Nova Scotia, (March 2000). http://www.nlc-bnc.ca/obj/s4/f2/dsk2/ftp01/MQ57336.pdf

The probability density above is defined in the “standardized” form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `kappa4.pdf(x, h, k, loc, scale)` is identically equivalent to `kappa4.pdf(y, h, k) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a “noncentral” distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import kappa4
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> h, k = 0.1, 0
>>> mean, var, skew, kurt = kappa4.stats(h, k, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(kappa4.ppf(0.01, h, k),
...                 kappa4.ppf(0.99, h, k), 100)
>>> ax.plot(x, kappa4.pdf(x, h, k),
...         'r-', lw=5, alpha=0.6, label='kappa4 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a “frozen” RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = kappa4(h, k)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

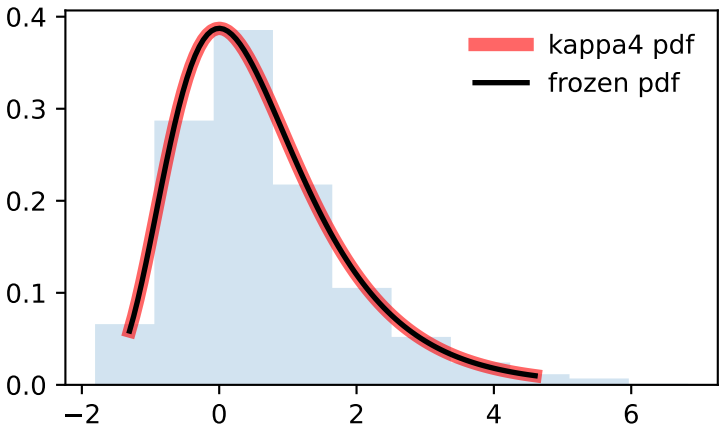
```
>>> vals = kappa4.ppf([0.001, 0.5, 0.999], h, k)
>>> np.allclose([0.001, 0.5, 0.999], kappa4.cdf(vals, h, k))
True
```

Generate random numbers:

```
>>> r = kappa4.rvs(h, k, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(h, k, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, h, k, loc=0, scale=1)	Probability density function.
logpdf(x, h, k, loc=0, scale=1)	Log of the probability density function.
cdf(x, h, k, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, h, k, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, h, k, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, h, k, loc=0, scale=1)	Log of the survival function.
ppf(q, h, k, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, h, k, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, h, k, loc=0, scale=1)	Non-central moment of order n
stats(h, k, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(h, k, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(h, k), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(h, k, loc=0, scale=1)	Median of the distribution.
mean(h, k, loc=0, scale=1)	Mean of the distribution.
var(h, k, loc=0, scale=1)	Variance of the distribution.
std(h, k, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, h, k, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.kappa3

scipy.stats.**kappa3 = <scipy.stats._continuous_distns.kappa3_gen object>**

Kappa 3 parameter distribution.

As an instance of the *rv_continuous* class, *kappa3* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *kappa3* is:

$$f(x, a) = a(a + x^a)^{-(a+1)/a}$$

for $x > 0$ and $a > 0$.

kappa3 takes `a` as a shape parameter for a.

References

P.W. Mielke and E.S. Johnson, "Three-Parameter Kappa Distribution Maximum Likelihood and Likelihood Ratio Tests", Methods in Weather Research, 701-707, (September, 1973), DOI:10.1175/1520-0493(1973)101<0701:TKDMLE>2.3.CO;2

B. Kumphon, "Maximum Entropy and Maximum Likelihood Estimation for the Three-Parameter Kappa Distribution", Open Journal of Statistics, vol 2, 415-419 (2012), DOI:10.4236/ojs.2012.24050

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `kappa3.pdf(x, a, loc, scale)` is identically equivalent to `kappa3.pdf(y, a) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import kappa3
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 1
>>> mean, var, skew, kurt = kappa3.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(kappa3.ppf(0.01, a),
...                 kappa3.ppf(0.99, a), 100)
>>> ax.plot(x, kappa3.pdf(x, a),
...         'r-', lw=5, alpha=0.6, label='kappa3 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = kappa3(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

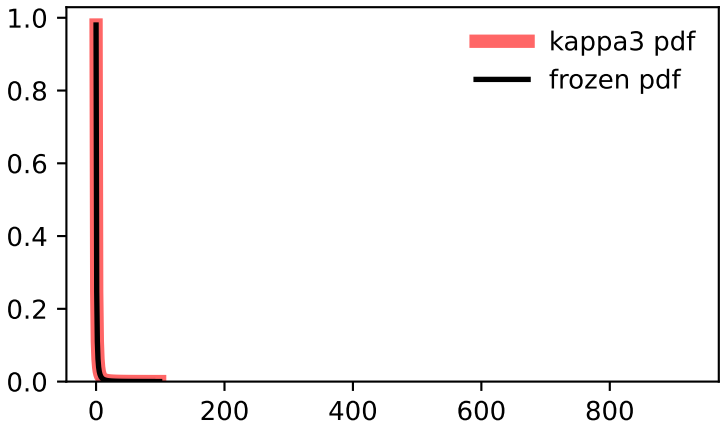
```
>>> vals = kappa3.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], kappa3.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = kappa3.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.ksone

scipy.stats.**ksone = <scipy.stats._continuous_distns.ksone_gen object>**

Kolmogorov-Smirnov one-sided test statistic distribution.

This is the distribution of the one-sided Kolmogorov-Smirnov (KS) statistics D_n^+ and D_n^- for a finite sample size `n` (the shape parameter).

As an instance of the *rv_continuous* class, *ksone* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

kstwobign, **kstwo**, **kstest**

Notes

D_n^+ and D_n^- are given by

$$D_n^+ = \sup_x(F_n(x) - F(x)),$$
$$D_n^- = \sup_x(F(x) - F_n(x)),$$

where F is a continuous CDF and F_n is an empirical CDF. *ksone* describes the distribution under the null hypothesis of the KS test that the empirical CDF corresponds to n i.i.d. random variates with CDF F.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `ksone.pdf(x, n, loc, scale)` is identically equivalent to `ksone.pdf(y, n) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import ksone
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> n = 1e+03
>>> mean, var, skew, kurt = ksone.stats(n, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(ksone.ppf(0.01, n),
...                 ksone.ppf(0.99, n), 100)
>>> ax.plot(x, ksone.pdf(x, n),
...         'r-', lw=5, alpha=0.6, label='ksone pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = ksone(n)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

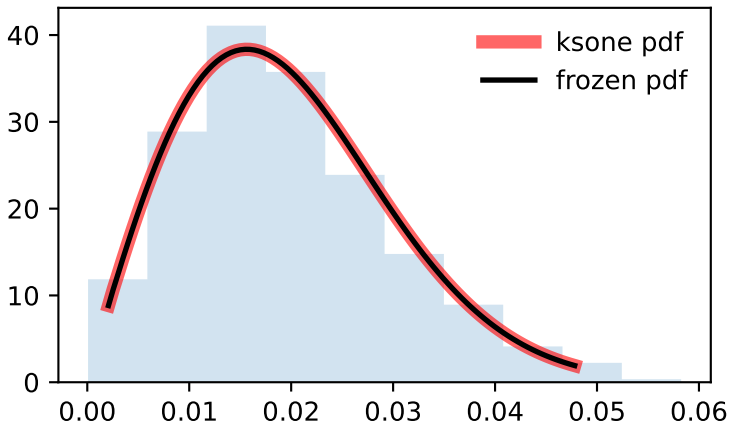
```
>>> vals = ksone.ppf([0.001, 0.5, 0.999], n)
>>> np.allclose([0.001, 0.5, 0.999], ksone.cdf(vals, n))
True
```

Generate random numbers:

```
>>> r = ksone.rvs(n, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(n, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, n, loc=0, scale=1)	Probability density function.
logpdf(x, n, loc=0, scale=1)	Log of the probability density function.
cdf(x, n, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, n, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, n, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, n, loc=0, scale=1)	Log of the survival function.
ppf(q, n, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, n, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, n, loc=0, scale=1)	Non-central moment of order n
stats(n, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(n, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(n,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(n, loc=0, scale=1)	Median of the distribution.
mean(n, loc=0, scale=1)	Mean of the distribution.
var(n, loc=0, scale=1)	Variance of the distribution.
std(n, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, n, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.kstwo

scipy.stats.**kstwo = <scipy.stats._continuous_distns.kstwo_gen object>**

Kolmogorov-Smirnov two-sided test statistic distribution.

This is the distribution of the two-sided Kolmogorov-Smirnov (KS) statistic D_n for a finite sample size `n` (the shape parameter).

As an instance of the *rv_continuous* class, *kstwo* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

kstwobign, **ksone**, **kstest**

Notes

D_n is given by

$$D_n = \sup_x |F_n(x) - F(x)|$$

where F is a (continuous) CDF and F_n is an empirical CDF. *kstwo* describes the distribution under the null hypothesis of the KS test that the empirical CDF corresponds to n i.i.d. random variates with CDF F.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `kstwo.pdf(x, n, loc, scale)` is identically equivalent to `kstwo.pdf(y, n) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import kstwo
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> n = 10
>>> mean, var, skew, kurt = kstwo.stats(n, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(kstwo.ppf(0.01, n),
...                 kstwo.ppf(0.99, n), 100)
>>> ax.plot(x, kstwo.pdf(x, n),
...         'r-', lw=5, alpha=0.6, label='kstwo pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = kstwo(n)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

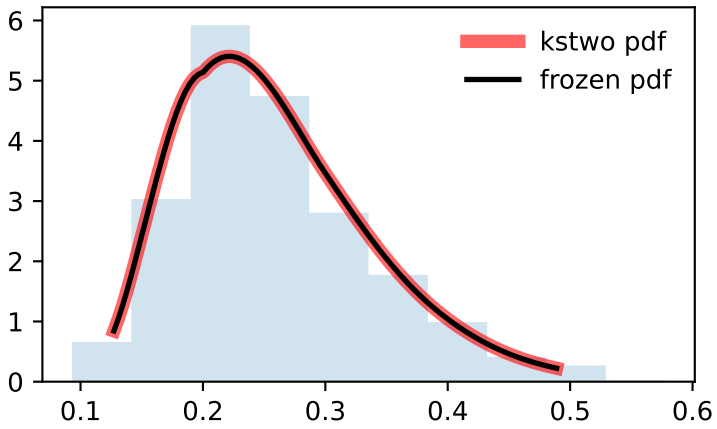
```
>>> vals = kstwo.ppf([0.001, 0.5, 0.999], n)
>>> np.allclose([0.001, 0.5, 0.999], kstwo.cdf(vals, n))
True
```

Generate random numbers:

```
>>> r = kstwo.rvs(n, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(n, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, n, loc=0, scale=1)	Probability density function.
logpdf(x, n, loc=0, scale=1)	Log of the probability density function.
cdf(x, n, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, n, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, n, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, n, loc=0, scale=1)	Log of the survival function.
ppf(q, n, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, n, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, n, loc=0, scale=1)	Non-central moment of order n
stats(n, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(n, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(n,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(n, loc=0, scale=1)	Median of the distribution.
mean(n, loc=0, scale=1)	Mean of the distribution.
var(n, loc=0, scale=1)	Variance of the distribution.
std(n, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, n, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.kstwobign

scipy.stats.**kstwobign = <scipy.stats._continuous_distns.kstwobign_gen object>**

Limiting distribution of scaled Kolmogorov-Smirnov two-sided test statistic.

This is the asymptotic distribution of the two-sided Kolmogorov-Smirnov statistic $\sqrt{n}D_n$ that measures the maximum absolute distance of the theoretical (continuous) CDF from the empirical CDF. (see *kstest*).

As an instance of the *rv_continuous* class, *kstwobign* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

ksone, **kstwo**, **kstest**

Notes

$\sqrt{n}D_n$ is given by

$$D_n = \sup_x |F_n(x) - F(x)|$$

where F is a continuous CDF and F_n is an empirical CDF. *kstwobign* describes the asymptotic distribution (i.e. the limit of $\sqrt{n}D_n$) under the null hypothesis of the KS test that the empirical CDF corresponds to i.i.d. random variates with CDF F.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `kstwobign.pdf(x, loc, scale)` is identically equivalent to `kstwobign.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import kstwobign
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = kstwobign.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(kstwobign.ppf(0.01),
...                 kstwobign.ppf(0.99), 100)
>>> ax.plot(x, kstwobign.pdf(x),
...         'r-', lw=5, alpha=0.6, label='kstwobign pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = kstwobign()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

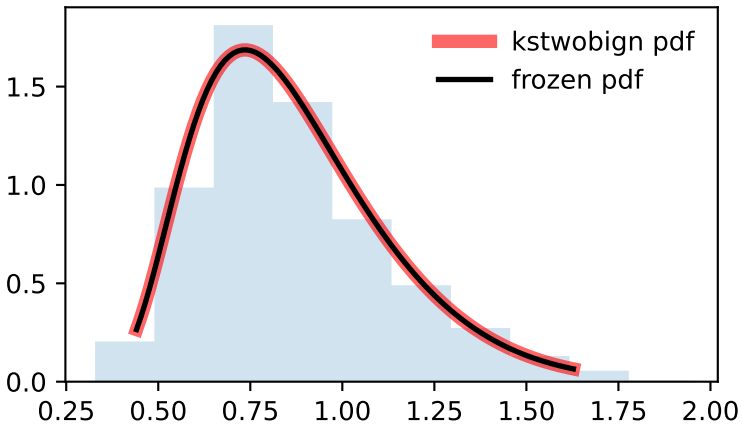
```
>>> vals = kstwobign.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], kstwobign.cdf(vals))
True
```

Generate random numbers:

```
>>> r = kstwobign.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.laplace

scipy.stats.**laplace = <scipy.stats._continuous_distns.laplace_gen object>**

A Laplace continuous random variable.

As an instance of the *rv_continuous* class, *laplace* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *laplace* is

$$f(x) = \frac{1}{2}\exp(-|x|)$$

for a real number x.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `laplace.pdf(x, loc, scale)` is identically equivalent to `laplace.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import laplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = laplace.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(laplace.ppf(0.01),
...                 laplace.ppf(0.99), 100)
>>> ax.plot(x, laplace.pdf(x),
...         'r-', lw=5, alpha=0.6, label='laplace pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = laplace()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

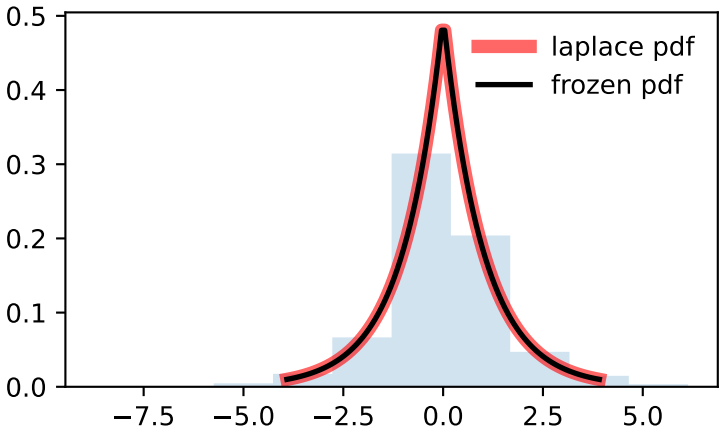
```
>>> vals = laplace.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], laplace.cdf(vals))
True
```

Generate random numbers:

```
>>> r = laplace.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.laplace_asymmetric

scipy.stats.**laplace_asymmetric = <scipy.stats._continuous_distns.laplace_asymmetric_gen ob**

An asymmetric Laplace continuous random variable.

As an instance of the *rv_continuous* class, *laplace_asymmetric* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

laplace

Laplace distribution

Notes

The probability density function for *laplace_asymmetric* is

$$f(x,\kappa) = \frac{1}{\kappa+\kappa^{-1}}\exp(-x\kappa), \quad x \geq 0$$
$$= \frac{1}{\kappa+\kappa^{-1}}\exp(x/\kappa), \quad x < 0$$

for $-\infty < x < \infty$, $\kappa > 0$.

laplace_asymmetric takes `kappa` as a shape parameter for κ. For $\kappa = 1$, it is identical to a Laplace distribution.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `laplace_asymmetric.pdf(x, kappa, loc, scale)` is identically equivalent to `laplace_asymmetric.pdf(y, kappa) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1], [2]

Examples

```
>>> from scipy.stats import laplace_asymmetric
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> kappa = 2
>>> mean, var, skew, kurt = laplace_asymmetric.stats(kappa, moments='mvsk
↪')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(laplace_asymmetric.ppf(0.01, kappa),
...                 laplace_asymmetric.ppf(0.99, kappa), 100)
>>> ax.plot(x, laplace_asymmetric.pdf(x, kappa),
...         'r-', lw=5, alpha=0.6, label='laplace_asymmetric pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = laplace_asymmetric(kappa)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

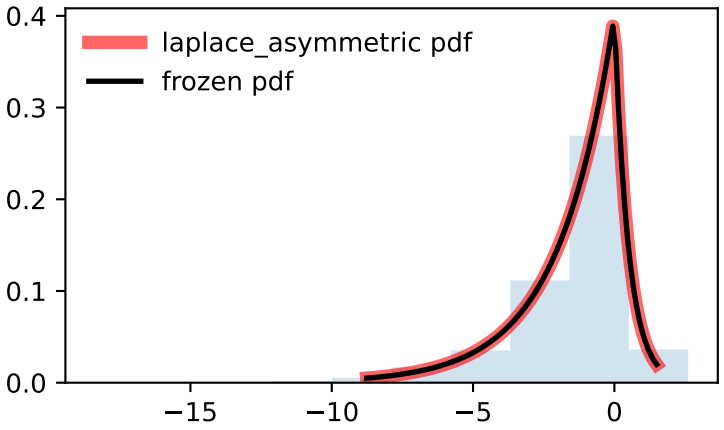
```
>>> vals = laplace_asymmetric.ppf([0.001, 0.5, 0.999], kappa)
>>> np.allclose([0.001, 0.5, 0.999], laplace_asymmetric.cdf(vals, kappa))
True
```

Generate random numbers:

```
>>> r = laplace_asymmetric.rvs(kappa, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(kappa, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, kappa, loc=0, scale=1)	Probability density function.
logpdf(x, kappa, loc=0, scale=1)	Log of the probability density function.
cdf(x, kappa, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, kappa, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, kappa, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, kappa, loc=0, scale=1)	Log of the survival function.
ppf(q, kappa, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, kappa, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, kappa, loc=0, scale=1)	Non-central moment of order n
stats(kappa, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(kappa, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(kappa,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(kappa, loc=0, scale=1)	Median of the distribution.
mean(kappa, loc=0, scale=1)	Mean of the distribution.
var(kappa, loc=0, scale=1)	Variance of the distribution.
std(kappa, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, kappa, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.levy

scipy.stats.**levy = <scipy.stats._continuous_distns.levy_gen object>**

A Levy continuous random variable.

As an instance of the *rv_continuous* class, *levy* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

levy_stable, **levy_l**

Notes

The probability density function for *levy* is:

$$f(x) = \frac{1}{\sqrt{2\pi x^3}} \exp\left(-\frac{1}{2x}\right)$$

for $x >= 0$.

This is the same as the Levy-stable distribution with $a = 1/2$ and $b = 1$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `levy.pdf(x, loc, scale)` is identically equivalent to `levy.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import levy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = levy.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(levy.ppf(0.01),
...                 levy.ppf(0.99), 100)
>>> ax.plot(x, levy.pdf(x),
...         'r-', lw=5, alpha=0.6, label='levy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = levy()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

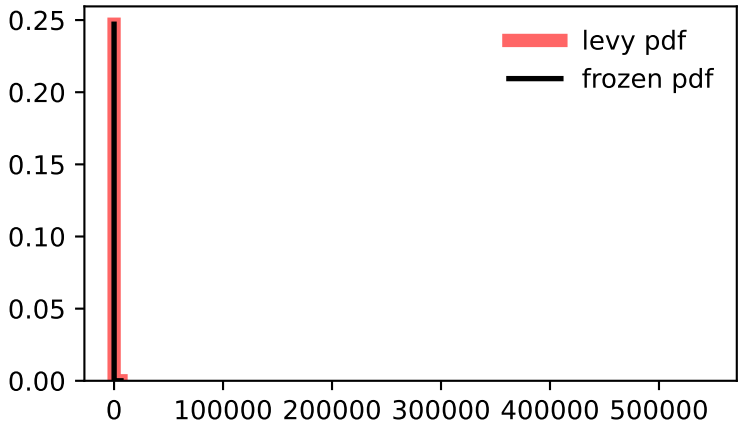
```
>>> vals = levy.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], levy.cdf(vals))
True
```

Generate random numbers:

```
>>> r = levy.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.levy_l

scipy.stats.**levy_l = <scipy.stats._continuous_distns.levy_l_gen object>**

A left-skewed Levy continuous random variable.

As an instance of the *rv_continuous* class, *levy_l* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

levy, **levy_stable**

Notes

The probability density function for *levy_l* is:

$$f(x) = \frac{1}{|x|\sqrt{2\pi|x|}} \exp\left(-\frac{1}{2|x|}\right)$$

for $x <= 0$.

This is the same as the Levy-stable distribution with $a = 1/2$ and $b = -1$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `levy_l.pdf(x, loc, scale)` is identically equivalent to `levy_l.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import levy_l
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = levy_l.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(levy_l.ppf(0.01),
...                 levy_l.ppf(0.99), 100)
>>> ax.plot(x, levy_l.pdf(x),
...         'r-', lw=5, alpha=0.6, label='levy_l pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = levy_l()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

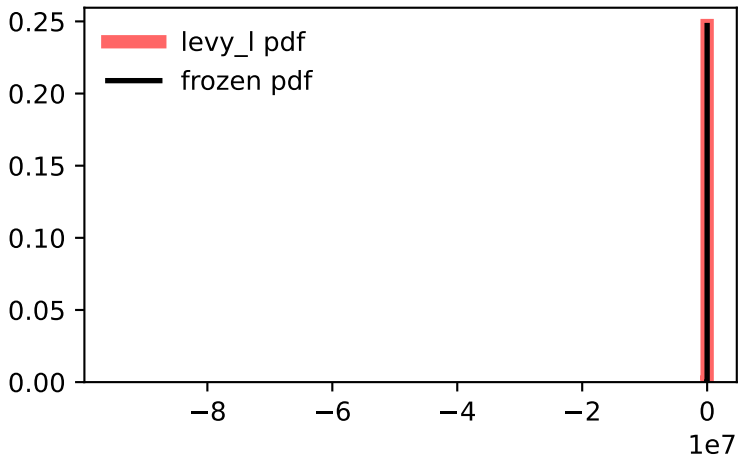
```
>>> vals = levy_l.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], levy_l.cdf(vals))
True
```

Generate random numbers:

```
>>> r = levy_l.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.levy_stable

scipy.stats.**levy_stable = <scipy.stats._continuous_distns.levy_stable_gen object>**

A Levy-stable continuous random variable.

As an instance of the *rv_continuous* class, *levy_stable* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

levy, **levy_l**

Notes

The distribution for *levy_stable* has characteristic function:

$$\varphi(t, \alpha, \beta, c, \mu) = e^{it\mu - |ct|^{\alpha}(1 - i\beta \operatorname{sign}(t)\Phi(\alpha, t))}$$

where:

$$\Phi = \begin{cases} \tan\left(\frac{\pi\alpha}{2}\right) & \alpha \neq 1 \\ -\frac{2}{\pi}\log|t| & \alpha = 1 \end{cases}$$

The probability density function for *levy_stable* is:

$$f(x) = \frac{1}{2\pi}\int_{-\infty}^{\infty} \varphi(t)e^{-ixt}\,dt$$

where $-\infty < t < \infty$. This integral does not have a known closed form.

For evaluation of pdf we use either Zolotarev S_0 parameterization with integration, direct integration of standard parameterization of characteristic function or FFT of characteristic function. If set to other than None and if number of points is greater than `levy_stable.pdf_fft_min_points_threshold` (defaults to None) we use FFT otherwise we use one of the other methods.

The default method is 'best' which uses Zolotarev's method if alpha = 1 and integration of characteristic function otherwise. The default method can be changed by setting `levy_stable.pdf_default_method` to either 'zolotarev', 'quadrature' or 'best'.

To increase accuracy of FFT calculation one can specify `levy_stable.pdf_fft_grid_spacing` (defaults to 0.001) and `pdf_fft_n_points_two_power` (defaults to a value that covers the input range * 4). Setting `pdf_fft_n_points_two_power` to 16 should be sufficiently accurate in most cases at the expense of CPU time.

For evaluation of cdf we use Zolatarev S_0 parameterization with integration or integral of the pdf FFT interpolated spline. The settings affecting FFT calculation are the same as for pdf calculation. Setting the threshold to `None` (default) will disable FFT. For cdf calculations the Zolatarev method is superior in accuracy, so FFT is disabled by default.

Fitting estimate uses quantile estimation method in [MC]. MLE estimation of parameters in fit method uses this quantile estimate initially. Note that MLE doesn't always converge if using FFT for pdf calculations; so it's best that `pdf_fft_min_points_threshold` is left unset.

Warning: For pdf calculations implementation of Zolatarev is unstable for values where alpha = 1 and beta != 0. In this case the quadrature method is recommended. FFT calculation is also considered experimental.

For cdf calculations FFT calculation is considered experimental. Use Zolatarev's method instead (default).

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `levy_stable.pdf(x, alpha, beta, loc, scale)` is identically equivalent to `levy_stable.pdf(y, alpha, beta) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[MC], [MS], [BS]

Examples

```
>>> from scipy.stats import levy_stable
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> alpha, beta = 1.8, -0.5
>>> mean, var, skew, kurt = levy_stable.stats(alpha, beta, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(levy_stable.ppf(0.01, alpha, beta),
...                 levy_stable.ppf(0.99, alpha, beta), 100)
>>> ax.plot(x, levy_stable.pdf(x, alpha, beta),
...         'r-', lw=5, alpha=0.6, label='levy_stable pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = levy_stable(alpha, beta)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

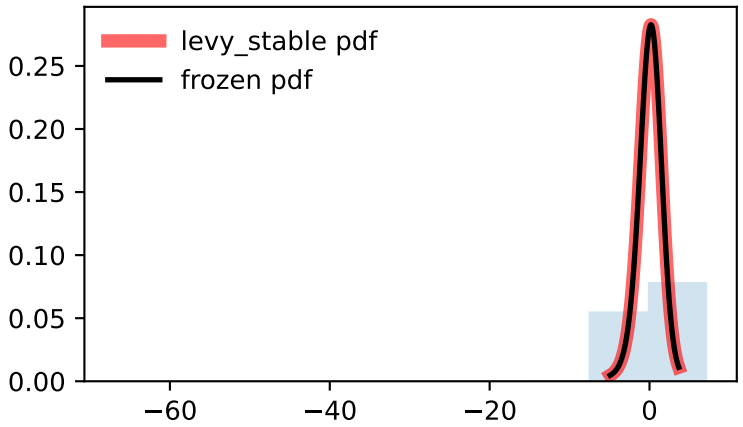
```
>>> vals = levy_stable.ppf([0.001, 0.5, 0.999], alpha, beta)
>>> np.allclose([0.001, 0.5, 0.999], levy_stable.cdf(vals, alpha, beta))
True
```

Generate random numbers:

```
>>> r = levy_stable.rvs(alpha, beta, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(alpha, beta, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, alpha, beta, loc=0, scale=1)	Probability density function.
logpdf(x, alpha, beta, loc=0, scale=1)	Log of the probability density function.
cdf(x, alpha, beta, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, alpha, beta, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, alpha, beta, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, alpha, beta, loc=0, scale=1)	Log of the survival function.
ppf(q, alpha, beta, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, alpha, beta, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, alpha, beta, loc=0, scale=1)	Non-central moment of order n
stats(alpha, beta, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(alpha, beta, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(alpha, beta), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(alpha, beta, loc=0, scale=1)	Median of the distribution.
mean(alpha, beta, loc=0, scale=1)	Mean of the distribution.
var(alpha, beta, loc=0, scale=1)	Variance of the distribution.
std(alpha, beta, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, alpha, beta, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.logistic

scipy.stats.**logistic = <scipy.stats._continuous_distns.logistic_gen object>**

A logistic (or Sech-squared) continuous random variable.

As an instance of the *rv_continuous* class, *logistic* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *logistic* is:

$$f(x) = \frac{\exp(-x)}{(1+\exp(-x))^2}$$

logistic is a special case of *genlogistic* with `c=1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `logistic.pdf(x, loc, scale)` is identically equivalent to `logistic.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import logistic
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = logistic.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(logistic.ppf(0.01),
...                 logistic.ppf(0.99), 100)
>>> ax.plot(x, logistic.pdf(x),
...         'r-', lw=5, alpha=0.6, label='logistic pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = logistic()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

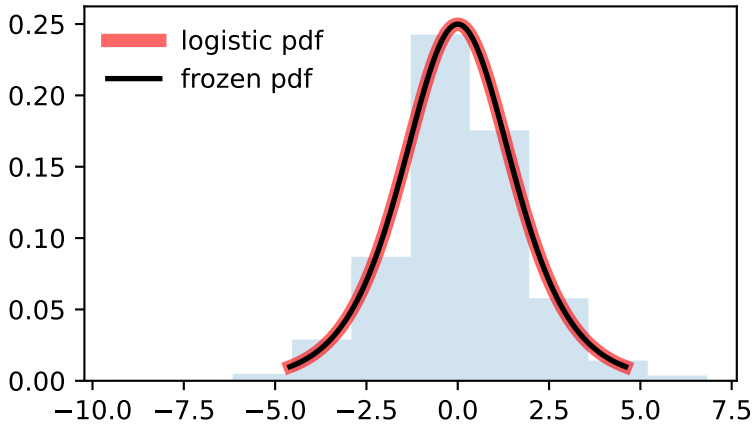
```
>>> vals = logistic.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], logistic.cdf(vals))
True
```

Generate random numbers:

```
>>> r = logistic.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.loggamma

scipy.stats.**loggamma = <scipy.stats._continuous_distns.loggamma_gen object>**

A log gamma continuous random variable.

As an instance of the *rv_continuous* class, *loggamma* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *loggamma* is:

$$f(x, c) = \frac{\exp(cx - \exp(x))}{\Gamma(c)}$$

for all $x, c > 0$. Here, Γ is the gamma function (*scipy.special.gamma*).

loggamma takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `loggamma.pdf(x, c, loc, scale)` is identically equivalent to `loggamma.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import loggamma
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 0.414
>>> mean, var, skew, kurt = loggamma.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(loggamma.ppf(0.01, c),
...                 loggamma.ppf(0.99, c), 100)
>>> ax.plot(x, loggamma.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='loggamma pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = loggamma(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

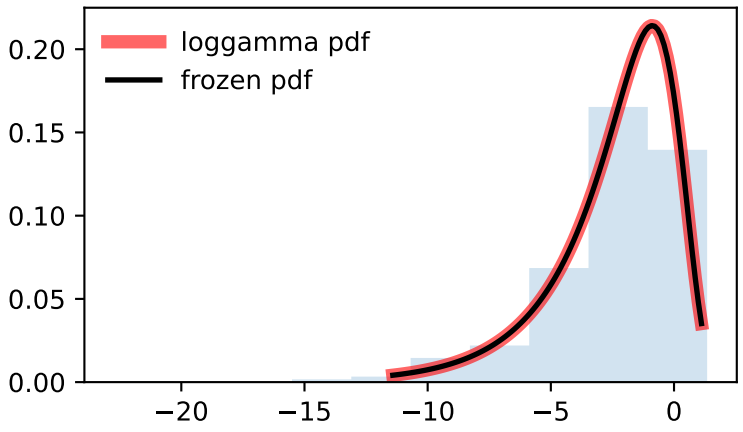
```
>>> vals = loggamma.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], loggamma.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = loggamma.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.loglaplace

scipy.stats.**loglaplace = <scipy.stats._continuous_distns.loglaplace_gen object>**

A log-Laplace continuous random variable.

As an instance of the *rv_continuous* class, *loglaplace* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *loglaplace* is:

$$f(x, c) = \begin{cases} \frac{c}{2} x^{c-1} & \text{for } 0 < x < 1 \\ \frac{c}{2} x^{-c-1} & \text{for } x \geq 1 \end{cases}$$

for $c > 0$.

loglaplace takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `loglaplace.pdf(x, c, loc, scale)` is identically equivalent to `loglaplace.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

T.J. Kozubowski and K. Podgorski, "A log-Laplace growth rate model", The Mathematical Scientist, vol. 28, pp. 49-60, 2003.

Examples

```
>>> from scipy.stats import loglaplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 3.25
>>> mean, var, skew, kurt = loglaplace.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(loglaplace.ppf(0.01, c),
...                 loglaplace.ppf(0.99, c), 100)
>>> ax.plot(x, loglaplace.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='loglaplace pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = loglaplace(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

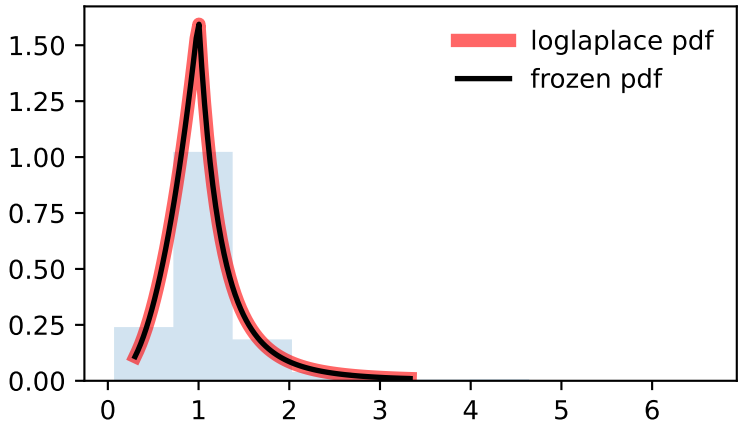
```
>>> vals = loglaplace.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], loglaplace.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = loglaplace.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.lognorm

scipy.stats.**lognorm = <scipy.stats._continuous_distns.lognorm_gen object>**

A lognormal continuous random variable.

As an instance of the *rv_continuous* class, *lognorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *lognorm* is:

$$f(x, s) = \frac{1}{sx\sqrt{2\pi}} \exp\left(-\frac{\log^2(x)}{2s^2}\right)$$

for $x > 0$, $s > 0$.

lognorm takes `s` as a shape parameter for s.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `lognorm.pdf(x, s, loc, scale)` is identically equivalent to `lognorm.pdf(y, s) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

A common parametrization for a lognormal random variable `Y` is in terms of the mean, `mu`, and standard deviation, `sigma`, of the unique normally distributed random variable `X` such that exp(X) = Y. This parametrization corresponds to setting `s = sigma` and `scale = exp(mu)`.

Examples

```
>>> from scipy.stats import lognorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> s = 0.954
>>> mean, var, skew, kurt = lognorm.stats(s, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(lognorm.ppf(0.01, s),
...                 lognorm.ppf(0.99, s), 100)
>>> ax.plot(x, lognorm.pdf(x, s),
...         'r-', lw=5, alpha=0.6, label='lognorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = lognorm(s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

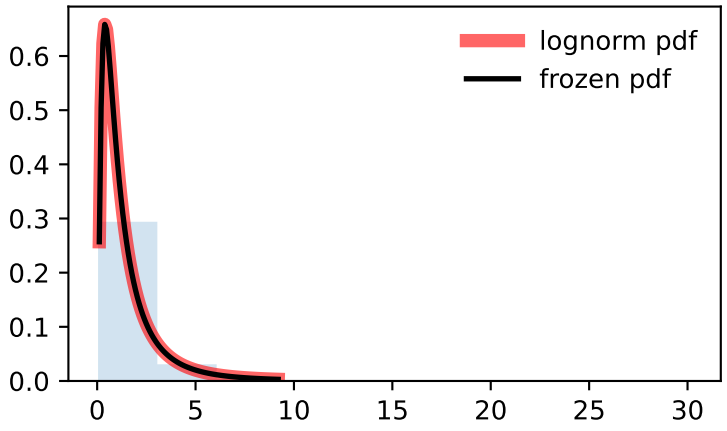
```
>>> vals = lognorm.ppf([0.001, 0.5, 0.999], s)
>>> np.allclose([0.001, 0.5, 0.999], lognorm.cdf(vals, s))
True
```

Generate random numbers:

```
>>> r = lognorm.rvs(s, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(s, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, s, loc=0, scale=1)	Probability density function.
logpdf(x, s, loc=0, scale=1)	Log of the probability density function.
cdf(x, s, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, s, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, s, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, s, loc=0, scale=1)	Log of the survival function.
ppf(q, s, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, s, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, s, loc=0, scale=1)	Non-central moment of order n
stats(s, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(s, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(s,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(s, loc=0, scale=1)	Median of the distribution.
mean(s, loc=0, scale=1)	Mean of the distribution.
var(s, loc=0, scale=1)	Variance of the distribution.
std(s, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, s, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.loguniform

scipy.stats.**loguniform = <scipy.stats._continuous_distns.reciprocal_gen object>**

A loguniform or reciprocal continuous random variable.

As an instance of the *rv_continuous* class, *loguniform* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for this class is:

$$f(x, a, b) = \frac{1}{x \log(b/a)}$$

for $a \leq x \leq b$, $b > a > 0$. This class takes a and b as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `loguniform.pdf(x, a, b, loc, scale)` is identically equivalent to `loguniform.pdf(y, a, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import loguniform
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b = 0.01, 1.25
>>> mean, var, skew, kurt = loguniform.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(loguniform.ppf(0.01, a, b),
...                 loguniform.ppf(0.99, a, b), 100)
>>> ax.plot(x, loguniform.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='loguniform pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = loguniform(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

```
>>> vals = loguniform.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], loguniform.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = loguniform.rvs(a, b, size=1000)
```

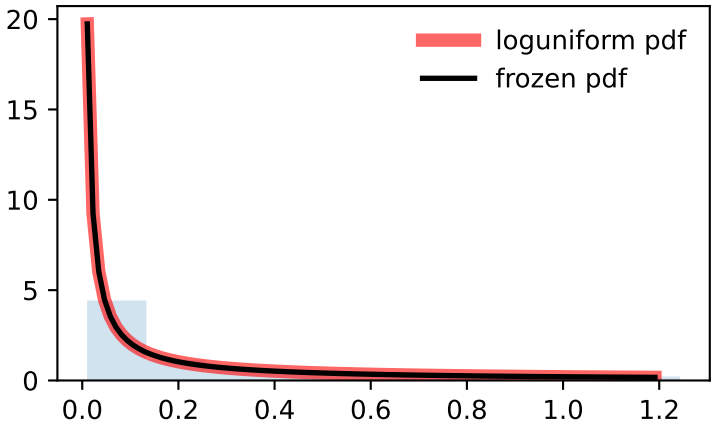
And compare the histogram:

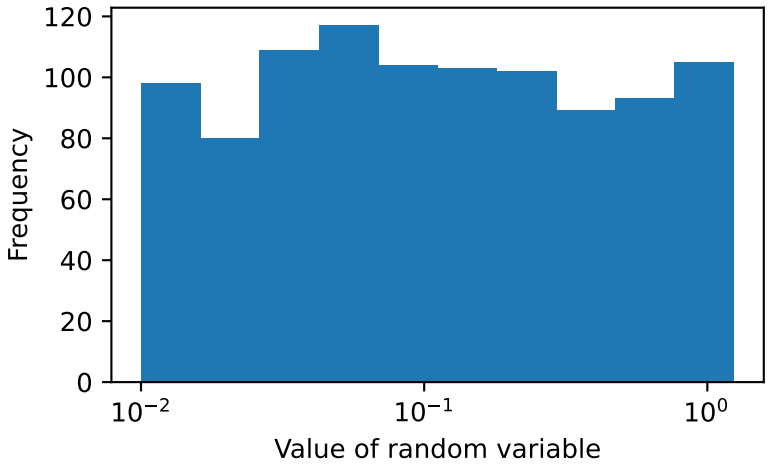
```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

This doesn't show the equal probability of `0.01`, `0.1` and `1`. This is best when the x-axis is log-scaled:

```
>>> import numpy as np
>>> fig, ax = plt.subplots(1, 1)
>>> ax.hist(np.log10(r))
>>> ax.set_ylabel("Frequency")
>>> ax.set_xlabel("Value of random variable")
>>> ax.xaxis.set_major_locator(plt.FixedLocator([-2, -1, 0]))
>>> ticks = ["$10^{{ {} }}$".format(i) for i in [-2, -1, 0]]
>>> ax.set_xticklabels(ticks)
>>> plt.show()
```

This random variable will be log-uniform regardless of the base chosen for `a` and `b`. Let's specify with base `2` instead:

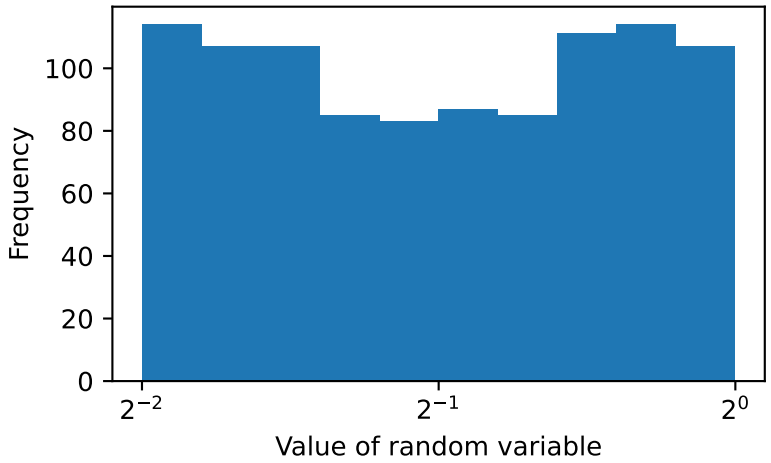

loguniform pdf
frozen pdf
20
15
10
5
0
0.0
0.2
0.4
0.6
0.8
1.0
1.2


120
100
80
60
40
20
0
Frequency
10^{-2}
10^{-1}
10^{0}
Value of random variable

```
>>> rvs = loguniform(2**-2, 2**0).rvs(size=1000)
```

Values of `1/4`, `1/2` and `1` are equally likely with this random variable. Here's the histogram:

```
>>> fig, ax = plt.subplots(1, 1)
>>> ax.hist(np.log2(rvs))
>>> ax.set_ylabel("Frequency")
>>> ax.set_xlabel("Value of random variable")
>>> ax.xaxis.set_major_locator(plt.FixedLocator([-2, -1, 0]))
>>> ticks = ["$2^{{ {} }}$".format(i) for i in [-2, -1, 0]]
>>> ax.set_xticklabels(ticks)
>>> plt.show()
```



Methods

rvs(a, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, loc=0, scale=1)	Non-central moment of order n
stats(a, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, loc=0, scale=1)	Median of the distribution.
mean(a, b, loc=0, scale=1)	Mean of the distribution.
var(a, b, loc=0, scale=1)	Variance of the distribution.
std(a, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.lomax

scipy.stats.**lomax = <scipy.stats._continuous_distns.lomax_gen object>**

A Lomax (Pareto of the second kind) continuous random variable.

As an instance of the *rv_continuous* class, *lomax* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *lomax* is:

$$f(x, c) = \frac{c}{(1+x)^{c+1}}$$

for $x \geq 0$, $c > 0$.

lomax takes `c` as a shape parameter for c.

lomax is a special case of *pareto* with `loc=-1.0`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `lomax.pdf(x, c, loc, scale)` is identically equivalent to `lomax.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of

a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import lomax
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 1.88
>>> mean, var, skew, kurt = lomax.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(lomax.ppf(0.01, c),
...                 lomax.ppf(0.99, c), 100)
>>> ax.plot(x, lomax.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='lomax pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = lomax(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

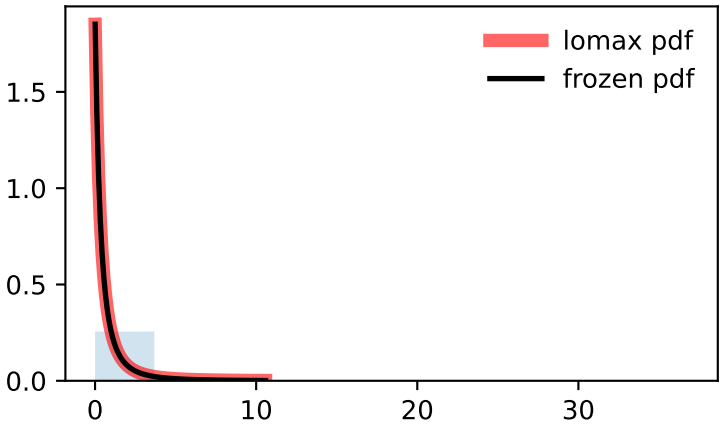
```
>>> vals = lomax.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], lomax.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = lomax.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.maxwell

scipy.stats.**maxwell = <scipy.stats._continuous_distns.maxwell_gen object>**

A Maxwell continuous random variable.

As an instance of the *rv_continuous* class, *maxwell* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

A special case of a *chi* distribution, with `df=3`, `loc=0.0`, and given `scale = a`, where `a` is the parameter used in the Mathworld description [1].

The probability density function for *maxwell* is:

$$f(x) = \sqrt{2/\pi}x^2\exp(-x^2/2)$$

for $x >= 0$.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `maxwell.pdf(x, loc, scale)` is identically equivalent to `maxwell.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import maxwell
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = maxwell.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(maxwell.ppf(0.01),
...                 maxwell.ppf(0.99), 100)
>>> ax.plot(x, maxwell.pdf(x),
...         'r-', lw=5, alpha=0.6, label='maxwell pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = maxwell()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

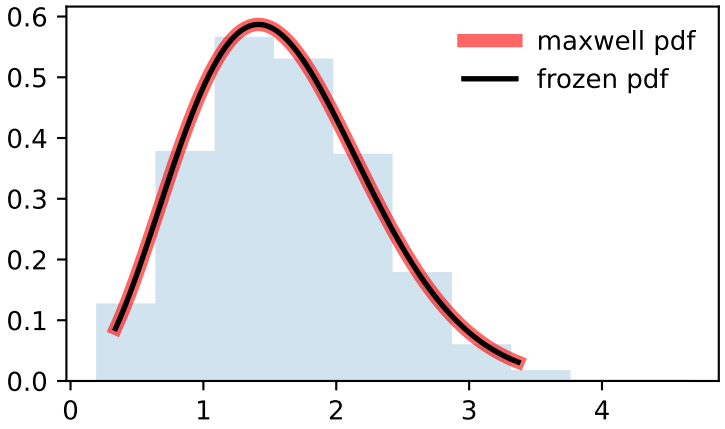
```
>>> vals = maxwell.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], maxwell.cdf(vals))
True
```

Generate random numbers:

```
>>> r = maxwell.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.mielke

scipy.stats.**mielke = <scipy.stats._continuous_distns.mielke_gen object>**

A Mielke Beta-Kappa / Dagum continuous random variable.

As an instance of the *rv_continuous* class, *mielke* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *mielke* is:

$$f(x, k, s) = \frac{k x^{k-1}}{(1+x^s)^{1+k/s}}$$

for $x > 0$ and $k, s > 0$. The distribution is sometimes called Dagum distribution ([2]). It was already defined in [3], called a Burr Type III distribution (*burr* with parameters `c=s` and `d=k/s`).

mielke takes `k` and `s` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `mielke.pdf(x, k, s, loc, scale)` is identically equivalent to `mielke.pdf(y, k, s) / scale` with `y = (x - loc) / scale`. Note that shifting the location

of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1], [2], [3]

Examples

```
>>> from scipy.stats import mielke
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> k, s = 10.4, 4.6
>>> mean, var, skew, kurt = mielke.stats(k, s, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(mielke.ppf(0.01, k, s),
...                 mielke.ppf(0.99, k, s), 100)
>>> ax.plot(x, mielke.pdf(x, k, s),
...         'r-', lw=5, alpha=0.6, label='mielke pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = mielke(k, s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

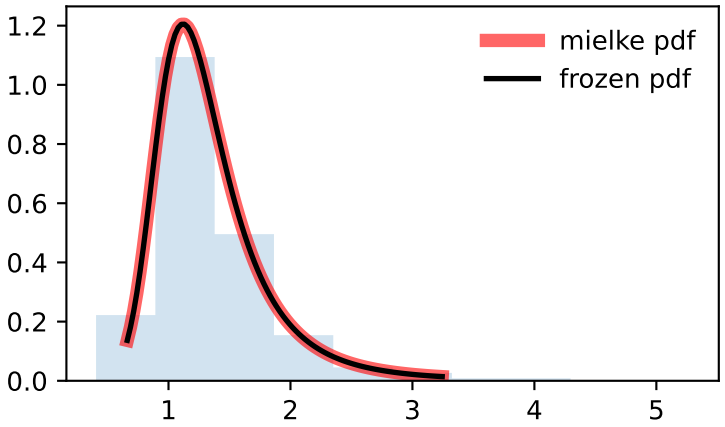
```
>>> vals = mielke.ppf([0.001, 0.5, 0.999], k, s)
>>> np.allclose([0.001, 0.5, 0.999], mielke.cdf(vals, k, s))
True
```

Generate random numbers:

```
>>> r = mielke.rvs(k, s, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(k, s, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, k, s, loc=0, scale=1)	Probability density function.
logpdf(x, k, s, loc=0, scale=1)	Log of the probability density function.
cdf(x, k, s, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, k, s, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, k, s, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, k, s, loc=0, scale=1)	Log of the survival function.
ppf(q, k, s, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, k, s, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, k, s, loc=0, scale=1)	Non-central moment of order n
stats(k, s, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(k, s, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(k, s), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(k, s, loc=0, scale=1)	Median of the distribution.
mean(k, s, loc=0, scale=1)	Mean of the distribution.
var(k, s, loc=0, scale=1)	Variance of the distribution.
std(k, s, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, k, s, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.moyal

scipy.stats.**moyal = <scipy.stats._continuous_distns.moyal_gen object>**

A Moyal continuous random variable.

As an instance of the *rv_continuous* class, *moyal* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *moyal* is:

$$f(x) = \exp(-(x + \exp(-x))/2)/\sqrt{2\pi}$$

for a real number x.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `moyal.pdf(x, loc, scale)` is identically equivalent to `moyal.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

This distribution has utility in high-energy physics and radiation detection. It describes the energy loss of a charged relativistic particle due to ionization of the medium [1]. It also provides an approximation for the Landau distribution. For an in depth description see [2]. For additional description, see [3].

References

New in version 1.1.0.

[1], [2], [3]

Examples

```
>>> from scipy.stats import moyal
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = moyal.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(moyal.ppf(0.01),
...                 moyal.ppf(0.99), 100)
>>> ax.plot(x, moyal.pdf(x),
...         'r-', lw=5, alpha=0.6, label='moyal pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = moyal()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

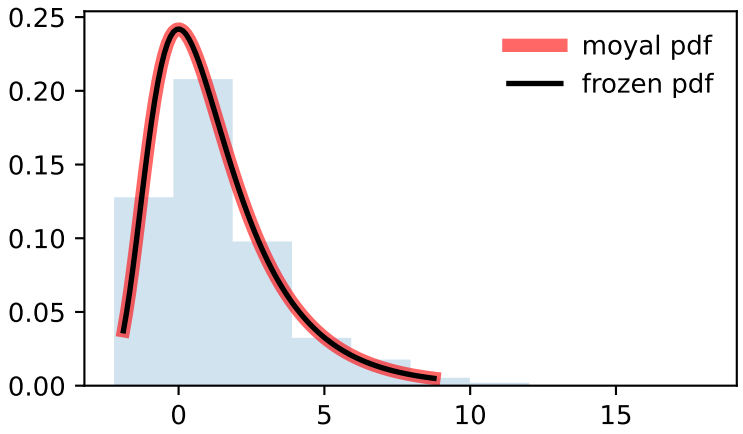
```
>>> vals = moyal.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], moyal.cdf(vals))
True
```

Generate random numbers:

```
>>> r = moyal.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.nakagami

scipy.stats.**nakagami = <scipy.stats._continuous_distns.nakagami_gen object>**

A Nakagami continuous random variable.

As an instance of the *rv_continuous* class, *nakagami* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *nakagami* is:

$$f(x, \nu) = \frac{2\nu^\nu}{\Gamma(\nu)} x^{2\nu-1} \exp(-\nu x^2)$$

for $x >= 0$, $\nu > 0$.

nakagami takes `nu` as a shape parameter for ν.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `nakagami.pdf(x, nu, loc, scale)` is identically equivalent to `nakagami.pdf(y, nu) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import nakagami
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> nu = 4.97
>>> mean, var, skew, kurt = nakagami.stats(nu, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(nakagami.ppf(0.01, nu),
...                 nakagami.ppf(0.99, nu), 100)
>>> ax.plot(x, nakagami.pdf(x, nu),
...         'r-', lw=5, alpha=0.6, label='nakagami pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = nakagami(nu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

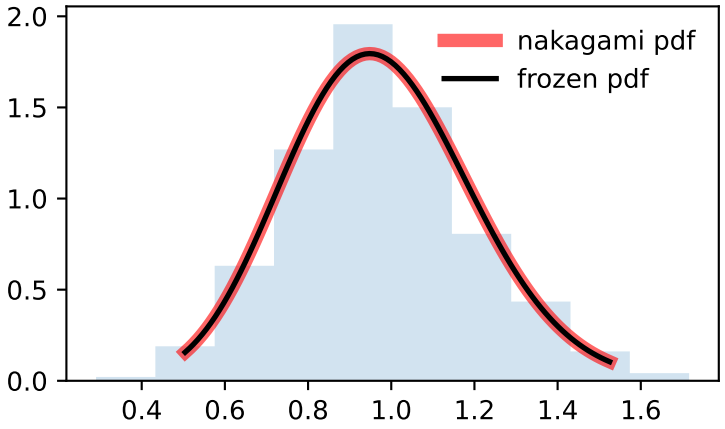
```
>>> vals = nakagami.ppf([0.001, 0.5, 0.999], nu)
>>> np.allclose([0.001, 0.5, 0.999], nakagami.cdf(vals, nu))
True
```

Generate random numbers:

```
>>> r = nakagami.rvs(nu, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(nu, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, nu, loc=0, scale=1)	Probability density function.
logpdf(x, nu, loc=0, scale=1)	Log of the probability density function.
cdf(x, nu, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, nu, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, nu, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, nu, loc=0, scale=1)	Log of the survival function.
ppf(q, nu, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, nu, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, nu, loc=0, scale=1)	Non-central moment of order n
stats(nu, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(nu, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(nu,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(nu, loc=0, scale=1)	Median of the distribution.
mean(nu, loc=0, scale=1)	Mean of the distribution.
var(nu, loc=0, scale=1)	Variance of the distribution.
std(nu, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, nu, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.ncx2

scipy.stats.**ncx2 = <scipy.stats._continuous_distns.ncx2_gen object>**

A non-central chi-squared continuous random variable.

As an instance of the *rv_continuous* class, *ncx2* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *ncx2* is:

$$f(x, k, \lambda) = \frac{1}{2}\exp(-(\lambda + x)/2)(x/\lambda)^{(k-2)/4} I_{(k-2)/2}(\sqrt{\lambda x})$$

for $x >= 0$ and $k, \lambda > 0$. k specifies the degrees of freedom (denoted `df` in the implementation) and λ is the non-centrality parameter (denoted `nc` in the implementation). I_ν denotes the modified Bessel function of first order of degree ν (*scipy.special.iv*).

ncx2 takes `df` and `nc` as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `ncx2.pdf(x, df, nc, loc, scale)` is identically equivalent to `ncx2.pdf(y, df, nc) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import ncx2
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> df, nc = 21, 1.06
>>> mean, var, skew, kurt = ncx2.stats(df, nc, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(ncx2.ppf(0.01, df, nc),
...                 ncx2.ppf(0.99, df, nc), 100)
>>> ax.plot(x, ncx2.pdf(x, df, nc),
...         'r-', lw=5, alpha=0.6, label='ncx2 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = ncx2(df, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

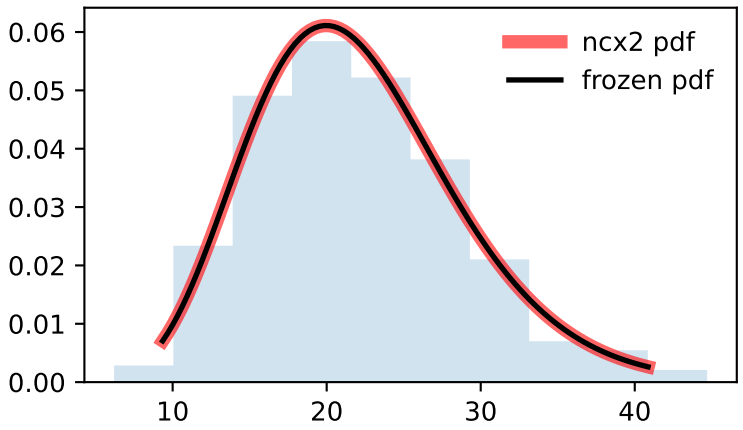
```
>>> vals = ncx2.ppf([0.001, 0.5, 0.999], df, nc)
>>> np.allclose([0.001, 0.5, 0.999], ncx2.cdf(vals, df, nc))
True
```

Generate random numbers:

```
>>> r = ncx2.rvs(df, nc, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(df, nc, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, df, nc, loc=0, scale=1)	Probability density function.
logpdf(x, df, nc, loc=0, scale=1)	Log of the probability density function.
cdf(x, df, nc, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, df, nc, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, df, nc, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, df, nc, loc=0, scale=1)	Log of the survival function.
ppf(q, df, nc, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, df, nc, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, df, nc, loc=0, scale=1)	Non-central moment of order n
stats(df, nc, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(df, nc, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(df, nc), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(df, nc, loc=0, scale=1)	Median of the distribution.
mean(df, nc, loc=0, scale=1)	Mean of the distribution.
var(df, nc, loc=0, scale=1)	Variance of the distribution.
std(df, nc, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, df, nc, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.ncf

scipy.stats.**ncf = <scipy.stats._continuous_distns.ncf_gen object>**

A non-central F distribution continuous random variable.

As an instance of the *rv_continuous* class, *ncf* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

scipy.stats.f

Fisher distribution

Notes

The probability density function for *ncf* is:

$$f(x, n_1, n_2, \lambda) = \exp\left(\frac{\lambda}{2} + \lambda n_1 \frac{x}{2(n_1 x + n_2)}\right) n_1^{n_1/2} n_2^{n_2/2} x^{n_1/2-1} \\ (n_2 + n_1 x)^{-(n_1+n_2)/2} \gamma(n_1/2)\gamma(1 + n_2/2) \\ \frac{L_{n_2/2}^{\frac{n_1}{2}-1}\left(-\lambda n_1 \frac{x}{2(n_1 x+n_2)}\right)}{B(n_1/2, n_2/2)\gamma\left(\frac{n_1+n_2}{2}\right)}$$

for $n_1, n_2 > 0$, $\lambda \geq 0$. Here n_1 is the degrees of freedom in the numerator, n_2 the degrees of freedom in the denominator, λ the non-centrality parameter, γ is the logarithm of the Gamma function, L_n^k is a generalized Laguerre polynomial and B is the beta function.

ncf takes `df1`, `df2` and `nc` as shape parameters. If `nc=0`, the distribution becomes equivalent to the Fisher distribution.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `ncf.pdf(x, dfn, dfd, nc, loc, scale)` is identically equivalent to `ncf.pdf(y, dfn, dfd, nc) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import ncf
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> dfn, dfd, nc = 27, 27, 0.416
>>> mean, var, skew, kurt = ncf.stats(dfn, dfd, nc, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(ncf.ppf(0.01, dfn, dfd, nc),
...                 ncf.ppf(0.99, dfn, dfd, nc), 100)
>>> ax.plot(x, ncf.pdf(x, dfn, dfd, nc),
...         'r-', lw=5, alpha=0.6, label='ncf pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = ncf(dfn, dfd, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

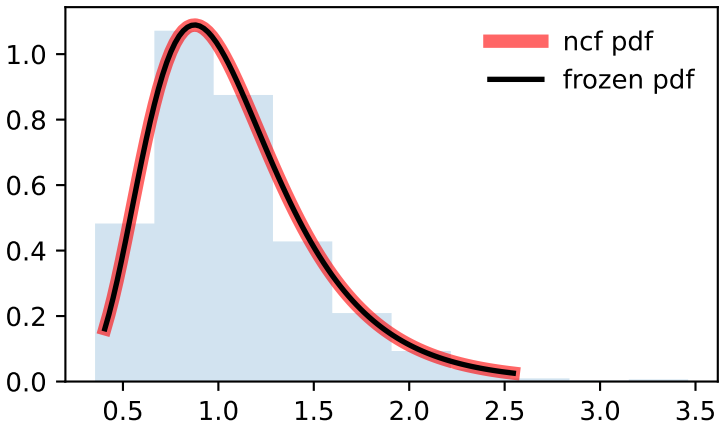
```
>>> vals = ncf.ppf([0.001, 0.5, 0.999], dfn, dfd, nc)
>>> np.allclose([0.001, 0.5, 0.999], ncf.cdf(vals, dfn, dfd, nc))
True
```

Generate random numbers:

```
>>> r = ncf.rvs(dfn, dfd, nc, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(dfn, dfd, nc, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, dfn, dfd, nc, loc=0, scale=1)	Probability density function.
logpdf(x, dfn, dfd, nc, loc=0, scale=1)	Log of the probability density function.
cdf(x, dfn, dfd, nc, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, dfn, dfd, nc, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, dfn, dfd, nc, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, dfn, dfd, nc, loc=0, scale=1)	Log of the survival function.
ppf(q, dfn, dfd, nc, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, dfn, dfd, nc, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, dfn, dfd, nc, loc=0, scale=1)	Non-central moment of order n
stats(dfn, dfd, nc, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(dfn, dfd, nc, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(dfn, dfd, nc), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(dfn, dfd, nc, loc=0, scale=1)	Median of the distribution.
mean(dfn, dfd, nc, loc=0, scale=1)	Mean of the distribution.
var(dfn, dfd, nc, loc=0, scale=1)	Variance of the distribution.
std(dfn, dfd, nc, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, dfn, dfd, nc, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.nct

scipy.stats.**nct = <scipy.stats._continuous_distns.nct_gen object>**

A non-central Student's t continuous random variable.

As an instance of the *rv_continuous* class, *nct* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

If Y is a standard normal random variable and V is an independent chi-square random variable (*chi2*) with k degrees of freedom, then

$$X = \frac{Y + c}{\sqrt{V/k}}$$

has a non-central Student's t distribution on the real line. The degrees of freedom parameter k (denoted `df` in the implementation) satisfies $k > 0$ and the noncentrality parameter c (denoted `nc` in the implementation) is a real number.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `nct.pdf(x, df, nc, loc, scale)` is identically equivalent

to `nct.pdf(y, df, nc) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import nct
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> df, nc = 14, 0.24
>>> mean, var, skew, kurt = nct.stats(df, nc, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(nct.ppf(0.01, df, nc),
...                 nct.ppf(0.99, df, nc), 100)
>>> ax.plot(x, nct.pdf(x, df, nc),
...         'r-', lw=5, alpha=0.6, label='nct pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = nct(df, nc)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

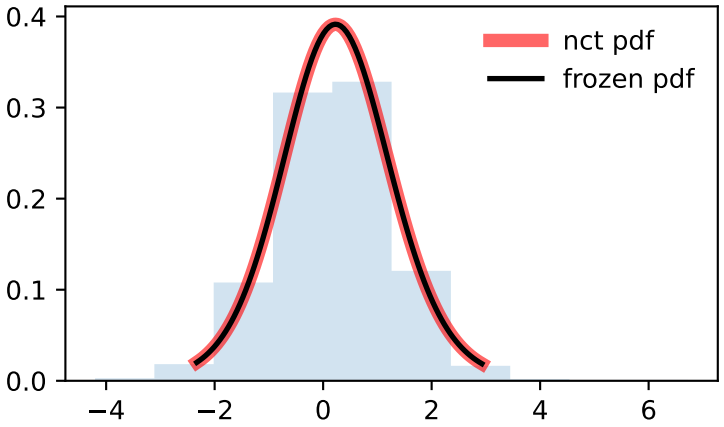
```
>>> vals = nct.ppf([0.001, 0.5, 0.999], df, nc)
>>> np.allclose([0.001, 0.5, 0.999], nct.cdf(vals, df, nc))
True
```

Generate random numbers:

```
>>> r = nct.rvs(df, nc, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(df, nc, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, df, nc, loc=0, scale=1)	Probability density function.
logpdf(x, df, nc, loc=0, scale=1)	Log of the probability density function.
cdf(x, df, nc, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, df, nc, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, df, nc, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, df, nc, loc=0, scale=1)	Log of the survival function.
ppf(q, df, nc, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, df, nc, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, df, nc, loc=0, scale=1)	Non-central moment of order n
stats(df, nc, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(df, nc, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(df, nc), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(df, nc, loc=0, scale=1)	Median of the distribution.
mean(df, nc, loc=0, scale=1)	Mean of the distribution.
var(df, nc, loc=0, scale=1)	Variance of the distribution.
std(df, nc, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, df, nc, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.norm

scipy.stats.**norm = <scipy.stats._continuous_distns.norm_gen object>**

A normal continuous random variable.

The location (`loc`) keyword specifies the mean. The scale (`scale`) keyword specifies the standard deviation.

As an instance of the *rv_continuous* class, *norm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *norm* is:

$$f(x) = \frac{\exp(-x^2/2)}{\sqrt{2\pi}}$$

for a real number x.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `norm.pdf(x, loc, scale)` is identically equivalent to `norm.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import norm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = norm.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(norm.ppf(0.01),
...                 norm.ppf(0.99), 100)
>>> ax.plot(x, norm.pdf(x),
...         'r-', lw=5, alpha=0.6, label='norm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = norm()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

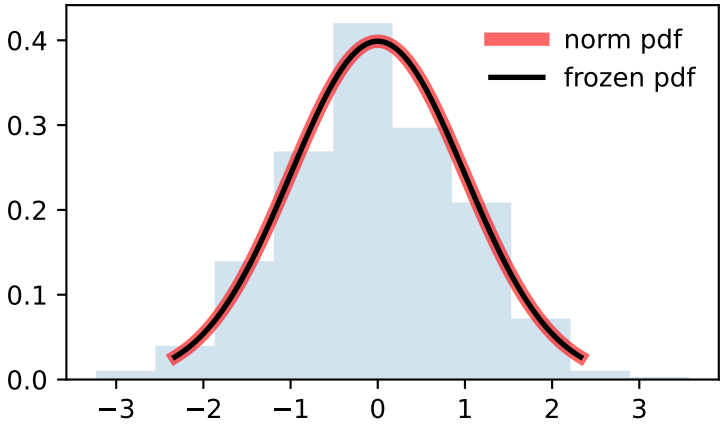
```
>>> vals = norm.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], norm.cdf(vals))
True
```

Generate random numbers:

```
>>> r = norm.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.norminvgauss

scipy.stats.**norminvgauss = <scipy.stats._continuous_distns.norminvgauss_gen object>**

A Normal Inverse Gaussian continuous random variable.

As an instance of the *rv_continuous* class, *norminvgauss* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *norminvgauss* is:

$$f(x, a, b) = \frac{a\, K_1(a\sqrt{1+x^2})}{\pi\sqrt{1+x^2}}\, \exp(\sqrt{a^2-b^2}+bx)$$

where x is a real number, the parameter a is the tail heaviness and b is the asymmetry parameter satisfying $a > 0$ and $|b| <= a$. K_1 is the modified Bessel function of second kind (*scipy.special.k1*).

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `norminvgauss.pdf(x, a, b, loc, scale)` is identically equivalent to `norminvgauss.pdf(y, a, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

A normal inverse Gaussian random variable *Y* with parameters *a* and *b* can be expressed as a normal mean-variance mixture: *Y = b * V + sqrt(V) * X* where *X* is *norm(0,1)* and *V* is *invgauss(mu=1/sqrt(a**2 - b**2))*. This representation is used to generate random variates.

References

O. Barndorff-Nielsen, "Hyperbolic Distributions and Distributions on Hyperbolae", Scandinavian Journal of Statistics, Vol. 5(3), pp. 151-157, 1978.

O. Barndorff-Nielsen, "Normal Inverse Gaussian Distributions and Stochastic Volatility Modelling", Scandinavian Journal of Statistics, Vol. 24, pp. 1-13, 1997.

Examples

```
>>> from scipy.stats import norminvgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b = 1.25, 0.5
>>> mean, var, skew, kurt = norminvgauss.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(norminvgauss.ppf(0.01, a, b),
...                 norminvgauss.ppf(0.99, a, b), 100)
>>> ax.plot(x, norminvgauss.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='norminvgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = norminvgauss(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

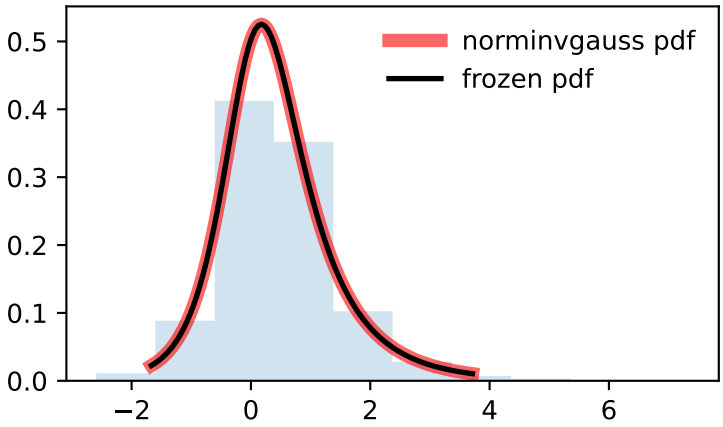
```
>>> vals = norminvgauss.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], norminvgauss.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = norminvgauss.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, loc=0, scale=1)	Non-central moment of order n
stats(a, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, loc=0, scale=1)	Median of the distribution.
mean(a, b, loc=0, scale=1)	Mean of the distribution.
var(a, b, loc=0, scale=1)	Variance of the distribution.
std(a, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.pareto

scipy.stats.**pareto = <scipy.stats._continuous_distns.pareto_gen object>**

A Pareto continuous random variable.

As an instance of the *rv_continuous* class, *pareto* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *pareto* is:

$$f(x, b) = \frac{b}{x^{b+1}}$$

for $x \geq 1$, $b > 0$.

pareto takes `b` as a shape parameter for b.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `pareto.pdf(x, b, loc, scale)` is identically equivalent to `pareto.pdf(y, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import pareto
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> b = 2.62
>>> mean, var, skew, kurt = pareto.stats(b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(pareto.ppf(0.01, b),
...                 pareto.ppf(0.99, b), 100)
>>> ax.plot(x, pareto.pdf(x, b),
...         'r-', lw=5, alpha=0.6, label='pareto pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = pareto(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

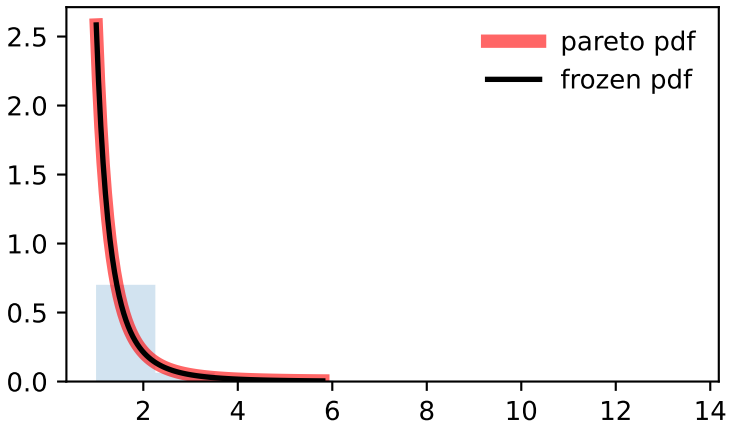
```
>>> vals = pareto.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], pareto.cdf(vals, b))
True
```

Generate random numbers:

```
>>> r = pareto.rvs(b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, b, loc=0, scale=1)	Probability density function.
logpdf(x, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, b, loc=0, scale=1)	Log of the survival function.
ppf(q, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, b, loc=0, scale=1)	Non-central moment of order n
stats(b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(b,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(b, loc=0, scale=1)	Median of the distribution.
mean(b, loc=0, scale=1)	Mean of the distribution.
var(b, loc=0, scale=1)	Variance of the distribution.
std(b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.pearson3

scipy.stats.**pearson3 = <scipy.stats._continuous_distns.pearson3_gen object>**

A pearson type III continuous random variable.

As an instance of the *rv_continuous* class, *pearson3* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *pearson3* is:

$$f(x, \kappa) = \frac{|\beta|}{\Gamma(\alpha)} (\beta(x - \zeta))^{\alpha - 1} \exp(-\beta(x - \zeta))$$

where:

$$\beta = \frac{2}{\kappa}$$
$$\alpha = \beta^2 = \frac{4}{\kappa^2}$$
$$\zeta = -\frac{\alpha}{\beta} = -\beta$$

Γ is the gamma function (*scipy.special.gamma*). Pass the skew κ into *pearson3* as the shape parameter `skew`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `pearson3.pdf(x, skew, loc, scale)` is identically equivalent to `pearson3.pdf(y, skew) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

R.W. Vogel and D.E. McMartin, "Probability Plot Goodness-of-Fit and Skewness Estimation Procedures for the Pearson Type 3 Distribution", Water Resources Research, Vol.27, 3149-3158 (1991).

L.R. Salvosa, "Tables of Pearson's Type III Function", Ann. Math. Statist., Vol.1, 191-198 (1930).

"Using Modern Computing Tools to Fit the Pearson Type III Distribution to Aviation Loads Data", Office of Aviation Research (2003).

Examples

```
>>> from scipy.stats import pearson3
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> skew = 0.1
>>> mean, var, skew, kurt = pearson3.stats(skew, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(pearson3.ppf(0.01, skew),
...                 pearson3.ppf(0.99, skew), 100)
>>> ax.plot(x, pearson3.pdf(x, skew),
...         'r-', lw=5, alpha=0.6, label='pearson3 pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = pearson3(skew)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

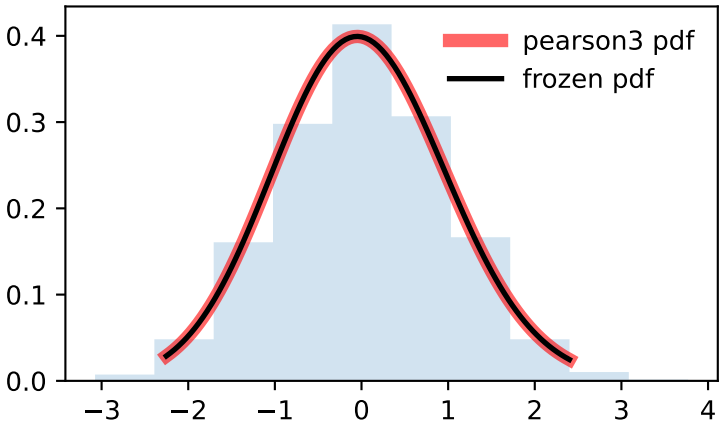
```
>>> vals = pearson3.ppf([0.001, 0.5, 0.999], skew)
>>> np.allclose([0.001, 0.5, 0.999], pearson3.cdf(vals, skew))
True
```

Generate random numbers:

```
>>> r = pearson3.rvs(skew, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(skew, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, skew, loc=0, scale=1)	Probability density function.
logpdf(x, skew, loc=0, scale=1)	Log of the probability density function.
cdf(x, skew, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, skew, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, skew, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, skew, loc=0, scale=1)	Log of the survival function.
ppf(q, skew, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, skew, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, skew, loc=0, scale=1)	Non-central moment of order n
stats(skew, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(skew, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(skew,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(skew, loc=0, scale=1)	Median of the distribution.
mean(skew, loc=0, scale=1)	Mean of the distribution.
var(skew, loc=0, scale=1)	Variance of the distribution.
std(skew, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, skew, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.powerlaw

scipy.stats.**powerlaw = <scipy.stats._continuous_distns.powerlaw_gen object>**

A power-function continuous random variable.

As an instance of the *rv_continuous* class, *powerlaw* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *powerlaw* is:

$$f(x, a) = ax^{a-1}$$

for $0 \leq x \leq 1$, $a > 0$.

powerlaw takes `a` as a shape parameter for a.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `powerlaw.pdf(x, a, loc, scale)` is identically equivalent to `powerlaw.pdf(y, a) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

powerlaw is a special case of *beta* with b=1.

Examples

```
>>> from scipy.stats import powerlaw
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 1.66
>>> mean, var, skew, kurt = powerlaw.stats(a, moments='mvsk')
```

Display the probability density function (pdf):

```
>>> x = np.linspace(powerlaw.ppf(0.01, a),
...                 powerlaw.ppf(0.99, a), 100)
>>> ax.plot(x, powerlaw.pdf(x, a),
...         'r-', lw=5, alpha=0.6, label='powerlaw pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```
>>> rv = powerlaw(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

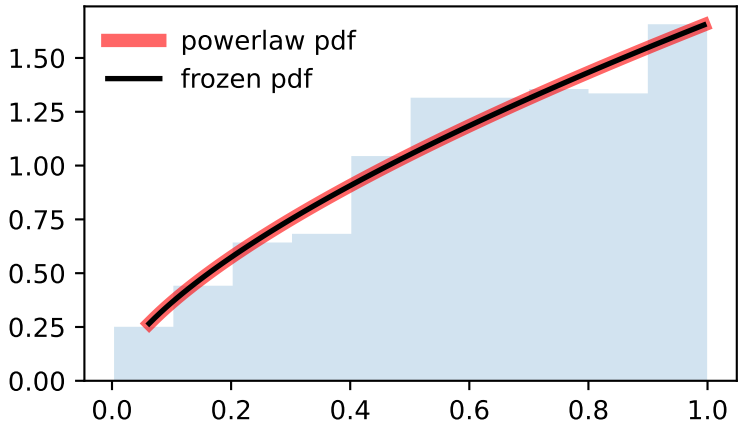
```
>>> vals = powerlaw.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], powerlaw.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = powerlaw.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.powerlognorm

scipy.stats.**powerlognorm = <scipy.stats._continuous_distns.powerlognorm_gen object>**

A power log-normal continuous random variable.

As an instance of the *rv_continuous* class, *powerlognorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *powerlognorm* is:

$$f(x, c, s) = \frac{c}{xs}\phi(\log(x)/s)(\Phi(-\log(x)/s))^{c-1}$$

where ϕ is the normal pdf, and Φ is the normal cdf, and $x > 0$, $s, c > 0$.

powerlognorm takes c and s as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `powerlognorm.pdf(x, c, s, loc, scale)` is identically equivalent to `powerlognorm.pdf(y, c, s) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import powerlognorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c, s = 2.14, 0.446
>>> mean, var, skew, kurt = powerlognorm.stats(c, s, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(powerlognorm.ppf(0.01, c, s),
...                 powerlognorm.ppf(0.99, c, s), 100)
>>> ax.plot(x, powerlognorm.pdf(x, c, s),
...         'r-', lw=5, alpha=0.6, label='powerlognorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = powerlognorm(c, s)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

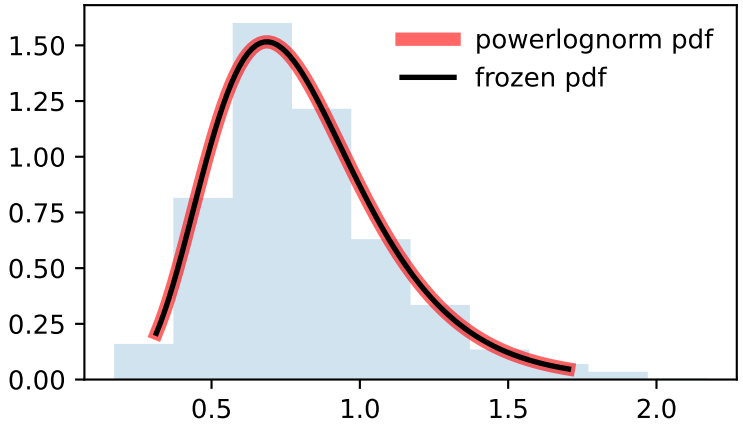
```
>>> vals = powerlognorm.ppf([0.001, 0.5, 0.999], c, s)
>>> np.allclose([0.001, 0.5, 0.999], powerlognorm.cdf(vals, c, s))
True
```

Generate random numbers:

```
>>> r = powerlognorm.rvs(c, s, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, s, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, s, loc=0, scale=1)	Probability density function.
logpdf(x, c, s, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, s, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, s, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, s, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, s, loc=0, scale=1)	Log of the survival function.
ppf(q, c, s, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, s, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, s, loc=0, scale=1)	Non-central moment of order n
stats(c, s, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, s, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c, s), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, s, loc=0, scale=1)	Median of the distribution.
mean(c, s, loc=0, scale=1)	Mean of the distribution.
var(c, s, loc=0, scale=1)	Variance of the distribution.
std(c, s, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, s, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.powernorm

scipy.stats.**powernorm = <scipy.stats._continuous_distns.powernorm_gen object>**

A power normal continuous random variable.

As an instance of the *rv_continuous* class, *powernorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *powernorm* is:

$$f(x, c) = c\phi(x)(\Phi(-x))^{c-1}$$

where ϕ is the normal pdf, and Φ is the normal cdf, and $x >= 0$, $c > 0$.

powernorm takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `powernorm.pdf(x, c, loc, scale)` is identically equivalent to `powernorm.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import powernorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 4.45
>>> mean, var, skew, kurt = powernorm.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(powernorm.ppf(0.01, c),
...                 powernorm.ppf(0.99, c), 100)
>>> ax.plot(x, powernorm.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='powernorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = powernorm(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

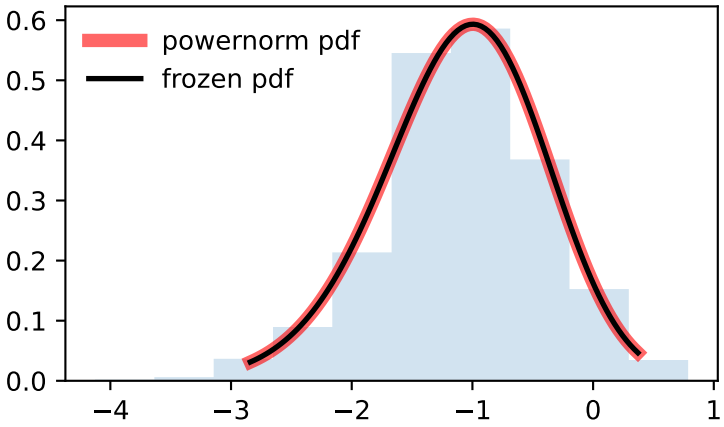
```
>>> vals = powernorm.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], powernorm.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = powernorm.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.rdist

scipy.stats.**rdist = <scipy.stats._continuous_distns.rdist_gen object>**

An R-distributed (symmetric beta) continuous random variable.

As an instance of the *rv_continuous* class, *rdist* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *rdist* is:

$$f(x, c) = \frac{(1 - x^2)^{c/2-1}}{B(1/2, c/2)}$$

for $-1 \leq x \leq 1$, $c > 0$. *rdist* is also called the symmetric beta distribution: if B has a *beta* distribution with parameters (c/2, c/2), then X = 2*B - 1 follows a R-distribution with parameter c.

rdist takes `c` as a shape parameter for c.

This distribution includes the following distribution kernels as special cases:

```
c = 2:  uniform
c = 3:  `semicircular`
c = 4:  Epanechnikov (parabolic)
c = 6:  quartic (biweight)
c = 8:  triweight
```

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rdist.pdf(x, c, loc, scale)` is identically equivalent to `rdist.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import rdist
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 1.6
>>> mean, var, skew, kurt = rdist.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(rdist.ppf(0.01, c),
...                 rdist.ppf(0.99, c), 100)
>>> ax.plot(x, rdist.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='rdist pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = rdist(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

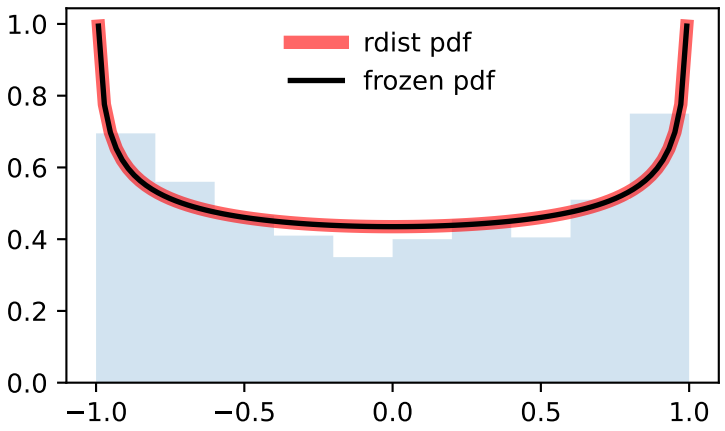
```
>>> vals = rdist.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], rdist.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = rdist.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.rayleigh

scipy.stats.**rayleigh = <scipy.stats._continuous_distns.rayleigh_gen object>**

A Rayleigh continuous random variable.

As an instance of the *rv_continuous* class, *rayleigh* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *rayleigh* is:

$$f(x) = x \exp(-x^2/2)$$

for $x \geq 0$.

rayleigh is a special case of *chi* with `df=2`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rayleigh.pdf(x, loc, scale)` is identically equivalent to `rayleigh.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import rayleigh
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = rayleigh.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(rayleigh.ppf(0.01),
...                 rayleigh.ppf(0.99), 100)
>>> ax.plot(x, rayleigh.pdf(x),
...         'r-', lw=5, alpha=0.6, label='rayleigh pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = rayleigh()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

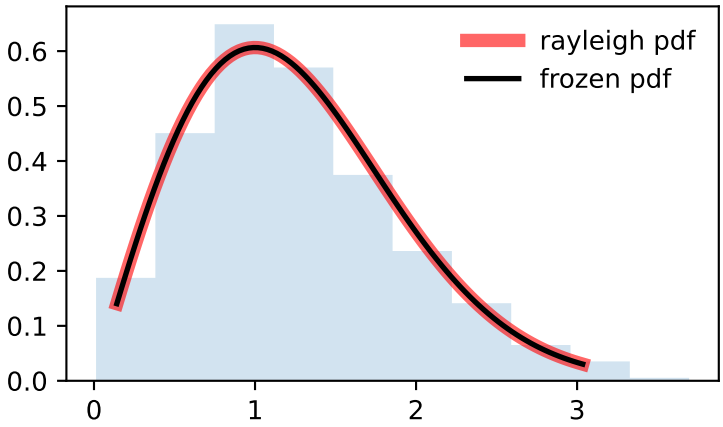
```
>>> vals = rayleigh.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], rayleigh.cdf(vals))
True
```

Generate random numbers:

```
>>> r = rayleigh.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.rice

scipy.stats.**rice = <scipy.stats._continuous_distns.rice_gen object>**

A Rice continuous random variable.

As an instance of the *rv_continuous* class, *rice* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *rice* is:

$$f(x, b) = x \exp(-\frac{x^2 + b^2}{2}) I_0(xb)$$

for $x >= 0$, $b > 0$. I_0 is the modified Bessel function of order zero (*scipy.special.i0*).

rice takes `b` as a shape parameter for b.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `rice.pdf(x, b, loc, scale)` is identically equivalent to `rice.pdf(y, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

The Rice distribution describes the length, r, of a 2-D vector with components $(U + u, V + v)$, where U, V are constant, u, v are independent Gaussian random variables with standard deviation s. Let $R = \sqrt{U^2 + V^2}$. Then the pdf of r is `rice.pdf(x, R/s, scale=s)`.

Examples

```
>>> from scipy.stats import rice
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> b = 0.775
>>> mean, var, skew, kurt = rice.stats(b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(rice.ppf(0.01, b),
...                 rice.ppf(0.99, b), 100)
>>> ax.plot(x, rice.pdf(x, b),
...         'r-', lw=5, alpha=0.6, label='rice pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = rice(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

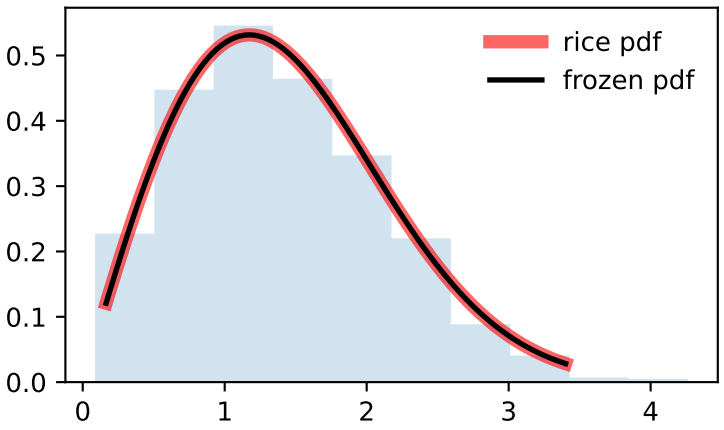
```
>>> vals = rice.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], rice.cdf(vals, b))
True
```

Generate random numbers:

```
>>> r = rice.rvs(b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, b, loc=0, scale=1)	Probability density function.
logpdf(x, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, b, loc=0, scale=1)	Log of the survival function.
ppf(q, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, b, loc=0, scale=1)	Non-central moment of order n
stats(b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(b,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(b, loc=0, scale=1)	Median of the distribution.
mean(b, loc=0, scale=1)	Mean of the distribution.
var(b, loc=0, scale=1)	Variance of the distribution.
std(b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.recipinvgauss

scipy.stats.**recipinvgauss = <scipy.stats._continuous_distns.recipinvgauss_gen object>**

A reciprocal inverse Gaussian continuous random variable.

As an instance of the *rv_continuous* class, *recipinvgauss* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *recipinvgauss* is:

$$f(x, \mu) = \frac{1}{\sqrt{2\pi x}} \exp\left(\frac{-(1-\mu x)^2}{2\mu^2 x}\right)$$

for $x \geq 0$.

recipinvgauss takes `mu` as a shape parameter for μ.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `recipinvgauss.pdf(x, mu, loc, scale)` is identically equivalent to `recipinvgauss.pdf(y, mu) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import recipinvgauss
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mu = 0.63
>>> mean, var, skew, kurt = recipinvgauss.stats(mu, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(recipinvgauss.ppf(0.01, mu),
...                 recipinvgauss.ppf(0.99, mu), 100)
>>> ax.plot(x, recipinvgauss.pdf(x, mu),
...         'r-', lw=5, alpha=0.6, label='recipinvgauss pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = recipinvgauss(mu)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

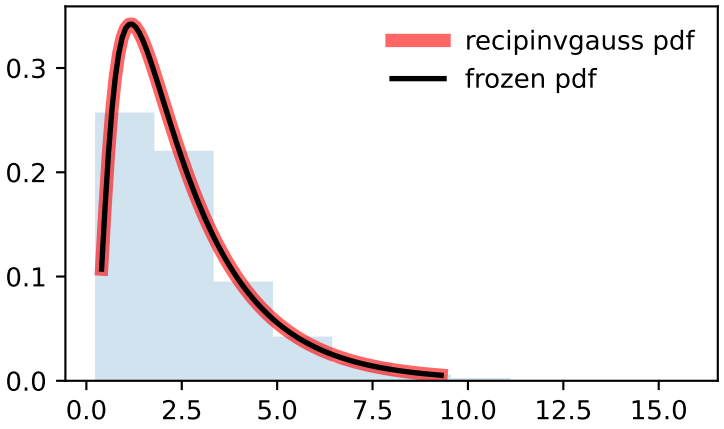
```
>>> vals = recipinvgauss.ppf([0.001, 0.5, 0.999], mu)
>>> np.allclose([0.001, 0.5, 0.999], recipinvgauss.cdf(vals, mu))
True
```

Generate random numbers:

```
>>> r = recipinvgauss.rvs(mu, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(mu, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, mu, loc=0, scale=1)	Probability density function.
logpdf(x, mu, loc=0, scale=1)	Log of the probability density function.
cdf(x, mu, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, mu, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, mu, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, mu, loc=0, scale=1)	Log of the survival function.
ppf(q, mu, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, mu, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, mu, loc=0, scale=1)	Non-central moment of order n
stats(mu, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(mu, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(mu,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(mu, loc=0, scale=1)	Median of the distribution.
mean(mu, loc=0, scale=1)	Mean of the distribution.
var(mu, loc=0, scale=1)	Variance of the distribution.
std(mu, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, mu, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.semicircular

scipy.stats.**semicircular = <scipy.stats._continuous_distns.semicircular_gen object>**

A semicircular continuous random variable.

As an instance of the *rv_continuous* class, *semicircular* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

rdist

Notes

The probability density function for *semicircular* is:

$$f(x) = \frac{2}{\pi}\sqrt{1-x^2}$$

for $-1 \leq x \leq 1$.

The distribution is a special case of *rdist* with *c* = *3*.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `semicircular.pdf(x, loc, scale)` is identically equivalent to `semicircular.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import semicircular
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = semicircular.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(semicircular.ppf(0.01),
...                 semicircular.ppf(0.99), 100)
>>> ax.plot(x, semicircular.pdf(x),
...         'r-', lw=5, alpha=0.6, label='semicircular pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = semicircular()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

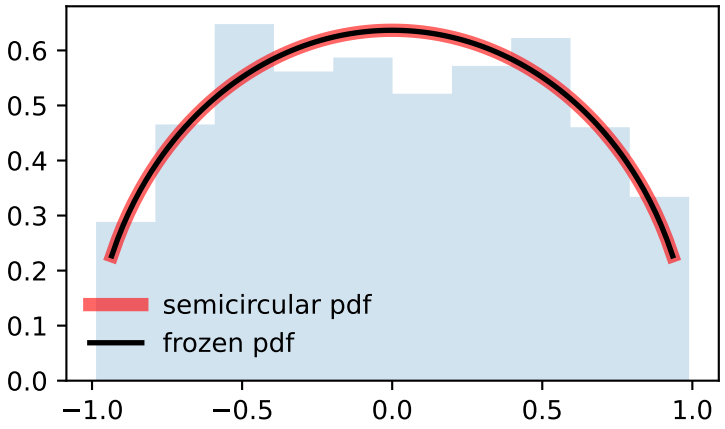
```
>>> vals = semicircular.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], semicircular.cdf(vals))
True
```

Generate random numbers:

```
>>> r = semicircular.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.skewcauchy

scipy.stats.**skewcauchy = <scipy.stats._continuous_distns.skewcauchy_gen object>**

A skewed Cauchy random variable.

As an instance of the *rv_continuous* class, *skewcauchy* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

cauchy

Cauchy distribution

Notes

The probability density function for *skewcauchy* is:

$$f(x) = \frac{1}{\pi\left(\frac{x^2}{(a\,\mathrm{sign}(x)+1)^2} + 1\right)}$$

for a real number x and skewness parameter $-1 < a < 1$.

When $a = 0$, the distribution reduces to the usual Cauchy distribution.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `skewcauchy.pdf(x, a, loc, scale)` is identically equivalent to `skewcauchy.pdf(y, a) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import skewcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 0.5
>>> mean, var, skew, kurt = skewcauchy.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(skewcauchy.ppf(0.01, a),
...                 skewcauchy.ppf(0.99, a), 100)
>>> ax.plot(x, skewcauchy.pdf(x, a),
...         'r-', lw=5, alpha=0.6, label='skewcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = skewcauchy(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

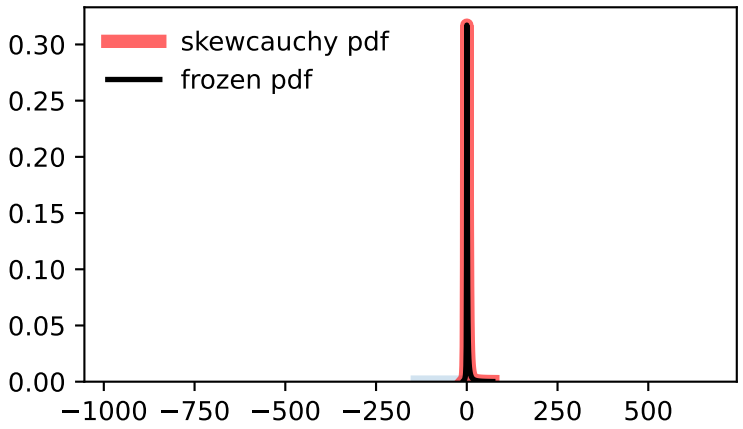
```
>>> vals = skewcauchy.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], skewcauchy.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = skewcauchy.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.skewnorm

scipy.stats.**skewnorm = <scipy.stats._continuous_distns.skew_norm_gen object>**

A skew-normal random variable.

As an instance of the *rv_continuous* class, *skewnorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The pdf is:

```
skewnorm.pdf(x, a) = 2 * norm.pdf(x) * norm.cdf(a*x)
```

skewnorm takes a real number a as a skewness parameter When `a = 0` the distribution is identical to a normal distribution (*norm*). *rvs* implements the method of [1].

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `skewnorm.pdf(x, a, loc, scale)` is identically equivalent to `skewnorm.pdf(y, a) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1]

Examples

```
>>> from scipy.stats import skewnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 4
>>> mean, var, skew, kurt = skewnorm.stats(a, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(skewnorm.ppf(0.01, a),
...                 skewnorm.ppf(0.99, a), 100)
>>> ax.plot(x, skewnorm.pdf(x, a),
...         'r-', lw=5, alpha=0.6, label='skewnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = skewnorm(a)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

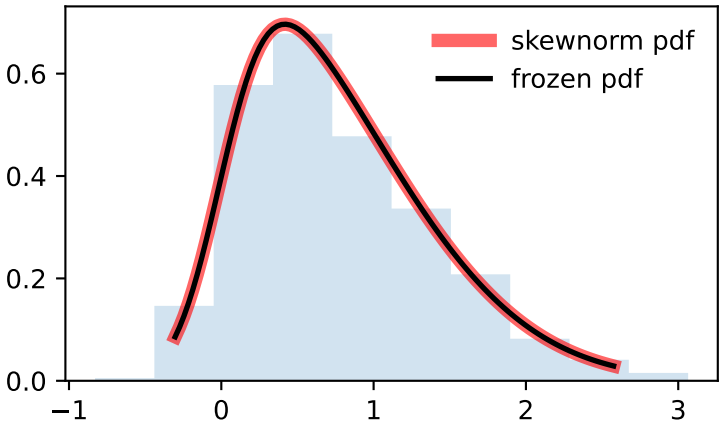
```
>>> vals = skewnorm.ppf([0.001, 0.5, 0.999], a)
>>> np.allclose([0.001, 0.5, 0.999], skewnorm.cdf(vals, a))
True
```

Generate random numbers:

```
>>> r = skewnorm.rvs(a, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, loc=0, scale=1)	Probability density function.
logpdf(x, a, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, loc=0, scale=1)	Log of the survival function.
ppf(q, a, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, loc=0, scale=1)	Non-central moment of order n
stats(a, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0, scale=1)	Median of the distribution.
mean(a, loc=0, scale=1)	Mean of the distribution.
var(a, loc=0, scale=1)	Variance of the distribution.
std(a, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.studentized_range

scipy.stats.**studentized_range = <scipy.stats._continuous_distns.studentized_range_gen objec**

A studentized range continuous random variable.

As an instance of the *rv_continuous* class, *studentized_range* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

t Student's t distribution

Notes

The probability density function for *studentized_range* is:

$$f(x; k, \nu) = \frac{k(k-1)\nu^{\nu/2}}{\Gamma(\nu/2)2^{\nu/2-1}} \int_0^\infty \int_{-\infty}^\infty s^\nu e^{-\nu s^2/2} \phi(z)\phi(sx+z)[\Phi(sx+z) - \Phi(z)]^{k-2}\, dz\, ds$$

for $x0$, $k > 1$, and $\nu > 0$.

studentized_range takes `k` for k and `df` for ν as shape parameters.

When ν exceeds 100,000, an asymptotic approximation (infinite degrees of freedom) is used to compute the cumulative distribution function [4].

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `studentized_range.pdf(x, k, df, loc, scale)` is identically equivalent to `studentized_range.pdf(y, k, df) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

[1], [2], [3], [4]

Examples

```
>>> from scipy.stats import studentized_range
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> k, df = 3, 10
>>> mean, var, skew, kurt = studentized_range.stats(k, df, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(studentized_range.ppf(0.01, k, df),
...                 studentized_range.ppf(0.99, k, df), 100)
>>> ax.plot(x, studentized_range.pdf(x, k, df),
...         'r-', lw=5, alpha=0.6, label='studentized_range pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = studentized_range(k, df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

```
>>> vals = studentized_range.ppf([0.001, 0.5, 0.999], k, df)
>>> np.allclose([0.001, 0.5, 0.999], studentized_range.cdf(vals, k, df))
True
```

Rather than using (`studentized_range.rvs`) to generate random variates, which is very slow for this distribution, we can approximate the inverse CDF using an interpolator, and then perform inverse transform sampling with this approximate inverse CDF.

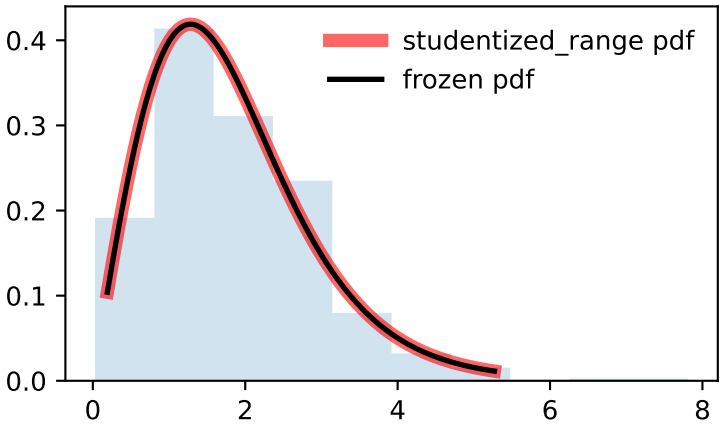
This distribution has an infinite but thin right tail, so we focus our attention on the leftmost 99.9 percent.

```
>>> a, b = studentized_range.ppf([0, .999], k, df)
>>> a, b
0, 7.41058083802274
```

```
>>> from scipy.interpolate import interp1d
>>> rng = np.random.default_rng()
>>> xs = np.linspace(a, b, 50)
>>> cdf = studentized_range.cdf(xs, k, df)
# Create an interpolant of the inverse CDF
>>> ppf = interp1d(cdf, xs, fill_value='extrapolate')
# Perform inverse transform sampling using the interpolant
>>> r = ppf(rng.uniform(size=1000))
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(k, df, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, k, df, loc=0, scale=1)	Probability density function.
logpdf(x, k, df, loc=0, scale=1)	Log of the probability density function.
cdf(x, k, df, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, k, df, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, k, df, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, k, df, loc=0, scale=1)	Log of the survival function.
ppf(q, k, df, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, k, df, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, k, df, loc=0, scale=1)	Non-central moment of order n
stats(k, df, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(k, df, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(k, df), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(k, df, loc=0, scale=1)	Median of the distribution.
mean(k, df, loc=0, scale=1)	Mean of the distribution.
var(k, df, loc=0, scale=1)	Variance of the distribution.
std(k, df, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, k, df, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.t

scipy.stats.**t = <scipy.stats._continuous_distns.t_gen object>**

A Student's t continuous random variable.

For the noncentral t distribution, see *nct*.

As an instance of the *rv_continuous* class, *t* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

nct

Notes

The probability density function for *t* is:

$$f(x, \nu) = \frac{\Gamma((\nu+1)/2)}{\sqrt{\pi\nu}\Gamma(\nu/2)}(1+x^2/\nu)^{-(\nu+1)/2}$$

where x is a real number and the degrees of freedom parameter ν (denoted `df` in the implementation) satisfies $\nu > 0$. Γ is the gamma function (*scipy.special.gamma*).

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `t.pdf(x, df, loc, scale)` is identically equivalent to `t.pdf(y, df) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import t
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> df = 2.74
>>> mean, var, skew, kurt = t.stats(df, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(t.ppf(0.01, df),
...                 t.ppf(0.99, df), 100)
>>> ax.plot(x, t.pdf(x, df),
...         'r-', lw=5, alpha=0.6, label='t pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = t(df)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

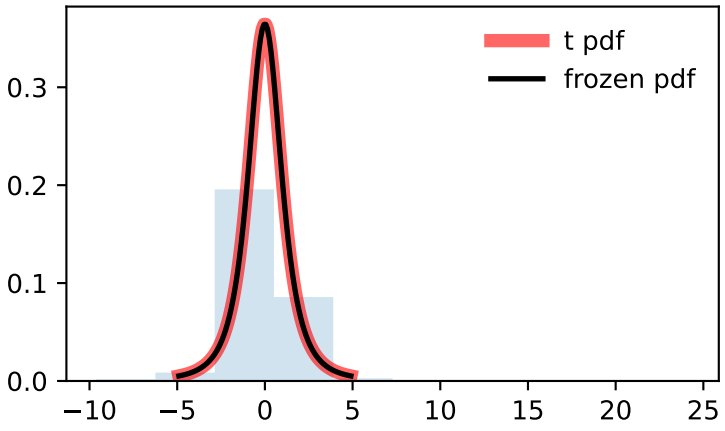
```
>>> vals = t.ppf([0.001, 0.5, 0.999], df)
>>> np.allclose([0.001, 0.5, 0.999], t.cdf(vals, df))
True
```

Generate random numbers:

```
>>> r = t.rvs(df, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(df, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, df, loc=0, scale=1)	Probability density function.
logpdf(x, df, loc=0, scale=1)	Log of the probability density function.
cdf(x, df, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, df, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, df, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, df, loc=0, scale=1)	Log of the survival function.
ppf(q, df, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, df, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, df, loc=0, scale=1)	Non-central moment of order n
stats(df, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(df, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(df,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(df, loc=0, scale=1)	Median of the distribution.
mean(df, loc=0, scale=1)	Mean of the distribution.
var(df, loc=0, scale=1)	Variance of the distribution.
std(df, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, df, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.trapezoid

scipy.stats.**trapezoid = <scipy.stats._continuous_distns.trapezoid_gen object>**

A trapezoidal continuous random variable.

As an instance of the *rv_continuous* class, *trapezoid* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The trapezoidal distribution can be represented with an up-sloping line from `loc` to `(loc + c*scale)`, then constant to `(loc + d*scale)` and then downsloping from `(loc + d*scale)` to `(loc+scale)`. This defines the trapezoid base from `loc` to `(loc+scale)` and the flat top from `c` to `d` proportional to the position along the base with `0 <= c <= d <= 1`. When `c=d`, this is equivalent to *triang* with the same values for *loc*, *scale* and *c*. The method of [1] is used for computing moments.

trapezoid takes c and d as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `trapezoid.pdf(x, c, d, loc, scale)` is identically equivalent to `trapezoid.pdf(y, c, d) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

The standard form is in the range [0, 1] with c the mode. The location parameter shifts the start to *loc*. The scale parameter changes the width from 1 to *scale*.

References

[1]

Examples

```
>>> from scipy.stats import trapezoid
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c, d = 0.2, 0.8
>>> mean, var, skew, kurt = trapezoid.stats(c, d, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(trapezoid.ppf(0.01, c, d),
...                 trapezoid.ppf(0.99, c, d), 100)
>>> ax.plot(x, trapezoid.pdf(x, c, d),
...         'r-', lw=5, alpha=0.6, label='trapezoid pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = trapezoid(c, d)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

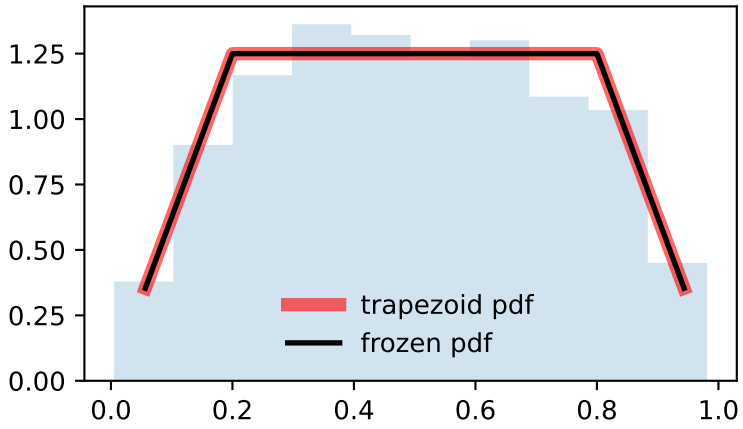
```
>>> vals = trapezoid.ppf([0.001, 0.5, 0.999], c, d)
>>> np.allclose([0.001, 0.5, 0.999], trapezoid.cdf(vals, c, d))
True
```

Generate random numbers:

```
>>> r = trapezoid.rvs(c, d, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, d, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, d, loc=0, scale=1)	Probability density function.
logpdf(x, c, d, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, d, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, d, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, d, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, d, loc=0, scale=1)	Log of the survival function.
ppf(q, c, d, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, d, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, d, loc=0, scale=1)	Non-central moment of order n
stats(c, d, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, d, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c, d), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, d, loc=0, scale=1)	Median of the distribution.
mean(c, d, loc=0, scale=1)	Mean of the distribution.
var(c, d, loc=0, scale=1)	Variance of the distribution.
std(c, d, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, d, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.triang

scipy.stats.**triang = <scipy.stats._continuous_distns.triang_gen object>**

A triangular continuous random variable.

As an instance of the *rv_continuous* class, *triang* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The triangular distribution can be represented with an up-sloping line from `loc` to `(loc + c*scale)` and then downsloping for `(loc + c*scale)` to `(loc + scale)`.

triang takes `c` as a shape parameter for *c*.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `triang.pdf(x, c, loc, scale)` is identically equivalent to `triang.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

The standard form is in the range [0, 1] with c the mode. The location parameter shifts the start to *loc*. The scale parameter changes the width from 1 to *scale*.

Examples

```
>>> from scipy.stats import triang
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 0.158
>>> mean, var, skew, kurt = triang.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(triang.ppf(0.01, c),
...                 triang.ppf(0.99, c), 100)
>>> ax.plot(x, triang.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='triang pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = triang(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

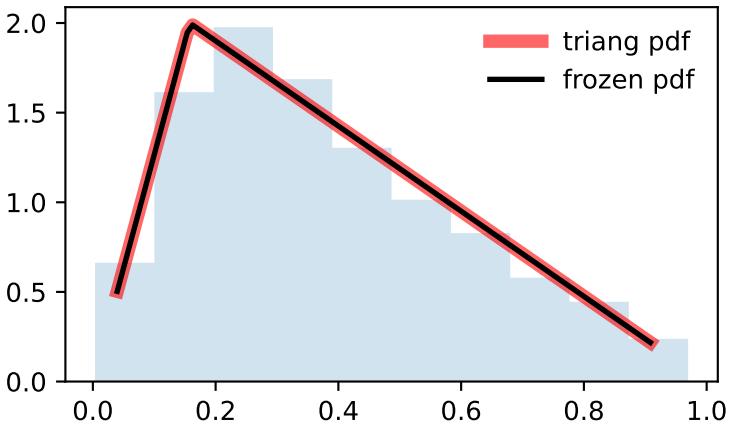
```
>>> vals = triang.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], triang.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = triang.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.truncexpon

scipy.stats.**truncexpon = <scipy.stats._continuous_distns.truncexpon_gen object>**

A truncated exponential continuous random variable.

As an instance of the *rv_continuous* class, *truncexpon* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *truncexpon* is:

$$f(x, b) = \frac{\exp(-x)}{1 - \exp(-b)}$$

for $0 <= x <= b$.

truncexpon takes `b` as a shape parameter for b.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `truncexpon.pdf(x, b, loc, scale)` is identically equivalent to `truncexpon.pdf(y, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import truncexpon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> b = 4.69
>>> mean, var, skew, kurt = truncexpon.stats(b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(truncexpon.ppf(0.01, b),
...                 truncexpon.ppf(0.99, b), 100)
>>> ax.plot(x, truncexpon.pdf(x, b),
...         'r-', lw=5, alpha=0.6, label='truncexpon pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = truncexpon(b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

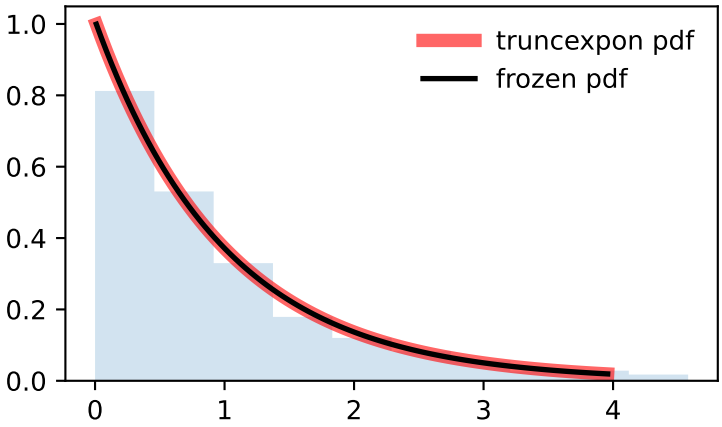
```
>>> vals = truncexpon.ppf([0.001, 0.5, 0.999], b)
>>> np.allclose([0.001, 0.5, 0.999], truncexpon.cdf(vals, b))
True
```

Generate random numbers:

```
>>> r = truncexpon.rvs(b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, b, loc=0, scale=1)	Probability density function.
logpdf(x, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, b, loc=0, scale=1)	Log of the survival function.
ppf(q, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, b, loc=0, scale=1)	Non-central moment of order n
stats(b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(b,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(b, loc=0, scale=1)	Median of the distribution.
mean(b, loc=0, scale=1)	Mean of the distribution.
var(b, loc=0, scale=1)	Variance of the distribution.
std(b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.truncnorm

scipy.stats.**truncnorm = <scipy.stats._continuous_distns.truncnorm_gen object>**

A truncated normal continuous random variable.

As an instance of the *rv_continuous* class, *truncnorm* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The standard form of this distribution is a standard normal truncated to the range [a, b] — notice that a and b are defined over the domain of the standard normal. To convert clip values for a specific mean and standard deviation, use:

```
a, b = (myclip_a - my_mean) / my_std, (myclip_b - my_mean) / my_std
```

truncnorm takes a and b as shape parameters.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `truncnorm.pdf(x, a, b, loc, scale)` is identically equivalent to `truncnorm.pdf(y, a, b) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import truncnorm
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, b = 0.1, 2
>>> mean, var, skew, kurt = truncnorm.stats(a, b, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(truncnorm.ppf(0.01, a, b),
...                 truncnorm.ppf(0.99, a, b), 100)
>>> ax.plot(x, truncnorm.pdf(x, a, b),
...         'r-', lw=5, alpha=0.6, label='truncnorm pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = truncnorm(a, b)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

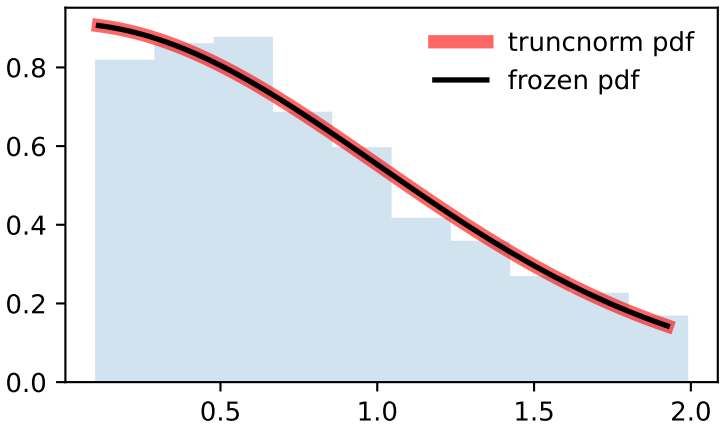
```
>>> vals = truncnorm.ppf([0.001, 0.5, 0.999], a, b)
>>> np.allclose([0.001, 0.5, 0.999], truncnorm.cdf(vals, a, b))
True
```

Generate random numbers:

```
>>> r = truncnorm.rvs(a, b, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(a, b, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, a, b, loc=0, scale=1)	Probability density function.
logpdf(x, a, b, loc=0, scale=1)	Log of the probability density function.
cdf(x, a, b, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, a, b, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, a, b, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, a, b, loc=0, scale=1)	Log of the survival function.
ppf(q, a, b, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, b, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, a, b, loc=0, scale=1)	Non-central moment of order n
stats(a, b, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, b, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(a, b), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(a, b, loc=0, scale=1)	Median of the distribution.
mean(a, b, loc=0, scale=1)	Mean of the distribution.
var(a, b, loc=0, scale=1)	Variance of the distribution.
std(a, b, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, a, b, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.tukeylambda

scipy.stats.**tukeylambda = <scipy.stats._continuous_distns.tukeylambda_gen object>**

A Tukey-Lamdba continuous random variable.

As an instance of the *rv_continuous* class, *tukeylambda* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

A flexible distribution, able to represent and interpolate between the following distributions:

- Cauchy ($lambda = -1$)
- logistic ($lambda = 0$)
- approx Normal ($lambda = 0.14$)
- uniform from -1 to 1 ($lambda = 1$)

tukeylambda takes a real number $lambda$ (denoted `lam` in the implementation) as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `tukeylambda.pdf(x, lam, loc, scale)` is identically equivalent to `tukeylambda.pdf(y, lam) / scale` with `y = (x - loc) / scale`. Note that

shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import tukeylambda
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> lam = 3.13
>>> mean, var, skew, kurt = tukeylambda.stats(lam, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(tukeylambda.ppf(0.01, lam),
...                 tukeylambda.ppf(0.99, lam), 100)
>>> ax.plot(x, tukeylambda.pdf(x, lam),
...         'r-', lw=5, alpha=0.6, label='tukeylambda pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = tukeylambda(lam)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

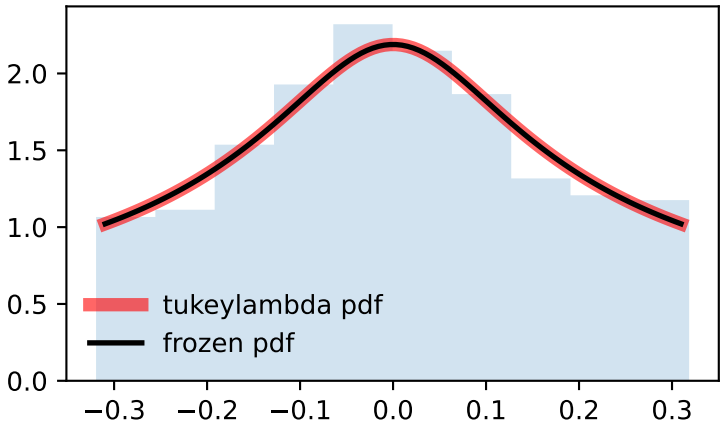
```
>>> vals = tukeylambda.ppf([0.001, 0.5, 0.999], lam)
>>> np.allclose([0.001, 0.5, 0.999], tukeylambda.cdf(vals, lam))
True
```

Generate random numbers:

```
>>> r = tukeylambda.rvs(lam, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(lam, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, lam, loc=0, scale=1)	Probability density function.
logpdf(x, lam, loc=0, scale=1)	Log of the probability density function.
cdf(x, lam, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, lam, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, lam, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, lam, loc=0, scale=1)	Log of the survival function.
ppf(q, lam, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, lam, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, lam, loc=0, scale=1)	Non-central moment of order n
stats(lam, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(lam, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(lam,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(lam, loc=0, scale=1)	Median of the distribution.
mean(lam, loc=0, scale=1)	Mean of the distribution.
var(lam, loc=0, scale=1)	Variance of the distribution.
std(lam, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, lam, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.uniform

scipy.stats.**uniform = <scipy.stats._continuous_distns.uniform_gen object>**

A uniform continuous random variable.

In the standard form, the distribution is uniform on `[0, 1]`. Using the parameters `loc` and `scale`, one obtains the uniform distribution on `[loc, loc + scale]`.

As an instance of the *rv_continuous* class, *uniform* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Examples

```
>>> from scipy.stats import uniform
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = uniform.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(uniform.ppf(0.01),
...                 uniform.ppf(0.99), 100)
>>> ax.plot(x, uniform.pdf(x),
...         'r-', lw=5, alpha=0.6, label='uniform pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = uniform()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

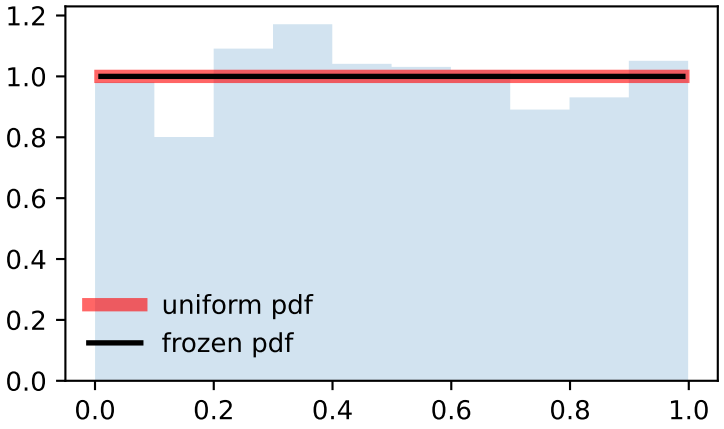
```
>>> vals = uniform.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], uniform.cdf(vals))
True
```

Generate random numbers:

```
>>> r = uniform.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.vonmises

scipy.stats.**vonmises = <scipy.stats._continuous_distns.vonmises_gen object>**

A Von Mises continuous random variable.

As an instance of the *rv_continuous* class, *vonmises* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *vonmises* and *vonmises_line* is:

$$f(x, \kappa) = \frac{\exp(\kappa \cos(x))}{2\pi I_0(\kappa)}$$

for $-\pi \leq x \leq \pi$, $\kappa > 0$. I_0 is the modified Bessel function of order zero (*scipy.special.i0*).

vonmises is a circular distribution which does not restrict the distribution to a fixed interval. Currently, there is no circular distribution framework in scipy. The `cdf` is implemented such that `cdf(x + 2*np.pi) == cdf(x) + 1`.

vonmises_line is the same distribution, defined on $[-\pi, \pi]$ on the real line. This is a regular (i.e. non-circular) distribution.

vonmises and *vonmises_line* take `kappa` as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `vonmises.pdf(x, kappa, loc, scale)` is identically equivalent to `vonmises.pdf(y, kappa) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import vonmises
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> kappa = 3.99
>>> mean, var, skew, kurt = vonmises.stats(kappa, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(vonmises.ppf(0.01, kappa),
...                 vonmises.ppf(0.99, kappa), 100)
>>> ax.plot(x, vonmises.pdf(x, kappa),
...         'r-', lw=5, alpha=0.6, label='vonmises pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = vonmises(kappa)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

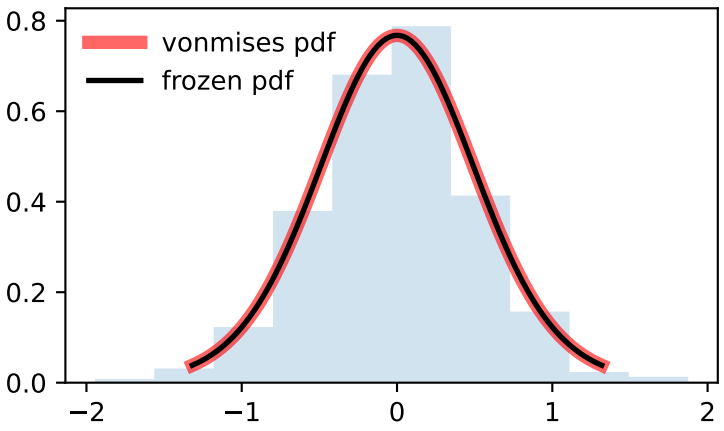
```
>>> vals = vonmises.ppf([0.001, 0.5, 0.999], kappa)
>>> np.allclose([0.001, 0.5, 0.999], vonmises.cdf(vals, kappa))
True
```

Generate random numbers:

```
>>> r = vonmises.rvs(kappa, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(kappa, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, kappa, loc=0, scale=1)	Probability density function.
logpdf(x, kappa, loc=0, scale=1)	Log of the probability density function.
cdf(x, kappa, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, kappa, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, kappa, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, kappa, loc=0, scale=1)	Log of the survival function.
ppf(q, kappa, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, kappa, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, kappa, loc=0, scale=1)	Non-central moment of order n
stats(kappa, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(kappa, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(kappa,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(kappa, loc=0, scale=1)	Median of the distribution.
mean(kappa, loc=0, scale=1)	Mean of the distribution.
var(kappa, loc=0, scale=1)	Variance of the distribution.
std(kappa, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, kappa, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.vonmises_line

scipy.stats.**vonmises_line = <scipy.stats._continuous_distns.vonmises_gen object>**

A Von Mises continuous random variable.

As an instance of the *rv_continuous* class, *vonmises_line* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *vonmises* and *vonmises_line* is:

$$f(x, \kappa) = \frac{\exp(\kappa \cos(x))}{2\pi I_0(\kappa)}$$

for $-\pi \leq x \leq \pi$, $\kappa > 0$. I_0 is the modified Bessel function of order zero (*scipy.special.i0*).

vonmises is a circular distribution which does not restrict the distribution to a fixed interval. Currently, there is no circular distribution framework in scipy. The `cdf` is implemented such that `cdf(x + 2*np.pi) == cdf(x) + 1`.

vonmises_line is the same distribution, defined on $[-\pi, \pi]$ on the real line. This is a regular (i.e. non-circular) distribution.

vonmises and *vonmises_line* take kappa as a shape parameter.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the loc and scale parameters. Specifically, vonmises_line.pdf(x, kappa, loc, scale) is identically equivalent to vonmises_line.pdf(y, kappa) / scale with y = (x - loc) / scale. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import vonmises_line
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> kappa = 3.99
>>> mean, var, skew, kurt = vonmises_line.stats(kappa, moments='mvsk')
```

Display the probability density function (pdf):

```
>>> x = np.linspace(vonmises_line.ppf(0.01, kappa),
...                 vonmises_line.ppf(0.99, kappa), 100)
>>> ax.plot(x, vonmises_line.pdf(x, kappa),
...         'r-', lw=5, alpha=0.6, label='vonmises_line pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen pdf:

```
>>> rv = vonmises_line(kappa)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of cdf and ppf:

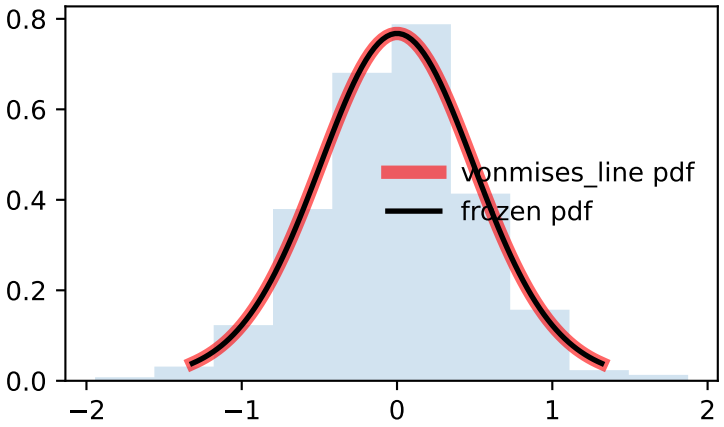
```
>>> vals = vonmises_line.ppf([0.001, 0.5, 0.999], kappa)
>>> np.allclose([0.001, 0.5, 0.999], vonmises_line.cdf(vals, kappa))
True
```

Generate random numbers:

```
>>> r = vonmises_line.rvs(kappa, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(kappa, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, kappa, loc=0, scale=1)	Probability density function.
logpdf(x, kappa, loc=0, scale=1)	Log of the probability density function.
cdf(x, kappa, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, kappa, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, kappa, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, kappa, loc=0, scale=1)	Log of the survival function.
ppf(q, kappa, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, kappa, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, kappa, loc=0, scale=1)	Non-central moment of order n
stats(kappa, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(kappa, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(kappa,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(kappa, loc=0, scale=1)	Median of the distribution.
mean(kappa, loc=0, scale=1)	Mean of the distribution.
var(kappa, loc=0, scale=1)	Variance of the distribution.
std(kappa, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, kappa, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.wald

scipy.stats.**wald = <scipy.stats._continuous_distns.wald_gen object>**

A Wald continuous random variable.

As an instance of the *rv_continuous* class, *wald* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *wald* is:

$$f(x) = \frac{1}{\sqrt{2\pi x^3}} \exp(-\frac{(x-1)^2}{2x})$$

for $x >= 0$.

wald is a special case of *invgauss* with `mu=1`.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `wald.pdf(x, loc, scale)` is identically equivalent to `wald.pdf(y) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import wald
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mean, var, skew, kurt = wald.stats(moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(wald.ppf(0.01),
...                 wald.ppf(0.99), 100)
>>> ax.plot(x, wald.pdf(x),
...         'r-', lw=5, alpha=0.6, label='wald pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = wald()
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

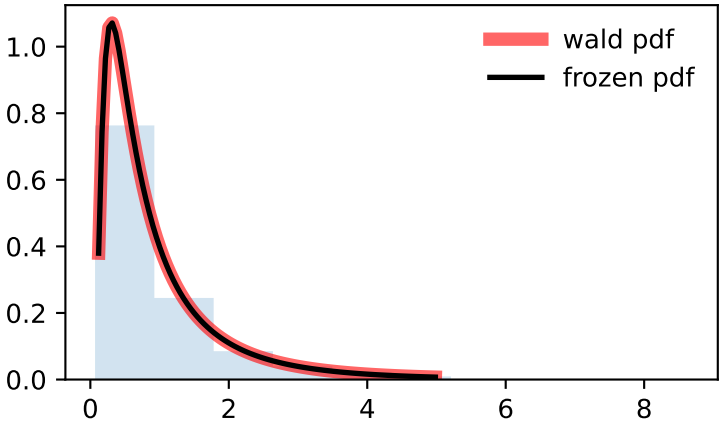
```
>>> vals = wald.ppf([0.001, 0.5, 0.999])
>>> np.allclose([0.001, 0.5, 0.999], wald.cdf(vals))
True
```

Generate random numbers:

```
>>> r = wald.rvs(size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, loc=0, scale=1)	Probability density function.
logpdf(x, loc=0, scale=1)	Log of the probability density function.
cdf(x, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, loc=0, scale=1)	Log of the survival function.
ppf(q, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, loc=0, scale=1)	Non-central moment of order n
stats(loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(loc=0, scale=1)	Median of the distribution.
mean(loc=0, scale=1)	Mean of the distribution.
var(loc=0, scale=1)	Variance of the distribution.
std(loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.weibull_min

scipy.stats.**weibull_min = <scipy.stats._continuous_distns.weibull_min_gen object>**

Weibull minimum continuous random variable.

The Weibull Minimum Extreme Value distribution, from extreme value theory (Fisher-Gnedenko theorem), is also often simply called the Weibull distribution. It arises as the limiting distribution of the rescaled minimum of iid random variables.

As an instance of the *rv_continuous* class, *weibull_min* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

weibull_max, ***numpy.random.Generator.weibull***, **exponweib**

Notes

The probability density function for *weibull_min* is:

$$f(x, c) = cx^{c-1} \exp(-x^c)$$

for $x > 0$, $c > 0$.

weibull_min takes `c` as a shape parameter for c. (named k in Wikipedia article and a in `numpy.random.weibull`). Special shape values are $c = 1$ and $c = 2$ where Weibull distribution reduces to the *expon* and *rayleigh* distributions respectively.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `weibull_min.pdf(x, c, loc, scale)` is identically equivalent to `weibull_min.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

https://en.wikipedia.org/wiki/Weibull_distribution

https://en.wikipedia.org/wiki/Fisher-Tippett-Gnedenko_theorem

Examples

```
>>> from scipy.stats import weibull_min
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 1.79
>>> mean, var, skew, kurt = weibull_min.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(weibull_min.ppf(0.01, c),
...                 weibull_min.ppf(0.99, c), 100)
>>> ax.plot(x, weibull_min.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='weibull_min pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = weibull_min(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

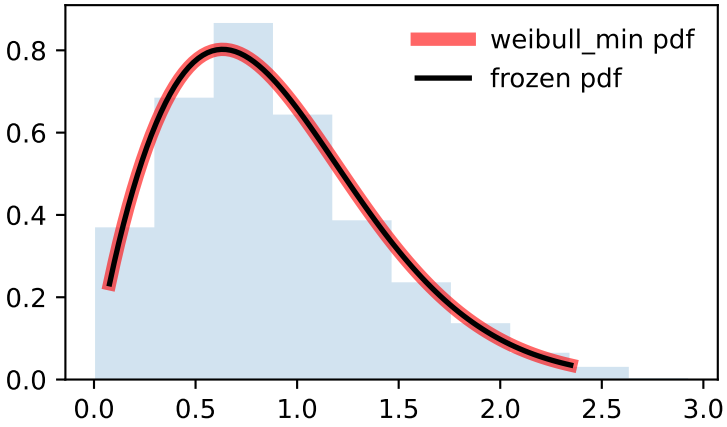
```
>>> vals = weibull_min.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], weibull_min.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = weibull_min.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.weibull_max

scipy.stats.**weibull_max = <scipy.stats._continuous_distns.weibull_max_gen object>**

Weibull maximum continuous random variable.

The Weibull Maximum Extreme Value distribution, from extreme value theory (Fisher-Gnedenko theorem), is the limiting distribution of rescaled maximum of iid random variables. This is the distribution of -X if X is from the *weibull_min* function.

As an instance of the *rv_continuous* class, *weibull_max* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

weibull_min

Notes

The probability density function for *weibull_max* is:

$$f(x, c) = c(-x)^{c-1} \exp(-(-x)^c)$$

for $x < 0$, $c > 0$.

weibull_max takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `weibull_max.pdf(x, c, loc, scale)` is identically equivalent to `weibull_max.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

References

https://en.wikipedia.org/wiki/Weibull_distribution

https://en.wikipedia.org/wiki/Fisher-Tippett-Gnedenko_theorem

Examples

```
>>> from scipy.stats import weibull_max
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 2.87
>>> mean, var, skew, kurt = weibull_max.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(weibull_max.ppf(0.01, c),
...                 weibull_max.ppf(0.99, c), 100)
>>> ax.plot(x, weibull_max.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='weibull_max pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = weibull_max(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

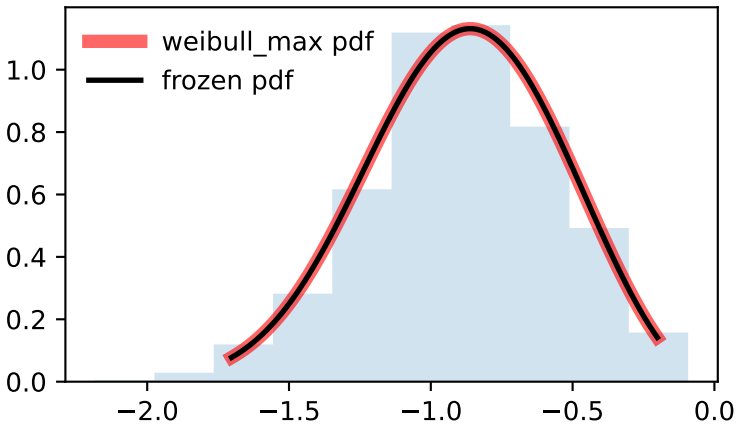
```
>>> vals = weibull_max.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], weibull_max.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = weibull_max.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.wrapcauchy

scipy.stats.**wrapcauchy = <scipy.stats._continuous_distns.wrapcauchy_gen object>**

A wrapped Cauchy continuous random variable.

As an instance of the *rv_continuous* class, *wrapcauchy* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability density function for *wrapcauchy* is:

$$f(x, c) = \frac{1 - c^2}{2\pi(1 + c^2 - 2c\cos(x))}$$

for $0 \leq x \leq 2\pi$, $0 < c < 1$.

wrapcauchy takes `c` as a shape parameter for c.

The probability density above is defined in the "standardized" form. To shift and/or scale the distribution use the `loc` and `scale` parameters. Specifically, `wrapcauchy.pdf(x, c, loc, scale)` is identically equivalent to `wrapcauchy.pdf(y, c) / scale` with `y = (x - loc) / scale`. Note that shifting the location of a distribution does not make it a "noncentral" distribution; noncentral generalizations of some distributions are available in separate classes.

Examples

```
>>> from scipy.stats import wrapcauchy
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> c = 0.0311
>>> mean, var, skew, kurt = wrapcauchy.stats(c, moments='mvsk')
```

Display the probability density function (`pdf`):

```
>>> x = np.linspace(wrapcauchy.ppf(0.01, c),
...                 wrapcauchy.ppf(0.99, c), 100)
>>> ax.plot(x, wrapcauchy.pdf(x, c),
...         'r-', lw=5, alpha=0.6, label='wrapcauchy pdf')
```

Alternatively, the distribution object can be called (as a function) to fix the shape, location and scale parameters. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pdf`:

```
>>> rv = wrapcauchy(c)
>>> ax.plot(x, rv.pdf(x), 'k-', lw=2, label='frozen pdf')
```

Check accuracy of `cdf` and `ppf`:

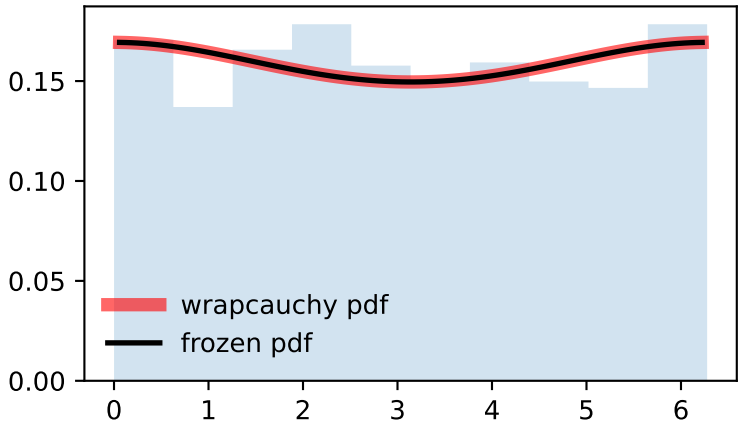
```
>>> vals = wrapcauchy.ppf([0.001, 0.5, 0.999], c)
>>> np.allclose([0.001, 0.5, 0.999], wrapcauchy.cdf(vals, c))
True
```

Generate random numbers:

```
>>> r = wrapcauchy.rvs(c, size=1000)
```

And compare the histogram:

```
>>> ax.hist(r, density=True, histtype='stepfilled', alpha=0.2)
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Methods

rvs(c, loc=0, scale=1, size=1, random_state=None)	Random variates.
pdf(x, c, loc=0, scale=1)	Probability density function.
logpdf(x, c, loc=0, scale=1)	Log of the probability density function.
cdf(x, c, loc=0, scale=1)	Cumulative distribution function.
logcdf(x, c, loc=0, scale=1)	Log of the cumulative distribution function.
sf(x, c, loc=0, scale=1)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(x, c, loc=0, scale=1)	Log of the survival function.
ppf(q, c, loc=0, scale=1)	Percent point function (inverse of `cdf` — percentiles).
isf(q, c, loc=0, scale=1)	Inverse survival function (inverse of `sf`).
moment(n, c, loc=0, scale=1)	Non-central moment of order n
stats(c, loc=0, scale=1, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(c, loc=0, scale=1)	(Differential) entropy of the RV.
fit(data)	Parameter estimates for generic data. See scipy.stats.rv_continuous.fit for detailed documentation of the keyword arguments.
expect(func, args=(c,), loc=0, scale=1, lb=None, ub=None, conditional=False, **kwds)	Expected value of a function (of one argument) with respect to the distribution.
median(c, loc=0, scale=1)	Median of the distribution.
mean(c, loc=0, scale=1)	Mean of the distribution.
var(c, loc=0, scale=1)	Variance of the distribution.
std(c, loc=0, scale=1)	Standard deviation of the distribution.
interval(alpha, c, loc=0, scale=1)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

Multivariate distributions

multivariate_normal	A multivariate normal random variable.
matrix_normal	A matrix normal random variable.
dirichlet	A Dirichlet random variable.
wishart	A Wishart random variable.
invwishart	An inverse Wishart random variable.
multinomial	A multinomial random variable.
special_ortho_group	A matrix-valued SO(N) random variable.
ortho_group	A matrix-valued O(N) random variable.
unitary_group	A matrix-valued U(N) random variable.
random_correlation	A random correlation matrix.
multivariate_t	A multivariate t-distributed random variable.
multivariate_hypergeom	A multivariate hypergeometric random variable.

scipy.stats.multivariate_normal

scipy.stats.**multivariate_normal = <scipy.stats._multivariate.multivariate_normal_gen object**

A multivariate normal random variable.

The *mean* keyword specifies the mean. The *cov* keyword specifies the covariance matrix.

Parameters

x [array_like] Quantiles, with the last axis of *x* denoting the components.
mean [array_like, optional] Mean of the distribution (default zero)
cov [array_like, optional] Covariance matrix of the distribution (default one)
allow_singular
[bool, optional] Whether to allow a singular covariance matrix. (Default: False)
random_state
[{None, int, `numpy.random.Generator`,]
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.
Alternatively, the object may be called (as a function) to fix the mean and covariance parameters, returning a "frozen" multivariate normal random variable:
rv = multivariate_normal(mean=None, cov=1, allow_singular=False)

- Frozen object with the same methods but holding the given mean and covariance fixed.

Notes

***Setting the parameter* mean *to* None *is equivalent to having* mean**

be the zero-vector. The parameter *cov* can be a scalar, in which case the covariance matrix is the identity times that value, a vector of diagonal entries for the covariance matrix, or a two-dimensional array_like.

The covariance matrix *cov* must be a (symmetric) positive semi-definite matrix. The determinant and inverse of *cov* are computed as the pseudo-determinant and pseudo-inverse, respectively, so that *cov* does not need to have full rank.

The probability density function for *multivariate_normal* is

$$f(x) = \frac{1}{\sqrt{(2\pi)^k \det \Sigma}} \exp\left(-\frac{1}{2}(x-\mu)^T \Sigma^{-1}(x-\mu)\right),$$

where μ is the mean, Σ the covariance matrix, and k is the dimension of the space where x takes values.

New in version 0.14.0.

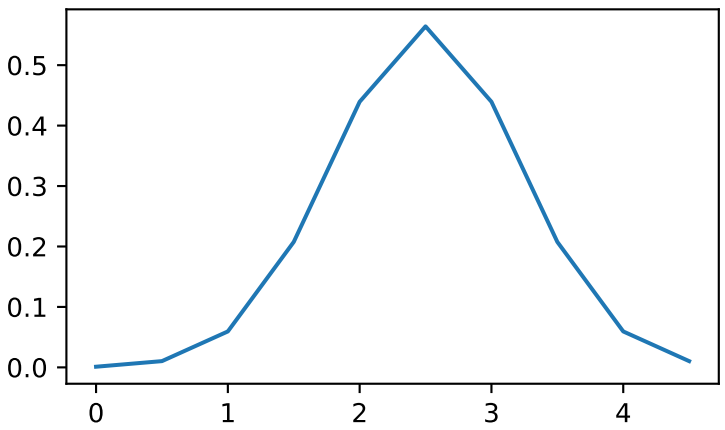
Examples

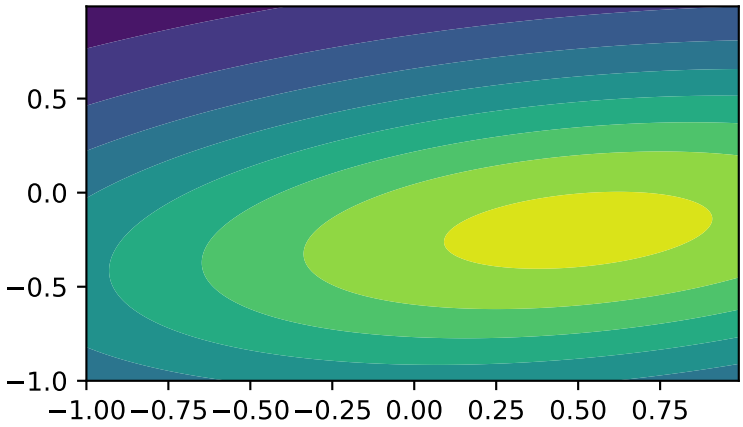
```
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import multivariate_normal
```

```
>>> x = np.linspace(0, 5, 10, endpoint=False)
>>> y = multivariate_normal.pdf(x, mean=2.5, cov=0.5); y
array([ 0.00108914,  0.01033349,  0.05946514,  0.20755375,  0.43939129,
        0.56418958,  0.43939129,  0.20755375,  0.05946514,  0.01033349])
>>> fig1 = plt.figure()
>>> ax = fig1.add_subplot(111)
>>> ax.plot(x, y)
```

The input quantiles can be any shape of array, as long as the last axis labels the components. This allows us for instance to display the frozen pdf for a non-isotropic random variable in 2D as follows:

```
>>> x, y = np.mgrid[-1:1:.01, -1:1:.01]
>>> pos = np.dstack((x, y))
>>> rv = multivariate_normal([0.5, -0.2], [[2.0, 0.3], [0.3, 0.5]])
>>> fig2 = plt.figure()
>>> ax2 = fig2.add_subplot(111)
>>> ax2.contourf(x, y, rv.pdf(pos))
```





Methods

``pdf(x, mean=None, cov=1, allow_singular=False)``	Probability density function.
``logpdf(x, mean=None, cov=1, allow_singular=False)``	Log of the probability density function.
``cdf(x, mean=None, cov=1, allow_singular=False, maxpts=1000000*dim, abseps=1e-5, releps=1e-5)``	Cumulative distribution function.
``logcdf(x, mean=None, cov=1, allow_singular=False, maxpts=1000000*dim, abseps=1e-5, releps=1e-5)``	Log of the cumulative distribution function.
``rvs(mean=None, cov=1, size=1, random_state=None)``	Draw random samples from a multivariate normal distribution.
``entropy()``	Compute the differential entropy of the multivariate normal.

scipy.stats.matrix_normal

scipy.stats.**matrix_normal = <scipy.stats._multivariate.matrix_normal_gen object>**

A matrix normal random variable.

The *mean* keyword specifies the mean. The *rowcov* keyword specifies the among-row covariance matrix. The 'colcov' keyword specifies the among-column covariance matrix.

Parameters

X [array_like] Quantiles, with the last two axes of *X* denoting the components.
mean [array_like, optional] Mean of the distribution (default: *None*)
rowcov [array_like, optional] Among-row covariance matrix of the distribution (default: *1*)
colcov [array_like, optional] Among-column covariance matrix of the distribution (default: *1*)
random_state
[{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used.
If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already

a `Generator` or `RandomState` instance then that instance is used.

Alternatively, the object may be called (as a function) to fix the mean and covariance parameters, returning a "frozen" matrix normal random variable:

rv = matrix_normal(mean=None, rowcov=1, colcov=1)

- Frozen object with the same methods but holding the given mean and covariance fixed.

Notes

If* mean *is set to* None *then a matrix of zeros is used for the mean.

The dimensions of this matrix are inferred from the shape of *rowcov* and *colcov*, if these are provided, or set to *1* if ambiguous.

rowcov and *colcov* can be two-dimensional array_likes specifying the covariance matrices directly. Alternatively, a one-dimensional array will be be interpreted as the entries of a diagonal matrix, and a scalar or zero-dimensional array will be interpreted as this value times the identity matrix.

The covariance matrices specified by *rowcov* and *colcov* must be (symmetric) positive definite. If the samples in *X* are $m \times n$, then *rowcov* must be $m \times m$ and *colcov* must be $n \times n$. *mean* must be the same shape as *X*.

The probability density function for *matrix_normal* is

$$f(X) = (2\pi)^{-\frac{mn}{2}}|U|^{-\frac{n}{2}}|V|^{-\frac{m}{2}}\exp\left(-\frac{1}{2}\mathrm{Tr}\left[U^{-1}(X-M)V^{-1}(X-M)^T\right]\right),$$

where M is the mean, U the among-row covariance matrix, V the among-column covariance matrix.

The *allow_singular* behaviour of the *multivariate_normal* distribution is not currently supported. Covariance matrices must be full rank.

The *matrix_normal* distribution is closely related to the *multivariate_normal* distribution. Specifically, $\mathrm{Vec}(X)$ (the vector formed by concatenating the columns of X) has a multivariate normal distribution with mean $\mathrm{Vec}(M)$ and covariance $V \otimes U$ (where $\otimes$ is the Kronecker product). Sampling and pdf evaluation are $\mathcal{O}(m^3 + n^3 + m^2n + mn^2)$ for the matrix normal, but $\mathcal{O}(m^3n^3)$ for the equivalent multivariate normal, making this equivalent form algorithmically inefficient.

New in version 0.17.0.

Examples

```
>>> from scipy.stats import matrix_normal
```

```
>>> M = np.arange(6).reshape(3,2); M
array([[0, 1],
       [2, 3],
       [4, 5]])
>>> U = np.diag([1,2,3]); U
array([[1, 0, 0],
       [0, 2, 0],
       [0, 0, 3]])
>>> V = 0.3*np.identity(2); V
array([[ 0.3,  0. ],
       [ 0. ,  0.3]])
```

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```
>>> X = M + 0.1; X
array([[ 0.1,  1.1],
       [ 2.1,  3.1],
       [ 4.1,  5.1]])
>>> matrix_normal.pdf(X, mean=M, rowcov=U, colcov=V)
0.023410202050005054
```

```
>>> # Equivalent multivariate normal
>>> from scipy.stats import multivariate_normal
>>> vectorised_X = X.T.flatten()
>>> equiv_mean = M.T.flatten()
>>> equiv_cov = np.kron(V,U)
>>> multivariate_normal.pdf(vectorised_X, mean=equiv_mean, cov=equiv_cov)
0.023410202050005054
```

Methods

``pdf(X, mean=None, rowcov=1, colcov=1)``	Probability density function.
``logpdf(X, mean=None, rowcov=1, colcov=1)``	Log of the probability density function.
``rvs(mean=None, rowcov=1, colcov=1, size=1, random_state=None)``	Draw random samples.

scipy.stats.dirichlet

scipy.stats.**dirichlet = <scipy.stats._multivariate.dirichlet_gen object>**

A Dirichlet random variable.

The *alpha* keyword specifies the concentration parameters of the distribution.

New in version 0.15.0.

Parameters

x [array_like] Quantiles, with the last axis of *x* denoting the components.

alpha [array_like] The concentration parameters. The number of entries determines the dimensionality of the distribution.

random_state [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional

If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Alternatively, the object may be called (as a function) to fix concentration parameters, returning a "frozen" Dirichlet random variable:
rv = dirichlet(alpha)

- Frozen object with the same methods but holding the given concentration parameters fixed.

Notes

Each α entry must be positive. The distribution has only support on the simplex defined by

$$\sum_{i=1}^{K} x_i = 1$$

where 0 < x_i < 1.

If the quantiles don't lie within the simplex, a ValueError is raised.

The probability density function for *dirichlet* is

$$f(x) = \frac{1}{\mathrm{B}(\boldsymbol{\alpha})} \prod_{i=1}^{K} x_i^{\alpha_i - 1}$$

where

$$\mathrm{B}(\boldsymbol{\alpha}) = \frac{\prod_{i=1}^{K} \Gamma(\alpha_i)}{\Gamma\left(\sum_{i=1}^{K} \alpha_i\right)}$$

and $\boldsymbol{\alpha} = (\alpha_1, \ldots, \alpha_K)$, the concentration parameters and K is the dimension of the space where x takes values.

Note that the dirichlet interface is somewhat inconsistent. The array returned by the rvs function is transposed with respect to the format expected by the pdf and logpdf.

Examples

```
>>> from scipy.stats import dirichlet
```

Generate a dirichlet random variable

```
>>> quantiles = np.array([0.2, 0.2, 0.6])  # specify quantiles
>>> alpha = np.array([0.4, 5, 15])  # specify concentration parameters
>>> dirichlet.pdf(quantiles, alpha)
0.2843831684937255
```

The same PDF but following a log scale

```
>>> dirichlet.logpdf(quantiles, alpha)
-1.2574327653159187
```

Once we specify the dirichlet distribution we can then calculate quantities of interest

```
>>> dirichlet.mean(alpha)  # get the mean of the distribution
array([0.01960784, 0.24509804, 0.73529412])
>>> dirichlet.var(alpha) # get variance
array([0.00089829, 0.00864603, 0.00909517])
>>> dirichlet.entropy(alpha)  # calculate the differential entropy
-4.3280162474082715
```

We can also return random samples from the distribution

```
>>> dirichlet.rvs(alpha, size=1, random_state=1)
array([[0.00766178, 0.24670518, 0.74563305]])
>>> dirichlet.rvs(alpha, size=2, random_state=2)
array([[0.01639427, 0.1292273 , 0.85437844],
       [0.00156917, 0.19033695, 0.80809388]])
```

Methods

``pdf(x, alpha)``	Probability density function.
``logpdf(x, alpha)``	Log of the probability density function.
``rvs(alpha, size=1, random_state=None)``	Draw random samples from a Dirichlet distribution.
``mean(alpha)``	The mean of the Dirichlet distribution
``var(alpha)``	The variance of the Dirichlet distribution
``entropy(alpha)``	Compute the differential entropy of the Dirichlet distribution.

scipy.stats.wishart

scipy.stats.**wishart = <scipy.stats._multivariate.wishart_gen object>**

A Wishart random variable.

The *df* keyword specifies the degrees of freedom. The *scale* keyword specifies the scale matrix, which must be symmetric and positive definite. In this context, the scale matrix is often interpreted in terms of a multivariate normal precision matrix (the inverse of the covariance matrix). These arguments must satisfy the relationship `df > scale.ndim - 1`, but see notes on using the *rvs* method with `df < scale.ndim`.

Parameters

x [array_like] Quantiles, with the last axis of *x* denoting the components.

df [int] Degrees of freedom, must be greater than or equal to dimension of the scale matrix

scale [array_like] Symmetric positive definite scale matrix of the distribution

random_state
[{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Alternatively, the object may be called (as a function) to fix the degrees of freedom and scale parameters, returning a "frozen" Wishart random variable:
rv = wishart(df=1, scale=1)

- Frozen object with the same methods but holding the given degrees of freedom and scale fixed.

See also:

invwishart, **chi2**

Notes

The scale matrix *scale* must be a symmetric positive definite matrix. Singular matrices, including the symmetric positive semi-definite case, are not supported.

The Wishart distribution is often denoted

$$W_p(\nu, \Sigma)$$

where ν is the degrees of freedom and Σ is the $p \times p$ scale matrix.

The probability density function for `wishart` has support over positive definite matrices S; if $S \sim W_p(\nu, \Sigma)$, then its PDF is given by:

$$f(S) = \frac{|S|^{\frac{\nu-p-1}{2}}}{2^{\frac{\nu p}{2}} |\Sigma|^{\frac{\nu}{2}} \Gamma_p\left(\frac{\nu}{2}\right)} \exp\left(-tr(\Sigma^{-1} S)/2\right)$$

If $S \sim W_p(\nu, \Sigma)$ (Wishart) then $S^{-1} \sim W_p^{-1}(\nu, \Sigma^{-1})$ (inverse Wishart).

If the scale matrix is 1-dimensional and equal to one, then the Wishart distribution $W_1(\nu, 1)$ collapses to the $\chi^2(\nu)$ distribution.

The algorithm [2] implemented by the *rvs* method may produce numerically singular matrices with $p - 1 < \nu < p$; the user may wish to check for this condition and generate replacement samples as necessary.

New in version 0.16.0.

References

[1], [2]

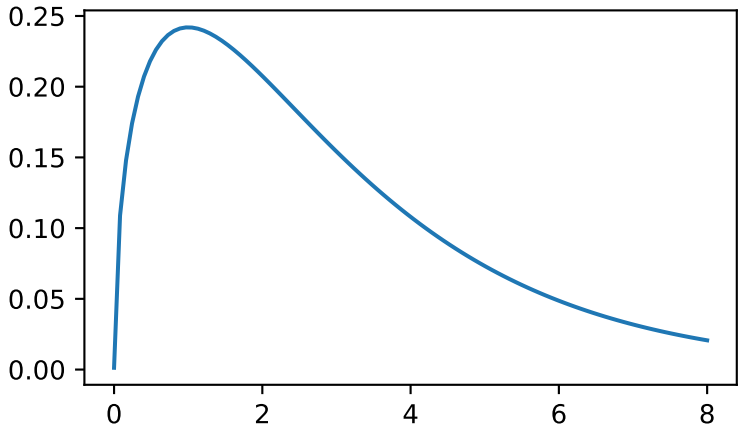
Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import wishart, chi2
>>> x = np.linspace(1e-5, 8, 100)
>>> w = wishart.pdf(x, df=3, scale=1); w[:5]
array([ 0.00126156,  0.10892176,  0.14793434,  0.17400548,  0.1929669 ])
>>> c = chi2.pdf(x, 3); c[:5]
array([ 0.00126156,  0.10892176,  0.14793434,  0.17400548,  0.1929669 ])
>>> plt.plot(x, w)
```

The input quantiles can be any shape of array, as long as the last axis labels the components.

Methods

``pdf(x, df, scale)``	Probability density function.
``logpdf(x, df, scale)``	Log of the probability density function.
``rvs(df, scale, size=1, random_state=None)``	Draw random samples from a Wishart distribution.
``entropy()``	Compute the differential entropy of the Wishart distribution.



scipy.stats.invwishart

scipy.stats.**invwishart = <scipy.stats._multivariate.invwishart_gen object>**

An inverse Wishart random variable.

The *df* keyword specifies the degrees of freedom. The *scale* keyword specifies the scale matrix, which must be symmetric and positive definite. In this context, the scale matrix is often interpreted in terms of a multivariate normal covariance matrix.

Parameters

x [array_like] Quantiles, with the last axis of *x* denoting the components.

df [int] Degrees of freedom, must be greater than or equal to dimension of the scale matrix

scale [array_like] Symmetric positive definite scale matrix of the distribution

random_state
[{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Alternatively, the object may be called (as a function) to fix the degrees of freedom and scale parameters, returning a "frozen" inverse Wishart random variable:
rv = invwishart(df=1, scale=1)

- Frozen object with the same methods but holding the given degrees of freedom and scale fixed.

See also:

`wishart`

Notes

The scale matrix *scale* must be a symmetric positive definite matrix. Singular matrices, including the symmetric positive semi-definite case, are not supported.

The inverse Wishart distribution is often denoted

$$W_p^{-1}(\nu, \Psi)$$

where ν is the degrees of freedom and Ψ is the $p \times p$ scale matrix.

The probability density function for *invwishart* has support over positive definite matrices S; if $S \sim W_p^{-1}(\nu, \Sigma)$, then its PDF is given by:

$$f(S) = \frac{|\Sigma|^{\frac{\nu}{2}}}{2^{\frac{\nu p}{2}} |S|^{\frac{\nu+p+1}{2}} \Gamma_p\left(\frac{\nu}{2}\right)} \exp\left(-tr(\Sigma S^{-1})/2\right)$$

If $S \sim W_p^{-1}(\nu, \Psi)$ (inverse Wishart) then $S^{-1} \sim W_p(\nu, \Psi^{-1})$ (Wishart).

If the scale matrix is 1-dimensional and equal to one, then the inverse Wishart distribution $W_1(\nu, 1)$ collapses to the inverse Gamma distribution with parameters shape = $\frac{\nu}{2}$ and scale = $\frac{1}{2}$.

New in version 0.16.0.

References

[1], [2]

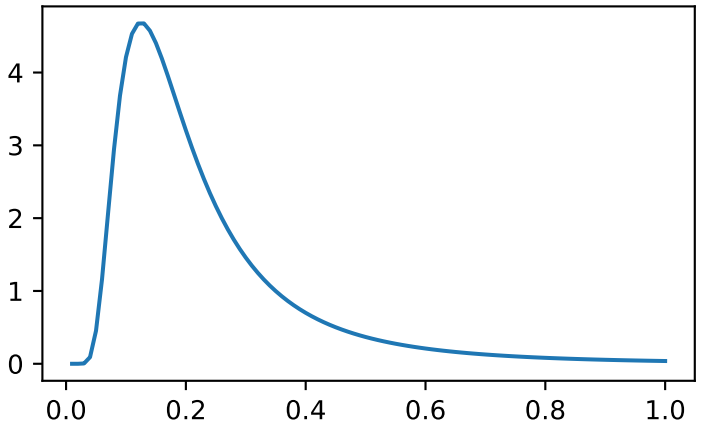
Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import invwishart, invgamma
>>> x = np.linspace(0.01, 1, 100)
>>> iw = invwishart.pdf(x, df=6, scale=1)
>>> iw[:3]
array([  1.20546865e-15,   5.42497807e-06,   4.45813929e-03])
>>> ig = invgamma.pdf(x, 6/2., scale=1./2)
>>> ig[:3]
array([  1.20546865e-15,   5.42497807e-06,   4.45813929e-03])
>>> plt.plot(x, iw)
```

The input quantiles can be any shape of array, as long as the last axis labels the components.

Methods

``pdf(x, df, scale)``	Probability density function.
``logpdf(x, df, scale)``	Log of the probability density function.
``rvs(df, scale, size=1, random_state=None)``	Draw random samples from an inverse Wishart distribution.



scipy.stats.multinomial

scipy.stats.**multinomial = <scipy.stats._multivariate.multinomial_gen object>**

A multinomial random variable.

Parameters

x [array_like] Quantiles, with the last axis of *x* denoting the components.

n [int] Number of trials

p [array_like] Probability of a trial falling into each category; should sum to 1

random_state
[{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

See also:

scipy.stats.binom

The binomial distribution.

numpy.random.Generator.multinomial

Sampling from the multinomial distribution.

scipy.stats.multivariate_hypergeom

The multivariate hypergeometric distribution.

Notes

n should be a positive integer. Each element of *p* should be in the interval $[0, 1]$ and the elements should sum to 1. If they do not sum to 1, the last element of the *p* array is not used and is replaced with the remaining probability left over from the earlier elements.

Alternatively, the object may be called (as a function) to fix the *n* and *p* parameters, returning a "frozen" multinomial random variable:

The probability mass function for *multinomial* is

$$f(x) = \frac{n!}{x_1! \cdots x_k!} p_1^{x_1} \cdots p_k^{x_k},$$

supported on $x = (x_1, \ldots, x_k)$ where each x_i is a nonnegative integer and their sum is n.

New in version 0.19.0.

Examples

```
>>> from scipy.stats import multinomial
>>> rv = multinomial(8, [0.3, 0.2, 0.5])
>>> rv.pmf([1, 3, 4])
0.042000000000000072
```

The multinomial distribution for $k = 2$ is identical to the corresponding binomial distribution (tiny numerical differences notwithstanding):

```
>>> from scipy.stats import binom
>>> multinomial.pmf([3, 4], n=7, p=[0.4, 0.6])
0.29030399999999973
>>> binom.pmf(3, 7, 0.4)
0.29030400000000012
```

The functions `pmf`, `logpmf`, `entropy`, and `cov` support broadcasting, under the convention that the vector parameters (`x` and `p`) are interpreted as if each row along the last axis is a single object. For instance:

```
>>> multinomial.pmf([[3, 4], [3, 5]], n=[7, 8], p=[.3, .7])
array([0.2268945,  0.25412184])
```

Here, `x.shape == (2, 2)`, `n.shape == (2,)`, and `p.shape == (2,)`, but following the rules mentioned above they behave as if the rows `[3, 4]` and `[3, 5]` in `x` and `[.3, .7]` in `p` were a single object, and as if we had `x.shape = (2,)`, `n.shape = (2,)`, and `p.shape = ()`. To obtain the individual elements without broadcasting, we would do this:

```
>>> multinomial.pmf([3, 4], n=7, p=[.3, .7])
0.2268945
>>> multinomial.pmf([3, 5], 8, p=[.3, .7])
0.25412184
```

This broadcasting also works for `cov`, where the output objects are square matrices of size `p.shape[-1]`. For example:

```
>>> multinomial.cov([4, 5], [[.3, .7], [.4, .6]])
array([[[ 0.84, -0.84],
```

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```
        [-0.84,  0.84]],
       [[ 1.2 , -1.2 ],
        [-1.2 ,  1.2 ]]])
```

In this example, `n.shape == (2,)` and `p.shape == (2, 2)`, and following the rules above, these broadcast as if `p.shape == (2,)`. Thus the result should also be of shape `(2,)`, but since each output is a 2×2 matrix, the result in fact has shape `(2, 2, 2)`, where `result[0]` is equal to `multinomial.cov(n=4, p=[.3, .7])` and `result[1]` is equal to `multinomial.cov(n=5, p=[.4, .6])`.

Methods

``pmf(x, n, p)``	Probability mass function.
``logpmf(x, n, p)``	Log of the probability mass function.
``rvs(n, p, size=1, random_state=None)``	Draw random samples from a multinomial distribution.
``entropy(n, p)``	Compute the entropy of the multinomial distribution.
``cov(n, p)``	Compute the covariance matrix of the multinomial distribution.

scipy.stats.special_ortho_group

scipy.stats.**special_ortho_group = <scipy.stats._multivariate.special_ortho_group_gen object**

A matrix-valued SO(N) random variable.

Return a random rotation matrix, drawn from the Haar distribution (the only uniform distribution on SO(n)).

The *dim* keyword specifies the dimension N.

Parameters

dim [scalar] Dimension of matrices

See also:

ortho_group, ***scipy.spatial.transform.Rotation.random***

Notes

This class is wrapping the random_rot code from the MDP Toolkit, https://github.com/mdp-toolkit/mdp-toolkit

Return a random rotation matrix, drawn from the Haar distribution (the only uniform distribution on SO(n)). The algorithm is described in the paper Stewart, G.W., "The efficient generation of random orthogonal matrices with an application to condition estimators", SIAM Journal on Numerical Analysis, 17(3), pp. 403-409, 1980. For more information see https://en.wikipedia.org/wiki/Orthogonal_matrix#Randomization

See also the similar *ortho_group*. For a random rotation in three dimensions, see `scipy.spatial.transform.Rotation.random`.

Examples

```
>>> from scipy.stats import special_ortho_group
>>> x = special_ortho_group.rvs(3)
```

```
>>> np.dot(x, x.T)
array([[  1.00000000e+00,   1.13231364e-17,  -2.86852790e-16],
       [  1.13231364e-17,   1.00000000e+00,  -1.46845020e-16],
       [ -2.86852790e-16,  -1.46845020e-16,   1.00000000e+00]])
```

```
>>> import scipy.linalg
>>> scipy.linalg.det(x)
1.0
```

This generates one random matrix from SO(3). It is orthogonal and has a determinant of 1.

Methods

``rvs(dim=None, size=1, random_state=None)``	Draw random samples from SO(N).

scipy.stats.ortho_group

scipy.stats.**ortho_group = <scipy.stats._multivariate.ortho_group_gen object>**

A matrix-valued O(N) random variable.

Return a random orthogonal matrix, drawn from the O(N) Haar distribution (the only uniform distribution on O(N)).

The *dim* keyword specifies the dimension N.

Parameters

dim [scalar] Dimension of matrices

Notes

This class is closely related to *special_ortho_group*.

Some care is taken to avoid numerical error, as per the paper by Mezzadri.

References

[1]

Examples

```
>>> from scipy.stats import ortho_group
>>> x = ortho_group.rvs(3)
```

```
>>> np.dot(x, x.T)
array([[  1.00000000e+00,   1.13231364e-17,  -2.86852790e-16],
       [  1.13231364e-17,   1.00000000e+00,  -1.46845020e-16],
       [ -2.86852790e-16,  -1.46845020e-16,   1.00000000e+00]])
```

```
>>> import scipy.linalg
>>> np.fabs(scipy.linalg.det(x))
1.0
```

This generates one random matrix from O(3). It is orthogonal and has a determinant of +1 or -1.

Methods

``rvs(dim=None, size=1, random_state=None)``	Draw random samples from O(N).

scipy.stats.unitary_group

scipy.stats.**unitary_group = <scipy.stats._multivariate.unitary_group_gen object>**

A matrix-valued U(N) random variable.

Return a random unitary matrix.

The *dim* keyword specifies the dimension N.

Parameters

dim [scalar] Dimension of matrices

Notes

This class is similar to *ortho_group*.

References

[1]

Examples

```
>>> from scipy.stats import unitary_group
>>> x = unitary_group.rvs(3)
```

```
>>> np.dot(x, x.conj().T)
array([[  1.00000000e+00,   1.13231364e-17,  -2.86852790e-16],
       [  1.13231364e-17,   1.00000000e+00,  -1.46845020e-16],
       [ -2.86852790e-16,  -1.46845020e-16,   1.00000000e+00]])
```

This generates one random matrix from U(3). The dot product confirms that it is unitary up to machine precision.

Methods

``rvs(dim=None, size=1, random_state=None)``	Draw random samples from U(N).

scipy.stats.random_correlation

scipy.stats.**random_correlation = <scipy.stats._multivariate.random_correlation_gen object>**

A random correlation matrix.

Return a random correlation matrix, given a vector of eigenvalues.

The *eigs* keyword specifies the eigenvalues of the correlation matrix, and implies the dimension.

Parameters

eigs [1d ndarray] Eigenvalues of correlation matrix.

Notes

Generates a random correlation matrix following a numerically stable algorithm spelled out by Davies & Higham. This algorithm uses a single O(N) similarity transformation to construct a symmetric positive semi-definite matrix, and applies a series of Givens rotations to scale it to have ones on the diagonal.

References

[1]

Examples

```
>>> from scipy.stats import random_correlation
>>> rng = np.random.default_rng()
>>> x = random_correlation.rvs((.5, .8, 1.2, 1.5), random_state=rng)
>>> x
array([[ 1.        , -0.07198934, -0.20411041, -0.24385796],
       [-0.07198934,  1.        ,  0.12968613, -0.29471382],
       [-0.20411041,  0.12968613,  1.        ,  0.2828693 ],
       [-0.24385796, -0.29471382,  0.2828693 ,  1.        ]])
```

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```
>>> import scipy.linalg
>>> e, v = scipy.linalg.eigh(x)
>>> e
array([ 0.5,  0.8,  1.2,  1.5])
```

Methods

``rvs(eigs=None, random_state=None)``	Draw random correlation matrices, all with eigenvalues eigs.

scipy.stats.multivariate_t

scipy.stats.**multivariate_t = <scipy.stats._multivariate.multivariate_t_gen object>**

A multivariate t-distributed random variable.

The *loc* parameter specifies the location. The *shape* parameter specifies the positive semidefinite shape matrix. The *df* parameter specifies the degrees of freedom.

In addition to calling the methods below, the object itself may be called as a function to fix the location, shape matrix, and degrees of freedom parameters, returning a "frozen" multivariate t-distribution random.

Parameters

x [array_like] Quantiles, with the last axis of *x* denoting the components.

loc [array_like, optional] Location of the distribution. (default `0`)

shape [array_like, optional] Positive semidefinite matrix of the distribution. (default `1`)

df [float, optional] Degrees of freedom of the distribution; must be greater than zero. If `np.inf` then results are multivariate normal. The default is `1`.

allow_singular
[bool, optional] Whether to allow a singular matrix. (default `False`)

random_state
[{None, int, `numpy.random.Generator`,]
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Notes

Setting the parameter *loc* to `None` is equivalent to having *loc* be the zero-vector. The parameter *shape* can be a scalar, in which case the shape matrix is the identity times that value, a vector of diagonal entries for the shape matrix, or a two-dimensional array_like. The matrix *shape* must be a (symmetric) positive semidefinite matrix. The determinant and inverse of *shape* are computed as the pseudo-determinant and pseudo-inverse, respectively, so that *shape* does not need to have full rank.

The probability density function for *`multivariate_t`* is

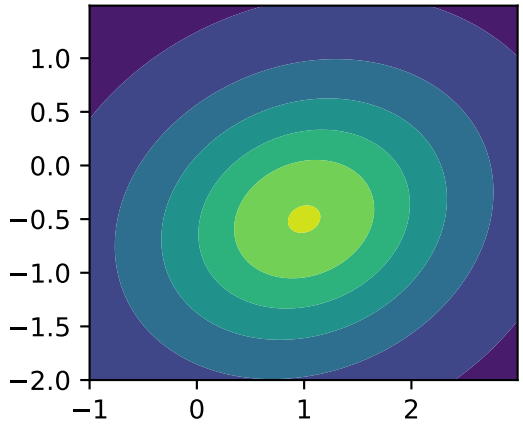
$$f(x) = \frac{\Gamma(\nu + p)/2}{\Gamma(\nu/2)\nu^{p/2}\pi^{p/2}|\Sigma|^{1/2}} \exp\left[1 + \frac{1}{\nu}(\mathbf{x} - \boldsymbol{\mu})^{\top}\boldsymbol{\Sigma}^{-1}(\mathbf{x} - \boldsymbol{\mu})\right]^{-(\nu+p)/2},$$

where p is the dimension of $\mathbf{x}$, $\boldsymbol{\mu}$ is the p-dimensional location, $\boldsymbol{\Sigma}$ the $p \times p$-dimensional shape matrix, and ν is the degrees of freedom.

New in version 1.6.0.

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import multivariate_t
>>> x, y = np.mgrid[-1:3:.01, -2:1.5:.01]
>>> pos = np.dstack((x, y))
>>> rv = multivariate_t([1.0, -0.5], [[2.1, 0.3], [0.3, 1.5]], df=2)
>>> fig, ax = plt.subplots(1, 1)
>>> ax.set_aspect('equal')
>>> plt.contourf(x, y, rv.pdf(pos))
```



Methods

``pdf(x, loc=None, shape=1, df=1, allow_singular=False)``	Probability density function.
``logpdf(x, loc=None, shape=1, df=1, allow_singular=False)``	Log of the probability density function.
``rvs(loc=None, shape=1, df=1, size=1, random_state=None)``	Draw random samples from a multivariate t-distribution.

scipy.stats.multivariate_hypergeom

scipy.stats.**multivariate_hypergeom = <scipy.stats._multivariate.multivariate_hypergeom_gen**

A multivariate hypergeometric random variable.

Parameters

m [array_like] The number of each type of object in the population. That is, $m[i]$ is the number of objects of type i.

n [array_like] The number of samples taken from the population.

random_state [{None, int, numpy.random.Generator,]

numpy.random.RandomState}, optional
If *seed* is None (or *np.random*), the numpy.random.RandomState singleton is used. If *seed* is an int, a new RandomState instance is used, seeded with *seed*. If *seed* is already a Generator or RandomState instance then that instance is used.

See also:

scipy.stats.hypergeom

The hypergeometric distribution.

scipy.stats.multinomial

The multinomial distribution.

Notes

m must be an array of positive integers. If the quantile i contains values out of the range $[0, m_i]$ where m_i is the number of objects of type i in the population or if the parameters are inconsistent with one another (e.g. `x.sum() != n`), methods return the appropriate value (e.g. `0` for `pmf`). If *m* or *n* contain negative values, the result will contain `nan` there.

The probability mass function for *multivariate_hypergeom* is

$$P(X_1 = x_1, X_2 = x_2, \ldots, X_k = x_k) = \frac{\binom{m_1}{x_1}\binom{m_2}{x_2}\cdots\binom{m_k}{x_k}}{\binom{M}{n}},$$
$$(x_1, x_2, \ldots, x_k) \in \mathbb{N}^k \text{ with } \sum_{i=1}^{k} x_i = n$$

where m_i are the number of objects of type i, M is the total number of objects in the population (sum of all the m_i), and n is the size of the sample to be taken from the population.

New in version 1.6.0.

References

[1], [2]

Examples

To evaluate the probability mass function of the multivariate hypergeometric distribution, with a dichotomous population of size 10 and 20, at a sample of size 12 with 8 objects of the first type and 4 objects of the second type, use:

```
>>> from scipy.stats import multivariate_hypergeom
>>> multivariate_hypergeom.pmf(x=[8, 4], m=[10, 20], n=12)
0.0025207176631464523
```

The *multivariate_hypergeom* distribution is identical to the corresponding *hypergeom* distribution (tiny numerical differences notwithstanding) when only two types (good and bad) of objects are present in the population as in the example above. Consider another example for a comparison with the hypergeometric distribution:

```
>>> from scipy.stats import hypergeom
>>> multivariate_hypergeom.pmf(x=[3, 1], m=[10, 5], n=4)
0.4395604395604395
>>> hypergeom.pmf(k=3, M=15, n=4, N=10)
0.43956043956044005
```

The functions `pmf`, `logpmf`, `mean`, `var`, `cov`, and `rvs` support broadcasting, under the convention that the vector parameters (`x`, `m`, and `n`) are interpreted as if each row along the last axis is a single object. For instance, we can combine the previous two calls to *`multivariate_hypergeom`* as

```
>>> multivariate_hypergeom.pmf(x=[[8, 4], [3, 1]], m=[[10, 20], [10, 5]],
...                            n=[12, 4])
array([0.00252072, 0.43956044])
```

This broadcasting also works for `cov`, where the output objects are square matrices of size `m.shape[-1]`. For example:

```
>>> multivariate_hypergeom.cov(m=[[7, 9], [10, 15]], n=[8, 12])
array([[[ 1.05, -1.05],
        [-1.05,  1.05]],
       [[ 1.56, -1.56],
        [-1.56,  1.56]]])
```

That is, `result[0]` is equal to `multivariate_hypergeom.cov(m=[7, 9], n=8)` and `result[1]` is equal to `multivariate_hypergeom.cov(m=[10, 15], n=12)`.

Alternatively, the object may be called (as a function) to fix the *m* and *n* parameters, returning a "frozen" multivariate hypergeometric random variable.

```
>>> rv = multivariate_hypergeom(m=[10, 20], n=12)
>>> rv.pmf(x=[8, 4])
0.0025207176631464523
```

Methods

``pmf(x, m, n)``	Probability mass function.
``logpmf(x, m, n)``	Log of the probability mass function.
``rvs(m, n, size=1, random_state=None)``	Draw random samples from a multivariate hypergeometric distribution.
``mean(m, n)``	Mean of the multivariate hypergeometric distribution.
``var(m, n)``	Variance of the multivariate hypergeometric distribution.
``cov(m, n)``	Compute the covariance matrix of the multivariate hypergeometric distribution.

Discrete distributions

bernoulli	A Bernoulli discrete random variable.
betabinom	A beta-binomial discrete random variable.
binom	A binomial discrete random variable.
boltzmann	A Boltzmann (Truncated Discrete Exponential) random variable.
dlaplace	A Laplacian discrete random variable.
geom	A geometric discrete random variable.
hypergeom	A hypergeometric discrete random variable.
logser	A Logarithmic (Log-Series, Series) discrete random variable.
nbinom	A negative binomial discrete random variable.
nchypergeom_fisher	A Fisher's noncentral hypergeometric discrete random variable.
nchypergeom_wallenius	A Wallenius' noncentral hypergeometric discrete random variable.
nhypergeom	A negative hypergeometric discrete random variable.
planck	A Planck discrete exponential random variable.
poisson	A Poisson discrete random variable.
randint	A uniform discrete random variable.
skellam	A Skellam discrete random variable.
yulesimon	A Yule-Simon discrete random variable.
zipf	A Zipf (Zeta) discrete random variable.
zipfian	A Zipfian discrete random variable.

scipy.stats.bernoulli

scipy.stats.**bernoulli = <scipy.stats._discrete_distns.bernoulli_gen object>**

A Bernoulli discrete random variable.

As an instance of the *rv_discrete* class, *bernoulli* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for *bernoulli* is:

$$f(k) = \begin{cases} 1-p & \text{if } k = 0 \\ p & \text{if } k = 1 \end{cases}$$

for k in $\{0, 1\}$, $0 \leq p \leq 1$

bernoulli takes p as shape parameter, where p is the probability of a single success and $1 - p$ is the probability of a single failure.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `bernoulli.pmf(k, p, loc)` is identically equivalent to `bernoulli.pmf(k - loc, p)`.

Examples

```
>>> from scipy.stats import bernoulli
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> p = 0.3
>>> mean, var, skew, kurt = bernoulli.stats(p, moments='mvsk')
```

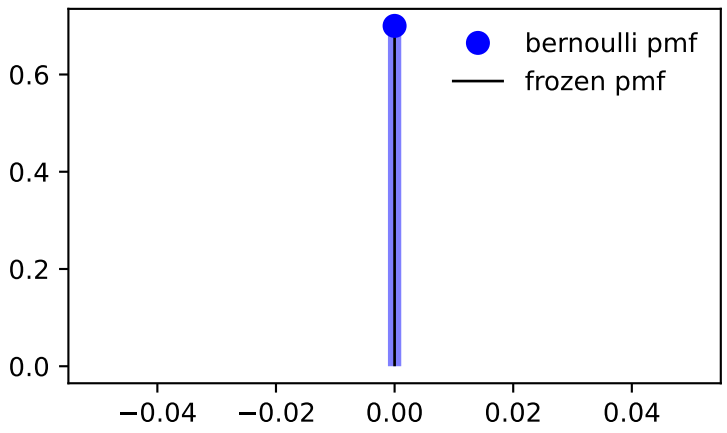
Display the probability mass function (`pmf`):

```
>>> x = np.arange(bernoulli.ppf(0.01, p),
...               bernoulli.ppf(0.99, p))
>>> ax.plot(x, bernoulli.pmf(x, p), 'bo', ms=8, label='bernoulli pmf')
>>> ax.vlines(x, 0, bernoulli.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = bernoulli(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = bernoulli.cdf(x, p)
>>> np.allclose(x, bernoulli.ppf(prob, p))
True
```

Generate random numbers:

```
>>> r = bernoulli.rvs(p, size=1000)
```

Methods

rvs(p, loc=0, size=1, random_state=None)	Random variates.
pmf(k, p, loc=0)	Probability mass function.
logpmf(k, p, loc=0)	Log of the probability mass function.
cdf(k, p, loc=0)	Cumulative distribution function.
logcdf(k, p, loc=0)	Log of the cumulative distribution function.
sf(k, p, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, p, loc=0)	Log of the survival function.
ppf(q, p, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, p, loc=0)	Inverse survival function (inverse of `sf`).
stats(p, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(p, loc=0)	(Differential) entropy of the RV.
expect(func, args=(p,), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(p, loc=0)	Median of the distribution.
mean(p, loc=0)	Mean of the distribution.
var(p, loc=0)	Variance of the distribution.
std(p, loc=0)	Standard deviation of the distribution.
interval(alpha, p, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.betabinom

scipy.stats.**betabinom = <scipy.stats._discrete_distns.betabinom_gen object>**

A beta-binomial discrete random variable.

As an instance of the *rv_discrete* class, *betabinom* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

beta, **binom**

Notes

The beta-binomial distribution is a binomial distribution with a probability of success *p* that follows a beta distribution.

The probability mass function for *betabinom* is:

$$f(k) = \binom{n}{k} \frac{B(k+a, n-k+b)}{B(a,b)}$$

for $k \in \{0, 1, \ldots, n\}$, $n \geq 0$, $a > 0$, $b > 0$, where $B(a, b)$ is the beta function.

betabinom takes n, a, and b as shape parameters.

References

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `betabinom.pmf(k, n, a, b, loc)` is identically equivalent to `betabinom.pmf(k - loc, n, a, b)`.

New in version 1.4.0.

[1]

Examples

```
>>> from scipy.stats import betabinom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> n, a, b = 5, 2.3, 0.63
>>> mean, var, skew, kurt = betabinom.stats(n, a, b, moments='mvsk')
```

Display the probability mass function (`pmf`):

```
>>> x = np.arange(betabinom.ppf(0.01, n, a, b),
...               betabinom.ppf(0.99, n, a, b))
>>> ax.plot(x, betabinom.pmf(x, n, a, b), 'bo', ms=8, label='betabinom pmf
↪')
>>> ax.vlines(x, 0, betabinom.pmf(x, n, a, b), colors='b', lw=5, alpha=0.
↪5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

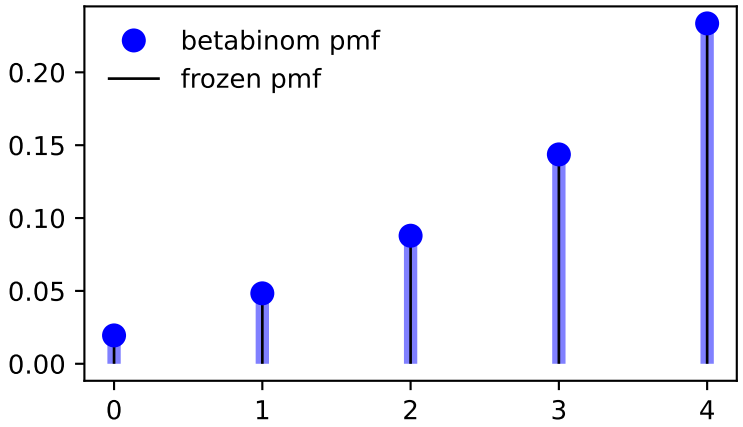
```
>>> rv = betabinom(n, a, b)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of `cdf` and `ppf`:

```
>>> prob = betabinom.cdf(x, n, a, b)
>>> np.allclose(x, betabinom.ppf(prob, n, a, b))
True
```

Generate random numbers:

```
>>> r = betabinom.rvs(n, a, b, size=1000)
```



Methods

rvs(n, a, b, loc=0, size=1, random_state=None)	Random variates.
pmf(k, n, a, b, loc=0)	Probability mass function.
logpmf(k, n, a, b, loc=0)	Log of the probability mass function.
cdf(k, n, a, b, loc=0)	Cumulative distribution function.
logcdf(k, n, a, b, loc=0)	Log of the cumulative distribution function.
sf(k, n, a, b, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, n, a, b, loc=0)	Log of the survival function.
ppf(q, n, a, b, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, n, a, b, loc=0)	Inverse survival function (inverse of `sf`).
stats(n, a, b, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(n, a, b, loc=0)	(Differential) entropy of the RV.
expect(func, args=(n, a, b), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(n, a, b, loc=0)	Median of the distribution.
mean(n, a, b, loc=0)	Mean of the distribution.
var(n, a, b, loc=0)	Variance of the distribution.
std(n, a, b, loc=0)	Standard deviation of the distribution.
interval(alpha, n, a, b, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.binom

scipy.stats.**binom = <scipy.stats._discrete_distns.binom_gen object>**

A binomial discrete random variable.

As an instance of the *rv_discrete* class, *binom* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

hypergeom, **nbinom**, **nhypergeom**

Notes

The probability mass function for *binom* is:

$$f(k) = \binom{n}{k} p^k (1-p)^{n-k}$$

for $k \in \{0, 1, \ldots, n\}$, $0 \leq p \leq 1$

binom takes n and p as shape parameters, where p is the probability of a single success and $1-p$ is the probability of a single failure.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `binom.pmf(k, n, p, loc)` is identically equivalent to `binom.pmf(k - loc, n, p)`.

Examples

```
>>> from scipy.stats import binom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> n, p = 5, 0.4
>>> mean, var, skew, kurt = binom.stats(n, p, moments='mvsk')
```

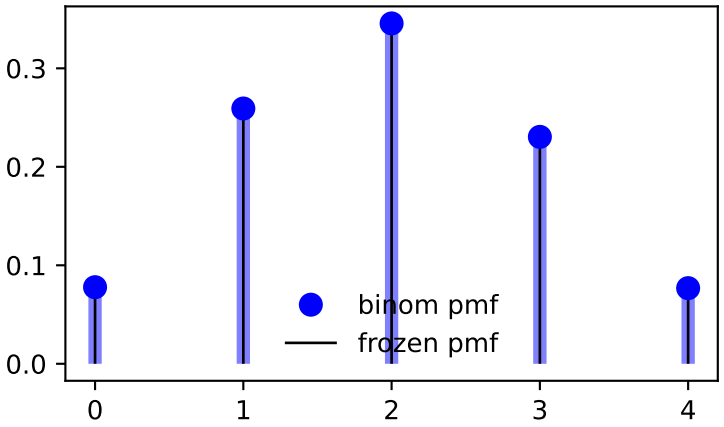
Display the probability mass function (`pmf`):

```
>>> x = np.arange(binom.ppf(0.01, n, p),
...               binom.ppf(0.99, n, p))
>>> ax.plot(x, binom.pmf(x, n, p), 'bo', ms=8, label='binom pmf')
>>> ax.vlines(x, 0, binom.pmf(x, n, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = binom(n, p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = binom.cdf(x, n, p)
>>> np.allclose(x, binom.ppf(prob, n, p))
True
```

Generate random numbers:

```
>>> r = binom.rvs(n, p, size=1000)
```

Methods

rvs(n, p, loc=0, size=1, random_state=None)	Random variates.
pmf(k, n, p, loc=0)	Probability mass function.
logpmf(k, n, p, loc=0)	Log of the probability mass function.
cdf(k, n, p, loc=0)	Cumulative distribution function.
logcdf(k, n, p, loc=0)	Log of the cumulative distribution function.
sf(k, n, p, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, n, p, loc=0)	Log of the survival function.
ppf(q, n, p, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, n, p, loc=0)	Inverse survival function (inverse of `sf`).
stats(n, p, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(n, p, loc=0)	(Differential) entropy of the RV.
expect(func, args=(n, p), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(n, p, loc=0)	Median of the distribution.
mean(n, p, loc=0)	Mean of the distribution.
var(n, p, loc=0)	Variance of the distribution.
std(n, p, loc=0)	Standard deviation of the distribution.
interval(alpha, n, p, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.boltzmann

scipy.stats.**boltzmann = <scipy.stats._discrete_distns.boltzmann_gen object>**

A Boltzmann (Truncated Discrete Exponential) random variable.

As an instance of the *rv_discrete* class, *boltzmann* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for *boltzmann* is:

$$f(k) = (1 - \exp(-\lambda)) \exp(-\lambda k)/(1 - \exp(-\lambda N))$$

for $k = 0, ..., N - 1$.

boltzmann takes $\lambda > 0$ and $N > 0$ as shape parameters.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `boltzmann.pmf(k, lambda_, N, loc)` is identically equivalent to `boltzmann.pmf(k - loc, lambda_, N)`.

Examples

```
>>> from scipy.stats import boltzmann
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> lambda_, N = 1.4, 19
>>> mean, var, skew, kurt = boltzmann.stats(lambda_, N, moments='mvsk')
```

Display the probability mass function (`pmf`):

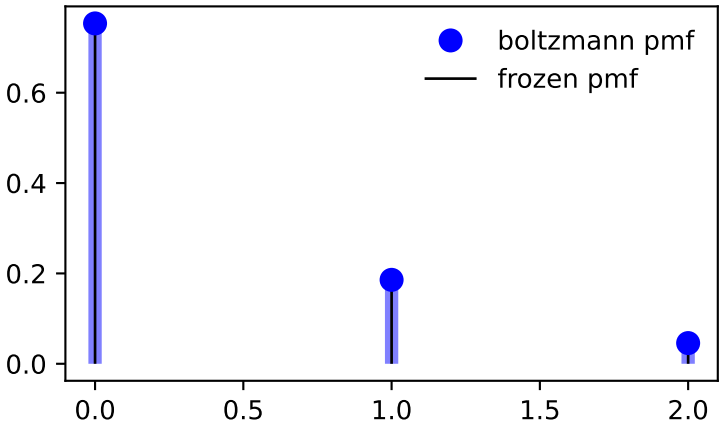
```
>>> x = np.arange(boltzmann.ppf(0.01, lambda_, N),
...               boltzmann.ppf(0.99, lambda_, N))
>>> ax.plot(x, boltzmann.pmf(x, lambda_, N), 'bo', ms=8, label='boltzmann␣
↪pmf')
>>> ax.vlines(x, 0, boltzmann.pmf(x, lambda_, N), colors='b', lw=5,␣
↪alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = boltzmann(lambda_, N)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of `cdf` and `ppf`:




```
>>> prob = boltzmann.cdf(x, lambda_, N)
>>> np.allclose(x, boltzmann.ppf(prob, lambda_, N))
True
```

Generate random numbers:

```
>>> r = boltzmann.rvs(lambda_, N, size=1000)
```

Methods

rvs(lambda_, N, loc=0, size=1, random_state=None)	Random variates.
pmf(k, lambda_, N, loc=0)	Probability mass function.
logpmf(k, lambda_, N, loc=0)	Log of the probability mass function.
cdf(k, lambda_, N, loc=0)	Cumulative distribution function.
logcdf(k, lambda_, N, loc=0)	Log of the cumulative distribution function.
sf(k, lambda_, N, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, lambda_, N, loc=0)	Log of the survival function.
ppf(q, lambda_, N, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, lambda_, N, loc=0)	Inverse survival function (inverse of `sf`).
stats(lambda_, N, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(lambda_, N, loc=0)	(Differential) entropy of the RV.
expect(func, args=(lambda_, N), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(lambda_, N, loc=0)	Median of the distribution.
mean(lambda_, N, loc=0)	Mean of the distribution.
var(lambda_, N, loc=0)	Variance of the distribution.
std(lambda_, N, loc=0)	Standard deviation of the distribution.
interval(alpha, lambda_, N, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.dlaplace

scipy.stats.**dlaplace = <scipy.stats._discrete_distns.dlaplace_gen object>**

A Laplacian discrete random variable.

As an instance of the *rv_discrete* class, *dlaplace* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for *dlaplace* is:

$$f(k) = \tanh(a/2)\exp(-a|k|)$$

for integers k and $a > 0$.

dlaplace takes a as shape parameter.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `dlaplace.pmf(k, a, loc)` is identically equivalent to `dlaplace.pmf(k - loc, a)`.

Examples

```
>>> from scipy.stats import dlaplace
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 0.8
>>> mean, var, skew, kurt = dlaplace.stats(a, moments='mvsk')
```

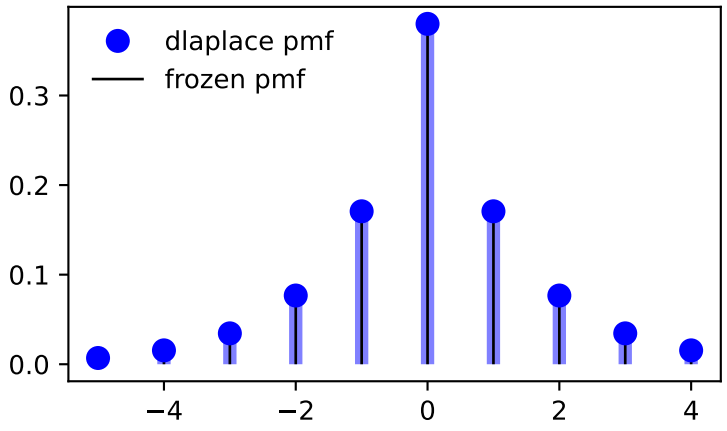
Display the probability mass function (`pmf`):

```
>>> x = np.arange(dlaplace.ppf(0.01, a),
...               dlaplace.ppf(0.99, a))
>>> ax.plot(x, dlaplace.pmf(x, a), 'bo', ms=8, label='dlaplace pmf')
>>> ax.vlines(x, 0, dlaplace.pmf(x, a), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = dlaplace(a)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = dlaplace.cdf(x, a)
>>> np.allclose(x, dlaplace.ppf(prob, a))
True
```

Generate random numbers:

```
>>> r = dlaplace.rvs(a, size=1000)
```

Methods

rvs(a, loc=0, size=1, random_state=None)	Random variates.
pmf(k, a, loc=0)	Probability mass function.
logpmf(k, a, loc=0)	Log of the probability mass function.
cdf(k, a, loc=0)	Cumulative distribution function.
logcdf(k, a, loc=0)	Log of the cumulative distribution function.
sf(k, a, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, a, loc=0)	Log of the survival function.
ppf(q, a, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0)	Inverse survival function (inverse of `sf`).
stats(a, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0)	(Differential) entropy of the RV.
expect(func, args=(a,), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0)	Median of the distribution.
mean(a, loc=0)	Mean of the distribution.
var(a, loc=0)	Variance of the distribution.
std(a, loc=0)	Standard deviation of the distribution.
interval(alpha, a, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.geom

scipy.stats.**geom = <scipy.stats._discrete_distns.geom_gen object>**

A geometric discrete random variable.

As an instance of the *rv_discrete* class, *geom* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

planck

Notes

The probability mass function for *geom* is:

$$f(k) = (1-p)^{k-1}p$$

for $k \geq 1, 0 < p \leq 1$

geom takes p as shape parameter, where p is the probability of a single success and $1-p$ is the probability of a single failure.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `geom.pmf(k, p, loc)` is identically equivalent to `geom.pmf(k - loc, p)`.

Examples

```
>>> from scipy.stats import geom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> p = 0.5
>>> mean, var, skew, kurt = geom.stats(p, moments='mvsk')
```

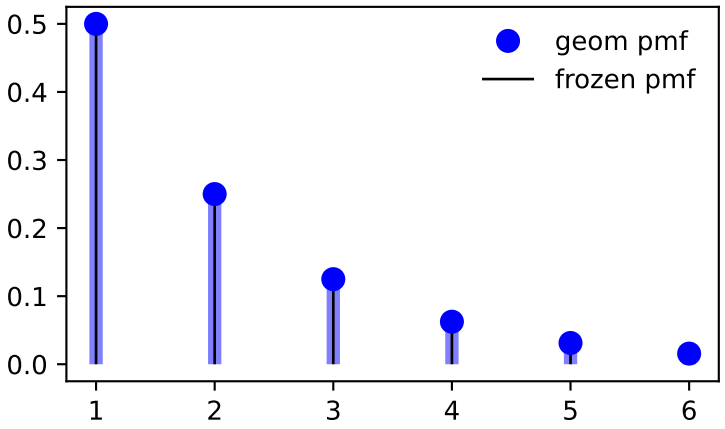
Display the probability mass function (`pmf`):

```
>>> x = np.arange(geom.ppf(0.01, p),
...               geom.ppf(0.99, p))
>>> ax.plot(x, geom.pmf(x, p), 'bo', ms=8, label='geom pmf')
>>> ax.vlines(x, 0, geom.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = geom(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = geom.cdf(x, p)
>>> np.allclose(x, geom.ppf(prob, p))
True
```

Generate random numbers:

```
>>> r = geom.rvs(p, size=1000)
```

Methods

rvs(p, loc=0, size=1, random_state=None)	Random variates.
pmf(k, p, loc=0)	Probability mass function.
logpmf(k, p, loc=0)	Log of the probability mass function.
cdf(k, p, loc=0)	Cumulative distribution function.
logcdf(k, p, loc=0)	Log of the cumulative distribution function.
sf(k, p, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, p, loc=0)	Log of the survival function.
ppf(q, p, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, p, loc=0)	Inverse survival function (inverse of `sf`).
stats(p, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(p, loc=0)	(Differential) entropy of the RV.
expect(func, args=(p,), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(p, loc=0)	Median of the distribution.
mean(p, loc=0)	Mean of the distribution.
var(p, loc=0)	Variance of the distribution.
std(p, loc=0)	Standard deviation of the distribution.
interval(alpha, p, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.hypergeom

scipy.stats.**hypergeom = <scipy.stats._discrete_distns.hypergeom_gen object>**

A hypergeometric discrete random variable.

The hypergeometric distribution models drawing objects from a bin. *M* is the total number of objects, *n* is total number of Type I objects. The random variate represents the number of Type I objects in *N* drawn without replacement from the total population.

As an instance of the *rv_discrete* class, *hypergeom* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

nhypergeom, **binom**, **nbinom**

Notes

The symbols used to denote the shape parameters (M, n, and N) are not universally accepted. See the Examples for a clarification of the definitions used here.

The probability mass function is defined as,

$$p(k, M, n, N) = \frac{\binom{n}{k}\binom{M-n}{N-k}}{\binom{M}{N}}$$

for $k \in [\max(0, N - M + n), \min(n, N)]$, where the binomial coefficients are defined as,

$$\binom{n}{k} \equiv \frac{n!}{k!(n-k)!}.$$

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `hypergeom.pmf(k, M, n, N, loc)` is identically equivalent to `hypergeom.pmf(k - loc, M, n, N)`.

Examples

```
>>> from scipy.stats import hypergeom
>>> import matplotlib.pyplot as plt
```

Suppose we have a collection of 20 animals, of which 7 are dogs. Then if we want to know the probability of finding a given number of dogs if we choose at random 12 of the 20 animals, we can initialize a frozen distribution and plot the probability mass function:

```
>>> [M, n, N] = [20, 7, 12]
>>> rv = hypergeom(M, n, N)
>>> x = np.arange(0, n+1)
>>> pmf_dogs = rv.pmf(x)
```

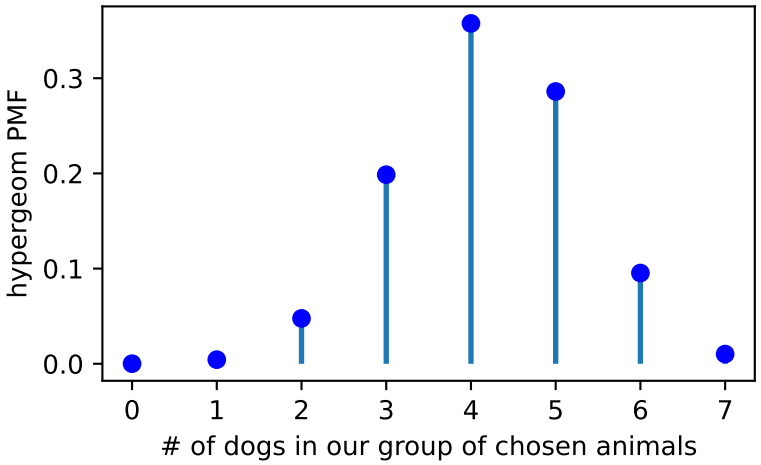
```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, pmf_dogs, 'bo')
>>> ax.vlines(x, 0, pmf_dogs, lw=2)
>>> ax.set_xlabel('# of dogs in our group of chosen animals')
>>> ax.set_ylabel('hypergeom PMF')
>>> plt.show()
```

Instead of using a frozen distribution we can also use *hypergeom* methods directly. To for example obtain the cumulative distribution function, use:

```
>>> prb = hypergeom.cdf(x, M, n, N)
```

And to generate random numbers:

```
>>> R = hypergeom.rvs(M, n, N, size=10)
```



Methods

rvs(M, n, N, loc=0, size=1, random_state=None)	Random variates.
pmf(k, M, n, N, loc=0)	Probability mass function.
logpmf(k, M, n, N, loc=0)	Log of the probability mass function.
cdf(k, M, n, N, loc=0)	Cumulative distribution function.
logcdf(k, M, n, N, loc=0)	Log of the cumulative distribution function.
sf(k, M, n, N, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, M, n, N, loc=0)	Log of the survival function.
ppf(q, M, n, N, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, M, n, N, loc=0)	Inverse survival function (inverse of `sf`).
stats(M, n, N, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(M, n, N, loc=0)	(Differential) entropy of the RV.
expect(func, args=(M, n, N), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(M, n, N, loc=0)	Median of the distribution.
mean(M, n, N, loc=0)	Mean of the distribution.
var(M, n, N, loc=0)	Variance of the distribution.
std(M, n, N, loc=0)	Standard deviation of the distribution.
interval(alpha, M, n, N, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.logser

scipy.stats.**logser = <scipy.stats._discrete_distns.logser_gen object>**

A Logarithmic (Log-Series, Series) discrete random variable.

As an instance of the *rv_discrete* class, *logser* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for *logser* is:

$$f(k) = -\frac{p^k}{k \log(1-p)}$$

for $k \geq 1, 0 < p < 1$

logser takes p as shape parameter, where p is the probability of a single success and $1 - p$ is the probability of a single failure.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `logser.pmf(k, p, loc)` is identically equivalent to `logser.pmf(k - loc, p)`.

Examples

```
>>> from scipy.stats import logser
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> p = 0.6
>>> mean, var, skew, kurt = logser.stats(p, moments='mvsk')
```

Display the probability mass function (`pmf`):

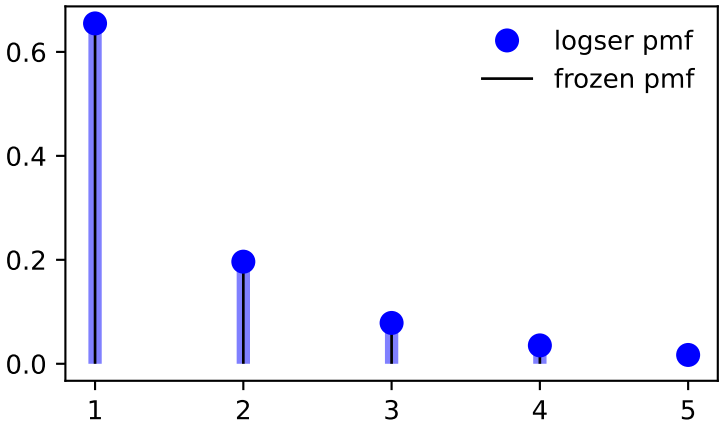
```
>>> x = np.arange(logser.ppf(0.01, p),
...               logser.ppf(0.99, p))
>>> ax.plot(x, logser.pmf(x, p), 'bo', ms=8, label='logser pmf')
>>> ax.vlines(x, 0, logser.pmf(x, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = logser(p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of `cdf` and `ppf`:




```
>>> prob = logser.cdf(x, p)
>>> np.allclose(x, logser.ppf(prob, p))
True
```

Generate random numbers:

```
>>> r = logser.rvs(p, size=1000)
```

Methods

rvs(p, loc=0, size=1, random_state=None)	Random variates.
pmf(k, p, loc=0)	Probability mass function.
logpmf(k, p, loc=0)	Log of the probability mass function.
cdf(k, p, loc=0)	Cumulative distribution function.
logcdf(k, p, loc=0)	Log of the cumulative distribution function.
sf(k, p, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, p, loc=0)	Log of the survival function.
ppf(q, p, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, p, loc=0)	Inverse survival function (inverse of `sf`).
stats(p, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(p, loc=0)	(Differential) entropy of the RV.
expect(func, args=(p,), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(p, loc=0)	Median of the distribution.
mean(p, loc=0)	Mean of the distribution.
var(p, loc=0)	Variance of the distribution.
std(p, loc=0)	Standard deviation of the distribution.
interval(alpha, p, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.nbinom

scipy.stats.**nbinom = <scipy.stats._discrete_distns.nbinom_gen object>**

A negative binomial discrete random variable.

As an instance of the *rv_discrete* class, *nbinom* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

hypergeom, **binom**, **nhypergeom**

Notes

Negative binomial distribution describes a sequence of i.i.d. Bernoulli trials, repeated until a predefined, non-random number of successes occurs.

The probability mass function of the number of failures for *nbinom* is:

$$f(k) = \binom{k+n-1}{n-1} p^n (1-p)^k$$

for $k \geq 0, 0 < p \leq 1$

nbinom takes n and p as shape parameters where n is the number of successes, p is the probability of a single success, and $1-p$ is the probability of a single failure.

Another common parameterization of the negative binomial distribution is in terms of the mean number of failures μ to achieve n successes. The mean μ is related to the probability of success as

$$p = \frac{n}{n+\mu}$$

The number of successes n may also be specified in terms of a "dispersion", "heterogeneity", or "aggregation" parameter α, which relates the mean μ to the variance σ^2, e.g. $\sigma^2 = \mu + \alpha\mu^2$. Regardless of the convention used for α,

$$p = \frac{\mu}{\sigma^2}$$
$$n = \frac{\mu^2}{\sigma^2 - \mu}$$

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `nbinom.pmf(k, n, p, loc)` is identically equivalent to `nbinom.pmf(k - loc, n, p)`.

Examples

```
>>> from scipy.stats import nbinom
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> n, p = 5, 0.5
>>> mean, var, skew, kurt = nbinom.stats(n, p, moments='mvsk')
```

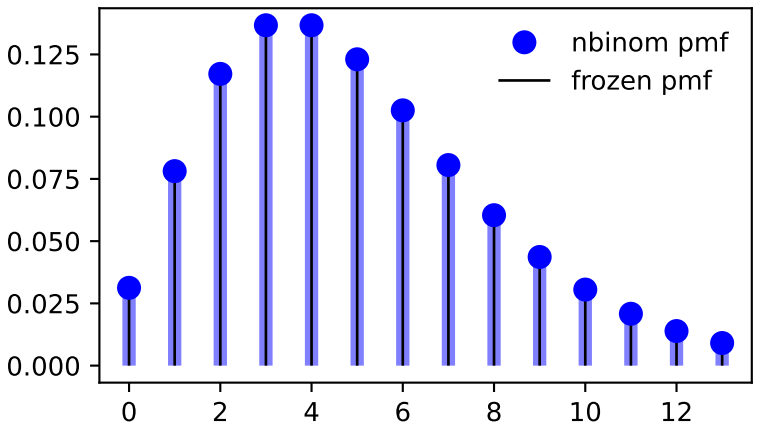
Display the probability mass function (`pmf`):

```
>>> x = np.arange(nbinom.ppf(0.01, n, p),
...               nbinom.ppf(0.99, n, p))
>>> ax.plot(x, nbinom.pmf(x, n, p), 'bo', ms=8, label='nbinom pmf')
>>> ax.vlines(x, 0, nbinom.pmf(x, n, p), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = nbinom(n, p)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = nbinom.cdf(x, n, p)
>>> np.allclose(x, nbinom.ppf(prob, n, p))
True
```

Generate random numbers:

```
>>> r = nbinom.rvs(n, p, size=1000)
```

Methods

rvs(n, p, loc=0, size=1, random_state=None)	Random variates.
pmf(k, n, p, loc=0)	Probability mass function.
logpmf(k, n, p, loc=0)	Log of the probability mass function.
cdf(k, n, p, loc=0)	Cumulative distribution function.
logcdf(k, n, p, loc=0)	Log of the cumulative distribution function.
sf(k, n, p, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, n, p, loc=0)	Log of the survival function.
ppf(q, n, p, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, n, p, loc=0)	Inverse survival function (inverse of `sf`).
stats(n, p, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(n, p, loc=0)	(Differential) entropy of the RV.
expect(func, args=(n, p), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(n, p, loc=0)	Median of the distribution.
mean(n, p, loc=0)	Mean of the distribution.
var(n, p, loc=0)	Variance of the distribution.
std(n, p, loc=0)	Standard deviation of the distribution.
interval(alpha, n, p, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.nchypergeom_fisher

scipy.stats.**nchypergeom_fisher = <scipy.stats._discrete_distns.nchypergeom_fisher_gen objec**

A Fisher's noncentral hypergeometric discrete random variable.

Fisher's noncentral hypergeometric distribution models drawing objects of two types from a bin. *M* is the total number of objects, *n* is the number of Type I objects, and *odds* is the odds ratio: the odds of selecting a Type I object rather than a Type II object when there is only one object of each type. The random variate represents the number of Type I objects drawn if we take a handful of objects from the bin at once and find out afterwards that we took *N* objects.

As an instance of the *rv_discrete* class, *nchypergeom_fisher* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

nchypergeom_wallenius, **hypergeom**, **nhypergeom**

Notes

Let mathematical symbols N, n, and M correspond with parameters *N*, *n*, and *M* (respectively) as defined above.

The probability mass function is defined as

$$p(x; M, n, N, \omega) = \frac{\binom{n}{x}\binom{M-n}{N-x}\omega^x}{P_0},$$

for $x \in [x_l, x_u]$, $M \in \mathbb{N}$, $n \in [0, M]$, $N \in [0, M]$, $\omega > 0$, where $x_l = \max(0, N - (M - n))$, $x_u = \min(N, n)$,

$$P_0 = \sum_{y=x_l}^{x_u} \binom{n}{y}\binom{M-n}{N-y}\omega^y,$$

and the binomial coefficients are defined as

$$\binom{n}{k} \equiv \frac{n!}{k!(n-k)!}.$$

nchypergeom_fisher uses the BiasedUrn package by Agner Fog with permission for it to be distributed under SciPy's license.

The symbols used to denote the shape parameters (N, n, and M) are not universally accepted; they are chosen for consistency with *hypergeom*.

Note that Fisher's noncentral hypergeometric distribution is distinct from Wallenius' noncentral hypergeometric distribution, which models drawing a pre-determined N objects from a bin one by one. When the odds ratio is unity, however, both distributions reduce to the ordinary hypergeometric distribution.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `nchypergeom_fisher.pmf(k, M, n, N, odds, loc)` is identically equivalent to `nchypergeom_fisher.pmf(k - loc, M, n, N, odds)`.

References

[1], [2]

Examples

```
>>> from scipy.stats import nchypergeom_fisher
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> M, n, N, odds = 140, 80, 60, 0.5
>>> mean, var, skew, kurt = nchypergeom_fisher.stats(M, n, N, odds,␣
↪moments='mvsk')
```

Display the probability mass function (`pmf`):

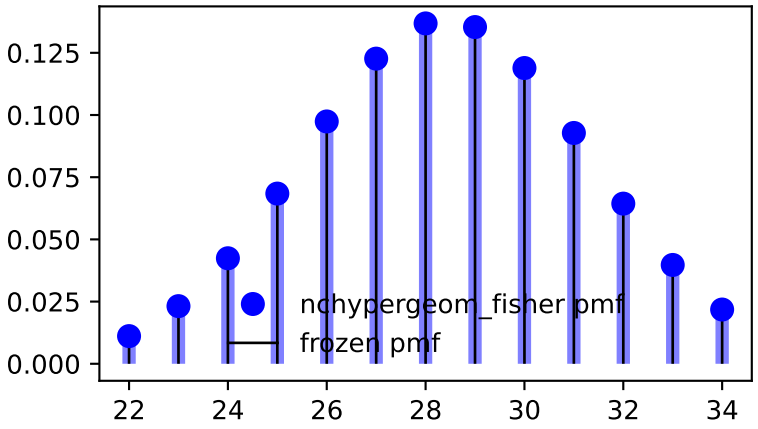
```
>>> x = np.arange(nchypergeom_fisher.ppf(0.01, M, n, N, odds),
...               nchypergeom_fisher.ppf(0.99, M, n, N, odds))
>>> ax.plot(x, nchypergeom_fisher.pmf(x, M, n, N, odds), 'bo', ms=8,␣
↪label='nchypergeom_fisher pmf')
>>> ax.vlines(x, 0, nchypergeom_fisher.pmf(x, M, n, N, odds), colors='b',␣
↪lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = nchypergeom_fisher(M, n, N, odds)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of `cdf` and `ppf`:




```
>>> prob = nchypergeom_fisher.cdf(x, M, n, N, odds)
>>> np.allclose(x, nchypergeom_fisher.ppf(prob, M, n, N, odds))
True
```

Generate random numbers:

```
>>> r = nchypergeom_fisher.rvs(M, n, N, odds, size=1000)
```

Methods

rvs(M, n, N, odds, loc=0, size=1, random_state=None)	Random variates.
pmf(k, M, n, N, odds, loc=0)	Probability mass function.
logpmf(k, M, n, N, odds, loc=0)	Log of the probability mass function.
cdf(k, M, n, N, odds, loc=0)	Cumulative distribution function.
logcdf(k, M, n, N, odds, loc=0)	Log of the cumulative distribution function.
sf(k, M, n, N, odds, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, M, n, N, odds, loc=0)	Log of the survival function.
ppf(q, M, n, N, odds, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, M, n, N, odds, loc=0)	Inverse survival function (inverse of `sf`).
stats(M, n, N, odds, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(M, n, N, odds, loc=0)	(Differential) entropy of the RV.
expect(func, args=(M, n, N, odds), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(M, n, N, odds, loc=0)	Median of the distribution.
mean(M, n, N, odds, loc=0)	Mean of the distribution.
var(M, n, N, odds, loc=0)	Variance of the distribution.
std(M, n, N, odds, loc=0)	Standard deviation of the distribution.
interval(alpha, M, n, N, odds, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.nchypergeom_wallenius

scipy.stats.**nchypergeom_wallenius = <scipy.stats._discrete_distns.nchypergeom_wallenius_ge**

A Wallenius' noncentral hypergeometric discrete random variable.

Wallenius' noncentral hypergeometric distribution models drawing objects of two types from a bin. *M* is the total number of objects, *n* is the number of Type I objects, and *odds* is the odds ratio: the odds of selecting a Type I object rather than a Type II object when there is only one object of each type. The random variate represents the number of Type I objects drawn if we draw a pre-determined *N* objects from a bin one by one.

As an instance of the *rv_discrete* class, *nchypergeom_wallenius* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

nchypergeom_fisher, **hypergeom**, **nhypergeom**

Notes

Let mathematical symbols N, n, and M correspond with parameters *N*, *n*, and *M* (respectively) as defined above.

The probability mass function is defined as

$$p(x; N, n, M) = \binom{n}{x}\binom{M-n}{N-x}\int_0^1 \left(1-t^{\omega/D}\right)^x \left(1-t^{1/D}\right)^{N-x} dt$$

for $x \in [x_l, x_u]$, $M \in \mathbb{N}$, $n \in [0, M]$, $N \in [0, M]$, $\omega > 0$, where $x_l = \max(0, N-(M-n))$, $x_u = \min(N, n)$,

$$D = \omega(n-x) + ((M-n)-(N-x)),$$

and the binomial coefficients are defined as

$$\binom{n}{k} \equiv \frac{n!}{k!(n-k)!}.$$

nchypergeom_wallenius uses the BiasedUrn package by Agner Fog with permission for it to be distributed under SciPy's license.

The symbols used to denote the shape parameters (*N*, *n*, and *M*) are not universally accepted; they are chosen for consistency with *hypergeom*.

Note that Wallenius' noncentral hypergeometric distribution is distinct from Fisher's noncentral hypergeometric distribution, which models take a handful of objects from the bin at once, finding out afterwards that *N* objects were taken. When the odds ratio is unity, however, both distributions reduce to the ordinary hypergeometric distribution.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `nchypergeom_wallenius.pmf(k, M, n, N, odds, loc)` is identically equivalent to `nchypergeom_wallenius.pmf(k - loc, M, n, N, odds)`.

References

[1], [2]

Examples

```
>>> from scipy.stats import nchypergeom_wallenius
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> M, n, N, odds = 140, 80, 60, 0.5
>>> mean, var, skew, kurt = nchypergeom_wallenius.stats(M, n, N, odds,␣
↪moments='mvsk')
```

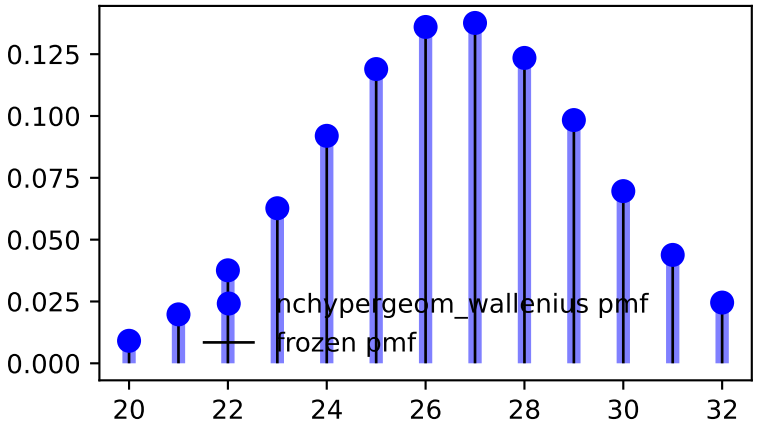
Display the probability mass function (`pmf`):

```
>>> x = np.arange(nchypergeom_wallenius.ppf(0.01, M, n, N, odds),
...               nchypergeom_wallenius.ppf(0.99, M, n, N, odds))
>>> ax.plot(x, nchypergeom_wallenius.pmf(x, M, n, N, odds), 'bo', ms=8,␣
↪label='nchypergeom_wallenius pmf')
>>> ax.vlines(x, 0, nchypergeom_wallenius.pmf(x, M, n, N, odds), colors='b
↪', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = nchypergeom_wallenius(M, n, N, odds)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = nchypergeom_wallenius.cdf(x, M, n, N, odds)
>>> np.allclose(x, nchypergeom_wallenius.ppf(prob, M, n, N, odds))
True
```

Generate random numbers:

```
>>> r = nchypergeom_wallenius.rvs(M, n, N, odds, size=1000)
```

Methods

rvs(M, n, N, odds, loc=0, size=1, random_state=None)	Random variates.
pmf(k, M, n, N, odds, loc=0)	Probability mass function.
logpmf(k, M, n, N, odds, loc=0)	Log of the probability mass function.
cdf(k, M, n, N, odds, loc=0)	Cumulative distribution function.
logcdf(k, M, n, N, odds, loc=0)	Log of the cumulative distribution function.
sf(k, M, n, N, odds, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, M, n, N, odds, loc=0)	Log of the survival function.
ppf(q, M, n, N, odds, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, M, n, N, odds, loc=0)	Inverse survival function (inverse of `sf`).
stats(M, n, N, odds, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(M, n, N, odds, loc=0)	(Differential) entropy of the RV.
expect(func, args=(M, n, N, odds), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(M, n, N, odds, loc=0)	Median of the distribution.
mean(M, n, N, odds, loc=0)	Mean of the distribution.
var(M, n, N, odds, loc=0)	Variance of the distribution.
std(M, n, N, odds, loc=0)	Standard deviation of the distribution.
interval(alpha, M, n, N, odds, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.nhypergeom

scipy.stats.**nhypergeom = <scipy.stats._discrete_distns.nhypergeom_gen object>**

A negative hypergeometric discrete random variable.

Consider a box containing M balls:, n red and $M - n$ blue. We randomly sample balls from the box, one at a time and *without* replacement, until we have picked r blue balls. *nhypergeom* is the distribution of the number of red balls k we have picked.

As an instance of the *rv_discrete* class, *nhypergeom* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

hypergeom, **binom**, **nbinom**

Notes

The symbols used to denote the shape parameters (*M*, *n*, and *r*) are not universally accepted. See the Examples for a clarification of the definitions used here.

The probability mass function is defined as,

$$f(k; M, n, r) = \frac{\binom{k+r-1}{k}\binom{M-r-k}{n-k}}{\binom{M}{n}}$$

for $k \in [0, n]$, $n \in [0, M]$, $r \in [0, M - n]$, and the binomial coefficient is:

$$\binom{n}{k} \equiv \frac{n!}{k!(n-k)!}.$$

It is equivalent to observing k successes in $k + r - 1$ samples with $k + r$'th sample being a failure. The former can be modelled as a hypergeometric distribution. The probability of the latter is simply the number of failures remaining $M - n - (r - 1)$ divided by the size of the remaining population $M - (k + r - 1)$. This relationship can be shown as:

$$NHG(k; M, n, r) = HG(k; M, n, k + r - 1)\frac{(M - n - (r - 1))}{(M - (k + r - 1))}$$

where NHG is probability mass function (PMF) of the negative hypergeometric distribution and HG is the PMF of the hypergeometric distribution.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `nhypergeom.pmf(k, M, n, r, loc)` is identically equivalent to `nhypergeom.pmf(k - loc, M, n, r)`.

References

[1], [2]

Examples

```
>>> from scipy.stats import nhypergeom
>>> import matplotlib.pyplot as plt
```

Suppose we have a collection of 20 animals, of which 7 are dogs. Then if we want to know the probability of finding a given number of dogs (successes) in a sample with exactly 12 animals that aren't dogs (failures), we can initialize a frozen distribution and plot the probability mass function:

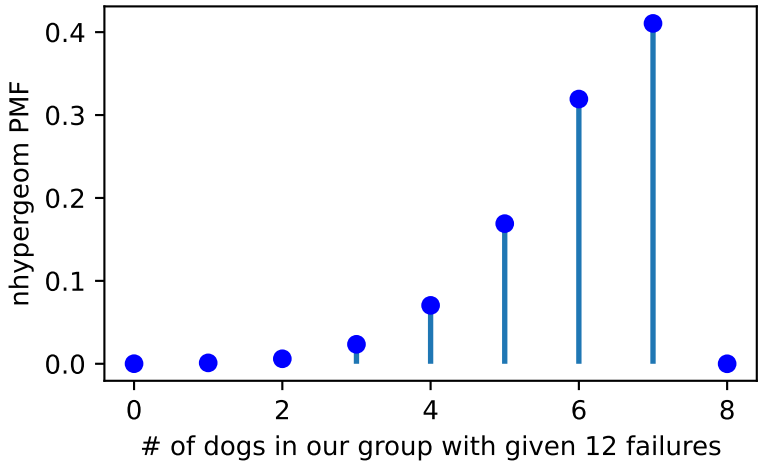
```
>>> M, n, r = [20, 7, 12]
>>> rv = nhypergeom(M, n, r)
>>> x = np.arange(0, n+2)
>>> pmf_dogs = rv.pmf(x)
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, pmf_dogs, 'bo')
>>> ax.vlines(x, 0, pmf_dogs, lw=2)
>>> ax.set_xlabel('# of dogs in our group with given 12 failures')
>>> ax.set_ylabel('nhypergeom PMF')
>>> plt.show()
```

Instead of using a frozen distribution we can also use *nhypergeom* methods directly. To for example obtain the probability mass function, use:

```
>>> prb = nhypergeom.pmf(x, M, n, r)
```

And to generate random numbers:




```
>>> R = nhypergeom.rvs(M, n, r, size=10)
```

To verify the relationship between *hypergeom* and *nhypergeom*, use:

```
>>> from scipy.stats import hypergeom, nhypergeom
>>> M, n, r = 45, 13, 8
>>> k = 6
>>> nhypergeom.pmf(k, M, n, r)
0.06180776620271643
>>> hypergeom.pmf(k, M, n, k+r-1) * (M - n - (r-1)) / (M - (k+r-1))
0.06180776620271644
```

Methods

rvs(M, n, r, loc=0, size=1, random_state=None)	Random variates.
pmf(k, M, n, r, loc=0)	Probability mass function.
logpmf(k, M, n, r, loc=0)	Log of the probability mass function.
cdf(k, M, n, r, loc=0)	Cumulative distribution function.
logcdf(k, M, n, r, loc=0)	Log of the cumulative distribution function.
sf(k, M, n, r, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, M, n, r, loc=0)	Log of the survival function.
ppf(q, M, n, r, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, M, n, r, loc=0)	Inverse survival function (inverse of `sf`).
stats(M, n, r, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(M, n, r, loc=0)	(Differential) entropy of the RV.
expect(func, args=(M, n, r), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(M, n, r, loc=0)	Median of the distribution.
mean(M, n, r, loc=0)	Mean of the distribution.
var(M, n, r, loc=0)	Variance of the distribution.
std(M, n, r, loc=0)	Standard deviation of the distribution.
interval(alpha, M, n, r, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.planck

scipy.stats.**planck = <scipy.stats._discrete_distns.planck_gen object>**

A Planck discrete exponential random variable.

As an instance of the *rv_discrete* class, *planck* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

geom

Notes

The probability mass function for *planck* is:

$$f(k) = (1 - \exp(-\lambda))\exp(-\lambda k)$$

for $k \geq 0$ and $\lambda > 0$.

planck takes λ as shape parameter. The Planck distribution can be written as a geometric distribution (*geom*) with $p = 1 - \exp(-\lambda)$ shifted by `loc = -1`.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `planck.pmf(k, lambda_, loc)` is identically equivalent to `planck.pmf(k - loc, lambda_)`.

Examples

```
>>> from scipy.stats import planck
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> lambda_ = 0.51
>>> mean, var, skew, kurt = planck.stats(lambda_, moments='mvsk')
```

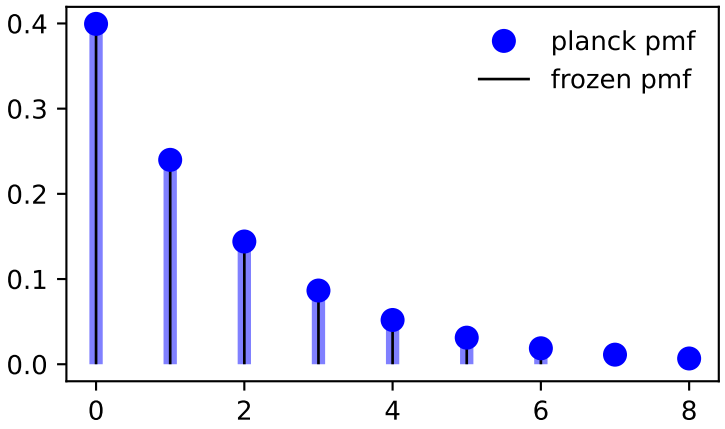
Display the probability mass function (`pmf`):

```
>>> x = np.arange(planck.ppf(0.01, lambda_),
...               planck.ppf(0.99, lambda_))
>>> ax.plot(x, planck.pmf(x, lambda_), 'bo', ms=8, label='planck pmf')
>>> ax.vlines(x, 0, planck.pmf(x, lambda_), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = planck(lambda_)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = planck.cdf(x, lambda_)
>>> np.allclose(x, planck.ppf(prob, lambda_))
True
```

Generate random numbers:

```
>>> r = planck.rvs(lambda_, size=1000)
```

Methods

rvs(lambda_, loc=0, size=1, random_state=None)	Random variates.
pmf(k, lambda_, loc=0)	Probability mass function.
logpmf(k, lambda_, loc=0)	Log of the probability mass function.
cdf(k, lambda_, loc=0)	Cumulative distribution function.
logcdf(k, lambda_, loc=0)	Log of the cumulative distribution function.
sf(k, lambda_, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, lambda_, loc=0)	Log of the survival function.
ppf(q, lambda_, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, lambda_, loc=0)	Inverse survival function (inverse of `sf`).
stats(lambda_, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(lambda_, loc=0)	(Differential) entropy of the RV.
expect(func, args=(lambda_,), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(lambda_, loc=0)	Median of the distribution.
mean(lambda_, loc=0)	Mean of the distribution.
var(lambda_, loc=0)	Variance of the distribution.
std(lambda_, loc=0)	Standard deviation of the distribution.
interval(alpha, lambda_, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.poisson

scipy.stats.**poisson = <scipy.stats._discrete_distns.poisson_gen object>**

A Poisson discrete random variable.

As an instance of the *rv_discrete* class, *poisson* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for *poisson* is:

$$f(k) = \exp(-\mu)\frac{\mu^k}{k!}$$

for $k \geq 0$.

poisson takes $\mu \geq 0$ as shape parameter. When $\mu = 0$, the `pmf` method returns `1.0` at quantile $k = 0$.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `poisson.pmf(k, mu, loc)` is identically equivalent to `poisson.pmf(k - loc, mu)`.

Examples

```
>>> from scipy.stats import poisson
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mu = 0.6
>>> mean, var, skew, kurt = poisson.stats(mu, moments='mvsk')
```

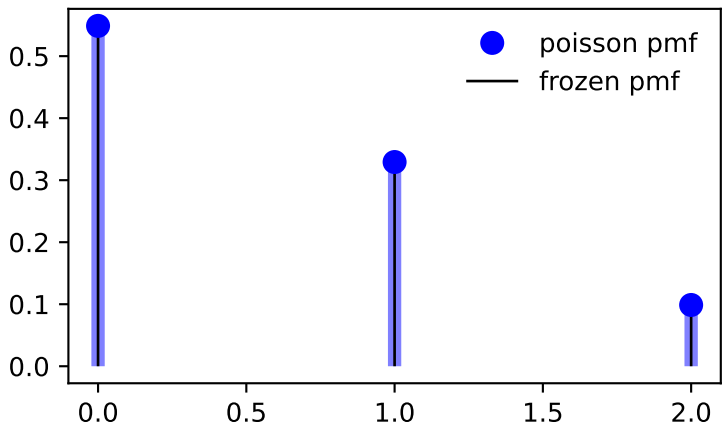
Display the probability mass function (`pmf`):

```
>>> x = np.arange(poisson.ppf(0.01, mu),
...               poisson.ppf(0.99, mu))
>>> ax.plot(x, poisson.pmf(x, mu), 'bo', ms=8, label='poisson pmf')
>>> ax.vlines(x, 0, poisson.pmf(x, mu), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = poisson(mu)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = poisson.cdf(x, mu)
>>> np.allclose(x, poisson.ppf(prob, mu))
True
```

Generate random numbers:

```
>>> r = poisson.rvs(mu, size=1000)
```

Methods

rvs(mu, loc=0, size=1, random_state=None)	Random variates.
pmf(k, mu, loc=0)	Probability mass function.
logpmf(k, mu, loc=0)	Log of the probability mass function.
cdf(k, mu, loc=0)	Cumulative distribution function.
logcdf(k, mu, loc=0)	Log of the cumulative distribution function.
sf(k, mu, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, mu, loc=0)	Log of the survival function.
ppf(q, mu, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, mu, loc=0)	Inverse survival function (inverse of `sf`).
stats(mu, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(mu, loc=0)	(Differential) entropy of the RV.
expect(func, args=(mu,), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(mu, loc=0)	Median of the distribution.
mean(mu, loc=0)	Mean of the distribution.
var(mu, loc=0)	Variance of the distribution.
std(mu, loc=0)	Standard deviation of the distribution.
interval(alpha, mu, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.randint

scipy.stats.**randint = <scipy.stats._discrete_distns.randint_gen object>**

A uniform discrete random variable.

As an instance of the *rv_discrete* class, *randint* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for *randint* is:

$$f(k) = \frac{1}{\texttt{high} - \texttt{low}}$$

for $k \in \{\texttt{low}, \ldots, \texttt{high} - 1\}$.

randint takes `low` and `high` as shape parameters.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `randint.pmf(k, low, high, loc)` is identically equivalent to `randint.pmf(k - loc, low, high)`.

Examples

```
>>> from scipy.stats import randint
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> low, high = 7, 31
>>> mean, var, skew, kurt = randint.stats(low, high, moments='mvsk')
```

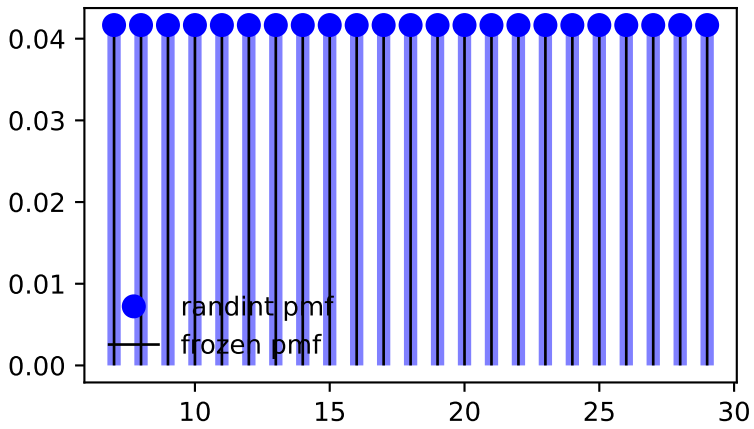
Display the probability mass function (`pmf`):

```
>>> x = np.arange(randint.ppf(0.01, low, high),
...               randint.ppf(0.99, low, high))
>>> ax.plot(x, randint.pmf(x, low, high), 'bo', ms=8, label='randint pmf')
>>> ax.vlines(x, 0, randint.pmf(x, low, high), colors='b', lw=5, alpha=0.
↪5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = randint(low, high)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = randint.cdf(x, low, high)
>>> np.allclose(x, randint.ppf(prob, low, high))
True
```

Generate random numbers:

```
>>> r = randint.rvs(low, high, size=1000)
```

Methods

rvs(low, high, loc=0, size=1, random_state=None)	Random variates.
pmf(k, low, high, loc=0)	Probability mass function.
logpmf(k, low, high, loc=0)	Log of the probability mass function.
cdf(k, low, high, loc=0)	Cumulative distribution function.
logcdf(k, low, high, loc=0)	Log of the cumulative distribution function.
sf(k, low, high, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, low, high, loc=0)	Log of the survival function.
ppf(q, low, high, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, low, high, loc=0)	Inverse survival function (inverse of `sf`).
stats(low, high, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(low, high, loc=0)	(Differential) entropy of the RV.
expect(func, args=(low, high), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(low, high, loc=0)	Median of the distribution.
mean(low, high, loc=0)	Mean of the distribution.
var(low, high, loc=0)	Variance of the distribution.
std(low, high, loc=0)	Standard deviation of the distribution.
interval(alpha, low, high, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.skellam

scipy.stats.**skellam = <scipy.stats._discrete_distns.skellam_gen object>**

A Skellam discrete random variable.

As an instance of the *rv_discrete* class, *skellam* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

Probability distribution of the difference of two correlated or uncorrelated Poisson random variables.

Let k_1 and k_2 be two Poisson-distributed r.v. with expected values λ_1 and λ_2. Then, $k_1 - k_2$ follows a Skellam distribution with parameters $\mu_1 = \lambda_1 - \rho\sqrt{\lambda_1\lambda_2}$ and $\mu_2 = \lambda_2 - \rho\sqrt{\lambda_1\lambda_2}$, where ρ is the correlation coefficient between k_1 and k_2. If the two Poisson-distributed r.v. are independent then $\rho = 0$.

Parameters μ_1 and μ_2 must be strictly positive.

For details see: https://en.wikipedia.org/wiki/Skellam_distribution

skellam takes μ_1 and μ_2 as shape parameters.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `skellam.pmf(k, mu1, mu2, loc)` is identically equivalent to `skellam.pmf(k - loc, mu1, mu2)`.

Examples

```
>>> from scipy.stats import skellam
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> mu1, mu2 = 15, 8
>>> mean, var, skew, kurt = skellam.stats(mu1, mu2, moments='mvsk')
```

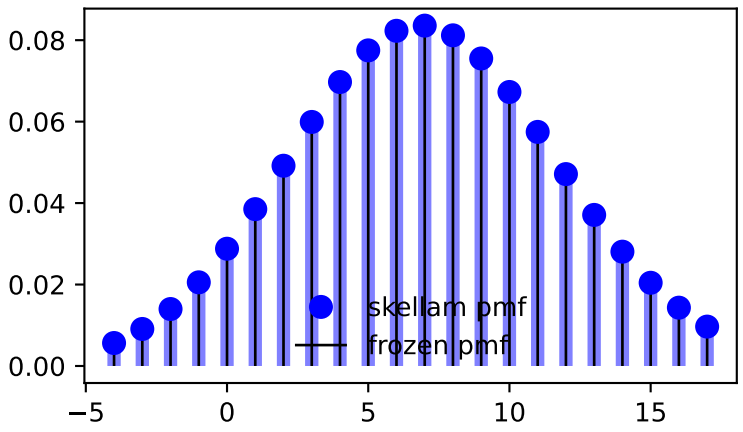
Display the probability mass function (`pmf`):

```
>>> x = np.arange(skellam.ppf(0.01, mu1, mu2),
...               skellam.ppf(0.99, mu1, mu2))
>>> ax.plot(x, skellam.pmf(x, mu1, mu2), 'bo', ms=8, label='skellam pmf')
>>> ax.vlines(x, 0, skellam.pmf(x, mu1, mu2), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = skellam(mu1, mu2)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = skellam.cdf(x, mu1, mu2)
>>> np.allclose(x, skellam.ppf(prob, mu1, mu2))
True
```

Generate random numbers:

```
>>> r = skellam.rvs(mu1, mu2, size=1000)
```

Methods

rvs(mu1, mu2, loc=0, size=1, random_state=None)	Random variates.
pmf(k, mu1, mu2, loc=0)	Probability mass function.
logpmf(k, mu1, mu2, loc=0)	Log of the probability mass function.
cdf(k, mu1, mu2, loc=0)	Cumulative distribution function.
logcdf(k, mu1, mu2, loc=0)	Log of the cumulative distribution function.
sf(k, mu1, mu2, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, mu1, mu2, loc=0)	Log of the survival function.
ppf(q, mu1, mu2, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, mu1, mu2, loc=0)	Inverse survival function (inverse of `sf`).
stats(mu1, mu2, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(mu1, mu2, loc=0)	(Differential) entropy of the RV.
expect(func, args=(mu1, mu2), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(mu1, mu2, loc=0)	Median of the distribution.
mean(mu1, mu2, loc=0)	Mean of the distribution.
var(mu1, mu2, loc=0)	Variance of the distribution.
std(mu1, mu2, loc=0)	Standard deviation of the distribution.
interval(alpha, mu1, mu2, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.yulesimon

scipy.stats.**yulesimon = <scipy.stats._discrete_distns.yulesimon_gen object>**

A Yule-Simon discrete random variable.

As an instance of the *rv_discrete* class, *yulesimon* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

Notes

The probability mass function for the *yulesimon* is:

$$f(k) = \alpha B(k, \alpha + 1)$$

for $k = 1, 2, 3, ...$, where $\alpha > 0$. Here B refers to the *scipy.special.beta* function.

The sampling of random variates is based on pg 553, Section 6.3 of [1]. Our notation maps to the referenced logic via $\alpha = a - 1$.

For details see the wikipedia entry [2].

References

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `yulesimon.pmf(k, alpha, loc)` is identically equivalent to `yulesimon.pmf(k - loc, alpha)`.

[1], [2]

Examples

```
>>> from scipy.stats import yulesimon
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> alpha = 11
>>> mean, var, skew, kurt = yulesimon.stats(alpha, moments='mvsk')
```

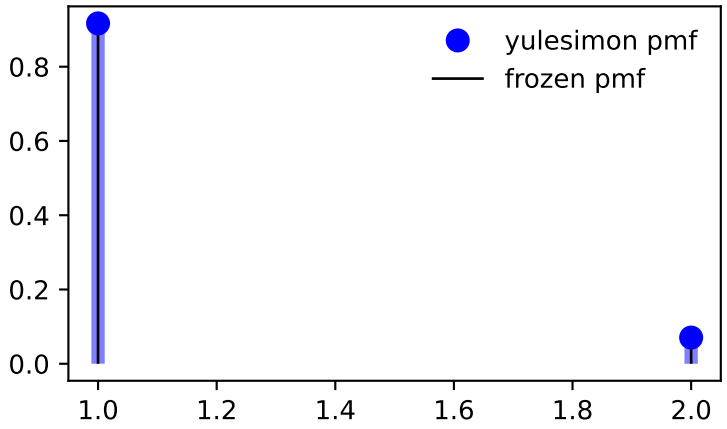
Display the probability mass function (`pmf`):

```
>>> x = np.arange(yulesimon.ppf(0.01, alpha),
...               yulesimon.ppf(0.99, alpha))
>>> ax.plot(x, yulesimon.pmf(x, alpha), 'bo', ms=8, label='yulesimon pmf')
>>> ax.vlines(x, 0, yulesimon.pmf(x, alpha), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = yulesimon(alpha)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = yulesimon.cdf(x, alpha)
>>> np.allclose(x, yulesimon.ppf(prob, alpha))
True
```

Generate random numbers:

```
>>> r = yulesimon.rvs(alpha, size=1000)
```

Methods

rvs(alpha, loc=0, size=1, random_state=None)	Random variates.
pmf(k, alpha, loc=0)	Probability mass function.
logpmf(k, alpha, loc=0)	Log of the probability mass function.
cdf(k, alpha, loc=0)	Cumulative distribution function.
logcdf(k, alpha, loc=0)	Log of the cumulative distribution function.
sf(k, alpha, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, alpha, loc=0)	Log of the survival function.
ppf(q, alpha, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, alpha, loc=0)	Inverse survival function (inverse of `sf`).
stats(alpha, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(alpha, loc=0)	(Differential) entropy of the RV.
expect(func, args=(alpha,), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(alpha, loc=0)	Median of the distribution.
mean(alpha, loc=0)	Mean of the distribution.
var(alpha, loc=0)	Variance of the distribution.
std(alpha, loc=0)	Standard deviation of the distribution.
interval(alpha, alpha, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.zipf

scipy.stats.**zipf = <scipy.stats._discrete_distns.zipf_gen object>**

A Zipf (Zeta) discrete random variable.

As an instance of the *rv_discrete* class, *zipf* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

zipfian

Notes

The probability mass function for *zipf* is:

$$f(k, a) = \frac{1}{\zeta(a) k^a}$$

for $k \geq 1$, $a > 1$.

zipf takes $a > 1$ as shape parameter. ζ is the Riemann zeta function (*scipy.special.zeta*)

The Zipf distribution is also known as the zeta distribution, which is a special case of the Zipfian distribution (*zipfian*).

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `zipf.pmf(k, a, loc)` is identically equivalent to `zipf.pmf(k - loc, a)`.

References

[1]

Examples

```
>>> from scipy.stats import zipf
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a = 6.5
>>> mean, var, skew, kurt = zipf.stats(a, moments='mvsk')
```

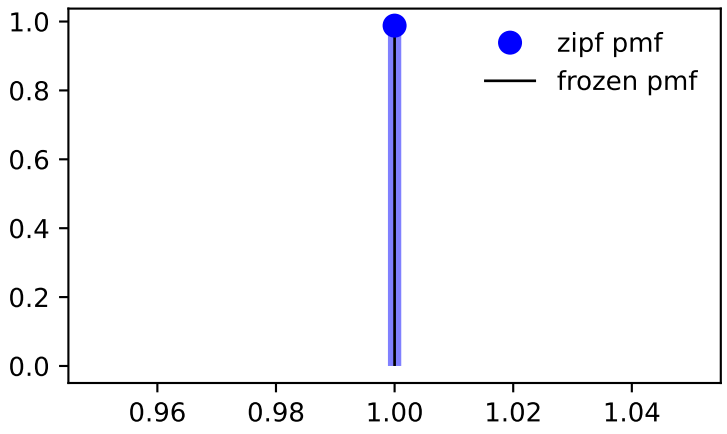
Display the probability mass function (`pmf`):

```
>>> x = np.arange(zipf.ppf(0.01, a),
...               zipf.ppf(0.99, a))
>>> ax.plot(x, zipf.pmf(x, a), 'bo', ms=8, label='zipf pmf')
>>> ax.vlines(x, 0, zipf.pmf(x, a), colors='b', lw=5, alpha=0.5)
```

Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = zipf(a)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...         label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```



Check accuracy of `cdf` and `ppf`:

```
>>> prob = zipf.cdf(x, a)
>>> np.allclose(x, zipf.ppf(prob, a))
True
```

Generate random numbers:

```
>>> r = zipf.rvs(a, size=1000)
```

Confirm that *zipf* is the large *n* limit of *zipfian*.

```
>>> from scipy.stats import zipfian
>>> k = np.arange(11)
>>> np.allclose(zipf.pmf(k, a), zipfian.pmf(k, a, n=10000000))
True
```

Methods

rvs(a, loc=0, size=1, random_state=None)	Random variates.
pmf(k, a, loc=0)	Probability mass function.
logpmf(k, a, loc=0)	Log of the probability mass function.
cdf(k, a, loc=0)	Cumulative distribution function.
logcdf(k, a, loc=0)	Log of the cumulative distribution function.
sf(k, a, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, a, loc=0)	Log of the survival function.
ppf(q, a, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, loc=0)	Inverse survival function (inverse of `sf`).
stats(a, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, loc=0)	(Differential) entropy of the RV.
expect(func, args=(a,), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(a, loc=0)	Median of the distribution.
mean(a, loc=0)	Mean of the distribution.
var(a, loc=0)	Variance of the distribution.
std(a, loc=0)	Standard deviation of the distribution.
interval(alpha, a, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

scipy.stats.zipfian

scipy.stats.**zipfian = <scipy.stats._discrete_distns.zipfian_gen object>**

A Zipfian discrete random variable.

As an instance of the *rv_discrete* class, *zipfian* object inherits from it a collection of generic methods (see below for the full list), and completes them with details specific for this particular distribution.

See also:

zipf

Notes

The probability mass function for *zipfian* is:

$$f(k, a, n) = \frac{1}{H_{n,a} k^a}$$

for $k \in \{1, 2, \ldots, n-1, n\}$, $a \geq 0$, $n \in \{1, 2, 3, \ldots\}$.

zipfian takes a and n as shape parameters. $H_{n,a}$ is the n^{th} generalized harmonic number of order a.

The Zipfian distribution reduces to the Zipf (zeta) distribution as $n \to \infty$.

The probability mass function above is defined in the "standardized" form. To shift distribution use the `loc` parameter. Specifically, `zipfian.pmf(k, a, n, loc)` is identically equivalent to `zipfian.pmf(k - loc, a, n)`.

References

[1], [2]

Examples

```
>>> from scipy.stats import zipfian
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots(1, 1)
```

Calculate the first four moments:

```
>>> a, n = 1.25, 10
>>> mean, var, skew, kurt = zipfian.stats(a, n, moments='mvsk')
```

Display the probability mass function (`pmf`):

```
>>> x = np.arange(zipfian.ppf(0.01, a, n),
...               zipfian.ppf(0.99, a, n))
>>> ax.plot(x, zipfian.pmf(x, a, n), 'bo', ms=8, label='zipfian pmf')
>>> ax.vlines(x, 0, zipfian.pmf(x, a, n), colors='b', lw=5, alpha=0.5)
```

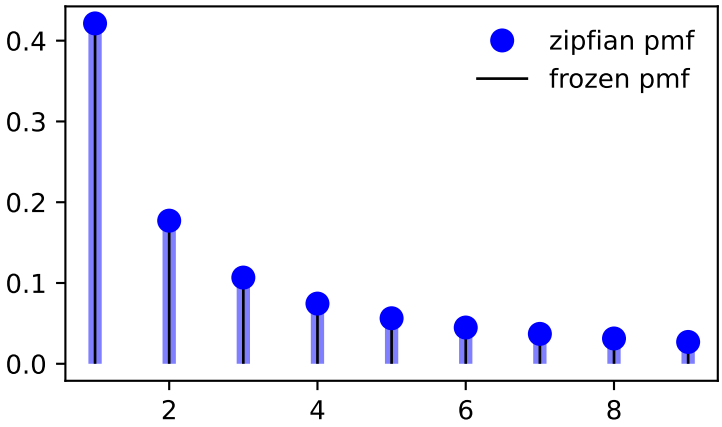
Alternatively, the distribution object can be called (as a function) to fix the shape and location. This returns a "frozen" RV object holding the given parameters fixed.

Freeze the distribution and display the frozen `pmf`:

```
>>> rv = zipfian(a, n)
>>> ax.vlines(x, 0, rv.pmf(x), colors='k', linestyles='-', lw=1,
...           label='frozen pmf')
>>> ax.legend(loc='best', frameon=False)
>>> plt.show()
```

Check accuracy of `cdf` and `ppf`:

```
>>> prob = zipfian.cdf(x, a, n)
>>> np.allclose(x, zipfian.ppf(prob, a, n))
True
```



Generate random numbers:

```
>>> r = zipfian.rvs(a, n, size=1000)
```

Confirm that *zipfian* reduces to *zipf* for large n, $a > 1$.

```
>>> from scipy.stats import zipf
>>> k = np.arange(11)
>>> np.allclose(zipfian.pmf(k, a=3.5, n=10000000), zipf.pmf(k, a=3.5))
True
```

Methods

rvs(a, n, loc=0, size=1, random_state=None)	Random variates.
pmf(k, a, n, loc=0)	Probability mass function.
logpmf(k, a, n, loc=0)	Log of the probability mass function.
cdf(k, a, n, loc=0)	Cumulative distribution function.
logcdf(k, a, n, loc=0)	Log of the cumulative distribution function.
sf(k, a, n, loc=0)	Survival function (also defined as `1 - cdf`, but *sf* is sometimes more accurate).
logsf(k, a, n, loc=0)	Log of the survival function.
ppf(q, a, n, loc=0)	Percent point function (inverse of `cdf` — percentiles).
isf(q, a, n, loc=0)	Inverse survival function (inverse of `sf`).
stats(a, n, loc=0, moments='mv')	Mean('m'), variance('v'), skew('s'), and/or kurtosis('k').
entropy(a, n, loc=0)	(Differential) entropy of the RV.
expect(func, args=(a, n), loc=0, lb=None, ub=None, conditional=False)	Expected value of a function (of one argument) with respect to the distribution.
median(a, n, loc=0)	Median of the distribution.
mean(a, n, loc=0)	Mean of the distribution.
var(a, n, loc=0)	Variance of the distribution.
std(a, n, loc=0)	Standard deviation of the distribution.
interval(alpha, a, n, loc=0)	Endpoints of the range that contains fraction alpha [0, 1] of the distribution

An overview of statistical functions is given below. Many of these functions have a similar version in *scipy.stats.mstats* which work for masked arrays.

Summary statistics

describe(a[, axis, ddof, bias, nan_policy])	Compute several descriptive statistics of the passed array.
gmean(a[, axis, dtype, weights])	Compute the geometric mean along the specified axis.
hmean(a[, axis, dtype])	Calculate the harmonic mean along the specified axis.
kurtosis(a[, axis, fisher, bias, nan_policy])	Compute the kurtosis (Fisher or Pearson) of a dataset.
mode(a[, axis, nan_policy])	Return an array of the modal (most common) value in the passed array.
moment(a[, moment, axis, nan_policy])	Calculate the nth moment about the mean for a sample.
skew(a[, axis, bias, nan_policy])	Compute the sample skewness of a data set.
kstat(data[, n])	Return the nth k-statistic (1<=n<=4 so far).
kstatvar(data[, n])	Return an unbiased estimator of the variance of the k-statistic.
tmean(a[, limits, inclusive, axis])	Compute the trimmed mean.
tvar(a[, limits, inclusive, axis, ddof])	Compute the trimmed variance.
tmin(a[, lowerlimit, axis, inclusive, …])	Compute the trimmed minimum.
tmax(a[, upperlimit, axis, inclusive, …])	Compute the trimmed maximum.
tstd(a[, limits, inclusive, axis, ddof])	Compute the trimmed sample standard deviation.
tsem(a[, limits, inclusive, axis, ddof])	Compute the trimmed standard error of the mean.
variation(a[, axis, nan_policy, ddof])	Compute the coefficient of variation.
find_repeats(arr)	Find repeats and repeat counts.
trim_mean(a, proportiontocut[, axis])	Return mean of array after trimming distribution from both tails.

continues on next page

Table 263 – continued from previous page

gstd(a[, axis, ddof])	Calculate the geometric standard deviation of an array.
iqr(x[, axis, rng, scale, nan_policy, …])	Compute the interquartile range of the data along the specified axis.
sem(a[, axis, ddof, nan_policy])	Compute standard error of the mean.
bayes_mvs(data[, alpha])	Bayesian confidence intervals for the mean, var, and std.
mvsdist(data)	'Frozen' distributions for mean, variance, and standard deviation of data.
entropy(pk[, qk, base, axis])	Calculate the entropy of a distribution for given probability values.
differential_entropy(values, *[, …])	Given a sample of a distribution, estimate the differential entropy.
median_absolute_deviation(*args, **kwds)	*median_absolute_deviation* is deprecated, use *median_abs_deviation* instead!
median_abs_deviation(x[, axis, center, …])	Compute the median absolute deviation of the data along the given axis.
bootstrap(data, statistic, *[, vectorized, …])	Compute a two-sided bootstrap confidence interval of a statistic.

scipy.stats.describe

scipy.stats.**describe**(*a*, *axis=0*, *ddof=1*, *bias=True*, *nan_policy='propagate'*)

Compute several descriptive statistics of the passed array.

Parameters

a [array_like] Input data.

axis [int or None, optional] Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.

ddof [int, optional] Delta degrees of freedom (only for variance). Default is 1.

bias [bool, optional] If False, then the skewness and kurtosis calculations are corrected for statistical bias.

nan_policy

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

nobs [int or ndarray of ints] Number of observations (length of data along *axis*). When 'omit' is chosen as nan_policy, the length along each axis slice is counted separately.

minmax: tuple of ndarrays or floats

Minimum and maximum value of *a* along the given axis.

mean [ndarray or float] Arithmetic mean of *a* along the given axis.

variance [ndarray or float] Unbiased variance of *a* along the given axis; denominator is number of observations minus one.

skewness [ndarray or float] Skewness of *a* along the given axis, based on moment calculations with denominator equal to the number of observations, i.e. no degrees of freedom correction.

kurtosis [ndarray or float] Kurtosis (Fisher) of *a* along the given axis. The kurtosis is normalized so that it is zero for the normal distribution. No degrees of freedom are used.

See also:

skew, **kurtosis**

Examples

```
>>> from scipy import stats
>>> a = np.arange(10)
>>> stats.describe(a)
DescribeResult(nobs=10, minmax=(0, 9), mean=4.5,
               variance=9.166666666666666, skewness=0.0,
               kurtosis=-1.2424242424242244)
>>> b = [[1, 2], [3, 4]]
>>> stats.describe(b)
DescribeResult(nobs=2, minmax=(array([1, 2]), array([3, 4])),
               mean=array([2., 3.]), variance=array([2., 2.]),
               skewness=array([0., 0.]), kurtosis=array([-2., -2.]))
```

scipy.stats.gmean

scipy.stats.**gmean**(*a*, *axis=0*, *dtype=None*, *weights=None*)

Compute the geometric mean along the specified axis.

Return the geometric average of the array elements. That is: n-th root of (x1 * x2 * … * xn)

Parameters

a	[array_like] Input array or object that can be converted to an array.
axis	[int or None, optional] Axis along which the geometric mean is computed. Default is 0. If None, compute over the whole array *a*.
dtype	[dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If dtype is not specified, it defaults to the dtype of a, unless a has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.
weights	[array_like, optional] The weights array can either be 1-D (in which case its length must be the size of *a* along the given *axis*) or of the same shape as *a*. Default is None, which gives each value a weight of 1.0.

Returns

gmean	[ndarray] See *dtype* parameter above.

See also:

numpy.mean

Arithmetic average

numpy.average

Weighted average

hmean

Harmonic mean

Notes

The geometric average is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity because masked arrays automatically mask any non-finite values.

References

[1]

Examples

```
>>> from scipy.stats import gmean
>>> gmean([1, 4])
2.0
>>> gmean([1, 2, 3, 4, 5, 6, 7])
3.3800151591412964
```

scipy.stats.hmean

scipy.stats.**hmean**(*a*, *axis=0*, *dtype=None*)

Calculate the harmonic mean along the specified axis.

That is: n / (1/x1 + 1/x2 + … + 1/xn)

Parameters

a	[array_like] Input array, masked array or object that can be converted to an array.
axis	[int or None, optional] Axis along which the harmonic mean is computed. Default is 0. If None, compute over the whole array *a*.
dtype	[dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer *dtype* with a precision less than that of the default platform integer. In that case, the default platform integer is used.

Returns

hmean	[ndarray] See *dtype* parameter above.

See also:

numpy.mean

Arithmetic average

numpy.average

Weighted average

gmean

Geometric mean

Notes

The harmonic mean is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity.

Examples

```
>>> from scipy.stats import hmean
>>> hmean([1, 4])
1.6000000000000001
>>> hmean([1, 2, 3, 4, 5, 6, 7])
2.6997245179063363
```

scipy.stats.kurtosis

scipy.stats.**kurtosis**(*a*, *axis=0*, *fisher=True*, *bias=True*, *nan_policy='propagate'*)

Compute the kurtosis (Fisher or Pearson) of a dataset.

Kurtosis is the fourth central moment divided by the square of the variance. If Fisher's definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.

If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators

Use *kurtosistest* to see if result is close enough to normal.

Parameters

a [array] Data for which the kurtosis is calculated.

axis [int or None, optional] Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array *a*.

fisher [bool, optional] If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

bias [bool, optional] If False, then the calculations are corrected for statistical bias.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

kurtosis [array] The kurtosis of values along an axis. If all values are equal, return -3 for Fisher's definition and 0 for Pearson's definition.

References

[1]

Examples

In Fisher's definiton, the kurtosis of the normal distribution is zero. In the following example, the kurtosis is close to zero, because it was calculated from the dataset, not from the continuous distribution.

```
>>> from scipy.stats import norm, kurtosis
>>> data = norm.rvs(size=1000, random_state=3)
>>> kurtosis(data)
-0.06928694200380558
```

The distribution with a higher kurtosis has a heavier tail. The zero valued kurtosis of the normal distribution in Fisher's definition can serve as a reference point.

```
>>> import matplotlib.pyplot as plt
>>> import scipy.stats as stats
>>> from scipy.stats import kurtosis
```

```
>>> x = np.linspace(-5, 5, 100)
>>> ax = plt.subplot()
>>> distnames = ['laplace', 'norm', 'uniform']
```

```
>>> for distname in distnames:
...     if distname == 'uniform':
...         dist = getattr(stats, distname)(loc=-2, scale=4)
...     else:
...         dist = getattr(stats, distname)
...     data = dist.rvs(size=1000)
...     kur = kurtosis(data, fisher=True)
...     y = dist.pdf(x)
...     ax.plot(x, y, label="{}, {}".format(distname, round(kur, 3)))
...     ax.legend()
```

The Laplace distribution has a heavier tail than the normal distribution. The uniform distribution (which has negative kurtosis) has the thinnest tail.

scipy.stats.mode

scipy.stats.**mode**(*a*, *axis=0*, *nan_policy='propagate'*)

Return an array of the modal (most common) value in the passed array.

If there is more than one such value, only the smallest is returned. The bin-count for the modal bins is also returned.

Parameters

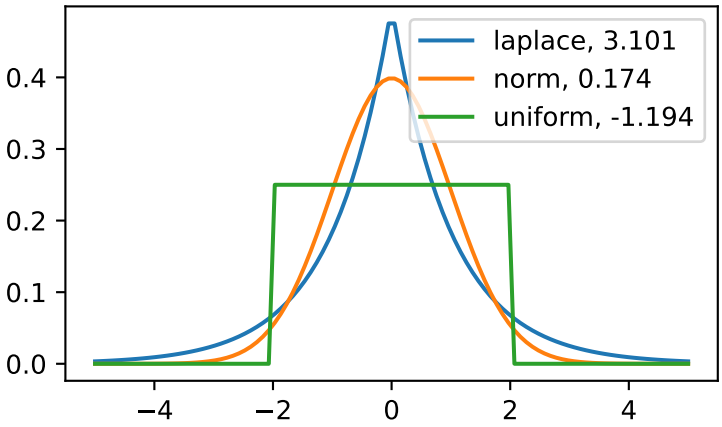
a [array_like] n-dimensional array of which to find mode(s).

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

nan_policy

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan



- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

mode	[ndarray] Array of modal values.
count	[ndarray] Array of counts for each mode.

Examples

```
>>> a = np.array([[6, 8, 3, 0],
...               [3, 2, 1, 7],
...               [8, 1, 8, 4],
...               [5, 3, 0, 5],
...               [4, 7, 5, 9]])
>>> from scipy import stats
>>> stats.mode(a)
ModeResult(mode=array([[3, 1, 0, 0]]), count=array([[1, 1, 1, 1]]))
```

To get mode of whole array, specify `axis=None`:

```
>>> stats.mode(a, axis=None)
ModeResult(mode=array([3]), count=array([3]))
```

scipy.stats.moment

`scipy.stats.`**`moment`**(*a*, *moment=1*, *axis=0*, *nan_policy='propagate'*)

Calculate the nth moment about the mean for a sample.

A moment is a specific quantitative measure of the shape of a set of points. It is often used to calculate coefficients of skewness and kurtosis due to its close relationship with them.

Parameters

a	[array_like] Input array.
moment	[int or array_like of ints, optional] Order of central moment that is returned. Default is 1.

axis [int or None, optional] Axis along which the central moment is computed. Default is 0. If None, compute over the whole array a.

nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):
- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

n-th central moment
[ndarray or float] The appropriate moment along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

See also:

kurtosis, **skew**, **describe**

Notes

The k-th central moment of a data sample is:

$$m_k = \frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^k$$

Where n is the number of samples and x-bar is the mean. This function uses exponentiation by squares [1] for efficiency.

References

[1]

Examples

```
>>> from scipy.stats import moment
>>> moment([1, 2, 3, 4, 5], moment=1)
0.0
>>> moment([1, 2, 3, 4, 5], moment=2)
2.0
```

scipy.stats.skew

scipy.stats.**skew**(*a*, *axis=0*, *bias=True*, *nan_policy='propagate'*)
Compute the sample skewness of a data set.

For normally distributed data, the skewness should be about zero. For unimodal continuous distributions, a skewness value greater than zero means that there is more weight in the right tail of the distribution. The function *skewtest* can be used to determine if the skewness value is close enough to zero, statistically speaking.

Parameters

a [ndarray] Input array.

axis [int or None, optional] Axis along which skewness is calculated. Default is 0. If None, compute over the whole array a.

bias [bool, optional] If False, then the calculations are corrected for statistical bias.

nan_policy

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

skewness [ndarray] The skewness of values along an axis, returning 0 where all values are equal.

Notes

The sample skewness is computed as the Fisher-Pearson coefficient of skewness, i.e.

$$g_1 = \frac{m_3}{m_2^{3/2}}$$

where

$$m_i = \frac{1}{N}\sum_{n=1}^{N}(x[n] - \bar{x})^i$$

is the biased sample ith central moment, and $\bar{x}$ is the sample mean. If `bias` is False, the calculations are corrected for bias and the value computed is the adjusted Fisher-Pearson standardized moment coefficient, i.e.

$$G_1 = \frac{k_3}{k_2^{3/2}} = \frac{\sqrt{N(N-1)}}{N-2}\frac{m_3}{m_2^{3/2}}.$$

References

[1]

Examples

```
>>> from scipy.stats import skew
>>> skew([1, 2, 3, 4, 5])
0.0
>>> skew([2, 8, 0, 4, 1, 9, 9, 0])
0.2650554122698573
```

scipy.stats.kstat

`scipy.stats.`**`kstat`**(*data*, *n=2*)

Return the nth k-statistic (1<=n<=4 so far).

The nth k-statistic k_n is the unique symmetric unbiased estimator of the nth cumulant kappa_n.

Parameters

data [array_like] Input array. Note that n-D input gets flattened.

n [int, {1, 2, 3, 4}, optional] Default is equal to 2.

Returns

kstat [float] The nth k-statistic.

See also:

kstatvar

Returns an unbiased estimator of the variance of the k-statistic.

moment

Returns the n-th central moment about the mean for a sample.

Notes

For a sample size n, the first few k-statistics are given by:

$$k_1 = \mu k_2 = \frac{n}{n-1} m_2 k_3 = \frac{n^2}{(n-1)(n-2)} m_3 k_4 = \frac{n^2[(n+1)m_4 - 3(n-1)m_2^2]}{(n-1)(n-2)(n-3)}$$

where μ is the sample mean, m_2 is the sample variance, and m_i is the i-th sample central moment.

References

http://mathworld.wolfram.com/k-Statistic.html

http://mathworld.wolfram.com/Cumulant.html

Examples

```
>>> from scipy import stats
>>> from numpy.random import default_rng
>>> rng = default_rng()
```

As sample size increases, n-th moment and n-th k-statistic converge to the same number (although they aren't identical). In the case of the normal distribution, they converge to zero.

```
>>> for n in [2, 3, 4, 5, 6, 7]:
...     x = rng.normal(size=10**n)
...     m, k = stats.moment(x, 3), stats.kstat(x, 3)
...     print("%.3g %.3g %.3g" % (m, k, m-k))
-0.631 -0.651 0.0194  # random
0.0282 0.0283 -8.49e-05
-0.0454 -0.0454 1.36e-05
7.53e-05 7.53e-05 -2.26e-09
0.00166 0.00166 -4.99e-09
-2.88e-06 -2.88e-06 8.63e-13
```

scipy.stats.kstatvar

scipy.stats.**kstatvar**(*data*, *n=2*)

Return an unbiased estimator of the variance of the k-statistic.

See *kstat* for more details of the k-statistic.

Parameters

data	[array_like] Input array. Note that n-D input gets flattened.
n	[int, {1, 2}, optional] Default is equal to 2.

Returns

kstatvar	[float] The nth k-statistic variance.

See also:

kstat

Returns the n-th k-statistic.

moment

Returns the n-th central moment about the mean for a sample.

Notes

The variances of the first few k-statistics are given by:

$$var(k_1) = \frac{\kappa^2}{n} var(k_2) = \frac{\kappa^4}{n} + \frac{2\kappa_2^2}{n-1} var(k_3) = \frac{\kappa^6}{n} + \frac{9\kappa_2\kappa_4}{n-1} + \frac{9\kappa_3^2}{n-1} + \frac{6n\kappa_2^3}{(n-1)(n-2)} var(k_4) = \frac{\kappa^8}{n} + \frac{16\kappa_2\kappa_6}{n-1} + \frac{48\kappa_3\kappa_5}{n-1}$$

scipy.stats.tmean

scipy.stats.**tmean**(*a*, *limits=None*, *inclusive=(True, True)*, *axis=None*)

Compute the trimmed mean.

This function finds the arithmetic mean of given values, ignoring values outside the given *limits*.

Parameters

a	[array_like] Array of values.
limits	[None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None (default), then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval.
inclusive	[(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
axis	[int or None, optional] Axis along which to compute test. Default is None.

Returns

tmean	[float] Trimmed mean.

See also:

trim_mean

Returns mean after trimming a proportion from both tails.

Examples

```
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tmean(x)
9.5
>>> stats.tmean(x, (3,17))
10.0
```

scipy.stats.tvar

scipy.stats.**tvar**(*a*, *limits=None*, *inclusive=(True, True)*, *axis=0*, *ddof=1*)

Compute the trimmed variance.

This function computes the sample variance of an array of values, while ignoring values which are outside of given *limits*.

Parameters

a	[array_like] Array of values.
limits	[None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.
inclusive	[(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
axis	[int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.
ddof	[int, optional] Delta degrees of freedom. Default is 1.

Returns

tvar	[float] Trimmed variance.

Notes

tvar computes the unbiased sample variance, i.e. it uses a correction factor `n / (n - 1)`.

Examples

```
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tvar(x)
35.0
>>> stats.tvar(x, (3,17))
20.0
```

scipy.stats.tmin

scipy.stats.**tmin**(*a*, *lowerlimit=None*, *axis=0*, *inclusive=True*, *nan_policy='propagate'*)

Compute the trimmed minimum.

This function finds the miminum value of an array *a* along the specified axis, but only considering values greater than a specified lower limit.

Parameters

a [array_like] Array of values.

lowerlimit [None or float, optional] Values in the input array less than the given limit will be ignored. When lowerlimit is None, then all values are used. The default value is None.

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive [{True, False}, optional] This flag determines whether values exactly equal to the lower limit are included. The default value is True.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

tmin [float, int or ndarray] Trimmed minimum.

Examples

```
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tmin(x)
0
```

```
>>> stats.tmin(x, 13)
13
```

```
>>> stats.tmin(x, 13, inclusive=False)
14
```

scipy.stats.tmax

scipy.stats.**tmax**(*a*, *upperlimit=None*, *axis=0*, *inclusive=True*, *nan_policy='propagate'*)

Compute the trimmed maximum.

This function computes the maximum value of an array along a given axis, while ignoring values larger than a specified upper limit.

Parameters

a [array_like] Array of values.

upperlimit [None or float, optional] Values in the input array greater than the given limit will be ignored. When upperlimit is None, then all values are used. The default value is None.

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive [{True, False}, optional] This flag determines whether values exactly equal to the upper limit are included. The default value is True.

nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):
- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

tmax [float, int or ndarray] Trimmed maximum.

Examples

```
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tmax(x)
19
```

```
>>> stats.tmax(x, 13)
13
```

```
>>> stats.tmax(x, 13, inclusive=False)
12
```

scipy.stats.tstd

scipy.stats.**tstd**(*a*, *limits=None*, *inclusive=(True, True)*, *axis=0*, *ddof=1*)

Compute the trimmed sample standard deviation.

This function finds the sample standard deviation of given values, ignoring values outside the given *limits*.

Parameters

a [array_like] Array of values.

limits [None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive [(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof [int, optional] Delta degrees of freedom. Default is 1.

Returns

tstd [float] Trimmed sample standard deviation.

Notes

tstd computes the unbiased sample standard deviation, i.e. it uses a correction factor `n / (n - 1)`.

Examples

```
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tstd(x)
5.9160797830996161
>>> stats.tstd(x, (3,17))
4.4721359549995796
```

scipy.stats.tsem

scipy.stats.**tsem**(*a*, *limits=None*, *inclusive=(True, True)*, *axis=0*, *ddof=1*)

Compute the trimmed standard error of the mean.

This function finds the standard error of the mean for given values, ignoring values outside the given *limits*.

Parameters

a [array_like] Array of values.

limits [None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.

inclusive [(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof [int, optional] Delta degrees of freedom. Default is 1.

Returns

tsem [float] Trimmed standard error of the mean.

Notes

tsem uses unbiased sample standard deviation, i.e. it uses a correction factor `n / (n - 1)`.

Examples

```
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.tsem(x)
1.3228756555322954
>>> stats.tsem(x, (3,17))
1.1547005383792515
```

scipy.stats.variation

scipy.stats.**variation**(*a*, *axis=0*, *nan_policy='propagate'*, *ddof=0*)

Compute the coefficient of variation.

The coefficient of variation is the standard deviation divided by the mean. This function is equivalent to:

```
np.std(x, axis=axis, ddof=ddof) / np.mean(x)
```

The default for `ddof` is 0, but many definitions of the coefficient of variation use the square root of the unbiased sample variance for the sample standard deviation, which corresponds to `ddof=1`.

Parameters

a [array_like] Input array.

axis [int or None, optional] Axis along which to calculate the coefficient of variation. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

ddof [int, optional] Delta degrees of freedom. Default is 0.

Returns

variation [ndarray] The calculated variation along the requested axis.

References

[1]

Examples

```
>>> from scipy.stats import variation
>>> variation([1, 2, 3, 4, 5])
0.47140452079103173
```

scipy.stats.find_repeats

scipy.stats.**find_repeats**(*arr*)

Find repeats and repeat counts.

Parameters

arr [array_like] Input array. This is cast to float64.

Returns

values [ndarray] The unique values from the (flattened) input that are repeated.

counts [ndarray] Number of times the corresponding 'value' is repeated.

Notes

In numpy >= 1.9 `numpy.unique` provides similar functionality. The main difference is that *`find_repeats`* only returns repeated values.

Examples

```
>>> from scipy import stats
>>> stats.find_repeats([2, 1, 2, 3, 2, 2, 5])
RepeatedResults(values=array([2.]), counts=array([4]))
```

```
>>> stats.find_repeats([[10, 20, 1, 2], [5, 5, 4, 4]])
RepeatedResults(values=array([4.,  5.]), counts=array([2, 2]))
```

scipy.stats.trim_mean

`scipy.stats.`**`trim_mean`**(*a*, *proportiontocut*, *axis=0*)

Return mean of array after trimming distribution from both tails.

If *proportiontocut* = 0.1, slices off 'leftmost' and 'rightmost' 10% of scores. The input is sorted before slicing. Slices off less if proportion results in a non-integer slice index (i.e., conservatively slices off *proportiontocut*).

Parameters

a [array_like] Input array.

proportiontocut [float] Fraction to cut off of both tails of the distribution.

axis [int or None, optional] Axis along which the trimmed means are computed. Default is 0. If None, compute over the whole array *a*.

Returns

trim_mean [ndarray] Mean of trimmed array.

See also:

`trimboth`

`tmean`

Compute the trimmed mean ignoring values outside given *limits*.

Examples

```
>>> from scipy import stats
>>> x = np.arange(20)
>>> stats.trim_mean(x, 0.1)
9.5
>>> x2 = x.reshape(5, 4)
>>> x2
array([[ 0,  1,  2,  3],
       [ 4,  5,  6,  7],
       [ 8,  9, 10, 11],
       [12, 13, 14, 15],
```

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```
       [16, 17, 18, 19]])
>>> stats.trim_mean(x2, 0.25)
array([  8.,   9.,  10.,  11.])
>>> stats.trim_mean(x2, 0.25, axis=1)
array([  1.5,   5.5,   9.5,  13.5,  17.5])
```

scipy.stats.gstd

scipy.stats.**gstd**(*a*, *axis=0*, *ddof=1*)

Calculate the geometric standard deviation of an array.

The geometric standard deviation describes the spread of a set of numbers where the geometric mean is preferred. It is a multiplicative factor, and so a dimensionless quantity.

It is defined as the exponent of the standard deviation of `log(a)`. Mathematically the population geometric standard deviation can be evaluated as:

```
gstd = exp(std(log(a)))
```

New in version 1.3.0.

Parameters

a [array_like] An array like object containing the sample data.

axis [int, tuple or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof [int, optional] Degree of freedom correction in the calculation of the geometric standard deviation. Default is 1.

Returns

ndarray or float
An array of the geometric standard deviation. If *axis* is None or *a* is a 1d array a float is returned.

Notes

As the calculation requires the use of logarithms the geometric standard deviation only supports strictly positive values. Any non-positive or infinite values will raise a *ValueError*. The geometric standard deviation is sometimes confused with the exponent of the standard deviation, `exp(std(a))`. Instead the geometric standard deviation is `exp(std(log(a)))`. The default value for *ddof* is different to the default value (0) used by other ddof containing functions, such as `np.std` and `np.nanstd`.

Examples

Find the geometric standard deviation of a log-normally distributed sample. Note that the standard deviation of the distribution is one, on a log scale this evaluates to approximately `exp(1)`.

```
>>> from scipy.stats import gstd
>>> rng = np.random.default_rng()
>>> sample = rng.lognormal(mean=0, sigma=1, size=1000)
>>> gstd(sample)
2.810010162475324
```

Compute the geometric standard deviation of a multidimensional array and of a given axis.

```
>>> a = np.arange(1, 25).reshape(2, 3, 4)
>>> gstd(a, axis=None)
2.2944076136018947
>>> gstd(a, axis=2)
array([[1.82424757, 1.22436866, 1.13183117],
       [1.09348306, 1.07244798, 1.05914985]])
>>> gstd(a, axis=(1,2))
array([2.12939215, 1.22120169])
```

The geometric standard deviation further handles masked arrays.

```
>>> a = np.arange(1, 25).reshape(2, 3, 4)
>>> ma = np.ma.masked_where(a > 16, a)
>>> ma
masked_array(
  data=[[[1, 2, 3, 4],
         [5, 6, 7, 8],
         [9, 10, 11, 12]],
        [[13, 14, 15, 16],
         [--, --, --, --],
         [--, --, --, --]]],
  mask=[[[False, False, False, False],
         [False, False, False, False],
         [False, False, False, False]],
        [[False, False, False, False],
         [ True,  True,  True,  True],
         [ True,  True,  True,  True]]],
  fill_value=999999)
>>> gstd(ma, axis=2)
masked_array(
  data=[[1.8242475707663655, 1.2243686572447428, 1.1318311657788478],
        [1.0934830582350938, --, --]],
  mask=[[False, False, False],
        [False,  True,  True]],
  fill_value=999999)
```

scipy.stats.iqr

scipy.stats.**iqr**(*x*, *axis=None*, *rng=(25, 75)*, *scale=1.0*, *nan_policy='propagate'*, *interpolation='linear'*, *keepdims=False*)

Compute the interquartile range of the data along the specified axis.

The interquartile range (IQR) is the difference between the 75th and 25th percentile of the data. It is a measure of the dispersion similar to standard deviation or variance, but is much more robust against outliers [2].

The `rng` parameter allows this function to compute other percentile ranges than the actual IQR. For example, setting `rng=(0, 100)` is equivalent to `numpy.ptp`.

The IQR of an empty array is *np.nan*.

New in version 0.18.0.

Parameters

x [array_like] Input array or object that can be converted to an array.

axis [int or sequence of int, optional] Axis along which the range is computed. The default is to compute the IQR for the entire array.

rng [Two-element sequence containing floats in range of [0,100] optional] Percentiles over which to compute the range. Each must be between 0 and 100, inclusive. The default is the true IQR: *(25, 75)*. The order of the elements is not important.

scale [scalar or str, optional] The numerical value of scale will be divided out of the final result. The following string values are recognized:
- 'raw' : No scaling, just return the raw IQR. **Deprecated!** Use *scale=1* instead.
- 'normal' : Scale by $2\sqrt{2}erf^{-1}(\frac{1}{2}) \approx 1.349$.

The default is 1.0. The use of scale='raw' is deprecated. Array-like scale is also allowed, as long as it broadcasts correctly to the output such that `out / scale` is a valid operation. The output dimensions depend on the input array, *x*, the *axis* argument, and the *keepdims* flag.

nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):
- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

interpolation
[{'linear', 'lower', 'higher', 'midpoint',]
'nearest'}, optional
Specifies the interpolation method to use when the percentile boundaries lie between two data points *i* and *j*. The following options are available (default is 'linear'):
- 'linear': *i + (j - i) * fraction*, where *fraction* is the fractional part of the index surrounded by *i* and *j*.
- 'lower': *i*.
- 'higher': *j*.
- 'nearest': *i* or *j* whichever is nearest.
- 'midpoint': *(i + j) / 2*.

keepdims [bool, optional] If this is set to *True*, the reduced axes are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original array *x*.

Returns

iqr [scalar or ndarray] If `axis=None`, a scalar is returned. If the input contains integers or floats of smaller precision than `np.float64`, then the output data-type is `np.float64`. Otherwise, the output data-type is the same as that of the input.

See also:

numpy.std*, *numpy.var

Notes

This function is heavily dependent on the version of `numpy` that is installed. Versions greater than 1.11.0b3 are highly recommended, as they include a number of enhancements and fixes to `numpy.percentile` and `numpy.nanpercentile` that affect the operation of this function. The following modifications apply:

Below 1.10.0

[*nan_policy* is poorly defined.] The default behavior of `numpy.percentile` is used for 'propagate'. This is a hybrid of 'omit' and 'propagate' that mostly yields a skewed version of 'omit' since NaNs are sorted to the end of the data. A warning is raised if there are NaNs in the data.

Below 1.9.0: `numpy.nanpercentile` does not exist.

This means that `numpy.percentile` is used regardless of *nan_policy* and a warning is issued. See previous item for a description of the behavior.

Below 1.9.0: **keepdims** ***and*** **interpolation** ***are not supported.***

The keywords get ignored with a warning if supplied with non-default values. However, multiple axes are still supported.

References

[1], [2], [3]

Examples

```
>>> from scipy.stats import iqr
>>> x = np.array([[10, 7, 4], [3, 2, 1]])
>>> x
array([[10,  7,  4],
       [ 3,  2,  1]])
>>> iqr(x)
4.0
>>> iqr(x, axis=0)
array([ 3.5,  2.5,  1.5])
>>> iqr(x, axis=1)
array([ 3.,  1.])
>>> iqr(x, axis=1, keepdims=True)
array([[ 3.],
       [ 1.]])
```

scipy.stats.sem

`scipy.stats.`**`sem`**(*a*, *axis=0*, *ddof=1*, *nan_policy='propagate'*)

Compute standard error of the mean.

Calculate the standard error of the mean (or standard error of measurement) of the values in the input array.

Parameters

a [array_like] An array containing the values for which the standard error is returned.

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof [int, optional] Delta degrees-of-freedom. How many degrees of freedom to adjust for bias in limited samples relative to the population estimate of variance. Defaults to 1.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

s [ndarray or float] The standard error of the mean in the sample(s), along the input axis.

Notes

The default value for *ddof* is different to the default (0) used by other ddof containing routines, such as np.std and np.nanstd.

Examples

Find standard error along the first axis:

```
>>> from scipy import stats
>>> a = np.arange(20).reshape(5,4)
>>> stats.sem(a)
array([ 2.8284,  2.8284,  2.8284,  2.8284])
```

Find standard error across the whole array, using n degrees of freedom:

```
>>> stats.sem(a, axis=None, ddof=0)
1.2893796958227628
```

scipy.stats.bayes_mvs

scipy.stats.**bayes_mvs**(*data*, *alpha=0.9*)

Bayesian confidence intervals for the mean, var, and std.

Parameters

data [array_like] Input data, if multi-dimensional it is flattened to 1-D by *bayes_mvs*. Requires 2 or more data points.

alpha [float, optional] Probability that the returned confidence interval contains the true parameter.

Returns

mean_cntr, var_cntr, std_cntr

[tuple] The three results are for the mean, variance and standard deviation, respectively. Each result is a tuple of the form:

```
(center, (lower, upper))
```

with *center* the mean of the conditional pdf of the value given the data, and *(lower, upper)* a confidence interval, centered on the median, containing the estimate to a probability `alpha`.

See also:

mvsdist

Notes

Each tuple of mean, variance, and standard deviation estimates represent the (center, (lower, upper)) with center the mean of the conditional pdf of the value given the data and (lower, upper) is a confidence interval centered on the median, containing the estimate to a probability `alpha`.

Converts data to 1-D and assumes all data has the same mean and variance. Uses Jeffrey's prior for variance and std.

Equivalent to `tuple((x.mean(), x.interval(alpha)) for x in mvsdist(dat))`

References

T.E. Oliphant, "A Bayesian perspective on estimating mean, variance, and standard-deviation from data", https://scholarsarchive.byu.edu/facpub/278, 2006.

Examples

First a basic example to demonstrate the outputs:

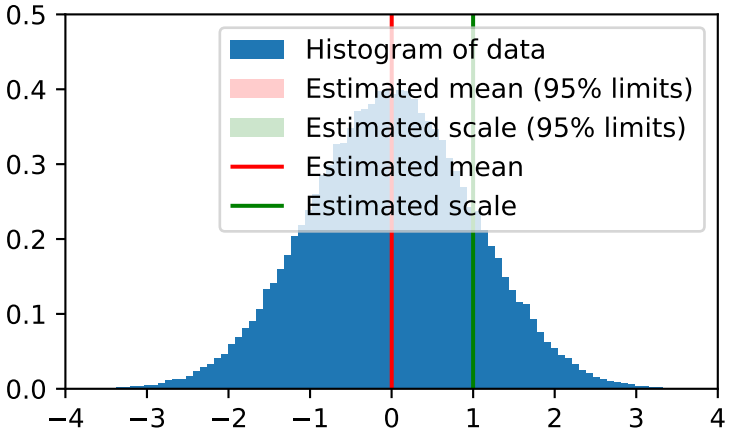
```
>>> from scipy import stats
>>> data = [6, 9, 12, 7, 8, 8, 13]
>>> mean, var, std = stats.bayes_mvs(data)
>>> mean
Mean(statistic=9.0, minmax=(7.103650222612533, 10.896349777387467))
>>> var
Variance(statistic=10.0, minmax=(3.176724206..., 24.45910382...))
>>> std
Std_dev(statistic=2.9724954732045084, minmax=(1.7823367265645143, 4.
↪945614605014631))
```

Now we generate some normally distributed random data, and get estimates of mean and standard deviation with 95% confidence intervals for those estimates:

```
>>> n_samples = 100000
>>> data = stats.norm.rvs(size=n_samples)
>>> res_mean, res_var, res_std = stats.bayes_mvs(data, alpha=0.95)
```

```
>>> import matplotlib.pyplot as plt
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.hist(data, bins=100, density=True, label='Histogram of data')
>>> ax.vlines(res_mean.statistic, 0, 0.5, colors='r', label='Estimated␣
↪mean')
>>> ax.axvspan(res_mean.minmax[0],res_mean.minmax[1], facecolor='r',
...            alpha=0.2, label=r'Estimated mean (95% limits)')
>>> ax.vlines(res_std.statistic, 0, 0.5, colors='g', label='Estimated␣
↪scale')
>>> ax.axvspan(res_std.minmax[0],res_std.minmax[1], facecolor='g',␣
↪alpha=0.2,
...            label=r'Estimated scale (95% limits)')
```

```
>>> ax.legend(fontsize=10)
>>> ax.set_xlim([-4, 4])
>>> ax.set_ylim([0, 0.5])
>>> plt.show()
```



scipy.stats.mvsdist

`scipy.stats.`**`mvsdist`**(*data*)

'Frozen' distributions for mean, variance, and standard deviation of data.

Parameters

data [array_like] Input array. Converted to 1-D using ravel. Requires 2 or more data-points.

Returns

mdist ["frozen" distribution object] Distribution object representing the mean of the data.
vdist ["frozen" distribution object] Distribution object representing the variance of the data.
sdist ["frozen" distribution object] Distribution object representing the standard deviation of the data.

See also:

`bayes_mvs`

Notes

The return values from `bayes_mvs(data)` is equivalent to `tuple((x.mean(), x.interval(0.90)) for x in mvsdist(data))`.

In other words, calling `<dist>.mean()` and `<dist>.interval(0.90)` on the three distribution objects returned from this function will give the same results that are returned from *bayes_mvs*.

References

T.E. Oliphant, "A Bayesian perspective on estimating mean, variance, and standard-deviation from data", https://scholarsarchive.byu.edu/facpub/278, 2006.

Examples

```
>>> from scipy import stats
>>> data = [6, 9, 12, 7, 8, 8, 13]
>>> mean, var, std = stats.mvsdist(data)
```

We now have frozen distribution objects "mean", "var" and "std" that we can examine:

```
>>> mean.mean()
9.0
>>> mean.interval(0.95)
(6.6120585482655692, 11.387941451734431)
>>> mean.std()
1.1952286093343936
```

scipy.stats.entropy

scipy.stats.**entropy**(*pk*, *qk=None*, *base=None*, *axis=0*)

Calculate the entropy of a distribution for given probability values.

If only probabilities *pk* are given, the entropy is calculated as `S = -sum(pk * log(pk), axis=axis)`.

If *qk* is not None, then compute the Kullback-Leibler divergence `S = sum(pk * log(pk / qk), axis=axis)`.

This routine will normalize *pk* and *qk* if they don't sum to 1.

Parameters

pk [sequence] Defines the (discrete) distribution. `pk[i]` is the (possibly unnormalized) probability of event `i`.

qk [sequence, optional] Sequence against which the relative entropy is computed. Should be in the same format as *pk*.

base [float, optional] The logarithmic base to use, defaults to `e` (natural logarithm).

axis: int, optional
The axis along which the entropy is calculated. Default is 0.

Returns

S [float] The calculated entropy.

Examples

```
>>> from scipy.stats import entropy
```

Bernoulli trial with different p. The outcome of a fair coin is the most uncertain:

```
>>> entropy([1/2, 1/2], base=2)
1.0
```

The outcome of a biased coin is less uncertain:

```
>>> entropy([9/10, 1/10], base=2)
0.46899559358928117
```

Relative entropy:

```
>>> entropy([1/2, 1/2], qk=[9/10, 1/10])
0.5108256237659907
```

scipy.stats.differential_entropy

scipy.stats.**differential_entropy**(*values*, *, *window_length=None*, *base=None*, *axis=0*, *method='auto'*)

Given a sample of a distribution, estimate the differential entropy.

Several estimation methods are available using the *method* parameter. By default, a method is selected based the size of the sample.

Parameters

values [sequence] Sample from a continuous distribution.

window_length [int, optional] Window length for computing Vasicek estimate. Must be an integer between 1 and half of the sample size. If `None` (the default), it uses the heuristic value

$$\lfloor \sqrt{n} + 0.5 \rfloor$$

where n is the sample size. This heuristic was originally proposed in [2] and has become common in the literature.

base [float, optional] The logarithmic base to use, defaults to `e` (natural logarithm).

axis [int, optional] The axis along which the differential entropy is calculated. Default is 0.

method [{'vasicek', 'van es', 'ebrahimi', 'correa', 'auto'}, optional] The method used to estimate the differential entropy from the sample. Default is `'auto'`. See Notes for more information.

Returns

entropy [float] The calculated differential entropy.

Notes

This function will converge to the true differential entropy in the limit

$$n \to \infty, \quad m \to \infty, \quad \frac{m}{n} \to 0$$

The optimal choice of `window_length` for a given sample size depends on the (unknown) distribution. Typically, the smoother the density of the distribution, the larger the optimal value of `window_length` [1].

The following options are available for the *method* parameter.

- `'vasicek'` uses the estimator presented in [1]. This is one of the first and most influential estimators of differential entropy.
- `'van es'` uses the bias-corrected estimator presented in [3], which is not only consistent but, under some conditions, asymptotically normal.
- `'ebrahimi'` uses an estimator presented in [4], which was shown in simulation to have smaller bias and mean squared error than the Vasicek estimator.
- `'correa'` uses the estimator presented in [5] based on local linear regression. In a simulation study, it had consistently smaller mean square error than the Vasiceck estimator, but it is more expensive to compute.

- `'auto'` selects the method automatically (default). Currently, this selects `'van es'` for very small samples (<10), `'ebrahimi'` for moderate sample sizes (11-1000), and `'vasicek'` for larger samples, but this behavior is subject to change in future versions.

All estimators are implemented as described in [6].

References

[1], [2], [3], [4], [5], [6]

Examples

```
>>> from scipy.stats import differential_entropy, norm
```

Entropy of a standard normal distribution:

```
>>> rng = np.random.default_rng()
>>> values = rng.standard_normal(100)
>>> differential_entropy(values)
1.3407817436640392
```

Compare with the true entropy:

```
>>> float(norm.entropy())
1.4189385332046727
```

For several sample sizes between 5 and 1000, compare the accuracy of the `'vasicek'`, `'van es'`, and `'ebrahimi'` methods. Specifically, compare the root mean squared error (over 1000 trials) between the estimate and the true differential entropy of the distribution.

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>>
>>>
>>> def rmse(res, expected):
...     '''Root mean squared error'''
...     return np.sqrt(np.mean((res - expected)**2))
>>>
>>>
>>> a, b = np.log10(5), np.log10(1000)
>>> ns = np.round(np.logspace(a, b, 10)).astype(int)
>>> reps = 1000  # number of repetitions for each sample size
>>> expected = stats.expon.entropy()
>>>
>>> method_errors = {'vasicek': [], 'van es': [], 'ebrahimi': []}
>>> for method in method_errors:
...     for n in ns:
...         rvs = stats.expon.rvs(size=(reps, n), random_state=rng)
...         res = stats.differential_entropy(rvs, method=method, axis=-1)
...         error = rmse(res, expected)
...         method_errors[method].append(error)
>>>
```

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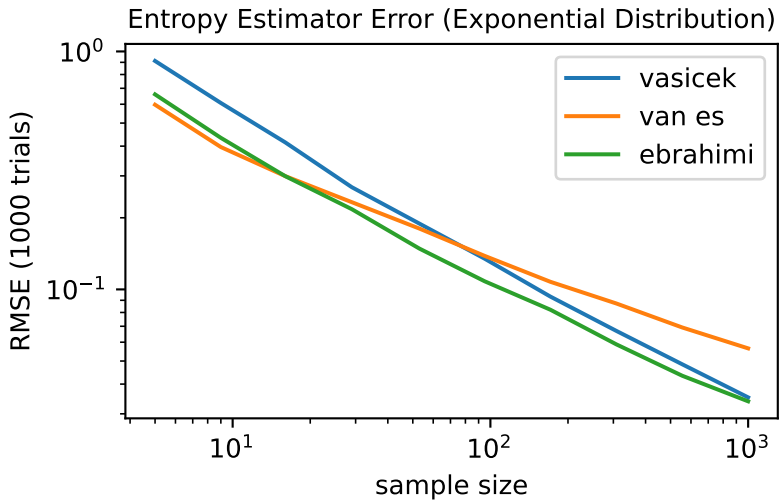
```
>>> for method, errors in method_errors.items():
...     plt.loglog(ns, errors, label=method)
>>>
>>> plt.legend()
>>> plt.xlabel('sample size')
>>> plt.ylabel('RMSE (1000 trials)')
>>> plt.title('Entropy Estimator Error (Exponential Distribution)')
```



scipy.stats.median_absolute_deviation

scipy.stats.**median_absolute_deviation**(**args*, ***kwds*)

median_absolute_deviation is deprecated, use *median_abs_deviation* instead!

To preserve the existing default behavior, use *scipy.stats.median_abs_deviation(..., scale=1/1.4826)*. The value 1.4826 is not numerically precise for scaling with a normal distribution. For a numerically precise value, use *scipy.stats.median_abs_deviation(..., scale='normal')*.

Compute the median absolute deviation of the data along the given axis.

The median absolute deviation (MAD, [1]) computes the median over the absolute deviations from the median. It is a measure of dispersion similar to the standard deviation but more robust to outliers [2].

The MAD of an empty array is `np.nan`.

New in version 1.3.0.

Parameters

x	[array_like] Input array or object that can be converted to an array.
axis	[int or None, optional] Axis along which the range is computed. Default is 0. If None, compute the MAD over the entire array.
center	[callable, optional] A function that will return the central value. The default is to use np.median. Any user defined function used will need to have the function signature `func(arr, axis)`.
scale	[int, optional] The scaling factor applied to the MAD. The default scale (1.4826) ensures consistency with the standard deviation for normally distributed data.

nan_policy
: [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):
- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

mad
: [scalar or ndarray] If `axis=None`, a scalar is returned. If the input contains integers or floats of smaller precision than `np.float64`, then the output data-type is `np.float64`. Otherwise, the output data-type is the same as that of the input.

See also:

numpy.std, ***numpy.var***, ***numpy.median***, **scipy.stats.iqr**, **scipy.stats.tmean**

scipy.stats.tstd, **scipy.stats.tvar**

Notes

The *center* argument only affects the calculation of the central value around which the MAD is calculated. That is, passing in `center=np.mean` will calculate the MAD around the mean - it will not calculate the *mean* absolute deviation.

References

[1], [2]

Examples

When comparing the behavior of *median_absolute_deviation* with `np.std`, the latter is affected when we change a single value of an array to have an outlier value while the MAD hardly changes:

```
>>> from scipy import stats
>>> x = stats.norm.rvs(size=100, scale=1, random_state=123456)
>>> x.std()
0.9973906394005013
>>> stats.median_absolute_deviation(x)
1.2280762773108278
>>> x[0] = 345.6
>>> x.std()
34.42304872314415
>>> stats.median_absolute_deviation(x)
1.2340335571164334
```

Axis handling example:

```
>>> x = np.array([[10, 7, 4], [3, 2, 1]])
>>> x
array([[10,  7,  4],
       [ 3,  2,  1]])
>>> stats.median_absolute_deviation(x)
```

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```
array([5.1891, 3.7065, 2.2239])
>>> stats.median_absolute_deviation(x, axis=None)
2.9652
```

scipy.stats.median_abs_deviation

scipy.stats.**median_abs_deviation**(*x*, *axis=0*, *center=<function median>*, *scale=1.0*, *nan_policy='propagate'*)

Compute the median absolute deviation of the data along the given axis.

The median absolute deviation (MAD, [1]) computes the median over the absolute deviations from the median. It is a measure of dispersion similar to the standard deviation but more robust to outliers [2].

The MAD of an empty array is `np.nan`.

New in version 1.5.0.

Parameters

x [array_like] Input array or object that can be converted to an array.

axis [int or None, optional] Axis along which the range is computed. Default is 0. If None, compute the MAD over the entire array.

center [callable, optional] A function that will return the central value. The default is to use np.median. Any user defined function used will need to have the function signature `func(arr, axis)`.

scale [scalar or str, optional] The numerical value of scale will be divided out of the final result. The default is 1.0. The string "normal" is also accepted, and results in *scale* being the inverse of the standard normal quantile function at 0.75, which is approximately 0.67449. Array-like scale is also allowed, as long as it broadcasts correctly to the output such that `out / scale` is a valid operation. The output dimensions depend on the input array, *x*, and the *axis* argument.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

mad [scalar or ndarray] If `axis=None`, a scalar is returned. If the input contains integers or floats of smaller precision than `np.float64`, then the output data-type is `np.float64`. Otherwise, the output data-type is the same as that of the input.

See also:

numpy.std, ***numpy.var***, ***numpy.median***, **scipy.stats.iqr**, **scipy.stats.tmean**

scipy.stats.tstd, **scipy.stats.tvar**

Notes

The *center* argument only affects the calculation of the central value around which the MAD is calculated. That is, passing in `center=np.mean` will calculate the MAD around the mean - it will not calculate the *mean* absolute deviation.

The input array may contain *inf*, but if *center* returns *inf*, the corresponding MAD for that data will be *nan*.

References

[1], [2]

Examples

When comparing the behavior of *median_abs_deviation* with `np.std`, the latter is affected when we change a single value of an array to have an outlier value while the MAD hardly changes:

```
>>> from scipy import stats
>>> x = stats.norm.rvs(size=100, scale=1, random_state=123456)
>>> x.std()
0.9973906394005013
>>> stats.median_abs_deviation(x)
0.82832610097857
>>> x[0] = 345.6
>>> x.std()
34.42304872314415
>>> stats.median_abs_deviation(x)
0.8323442311590675
```

Axis handling example:

```
>>> x = np.array([[10, 7, 4], [3, 2, 1]])
>>> x
array([[10,  7,  4],
       [ 3,  2,  1]])
>>> stats.median_abs_deviation(x)
array([3.5, 2.5, 1.5])
>>> stats.median_abs_deviation(x, axis=None)
2.0
```

Scale normal example:

```
>>> x = stats.norm.rvs(size=1000000, scale=2, random_state=123456)
>>> stats.median_abs_deviation(x)
1.3487398527041636
>>> stats.median_abs_deviation(x, scale='normal')
1.9996446978061115
```

scipy.stats.bootstrap

scipy.stats.**bootstrap**(*data*, *statistic*, ***, *vectorized=True*, *paired=False*, *axis=0*, *confidence_level=0.95*, *n_resamples=9999*, *batch=None*, *method='BCa'*, *random_state=None*)

Compute a two-sided bootstrap confidence interval of a statistic.

When *method* is `'percentile'`, a bootstrap confidence interval is computed according to the following procedure.

1. Resample the data: for each sample in *data* and for each of *n_resamples*, take a random sample of the original sample (with replacement) of the same size as the original sample.
2. Compute the bootstrap distribution of the statistic: for each set of resamples, compute the test statistic.
3. Determine the confidence interval: find the interval of the bootstrap distribution that is
   - symmetric about the median and
   - contains *confidence_level* of the resampled statistic values.

While the `'percentile'` method is the most intuitive, it is rarely used in practice. Two more common methods are available, `'basic'` ('reverse percentile') and `'BCa'` ('bias-corrected and accelerated'); they differ in how step 3 is performed.

If the samples in *data* are taken at random from their respective distributions n times, the confidence interval returned by *bootstrap* will contain the true value of the statistic for those distributions approximately *confidence_level* $\times n$ times.

Parameters

data [sequence of array-like] Each element of data is a sample from an underlying distribution.

statistic [callable] Statistic for which the confidence interval is to be calculated. *statistic* must be a callable that accepts `len(data)` samples as separate arguments and returns the resulting statistic. If *vectorized* is set `True`, *statistic* must also accept a keyword argument *axis* and be vectorized to compute the statistic along the provided *axis*.

vectorized [bool, default: `True`] If *vectorized* is set `False`, *statistic* will not be passed keyword argument *axis*, and is assumed to calculate the statistic only for 1D samples.

paired [bool, default: `False`] Whether the statistic treats corresponding elements of the samples in *data* as paired.

axis [int, default: `0`] The axis of the samples in *data* along which the *statistic* is calculated.

confidence_level [float, default: `0.95`] The confidence level of the confidence interval.

n_resamples [int, default: `9999`] The number of resamples performed to form the bootstrap distribution of the statistic.

batch [int, optional] The number of resamples to process in each vectorized call to *statistic*. Memory usage is O(*batch*`*`*n*`), where `n` is the sample size. Default is `None`, in which case `batch = n_resamples` (or `batch = max(n_resamples, n)` for `method='BCa'`).

method [{'percentile', 'basic', 'bca'}, default: `'BCa'`] Whether to return the 'percentile' bootstrap confidence interval (`'percentile'`), the 'reverse' or the bias-corrected and accelerated bootstrap confidence interval (`'BCa'`). Note that only `'percentile'` and `'basic'` support multi-sample statistics at this time.

random_state [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional
If *seed* is `None` (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.
Pseudorandom number generator state used to generate resamples.

Returns

res [BootstrapResult] An object with attributes:

confidence_interval
[ConfidenceInterval] The bootstrap confidence interval as an instance of `collections.namedtuple` with attributes *low* and *high*.

standard_error
[float or ndarray] The bootstrap standard error, that is, the sample standard deviation of the bootstrap distribution

References

[1], [2], [3]

Examples

Suppose we have sampled data from an unknown distribution.

```
>>> import numpy as np
>>> rng = np.random.default_rng()
>>> from scipy.stats import norm
>>> dist = norm(loc=2, scale=4)  # our "unknown" distribution
>>> data = dist.rvs(size=100, random_state=rng)
```

We are interested int the standard deviation of the distribution.

```
>>> std_true = dist.std()      # the true value of the statistic
>>> print(std_true)
4.0
>>> std_sample = np.std(data)  # the sample statistic
>>> print(std_sample)
3.9460644295563863
```

We can calculate a 90% confidence interval of the statistic using *bootstrap*.

```
>>> from scipy.stats import bootstrap
>>> data = (data,)  # samples must be in a sequence
>>> res = bootstrap(data, np.std, confidence_level=0.9,
...                 random_state=rng)
>>> print(res.confidence_interval)
ConfidenceInterval(low=3.57655333533867, high=4.382043696342881)
```

If we sample from the distribution 1000 times and form a bootstrap confidence interval for each sample, the confidence interval contains the true value of the statistic approximately 900 times.

```
>>> n_trials = 1000
>>> ci_contains_true_std = 0
>>> for i in range(n_trials):
...     data = (dist.rvs(size=100, random_state=rng),)
...     ci = bootstrap(data, np.std, confidence_level=0.9, n_
↪resamples=1000,
...                    random_state=rng).confidence_interval
...     if ci[0] < std_true < ci[1]:
```

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```
...         ci_contains_true_std += 1
>>> print(ci_contains_true_std)
875
```

Rather than writing a loop, we can also determine the confidence intervals for all 1000 samples at once.

```
>>> data = (dist.rvs(size=(n_trials, 100), random_state=rng),)
>>> res = bootstrap(data, np.std, axis=-1, confidence_level=0.9,
...                 n_resamples=1000, random_state=rng)
>>> ci_l, ci_u = res.confidence_interval
```

Here, *ci_l* and *ci_u* contain the confidence interval for each of the `n_trials = 1000` samples.

```
>>> print(ci_l[995:])
[3.77729695 3.75090233 3.45829131 3.34078217 3.48072829]
>>> print(ci_u[995:])
[4.88316666 4.86924034 4.32032996 4.2822427  4.59360598]
```

And again, approximately 90% contain the true value, `std_true = 4`.

```
>>> print(np.sum((ci_l < std_true) & (std_true < ci_u)))
900
```

bootstrap can also be used to estimate confidence intervals of multi-sample statistics, including those calculated by hypothesis tests. *scipy.stats.mood* perform's Mood's test for equal scale parameters, and it returns two outputs: a statistic, and a p-value. To get a confidence interval for the test statistic, we first wrap *scipy.stats.mood* in a function that accepts two sample arguments, accepts an *axis* keyword argument, and returns only the statistic.

```
>>> from scipy.stats import mood
>>> def my_statistic(sample1, sample2, axis):
...     statistic, _ = mood(sample1, sample2, axis=-1)
...     return statistic
```

Here, we use the 'percentile' method with the default 95% confidence level.

```
>>> sample1 = norm.rvs(scale=1, size=100, random_state=rng)
>>> sample2 = norm.rvs(scale=2, size=100, random_state=rng)
>>> data = (sample1, sample2)
>>> res = bootstrap(data, my_statistic, method='basic', random_state=rng)
>>> print(mood(sample1, sample2)[0])  # element 0 is the statistic
-5.521109549096542
>>> print(res.confidence_interval)
ConfidenceInterval(low=-7.255994487314675, high=-4.016202624747605)
```

The bootstrap estimate of the standard error is also available.

```
>>> print(res.standard_error)
0.8344963846318795
```

Paired-sample statistics work, too. For example, consider the Pearson correlation coefficient.

```
>>> from scipy.stats import pearsonr
>>> n = 100
>>> x = np.linspace(0, 10, n)
>>> y = x + rng.uniform(size=n)
>>> print(pearsonr(x, y)[0])  # element 0 is the statistic
0.9962357936065914
```

We wrap *pearsonr* so that it returns only the statistic.

```
>>> def my_statistic(x, y):
...     return pearsonr(x, y)[0]
```

We call *bootstrap* using `paired=True`. Also, since `my_statistic` isn't vectorized to calculate the statistic along a given axis, we pass in `vectorized=False`.

```
>>> res = bootstrap((x, y), my_statistic, vectorized=False, paired=True,
...                 random_state=rng)
>>> print(res.confidence_interval)
ConfidenceInterval(low=0.9950085825848624, high=0.9971212407917498)
```

Frequency statistics

cumfreq(a[, numbins, defaultreallimits, weights])	Return a cumulative frequency histogram, using the histogram function.
itemfreq(*args, **kwds)	*itemfreq* is deprecated! *itemfreq* is deprecated and will be removed in a future version.
percentileofscore(a, score[, kind])	Compute the percentile rank of a score relative to a list of scores.
scoreatpercentile(a, per[, limit, …])	Calculate the score at a given percentile of the input sequence.
relfreq(a[, numbins, defaultreallimits, weights])	Return a relative frequency histogram, using the histogram function.

scipy.stats.cumfreq

scipy.stats.**cumfreq**(*a*, *numbins=10*, *defaultreallimits=None*, *weights=None*)

Return a cumulative frequency histogram, using the histogram function.

A cumulative histogram is a mapping that counts the cumulative number of observations in all of the bins up to the specified bin.

Parameters

a [array_like] Input array.

numbins [int, optional] The number of bins to use for the histogram. Default is 10.

defaultreallimits [tuple (lower, upper), optional] The lower and upper values for the range of the histogram. If no value is given, a range slightly larger than the range of the values in *a* is used. Specifically `(a.min() - s, a.max() + s)`, where `s = (1/2)(a.max() - a.min()) / (numbins - 1)`.

weights [array_like, optional] The weights for each value in *a*. Default is None, which gives each value a weight of 1.0

Returns

cumcount [ndarray] Binned values of cumulative frequency.
lowerlimit [float] Lower real limit
binsize [float] Width of each bin.
extrapoints [int] Extra points.

Examples

```
>>> import matplotlib.pyplot as plt
>>> from numpy.random import default_rng
>>> from scipy import stats
>>> rng = default_rng()
>>> x = [1, 4, 2, 1, 3, 1]
>>> res = stats.cumfreq(x, numbins=4, defaultreallimits=(1.5, 5))
>>> res.cumcount
array([ 1.,  2.,  3.,  3.])
>>> res.extrapoints
3
```

Create a normal distribution with 1000 random values

```
>>> samples = stats.norm.rvs(size=1000, random_state=rng)
```

Calculate cumulative frequencies

```
>>> res = stats.cumfreq(samples, numbins=25)
```

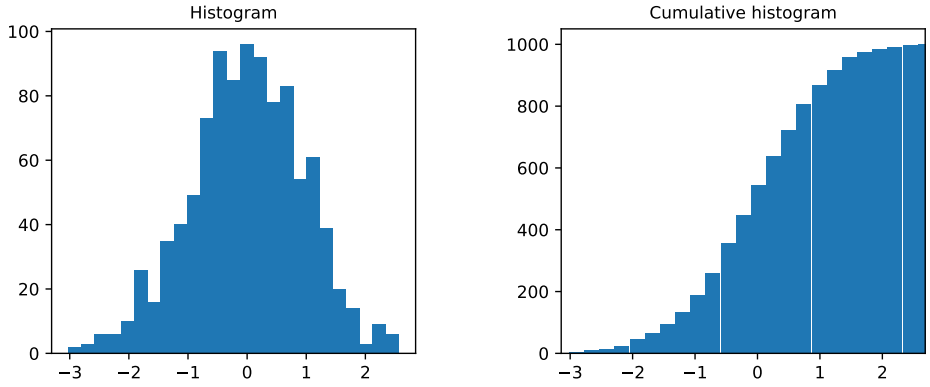
Calculate space of values for x

```
>>> x = res.lowerlimit + np.linspace(0, res.binsize*res.cumcount.size,
...                                  res.cumcount.size)
```

Plot histogram and cumulative histogram

```
>>> fig = plt.figure(figsize=(10, 4))
>>> ax1 = fig.add_subplot(1, 2, 1)
>>> ax2 = fig.add_subplot(1, 2, 2)
>>> ax1.hist(samples, bins=25)
>>> ax1.set_title('Histogram')
>>> ax2.bar(x, res.cumcount, width=res.binsize)
>>> ax2.set_title('Cumulative histogram')
>>> ax2.set_xlim([x.min(), x.max()])
```

```
>>> plt.show()
```



scipy.stats.itemfreq

scipy.stats.**itemfreq**(**args*, ***kwds*)

itemfreq is deprecated! *itemfreq* is deprecated and will be removed in a future version. Use instead *np.unique(..., return_counts=True)*

Return a 2-D array of item frequencies.

Parameters

a [(N,) array_like] Input array.

Returns

itemfreq [(K, 2) ndarray] A 2-D frequency table. Column 1 contains sorted, unique values from *a*, column 2 contains their respective counts.

Examples

```
>>> from scipy import stats
>>> a = np.array([1, 1, 5, 0, 1, 2, 2, 0, 1, 4])
>>> stats.itemfreq(a)
array([[ 0.,  2.],
       [ 1.,  4.],
       [ 2.,  2.],
       [ 4.,  1.],
       [ 5.,  1.]])
>>> np.bincount(a)
array([2, 4, 2, 0, 1, 1])
```

```
>>> stats.itemfreq(a/10.)
array([[ 0. ,  2. ],
       [ 0.1,  4. ],
       [ 0.2,  2. ],
       [ 0.4,  1. ],
       [ 0.5,  1. ]])
```

scipy.stats.percentileofscore

scipy.stats.**percentileofscore**(*a*, *score*, *kind='rank'*)

Compute the percentile rank of a score relative to a list of scores.

A *percentileofscore* of, for example, 80% means that 80% of the scores in *a* are below the given score. In the case of gaps or ties, the exact definition depends on the optional keyword, *kind*.

Parameters

a [array_like] Array of scores to which *score* is compared.

score [int or float] Score that is compared to the elements in *a*.

kind [{'rank', 'weak', 'strict', 'mean'}, optional] Specifies the interpretation of the resulting score. The following options are available (default is 'rank'):

- 'rank': Average percentage ranking of score. In case of multiple matches, average the percentage rankings of all matching scores.
- 'weak': This kind corresponds to the definition of a cumulative distribution function. A percentileofscore of 80% means that 80% of values are less than or equal to the provided score.
- 'strict': Similar to "weak", except that only values that are strictly less than the given score are counted.
- 'mean': The average of the "weak" and "strict" scores, often used in testing. See https://en.wikipedia.org/wiki/Percentile_rank

Returns

pcos [float] Percentile-position of score (0-100) relative to *a*.

See also:

numpy.percentile

Examples

Three-quarters of the given values lie below a given score:

```
>>> from scipy import stats
>>> stats.percentileofscore([1, 2, 3, 4], 3)
75.0
```

With multiple matches, note how the scores of the two matches, 0.6 and 0.8 respectively, are averaged:

```
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3)
70.0
```

Only 2/5 values are strictly less than 3:

```
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='strict')
40.0
```

But 4/5 values are less than or equal to 3:

```
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='weak')
80.0
```

The average between the weak and the strict scores is:

```
>>> stats.percentileofscore([1, 2, 3, 3, 4], 3, kind='mean')
60.0
```

scipy.stats.scoreatpercentile

scipy.stats.**scoreatpercentile**(*a*, *per*, *limit=()*, *interpolation_method='fraction'*, *axis=None*)

Calculate the score at a given percentile of the input sequence.

For example, the score at *per=50* is the median. If the desired quantile lies between two data points, we interpolate between them, according to the value of *interpolation*. If the parameter *limit* is provided, it should be a tuple (lower, upper) of two values.

Parameters

a [array_like] A 1-D array of values from which to extract score.

per [array_like] Percentile(s) at which to extract score. Values should be in range [0,100].

limit [tuple, optional] Tuple of two scalars, the lower and upper limits within which to compute the percentile. Values of *a* outside this (closed) interval will be ignored.

interpolation_method

[{'fraction', 'lower', 'higher'}, optional] Specifies the interpolation method to use, when the desired quantile lies between two data points *i* and *j* The following options are available (default is 'fraction'):

- 'fraction': `i + (j - i) * fraction` where `fraction` is the fractional part of the index surrounded by `i` and `j`
- 'lower': `i`
- 'higher': `j`

axis [int, optional] Axis along which the percentiles are computed. Default is None. If None, compute over the whole array *a*.

Returns

score [float or ndarray] Score at percentile(s).

See also:

percentileofscore, ***numpy.percentile***

Notes

This function will become obsolete in the future. For NumPy 1.9 and higher, `numpy.percentile` provides all the functionality that *scoreatpercentile* provides. And it's significantly faster. Therefore it's recommended to use `numpy.percentile` for users that have numpy >= 1.9.

Examples

```
>>> from scipy import stats
>>> a = np.arange(100)
>>> stats.scoreatpercentile(a, 50)
49.5
```

scipy.stats.relfreq

scipy.stats.**relfreq**(*a*, *numbins=10*, *defaultreallimits=None*, *weights=None*)

Return a relative frequency histogram, using the histogram function.

A relative frequency histogram is a mapping of the number of observations in each of the bins relative to the total of observations.

Parameters

a [array_like] Input array.

numbins [int, optional] The number of bins to use for the histogram. Default is 10.

defaultreallimits [tuple (lower, upper), optional] The lower and upper values for the range of the histogram. If no value is given, a range slightly larger than the range of the values in a is used. Specifically `(a.min() - s, a.max() + s)`, where `s = (1/2)(a.max() - a.min()) / (numbins - 1)`.

weights [array_like, optional] The weights for each value in *a*. Default is None, which gives each value a weight of 1.0

Returns

frequency [ndarray] Binned values of relative frequency.

lowerlimit [float] Lower real limit.

binsize [float] Width of each bin.

extrapoints [int] Extra points.

Examples

```
>>> import matplotlib.pyplot as plt
>>> from numpy.random import default_rng
>>> from scipy import stats
>>> rng = default_rng()
>>> a = np.array([2, 4, 1, 2, 3, 2])
>>> res = stats.relfreq(a, numbins=4)
>>> res.frequency
array([ 0.16666667, 0.5       , 0.16666667,  0.16666667])
>>> np.sum(res.frequency)  # relative frequencies should add up to 1
1.0
```

Create a normal distribution with 1000 random values

```
>>> samples = stats.norm.rvs(size=1000, random_state=rng)
```

Calculate relative frequencies

```
>>> res = stats.relfreq(samples, numbins=25)
```

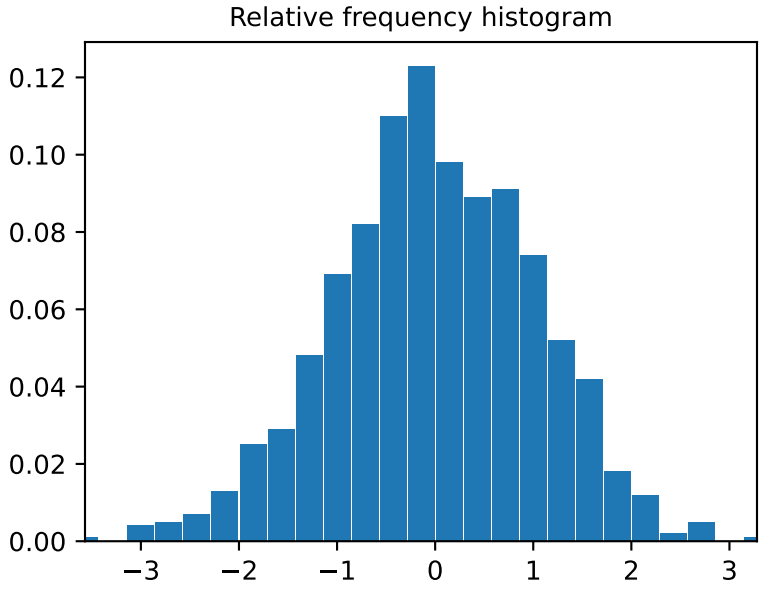
Calculate space of values for x

```
>>> x = res.lowerlimit + np.linspace(0, res.binsize*res.frequency.size,
...                                  res.frequency.size)
```

Plot relative frequency histogram

```
>>> fig = plt.figure(figsize=(5, 4))
>>> ax = fig.add_subplot(1, 1, 1)
>>> ax.bar(x, res.frequency, width=res.binsize)
>>> ax.set_title('Relative frequency histogram')
>>> ax.set_xlim([x.min(), x.max()])
```

```
>>> plt.show()
```



binned_statistic(x, values[, statistic, …])	Compute a binned statistic for one or more sets of data.
binned_statistic_2d(x, y, values[, …])	Compute a bidimensional binned statistic for one or more sets of data.
binned_statistic_dd(sample, values[, …])	Compute a multidimensional binned statistic for a set of data.

scipy.stats.binned_statistic

scipy.stats.**binned_statistic**(*x*, *values*, *statistic='mean'*, *bins=10*, *range=None*)

Compute a binned statistic for one or more sets of data.

This is a generalization of a histogram function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values (or set of values) within each bin.

Parameters

x [(N,) array_like] A sequence of values to be binned.

values [(N,) array_like or list of (N,) array_like] The data on which the statistic will be computed. This must be the same shape as *x*, or a set of sequences - each the same shape as *x*. If *values*

is a set of sequences, the statistic will be computed on each independently.

statistic [string or callable, optional] The statistic to compute (default is 'mean'). The following statistics are available:

- 'mean' : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
- 'std' : compute the standard deviation within each bin. This is implicitly calculated with ddof=0.
- 'median' : compute the median of values for points within each bin. Empty bins will be represented by NaN.
- 'count' : compute the count of points within each bin. This is identical to an unweighted histogram. *values* array is not referenced.
- 'sum' : compute the sum of values for points within each bin. This is identical to a weighted histogram.
- 'min' : compute the minimum of values for points within each bin. Empty bins will be represented by NaN.
- 'max' : compute the maximum of values for point within each bin. Empty bins will be represented by NaN.
- function : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by function([]), or NaN if this returns an error.

bins [int or sequence of scalars, optional] If *bins* is an int, it defines the number of equal-width bins in the given range (10 by default). If *bins* is a sequence, it defines the bin edges, including the rightmost edge, allowing for non-uniform bin widths. Values in *x* that are smaller than lowest bin edge are assigned to bin number 0, values beyond the highest bin are assigned to `bins[-1]`. If the bin edges are specified, the number of bins will be, (nx = len(bins)-1).

range [(float, float) or [(float, float)], optional] The lower and upper range of the bins. If not provided, range is simply `(x.min(), x.max())`. Values outside the range are ignored.

Returns

statistic [array] The values of the selected statistic in each bin.

bin_edges [array of dtype float] Return the bin edges `(length(statistic)+1)`.

binnumber: 1-D ndarray of ints

Indices of the bins (corresponding to *bin_edges*) in which each value of *x* belongs. Same length as *values*. A binnumber of *i* means the corresponding value is between (bin_edges[i-1], bin_edges[i]).

See also:

numpy.digitize, ***numpy.histogram***, **binned_statistic_2d**, **binned_statistic_dd**

Notes

All but the last (righthand-most) bin is half-open. In other words, if *bins* is `[1, 2, 3, 4]`, then the first bin is `[1, 2)` (including 1, but excluding 2) and the second `[2, 3)`. The last bin, however, is `[3, 4]`, which *includes* 4.

New in version 0.11.0.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

First some basic examples:

Create two evenly spaced bins in the range of the given sample, and sum the corresponding values in each of those bins:

```
>>> values = [1.0, 1.0, 2.0, 1.5, 3.0]
>>> stats.binned_statistic([1, 1, 2, 5, 7], values, 'sum', bins=2)
BinnedStatisticResult(statistic=array([4. , 4.5]),
       bin_edges=array([1., 4., 7.]), binnumber=array([1, 1, 1, 2, 2]))
```

Multiple arrays of values can also be passed. The statistic is calculated on each set independently:

```
>>> values = [[1.0, 1.0, 2.0, 1.5, 3.0], [2.0, 2.0, 4.0, 3.0, 6.0]]
>>> stats.binned_statistic([1, 1, 2, 5, 7], values, 'sum', bins=2)
BinnedStatisticResult(statistic=array([[4. , 4.5],
       [8. , 9. ]]), bin_edges=array([1., 4., 7.]),
       binnumber=array([1, 1, 1, 2, 2]))
```

```
>>> stats.binned_statistic([1, 2, 1, 2, 4], np.arange(5), statistic='mean
↪',
...                         bins=3)
BinnedStatisticResult(statistic=array([1., 2., 4.]),
       bin_edges=array([1., 2., 3., 4.]),
       binnumber=array([1, 2, 1, 2, 3]))
```

As a second example, we now generate some random data of sailing boat speed as a function of wind speed, and then determine how fast our boat is for certain wind speeds:

```
>>> rng = np.random.default_rng()
>>> windspeed = 8 * rng.random(500)
>>> boatspeed = .3 * windspeed**.5 + .2 * rng.random(500)
>>> bin_means, bin_edges, binnumber = stats.binned_statistic(windspeed,
...                 boatspeed, statistic='median', bins=[1,2,3,4,5,6,7])
>>> plt.figure()
>>> plt.plot(windspeed, boatspeed, 'b.', label='raw data')
>>> plt.hlines(bin_means, bin_edges[:-1], bin_edges[1:], colors='g', lw=5,
...            label='binned statistic of data')
>>> plt.legend()
```

Now we can use `binnumber` to select all datapoints with a windspeed below 1:

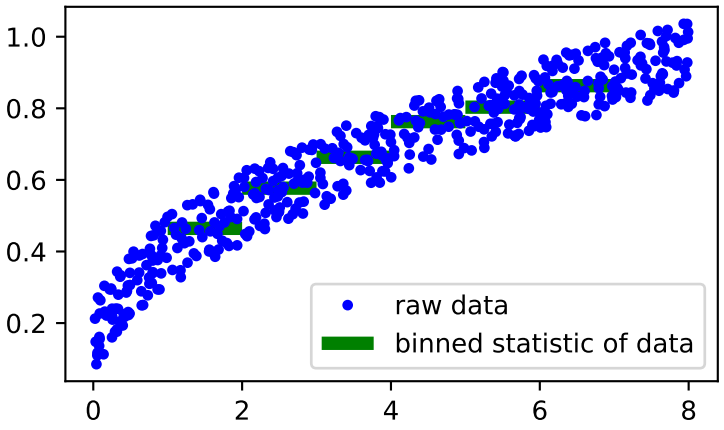
```
>>> low_boatspeed = boatspeed[binnumber == 0]
```

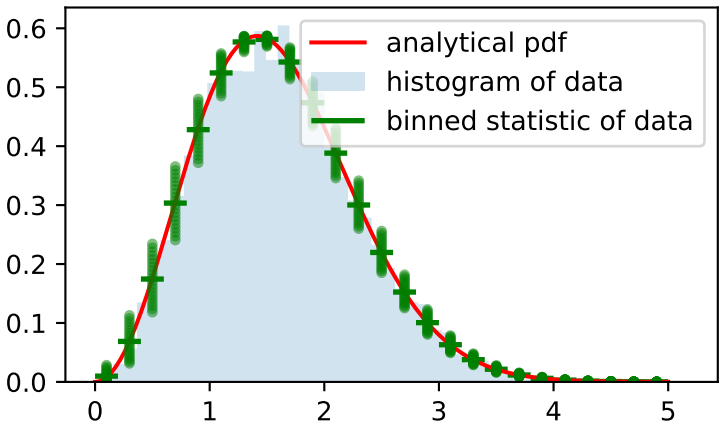
As a final example, we will use `bin_edges` and `binnumber` to make a plot of a distribution that shows the mean and distribution around that mean per bin, on top of a regular histogram and the probability distribution function:

```
>>> x = np.linspace(0, 5, num=500)
>>> x_pdf = stats.maxwell.pdf(x)
>>> samples = stats.maxwell.rvs(size=10000)
```

```
>>> bin_means, bin_edges, binnumber = stats.binned_statistic(x, x_pdf,
...         statistic='mean', bins=25)
>>> bin_width = (bin_edges[1] - bin_edges[0])
>>> bin_centers = bin_edges[1:] - bin_width/2
```

```
>>> plt.figure()
>>> plt.hist(samples, bins=50, density=True, histtype='stepfilled',
...          alpha=0.2, label='histogram of data')
>>> plt.plot(x, x_pdf, 'r-', label='analytical pdf')
>>> plt.hlines(bin_means, bin_edges[:-1], bin_edges[1:], colors='g', lw=2,
...            label='binned statistic of data')
>>> plt.plot((binnumber - 0.5) * bin_width, x_pdf, 'g.', alpha=0.5)
>>> plt.legend(fontsize=10)
>>> plt.show()
```





scipy.stats.binned_statistic_2d

scipy.stats.**binned_statistic_2d**(*x*, *y*, *values*, *statistic='mean'*, *bins=10*, *range=None*, *expand_binnumbers=False*)

Compute a bidimensional binned statistic for one or more sets of data.

This is a generalization of a histogram2d function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values (or set of values) within each bin.

Parameters

x [(N,) array_like] A sequence of values to be binned along the first dimension.

y [(N,) array_like] A sequence of values to be binned along the second dimension.

values [(N,) array_like or list of (N,) array_like] The data on which the statistic will be computed. This must be the same shape as *x*, or a list of sequences - each with the same shape as *x*. If *values* is such a list, the statistic will be computed on each independently.

statistic [string or callable, optional] The statistic to compute (default is 'mean'). The following statistics are available:

- 'mean' : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
- 'std' : compute the standard deviation within each bin. This is implicitly calculated with ddof=0.
- 'median' : compute the median of values for points within each bin. Empty bins will be represented by NaN.
- 'count' : compute the count of points within each bin. This is identical to an unweighted histogram. *values* array is not referenced.
- 'sum' : compute the sum of values for points within each bin. This is identical to a weighted histogram.
- 'min' : compute the minimum of values for points within each bin. Empty bins will be represented by NaN.
- 'max' : compute the maximum of values for point within each bin. Empty bins will be represented by NaN.
- function : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by function([]), or NaN if this returns an error.

bins [int or [int, int] or array_like or [array, array], optional] The bin specification:

- the number of bins for the two dimensions (nx = ny = bins),
- the number of bins in each dimension (nx, ny = bins),
- the bin edges for the two dimensions (x_edge = y_edge = bins),
- the bin edges in each dimension (x_edge, y_edge = bins).

If the bin edges are specified, the number of bins will be, (nx = len(x_edge)-1, ny = len(y_edge)-1).

range [(2,2) array_like, optional] The leftmost and rightmost edges of the bins along each dimension (if not specified explicitly in the *bins* parameters): [[xmin, xmax], [ymin, ymax]]. All values outside of this range will be considered outliers and not tallied in the histogram.

expand_binnumbers

[bool, optional] 'False' (default): the returned *binnumber* is a shape (N,) array of linearized bin indices. 'True': the returned *binnumber* is 'unraveled' into a shape (2,N) ndarray, where each row gives the bin numbers in the corresponding dimension. See the *binnumber* returned value, and the *Examples* section.

New in version 0.17.0.

Returns

statistic [(nx, ny) ndarray] The values of the selected statistic in each two-dimensional bin.

x_edge [(nx + 1) ndarray] The bin edges along the first dimension.

y_edge [(ny + 1) ndarray] The bin edges along the second dimension.

binnumber [(N,) array of ints or (2,N) ndarray of ints] This assigns to each element of *sample* an integer that represents the bin in which this observation falls. The representation depends on the *expand_binnumbers* argument. See *Notes* for details.

See also:

numpy.digitize, ***numpy.histogram2d***, **binned_statistic**, **binned_statistic_dd**

Notes

Binedges: All but the last (righthand-most) bin is half-open. In other words, if *bins* is `[1, 2, 3, 4]`, then the first bin is `[1, 2)` (including 1, but excluding 2) and the second `[2, 3)`. The last bin, however, is `[3, 4]`, which *includes* 4.

binnumber: This returned argument assigns to each element of *sample* an integer that represents the bin in which it belongs. The representation depends on the *expand_binnumbers* argument. If 'False' (default): The returned *binnumber* is a shape (N,) array of linearized indices mapping each element of *sample* to its corresponding bin (using row-major ordering). If 'True': The returned *binnumber* is a shape (2,N) ndarray where each row indicates bin placements for each dimension respectively. In each dimension, a binnumber of *i* means the corresponding value is between (D_edge[i-1], D_edge[i]), where 'D' is either 'x' or 'y'.

New in version 0.11.0.

Examples

```
>>> from scipy import stats
```

Calculate the counts with explicit bin-edges:

```
>>> x = [0.1, 0.1, 0.1, 0.6]
>>> y = [2.1, 2.6, 2.1, 2.1]
>>> binx = [0.0, 0.5, 1.0]
>>> biny = [2.0, 2.5, 3.0]
>>> ret = stats.binned_statistic_2d(x, y, None, 'count', bins=[binx,␣
↪biny])
>>> ret.statistic
array([[2., 1.],
       [1., 0.]])
```

The bin in which each sample is placed is given by the *binnumber* returned parameter. By default, these are the linearized bin indices:

```
>>> ret.binnumber
array([5, 6, 5, 9])
```

The bin indices can also be expanded into separate entries for each dimension using the *expand_binnumbers* parameter:

```
>>> ret = stats.binned_statistic_2d(x, y, None, 'count', bins=[binx,␣
↪biny],
...                                 expand_binnumbers=True)
```

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```
>>> ret.binnumber
array([[1, 1, 1, 2],
       [1, 2, 1, 1]])
```

Which shows that the first three elements belong in the xbin 1, and the fourth into xbin 2; and so on for y.

scipy.stats.binned_statistic_dd

scipy.stats.**binned_statistic_dd**(*sample*, *values*, *statistic='mean'*, *bins=10*, *range=None*, *expand_binnumbers=False*, *binned_statistic_result=None*)

Compute a multidimensional binned statistic for a set of data.

This is a generalization of a histogramdd function. A histogram divides the space into bins, and returns the count of the number of points in each bin. This function allows the computation of the sum, mean, median, or other statistic of the values within each bin.

Parameters

sample [array_like] Data to histogram passed as a sequence of N arrays of length D, or as an (N,D) array.

values [(N,) array_like or list of (N,) array_like] The data on which the statistic will be computed. This must be the same shape as *sample*, or a list of sequences - each with the same shape as *sample*. If *values* is such a list, the statistic will be computed on each independently.

statistic [string or callable, optional] The statistic to compute (default is 'mean'). The following statistics are available:

- 'mean' : compute the mean of values for points within each bin. Empty bins will be represented by NaN.
- 'median' : compute the median of values for points within each bin. Empty bins will be represented by NaN.
- 'count' : compute the count of points within each bin. This is identical to an unweighted histogram. *values* array is not referenced.
- 'sum' : compute the sum of values for points within each bin. This is identical to a weighted histogram.
- 'std' : compute the standard deviation within each bin. This is implicitly calculated with ddof=0. If the number of values within a given bin is 0 or 1, the computed standard deviation value will be 0 for the bin.
- 'min' : compute the minimum of values for points within each bin. Empty bins will be represented by NaN.
- 'max' : compute the maximum of values for point within each bin. Empty bins will be represented by NaN.
- function : a user-defined function which takes a 1D array of values, and outputs a single numerical statistic. This function will be called on the values in each bin. Empty bins will be represented by function([]), or NaN if this returns an error.

bins [sequence or positive int, optional] The bin specification must be in one of the following forms:

- A sequence of arrays describing the bin edges along each dimension.
- The number of bins for each dimension (nx, ny, … = bins).
- The number of bins for all dimensions (nx = ny = … = bins).

range [sequence, optional] A sequence of lower and upper bin edges to be used if the edges are not given explicitly in *bins*. Defaults to the minimum and maximum values along each dimension.

expand_binnumbers

[bool, optional] 'False' (default): the returned *binnumber* is a shape (N,) array of linearized bin indices. 'True': the returned *binnumber* is 'unraveled' into a shape (D,N) ndarray, where each row gives the bin numbers in the corresponding dimension. See the *binnumber* returned value, and the *Examples* section of *binned_statistic_2d*.

binned_statistic_result
[binnedStatisticddResult] Result of a previous call to the function in order to reuse bin edges and bin numbers with new values and/or a different statistic. To reuse bin numbers, *expand_binnumbers* must have been set to False (the default)
New in version 0.17.0.

Returns

statistic [ndarray, shape(nx1, nx2, nx3,...)] The values of the selected statistic in each two-dimensional bin.
bin_edges [list of ndarrays] A list of D arrays describing the (nxi + 1) bin edges for each dimension.
binnumber
[(N,) array of ints or (D,N) ndarray of ints] This assigns to each element of *sample* an integer that represents the bin in which this observation falls. The representation depends on the *expand_binnumbers* argument. See *Notes* for details.

See also:

numpy.digitize, ***numpy.histogramdd***, **binned_statistic**, **binned_statistic_2d**

Notes

Binedges: All but the last (righthand-most) bin is half-open in each dimension. In other words, if *bins* is `[1, 2, 3, 4]`, then the first bin is `[1, 2)` (including 1, but excluding 2) and the second `[2, 3)`. The last bin, however, is `[3, 4]`, which *includes* 4.

binnumber: This returned argument assigns to each element of *sample* an integer that represents the bin in which it belongs. The representation depends on the *expand_binnumbers* argument. If 'False' (default): The returned *binnumber* is a shape (N,) array of linearized indices mapping each element of *sample* to its corresponding bin (using row-major ordering). If 'True': The returned *binnumber* is a shape (D,N) ndarray where each row indicates bin placements for each dimension respectively. In each dimension, a binnumber of *i* means the corresponding value is between (bin_edges[D][i-1], bin_edges[D][i]), for each dimension 'D'.

New in version 0.11.0.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.mplot3d import Axes3D
```

Take an array of 600 (x, y) coordinates as an example. *binned_statistic_dd* can handle arrays of higher dimension *D*. But a plot of dimension *D+1* is required.

```
>>> mu = np.array([0., 1.])
>>> sigma = np.array([[1., -0.5],[-0.5, 1.5]])
>>> multinormal = stats.multivariate_normal(mu, sigma)
>>> data = multinormal.rvs(size=600, random_state=235412)
>>> data.shape
(600, 2)
```

Create bins and count how many arrays fall in each bin:

```
>>> N = 60
>>> x = np.linspace(-3, 3, N)
>>> y = np.linspace(-3, 4, N)
>>> ret = stats.binned_statistic_dd(data, np.arange(600), bins=[x, y],
...                                 statistic='count')
>>> bincounts = ret.statistic
```

Set the volume and the location of bars:

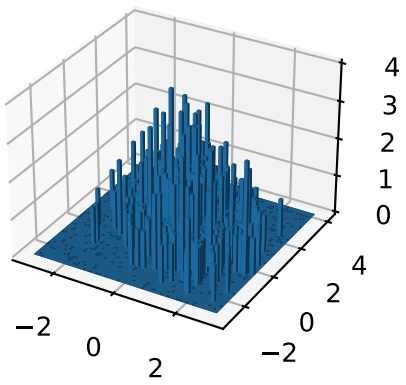
```
>>> dx = x[1] - x[0]
>>> dy = y[1] - y[0]
>>> x, y = np.meshgrid(x[:-1]+dx/2, y[:-1]+dy/2)
>>> z = 0
```

```
>>> bincounts = bincounts.ravel()
>>> x = x.ravel()
>>> y = y.ravel()
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111, projection='3d')
>>> with np.errstate(divide='ignore'):   # silence random axes3d warning
...     ax.bar3d(x, y, z, dx, dy, bincounts)
```

Reuse bin numbers and bin edges with new values:

```
>>> ret2 = stats.binned_statistic_dd(data, -np.arange(600),
...                                  binned_statistic_result=ret,
...                                  statistic='mean')
```



Correlation functions

f_oneway(*args[, axis])	Perform one-way ANOVA.
alexandergovern(*args[, nan_policy])	Performs the Alexander Govern test.
pearsonr(x, y)	Pearson correlation coefficient and p-value for testing non-correlation.
spearmanr(a[, b, axis, nan_policy, alternative])	Calculate a Spearman correlation coefficient with associated p-value.
pointbiserialr(x, y)	Calculate a point biserial correlation coefficient and its p-value.
kendalltau(x, y[, initial_lexsort, …])	Calculate Kendall's tau, a correlation measure for ordinal data.
weightedtau(x, y[, rank, weigher, additive])	Compute a weighted version of Kendall's τ.
somersd(x[, y])	Calculates Somers' D, an asymmetric measure of ordinal association.
linregress(x[, y, alternative])	Calculate a linear least-squares regression for two sets of measurements.
siegelslopes(y[, x, method])	Computes the Siegel estimator for a set of points (x, y).
theilslopes(y[, x, alpha])	Computes the Theil-Sen estimator for a set of points (x, y).
multiscale_graphcorr(x, y[, …])	Computes the Multiscale Graph Correlation (MGC) test statistic.

scipy.stats.f_oneway

scipy.stats.**f_oneway**(**args*, *axis=0*)

Perform one-way ANOVA.

The one-way ANOVA tests the null hypothesis that two or more groups have the same population mean. The test is applied to samples from two or more groups, possibly with differing sizes.

Parameters

sample1, sample2, …
: [array_like] The sample measurements for each group. There must be at least two arguments. If the arrays are multidimensional, then all the dimensions of the array must be the same except for *axis*.

axis
: [int, optional] Axis of the input arrays along which the test is applied. Default is 0.

Returns

statistic
: [float] The computed F statistic of the test.

pvalue
: [float] The associated p-value from the F distribution.

Warns

F_onewayConstantInputWarning
: Raised if each of the input arrays is constant array. In this case the F statistic is either infinite or isn't defined, so `np.inf` or `np.nan` is returned.

F_onewayBadInputSizesWarning
: Raised if the length of any input array is 0, or if all the input arrays have length 1. `np.nan` is returned for the F statistic and the p-value in these cases.

Notes

The ANOVA test has important assumptions that must be satisfied in order for the associated p-value to be valid.

1. The samples are independent.
2. Each sample is from a normally distributed population.
3. The population standard deviations of the groups are all equal. This property is known as homoscedasticity.

If these assumptions are not true for a given set of data, it may still be possible to use the Kruskal-Wallis H-test (*scipy.stats.kruskal*) or the Alexander-Govern test (*scipy.stats.alexandergovern*) although with some loss of power.

The length of each group must be at least one, and there must be at least one group with length greater than one. If these conditions are not satisfied, a warning is generated and (`np.nan`, `np.nan`) is returned.

If each group contains constant values, and there exist at least two groups with different values, the function generates a warning and returns (`np.inf`, 0).

If all values in all groups are the same, function generates a warning and returns (`np.nan`, `np.nan`).

The algorithm is from Heiman [2], pp.394-7.

References

[1], [2], [3]

Examples

```
>>> from scipy.stats import f_oneway
```

Here are some data [3] on a shell measurement (the length of the anterior adductor muscle scar, standardized by dividing by length) in the mussel Mytilus trossulus from five locations: Tillamook, Oregon; Newport, Oregon; Petersburg, Alaska; Magadan, Russia; and Tvarminne, Finland, taken from a much larger data set used in McDonald et al. (1991).

```
>>> tillamook = [0.0571, 0.0813, 0.0831, 0.0976, 0.0817, 0.0859, 0.0735,
...              0.0659, 0.0923, 0.0836]
>>> newport = [0.0873, 0.0662, 0.0672, 0.0819, 0.0749, 0.0649, 0.0835,
...            0.0725]
>>> petersburg = [0.0974, 0.1352, 0.0817, 0.1016, 0.0968, 0.1064, 0.105]
>>> magadan = [0.1033, 0.0915, 0.0781, 0.0685, 0.0677, 0.0697, 0.0764,
...            0.0689]
>>> tvarminne = [0.0703, 0.1026, 0.0956, 0.0973, 0.1039, 0.1045]
>>> f_oneway(tillamook, newport, petersburg, magadan, tvarminne)
F_onewayResult(statistic=7.121019471642447, pvalue=0.0002812242314534544)
```

f_oneway accepts multidimensional input arrays. When the inputs are multidimensional and *axis* is not given, the test is performed along the first axis of the input arrays. For the following data, the test is performed three times, once for each column.

```
>>> a = np.array([[9.87, 9.03, 6.81],
...               [7.18, 8.35, 7.00],
...               [8.39, 7.58, 7.68],
...               [7.45, 6.33, 9.35],
```

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```
...                [6.41, 7.10, 9.33],
...                [8.00, 8.24, 8.44]])
>>> b = np.array([[6.35, 7.30, 7.16],
...                [6.65, 6.68, 7.63],
...                [5.72, 7.73, 6.72],
...                [7.01, 9.19, 7.41],
...                [7.75, 7.87, 8.30],
...                [6.90, 7.97, 6.97]])
>>> c = np.array([[3.31, 8.77, 1.01],
...                [8.25, 3.24, 3.62],
...                [6.32, 8.81, 5.19],
...                [7.48, 8.83, 8.91],
...                [8.59, 6.01, 6.07],
...                [3.07, 9.72, 7.48]])
>>> F, p = f_oneway(a, b, c)
>>> F
array([1.75676344, 0.03701228, 3.76439349])
>>> p
array([0.20630784, 0.96375203, 0.04733157])
```

scipy.stats.alexandergovern

`scipy.stats.`**`alexandergovern`**(**args*, *nan_policy='propagate'*)

Performs the Alexander Govern test.

The Alexander-Govern approximation tests the equality of k independent means in the face of heterogeneity of variance. The test is applied to samples from two or more groups, possibly with differing sizes.

Parameters

sample1, sample2, …
: [array_like] The sample measurements for each group. There must be at least two samples.

nan_policy
: [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):
- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

statistic [float] The computed A statistic of the test.
pvalue [float] The associated p-value from the chi-squared distribution.

Warns

AlexanderGovernConstantInputWarning
: Raised if an input is a constant array. The statistic is not defined in this case, so `np.nan` is returned.

See also:

`f_oneway`

one-way ANOVA

Notes

The use of this test relies on several assumptions.

1. The samples are independent.
2. Each sample is from a normally distributed population.
3. Unlike *f_oneway*, this test does not assume on homoscedasticity, instead relaxing the assumption of equal variances.

Input samples must be finite, one dimensional, and with size greater than one.

References

[1]

Examples

```
>>> from scipy.stats import alexandergovern
```

Here are some data on annual percentage rate of interest charged on new car loans at nine of the largest banks in four American cities taken from the National Institute of Standards and Technology's ANOVA dataset.

We use *alexandergovern* to test the null hypothesis that all cities have the same mean APR against the alternative that the cities do not all have the same mean APR. We decide that a sigificance level of 5% is required to reject the null hypothesis in favor of the alternative.

```
>>> atlanta = [13.75, 13.75, 13.5, 13.5, 13.0, 13.0, 13.0, 12.75, 12.5]
>>> chicago = [14.25, 13.0, 12.75, 12.5, 12.5, 12.4, 12.3, 11.9, 11.9]
>>> houston = [14.0, 14.0, 13.51, 13.5, 13.5, 13.25, 13.0, 12.5, 12.5]
>>> memphis = [15.0, 14.0, 13.75, 13.59, 13.25, 12.97, 12.5, 12.25,
...           11.89]
>>> alexandergovern(atlanta, chicago, houston, memphis)
AlexanderGovernResult(statistic=4.65087071883494,
                      pvalue=0.19922132490385214)
```

The p-value is 0.1992, indicating a nearly 20% chance of observing such an extreme value of the test statistic under the null hypothesis. This exceeds 5%, so we do not reject the null hypothesis in favor of the alternative.

scipy.stats.pearsonr

scipy.stats.**pearsonr**(*x*, *y*)

Pearson correlation coefficient and p-value for testing non-correlation.

The Pearson correlation coefficient [1] measures the linear relationship between two datasets. The calculation of the p-value relies on the assumption that each dataset is normally distributed. (See Kowalski [3] for a discussion of the effects of non-normality of the input on the distribution of the correlation coefficient.) Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as x increases, so does y. Negative correlations imply that as x increases, y decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Pearson correlation at least as extreme as the one computed from these datasets.

Parameters

x [(N,) array_like] Input array.
y [(N,) array_like] Input array.

Returns

r [float] Pearson's correlation coefficient.
p-value [float] Two-tailed p-value.

Warns

PearsonRConstantInputWarning
Raised if an input is a constant array. The correlation coefficient is not defined in this case, so `np.nan` is returned.

PearsonRNearConstantInputWarning
Raised if an input is "nearly" constant. The array `x` is considered nearly constant if `norm(x - mean(x)) < 1e-13 * abs(mean(x))`. Numerical errors in the calculation `x - mean(x)` in this case might result in an inaccurate calculation of r.

See also:

spearmanr

Spearman rank-order correlation coefficient.

kendalltau

Kendall's tau, a correlation measure for ordinal data.

Notes

The correlation coefficient is calculated as follows:

$$r = \frac{\sum(x - m_x)(y - m_y)}{\sqrt{\sum(x - m_x)^2 \sum(y - m_y)^2}}$$

where m_x is the mean of the vector x and m_y is the mean of the vector y.

Under the assumption that x and m_y are drawn from independent normal distributions (so the population correlation coefficient is 0), the probability density function of the sample correlation coefficient r is ([1], [2]):

$$f(r) = \frac{(1 - r^2)^{n/2-2}}{\mathrm{B}(\frac{1}{2}, \frac{n}{2} - 1)}$$

where n is the number of samples, and B is the beta function. This is sometimes referred to as the exact distribution of r. This is the distribution that is used in *pearsonr* to compute the p-value. The distribution is a beta distribution on the interval [-1, 1], with equal shape parameters a = b = n/2 - 1. In terms of SciPy's implementation of the beta distribution, the distribution of r is:

```
dist = scipy.stats.beta(n/2 - 1, n/2 - 1, loc=-1, scale=2)
```

The p-value returned by *pearsonr* is a two-sided p-value. For a given sample with correlation coefficient r, the p-value is the probability that abs(r') of a random sample x' and y' drawn from the population with zero correlation would be greater than or equal to abs(r). In terms of the object `dist` shown above, the p-value for a given r and length n can be computed as:

```
p = 2*dist.cdf(-abs(r))
```

When n is 2, the above continuous distribution is not well-defined. One can interpret the limit of the beta distribution as the shape parameters a and b approach a = b = 0 as a discrete distribution with equal probability masses at r = 1 and r = -1. More directly, one can observe that, given the data x = [x1, x2] and y = [y1, y2], and assuming x1 != x2 and y1 != y2, the only possible values for r are 1 and -1. Because abs(r') for any sample x' and y' with length 2 will be 1, the two-sided p-value for a sample of length 2 is always 1.

References

[1], [2], [3]

Examples

```
>>> from scipy import stats
>>> a = np.array([0, 0, 0, 1, 1, 1, 1])
>>> b = np.arange(7)
>>> stats.pearsonr(a, b)
(0.8660254037844386, 0.011724811003954649)
```

```
>>> stats.pearsonr([1, 2, 3, 4, 5], [10, 9, 2.5, 6, 4])
(-0.7426106572325057, 0.1505558088534455)
```

scipy.stats.spearmanr

scipy.stats.**spearmanr**(*a*, *b=None*, *axis=0*, *nan_policy='propagate'*, *alternative='two-sided'*)

Calculate a Spearman correlation coefficient with associated p-value.

The Spearman rank-order correlation coefficient is a nonparametric measure of the monotonicity of the relationship between two datasets. Unlike the Pearson correlation, the Spearman correlation does not assume that both datasets are normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact monotonic relationship. Positive correlations imply that as x increases, so does y. Negative correlations imply that as x increases, y decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Spearman correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters

a, b [1D or 2D array_like, b is optional] One or two 1-D or 2-D arrays containing multiple variables and observations. When these are 1-D, each represents a vector of observations of a single variable. For the behavior in the 2-D case, see under `axis`, below. Both arrays need to have the same length in the `axis` dimension.

axis [int or None, optional] If axis=0 (default), then each column represents a variable, with observations in the rows. If axis=1, the relationship is transposed: each row represents a variable, while the columns contain observations. If axis=None, then both arrays will be raveled.

nan_policy

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

alternative
[{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. Default is 'two-sided'. The following options are available:
- 'two-sided': the correlation is nonzero
- 'less': the correlation is negative (less than zero)
- 'greater': the correlation is positive (greater than zero)

New in version 1.7.0.

Returns

correlation
[float or ndarray (2-D square)] Spearman correlation matrix or correlation coefficient (if only 2 variables are given as parameters. Correlation matrix is square with length equal to total number of variables (columns or rows) in `a` and `b` combined.

pvalue [float] The p-value for a hypothesis test whose null hypotheisis is that two sets of data are uncorrelated. See *alternative* above for alternative hypotheses. *pvalue* has the same shape as *correlation*.

References

[1]

Examples

```
>>> from scipy import stats
>>> stats.spearmanr([1,2,3,4,5], [5,6,7,8,7])
SpearmanrResult(correlation=0.82078..., pvalue=0.08858...)
>>> rng = np.random.default_rng()
>>> x2n = rng.standard_normal((100, 2))
>>> y2n = rng.standard_normal((100, 2))
>>> stats.spearmanr(x2n)
SpearmanrResult(correlation=-0.07960396039603959, pvalue=0.
↪4311168705769747)
>>> stats.spearmanr(x2n[:,0], x2n[:,1])
SpearmanrResult(correlation=-0.07960396039603959, pvalue=0.
↪4311168705769747)
>>> rho, pval = stats.spearmanr(x2n, y2n)
>>> rho
array([[ 1.        , -0.07960396, -0.08314431,  0.09662166],
       [-0.07960396,  1.        , -0.14448245,  0.16738074],
       [-0.08314431, -0.14448245,  1.        ,  0.03234323],
       [ 0.09662166,  0.16738074,  0.03234323,  1.        ]])
>>> pval
array([[0.        , 0.43111687, 0.41084066, 0.33891628],
       [0.43111687, 0.        , 0.15151618, 0.09600687],
       [0.41084066, 0.15151618, 0.        , 0.74938561],
       [0.33891628, 0.09600687, 0.74938561, 0.        ]])
>>> rho, pval = stats.spearmanr(x2n.T, y2n.T, axis=1)
>>> rho
array([[ 1.        , -0.07960396, -0.08314431,  0.09662166],
       [-0.07960396,  1.        , -0.14448245,  0.16738074],
       [-0.08314431, -0.14448245,  1.        ,  0.03234323],
```

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```
       [ 0.09662166,  0.16738074,  0.03234323,  1.        ]])
>>> stats.spearmanr(x2n, y2n, axis=None)
SpearmanrResult(correlation=0.044981624540613524, pvalue=0.
↪5270803651336189)
>>> stats.spearmanr(x2n.ravel(), y2n.ravel())
SpearmanrResult(correlation=0.044981624540613524, pvalue=0.
↪5270803651336189)
```

```
>>> rng = np.random.default_rng()
>>> xint = rng.integers(10, size=(100, 2))
>>> stats.spearmanr(xint)
SpearmanrResult(correlation=0.09800224850707953, pvalue=0.
↪3320271757932076)
```

scipy.stats.pointbiserialr

scipy.stats.**pointbiserialr**(*x*, *y*)

Calculate a point biserial correlation coefficient and its p-value.

The point biserial correlation is used to measure the relationship between a binary variable, x, and a continuous variable, y. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply a determinative relationship.

This function uses a shortcut formula but produces the same result as *pearsonr*.

Parameters

x [array_like of bools] Input array.
y [array_like] Input array.

Returns

correlation [float] R value.
pvalue [float] Two-sided p-value.

Notes

pointbiserialr uses a t-test with `n-1` degrees of freedom. It is equivalent to *pearsonr*.

The value of the point-biserial correlation can be calculated from:

$$r_{pb} = \frac{\overline{Y_1} - \overline{Y_0}}{s_y} \sqrt{\frac{N_1 N_2}{N(N-1))}}$$

Where Y_0 and Y_1 are means of the metric observations coded 0 and 1 respectively; N_0 and N_1 are number of observations coded 0 and 1 respectively; N is the total number of observations and s_y is the standard deviation of all the metric observations.

A value of r_{pb} that is significantly different from zero is completely equivalent to a significant difference in means between the two groups. Thus, an independent groups t Test with $N - 2$ degrees of freedom may be used to test whether r_{pb} is nonzero. The relation between the t-statistic for comparing two independent groups and r_{pb} is given by:

$$t = \sqrt{N - 2} \frac{r_{pb}}{\sqrt{1 - r_{pb}^2}}$$

References

[1], [2], [3]

Examples

```
>>> from scipy import stats
>>> a = np.array([0, 0, 0, 1, 1, 1, 1])
>>> b = np.arange(7)
>>> stats.pointbiserialr(a, b)
(0.8660254037844386, 0.011724811003954652)
>>> stats.pearsonr(a, b)
(0.86602540378443871, 0.011724811003954626)
>>> np.corrcoef(a, b)
array([[ 1.       ,  0.8660254],
       [ 0.8660254,  1.       ]])
```

scipy.stats.kendalltau

scipy.stats.**kendalltau**(*x*, *y*, *initial_lexsort=None*, *nan_policy='propagate'*, *method='auto'*, *variant='b'*)

Calculate Kendall's tau, a correlation measure for ordinal data.

Kendall's tau is a measure of the correspondence between two rankings. Values close to 1 indicate strong agreement, and values close to -1 indicate strong disagreement. This implements two variants of Kendall's tau: tau-b (the default) and tau-c (also known as Stuart's tau-c). These differ only in how they are normalized to lie within the range -1 to 1; the hypothesis tests (their p-values) are identical. Kendall's original tau-a is not implemented separately because both tau-b and tau-c reduce to tau-a in the absence of ties.

Parameters

x, y [array_like] Arrays of rankings, of the same shape. If arrays are not 1-D, they will be flattened to 1-D.

initial_lexsort
[bool, optional] Unused (deprecated).

nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):
- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

method [{'auto', 'asymptotic', 'exact'}, optional] Defines which method is used to calculate the p-value [5]. The following options are available (default is 'auto'):
- 'auto': selects the appropriate method based on a trade-off between speed and accuracy
- 'asymptotic': uses a normal approximation valid for large samples
- 'exact': computes the exact p-value, but can only be used if no ties are present. As the sample size increases, the 'exact' computation time may grow and the result may lose some precision.

variant: {'b', 'c'}, optional
Defines which variant of Kendall's tau is returned. Default is 'b'.

Returns

correlation
[float] The tau statistic.

pvalue [float] The two-sided p-value for a hypothesis test whose null hypothesis is an absence of association, tau = 0.

See also:

spearmanr

Calculates a Spearman rank-order correlation coefficient.

theilslopes

Computes the Theil-Sen estimator for a set of points (x, y).

weightedtau

Computes a weighted version of Kendall's tau.

Notes

The definition of Kendall's tau that is used is [2]:

```
tau_b = (P - Q) / sqrt((P + Q + T) * (P + Q + U))

tau_c = 2 (P - Q) / (n**2 * (m - 1) / m)
```

where P is the number of concordant pairs, Q the number of discordant pairs, T the number of ties only in *x*, and U the number of ties only in *y*. If a tie occurs for the same pair in both *x* and *y*, it is not added to either T or U. n is the total number of samples, and m is the number of unique values in either *x* or *y*, whichever is smaller.

References

[1], [2], [3], [4], [5]

Examples

```
>>> from scipy import stats
>>> x1 = [12, 2, 1, 12, 2]
>>> x2 = [1, 4, 7, 1, 0]
>>> tau, p_value = stats.kendalltau(x1, x2)
>>> tau
-0.47140452079103173
>>> p_value
0.2827454599327748
```

scipy.stats.weightedtau

scipy.stats.**weightedtau**(*x*, *y*, *rank=True*, *weigher=None*, *additive=True*)

Compute a weighted version of Kendall's τ.

The weighted τ is a weighted version of Kendall's τ in which exchanges of high weight are more influential than exchanges of low weight. The default parameters compute the additive hyperbolic version of the index, τ_h, which has been shown to provide the best balance between important and unimportant elements [1].

The weighting is defined by means of a rank array, which assigns a nonnegative rank to each element (higher importance ranks being associated with smaller values, e.g., 0 is the highest possible rank), and a weigher function, which assigns a weight based on the rank to each element. The weight of an exchange is then the sum or the product

of the weights of the ranks of the exchanged elements. The default parameters compute τ_{h}: an exchange between elements with rank r and s (starting from zero) has weight $1/(r+1) + 1/(s+1)$.

Specifying a rank array is meaningful only if you have in mind an external criterion of importance. If, as it usually happens, you do not have in mind a specific rank, the weighted τ is defined by averaging the values obtained using the decreasing lexicographical rank by (*x*, *y*) and by (*y*, *x*). This is the behavior with default parameters. Note that the convention used here for ranking (lower values imply higher importance) is opposite to that used by other SciPy statistical functions.

Parameters

x, y [array_like] Arrays of scores, of the same shape. If arrays are not 1-D, they will be flattened to 1-D.

rank [array_like of ints or bool, optional] A nonnegative rank assigned to each element. If it is None, the decreasing lexicographical rank by (*x*, *y*) will be used: elements of higher rank will be those with larger *x*-values, using *y*-values to break ties (in particular, swapping *x* and *y* will give a different result). If it is False, the element indices will be used directly as ranks. The default is True, in which case this function returns the average of the values obtained using the decreasing lexicographical rank by (*x*, *y*) and by (*y*, *x*).

weigher [callable, optional] The weigher function. Must map nonnegative integers (zero representing the most important element) to a nonnegative weight. The default, None, provides hyperbolic weighing, that is, rank r is mapped to weight $1/(r+1)$.

additive [bool, optional] If True, the weight of an exchange is computed by adding the weights of the ranks of the exchanged elements; otherwise, the weights are multiplied. The default is True.

Returns

correlation
[float] The weighted τ correlation index.

pvalue [float] Presently `np.nan`, as the null statistics is unknown (even in the additive hyperbolic case).

See also:

kendalltau

Calculates Kendall's tau.

spearmanr

Calculates a Spearman rank-order correlation coefficient.

theilslopes

Computes the Theil-Sen estimator for a set of points (x, y).

Notes

This function uses an $O(n \log n)$, mergesort-based algorithm [1] that is a weighted extension of Knight's algorithm for Kendall's τ [2]. It can compute Shieh's weighted τ [3] between rankings without ties (i.e., permutations) by setting *additive* and *rank* to False, as the definition given in [1] is a generalization of Shieh's.

NaNs are considered the smallest possible score.

New in version 0.19.0.

References

[1], [2], [3]

Examples

```
>>> from scipy import stats
>>> x = [12, 2, 1, 12, 2]
>>> y = [1, 4, 7, 1, 0]
>>> tau, p_value = stats.weightedtau(x, y)
>>> tau
-0.56694968153682723
>>> p_value
nan
>>> tau, p_value = stats.weightedtau(x, y, additive=False)
>>> tau
-0.62205716951801038
```

NaNs are considered the smallest possible score:

```
>>> x = [12, 2, 1, 12, 2]
>>> y = [1, 4, 7, 1, np.nan]
>>> tau, _ = stats.weightedtau(x, y)
>>> tau
-0.56694968153682723
```

This is exactly Kendall's tau:

```
>>> x = [12, 2, 1, 12, 2]
>>> y = [1, 4, 7, 1, 0]
>>> tau, _ = stats.weightedtau(x, y, weigher=lambda x: 1)
>>> tau
-0.47140452079103173
```

```
>>> x = [12, 2, 1, 12, 2]
>>> y = [1, 4, 7, 1, 0]
>>> stats.weightedtau(x, y, rank=None)
WeightedTauResult(correlation=-0.4157652301037516, pvalue=nan)
>>> stats.weightedtau(y, x, rank=None)
WeightedTauResult(correlation=-0.7181341329699028, pvalue=nan)
```

scipy.stats.somersd

scipy.stats.**somersd**(*x*, *y=None*)

Calculates Somers' D, an asymmetric measure of ordinal association.

Like Kendall's τ, Somers' D is a measure of the correspondence between two rankings. Both statistics consider the difference between the number of concordant and discordant pairs in two rankings X and Y, and both are normalized such that values close to 1 indicate strong agreement and values close to -1 indicate strong disagreement. They differ in how they are normalized. To show the relationship, Somers' D can be defined in terms of Kendall's τ_a:

$$D(Y|X) = \frac{\tau_a(X, Y)}{\tau_a(X, X)}$$

Suppose the first ranking X has r distinct ranks and the second ranking Y has s distinct ranks. These two lists of n rankings can also be viewed as an $r \times s$ contingency table in which element i, j is the number of rank pairs with rank i in ranking X and rank j in ranking Y. Accordingly, `somersd` also allows the input data to be supplied as a single, 2D contingency table instead of as two separate, 1D rankings.

Note that the definition of Somers' D is asymmetric: in general, $D(Y|X) \neq D(X|Y)$. `somersd(x, y)` calculates Somers' $D(Y|X)$: the "row" variable X is treated as an independent variable, and the "column" variable Y is dependent. For Somers' $D(X|Y)$, swap the input lists or transpose the input table.

Parameters

x: array_like
: 1D array of rankings, treated as the (row) independent variable. Alternatively, a 2D contingency table.

y: array_like
: If *x* is a 1D array of rankings, *y* is a 1D array of rankings of the same length, treated as the (column) dependent variable. If *x* is 2D, *y* is ignored.

Returns

res [SomersDResult] A *SomersDResult* object with the following fields:

correlation
: [float] The Somers' D statistic.

pvalue
: [float] The two-sided p-value for a hypothesis test whose null hypothesis is an absence of association, $D = 0$. See notes for more information.

table
: [2D array] The contingency table formed from rankings *x* and *y* (or the provided contingency table, if *x* is a 2D array)

See also:

kendalltau

Calculates Kendall's tau, another correlation measure.

weightedtau

Computes a weighted version of Kendall's tau.

spearmanr

Calculates a Spearman rank-order correlation coefficient.

pearsonr

Calculates a Pearson correlation coefficient.

Notes

This function follows the contingency table approach of [2] and [3]. *p*-values are computed based on an asymptotic approximation of the test statistic distribution under the null hypothesis $D = 0$.

Theoretically, hypothesis tests based on Kendall's tau and Somers' D should be identical. However, the *p*-values returned by `kendalltau` are based on the null hypothesis of *independence* between X and Y (i.e. the population from which pairs in X and Y are sampled contains equal numbers of all possible pairs), which is more specific than the null hypothesis $D = 0$ used here. If the null hypothesis of independence is desired, it is acceptable to use the *p*-value returned by `kendalltau` with the statistic returned by `somersd` and vice versa. For more information, see [2].

Contingency tables are formatted according to the convention used by SAS and R: the first ranking supplied (`x`) is the "row" variable, and the second ranking supplied (`y`) is the "column" variable. This is opposite the convention of Somers' original paper [1].

References

[1], [2], [3], [4]

Examples

We calculate Somers' D for the example given in [4], in which a hotel chain owner seeks to determine the association between hotel room cleanliness and customer satisfaction. The independent variable, hotel room cleanliness, is ranked on an ordinal scale: "below average (1)", "average (2)", or "above average (3)". The dependent variable, customer satisfaction, is ranked on a second scale: "very dissatisfied (1)", "moderately dissatisfied (2)", "neither dissatisfied nor satisfied (3)", "moderately satisfied (4)", or "very satisfied (5)". 189 customers respond to the survey, and the results are cast into a contingency table with the hotel room cleanliness as the "row" variable and customer satisfaction as the "column" variable.

	(1)	(2)	(3)	(4)	(5)
(1)	27	25	14	7	0
(2)	7	14	18	35	12
(3)	1	3	2	7	17

For example, 27 customers assigned their room a cleanliness ranking of "below average (1)" and a corresponding satisfaction of "very dissatisfied (1)". We perform the analysis as follows.

```
>>> from scipy.stats import somersd
>>> table = [[27, 25, 14, 7, 0], [7, 14, 18, 35, 12], [1, 3, 2, 7, 17]]
>>> res = somersd(table)
>>> res.statistic
0.6032766111513396
>>> res.pvalue
1.0007091191074533e-27
```

The value of the Somers' D statistic is approximately 0.6, indicating a positive correlation between room cleanliness and customer satisfaction in the sample. The *p*-value is very small, indicating a very small probability of observing such an extreme value of the statistic under the null hypothesis that the statistic of the entire population (from which our sample of 189 customers is drawn) is zero. This supports the alternative hypothesis that the true value of Somers' D for the population is nonzero.

scipy.stats.linregress

scipy.stats.**linregress**(*x*, *y=None*, *alternative='two-sided'*)

Calculate a linear least-squares regression for two sets of measurements.

Parameters

x, y [array_like] Two sets of measurements. Both arrays should have the same length. If only *x* is given (and `y=None`), then it must be a two-dimensional array where one dimension has length 2. The two sets of measurements are then found by splitting the array along the length-2 dimension. In the case where `y=None` and *x* is a 2x2 array, `linregress(x)` is equivalent to `linregress(x[0], x[1])`.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. Default is 'two-sided'. The following options are available:
- 'two-sided': the slope of the regression line is nonzero
- 'less': the slope of the regression line is less than zero
- 'greater': the slope of the regression line is greater than zero

New in version 1.7.0.

Returns

result [`LinregressResult` instance] The return value is an object with the following attributes:

slope [float] Slope of the regression line.

intercept [float] Intercept of the regression line.

rvalue [float] Correlation coefficient.

pvalue [float] The p-value for a hypothesis test whose null hypothesis is that the slope is zero, using Wald Test with t-distribution of the test statistic. See *alternative* above for alternative hypotheses.

stderr [float] Standard error of the estimated slope (gradient), under the assumption of residual normality.

intercept_stderr [float] Standard error of the estimated intercept, under the assumption of residual normality.

See also:

scipy.optimize.curve_fit

Use non-linear least squares to fit a function to data.

scipy.optimize.leastsq

Minimize the sum of squares of a set of equations.

Notes

Missing values are considered pair-wise: if a value is missing in *x*, the corresponding value in *y* is masked.

For compatibility with older versions of SciPy, the return value acts like a `namedtuple` of length 5, with fields `slope`, `intercept`, `rvalue`, `pvalue` and `stderr`, so one can continue to write:

```
slope, intercept, r, p, se = linregress(x, y)
```

With that style, however, the standard error of the intercept is not available. To have access to all the computed values, including the standard error of the intercept, use the return value as an object with attributes, e.g.:

```
result = linregress(x, y)
print(result.intercept, result.intercept_stderr)
```

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy import stats
>>> rng = np.random.default_rng()
```

Generate some data:

```
>>> x = rng.random(10)
>>> y = 1.6*x + rng.random(10)
```

Perform the linear regression:

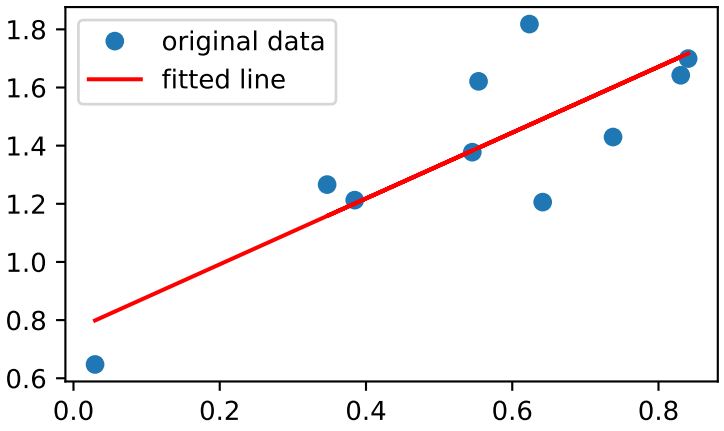
```
>>> res = stats.linregress(x, y)
```

Coefficient of determination (R-squared):

```
>>> print(f"R-squared: {res.rvalue**2:.6f}")
R-squared: 0.717533
```

Plot the data along with the fitted line:

```
>>> plt.plot(x, y, 'o', label='original data')
>>> plt.plot(x, res.intercept + res.slope*x, 'r', label='fitted line')
>>> plt.legend()
>>> plt.show()
```



Calculate 95% confidence interval on slope and intercept:

```
>>> # Two-sided inverse Students t-distribution
>>> # p - probability, df - degrees of freedom
>>> from scipy.stats import t
>>> tinv = lambda p, df: abs(t.ppf(p/2, df))
```

```
>>> ts = tinv(0.05, len(x)-2)
>>> print(f"slope (95%): {res.slope:.6f} +/- {ts*res.stderr:.6f}")
slope (95%): 1.453392 +/- 0.743465
>>> print(f"intercept (95%): {res.intercept:.6f}"
...       f" +/- {ts*res.intercept_stderr:.6f}")
intercept (95%): 0.616950 +/- 0.544475
```

scipy.stats.siegelslopes

scipy.stats.**siegelslopes**(*y*, *x=None*, *method='hierarchical'*)

Computes the Siegel estimator for a set of points (x, y).

siegelslopes implements a method for robust linear regression using repeated medians (see [1]) to fit a line to the points (x, y). The method is robust to outliers with an asymptotic breakdown point of 50%.

Parameters

y [array_like] Dependent variable.

x [array_like or None, optional] Independent variable. If None, use `arange(len(y))` instead.

method [{'hierarchical', 'separate'}] If 'hierarchical', estimate the intercept using the estimated slope `medslope` (default option). If 'separate', estimate the intercept independent of the estimated slope. See Notes for details.

Returns

medslope [float] Estimate of the slope of the regression line.

medintercept [float] Estimate of the intercept of the regression line.

See also:

theilslopes

a similar technique without repeated medians

Notes

With `n = len(y)`, compute `m_j` as the median of the slopes from the point `(x[j], y[j])` to all other *n-1* points. `medslope` is then the median of all slopes `m_j`. Two ways are given to estimate the intercept in [1] which can be chosen via the parameter `method`. The hierarchical approach uses the estimated slope `medslope` and computes `medintercept` as the median of `y - medslope*x`. The other approach estimates the intercept separately as follows: for each point `(x[j], y[j])`, compute the intercepts of all the *n-1* lines through the remaining points and take the median `i_j`. `medintercept` is the median of the `i_j`.

The implementation computes *n* times the median of a vector of size *n* which can be slow for large vectors. There are more efficient algorithms (see [2]) which are not implemented here.

References

[1], [2]

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

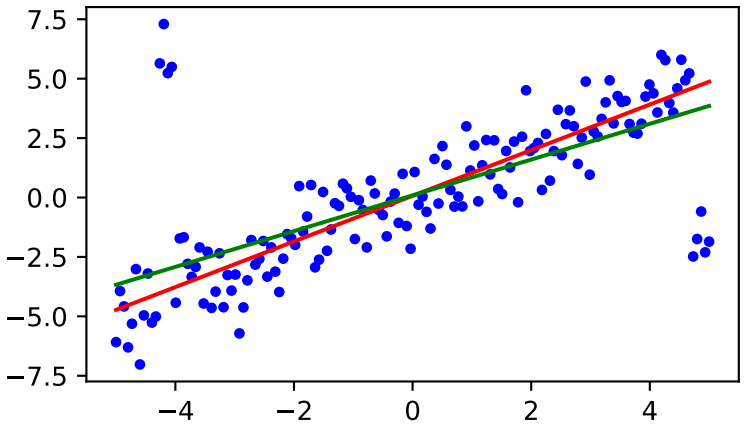
```
>>> x = np.linspace(-5, 5, num=150)
>>> y = x + np.random.normal(size=x.size)
>>> y[11:15] += 10  # add outliers
>>> y[-5:] -= 7
```

Compute the slope and intercept. For comparison, also compute the least-squares fit with *linregress*:

```
>>> res = stats.siegelslopes(y, x)
>>> lsq_res = stats.linregress(x, y)
```

Plot the results. The Siegel regression line is shown in red. The green line shows the least-squares fit for comparison.

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, y, 'b.')
>>> ax.plot(x, res[1] + res[0] * x, 'r-')
>>> ax.plot(x, lsq_res[1] + lsq_res[0] * x, 'g-')
>>> plt.show()
```



scipy.stats.theilslopes

scipy.stats.**theilslopes**(*y*, *x=None*, *alpha=0.95*)

Computes the Theil-Sen estimator for a set of points (x, y).

theilslopes implements a method for robust linear regression. It computes the slope as the median of all slopes between paired values.

Parameters

y [array_like] Dependent variable.

x [array_like or None, optional] Independent variable. If None, use `arange(len(y))` instead.

alpha [float, optional] Confidence degree between 0 and 1. Default is 95% confidence. Note that *alpha* is symmetric around 0.5, i.e. both 0.1 and 0.9 are interpreted as "find the 90% confidence interval".

Returns

medslope [float] Theil slope.

medintercept [float] Intercept of the Theil line, as `median(y) - medslope*median(x)`.

lo_slope [float] Lower bound of the confidence interval on *medslope*.

up_slope [float] Upper bound of the confidence interval on *medslope*.

See also:

siegelslopes

a similar technique using repeated medians

Notes

The implementation of *theilslopes* follows [1]. The intercept is not defined in [1], and here it is defined as `median(y) - medslope*median(x)`, which is given in [3]. Other definitions of the intercept exist in the literature. A confidence interval for the intercept is not given as this question is not addressed in [1].

References

[1], [2], [3]

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

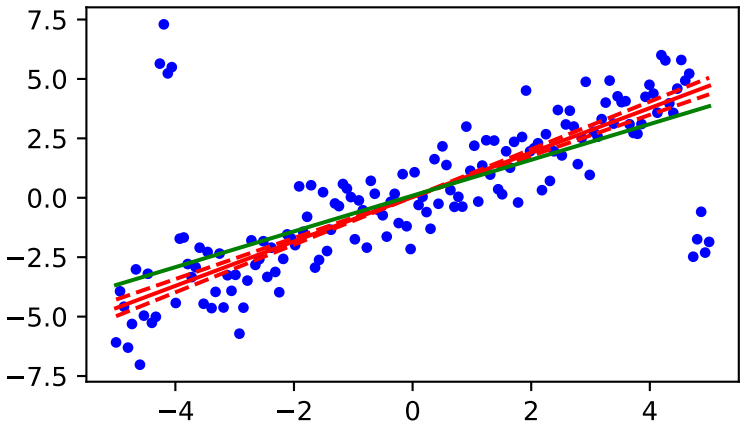
```
>>> x = np.linspace(-5, 5, num=150)
>>> y = x + np.random.normal(size=x.size)
>>> y[11:15] += 10  # add outliers
>>> y[-5:] -= 7
```

Compute the slope, intercept and 90% confidence interval. For comparison, also compute the least-squares fit with *linregress*:

```
>>> res = stats.theilslopes(y, x, 0.90)
>>> lsq_res = stats.linregress(x, y)
```

Plot the results. The Theil-Sen regression line is shown in red, with the dashed red lines illustrating the confidence interval of the slope (note that the dashed red lines are not the confidence interval of the regression as the confidence interval of the intercept is not included). The green line shows the least-squares fit for comparison.

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(x, y, 'b.')
>>> ax.plot(x, res[1] + res[0] * x, 'r-')
>>> ax.plot(x, res[1] + res[2] * x, 'r--')
>>> ax.plot(x, res[1] + res[3] * x, 'r--')
>>> ax.plot(x, lsq_res[1] + lsq_res[0] * x, 'g-')
>>> plt.show()
```



scipy.stats.multiscale_graphcorr

scipy.stats.**multiscale_graphcorr**(*x*, *y*, *compute_distance=<function _euclidean_dist>*, *reps=1000*, *workers=1*, *is_twosamp=False*, *random_state=None*)

Computes the Multiscale Graph Correlation (MGC) test statistic.

Specifically, for each point, MGC finds the k-nearest neighbors for one property (e.g. cloud density), and the l-nearest neighbors for the other property (e.g. grass wetness) [1]. This pair (k, l) is called the "scale". A priori, however, it is not know which scales will be most informative. So, MGC computes all distance pairs, and then efficiently computes the distance correlations for all scales. The local correlations illustrate which scales are relatively informative about the relationship. The key, therefore, to successfully discover and decipher relationships between disparate data modalities is to adaptively determine which scales are the most informative, and the geometric implication for the most informative scales. Doing so not only provides an estimate of whether the modalities are related, but also provides insight into how the determination was made. This is especially important in high-dimensional data, where simple visualizations do not reveal relationships to the unaided human eye. Characterizations of this implementation in particular have been derived from and benchmarked within in [2].

Parameters

x, y [ndarray] If `x` and `y` have shapes `(n, p)` and `(n, q)` where *n* is the number of samples and *p* and *q* are the number of dimensions, then the MGC independence test will be run. Alternatively, `x` and `y` can have shapes `(n, n)` if they are distance or similarity matrices, and `compute_distance` must be sent to `None`. If `x` and `y` have shapes `(n, p)` and `(m, p)`, an unpaired two-sample MGC test will be run.

compute_distance
[callable, optional] A function that computes the distance or similarity among the samples within each data matrix. Set to `None` if `x` and `y` are already distance matrices. The default uses the euclidean norm metric. If you are calling a custom function, either create the distance matrix before-hand or create a function of the form `compute_distance(x)` where *x* is the data matrix for which pairwise distances are calculated.

reps [int, optional] The number of replications used to estimate the null when using the permutation test. The default is `1000`.

workers [int or map-like callable, optional] If `workers` is an int the population is subdivided into `workers` sections and evaluated in parallel (uses `multiprocessing.Pool <multiprocessing>`). Supply `-1` to use all cores available to the Process. Alternatively supply a map-like callable, such as `multiprocessing.Pool.map` for evaluating the p-value in parallel. This evaluation is carried out as `workers(func, iterable)`. Requires that *func* be pickleable. The default is `1`.

is_twosamp
[bool, optional] If *True*, a two sample test will be run. If `x` and `y` have shapes `(n, p)` and `(m, p)`, this optional will be overriden and set to `True`. Set to `True` if `x` and `y` both have shapes `(n, p)` and a two sample test is desired. The default is `False`. Note that this will not run if inputs are distance matrices.

random_state
[{None, int, `numpy.random.Generator`,]
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.

Returns

stat [float] The sample MGC test statistic within *[-1, 1]*.

pvalue [float] The p-value obtained via permutation.

mgc_dict [dict] Contains additional useful additional returns containing the following keys:

- **mgc_map** [ndarray] A 2D representation of the latent geometry of the relationship. of the relationship.
- **opt_scale** [(int, int)] The estimated optimal scale as a *(x, y)* pair.
- **null_dist** [list] The null distribution derived from the permuted matrices

See also:

pearsonr

Pearson correlation coefficient and p-value for testing non-correlation.

kendalltau

Calculates Kendall's tau.

spearmanr

Calculates a Spearman rank-order correlation coefficient.

Notes

A description of the process of MGC and applications on neuroscience data can be found in [1]. It is performed using the following steps:

1. Two distance matrices D^X and D^Y are computed and modified to be mean zero columnwise. This results in two $n \times n$ distance matrices A and B (the centering and unbiased modification) [3].

2. For all values k and l from $1, ..., n$,

   - The k-nearest neighbor and l-nearest neighbor graphs are calculated for each property. Here, $G_k(i, j)$ indicates the k-smallest values of the i-th row of A and $H_l(i, j)$ indicates the l smallested values of the i-th row of B

   - Let $\circ$ denotes the entry-wise matrix product, then local correlations are summed and normalized using the following statistic:

$$c^{kl} = \frac{\sum_{ij} AG_kBH_l}{\sqrt{\sum_{ij} A^2G_k \times \sum_{ij} B^2H_l}}$$

1. The MGC test statistic is the smoothed optimal local correlation of $\{c^{kl}\}$. Denote the smoothing operation as $R(\cdot)$ (which essentially set all isolated large correlations) as 0 and connected large correlations the same as before, see [3].) MGC is,

$$MGC_n(x, y) = \max_{(k,l)} R\left(c^{kl}\left(x_n, y_n\right)\right)$$

The test statistic returns a value between $(-1, 1)$ since it is normalized.

The p-value returned is calculated using a permutation test. This process is completed by first randomly permuting y to estimate the null distribution and then calculating the probability of observing a test statistic, under the null, at least as extreme as the observed test statistic.

MGC requires at least 5 samples to run with reliable results. It can also handle high-dimensional data sets. In addition, by manipulating the input data matrices, the two-sample testing problem can be reduced to the independence testing problem [4]. Given sample data U and V of sizes $p \times n$ $p \times m$, data matrix X and Y can be created as follows:

$$X = [U|V] \in \mathcal{R}^{p \times (n+m)} Y = [0_{1 \times n}|1_{1 \times m}] \in \mathcal{R}^{(n+m)}$$

Then, the MGC statistic can be calculated as normal. This methodology can be extended to similar tests such as distance correlation [4].

New in version 1.4.0.

References

[1], [2], [3], [4]

Examples

```
>>> from scipy.stats import multiscale_graphcorr
>>> x = np.arange(100)
>>> y = x
>>> stat, pvalue, _ = multiscale_graphcorr(x, y, workers=-1)
>>> '%.1f, %.3f' % (stat, pvalue)
'1.0, 0.001'
```

Alternatively,

```
>>> x = np.arange(100)
>>> y = x
>>> mgc = multiscale_graphcorr(x, y)
>>> '%.1f, %.3f' % (mgc.stat, mgc.pvalue)
'1.0, 0.001'
```

To run an unpaired two-sample test,

```
>>> x = np.arange(100)
>>> y = np.arange(79)
>>> mgc = multiscale_graphcorr(x, y)
>>> '%.3f, %.2f' % (mgc.stat, mgc.pvalue)
'0.033, 0.02'
```

or, if shape of the inputs are the same,

```
>>> x = np.arange(100)
>>> y = x
>>> mgc = multiscale_graphcorr(x, y, is_twosamp=True)
>>> '%.3f, %.1f' % (mgc.stat, mgc.pvalue)
'-0.008, 1.0'
```

Statistical tests

ttest_1samp(a, popmean[, axis, nan_policy, …])	Calculate the T-test for the mean of ONE group of scores.
ttest_ind(a, b[, axis, equal_var, …])	Calculate the T-test for the means of *two independent* samples of scores.
ttest_ind_from_stats(mean1, std1, nobs1, …)	T-test for means of two independent samples from descriptive statistics.
ttest_rel(a, b[, axis, nan_policy, alternative])	Calculate the t-test on TWO RELATED samples of scores, a and b.
chisquare(f_obs[, f_exp, ddof, axis])	Calculate a one-way chi-square test.
cramervonmises(rvs, cdf[, args])	Perform the one-sample Cramér-von Mises test for goodness of fit.
cramervonmises_2samp(x, y[, method])	Perform the two-sample Cramér-von Mises test for goodness of fit.
power_divergence(f_obs[, f_exp, ddof, axis, …])	Cressie-Read power divergence statistic and goodness of fit test.
kstest(rvs, cdf[, args, N, alternative, mode])	Performs the (one-sample or two-sample) Kolmogorov-Smirnov test for goodness of fit.
ks_1samp(x, cdf[, args, alternative, mode])	Performs the one-sample Kolmogorov-Smirnov test for goodness of fit.
ks_2samp(data1, data2[, alternative, mode])	Performs the two-sample Kolmogorov-Smirnov test for goodness of fit.
epps_singleton_2samp(x, y[, t])	Compute the Epps-Singleton (ES) test statistic.
mannwhitneyu(x, y[, use_continuity, …])	Perform the Mann-Whitney U rank test on two independent samples.
tiecorrect(rankvals)	Tie correction factor for Mann-Whitney U and Kruskal-Wallis H tests.

continues on next page

Table 267 – continued from previous page

rankdata(a[, method, axis])	Assign ranks to data, dealing with ties appropriately.
ranksums(x, y[, alternative])	Compute the Wilcoxon rank-sum statistic for two samples.
wilcoxon(x[, y, zero_method, correction, …])	Calculate the Wilcoxon signed-rank test.
kruskal(*args[, nan_policy])	Compute the Kruskal-Wallis H-test for independent samples.
friedmanchisquare(*args)	Compute the Friedman test for repeated measurements.
brunnermunzel(x, y[, alternative, …])	Compute the Brunner-Munzel test on samples x and y.
combine_pvalues(pvalues[, method, weights])	Combine p-values from independent tests bearing upon the same hypothesis.
jarque_bera(x)	Perform the Jarque-Bera goodness of fit test on sample data.
page_trend_test(data[, ranked, …])	Perform Page's Test, a measure of trend in observations between treatments.

scipy.stats.ttest_1samp

scipy.stats.**ttest_1samp**(*a*, *popmean*, *axis=0*, *nan_policy='propagate'*, *alternative='two-sided'*)

Calculate the T-test for the mean of ONE group of scores.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations *a* is equal to the given population mean, *popmean*.

Parameters

a [array_like] Sample observation.

popmean [float or array_like] Expected value in null hypothesis. If array_like, then it must have the same shape as *a* excluding the axis dimension.

axis [int or None, optional] Axis along which to compute test; default is 0. If None, compute over the whole array *a*.

nan_policy

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

alternative

[{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. The following options are available (default is 'two-sided'):

- 'two-sided'
- 'less': one-sided
- 'greater': one-sided

New in version 1.6.0.

Returns

statistic [float or array] t-statistic.

pvalue [float or array] Two-sided p-value.

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50, 2), random_state=rng)
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don't reject it in the first case.

```
>>> stats.ttest_1samp(rvs, 5.0)
Ttest_1sampResult(statistic=array([-2.09794637, -1.75977004]),␣
↪pvalue=array([0.04108952, 0.08468867]))
>>> stats.ttest_1samp(rvs, 0.0)
Ttest_1sampResult(statistic=array([1.64495065, 1.62095307]),␣
↪pvalue=array([0.10638103, 0.11144602]))
```

Examples using axis and non-scalar dimension for population mean.

```
>>> result = stats.ttest_1samp(rvs, [5.0, 0.0])
>>> result.statistic
array([-2.09794637,  1.62095307])
>>> result.pvalue
array([0.04108952, 0.11144602])
```

```
>>> result = stats.ttest_1samp(rvs.T, [5.0, 0.0], axis=1)
>>> result.statistic
array([-2.09794637,  1.62095307])
>>> result.pvalue
array([0.04108952, 0.11144602])
```

```
>>> result = stats.ttest_1samp(rvs, [[5.0], [0.0]])
>>> result.statistic
array([[-2.09794637, -1.75977004],
       [ 1.64495065,  1.62095307]])
>>> result.pvalue
array([[0.04108952, 0.08468867],
       [0.10638103, 0.11144602]])
```

scipy.stats.ttest_ind

scipy.stats.**ttest_ind**(*a*, *b*, *axis=0*, *equal_var=True*, *nan_policy='propagate'*, *permutations=None*, *random_state=None*, *alternative='two-sided'*, *trim=0*)

Calculate the T-test for the means of *two independent* samples of scores.

This is a two-sided test for the null hypothesis that 2 independent samples have identical average (expected) values. This test assumes that the populations have identical variances by default.

Parameters

a, b [array_like] The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

equal_var [bool, optional] If True (default), perform a standard independent 2 sample test that assumes equal population variances [1]. If False, perform Welch's t-test, which does not assume equal

population variance [2].
New in version 0.11.0.

nan_policy

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

The 'omit' option is not currently available for permutation tests or one-sided asympyotic tests.

permutations

[non-negative int, np.inf, or None (default), optional] If 0 or None (default), use the t-distribution to calculate p-values. Otherwise, *permutations* is the number of random permutations that will be used to estimate p-values using a permutation test. If *permutations* equals or exceeds the number of distinct partitions of the pooled data, an exact test is performed instead (i.e. each distinct partition is used exactly once). See Notes for details.
New in version 1.7.0.

random_state

[{None, int, `numpy.random.Generator`,
`numpy.random.RandomState`}, optional
If *seed* is None (or *np.random*), the `numpy.random.RandomState` singleton is used. If *seed* is an int, a new `RandomState` instance is used, seeded with *seed*. If *seed* is already a `Generator` or `RandomState` instance then that instance is used.
Pseudorandom number generator state used to generate permutations (used only when *permutations* is not None).
New in version 1.7.0.

alternative

[{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. The following options are available (default is 'two-sided'):

- 'two-sided'
- 'less': one-sided
- 'greater': one-sided

New in version 1.6.0.

trim [float, optional] If nonzero, performs a trimmed (Yuen's) t-test. Defines the fraction of elements to be trimmed from each end of the input samples. If 0 (default), no elements will be trimmed from either side. The number of trimmed elements from each tail is the floor of the trim times the number of elements. Valid range is [0, .5).
New in version 1.7.

Returns

statistic [float or array] The calculated t-statistic.
pvalue [float or array] The two-tailed p-value.

Notes

Suppose we observe two independent samples, e.g. flower petal lengths, and we are considering whether the two samples were drawn from the same population (e.g. the same species of flower or two species with similar petal characteristics) or two different populations.

The t-test quantifies the difference between the arithmetic means of the two samples. The p-value quantifies the probability of observing as or more extreme values assuming the null hypothesis, that the samples are drawn from populations with the same population means, is true. A p-value larger than a chosen threshold (e.g. 5% or 1%) indicates that our observation is not so unlikely to have occurred by chance. Therefore, we do not reject the null

hypothesis of equal population means. If the p-value is smaller than our threshold, then we have evidence against the null hypothesis of equal population means.

By default, the p-value is determined by comparing the t-statistic of the observed data against a theoretical t-distribution. When `1 < permutations < binom(n, k)`, where

- `k` is the number of observations in *a*,
- `n` is the total number of observations in *a* and *b*, and
- `binom(n, k)` is the binomial coefficient (`n` choose `k`),

the data are pooled (concatenated), randomly assigned to either group *a* or *b*, and the t-statistic is calculated. This process is performed repeatedly (*permutation* times), generating a distribution of the t-statistic under the null hypothesis, and the t-statistic of the observed data is compared to this distribution to determine the p-value. When `permutations >= binom(n, k)`, an exact test is performed: the data are partitioned between the groups in each distinct way exactly once.

The permutation test can be computationally expensive and not necessarily more accurate than the analytical test, but it does not make strong assumptions about the shape of the underlying distribution.

Use of trimming is commonly referred to as the trimmed t-test. At times called Yuen's t-test, this is an extension of Welch's t-test, with the difference being the use of winsorized means in calculation of the variance and the trimmed sample size in calculation of the statistic. Trimming is reccomended if the underlying distribution is long-tailed or contaminated with outliers [4].

References

[1], [2], [3], [4], [5]

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
```

Test with sample with identical means:

```
>>> rvs1 = stats.norm.rvs(loc=5, scale=10, size=500, random_state=rng)
>>> rvs2 = stats.norm.rvs(loc=5, scale=10, size=500, random_state=rng)
>>> stats.ttest_ind(rvs1, rvs2)
Ttest_indResult(statistic=-0.4390847099199348, pvalue=0.6606952038870015)
>>> stats.ttest_ind(rvs1, rvs2, equal_var=False)
Ttest_indResult(statistic=-0.4390847099199348, pvalue=0.6606952553131064)
```

ttest_ind underestimates p for unequal variances:

```
>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500, random_state=rng)
>>> stats.ttest_ind(rvs1, rvs3)
Ttest_indResult(statistic=-1.6370984482905417, pvalue=0.1019251574705033)
>>> stats.ttest_ind(rvs1, rvs3, equal_var=False)
Ttest_indResult(statistic=-1.637098448290542, pvalue=0.10202110497954867)
```

When `n1 != n2`, the equal variance t-statistic is no longer equal to the unequal variance t-statistic:

```
>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100, random_state=rng)
>>> stats.ttest_ind(rvs1, rvs4)
Ttest_indResult(statistic=-1.9481646859513422, pvalue=0.05186270935842703)
>>> stats.ttest_ind(rvs1, rvs4, equal_var=False)
Ttest_indResult(statistic=-1.3146566100751664, pvalue=0.1913495266513811)
```

T-test with different means, variance, and n:

```
>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100, random_state=rng)
>>> stats.ttest_ind(rvs1, rvs5)
Ttest_indResult(statistic=-2.8415950600298774, pvalue=0.
↪0046418707568707885)
>>> stats.ttest_ind(rvs1, rvs5, equal_var=False)
Ttest_indResult(statistic=-1.8686598649188084, pvalue=0.06434714193919686)
```

When performing a permutation test, more permutations typically yields more accurate results. Use a `np.random.Generator` to ensure reproducibility:

```
>>> stats.ttest_ind(rvs1, rvs5, permutations=10000,
...                 random_state=rng)
Ttest_indResult(statistic=-2.8415950600298774, pvalue=0.0052)
```

Take these two samples, one of which has an extreme tail.

```
>>> a = (56, 128.6, 12, 123.8, 64.34, 78, 763.3)
>>> b = (1.1, 2.9, 4.2)
```

Use the *trim* keyword to perform a trimmed (Yuen) t-test. For example, using 20% trimming, `trim=.2`, the test will reduce the impact of one (`np.floor(trim*len(a))`) element from each tail of sample *a*. It will have no effect on sample *b* because `np.floor(trim*len(b))` is 0.

```
>>> stats.ttest_ind(a, b, trim=.2)
Ttest_indResult(statistic=3.4463884028073513,
                pvalue=0.01369338726499547)
```

scipy.stats.ttest_ind_from_stats

scipy.stats.**ttest_ind_from_stats**(*mean1*, *std1*, *nobs1*, *mean2*, *std2*, *nobs2*, *equal_var=True*, *alternative='two-sided'*)

T-test for means of two independent samples from descriptive statistics.

This is a two-sided test for the null hypothesis that two independent samples have identical average (expected) values.

Parameters

mean1 [array_like] The mean(s) of sample 1.
std1 [array_like] The standard deviation(s) of sample 1.
nobs1 [array_like] The number(s) of observations of sample 1.
mean2 [array_like] The mean(s) of sample 2.
std2 [array_like] The standard deviations(s) of sample 2.
nobs2 [array_like] The number(s) of observations of sample 2.
equal_var [bool, optional] If True (default), perform a standard independent 2 sample test that assumes equal population variances [1]. If False, perform Welch's t-test, which does not assume equal population variance [2].

alternative
[{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. The following options are available (default is 'two-sided'):
- 'two-sided'
- 'less': one-sided
- 'greater': one-sided

New in version 1.6.0.

Returns

statistic [float or array] The calculated t-statistics.
pvalue [float or array] The two-tailed p-value.

See also:

`scipy.stats.ttest_ind`

Notes

New in version 0.16.0.

References

[1], [2]

Examples

Suppose we have the summary data for two samples, as follows:

```
                 Sample   Sample
           Size   Mean   Variance
Sample 1    13    15.0     87.5
Sample 2    11    12.0     39.0
```

Apply the t-test to this data (with the assumption that the population variances are equal):

```
>>> from scipy.stats import ttest_ind_from_stats
>>> ttest_ind_from_stats(mean1=15.0, std1=np.sqrt(87.5), nobs1=13,
...                      mean2=12.0, std2=np.sqrt(39.0), nobs2=11)
Ttest_indResult(statistic=0.9051358093310269, pvalue=0.3751996797581487)
```

For comparison, here is the data from which those summary statistics were taken. With this data, we can compute the same result using *scipy.stats.ttest_ind*:

```
>>> a = np.array([1, 3, 4, 6, 11, 13, 15, 19, 22, 24, 25, 26, 26])
>>> b = np.array([2, 4, 6, 9, 11, 13, 14, 15, 18, 19, 21])
>>> from scipy.stats import ttest_ind
>>> ttest_ind(a, b)
Ttest_indResult(statistic=0.905135809331027, pvalue=0.3751996797581486)
```

Suppose we instead have binary data and would like to apply a t-test to compare the proportion of 1s in two independent groups:

```
                  Number of    Sample     Sample
            Size    ones        Mean     Variance
Sample 1    150      30         0.2        0.16
Sample 2    200      45         0.225      0.174375
```

The sample mean $\hat{p}$ is the proportion of ones in the sample and the variance for a binary observation is estimated by $\hat{p}(1-\hat{p})$.

```
>>> ttest_ind_from_stats(mean1=0.2, std1=np.sqrt(0.16), nobs1=150,
...                      mean2=0.225, std2=np.sqrt(0.17437), nobs2=200)
Ttest_indResult(statistic=-0.564327545549774, pvalue=0.5728947691244874)
```

For comparison, we could compute the t statistic and p-value using arrays of 0s and 1s and *scipy.stat.ttest_ind*, as above.

```
>>> group1 = np.array([1]*30 + [0]*(150-30))
>>> group2 = np.array([1]*45 + [0]*(200-45))
>>> ttest_ind(group1, group2)
Ttest_indResult(statistic=-0.5627179589855622, pvalue=0.573989277115258)
```

scipy.stats.ttest_rel

scipy.stats.**ttest_rel**(*a*, *b*, *axis=0*, *nan_policy='propagate'*, *alternative='two-sided'*)

Calculate the t-test on TWO RELATED samples of scores, a and b.

This is a two-sided test for the null hypothesis that 2 related or repeated samples have identical average (expected) values.

Parameters

a, b [array_like] The arrays must have the same shape.

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. The following options are available (default is 'two-sided'):

- 'two-sided'
- 'less': one-sided
- 'greater': one-sided

New in version 1.6.0.

Returns

statistic [float or array] t-statistic.

pvalue [float or array] Two-sided p-value.

Notes

Examples for use are scores of the same set of student in different exams, or repeated sampling from the same units. The test measures whether the average score differs significantly across samples (e.g. exams). If we observe a large p-value, for example greater than 0.05 or 0.1 then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages. Small p-values are associated with large t-statistics.

References

https://en.wikipedia.org/wiki/T-test#Dependent_t-test_for_paired_samples

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
```

```
>>> rvs1 = stats.norm.rvs(loc=5, scale=10, size=500, random_state=rng)
>>> rvs2 = (stats.norm.rvs(loc=5, scale=10, size=500, random_state=rng)
...         + stats.norm.rvs(scale=0.2, size=500, random_state=rng))
>>> stats.ttest_rel(rvs1, rvs2)
Ttest_relResult(statistic=-0.4549717054410304, pvalue=0.6493274702088672)
>>> rvs3 = (stats.norm.rvs(loc=8, scale=10, size=500, random_state=rng)
...         + stats.norm.rvs(scale=0.2, size=500, random_state=rng))
>>> stats.ttest_rel(rvs1, rvs3)
Ttest_relResult(statistic=-5.879467544540889, pvalue=7.540777129099917e-
↪09)
```

scipy.stats.chisquare

scipy.stats.**chisquare**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*)

Calculate a one-way chi-square test.

The chi-square test tests the null hypothesis that the categorical data has the given frequencies.

Parameters

f_obs [array_like] Observed frequencies in each category.

f_exp [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof [int, optional] "Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis [int or None, optional] The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

Returns

chisq [float or ndarray] The chi-squared test statistic. The value is a float if *axis* is None or *f_obs* and *f_exp* are 1-D.

p [float or ndarray] The p-value of the test. The value is a float if *ddof* and the return value *chisq* are scalars.

See also:

scipy.stats.power_divergence

scipy.stats.fisher_exact

Fisher exact test on a 2x2 contingency table.

scipy.stats.barnard_exact

An unconditional exact test. An alternative to chi-squared test for small sample sizes.

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5. According to [3], the total number of samples is recommended to be greater than 13, otherwise exact tests (such as Barnard's Exact test) should be used because they do not overreject.

Also, the sum of the observed and expected frequencies must be the same for the test to be valid; *chisquare* raises an error if the sums do not agree within a relative tolerance of `1e-8`.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not chi-square, in which case this test is not appropriate.

References

[1], [2], [3]

Examples

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```
>>> from scipy.stats import chisquare
>>> chisquare([16, 18, 16, 14, 12, 12])
(2.0, 0.84914503608460956)
```

With *f_exp* the expected frequencies can be given.

```
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])
(3.5, 0.62338762774958223)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> chisquare(obs)
(array([ 2.        ,  6.66666667]), array([ 0.84914504,  0.24663415]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> chisquare(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> chisquare(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.7357588823428847)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with *ddof*.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we use `axis=1`:

```
>>> chisquare([16, 18, 16, 14, 12, 12],
...           f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
...           axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

scipy.stats.cramervonmises

`scipy.stats.`**`cramervonmises`**(*rvs*, *cdf*, *args=()*)

Perform the one-sample Cramér-von Mises test for goodness of fit.

This performs a test of the goodness of fit of a cumulative distribution function (cdf) F compared to the empirical distribution function F_n of observed random variates $X_1, ..., X_n$ that are assumed to be independent and identically distributed ([1]). The null hypothesis is that the X_i have cumulative distribution F.

Parameters

rvs : [array_like] A 1-D array of observed values of the random variables X_i.

cdf : [str or callable] The cumulative distribution function F to test the observations against. If a string, it should be the name of a distribution in *scipy.stats*. If a callable, that callable is used to calculate the cdf: `cdf(x, *args) -> float`.

args : [tuple, optional] Distribution parameters. These are assumed to be known; see Notes.

Returns

res : [object with attributes]

- **statistic** : [float] Cramér-von Mises statistic.
- **pvalue** : [float] The p-value.

See also:

kstest, **cramervonmises_2samp**

Notes

New in version 1.6.0.

The p-value relies on the approximation given by equation 1.8 in [2]. It is important to keep in mind that the p-value is only accurate if one tests a simple hypothesis, i.e. the parameters of the reference distribution are known. If the parameters are estimated from the data (composite hypothesis), the computed p-value is not reliable.

References

[1], [2]

Examples

Suppose we wish to test whether data generated by `scipy.stats.norm.rvs` were, in fact, drawn from the standard normal distribution. We choose a significance level of alpha=0.05.

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
>>> x = stats.norm.rvs(size=500, random_state=rng)
>>> res = stats.cramervonmises(x, 'norm')
>>> res.statistic, res.pvalue
(0.49121480855028343, 0.04189256516661377)
```

The p-value 0.79 exceeds our chosen significance level, so we do not reject the null hypothesis that the observed sample is drawn from the standard normal distribution.

Now suppose we wish to check whether the same samples shifted by 2.1 is consistent with being drawn from a normal distribution with a mean of 2.

```
>>> y = x + 2.1
>>> res = stats.cramervonmises(y, 'norm', args=(2,))
>>> res.statistic, res.pvalue
(0.07400330012187435, 0.7274595666160468)
```

Here we have used the *args* keyword to specify the mean (`loc`) of the normal distribution to test the data against. This is equivalent to the following, in which we create a frozen normal distribution with mean 2.1, then pass its `cdf` method as an argument.

```
>>> frozen_dist = stats.norm(loc=2)
>>> res = stats.cramervonmises(y, frozen_dist.cdf)
>>> res.statistic, res.pvalue
(0.07400330012187435, 0.7274595666160468)
```

In either case, we would reject the null hypothesis that the observed sample is drawn from a normal distribution with a mean of 2 (and default variance of 1) because the p-value 0.04 is less than our chosen significance level.

scipy.stats.cramervonmises_2samp

scipy.stats.**cramervonmises_2samp**(*x*, *y*, *method='auto'*)

Perform the two-sample Cramér-von Mises test for goodness of fit.

This is the two-sample version of the Cramér-von Mises test ([1]): for two independent samples $X_1, ..., X_n$ and $Y_1, ..., Y_m$, the null hypothesis is that the samples come from the same (unspecified) continuous distribution.

Parameters

x [array_like] A 1-D array of observed values of the random variables X_i.
y [array_like] A 1-D array of observed values of the random variables Y_i.
method [{'auto', 'asymptotic', 'exact'}, optional] The method used to compute the p-value, see Notes for details. The default is 'auto'.

Returns

res [object with attributes]
statistic [float] Cramér-von Mises statistic.
pvalue [float] The p-value.

See also:

cramervonmises, **anderson_ksamp**, **epps_singleton_2samp**, **ks_2samp**

Notes

New in version 1.7.0.

The statistic is computed according to equation 9 in [2]. The calculation of the p-value depends on the keyword *method*:

- `asymptotic`: The p-value is approximated by using the limiting distribution of the test statistic.
- `exact`: The exact p-value is computed by enumerating all possible combinations of the test statistic, see [2].

The exact calculation will be very slow even for moderate sample sizes as the number of combinations increases rapidly with the size of the samples. If `method=='auto'`, the exact approach is used if both samples contain less than 10 observations, otherwise the asymptotic distribution is used.

If the underlying distribution is not continuous, the p-value is likely to be conservative (Section 6.2 in [3]). When ranking the data to compute the test statistic, midranks are used if there are ties.

References

[1], [2], [3]

Examples

Suppose we wish to test whether two samples generated by `scipy.stats.norm.rvs` have the same distribution. We choose a significance level of alpha=0.05.

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
>>> x = stats.norm.rvs(size=100, random_state=rng)
>>> y = stats.norm.rvs(size=70, random_state=rng)
>>> res = stats.cramervonmises_2samp(x, y)
```

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```
>>> res.statistic, res.pvalue
(0.29376470588235293, 0.1412873014573014)
```

The p-value exceeds our chosen significance level, so we do not reject the null hypothesis that the observed samples are drawn from the same distribution.

For small sample sizes, one can compute the exact p-values:

```
>>> x = stats.norm.rvs(size=7, random_state=rng)
>>> y = stats.t.rvs(df=2, size=6, random_state=rng)
>>> res = stats.cramervonmises_2samp(x, y, method='exact')
>>> res.statistic, res.pvalue
(0.197802197802198, 0.31643356643356646)
```

The p-value based on the asymptotic distribution is a good approximation even though the sample size is small.

```
>>> res = stats.cramervonmises_2samp(x, y, method='asymptotic')
>>> res.statistic, res.pvalue
(0.197802197802198, 0.2966041181527128)
```

Independent of the method, one would not reject the null hypothesis at the chosen significance level in this example.

scipy.stats.power_divergence

scipy.stats.**power_divergence**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*, *lambda_=None*)

Cressie-Read power divergence statistic and goodness of fit test.

This function tests the null hypothesis that the categorical data has the given frequencies, using the Cressie-Read power divergence statistic.

Parameters

f_obs [array_like] Observed frequencies in each category.

f_exp [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof [int, optional] "Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis [int or None, optional] The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

lambda_ [float or str, optional] The power in the Cressie-Read power divergence statistic. The default is 1. For convenience, *lambda_* may be assigned one of the following strings, in which case the corresponding numerical value is used:

```
String              Value   Description
"pearson"             1     Pearson's chi-squared␣
↪statistic.
                            In this case, the function is
                            equivalent to `stats.
↪chisquare`.
"log-likelihood"      0     Log-likelihood ratio. Also␣
↪known as
                            the G-test [Rf6c2a1ea428c-3]_.
```

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```
"freeman-tukey"      -1/2   Freeman-Tukey statistic.
"mod-log-likelihood" -1     Modified log-likelihood ratio.
"neyman"             -2     Neyman's statistic.
"cressie-read"        2/3   The power recommended in␣
↪[Rf6c2a1ea428c-5]_.
```

Returns

statistic [float or ndarray] The Cressie-Read power divergence test statistic. The value is a float if *axis* is None or if` *f_obs* and *f_exp* are 1-D.

pvalue [float or ndarray] The p-value of the test. The value is a float if *ddof* and the return value `stat` are scalars.

See also:

`chisquare`

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

Also, the sum of the observed and expected frequencies must be the same for the test to be valid; *`power_divergence`* raises an error if the sums do not agree within a relative tolerance of `1e-8`.

When *lambda_* is less than zero, the formula for the statistic involves dividing by *f_obs*, so a warning or error may be generated if any value in *f_obs* is 0.

Similarly, a warning or error may be generated if any value in *f_exp* is zero when *lambda_* >= 0.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

This function handles masked arrays. If an element of *f_obs* or *f_exp* is masked, then data at that position is ignored, and does not count towards the size of the data set.

New in version 0.13.0.

References

[1], [2], [3], [4], [5]

Examples

(See *`chisquare`* for more examples.)

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies. Here we perform a G-test (i.e. use the log-likelihood ratio statistic):

```
>>> from scipy.stats import power_divergence
>>> power_divergence([16, 18, 16, 14, 12, 12], lambda_='log-likelihood')
(2.006573162632538, 0.84823476779463769)
```

The expected frequencies can be given with the *f_exp* argument:

```
>>> power_divergence([16, 18, 16, 14, 12, 12],
...                  f_exp=[16, 16, 16, 16, 16, 8],
...                  lambda_='log-likelihood')
(3.3281031458963746, 0.6495419288047497)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> power_divergence(obs, lambda_="log-likelihood")
(array([ 2.00657316,  6.77634498]), array([ 0.84823477,  0.23781225]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> power_divergence(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> power_divergence(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.7357588823428847)
```

The calculation of the p-values is done by broadcasting the test statistic with *ddof*.

```
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we must use `axis=1`:

```
>>> power_divergence([16, 18, 16, 14, 12, 12],
...                  f_exp=[[16, 16, 16, 16, 16, 8],
...                         [8, 20, 20, 16, 12, 12]],
...                  axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

scipy.stats.kstest

`scipy.stats.`**`kstest`**(*rvs*, *cdf*, *args=()*, *N=20*, *alternative='two-sided'*, *mode='auto'*)

Performs the (one-sample or two-sample) Kolmogorov-Smirnov test for goodness of fit.

The one-sample test compares the underlying distribution F(x) of a sample against a given distribution G(x). The two-sample test compares the underlying distributions of two independent samples. Both tests are valid only for continuous distributions.

Parameters

rvs [str, array_like, or callable] If an array, it should be a 1-D array of observations of random variables. If a callable, it should be a function to generate random variables; it is required to

have a keyword argument *size*. If a string, it should be the name of a distribution in *scipy.stats*, which will be used to generate random variables.

cdf [str, array_like or callable] If array_like, it should be a 1-D array of observations of random variables, and the two-sample test is performed (and rvs must be array_like). If a callable, that callable is used to calculate the cdf. If a string, it should be the name of a distribution in *scipy.stats*, which will be used as the cdf function.

args [tuple, sequence, optional] Distribution parameters, used if *rvs* or *cdf* are strings or callables.

N [int, optional] Sample size if *rvs* is string or callable. Default is 20.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the null and alternative hypotheses. Default is 'two-sided'. Please see explanations in the Notes below.

mode [{'auto', 'exact', 'approx', 'asymp'}, optional] Defines the distribution used for calculating the p-value. The following options are available (default is 'auto'):

- 'auto' : selects one of the other options.
- 'exact' : uses the exact distribution of test statistic.
- 'approx' : approximates the two-sided probability with twice the one-sided probability
- 'asymp': uses asymptotic distribution of test statistic

Returns

statistic [float] KS test statistic, either D, D+ or D-.

pvalue [float] One-tailed or two-tailed p-value.

See also:

ks_2samp

Notes

There are three options for the null and corresponding alternative hypothesis that can be selected using the *alternative* parameter.

- *two-sided*: The null hypothesis is that the two distributions are identical, F(x)=G(x) for all x; the alternative is that they are not identical.
- *less*: The null hypothesis is that F(x) >= G(x) for all x; the alternative is that F(x) < G(x) for at least one x.
- *greater*: The null hypothesis is that F(x) <= G(x) for all x; the alternative is that F(x) > G(x) for at least one x.

Note that the alternative hypotheses describe the *CDFs* of the underlying distributions, not the observed values. For example, suppose x1 ~ F and x2 ~ G. If F(x) > G(x) for all x, the values in x1 tend to be less than those in x2.

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
```

```
>>> x = np.linspace(-15, 15, 9)
>>> stats.kstest(x, 'norm')
KstestResult(statistic=0.444356027159..., pvalue=0.038850140086...)
```

```
>>> stats.kstest(stats.norm.rvs(size=100, random_state=rng), stats.norm.
↪cdf)
KstestResult(statistic=0.165471391799..., pvalue=0.007331283245...)
```

The above lines are equivalent to:

```
>>> stats.kstest(stats.norm.rvs, 'norm', N=100)
KstestResult(statistic=0.113810164200..., pvalue=0.138690052319...)  #␣
↪may vary
```

Test against one-sided alternative hypothesis

Shift distribution to larger values, so that `CDF(x) < norm.cdf(x)`:

```
>>> x = stats.norm.rvs(loc=0.2, size=100, random_state=rng)
>>> stats.kstest(x, 'norm', alternative='less')
KstestResult(statistic=0.1002033514..., pvalue=0.1255446444...)
```

Reject null hypothesis in favor of alternative hypothesis: less

```
>>> stats.kstest(x, 'norm', alternative='greater')
KstestResult(statistic=0.018749806388..., pvalue=0.920581859791...)
```

Don't reject null hypothesis in favor of alternative hypothesis: greater

```
>>> stats.kstest(x, 'norm')
KstestResult(statistic=0.100203351482..., pvalue=0.250616879765...)
```

Testing t distributed random variables against normal distribution

With 100 degrees of freedom the t distribution looks close to the normal distribution, and the K-S test does not reject the hypothesis that the sample came from the normal distribution:

```
>>> stats.kstest(stats.t.rvs(100, size=100, random_state=rng), 'norm')
KstestResult(statistic=0.064273776544..., pvalue=0.778737758305...)
```

With 3 degrees of freedom the t distribution looks sufficiently different from the normal distribution, that we can reject the hypothesis that the sample came from the normal distribution at the 10% level:

```
>>> stats.kstest(stats.t.rvs(3, size=100, random_state=rng), 'norm')
KstestResult(statistic=0.128678487493..., pvalue=0.066569081515...)
```

scipy.stats.ks_1samp

`scipy.stats.`**`ks_1samp`**(*x*, *cdf*, *args=()*, *alternative='two-sided'*, *mode='auto'*)

Performs the one-sample Kolmogorov-Smirnov test for goodness of fit.

This test compares the underlying distribution F(x) of a sample against a given continuous distribution G(x). See Notes for a description of the available null and alternative hypotheses.

Parameters

x [array_like] a 1-D array of observations of iid random variables.

cdf [callable] callable used to calculate the cdf.

args [tuple, sequence, optional] Distribution parameters, used with *cdf*.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the null and alternative hypotheses. Default is 'two-sided'. Please see explanations in the Notes below.

mode [{'auto', 'exact', 'approx', 'asymp'}, optional] Defines the distribution used for calculating the p-value. The following options are available (default is 'auto'):

- 'auto' : selects one of the other options.
- 'exact' : uses the exact distribution of test statistic.

- 'approx' : approximates the two-sided probability with twice the one-sided probability
- 'asymp': uses asymptotic distribution of test statistic

Returns

statistic [float] KS test statistic, either D, D+ or D- (depending on the value of 'alternative')
pvalue [float] One-tailed or two-tailed p-value.

See also:

ks_2samp, **kstest**

Notes

There are three options for the null and corresponding alternative hypothesis that can be selected using the *alternative* parameter.

- *two-sided*: The null hypothesis is that the two distributions are identical, F(x)=G(x) for all x; the alternative is that they are not identical.
- *less*: The null hypothesis is that F(x) >= G(x) for all x; the alternative is that F(x) < G(x) for at least one x.
- *greater*: The null hypothesis is that F(x) <= G(x) for all x; the alternative is that F(x) > G(x) for at least one x.

Note that the alternative hypotheses describe the *CDFs* of the underlying distributions, not the observed values. For example, suppose x1 ~ F and x2 ~ G. If F(x) > G(x) for all x, the values in x1 tend to be less than those in x2.

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
```

```
>>> x = np.linspace(-15, 15, 9)
>>> stats.ks_1samp(x, stats.norm.cdf)
(0.44435602715924361, 0.038850142705171065)
```

```
>>> stats.ks_1samp(stats.norm.rvs(size=100, random_state=rng),
...                stats.norm.cdf)
KstestResult(statistic=0.165471391799..., pvalue=0.007331283245...)
```

Test against one-sided alternative hypothesis

Shift distribution to larger values, so that `` CDF(x) < norm.cdf(x)``:

```
>>> x = stats.norm.rvs(loc=0.2, size=100, random_state=rng)
>>> stats.ks_1samp(x, stats.norm.cdf, alternative='less')
KstestResult(statistic=0.100203351482..., pvalue=0.125544644447...)
```

Reject null hypothesis in favor of alternative hypothesis: less

```
>>> stats.ks_1samp(x, stats.norm.cdf, alternative='greater')
KstestResult(statistic=0.018749806388..., pvalue=0.920581859791...)
```

Reject null hypothesis in favor of alternative hypothesis: greater

```
>>> stats.ks_1samp(x, stats.norm.cdf)
KstestResult(statistic=0.100203351482..., pvalue=0.250616879765...)
```

Don't reject null hypothesis in favor of alternative hypothesis: two-sided

Testing t distributed random variables against normal distribution

With 100 degrees of freedom the t distribution looks close to the normal distribution, and the K-S test does not reject the hypothesis that the sample came from the normal distribution:

```
>>> stats.ks_1samp(stats.t.rvs(100,size=100, random_state=rng),
...                stats.norm.cdf)
KstestResult(statistic=0.064273776544..., pvalue=0.778737758305...)
```

With 3 degrees of freedom the t distribution looks sufficiently different from the normal distribution, that we can reject the hypothesis that the sample came from the normal distribution at the 10% level:

```
>>> stats.ks_1samp(stats.t.rvs(3,size=100, random_state=rng),
...                stats.norm.cdf)
KstestResult(statistic=0.128678487493..., pvalue=0.066569081515...)
```

scipy.stats.ks_2samp

scipy.stats.**ks_2samp**(*data1*, *data2*, *alternative='two-sided'*, *mode='auto'*)

Performs the two-sample Kolmogorov-Smirnov test for goodness of fit.

This test compares the underlying continuous distributions F(x) and G(x) of two independent samples. See Notes for a description of the available null and alternative hypotheses.

Parameters

data1, data2
: [array_like, 1-Dimensional] Two arrays of sample observations assumed to be drawn from a continuous distribution, sample sizes can be different.

alternative
: [{'two-sided', 'less', 'greater'}, optional] Defines the null and alternative hypotheses. Default is 'two-sided'. Please see explanations in the Notes below.

mode
: [{'auto', 'exact', 'asymp'}, optional] Defines the method used for calculating the p-value. The following options are available (default is 'auto'):
- 'auto' : use 'exact' for small size arrays, 'asymp' for large
- 'exact' : use exact distribution of test statistic
- 'asymp' : use asymptotic distribution of test statistic

Returns

statistic
: [float] KS statistic.

pvalue
: [float] One-tailed or two-tailed p-value.

See also:

kstest, **ks_1samp**, **epps_singleton_2samp**, **anderson_ksamp**

Notes

There are three options for the null and corresponding alternative hypothesis that can be selected using the *alternative* parameter.

- *two-sided*: The null hypothesis is that the two distributions are identical, F(x)=G(x) for all x; the alternative is that they are not identical.
- *less*: The null hypothesis is that F(x) >= G(x) for all x; the alternative is that F(x) < G(x) for at least one x.
- *greater*: The null hypothesis is that F(x) <= G(x) for all x; the alternative is that F(x) > G(x) for at least one x.

Note that the alternative hypotheses describe the *CDFs* of the underlying distributions, not the observed values. For example, suppose x1 ~ F and x2 ~ G. If F(x) > G(x) for all x, the values in x1 tend to be less than those in x2.

If the KS statistic is small or the p-value is high, then we cannot reject the null hypothesis in favor of the alternative.

If the mode is 'auto', the computation is exact if the sample sizes are less than 10000. For larger sizes, the computation uses the Kolmogorov-Smirnov distributions to compute an approximate value.

The 'two-sided' 'exact' computation computes the complementary probability and then subtracts from 1. As such, the minimum probability it can return is about 1e-16. While the algorithm itself is exact, numerical errors may accumulate for large sample sizes. It is most suited to situations in which one of the sample sizes is only a few thousand.

We generally follow Hodges' treatment of Drion/Gnedenko/Korolyuk [1].

References

[1]

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
```

```
>>> n1 = 200  # size of first sample
>>> n2 = 300  # size of second sample
```

For a different distribution, we can reject the null hypothesis since the pvalue is below 1%:

```
>>> rvs1 = stats.norm.rvs(size=n1, loc=0., scale=1, random_state=rng)
>>> rvs2 = stats.norm.rvs(size=n2, loc=0.5, scale=1.5, random_state=rng)
>>> stats.ks_2samp(rvs1, rvs2)
 KstestResult(statistic=0.2483333333333332, pvalue=5.846586728086578e-07)
```

For a slightly different distribution, we cannot reject the null hypothesis at a 10% or lower alpha since the p-value at 0.144 is higher than 10%

```
>>> rvs3 = stats.norm.rvs(size=n2, loc=0.01, scale=1.0, random_state=rng)
>>> stats.ks_2samp(rvs1, rvs3)
KstestResult(statistic=0.07833333333333334, pvalue=0.4379658456442945)
```

For an identical distribution, we cannot reject the null hypothesis since the p-value is high, 41%:

```
>>> rvs4 = stats.norm.rvs(size=n2, loc=0.0, scale=1.0, random_state=rng)
>>> stats.ks_2samp(rvs1, rvs4)
KstestResult(statistic=0.12166666666666667, pvalue=0.05401863039081145)
```

scipy.stats.epps_singleton_2samp

scipy.stats.**epps_singleton_2samp**(*x*, *y*, *t=(0.4, 0.8)*)

Compute the Epps-Singleton (ES) test statistic.

Test the null hypothesis that two samples have the same underlying probability distribution.

Parameters

x, y [array-like] The two samples of observations to be tested. Input must not have more than one dimension. Samples can have different lengths.

t [array-like, optional] The points (t1, …, tn) where the empirical characteristic function is to be evaluated. It should be positive distinct numbers. The default value (0.4, 0.8) is proposed in [1]. Input must not have more than one dimension.

Returns

statistic [float] The test statistic.

pvalue [float] The associated p-value based on the asymptotic chi2-distribution.

See also:

ks_2samp, **anderson_ksamp**

Notes

Testing whether two samples are generated by the same underlying distribution is a classical question in statistics. A widely used test is the Kolmogorov-Smirnov (KS) test which relies on the empirical distribution function. Epps and Singleton introduce a test based on the empirical characteristic function in [1].

One advantage of the ES test compared to the KS test is that is does not assume a continuous distribution. In [1], the authors conclude that the test also has a higher power than the KS test in many examples. They recommend the use of the ES test for discrete samples as well as continuous samples with at least 25 observations each, whereas *anderson_ksamp* is recommended for smaller sample sizes in the continuous case.

The p-value is computed from the asymptotic distribution of the test statistic which follows a *chi2* distribution. If the sample size of both *x* and *y* is below 25, the small sample correction proposed in [1] is applied to the test statistic.

The default values of *t* are determined in [1] by considering various distributions and finding good values that lead to a high power of the test in general. Table III in [1] gives the optimal values for the distributions tested in that study. The values of *t* are scaled by the semi-interquartile range in the implementation, see [1].

References

[1], [2]

scipy.stats.mannwhitneyu

scipy.stats.**mannwhitneyu**(*x*, *y*, *use_continuity=True*, *alternative='two-sided'*, *axis=0*, *method='auto'*)

Perform the Mann-Whitney U rank test on two independent samples.

The Mann-Whitney U test is a nonparametric test of the null hypothesis that the distribution underlying sample *x* is the same as the distribution underlying sample *y*. It is often used as a test of of difference in location between distributions.

Parameters

x, y [array-like] N-d arrays of samples. The arrays must be broadcastable except along the dimension given by *axis*.

use_continuity [bool, optional] Whether a continuity correction (1/2) should be applied. Default is True when *method* is `'asymptotic'`; has no effect otherwise.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. Default is 'two-sided'. Let *F(u)* and *G(u)* be the cumulative distribution functions of the distributions underlying *x* and *y*, respectively. Then the following alternative hypotheses are available:

- 'two-sided': the distributions are not equal, i.e. $F(u) \neq G(u)$ for at least one u.
- 'less': the distribution underlying *x* is stochastically less than the distribution underlying *y*, i.e. $F(u) > G(u)$ for all u.
- 'greater': the distribution underlying *x* is stochastically greater than the distribution underlying *y*, i.e. $F(u) < G(u)$ for all u.

Under a more restrictive set of assumptions, the alternative hypotheses can be expressed in terms of the locations of the distributions; see [5] section 5.1.

axis [int, optional] Axis along which to perform the test. Default is 0.

method [{'auto', 'asymptotic', 'exact'}, optional] Selects the method used to calculate the *p*-value. Default is 'auto'. The following options are available.

- `'asymptotic'`: compares the standardized test statistic against the normal distribution, correcting for ties.
- `'exact'`: computes the exact *p*-value by comparing the observed U statistic against the exact distribution of the U statistic under the null hypothesis. No correction is made for ties.
- `'auto'`: chooses `'exact'` when the size of one of the samples is less than 8 and there are no ties; chooses `'asymptotic'` otherwise.

Returns

res [MannwhitneyuResult] An object containing attributes:

statistic [float] The Mann-Whitney U statistic corresponding with sample *x*. See Notes for the test statistic corresponding with sample *y*.

pvalue [float] The associated *p*-value for the chosen *alternative*.

See also:

scipy.stats.wilcoxon, **scipy.stats.ranksums**, **scipy.stats.ttest_ind**

Notes

If `U1` is the statistic corresponding with sample *x*, then the statistic corresponding with sample *y* is *U2 = `x.shape[axis] * y.shape[axis] - U1`*.

mannwhitneyu is for independent samples. For related / paired samples, consider *scipy.stats.wilcoxon*.

method `'exact'` is recommended when there are no ties and when either sample size is less than 8 [1]. The implementation follows the recurrence relation originally proposed in [1] as it is described in [3]. Note that the exact method is *not* corrected for ties, but *mannwhitneyu* will not raise errors or warnings if there are ties in the data.

The Mann-Whitney U test is a non-parametric version of the t-test for independent samples. When the the means of samples from the populations are normally distributed, consider *scipy.stats.ttest_ind*.

References

[1], [2], [3], [4], [5]

Examples

We follow the example from [4]: nine randomly sampled young adults were diagnosed with type II diabetes at the ages below.

```
>>> males = [19, 22, 16, 29, 24]
>>> females = [20, 11, 17, 12]
```

We use the Mann-Whitney U test to assess whether there is a statistically significant difference in the diagnosis age of males and females. The null hypothesis is that the distribution of male diagnosis ages is the same as the distribution of female diagnosis ages. We decide that a confidence level of 95% is required to reject the null hypothesis in favor of the alternative that that the distributions are different. Since the number of samples is very small and there are no ties in the data, we can compare the observed test statistic against the *exact* distribution of the test statistic under the null hypothesis.

```
>>> from scipy.stats import mannwhitneyu
>>> U1, p = mannwhitneyu(males, females, method="exact")
>>> print(U1)
17.0
```

mannwhitneyu always reports the statistic associated with the first sample, which, in this case, is males. This agrees with $U_M = 17$ reported in [4]. The statistic associated with the second statistic can be calculated:

```
>>> nx, ny = len(males), len(females)
>>> U2 = nx*ny - U1
>>> print(U2)
3.0
```

This agrees with $U_F = 3$ reported in [4]. The two-sided *p*-value can be calculated from either statistic, and the value produced by *mannwhitneyu* agrees with $p = 0.11$ reported in [4].

```
>>> print(p)
0.1111111111111111
```

The exact distribution of the test statistic is asymptotically normal, so the example continues by comparing the exact *p*-value against the *p*-value produced using the normal approximation.

```
>>> _, pnorm = mannwhitneyu(males, females, method="asymptotic")
>>> print(pnorm)
0.11134688653314041
```

Here *mannwhitneyu*'s reported *p*-value appears to conflict with the value $p = 0.09$ given in [4]. The reason is that [4] does not apply the continuity correction performed by *mannwhitneyu*; *mannwhitneyu* reduces the distance between the test statistic and the mean $\mu = n_x n_y/2$ by 0.5 to correct for the fact that the discrete statistic is being compared against a continuous distribution. Here, the U statistic used is less than the mean, so we reduce the distance by adding 0.5 in the numerator.

```
>>> import numpy as np
>>> from scipy.stats import norm
>>> U = min(U1, U2)
>>> N = nx + ny
>>> z = (U - nx*ny/2 + 0.5) / np.sqrt(nx*ny * (N + 1)/ 12)
>>> p = 2 * norm.cdf(z)  # use CDF to get p-value from smaller statistic
>>> print(p)
0.11134688653314041
```

If desired, we can disable the continuity correction to get a result that agrees with that reported in [4].

```
>>> _, pnorm = mannwhitneyu(males, females, use_continuity=False,
...                         method="asymptotic")
>>> print(pnorm)
0.0864107329737
```

Regardless of whether we perform an exact or asymptotic test, the probability of the test statistic being as extreme or more extreme by chance exceeds 5%, so we do not consider the results statistically significant.

Suppose that, before seeing the data, we had hypothesized that females would tend to be diagnosed at a younger age than males. In that case, it would be natural to provide the female ages as the first input, and we would have performed a one-sided test using `alternative = 'less'`: females are diagnosed at an age that is stochastically less than that of males.

```
>>> res = mannwhitneyu(females, males, alternative="less", method="exact")
>>> print(res)
MannwhitneyuResult(statistic=3.0, pvalue=0.05555555555555555)
```

Again, the probability of getting a sufficiently low value of the test statistic by chance under the null hypothesis is greater than 5%, so we do not reject the null hypothesis in favor of our alternative.

If it is reasonable to assume that the means of samples from the populations are normally distributed, we could have used a t-test to perform the analysis.

```
>>> from scipy.stats import ttest_ind
>>> res = ttest_ind(females, males, alternative="less")
>>> print(res)
Ttest_indResult(statistic=-2.239334696520584, pvalue=0.030068441095757924)
```

Under this assumption, the *p*-value would be low enough to reject the null hypothesis in favor of the alternative.

scipy.stats.tiecorrect

scipy.stats.**tiecorrect**(*rankvals*)

Tie correction factor for Mann-Whitney U and Kruskal-Wallis H tests.

Parameters

rankvals [array_like] A 1-D sequence of ranks. Typically this will be the array returned by *rankdata*.

Returns

factor [float] Correction factor for U or H.

See also:

rankdata

Assign ranks to the data

mannwhitneyu

Mann-Whitney rank test

kruskal

Kruskal-Wallis H test

References

[1]

Examples

```
>>> from scipy.stats import tiecorrect, rankdata
>>> tiecorrect([1, 2.5, 2.5, 4])
0.9
>>> ranks = rankdata([1, 3, 2, 4, 5, 7, 2, 8, 4])
>>> ranks
array([ 1. ,  4. ,  2.5,  5.5,  7. ,  8. ,  2.5,  9. ,  5.5])
>>> tiecorrect(ranks)
0.9833333333333333
```

scipy.stats.rankdata

scipy.stats.**rankdata**(*a*, *method='average'*, ***, *axis=None*)

Assign ranks to data, dealing with ties appropriately.

By default (`axis=None`), the data array is first flattened, and a flat array of ranks is returned. Separately reshape the rank array to the shape of the data array if desired (see Examples).

Ranks begin at 1. The *method* argument controls how ranks are assigned to equal values. See [1] for further discussion of ranking methods.

Parameters

a [array_like] The array of values to be ranked.

method [{'average', 'min', 'max', 'dense', 'ordinal'}, optional] The method used to assign ranks to tied elements. The following methods are available (default is 'average'):

- 'average': The average of the ranks that would have been assigned to all the tied values is assigned to each value.
- 'min': The minimum of the ranks that would have been assigned to all the tied values is assigned to each value. (This is also referred to as "competition" ranking.)
- 'max': The maximum of the ranks that would have been assigned to all the tied values is assigned to each value.
- 'dense': Like 'min', but the rank of the next highest element is assigned the rank immediately after those assigned to the tied elements.
- 'ordinal': All values are given a distinct rank, corresponding to the order that the values occur in *a*.

axis [{None, int}, optional] Axis along which to perform the ranking. If `None`, the data array is first flattened.

Returns

ranks [ndarray] An array of size equal to the size of *a*, containing rank scores.

References

[1]

Examples

```
>>> from scipy.stats import rankdata
>>> rankdata([0, 2, 3, 2])
array([ 1. ,  2.5,  4. ,  2.5])
>>> rankdata([0, 2, 3, 2], method='min')
array([ 1,  2,  4,  2])
>>> rankdata([0, 2, 3, 2], method='max')
array([ 1,  3,  4,  3])
>>> rankdata([0, 2, 3, 2], method='dense')
array([ 1,  2,  3,  2])
>>> rankdata([0, 2, 3, 2], method='ordinal')
array([ 1,  2,  4,  3])
>>> rankdata([[0, 2], [3, 2]]).reshape(2,2)
array([[1. , 2.5],
       [4. , 2.5]])
>>> rankdata([[0, 2, 2], [3, 2, 5]], axis=1)
array([[1. , 2.5, 2.5],
       [2. , 1. , 3. ]])
```

scipy.stats.ranksums

`scipy.stats.`**`ranksums`**(*x*, *y*, *alternative='two-sided'*)

Compute the Wilcoxon rank-sum statistic for two samples.

The Wilcoxon rank-sum test tests the null hypothesis that two sets of measurements are drawn from the same distribution. The alternative hypothesis is that values in one sample are more likely to be larger than the values in the other sample.

This test should be used to compare two samples from continuous distributions. It does not handle ties between measurements in x and y. For tie-handling and an optional continuity correction see *scipy.stats.mannwhitneyu*.

Parameters

x,y [array_like] The data from the two samples.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. Default is 'two-sided'. The following options are available:

- 'two-sided': one of the distributions (underlying *x* or *y*) is stochastically greater than the other.
- 'less': the distribution underlying *x* is stochastically less than the distribution underlying *y*.
- 'greater': the distribution underlying *x* is stochastically greater than the distribution underlying *y*.

New in version 1.7.0.

Returns

statistic [float] The test statistic under the large-sample approximation that the rank sum statistic is normally distributed.

pvalue [float] The p-value of the test.

References

[1]

Examples

We can test the hypothesis that two independent unequal-sized samples are drawn from the same distribution with computing the Wilcoxon rank-sum statistic.

```
>>> from scipy.stats import ranksums
>>> rng = np.random.default_rng()
>>> sample1 = rng.uniform(-1, 1, 200)
>>> sample2 = rng.uniform(-0.5, 1.5, 300) # a shifted distribution
>>> ranksums(sample1, sample2)
RanksumsResult(statistic=-7.887059, pvalue=3.09390448e-15)  # may vary
>>> ranksums(sample1, sample2, alternative='less')
RanksumsResult(statistic=-7.750585297581713, pvalue=4.573497606342543e-
↪15) # may vary
>>> ranksums(sample1, sample2, alternative='greater')
RanksumsResult(statistic=-7.750585297581713, pvalue=0.9999999999999954) #␣
↪may vary
```

The p-value of less than `0.05` indicates that this test rejects the hypothesis at the 5% significance level.

scipy.stats.wilcoxon

`scipy.stats.`**`wilcoxon`**(*x*, *y=None*, *zero_method='wilcox'*, *correction=False*, *alternative='two-sided'*, *mode='auto'*)

Calculate the Wilcoxon signed-rank test.

The Wilcoxon signed-rank test tests the null hypothesis that two related paired samples come from the same distribution. In particular, it tests whether the distribution of the differences x - y is symmetric about zero. It is a non-parametric version of the paired T-test.

Parameters

x [array_like] Either the first set of measurements (in which case `y` is the second set of measurements), or the differences between two sets of measurements (in which case `y` is not to be specified.) Must be one-dimensional.

y [array_like, optional] Either the second set of measurements (if `x` is the first set of measurements), or not specified (if `x` is the differences between two sets of measurements.) Must be one-dimensional.

zero_method
[{"pratt", "wilcox", "zsplit"}, optional] The following options are available (default is "wilcox"):
- "pratt": Includes zero-differences in the ranking process, but drops the ranks of the zeros, see [4], (more conservative).
- "wilcox": Discards all zero-differences, the default.
- "zsplit": Includes zero-differences in the ranking process and split the zero rank between positive and negative ones.

correction [bool, optional] If True, apply continuity correction by adjusting the Wilcoxon rank statistic by 0.5 towards the mean value when computing the z-statistic if a normal approximation is used. Default is False.

alternative
[{"two-sided", "greater", "less"}, optional] The alternative hypothesis to be tested, see Notes. Default is "two-sided".

mode [{"auto", "exact", "approx"}] Method to calculate the p-value, see Notes. Default is "auto".

Returns

statistic [float] If `alternative` is "two-sided", the sum of the ranks of the differences above or below zero, whichever is smaller. Otherwise the sum of the ranks of the differences above zero.

pvalue [float] The p-value for the test depending on `alternative` and `mode`.

See also:

`kruskal`, **`mannwhitneyu`**

Notes

The test has been introduced in [4]. Given n independent samples (xi, yi) from a bivariate distribution (i.e. paired samples), it computes the differences di = xi - yi. One assumption of the test is that the differences are symmetric, see [2]. The two-sided test has the null hypothesis that the median of the differences is zero against the alternative that it is different from zero. The one-sided test has the null hypothesis that the median is positive against the alternative that it is negative (`alternative == 'less'`), or vice versa (`alternative == 'greater.'`).

To derive the p-value, the exact distribution (`mode == 'exact'`) can be used for sample sizes of up to 25. The default `mode == 'auto'` uses the exact distribution if there are at most 25 observations and no ties, otherwise a normal approximation is used (`mode == 'approx'`).

The treatment of ties can be controlled by the parameter *zero_method*. If `zero_method == 'pratt'`, the normal approximation is adjusted as in [5]. A typical rule is to require that n > 20 ([2], p. 383).

References

[1], [2], [3], [4], [5]

Examples

In [4], the differences in height between cross- and self-fertilized corn plants is given as follows:

```
>>> d = [6, 8, 14, 16, 23, 24, 28, 29, 41, -48, 49, 56, 60, -67, 75]
```

Cross-fertilized plants appear to be be higher. To test the null hypothesis that there is no height difference, we can apply the two-sided test:

```
>>> from scipy.stats import wilcoxon
>>> w, p = wilcoxon(d)
>>> w, p
(24.0, 0.041259765625)
```

Hence, we would reject the null hypothesis at a confidence level of 5%, concluding that there is a difference in height between the groups. To confirm that the median of the differences can be assumed to be positive, we use:

```
>>> w, p = wilcoxon(d, alternative='greater')
>>> w, p
(96.0, 0.0206298828125)
```

This shows that the null hypothesis that the median is negative can be rejected at a confidence level of 5% in favor of the alternative that the median is greater than zero. The p-values above are exact. Using the normal approximation gives very similar values:

```
>>> w, p = wilcoxon(d, mode='approx')
>>> w, p
(24.0, 0.04088813291185591)
```

Note that the statistic changed to 96 in the one-sided case (the sum of ranks of positive differences) whereas it is 24 in the two-sided case (the minimum of sum of ranks above and below zero).

scipy.stats.kruskal

scipy.stats.**kruskal**(**args*, *nan_policy='propagate'*)

Compute the Kruskal-Wallis H-test for independent samples.

The Kruskal-Wallis H-test tests the null hypothesis that the population median of all of the groups are equal. It is a non-parametric version of ANOVA. The test works on 2 or more independent samples, which may have different sizes. Note that rejecting the null hypothesis does not indicate which of the groups differs. Post hoc comparisons between groups are required to determine which groups are different.

Parameters

sample1, sample2, …
: [array_like] Two or more arrays with the sample measurements can be given as arguments. Samples must be one-dimensional.

nan_policy
: [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):
- 'propagate': returns nan
- 'raise': throws an error

- 'omit': performs the calculations ignoring nan values

Returns

statistic [float] The Kruskal-Wallis H statistic, corrected for ties.
pvalue [float] The p-value for the test using the assumption that H has a chi square distribution. The p-value returned is the survival function of the chi square distribution evaluated at H.

See also:

f_oneway

1-way ANOVA.

mannwhitneyu

Mann-Whitney rank test on two samples.

friedmanchisquare

Friedman test for repeated measurements.

Notes

Due to the assumption that H has a chi square distribution, the number of samples in each group must not be too small. A typical rule is that each sample must have at least 5 measurements.

References

[1], [2]

Examples

```
>>> from scipy import stats
>>> x = [1, 3, 5, 7, 9]
>>> y = [2, 4, 6, 8, 10]
>>> stats.kruskal(x, y)
KruskalResult(statistic=0.2727272727272734, pvalue=0.6015081344405895)
```

```
>>> x = [1, 1, 1]
>>> y = [2, 2, 2]
>>> z = [2, 2]
>>> stats.kruskal(x, y, z)
KruskalResult(statistic=7.0, pvalue=0.0301973834223185)
```

scipy.stats.friedmanchisquare

scipy.stats.**friedmanchisquare**(**args*)

Compute the Friedman test for repeated measurements.

The Friedman test tests the null hypothesis that repeated measurements of the same individuals have the same distribution. It is often used to test for consistency among measurements obtained in different ways. For example, if two measurement techniques are used on the same set of individuals, the Friedman test can be used to determine if the two measurement techniques are consistent.

Parameters

measurements1, measurements2, measurements3…
[array_like] Arrays of measurements. All of the arrays must have the same number of elements. At least 3 sets of measurements must be given.

Returns

statistic [float] The test statistic, correcting for ties.
pvalue [float] The associated p-value assuming that the test statistic has a chi squared distribution.

Notes

Due to the assumption that the test statistic has a chi squared distribution, the p-value is only reliable for n > 10 and more than 6 repeated measurements.

References

[1]

scipy.stats.brunnermunzel

`scipy.stats.`**`brunnermunzel`**(*x*, *y*, *alternative='two-sided'*, *distribution='t'*, *nan_policy='propagate'*)

Compute the Brunner-Munzel test on samples x and y.

The Brunner-Munzel test is a nonparametric test of the null hypothesis that when values are taken one by one from each group, the probabilities of getting large values in both groups are equal. Unlike the Wilcoxon-Mann-Whitney's U test, this does not require the assumption of equivariance of two groups. Note that this does not assume the distributions are same. This test works on two independent samples, which may have different sizes.

Parameters

x, y [array_like] Array of samples, should be one-dimensional.
alternative
[{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. The following options are available (default is 'two-sided'):
- 'two-sided'
- 'less': one-sided
- 'greater': one-sided

distribution
[{'t', 'normal'}, optional] Defines how to get the p-value. The following options are available (default is 't'):
- 't': get the p-value by t-distribution
- 'normal': get the p-value by standard normal distribution.

nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):
- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

statistic [float] The Brunner-Munzer W statistic.
pvalue [float] p-value assuming an t distribution. One-sided or two-sided, depending on the choice of *alternative* and *distribution*.

See also:

mannwhitneyu

Mann-Whitney rank test on two samples.

Notes

Brunner and Munzel recommended to estimate the p-value by t-distribution when the size of data is 50 or less. If the size is lower than 10, it would be better to use permuted Brunner Munzel test (see [2]).

References

[1], [2]

Examples

```
>>> from scipy import stats
>>> x1 = [1,2,1,1,1,1,1,1,1,1,2,4,1,1]
>>> x2 = [3,3,4,3,1,2,3,1,1,5,4]
>>> w, p_value = stats.brunnermunzel(x1, x2)
>>> w
3.1374674823029505
>>> p_value
0.0057862086661515377
```

scipy.stats.combine_pvalues

scipy.stats.**combine_pvalues**(*pvalues*, *method='fisher'*, *weights=None*)

Combine p-values from independent tests bearing upon the same hypothesis.

Parameters

pvalues [array_like, 1-D] Array of p-values assumed to come from independent tests.

method [{'fisher', 'pearson', 'tippett', 'stouffer',] 'mudholkar_george'}, optional
Name of method to use to combine p-values. The following methods are available (default is 'fisher'):

- 'fisher': Fisher's method (Fisher's combined probability test), the sum of the logarithm of the p-values
- 'pearson': Pearson's method (similar to Fisher's but uses sum of the complement of the p-values inside the logarithms)
- 'tippett': Tippett's method (minimum of p-values)
- 'stouffer': Stouffer's Z-score method
- 'mudholkar_george': the difference of Fisher's and Pearson's methods divided by 2

weights [array_like, 1-D, optional] Optional array of weights used only for Stouffer's Z-score method.

Returns

statistic: float
The statistic calculated by the specified method.

pval: float The combined p-value.

Notes

Fisher's method (also known as Fisher's combined probability test) [1] uses a chi-squared statistic to compute a combined p-value. The closely related Stouffer's Z-score method [2] uses Z-scores rather than p-values. The advantage of Stouffer's method is that it is straightforward to introduce weights, which can make Stouffer's method more powerful than Fisher's method when the p-values are from studies of different size [6] [7]. The Pearson's method uses $log(1 - p_i)$ inside the sum whereas Fisher's method uses $log(p_i)$ [4]. For Fisher's and Pearson's method, the sum of the logarithms is multiplied by -2 in the implementation. This quantity has a chi-square distribution that determines the p-value. The *mudholkar_george* method is the difference of the Fisher's and Pearson's test statistics, each of which include the -2 factor [4]. However, the *mudholkar_george* method does not include these -2 factors. The test statistic of *mudholkar_george* is the sum of logisitic random variables and equation 3.6 in [3] is used to approximate the p-value based on Student's t-distribution.

Fisher's method may be extended to combine p-values from dependent tests [5]. Extensions such as Brown's method and Kost's method are not currently implemented.

New in version 0.15.0.

References

[1], [2], [3], [4], [5], [6], [7]

scipy.stats.jarque_bera

scipy.stats.**jarque_bera**(*x*)

Perform the Jarque-Bera goodness of fit test on sample data.

The Jarque-Bera test tests whether the sample data has the skewness and kurtosis matching a normal distribution.

Note that this test only works for a large enough number of data samples (>2000) as the test statistic asymptotically has a Chi-squared distribution with 2 degrees of freedom.

Parameters

x [array_like] Observations of a random variable.

Returns

jb_value [float] The test statistic.
p [float] The p-value for the hypothesis test.

References

[1]

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
>>> x = rng.normal(0, 1, 100000)
>>> jarque_bera_test = stats.jarque_bera(x)
>>> jarque_bera_test
Jarque_beraResult(statistic=3.3415184718131554, pvalue=0.
↪18810419594996775)
>>> jarque_bera_test.statistic
```

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```
3.3415184718131554
>>> jarque_bera_test.pvalue
0.18810419594996775
```

scipy.stats.page_trend_test

scipy.stats.**page_trend_test**(*data*, *ranked=False*, *predicted_ranks=None*, *method='auto'*)

Perform Page's Test, a measure of trend in observations between treatments.

Page's Test (also known as Page's L test) is useful when:

- there are $n \geq 3$ treatments,
- $m \geq 2$ subjects are observed for each treatment, and
- the observations are hypothesized to have a particular order.

Specifically, the test considers the null hypothesis that

$$m_1 = m_2 = m_3 \cdots = m_n,$$

where m_j is the mean of the observed quantity under treatment j, against the alternative hypothesis that

$$m_1 \leq m_2 \leq m_3 \leq \cdots \leq m_n,$$

where at least one inequality is strict.

As noted by [4], Page's L test has greater statistical power than the Friedman test against the alternative that there is a difference in trend, as Friedman's test only considers a difference in the means of the observations without considering their order. Whereas Spearman ρ considers the correlation between the ranked observations of two variables (e.g. the airspeed velocity of a swallow vs. the weight of the coconut it carries), Page's L is concerned with a trend in an observation (e.g. the airspeed velocity of a swallow) across several distinct treatments (e.g. carrying each of five coconuts of different weight) even as the observation is repeated with multiple subjects (e.g. one European swallow and one African swallow).

Parameters

data [array-like] A $m \times n$ array; the element in row i and column j is the observation corresponding with subject i and treatment j. By default, the columns are assumed to be arranged in order of increasing predicted mean.

ranked [boolean, optional] By default, *data* is assumed to be observations rather than ranks; it will be ranked with *scipy.stats.rankdata* along `axis=1`. If *data* is provided in the form of ranks, pass argument `True`.

predicted_ranks [array-like, optional] The predicted ranks of the column means. If not specified, the columns are assumed to be arranged in order of increasing predicted mean, so the default *predicted_ranks* are $[1, 2, \ldots, n-1, n]$.

method [{'auto', 'asymptotic', 'exact'}, optional] Selects the method used to calculate the *p*-value. The following options are available.

- 'auto': selects between 'exact' and 'asymptotic' to achieve reasonably accurate results in reasonable time (default)
- 'asymptotic': compares the standardized test statistic against the normal distribution
- 'exact': computes the exact *p*-value by comparing the observed L statistic against those realized by all possible permutations of ranks (under the null hypothesis that each permutation is equally likely)

Returns

res [PageTrendTestResult] An object containing attributes:
- **statistic** [float] Page's L test statistic.
- **pvalue** [float] The associated p-value
- **method** [{'asymptotic', 'exact'}] The method used to compute the p-value

See also:

rankdata, **friedmanchisquare**, **spearmanr**

Notes

As noted in [1], "the n 'treatments' could just as well represent n objects or events or performances or persons or trials ranked." Similarly, the m 'subjects' could equally stand for m "groupings by ability or some other control variable, or judges doing the ranking, or random replications of some other sort."

The procedure for calculating the L statistic, adapted from [1], is:

1. "Predetermine with careful logic the appropriate hypotheses concerning the predicted ording of the experimental results. If no reasonable basis for ordering any treatments is known, the L test is not appropriate."
2. "As in other experiments, determine at what level of confidence you will reject the null hypothesis that there is no agreement of experimental results with the monotonic hypothesis."
3. "Cast the experimental material into a two-way table of n columns (treatments, objects ranked, conditions) and m rows (subjects, replication groups, levels of control variables)."
4. "When experimental observations are recorded, rank them across each row", e.g. `ranks = scipy.stats.rankdata(data, axis=1)`.
5. "Add the ranks in each column", e.g. `colsums = np.sum(ranks, axis=0)`.
6. "Multiply each sum of ranks by the predicted rank for that same column", e.g. `products = predicted_ranks * colsums`.
7. "Sum all such products", e.g. `L = products.sum()`.

[1] continues by suggesting use of the standardized statistic

$$\chi_L^2 = \frac{\left[12L - 3mn(n+1)^2\right]^2}{mn^2(n^2-1)(n+1)}$$

"which is distributed approximately as chi-square with 1 degree of freedom. The ordinary use of χ^2 tables would be equivalent to a two-sided test of agreement. If a one-sided test is desired, *as will almost always be the case*, the probability discovered in the chi-square table should be *halved*."

However, this standardized statistic does not distinguish between the observed values being well correlated with the predicted ranks and being _anti_-correlated with the predicted ranks. Instead, we follow [2] and calculate the standardized statistic

$$\Lambda = \frac{L - E_0}{\sqrt{V_0}},$$

where $E_0 = \frac{1}{4}mn(n+1)^2$ and $V_0 = \frac{1}{144}mn^2(n+1)(n^2-1)$, "which is asymptotically normal under the null hypothesis".

The *p*-value for `method='exact'` is generated by comparing the observed value of L against the L values generated for all $(n!)^m$ possible permutations of ranks. The calculation is performed using the recursive method of [5].

The *p*-values are not adjusted for the possibility of ties. When ties are present, the reported `'exact'` *p*-values may be somewhat larger (i.e. more conservative) than the true *p*-value [2]. The `'asymptotic'` *p*-values, however, tend to be smaller (i.e. less conservative) than the `'exact'` *p*-values.

References

[1], [2], [3], [4], [5]

Examples

We use the example from [3]: 10 students are asked to rate three teaching methods - tutorial, lecture, and seminar - on a scale of 1-5, with 1 being the lowest and 5 being the highest. We have decided that a confidence level of 99% is required to reject the null hypothesis in favor of our alternative: that the seminar will have the highest ratings and the tutorial will have the lowest. Initially, the data have been tabulated with each row representing an individual student's ratings of the three methods in the following order: tutorial, lecture, seminar.

```
>>> table = [[3, 4, 3],
...          [2, 2, 4],
...          [3, 3, 5],
...          [1, 3, 2],
...          [2, 3, 2],
...          [2, 4, 5],
...          [1, 2, 4],
...          [3, 4, 4],
...          [2, 4, 5],
...          [1, 3, 4]]
```

Because the tutorial is hypothesized to have the lowest ratings, the column corresponding with tutorial rankings should be first; the seminar is hypothesized to have the highest ratings, so its column should be last. Since the columns are already arranged in this order of increasing predicted mean, we can pass the table directly into *page_trend_test*.

```
>>> from scipy.stats import page_trend_test
>>> res = page_trend_test(table)
>>> res
PageTrendTestResult(statistic=133.5, pvalue=0.0018191161948127822,
                    method='exact')
```

This *p*-value indicates that there is a 0.1819% chance that the L statistic would reach such an extreme value under the null hypothesis. Because 0.1819% is less than 1%, we have evidence to reject the null hypothesis in favor of our alternative at a 99% confidence level.

The value of the L statistic is 133.5. To check this manually, we rank the data such that high scores correspond with high ranks, settling ties with an average rank:

```
>>> from scipy.stats import rankdata
>>> ranks = rankdata(table, axis=1)
>>> ranks
array([[1.5, 3. , 1.5],
       [1.5, 1.5, 3. ],
       [1.5, 1.5, 3. ],
       [1. , 3. , 2. ],
       [1.5, 3. , 1.5],
       [1. , 2. , 3. ],
       [1. , 2. , 3. ],
       [1. , 2.5, 2.5],
       [1. , 2. , 3. ],
       [1. , 2. , 3. ]])
```

We add the ranks within each column, multiply the sums by the predicted ranks, and sum the products.

```
>>> import numpy as np
>>> m, n = ranks.shape
>>> predicted_ranks = np.arange(1, n+1)
>>> L = (predicted_ranks * np.sum(ranks, axis=0)).sum()
>>> res.statistic == L
True
```

As presented in [3], the asymptotic approximation of the *p*-value is the survival function of the normal distribution evaluated at the standardized test statistic:

```
>>> from scipy.stats import norm
>>> E0 = (m*n*(n+1)**2)/4
>>> V0 = (m*n**2*(n+1)*(n**2-1))/144
>>> Lambda = (L-E0)/np.sqrt(V0)
>>> p = norm.sf(Lambda)
>>> p
0.0012693433690751756
```

This does not precisely match the *p*-value reported by *page_trend_test* above. The asymptotic distribution is not very accurate, nor conservative, for $m \leq 12$ and $n \leq 8$, so *page_trend_test* chose to use `method='exact'` based on the dimensions of the table and the recommendations in Page's original paper [1]. To override *page_trend_test*'s choice, provide the *method* argument.

```
>>> res = page_trend_test(table, method="asymptotic")
>>> res
PageTrendTestResult(statistic=133.5, pvalue=0.0012693433690751756,
                    method='asymptotic')
```

If the data are already ranked, we can pass in the `ranks` instead of the `table` to save computation time.

```
>>> res = page_trend_test(ranks,             # ranks of data
...                       ranked=True,       # data is already ranked
...                       )
>>> res
PageTrendTestResult(statistic=133.5, pvalue=0.0018191161948127822,
                    method='exact')
```

Suppose the raw data had been tabulated in an order different from the order of predicted means, say lecture, seminar, tutorial.

```
>>> table = np.asarray(table)[:, [1, 2, 0]]
```

Since the arrangement of this table is not consistent with the assumed ordering, we can either rearrange the table or provide the *predicted_ranks*. Remembering that the lecture is predicted to have the middle rank, the seminar the highest, and tutorial the lowest, we pass:

```
>>> res = page_trend_test(table,             # data as originally␣
↪tabulated
...                       predicted_ranks=[2, 3, 1],  # our predicted␣
↪order
...                       )
>>> res
```

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```
PageTrendTestResult(statistic=133.5, pvalue=0.0018191161948127822,
                    method='exact')
```

ansari(x, y[, alternative])	Perform the Ansari-Bradley test for equal scale parameters.
bartlett(*args)	Perform Bartlett's test for equal variances.
levene(*args[, center, proportiontocut])	Perform Levene test for equal variances.
shapiro(x)	Perform the Shapiro-Wilk test for normality.
anderson(x[, dist])	Anderson-Darling test for data coming from a particular distribution.
anderson_ksamp(samples[, midrank])	The Anderson-Darling test for k-samples.
binom_test(x[, n, p, alternative])	Perform a test that the probability of success is p.
binomtest(k, n[, p, alternative])	Perform a test that the probability of success is p.
fligner(*args[, center, proportiontocut])	Perform Fligner-Killeen test for equality of variance.
median_test(*args[, ties, correction, …])	Perform a Mood's median test.
mood(x, y[, axis, alternative])	Perform Mood's test for equal scale parameters.
skewtest(a[, axis, nan_policy, alternative])	Test whether the skew is different from the normal distribution.
kurtosistest(a[, axis, nan_policy, alternative])	Test whether a dataset has normal kurtosis.
normaltest(a[, axis, nan_policy])	Test whether a sample differs from a normal distribution.

scipy.stats.ansari

scipy.stats.**ansari**(*x*, *y*, *alternative='two-sided'*)

Perform the Ansari-Bradley test for equal scale parameters.

The Ansari-Bradley test ([1], [2]) is a non-parametric test for the equality of the scale parameter of the distributions from which two samples were drawn. The null hypothesis states that the ratio of the scale of the distribution underlying *x* to the scale of the distribution underlying *y* is 1.

Parameters

x, y [array_like] Arrays of sample data.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. Default is 'two-sided'. The following options are available:
- 'two-sided': the ratio of scales is not equal to 1.
- 'less': the ratio of scales is less than 1.
- 'greater': the ratio of scales is greater than 1.

New in version 1.7.0.

Returns

statistic [float] The Ansari-Bradley test statistic.

pvalue [float] The p-value of the hypothesis test.

See also:

fligner

A non-parametric test for the equality of k variances

mood

A non-parametric test for the equality of two scale parameters

Notes

The p-value given is exact when the sample sizes are both less than 55 and there are no ties, otherwise a normal approximation for the p-value is used.

References

[1], [2], [3]

Examples

```
>>> from scipy.stats import ansari
>>> rng = np.random.default_rng()
```

For these examples, we'll create three random data sets. The first two, with sizes 35 and 25, are drawn from a normal distribution with mean 0 and standard deviation 2. The third data set has size 25 and is drawn from a normal distribution with standard deviation 1.25.

```
>>> x1 = rng.normal(loc=0, scale=2, size=35)
>>> x2 = rng.normal(loc=0, scale=2, size=25)
>>> x3 = rng.normal(loc=0, scale=1.25, size=25)
```

First we apply *ansari* to *x1* and *x2*. These samples are drawn from the same distribution, so we expect the Ansari-Bradley test should not lead us to conclude that the scales of the distributions are different.

```
>>> ansari(x1, x2)
AnsariResult(statistic=541.0, pvalue=0.9762532927399098)
```

With a p-value close to 1, we cannot conclude that there is a significant difference in the scales (as expected).

Now apply the test to *x1* and *x3*:

```
>>> ansari(x1, x3)
AnsariResult(statistic=425.0, pvalue=0.0003087020407974518)
```

The probability of observing such an extreme value of the statistic under the null hypothesis of equal scales is only 0.03087%. We take this as evidence against the null hypothesis in favor of the alternative: the scales of the distributions from which the samples were drawn are not equal.

We can use the *alternative* parameter to perform a one-tailed test. In the above example, the scale of *x1* is greater than *x3* and so the ratio of scales of *x1* and *x3* is greater than 1. This means that the p-value when `alternative='greater'` should be near 0 and hence we should be able to reject the null hypothesis:

```
>>> ansari(x1, x3, alternative='greater')
AnsariResult(statistic=425.0, pvalue=0.0001543510203987259)
```

As we can see, the p-value is indeed quite low. Use of `alternative='less'` should thus yield a large p-value:

```
>>> ansari(x1, x3, alternative='less')
AnsariResult(statistic=425.0, pvalue=0.9998643258449039)
```

scipy.stats.bartlett

scipy.stats.**bartlett**(**args*)

Perform Bartlett's test for equal variances.

Bartlett's test tests the null hypothesis that all input samples are from populations with equal variances. For samples from significantly non-normal populations, Levene's test `levene` is more robust.

Parameters

sample1, sample2,…
: [array_like] arrays of sample data. Only 1d arrays are accepted, they may have different lengths.

Returns

statistic : [float] The test statistic.
pvalue : [float] The p-value of the test.

See also:

fligner

A non-parametric test for the equality of k variances

levene

A robust parametric test for equality of k variances

Notes

Conover et al. (1981) examine many of the existing parametric and nonparametric tests by extensive simulations and they conclude that the tests proposed by Fligner and Killeen (1976) and Levene (1960) appear to be superior in terms of robustness of departures from normality and power ([3]).

References

[1], [2], [3], [4]

Examples

Test whether or not the lists *a*, *b* and *c* come from populations with equal variances.

```
>>> from scipy.stats import bartlett
>>> a = [8.88, 9.12, 9.04, 8.98, 9.00, 9.08, 9.01, 8.85, 9.06, 8.99]
>>> b = [8.88, 8.95, 9.29, 9.44, 9.15, 9.58, 8.36, 9.18, 8.67, 9.05]
>>> c = [8.95, 9.12, 8.95, 8.85, 9.03, 8.84, 9.07, 8.98, 8.86, 8.98]
>>> stat, p = bartlett(a, b, c)
>>> p
1.1254782518834628e-05
```

The very small p-value suggests that the populations do not have equal variances.

This is not surprising, given that the sample variance of *b* is much larger than that of *a* and *c*:

```
>>> [np.var(x, ddof=1) for x in [a, b, c]]
[0.007054444444444413, 0.13073888888888888, 0.008890000000000002]
```

scipy.stats.levene

scipy.stats.**levene**(**args*, *center='median'*, *proportiontocut=0.05*)

Perform Levene test for equal variances.

The Levene test tests the null hypothesis that all input samples are from populations with equal variances. Levene's test is an alternative to Bartlett's test `bartlett` in the case where there are significant deviations from normality.

Parameters

sample1, sample2, …
: [array_like] The sample data, possibly with different lengths. Only one-dimensional samples are accepted.

center
: [{'mean', 'median', 'trimmed'}, optional] Which function of the data to use in the test. The default is 'median'.

proportiontocut
: [float, optional] When *center* is 'trimmed', this gives the proportion of data points to cut from each end. (See `scipy.stats.trim_mean`.) Default is 0.05.

Returns

statistic
: [float] The test statistic.

pvalue
: [float] The p-value for the test.

Notes

Three variations of Levene's test are possible. The possibilities and their recommended usages are:

- 'median' : Recommended for skewed (non-normal) distributions>
- 'mean' : Recommended for symmetric, moderate-tailed distributions.
- 'trimmed' : Recommended for heavy-tailed distributions.

The test version using the mean was proposed in the original article of Levene ([2]) while the median and trimmed mean have been studied by Brown and Forsythe ([3]), sometimes also referred to as Brown-Forsythe test.

References

[1], [2], [3]

Examples

Test whether or not the lists *a*, *b* and *c* come from populations with equal variances.

```
>>> from scipy.stats import levene
>>> a = [8.88, 9.12, 9.04, 8.98, 9.00, 9.08, 9.01, 8.85, 9.06, 8.99]
>>> b = [8.88, 8.95, 9.29, 9.44, 9.15, 9.58, 8.36, 9.18, 8.67, 9.05]
>>> c = [8.95, 9.12, 8.95, 8.85, 9.03, 8.84, 9.07, 8.98, 8.86, 8.98]
>>> stat, p = levene(a, b, c)
>>> p
0.002431505967249681
```

The small p-value suggests that the populations do not have equal variances.

This is not surprising, given that the sample variance of *b* is much larger than that of *a* and *c*:

```
>>> [np.var(x, ddof=1) for x in [a, b, c]]
[0.007054444444444413, 0.13073888888888888, 0.008890000000000002]
```

scipy.stats.shapiro

scipy.stats.**shapiro**(*x*)

Perform the Shapiro-Wilk test for normality.

The Shapiro-Wilk test tests the null hypothesis that the data was drawn from a normal distribution.

Parameters

x [array_like] Array of sample data.

Returns

statistic [float] The test statistic.
p-value [float] The p-value for the hypothesis test.

See also:

anderson

The Anderson-Darling test for normality

kstest

The Kolmogorov-Smirnov test for goodness of fit.

Notes

The algorithm used is described in [4] but censoring parameters as described are not implemented. For N > 5000 the W test statistic is accurate but the p-value may not be.

The chance of rejecting the null hypothesis when it is true is close to 5% regardless of sample size.

References

[1], [2], [3], [4]

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
>>> x = stats.norm.rvs(loc=5, scale=3, size=100, random_state=rng)
>>> shapiro_test = stats.shapiro(x)
>>> shapiro_test
ShapiroResult(statistic=0.9813305735588074, pvalue=0.16855233907699585)
>>> shapiro_test.statistic
0.9813305735588074
>>> shapiro_test.pvalue
0.16855233907699585
```

scipy.stats.anderson

scipy.stats.**anderson**(*x*, *dist='norm'*)

Anderson-Darling test for data coming from a particular distribution.

The Anderson-Darling test tests the null hypothesis that a sample is drawn from a population that follows a particular distribution. For the Anderson-Darling test, the critical values depend on which distribution is being tested against. This function works for normal, exponential, logistic, or Gumbel (Extreme Value Type I) distributions.

Parameters

x [array_like] Array of sample data.

dist [{'norm', 'expon', 'logistic', 'gumbel', 'gumbel_l', 'gumbel_r', 'extreme1'}, optional] The type of distribution to test against. The default is 'norm'. The names 'extreme1', 'gumbel_l' and 'gumbel' are synonyms for the same distribution.

Returns

statistic [float] The Anderson-Darling test statistic.

critical_values
[list] The critical values for this distribution.

significance_level
[list] The significance levels for the corresponding critical values in percents. The function returns critical values for a differing set of significance levels depending on the distribution that is being tested against.

See also:

kstest

The Kolmogorov-Smirnov test for goodness-of-fit.

Notes

Critical values provided are for the following significance levels:

normal/exponential

15%, 10%, 5%, 2.5%, 1%

logistic

25%, 10%, 5%, 2.5%, 1%, 0.5%

Gumbel

25%, 10%, 5%, 2.5%, 1%

If the returned statistic is larger than these critical values then for the corresponding significance level, the null hypothesis that the data come from the chosen distribution can be rejected. The returned statistic is referred to as 'A2' in the references.

References

[1], [2], [3], [4], [5], [6]

scipy.stats.anderson_ksamp

scipy.stats.**anderson_ksamp**(*samples*, *midrank=True*)

The Anderson-Darling test for k-samples.

The k-sample Anderson-Darling test is a modification of the one-sample Anderson-Darling test. It tests the null hypothesis that k-samples are drawn from the same population without having to specify the distribution function of that population. The critical values depend on the number of samples.

Parameters

samples [sequence of 1-D array_like] Array of sample data in arrays.

midrank [bool, optional] Type of Anderson-Darling test which is computed. Default (True) is the midrank test applicable to continuous and discrete populations. If False, the right side empirical distribution is used.

Returns

statistic [float] Normalized k-sample Anderson-Darling test statistic.

critical_values
[array] The critical values for significance levels 25%, 10%, 5%, 2.5%, 1%, 0.5%, 0.1%.

significance_level
[float] An approximate significance level at which the null hypothesis for the provided samples can be rejected. The value is floored / capped at 0.1% / 25%.

Raises

ValueError
If less than 2 samples are provided, a sample is empty, or no distinct observations are in the samples.

See also:

ks_2samp

2 sample Kolmogorov-Smirnov test

anderson

1 sample Anderson-Darling test

Notes

[1] defines three versions of the k-sample Anderson-Darling test: one for continuous distributions and two for discrete distributions, in which ties between samples may occur. The default of this routine is to compute the version based on the midrank empirical distribution function. This test is applicable to continuous and discrete data. If midrank is set to False, the right side empirical distribution is used for a test for discrete data. According to [1], the two discrete test statistics differ only slightly if a few collisions due to round-off errors occur in the test not adjusted for ties between samples.

The critical values corresponding to the significance levels from 0.01 to 0.25 are taken from [1]. p-values are floored / capped at 0.1% / 25%. Since the range of critical values might be extended in future releases, it is recommended not to test `p == 0.25`, but rather `p >= 0.25` (analogously for the lower bound).

New in version 0.14.0.

References

[1]

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
```

The null hypothesis that the two random samples come from the same distribution can be rejected at the 5% level because the returned test value is greater than the critical value for 5% (1.961) but not at the 2.5% level. The interpolation gives an approximate significance level of 3.2%:

```
>>> stats.anderson_ksamp([rng.normal(size=50),
... rng.normal(loc=0.5, size=30)])
(1.974403288713695,
  array([0.325, 1.226, 1.961, 2.718, 3.752, 4.592, 6.546]),
  0.04991293614572478)
```

The null hypothesis cannot be rejected for three samples from an identical distribution. The reported p-value (25%) has been capped and may not be very accurate (since it corresponds to the value 0.449 whereas the statistic is -0.731):

```
>>> stats.anderson_ksamp([rng.normal(size=50),
... rng.normal(size=30), rng.normal(size=20)])
(-0.29103725200789504,
  array([ 0.44925884,  1.3052767 ,  1.9434184 ,  2.57696569,  3.41634856,
  4.07210043, 5.56419101]),
  0.25)
```

scipy.stats.binom_test

scipy.stats.**binom_test**(*x*, *n=None*, *p=0.5*, *alternative='two-sided'*)

Perform a test that the probability of success is p.

Note: *binom_test* is deprecated; it is recommended that *binomtest* be used instead.

This is an exact, two-sided test of the null hypothesis that the probability of success in a Bernoulli experiment is *p*.

Parameters

x [int or array_like] The number of successes, or if x has length 2, it is the number of successes and the number of failures.

n [int] The number of trials. This is ignored if x gives both the number of successes and failures.

p [float, optional] The hypothesized probability of success. `0 <= p <= 1`. The default value is `p = 0.5`.

alternative [{'two-sided', 'greater', 'less'}, optional] Indicates the alternative hypothesis. The default value is 'two-sided'.

Returns

p-value [float] The p-value of the hypothesis test.

References

[1]

Examples

```
>>> from scipy import stats
```

A car manufacturer claims that no more than 10% of their cars are unsafe. 15 cars are inspected for safety, 3 were found to be unsafe. Test the manufacturer's claim:

```
>>> stats.binom_test(3, n=15, p=0.1, alternative='greater')
0.18406106910639114
```

The null hypothesis cannot be rejected at the 5% level of significance because the returned p-value is greater than the critical value of 5%.

scipy.stats.binomtest

scipy.stats.**binomtest**(*k*, *n*, *p=0.5*, *alternative='two-sided'*)

Perform a test that the probability of success is p.

The binomial test [1] is a test of the null hypothesis that the probability of success in a Bernoulli experiment is *p*.

Details of the test can be found in many texts on statistics, such as section 24.5 of [2].

Parameters

k [int] The number of successes.

n [int] The number of trials.

p [float, optional] The hypothesized probability of success, i.e. the expected proportion of successes. The value must be in the interval `0 <= p <= 1`. The default value is `p = 0.5`.

alternative

[{'two-sided', 'greater', 'less'}, optional] Indicates the alternative hypothesis. The default value is 'two-sided'.

Returns

result [*BinomTestResult* instance] The return value is an object with the following attributes:

k [int] The number of successes (copied from *binomtest* input).

n [int] The number of trials (copied from *binomtest* input).

alternative

[str] Indicates the alternative hypothesis specified in the input to *binomtest*. It will be one of `'two-sided'`, `'greater'`, or `'less'`.

pvalue [float] The p-value of the hypothesis test.

proportion_estimate

[float] The estimate of the proportion of successes.

The object has the following methods:

proportion_ci(confidence_level=0.95, method='exact') :

Compute the confidence interval for `proportion_estimate`.

Notes

New in version 1.7.0.

References

[1], [2]

Examples

```
>>> from scipy.stats import binomtest
```

A car manufacturer claims that no more than 10% of their cars are unsafe. 15 cars are inspected for safety, 3 were found to be unsafe. Test the manufacturer's claim:

```
>>> result = binomtest(3, n=15, p=0.1, alternative='greater')
>>> result.pvalue
0.18406106910639114
```

The null hypothesis cannot be rejected at the 5% level of significance because the returned p-value is greater than the critical value of 5%.

The estimated proportion is simply `3/15`:

```
>>> result.proportion_estimate
0.2
```

We can use the *proportion_ci()* method of the result to compute the confidence interval of the estimate:

```
>>> result.proportion_ci(confidence_level=0.95)
ConfidenceInterval(low=0.05684686759024681, high=1.0)
```

scipy.stats.fligner

`scipy.stats.`**`fligner`**(**args*, *center='median'*, *proportiontocut=0.05*)

Perform Fligner-Killeen test for equality of variance.

Fligner's test tests the null hypothesis that all input samples are from populations with equal variances. Fligner-Killeen's test is distribution free when populations are identical [2].

Parameters

sample1, sample2, …
: [array_like] Arrays of sample data. Need not be the same length.

center
: [{'mean', 'median', 'trimmed'}, optional] Keyword argument controlling which function of the data is used in computing the test statistic. The default is 'median'.

proportiontocut
: [float, optional] When *center* is 'trimmed', this gives the proportion of data points to cut from each end. (See *scipy.stats.trim_mean*.) Default is 0.05.

Returns

statistic
: [float] The test statistic.

pvalue
: [float] The p-value for the hypothesis test.

See also:

bartlett

A parametric test for equality of k variances in normal samples

levene

A robust parametric test for equality of k variances

Notes

As with Levene's test there are three variants of Fligner's test that differ by the measure of central tendency used in the test. See *levene* for more information.

Conover et al. (1981) examine many of the existing parametric and nonparametric tests by extensive simulations and they conclude that the tests proposed by Fligner and Killeen (1976) and Levene (1960) appear to be superior in terms of robustness of departures from normality and power [3].

References

[1], [2], [3], [4]

Examples

Test whether or not the lists *a*, *b* and *c* come from populations with equal variances.

```
>>> from scipy.stats import fligner
>>> a = [8.88, 9.12, 9.04, 8.98, 9.00, 9.08, 9.01, 8.85, 9.06, 8.99]
>>> b = [8.88, 8.95, 9.29, 9.44, 9.15, 9.58, 8.36, 9.18, 8.67, 9.05]
>>> c = [8.95, 9.12, 8.95, 8.85, 9.03, 8.84, 9.07, 8.98, 8.86, 8.98]
>>> stat, p = fligner(a, b, c)
>>> p
0.00450826080004775
```

The small p-value suggests that the populations do not have equal variances.

This is not surprising, given that the sample variance of *b* is much larger than that of *a* and *c*:

```
>>> [np.var(x, ddof=1) for x in [a, b, c]]
[0.007054444444444413, 0.13073888888888888, 0.008890000000000002]
```

scipy.stats.median_test

scipy.stats.**median_test**(**args*, *ties='below'*, *correction=True*, *lambda_=1*, *nan_policy='propagate'*)

Perform a Mood's median test.

Test that two or more samples come from populations with the same median.

Let `n = len(args)` be the number of samples. The "grand median" of all the data is computed, and a contingency table is formed by classifying the values in each sample as being above or below the grand median. The contingency table, along with *correction* and *lambda_*, are passed to *scipy.stats.chi2_contingency* to compute the test statistic and p-value.

Parameters

sample1, sample2, …
: [array_like] The set of samples. There must be at least two samples. Each sample must be a one-dimensional sequence containing at least one value. The samples are not required to have the same length.

ties
: [str, optional] Determines how values equal to the grand median are classified in the contingency table. The string must be one of:

```
"below":
    Values equal to the grand median are counted as "below
↪".
"above":
    Values equal to the grand median are counted as "above
↪".
"ignore":
    Values equal to the grand median are not counted.
```

The default is "below".

correction
: [bool, optional] If True, *and* there are just two samples, apply Yates' correction for continuity when computing the test statistic associated with the contingency table. Default is True.

lambda_
: [float or str, optional] By default, the statistic computed in this test is Pearson's chi-squared statistic. *lambda_* allows a statistic from the Cressie-Read power divergence family to be used instead. See *power_divergence* for details. Default is 1 (Pearson's chi-squared statistic).

nan_policy
: [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

stat
: [float] The test statistic. The statistic that is returned is determined by *lambda_*. The default is Pearson's chi-squared statistic.

p
: [float] The p-value of the test.

m
: [float] The grand median.

table
: [ndarray] The contingency table. The shape of the table is (2, n), where n is the number of samples. The first row holds the counts of the values above the grand median, and the second row holds the counts of the values below the grand median. The table allows further analysis with, for example, *scipy.stats.chi2_contingency*, or with *scipy.stats.fisher_exact* if there are two samples, without having to recompute the table. If `nan_policy` is "propagate" and there are nans in the input, the return value for `table` is `None`.

See also:

kruskal

Compute the Kruskal-Wallis H-test for independent samples.

mannwhitneyu

Computes the Mann-Whitney rank test on samples x and y.

Notes

New in version 0.15.0.

References

[1], [2]

Examples

A biologist runs an experiment in which there are three groups of plants. Group 1 has 16 plants, group 2 has 15 plants, and group 3 has 17 plants. Each plant produces a number of seeds. The seed counts for each group are:

```
Group 1: 10 14 14 18 20 22 24 25 31 31 32 39 43 43 48 49
Group 2: 28 30 31 33 34 35 36 40 44 55 57 61 91 92 99
Group 3:  0  3  9 22 23 25 25 33 34 34 40 45 46 48 62 67 84
```

The following code applies Mood's median test to these samples.

```
>>> g1 = [10, 14, 14, 18, 20, 22, 24, 25, 31, 31, 32, 39, 43, 43, 48, 49]
>>> g2 = [28, 30, 31, 33, 34, 35, 36, 40, 44, 55, 57, 61, 91, 92, 99]
>>> g3 = [0, 3, 9, 22, 23, 25, 25, 33, 34, 34, 40, 45, 46, 48, 62, 67, 84]
>>> from scipy.stats import median_test
>>> stat, p, med, tbl = median_test(g1, g2, g3)
```

The median is

```
>>> med
34.0
```

and the contingency table is

```
>>> tbl
array([[ 5, 10,  7],
       [11,  5, 10]])
```

p is too large to conclude that the medians are not the same:

```
>>> p
0.12609082774093244
```

The "G-test" can be performed by passing `lambda_="log-likelihood"` to *median_test*.

```
>>> g, p, med, tbl = median_test(g1, g2, g3, lambda_="log-likelihood")
>>> p
0.12224779737117837
```

The median occurs several times in the data, so we'll get a different result if, for example, `ties="above"` is used:

```
>>> stat, p, med, tbl = median_test(g1, g2, g3, ties="above")
>>> p
0.063873276069553273
```

```
>>> tbl
array([[ 5, 11,  9],
       [11,  4,  8]])
```

This example demonstrates that if the data set is not large and there are values equal to the median, the p-value can be sensitive to the choice of *ties*.

scipy.stats.mood

scipy.stats.**mood**(*x*, *y*, *axis=0*, *alternative='two-sided'*)

Perform Mood's test for equal scale parameters.

Mood's two-sample test for scale parameters is a non-parametric test for the null hypothesis that two samples are drawn from the same distribution with the same scale parameter.

Parameters

x, y [array_like] Arrays of sample data.

axis [int, optional] The axis along which the samples are tested. *x* and *y* can be of different length along *axis*. If *axis* is None, *x* and *y* are flattened and the test is done on all values in the flattened arrays.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. Default is 'two-sided'. The following options are available:

- 'two-sided': the scales of the distributions underlying *x* and *y* are different.
- 'less': the scale of the distribution underlying *x* is less than the scale of the distribution underlying *y*.
- 'greater': the scale of the distribution underlying *x* is greater than the scale of the distribution underlying *y*.

New in version 1.7.0.

Returns

z [scalar or ndarray] The z-score for the hypothesis test. For 1-D inputs a scalar is returned.

p-value [scalar ndarray] The p-value for the hypothesis test.

See also:

fligner

A non-parametric test for the equality of k variances

ansari

A non-parametric test for the equality of 2 variances

bartlett

A parametric test for equality of k variances in normal samples

levene

A parametric test for equality of k variances

Notes

The data are assumed to be drawn from probability distributions `f(x)` and `f(x/s) / s` respectively, for some probability density function f. The null hypothesis is that `s == 1`.

For multi-dimensional arrays, if the inputs are of shapes `(n0, n1, n2, n3)` and `(n0, m1, n2, n3)`, then if `axis=1`, the resulting z and p values will have shape `(n0, n2, n3)`. Note that `n1` and `m1` don't have to be equal, but the other dimensions do.

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
>>> x2 = rng.standard_normal((2, 45, 6, 7))
>>> x1 = rng.standard_normal((2, 30, 6, 7))
>>> z, p = stats.mood(x1, x2, axis=1)
>>> p.shape
(2, 6, 7)
```

Find the number of points where the difference in scale is not significant:

```
>>> (p > 0.1).sum()
78
```

Perform the test with different scales:

```
>>> x1 = rng.standard_normal((2, 30))
>>> x2 = rng.standard_normal((2, 35)) * 10.0
>>> stats.mood(x1, x2, axis=1)
(array([-5.76174136, -6.12650783]), array([8.32505043e-09, 8.98287869e-
↪10]))
```

scipy.stats.skewtest

scipy.stats.**skewtest**(*a*, *axis=0*, *nan_policy='propagate'*, *alternative='two-sided'*)

Test whether the skew is different from the normal distribution.

This function tests the null hypothesis that the skewness of the population that the sample was drawn from is the same as that of a corresponding normal distribution.

Parameters

a [array] The data to be tested.

axis [int or None, optional] Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. Default is 'two-sided'. The following options are available:

- 'two-sided': the skewness of the distribution underlying the sample is different from that of the normal distribution (i.e. 0)
- 'less': the skewness of the distribution underlying the sample is less than that of the normal distribution
- 'greater': the skewness of the distribution underlying the sample is greater than that of the normal distribution

New in version 1.7.0.

Returns

statistic [float] The computed z-score for this test.
pvalue [float] The p-value for the hypothesis test.

Notes

The sample size must be at least 8.

References

[1]

Examples

```
>>> from scipy.stats import skewtest
>>> skewtest([1, 2, 3, 4, 5, 6, 7, 8])
SkewtestResult(statistic=1.0108048609177787, pvalue=0.3121098361421897)
>>> skewtest([2, 8, 0, 4, 1, 9, 9, 0])
SkewtestResult(statistic=0.44626385374196975, pvalue=0.6554066631275459)
>>> skewtest([1, 2, 3, 4, 5, 6, 7, 8000])
SkewtestResult(statistic=3.571773510360407, pvalue=0.0003545719905823133)
>>> skewtest([100, 100, 100, 100, 100, 100, 100, 101])
SkewtestResult(statistic=3.5717766638478072, pvalue=0.00035456772028163 4)
>>> skewtest([1, 2, 3, 4, 5, 6, 7, 8], alternative='less')
SkewtestResult(statistic=1.0108048609177787, pvalue=0.8439450819289052)
>>> skewtest([1, 2, 3, 4, 5, 6, 7, 8], alternative='greater')
SkewtestResult(statistic=1.0108048609177787, pvalue=0.15605491807109484)
```

scipy.stats.kurtosistest

`scipy.stats.`**`kurtosistest`**(*a*, *axis=0*, *nan_policy='propagate'*, *alternative='two-sided'*)

Test whether a dataset has normal kurtosis.

This function tests the null hypothesis that the kurtosis of the population from which the sample was drawn is that of the normal distribution.

Parameters

a [array] Array of the sample data.
axis [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.
nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan

- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

alternative

[{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. The following options are available (default is 'two-sided'):

- 'two-sided': the kurtosis of the distribution underlying the sample is different from that of the normal distribution
- 'less': the kurtosis of the distribution underlying the sample is less than that of the normal distribution
- 'greater': the kurtosis of the distribution underlying the sample is greater than that of the normal distribution

New in version 1.7.0.

Returns

statistic [float] The computed z-score for this test.

pvalue [float] The p-value for the hypothesis test.

Notes

Valid only for n>20. This function uses the method described in [1].

References

[1]

Examples

```
>>> from scipy.stats import kurtosistest
>>> kurtosistest(list(range(20)))
KurtosistestResult(statistic=-1.7058104152122062, pvalue=0.
↪08804338332528348)
>>> kurtosistest(list(range(20)), alternative='less')
KurtosistestResult(statistic=-1.7058104152122062, pvalue=0.
↪04402169166264174)
>>> kurtosistest(list(range(20)), alternative='greater')
KurtosistestResult(statistic=-1.7058104152122062, pvalue=0.
↪9559783083373583)
```

```
>>> rng = np.random.default_rng()
>>> s = rng.normal(0, 1, 1000)
>>> kurtosistest(s)
KurtosistestResult(statistic=-1.475047944490622, pvalue=0.
↪14019965402996987)
```

scipy.stats.normaltest

scipy.stats.**normaltest**(*a*, *axis=0*, *nan_policy='propagate'*)

Test whether a sample differs from a normal distribution.

This function tests the null hypothesis that a sample comes from a normal distribution. It is based on D'Agostino and Pearson's [1], [2] test that combines skew and kurtosis to produce an omnibus test of normality.

Parameters

a [array_like] The array containing the sample to be tested.

axis [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': returns nan
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Returns

statistic [float or array] `s^2 + k^2`, where `s` is the z-score returned by *skewtest* and `k` is the z-score returned by *kurtosistest*.

pvalue [float or array] A 2-sided chi squared probability for the hypothesis test.

References

[1], [2]

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
>>> pts = 1000
>>> a = rng.normal(0, 1, size=pts)
>>> b = rng.normal(2, 1, size=pts)
>>> x = np.concatenate((a, b))
>>> k2, p = stats.normaltest(x)
>>> alpha = 1e-3
>>> print("p = {:g}".format(p))
p = 8.4713e-19
>>> if p < alpha:  # null hypothesis: x comes from a normal distribution
...     print("The null hypothesis can be rejected")
... else:
...     print("The null hypothesis cannot be rejected")
The null hypothesis can be rejected
```

Quasi-Monte Carlo

Quasi-Monte Carlo submodule (`scipy.stats.qmc`)

This module provides Quasi-Monte Carlo generators and associated helper functions.

Quasi-Monte Carlo

Engines

QMCEngine(d, *[, seed])	A generic Quasi-Monte Carlo sampler class meant for subclassing.
Sobol(d, *[, scramble, seed])	Engine for generating (scrambled) Sobol' sequences.
Halton(d, *[, scramble, seed])	Halton sequence.
LatinHypercube(d, *[, centered, seed])	Latin hypercube sampling (LHS).
MultinomialQMC(pvals, *[, engine, seed])	QMC sampling from a multinomial distribution.
MultivariateNormalQMC(mean[, cov, cov_root, …])	QMC sampling from a multivariate Normal $N(\mu, \Sigma)$.

scipy.stats.qmc.QMCEngine

class scipy.stats.qmc.**QMCEngine**(*d*, *, *seed=None*)

A generic Quasi-Monte Carlo sampler class meant for subclassing.

QMCEngine is a base class to construct a specific Quasi-Monte Carlo sampler. It cannot be used directly as a sampler.

Parameters

d [int] Dimension of the parameter space.

seed [{None, int, `numpy.random.Generator`}, optional] If *seed* is None the `numpy.random.Generator` singleton is used. If *seed* is an int, a new `Generator` instance is used, seeded with *seed*. If *seed* is already a `Generator` instance then that instance is used.

Notes

By convention samples are distributed over the half-open interval `[0, 1)`. Instances of the class can access the attributes: `d` for the dimension; and `rng` for the random number generator (used for the `seed`).

Subclassing

When subclassing *QMCEngine* to create a new sampler, `__init__` and `random` must be redefined.

- `__init__(d, seed=None)`: at least fix the dimension. If the sampler does not take advantage of a `seed` (deterministic methods like Halton), this parameter can be omitted.
- `random(n)`: draw `n` from the engine and increase the counter `num_generated` by `n`.

Optionally, two other methods can be overwritten by subclasses:

- `reset`: Reset the engine to it's original state.
- `fast_forward`: If the sequence is deterministic (like Halton sequence), then `fast_forward(n)` is skipping the `n` first draw.

Examples

To create a random sampler based on `np.random.random`, we would do the following:

```
>>> from scipy.stats import qmc
>>> class RandomEngine(qmc.QMCEngine):
...     def __init__(self, d, seed=None):
...         super().__init__(d=d, seed=seed)
...
...
...     def random(self, n=1):
...         self.num_generated += n
...         return self.rng.random((n, self.d))
...
...
...     def reset(self):
...         super().__init__(d=self.d, seed=self.rng_seed)
...         return self
...
...
...     def fast_forward(self, n):
...         self.random(n)
...         return self
```

After subclassing *QMCEngine* to define the sampling strategy we want to use, we can create an instance to sample from.

```
>>> engine = RandomEngine(2)
>>> engine.random(5)
array([[0.22733602, 0.31675834],  # random
       [0.79736546, 0.67625467],
       [0.39110955, 0.33281393],
       [0.59830875, 0.18673419],
       [0.67275604, 0.94180287]])
```

We can also reset the state of the generator and resample again.

```
>>> _ = engine.reset()
>>> engine.random(5)
array([[0.22733602, 0.31675834],  # random
       [0.79736546, 0.67625467],
       [0.39110955, 0.33281393],
       [0.59830875, 0.18673419],
       [0.67275604, 0.94180287]])
```

Methods

fast_forward(n)	Fast-forward the sequence by *n* positions.
random([n])	Draw *n* in the half-open interval `[0, 1)`.
reset()	Reset the engine to base state.

scipy.stats.qmc.QMCEngine.fast_forward

QMCEngine.**fast_forward**(*n*)

Fast-forward the sequence by *n* positions.

Parameters

n [int] Number of points to skip in the sequence.

Returns

engine [QMCEngine] Engine reset to its base state.

scipy.stats.qmc.QMCEngine.random

abstract QMCEngine.**random**(*n=1*)

Draw *n* in the half-open interval `[0, 1)`.

Parameters

n [int, optional] Number of samples to generate in the parameter space. Default is 1.

Returns

sample [array_like (n, d)] QMC sample.

scipy.stats.qmc.QMCEngine.reset

QMCEngine.**reset**()

Reset the engine to base state.

Returns

engine [QMCEngine] Engine reset to its base state.

scipy.stats.qmc.Sobol

class scipy.stats.qmc.**Sobol**(*d*, ***, *scramble=True*, *seed=None*)

Engine for generating (scrambled) Sobol' sequences.

Sobol' sequences are low-discrepancy, quasi-random numbers. Points can be drawn using two methods:

- *random_base2*: safely draw $n = 2^m$ points. This method guarantees the balance properties of the sequence.
- *random*: draw an arbitrary number of points from the sequence. See warning below.

Parameters

d	[int] Dimensionality of the sequence. Max dimensionality is 21201.
scramble	[bool, optional] If True, use Owen scrambling. Otherwise no scrambling is done. Default is True.
seed	[{None, int, `numpy.random.Generator`}, optional] If *seed* is None the `numpy.random.Generator` singleton is used. If *seed* is an int, a new `Generator` instance is used, seeded with *seed*. If *seed* is already a `Generator` instance then that instance is used.

Notes

Sobol' sequences [1] provide $n = 2^m$ low discrepancy points in $[0, 1)^d$. Scrambling them [2] makes them suitable for singular integrands, provides a means of error estimation, and can improve their rate of convergence.

There are many versions of Sobol' sequences depending on their 'direction numbers'. This code uses direction numbers from [3]. Hence, the maximum number of dimension is 21201. The direction numbers have been precomputed with search criterion 6 and can be retrieved at https://web.maths.unsw.edu.au/~fkuo/sobol/.

Warning: Sobol' sequences are a quadrature rule and they lose their balance properties if one uses a sample size that is not a power of 2, or skips the first point, or thins the sequence [4].

If $n = 2^m$ points are not enough then one should take 2^M points for $M > m$. When scrambling, the number R of independent replicates does not have to be a power of 2.

Sobol' sequences are generated to some number B of bits. After 2^B points have been generated, the sequence will repeat. Currently $B = 30$.

References

[1], [2], [3], [4]

Examples

Generate samples from a low discrepancy sequence of Sobol'.

```
>>> from scipy.stats import qmc
>>> sampler = qmc.Sobol(d=2, scramble=False)
>>> sample = sampler.random_base2(m=3)
>>> sample
array([[0.   , 0.   ],
       [0.5  , 0.5  ],
       [0.75 , 0.25 ],
       [0.25 , 0.75 ],
       [0.375, 0.375],
       [0.875, 0.875],
       [0.625, 0.125],
       [0.125, 0.625]])
```

Compute the quality of the sample using the discrepancy criterion.

```
>>> qmc.discrepancy(sample)
0.013882107204860938
```

To continue an existing design, extra points can be obtained by calling again *random_base2*. Alternatively, you can skip some points like:

```
>>> _ = sampler.reset()
>>> _ = sampler.fast_forward(4)
>>> sample_continued = sampler.random_base2(m=2)
>>> sample_continued
array([[0.375, 0.375],
       [0.875, 0.875],
       [0.625, 0.125],
       [0.125, 0.625]])
```

Finally, samples can be scaled to bounds.

```
>>> l_bounds = [0, 2]
>>> u_bounds = [10, 5]
>>> qmc.scale(sample_continued, l_bounds, u_bounds)
array([[3.75 , 3.125],
       [8.75 , 4.625],
       [6.25 , 2.375],
       [1.25 , 3.875]])
```

Methods

fast_forward(n)	Fast-forward the sequence by *n* positions.
random([n])	Draw next point(s) in the Sobol' sequence.
random_base2(m)	Draw point(s) from the Sobol' sequence.
reset()	Reset the engine to base state.

scipy.stats.qmc.Sobol.fast_forward

Sobol.**fast_forward**(*n*)

Fast-forward the sequence by *n* positions.

Parameters

n [int] Number of points to skip in the sequence.

Returns

engine: Sobol

The fast-forwarded engine.

scipy.stats.qmc.Sobol.random

Sobol.**random**(*n=1*)

Draw next point(s) in the Sobol' sequence.

Parameters

n [int, optional] Number of samples to generate in the parameter space. Default is 1.

Returns

sample [array_like (n, d)] Sobol' sample.

scipy.stats.qmc.Sobol.random_base2

Sobol.**random_base2**(*m*)

Draw point(s) from the Sobol' sequence.

This function draws $n = 2^m$ points in the parameter space ensuring the balance properties of the sequence.

Parameters

m [int] Logarithm in base 2 of the number of samples; i.e., n = 2^m.

Returns

sample [array_like (n, d)] Sobol' sample.

scipy.stats.qmc.Sobol.reset

Sobol.**reset**()

Reset the engine to base state.

Returns

engine [Sobol] Engine reset to its base state.

scipy.stats.qmc.Halton

class scipy.stats.qmc.**Halton**(*d*, ***, *scramble=True*, *seed=None*)

Halton sequence.

Pseudo-random number generator that generalize the Van der Corput sequence for multiple dimensions. The Halton sequence uses the base-two Van der Corput sequence for the first dimension, base-three for its second and base-n for its n-dimension.

Parameters

d [int] Dimension of the parameter space.

scramble [bool, optional] If True, use Owen scrambling. Otherwise no scrambling is done. Default is True.

seed [{None, int, `numpy.random.Generator`}, optional] If *seed* is None the `numpy.random.Generator` singleton is used. If *seed* is an int, a new `Generator` instance is used, seeded with *seed*. If *seed* is already a `Generator` instance then that instance is used.

Notes

The Halton sequence has severe striping artifacts for even modestly large dimensions. These can be ameliorated by scrambling. Scrambling also supports replication-based error estimates and extends applicabiltiy to unbounded integrands.

References

[1], [2]

Examples

Generate samples from a low discrepancy sequence of Halton.

```
>>> from scipy.stats import qmc
>>> sampler = qmc.Halton(d=2, scramble=False)
>>> sample = sampler.random(n=5)
>>> sample
array([[0.        , 0.        ],
       [0.5       , 0.33333333],
       [0.25      , 0.66666667],
       [0.75      , 0.11111111],
       [0.125     , 0.44444444]])
```

Compute the quality of the sample using the discrepancy criterion.

```
>>> qmc.discrepancy(sample)
0.088893711419753
```

If some wants to continue an existing design, extra points can be obtained by calling again *random*. Alternatively, you can skip some points like:

```
>>> _ = sampler.fast_forward(5)
>>> sample_continued = sampler.random(n=5)
>>> sample_continued
array([[0.3125    , 0.37037037],
       [0.8125    , 0.7037037 ],
       [0.1875    , 0.14814815],
       [0.6875    , 0.48148148],
       [0.4375    , 0.81481481]])
```

Finally, samples can be scaled to bounds.

```
>>> l_bounds = [0, 2]
>>> u_bounds = [10, 5]
>>> qmc.scale(sample_continued, l_bounds, u_bounds)
array([[3.125     , 3.11111111],
       [8.125     , 4.11111111],
       [1.875     , 2.44444444],
       [6.875     , 3.44444444],
       [4.375     , 4.44444444]])
```

Methods

fast_forward(n)	Fast-forward the sequence by *n* positions.
random([n])	Draw *n* in the half-open interval `[0, 1)`.
reset()	Reset the engine to base state.

scipy.stats.qmc.Halton.fast_forward

Halton.**fast_forward**(*n*)

Fast-forward the sequence by *n* positions.

Parameters

n [int] Number of points to skip in the sequence.

Returns

engine [QMCEngine] Engine reset to its base state.

scipy.stats.qmc.Halton.random

Halton.**random**(*n=1*)

Draw *n* in the half-open interval `[0, 1)`.

Parameters

n [int, optional] Number of samples to generate in the parameter space. Default is 1.

Returns

sample [array_like (n, d)] QMC sample.

scipy.stats.qmc.Halton.reset

Halton.**reset**()

Reset the engine to base state.

Returns

engine [QMCEngine] Engine reset to its base state.

scipy.stats.qmc.LatinHypercube

class scipy.stats.qmc.**LatinHypercube**(*d*, ***, *centered=False*, *seed=None*)

Latin hypercube sampling (LHS).

A Latin hypercube sample [1] generates n points in $[0, 1)^d$. Each univariate marginal distribution is stratified, placing exactly one point in $[j/n, (j+1)/n)$ for $j = 0, 1, ..., n-1$. They are still applicable when $n << d$. LHS is extremely effective on integrands that are nearly additive [2]. LHS on n points never has more variance than plain MC on $n-1$ points [3]. There is a central limit theorem for LHS [4], but not necessarily for optimized LHS.

Parameters

d [int] Dimension of the parameter space.

centered [bool, optional] Center the point within the multi-dimensional grid. Default is False.

seed [{None, int, `numpy.random.Generator`}, optional] If *seed* is None the `numpy.random.Generator` singleton is used. If *seed* is an int, a new `Generator` instance is used, seeded with *seed*. If *seed* is already a `Generator` instance then that instance is used.

References

[1], [2], [3], [4]

Examples

Generate samples from a Latin hypercube generator.

```
>>> from scipy.stats import qmc
>>> sampler = qmc.LatinHypercube(d=2)
>>> sample = sampler.random(n=5)
>>> sample
array([[0.1545328 , 0.53664833],  # random
       [0.84052691, 0.06474907],
       [0.52177809, 0.93343721],
       [0.68033825, 0.36265316],
       [0.26544879, 0.61163943]])
```

Compute the quality of the sample using the discrepancy criterion.

```
>>> qmc.discrepancy(sample)
0.019558034794794565  # random
```

Finally, samples can be scaled to bounds.

```
>>> l_bounds = [0, 2]
>>> u_bounds = [10, 5]
>>> qmc.scale(sample, l_bounds, u_bounds)
array([[1.54532796, 3.609945  ],  # random
       [8.40526909, 2.1942472 ],
       [5.2177809 , 4.80031164],
       [6.80338249, 3.08795949],
       [2.65448791, 3.83491828]])
```

Methods

fast_forward(n)	Fast-forward the sequence by *n* positions.
random([n])	Draw *n* in the half-open interval `[0, 1)`.
reset()	Reset the engine to base state.

scipy.stats.qmc.LatinHypercube.fast_forward

LatinHypercube.**fast_forward**(*n*)

Fast-forward the sequence by *n* positions.

Parameters

n [int] Number of points to skip in the sequence.

Returns

engine [QMCEngine] Engine reset to its base state.

scipy.stats.qmc.LatinHypercube.random

LatinHypercube.**random**(*n=1*)

Draw *n* in the half-open interval `[0, 1)`.

Parameters

n [int, optional] Number of samples to generate in the parameter space. Default is 1.

Returns

sample [array_like (n, d)] LHS sample.

scipy.stats.qmc.LatinHypercube.reset

LatinHypercube.**reset**()

Reset the engine to base state.

Returns

engine [QMCEngine] Engine reset to its base state.

scipy.stats.qmc.MultinomialQMC

class scipy.stats.qmc.**MultinomialQMC**(*pvals*, *, *engine=None*, *seed=None*)

QMC sampling from a multinomial distribution.

Parameters

pvals [array_like (k,)] Vector of probabilities of size `k`, where `k` is the number of categories. Elements must be non-negative and sum to 1.

engine [QMCEngine, optional] Quasi-Monte Carlo engine sampler. If None, *Sobol* is used.

seed [{None, int, `numpy.random.Generator`}, optional] If *seed* is None the `numpy.random.Generator` singleton is used. If *seed* is an int, a new `Generator` instance is used, seeded with *seed*. If *seed* is already a `Generator` instance then that instance is used.

Examples

```
>>> from scipy.stats import qmc
>>> engine = qmc.MultinomialQMC(pvals=[0.2, 0.4, 0.4])
>>> sample = engine.random(10)
```

Methods

fast_forward(n)	Fast-forward the sequence by *n* positions.
random([n])	Draw *n* QMC samples from the multinomial distribution.
reset()	Reset the engine to base state.

scipy.stats.qmc.MultinomialQMC.fast_forward

MultinomialQMC.**fast_forward**(*n*)

Fast-forward the sequence by *n* positions.

Parameters

n [int] Number of points to skip in the sequence.

Returns

engine [QMCEngine] Engine reset to its base state.

scipy.stats.qmc.MultinomialQMC.random

MultinomialQMC.**random**(*n=1*)

Draw *n* QMC samples from the multinomial distribution.

Parameters

n [int, optional] Number of samples to generate in the parameter space. Default is 1.

Returns

samples [array_like (pvals,)] Vector of size `p` summing to *n*.

scipy.stats.qmc.MultinomialQMC.reset

MultinomialQMC.**reset**()

Reset the engine to base state.

Returns

engine [MultinomialQMC] Engine reset to its base state.

scipy.stats.qmc.MultivariateNormalQMC

class scipy.stats.qmc.**MultivariateNormalQMC**(*mean*, *cov=None*, ***, *cov_root=None*, *inv_transform=True*, *engine=None*, *seed=None*)

QMC sampling from a multivariate Normal $N(\mu, \Sigma)$.

Parameters

mean [array_like (d,)] The mean vector. Where `d` is the dimension.

cov [array_like (d, d), optional] The covariance matrix. If omitted, use *cov_root* instead. If both *cov* and *cov_root* are omitted, use the identity matrix.

cov_root [array_like (d, d'), optional] A root decomposition of the covariance matrix, where `d'` may be less than `d` if the covariance is not full rank. If omitted, use *cov*.

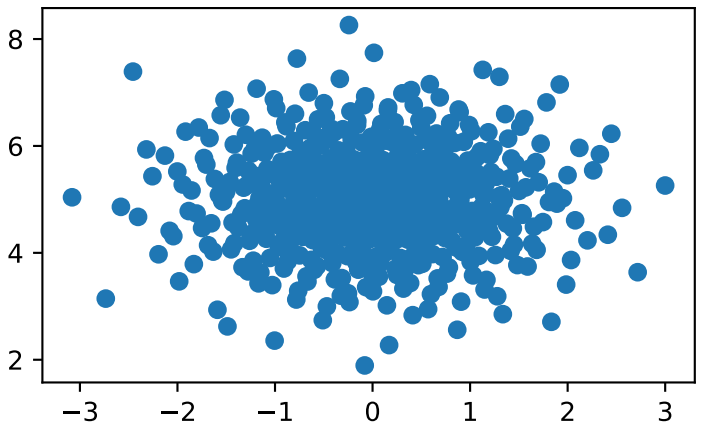
inv_transform [bool, optional] If True, use inverse transform instead of Box-Muller. Default is True.

engine [QMCEngine, optional] Quasi-Monte Carlo engine sampler. If None, *Sobol* is used.

seed [{None, int, `numpy.random.Generator`}, optional] If *seed* is None the `numpy.random.Generator` singleton is used. If *seed* is an int, a new `Generator` instance is used, seeded with *seed*. If *seed* is already a `Generator` instance then that instance is used.

Examples

```
>>> import matplotlib.pyplot as plt
>>> from scipy.stats import qmc
>>> engine = qmc.MultivariateNormalQMC(mean=[0, 5], cov=[[1, 0], [0, 1]])
>>> sample = engine.random(512)
>>> _ = plt.scatter(sample[:, 0], sample[:, 1])
>>> plt.show()
```



Methods

fast_forward(n)	Fast-forward the sequence by *n* positions.
random([n])	Draw *n* QMC samples from the multivariate Normal.
reset()	Reset the engine to base state.

scipy.stats.qmc.MultivariateNormalQMC.fast_forward

MultivariateNormalQMC.**fast_forward**(*n*)

Fast-forward the sequence by *n* positions.

Parameters

n [int] Number of points to skip in the sequence.

Returns

engine [QMCEngine] Engine reset to its base state.

scipy.stats.qmc.MultivariateNormalQMC.random

MultivariateNormalQMC.**random**(*n=1*)

Draw *n* QMC samples from the multivariate Normal.

Parameters

n [int, optional] Number of samples to generate in the parameter space. Default is 1.

Returns

sample [array_like (n, d)] Sample.

scipy.stats.qmc.MultivariateNormalQMC.reset

MultivariateNormalQMC.**reset**()

Reset the engine to base state.

Returns

engine [MultivariateNormalQMC] Engine reset to its base state.

Helpers

discrepancy(sample, *[, iterative, method, …])	Discrepancy of a given sample.
update_discrepancy(x_new, sample, initial_disc)	Update the centered discrepancy with a new sample.
scale(sample, l_bounds, u_bounds, *[, reverse])	Sample scaling from unit hypercube to different bounds.

scipy.stats.qmc.discrepancy

scipy.stats.qmc.**discrepancy**(*sample*, ***, *iterative=False*, *method='CD'*, *workers=1*)

Discrepancy of a given sample.

Parameters

sample [array_like (n, d)] The sample to compute the discrepancy from.

iterative [bool, optional] Must be False if not using it for updating the discrepancy. Default is False. Refer to the notes for more details.

method [str, optional] Type of discrepancy, can be `CD`, `WD`, `MD` or `L2-star`. Refer to the notes for more details. Default is `CD`.

workers [int, optional] Number of workers to use for parallel processing. If -1 is given all CPU threads are used. Default is 1.

Returns

discrepancy
[float] Discrepancy.

Notes

The discrepancy is a uniformity criterion used to assess the space filling of a number of samples in a hypercube. A discrepancy quantifies the distance between the continuous uniform distribution on a hypercube and the discrete uniform distribution on n distinct sample points.

The lower the value is, the better the coverage of the parameter space is.

For a collection of subsets of the hypercube, the discrepancy is the difference between the fraction of sample points in one of those subsets and the volume of that subset. There are different definitions of discrepancy corresponding to different collections of subsets. Some versions take a root mean square difference over subsets instead of a maximum.

A measure of uniformity is reasonable if it satisfies the following criteria [1]:

1. It is invariant under permuting factors and/or runs.
2. It is invariant under rotation of the coordinates.
3. It can measure not only uniformity of the sample over the hypercube, but also the projection uniformity of the sample over non-empty subset of lower dimension hypercubes.
4. There is some reasonable geometric meaning.
5. It is easy to compute.
6. It satisfies the Koksma-Hlawka-like inequality.
7. It is consistent with other criteria in experimental design.

Four methods are available:

- `CD`: Centered Discrepancy - subspace involves a corner of the hypercube
- `WD`: Wrap-around Discrepancy - subspace can wrap around bounds
- `MD`: Mixture Discrepancy - mix between CD/WD covering more criteria
- `L2-star`: L2-star discrepancy - like CD BUT variant to rotation

See [2] for precise definitions of each method.

Lastly, using `iterative=True`, it is possible to compute the discrepancy as if we had $n+1$ samples. This is useful if we want to add a point to a sampling and check the candidate which would give the lowest discrepancy. Then you could just update the discrepancy with each candidate using *`update_discrepancy`*. This method is faster than computing the discrepancy for a large number of candidates.

References

[1], [2], [3]

Examples

Calculate the quality of the sample using the discrepancy:

```
>>> from scipy.stats import qmc
>>> space = np.array([[1, 3], [2, 6], [3, 2], [4, 5], [5, 1], [6, 4]])
>>> l_bounds = [0.5, 0.5]
>>> u_bounds = [6.5, 6.5]
>>> space = qmc.scale(space, l_bounds, u_bounds, reverse=True)
>>> space
array([[0.08333333, 0.41666667],
       [0.25      , 0.91666667],
       [0.41666667, 0.25      ],
       [0.58333333, 0.75      ],
       [0.75      , 0.08333333],
       [0.91666667, 0.58333333]])
>>> qmc.discrepancy(space)
0.008142039609053464
```

We can also compute iteratively the `CD` discrepancy by using `iterative=True`.

```
>>> disc_init = qmc.discrepancy(space[:-1], iterative=True)
>>> disc_init
0.04769081147119336
>>> qmc.update_discrepancy(space[-1], space[:-1], disc_init)
0.008142039609053513
```

scipy.stats.qmc.update_discrepancy

scipy.stats.qmc.**update_discrepancy**(*x_new*, *sample*, *initial_disc*)

Update the centered discrepancy with a new sample.

Parameters

x_new [array_like (1, d)] The new sample to add in *sample*.
sample [array_like (n, d)] The initial sample.
initial_disc [float] Centered discrepancy of the *sample*.

Returns

discrepancy [float] Centered discrepancy of the sample composed of *x_new* and *sample*.

Examples

We can also compute iteratively the discrepancy by using `iterative=True`.

```
>>> from scipy.stats import qmc
>>> space = np.array([[1, 3], [2, 6], [3, 2], [4, 5], [5, 1], [6, 4]])
>>> l_bounds = [0.5, 0.5]
>>> u_bounds = [6.5, 6.5]
>>> space = qmc.scale(space, l_bounds, u_bounds, reverse=True)
>>> disc_init = qmc.discrepancy(space[:-1], iterative=True)
>>> disc_init
0.04769081147119336
>>> qmc.update_discrepancy(space[-1], space[:-1], disc_init)
0.008142039609053513
```

scipy.stats.qmc.scale

`scipy.stats.qmc.`**`scale`**(*sample*, *l_bounds*, *u_bounds*, ***, *reverse=False*)

Sample scaling from unit hypercube to different bounds.

To convert a sample from $[0, 1)$ to $[a, b), b > a$, with a the lower bounds and b the upper bounds. The following transformation is used:

$$(b - a) \cdot \text{sample} + a$$

Parameters

sample [array_like (n, d)] Sample to scale.

l_bounds, u_bounds [array_like (d,)] Lower and upper bounds (resp. a, b) of transformed data. If *reverse* is True, range of the original data to transform to the unit hypercube.

reverse [bool, optional] Reverse the transformation from different bounds to the unit hypercube. Default is False.

Returns

sample [array_like (n, d)] Scaled sample.

Examples

Transform 3 samples in the unit hypercube to bounds:

```
>>> from scipy.stats import qmc
>>> l_bounds = [-2, 0]
>>> u_bounds = [6, 5]
>>> sample = [[0.5 , 0.75],
...           [0.5 , 0.5],
...           [0.75, 0.25]]
>>> sample_scaled = qmc.scale(sample, l_bounds, u_bounds)
>>> sample_scaled
array([[2.  , 3.75],
       [2.  , 2.5 ],
       [4.  , 1.25]])
```

And convert back to the unit hypercube:

```
>>> sample_ = qmc.scale(sample_scaled, l_bounds, u_bounds, reverse=True)
>>> sample_
array([[0.5 , 0.75],
       [0.5 , 0.5 ],
       [0.75, 0.25]])
```

Introduction to Quasi-Monte Carlo

Quasi-Monte Carlo (QMC) methods [1], [2], [3] provide an $n \times d$ array of numbers in $[0, 1]$. They can be used in place of n points from the $U[0, 1]^d$ distribution. Compared to random points, QMC points are designed to have fewer gaps and clumps. This is quantified by discrepancy measures [4]. From the Koksma-Hlawka inequality [5] we know that low discrepancy reduces a bound on integration error. Averaging a function f over n QMC points can achieve an integration error close to $O(n^{-1})$ for well behaved functions [2].

Most QMC constructions are designed for special values of n such as powers of 2 or large primes. Changing the sample size by even one can degrade their performance, even their rate of convergence [6]. For instance $n = 100$ points may give less accuracy than $n = 64$ if the method was designed for $n = 2^m$.

Some QMC constructions are extensible in n: we can find another special sample size $n' > n$ and often an infinite sequence of increasing special sample sizes. Some QMC constructions are extensible in d: we can increase the dimension, possibly to some upper bound, and typically without requiring special values of d. Some QMC methods are extensible in both n and d.

QMC points are deterministic. That makes it hard to estimate the accuracy of integrals estimated by averages over QMC points. Randomized QMC (RQMC) [7] points are constructed so that each point is individually $U[0, 1]^d$ while collectively the n points retain their low discrepancy. One can make R independent replications of RQMC points to see how stable a computation is. From R independent values, a t-test (or bootstrap t-test [8]) then gives approximate confidence intervals on the mean value. Some RQMC methods produce a root mean squared error that is actually $o(1/n)$ and smaller than the rate seen in unrandomized QMC. An intuitive explanation is that the error is a sum of many small ones and random errors cancel in a way that deterministic ones do not. RQMC also has advantages on integrands that are singular or, for other reasons, fail to be Riemann integrable.

(R)QMC cannot beat Bahkvalov's curse of dimension (see [9]). For any random or deterministic method, there are worst case functions that will give it poor performance in high dimensions. A worst case function for QMC might be 0 at all n points but very large elsewhere. Worst case analyses get very pessimistic in high dimensions. (R)QMC can bring a great improvement over MC when the functions on which it is used are not worst case. For instance (R)QMC can be especially effective on integrands that are well approximated by sums of functions of some small number of their input variables at a time [10], [11]. That property is often a surprising finding about those functions.

Also, to see an improvement over IID MC, (R)QMC requires a bit of smoothness of the integrand, roughly the mixed first order derivative in each direction, $\partial^d f/\partial x_1 \cdots \partial x_d$, must be integral. For instance, a function that is 1 inside the hypersphere and 0 outside of it has infinite variation in the sense of Hardy and Krause for any dimension $d = 2$.

Scrambled nets are a kind of RQMC that have some valuable robustness properties [12]. If the integrand is square integrable, they give variance $var_{SNET} = o(1/n)$. There is a finite upper bound on var_{SNET}/var_{MC} that holds simultaneously for every square integrable integrand. Scrambled nets satisfy a strong law of large numbers for f in L^p when $p > 1$. In some special cases there is a central limit theorem [13]. For smooth enough integrands they can achieve RMSE nearly $O(n^{-3})$. See [12] for references about these properties.

The main kinds of QMC methods are lattice rules [14] and digital nets and sequences [2], [15]. The theories meet up in polynomial lattice rules [16] which can produce digital nets. Lattice rules require some form of search for good constructions. For digital nets there are widely used default constructions.

The most widely used QMC methods are Sobol' sequences [17]. These are digital nets. They are extensible in both n and d. They can be scrambled. The special sample sizes are powers of 2. Another popular method are Halton sequences [18].

The constructions resemble those of digital nets. The earlier dimensions have much better equidistribution properties than later ones. There are essentially no special sample sizes. They are not thought to be as accurate as Sobol' sequences. They can be scrambled. The nets of Faure [19] are also widely used. All dimensions are equally good, but the special sample sizes grow rapidly with dimension d. They can be scrambled. The nets of Niederreiter and Xing [20] have the best asymptotic properties but have not shown good empirical performance [21].

Higher order digital nets are formed by a digit interleaving process in the digits of the constructed points. They can achieve higher levels of asymptotic accuracy given higher smoothness conditions on f and they can be scrambled [22]. There is little or no empirical work showing the improved rate to be attained.

Using QMC is like using the entire period of a small random number generator. The constructions are similar and so therefore are the computational costs [23].

(R)QMC is sometimes improved by passing the points through a baker's transformation (tent function) prior to using them. That function has the form $1 - 2|x - 1/2|$. As x goes from 0 to 1, this function goes from 0 to 1 and then back. It is very useful to produce a periodic function for lattice rules [14], and sometimes it improves the convergence rate [24].

It is not straightforward to apply QMC methods to Markov chain Monte Carlo (MCMC). We can think of MCMC as using $n = 1$ point in $[0, 1]^d$ for very large d, with ergodic results corresponding to $d \to \infty$. One proposal is in [25] and under strong conditions an improved rate of convergence has been shown [26].

Returning to Sobol' points: there are many versions depending on what are called direction numbers. Those are the result of searches and are tabulated. A very widely used set of direction numbers come from [27]. It is extensible in dimension up to $d = 21201$.

References

Masked statistics functions

Statistical functions for masked arrays (`scipy.stats.mstats`)

This module contains a large number of statistical functions that can be used with masked arrays.

Most of these functions are similar to those in `scipy.stats` but might have small differences in the API or in the algorithm used. Since this is a relatively new package, some API changes are still possible.

Summary statistics

`describe`(a[, axis, ddof, bias])	Computes several descriptive statistics of the passed array.
`gmean`(a[, axis, dtype, weights])	Compute the geometric mean along the specified axis.
`hmean`(a[, axis, dtype])	Calculate the harmonic mean along the specified axis.
`kurtosis`(a[, axis, fisher, bias])	Computes the kurtosis (Fisher or Pearson) of a dataset.
`mode`(a[, axis])	Returns an array of the modal (most common) value in the passed array.
`mquantiles`(a[, prob, alphap, betap, axis, limit])	Computes empirical quantiles for a data array.
`hdmedian`(data[, axis, var])	Returns the Harrell-Davis estimate of the median along the given axis.
`hdquantiles`(data[, prob, axis, var])	Computes quantile estimates with the Harrell-Davis method.
`hdquantiles_sd`(data[, prob, axis])	The standard error of the Harrell-Davis quantile estimates by jackknife.
`idealfourths`(data[, axis])	Returns an estimate of the lower and upper quartiles.

continues on next page

Table 277 – continued from previous page

plotting_positions(data[, alpha, beta])	Returns plotting positions (or empirical percentile points) for the data.
meppf(data[, alpha, beta])	Returns plotting positions (or empirical percentile points) for the data.
moment(a[, moment, axis])	Calculates the nth moment about the mean for a sample.
skew(a[, axis, bias])	Computes the skewness of a data set.
tmean(a[, limits, inclusive, axis])	Compute the trimmed mean.
tvar(a[, limits, inclusive, axis, ddof])	Compute the trimmed variance
tmin(a[, lowerlimit, axis, inclusive])	Compute the trimmed minimum
tmax(a[, upperlimit, axis, inclusive])	Compute the trimmed maximum
tsem(a[, limits, inclusive, axis, ddof])	Compute the trimmed standard error of the mean.
variation(a[, axis, ddof])	Compute the coefficient of variation.
find_repeats(arr)	Find repeats in arr and return a tuple (repeats, repeat_count).
sem(a[, axis, ddof])	Calculates the standard error of the mean of the input array.
trimmed_mean(a[, limits, inclusive, …])	Returns the trimmed mean of the data along the given axis.
trimmed_mean_ci(data[, limits, inclusive, …])	Selected confidence interval of the trimmed mean along the given axis.
trimmed_std(a[, limits, inclusive, …])	Returns the trimmed standard deviation of the data along the given axis.
trimmed_var(a[, limits, inclusive, …])	Returns the trimmed variance of the data along the given axis.

scipy.stats.mstats.describe

scipy.stats.mstats.**describe**(*a*, *axis=0*, *ddof=0*, *bias=True*)

Computes several descriptive statistics of the passed array.

Parameters

a	[array_like] Data array
axis	[int or None, optional] Axis along which to calculate statistics. Default 0. If None, compute over the whole array *a*.
ddof	[int, optional] degree of freedom (default 0); note that default ddof is different from the same routine in stats.describe
bias	[bool, optional] If False, then the skewness and kurtosis calculations are corrected for statistical bias.

Returns

nobs	[int] (size of the data (discarding missing values)
minmax	[(int, int)] min, max
mean	[float] arithmetic mean
variance	[float] unbiased variance
skewness	[float] biased skewness
kurtosis	[float] biased kurtosis

Examples

```
>>> from scipy.stats.mstats import describe
>>> ma = np.ma.array(range(6), mask=[0, 0, 0, 1, 1, 1])
>>> describe(ma)
DescribeResult(nobs=3, minmax=(masked_array(data=0,
             mask=False,
       fill_value=999999), masked_array(data=2,
             mask=False,
       fill_value=999999)), mean=1.0, variance=0.6666666666666666,
       skewness=masked_array(data=0., mask=False, fill_value=1e+20),
        kurtosis=-1.5)
```

scipy.stats.mstats.gmean

scipy.stats.mstats.**gmean**(*a*, *axis=0*, *dtype=None*, *weights=None*)

Compute the geometric mean along the specified axis.

Return the geometric average of the array elements. That is: n-th root of (x1 * x2 * … * xn)

Parameters

a [array_like] Input array or object that can be converted to an array.

axis [int or None, optional] Axis along which the geometric mean is computed. Default is 0. If None, compute over the whole array *a*.

dtype [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If dtype is not specified, it defaults to the dtype of a, unless a has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.

weights [array_like, optional] The weights array can either be 1-D (in which case its length must be the size of *a* along the given *axis*) or of the same shape as *a*. Default is None, which gives each value a weight of 1.0.

Returns

gmean [ndarray] See *dtype* parameter above.

See also:

numpy.mean

Arithmetic average

numpy.average

Weighted average

hmean

Harmonic mean

Notes

The geometric average is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity because masked arrays automatically mask any non-finite values.

References

[1]

Examples

```
>>> from scipy.stats import gmean
>>> gmean([1, 4])
2.0
>>> gmean([1, 2, 3, 4, 5, 6, 7])
3.3800151591412964
```

scipy.stats.mstats.hmean

scipy.stats.mstats.**hmean**(*a*, *axis=0*, *dtype=None*)

Calculate the harmonic mean along the specified axis.

That is: n / (1/x1 + 1/x2 + … + 1/xn)

Parameters

a	[array_like] Input array, masked array or object that can be converted to an array.
axis	[int or None, optional] Axis along which the harmonic mean is computed. Default is 0. If None, compute over the whole array *a*.
dtype	[dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer *dtype* with a precision less than that of the default platform integer. In that case, the default platform integer is used.

Returns

hmean	[ndarray] See *dtype* parameter above.

See also:

numpy.mean

Arithmetic average

numpy.average

Weighted average

gmean

Geometric mean

Notes

The harmonic mean is computed over a single dimension of the input array, axis=0 by default, or all values in the array if axis=None. float64 intermediate and return values are used for integer inputs.

Use masked arrays to ignore any non-finite values in the input or that arise in the calculations such as Not a Number and infinity.

Examples

```
>>> from scipy.stats import hmean
>>> hmean([1, 4])
1.6000000000000001
>>> hmean([1, 2, 3, 4, 5, 6, 7])
2.6997245179063363
```

scipy.stats.mstats.kurtosis

scipy.stats.mstats.**kurtosis**(*a*, *axis=0*, *fisher=True*, *bias=True*)

Computes the kurtosis (Fisher or Pearson) of a dataset.

Kurtosis is the fourth central moment divided by the square of the variance. If Fisher's definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.

If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators

Use *kurtosistest* to see if result is close enough to normal.

Parameters

a	[array] data for which the kurtosis is calculated
axis	[int or None, optional] Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array *a*.
fisher	[bool, optional] If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).
bias	[bool, optional] If False, then the calculations are corrected for statistical bias.

Returns

kurtosis	[array] The kurtosis of values along an axis. If all values are equal, return -3 for Fisher's definition and 0 for Pearson's definition.

Notes

For more details about *kurtosis*, see *stats.kurtosis*.

scipy.stats.mstats.mode

scipy.stats.mstats.**mode**(*a*, *axis=0*)

Returns an array of the modal (most common) value in the passed array.

Parameters

a	[array_like] n-dimensional array of which to find mode(s).
axis	[int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

Returns

mode	[ndarray] Array of modal values.
count	[ndarray] Array of counts for each mode.

Notes

For more details, see *stats.mode*.

Examples

```
>>> from scipy import stats
>>> from scipy.stats import mstats
>>> m_arr = np.ma.array([1, 1, 0, 0, 0, 0], mask=[0, 0, 1, 1, 1, 0])
>>> stats.mode(m_arr)
ModeResult(mode=array([0]), count=array([4]))
>>> mstats.mode(m_arr)
ModeResult(mode=array([1.]), count=array([2.]))
```

scipy.stats.mstats.mquantiles

scipy.stats.mstats.**mquantiles**(*a*, *prob=[0.25, 0.5, 0.75]*, *alphap=0.4*, *betap=0.4*, *axis=None*, *limit=()*)

Computes empirical quantiles for a data array.

Samples quantile are defined by `Q(p) = (1-gamma)*x[j] + gamma*x[j+1]`, where `x[j]` is the j-th order statistic, and gamma is a function of `j = floor(n*p + m)`, `m = alphap + p*(1 - alphap - betap)` and `g = n*p + m - j`.

Reinterpreting the above equations to compare to **R** lead to the equation: `p(k) = (k - alphap)/(n + 1 - alphap - betap)`

Typical values of (alphap,betap) are:

- (0,1) : `p(k) = k/n` : linear interpolation of cdf (**R** type 4)
- (.5,.5) : `p(k) = (k - 1/2.)/n` : piecewise linear function (**R** type 5)
- (0,0) : `p(k) = k/(n+1)` : (**R** type 6)
- (1,1) : `p(k) = (k-1)/(n-1)`: p(k) = mode[F(x[k])]. (**R** type 7, **R** default)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`: Then p(k) ~ median[F(x[k])]. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (**R** type 8)

- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`: Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (**R** type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM

Parameters

a	[array_like] Input data, as a sequence or array of dimension at most 2.
prob	[array_like, optional] List of quantiles to compute.
alphap	[float, optional] Plotting positions parameter, default is 0.4.
betap	[float, optional] Plotting positions parameter, default is 0.4.
axis	[int, optional] Axis along which to perform the trimming. If None (default), the input array is first flattened.
limit	[tuple, optional] Tuple of (lower, upper) values. Values of *a* outside this open interval are ignored.

Returns

mquantiles
: [MaskedArray] An array containing the calculated quantiles.

Notes

This formulation is very similar to **R** except the calculation of `m` from `alphap` and `betap`, where in **R** `m` is defined with each type.

References

[1], [2]

Examples

```
>>> from scipy.stats.mstats import mquantiles
>>> a = np.array([6., 47., 49., 15., 42., 41., 7., 39., 43., 40., 36.])
>>> mquantiles(a)
array([ 19.2,  40. ,  42.8])
```

Using a 2D array, specifying axis and limit.

```
>>> data = np.array([[   6.,    7.,    1.],
...                  [  47.,   15.,    2.],
...                  [  49.,   36.,    3.],
...                  [  15.,   39.,    4.],
...                  [  42.,   40., -999.],
...                  [  41.,   41., -999.],
...                  [   7., -999., -999.],
...                  [  39., -999., -999.],
...                  [  43., -999., -999.],
...                  [  40., -999., -999.],
...                  [  36., -999., -999.]])
>>> print(mquantiles(data, axis=0, limit=(0, 50)))
```

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```
[[19.2  14.6   1.45]
 [40.   37.5   2.5 ]
 [42.8  40.05  3.55]]
```

```
>>> data[:, 2] = -999.
>>> print(mquantiles(data, axis=0, limit=(0, 50)))
[[19.200000000000003 14.6 --]
 [40.0 37.5 --]
 [42.800000000000004 40.05 --]]
```

scipy.stats.mstats.hdmedian

scipy.stats.mstats.**hdmedian**(*data*, *axis=- 1*, *var=False*)

Returns the Harrell-Davis estimate of the median along the given axis.

Parameters

data [ndarray] Data array.
axis [int, optional] Axis along which to compute the quantiles. If None, use a flattened array.
var [bool, optional] Whether to return the variance of the estimate.

Returns

hdmedian [MaskedArray] The median values. If `var=True`, the variance is returned inside the masked array. E.g. for a 1-D array the shape change from (1,) to (2,).

scipy.stats.mstats.hdquantiles

scipy.stats.mstats.**hdquantiles**(*data*, *prob=[0.25, 0.5, 0.75]*, *axis=None*, *var=False*)

Computes quantile estimates with the Harrell-Davis method.

The quantile estimates are calculated as a weighted linear combination of order statistics.

Parameters

data [array_like] Data array.
prob [sequence, optional] Sequence of quantiles to compute.
axis [int or None, optional] Axis along which to compute the quantiles. If None, use a flattened array.
var [bool, optional] Whether to return the variance of the estimate.

Returns

hdquantiles
[MaskedArray] A (p,) array of quantiles (if *var* is False), or a (2,p) array of quantiles and variances (if *var* is True), where `p` is the number of quantiles.

See also:

hdquantiles_sd

scipy.stats.mstats.hdquantiles_sd

scipy.stats.mstats.**hdquantiles_sd**(*data*, *prob=[0.25, 0.5, 0.75]*, *axis=None*)

The standard error of the Harrell-Davis quantile estimates by jackknife.

Parameters

data [array_like] Data array.
prob [sequence, optional] Sequence of quantiles to compute.
axis [int, optional] Axis along which to compute the quantiles. If None, use a flattened array.

Returns

hdquantiles_sd
[MaskedArray] Standard error of the Harrell-Davis quantile estimates.

See also:

hdquantiles

scipy.stats.mstats.idealfourths

scipy.stats.mstats.**idealfourths**(*data*, *axis=None*)

Returns an estimate of the lower and upper quartiles.

Uses the ideal fourths algorithm.

Parameters

data [array_like] Input array.
axis [int, optional] Axis along which the quartiles are estimated. If None, the arrays are flattened.

Returns

idealfourths
[{list of floats, masked array}] Returns the two internal values that divide *data* into four parts using the ideal fourths algorithm either along the flattened array (if *axis* is None) or along *axis* of *data*.

scipy.stats.mstats.plotting_positions

scipy.stats.mstats.**plotting_positions**(*data*, *alpha=0.4*, *beta=0.4*)

Returns plotting positions (or empirical percentile points) for the data.

Plotting positions are defined as `(i-alpha)/(n+1-alpha-beta)`, where:

- i is the rank order statistics
- n is the number of unmasked values along the given axis
- *alpha* and *beta* are two parameters.

Typical values for* alpha *and* beta *are:

- (0,1) : `p(k) = k/n`, linear interpolation of cdf (R, type 4)
- (.5,.5) : `p(k) = (k-1/2.)/n`, piecewise linear function (R, type 5)
- (0,0) : `p(k) = k/(n+1)`, Weibull (R type 6)

- (1,1) : `p(k) = (k-1)/(n-1)`, in this case, `p(k) = mode[F(x[k])]`. That's R default (R type 7)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`, then `p(k) ~ median[F(x[k])]`. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (R type 8)
- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`, Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM
- (.3175, .3175): used in scipy.stats.probplot

Parameters

data	[array_like] Input data, as a sequence or array of dimension at most 2.
alpha	[float, optional] Plotting positions parameter. Default is 0.4.
beta	[float, optional] Plotting positions parameter. Default is 0.4.

Returns

positions	[MaskedArray] The calculated plotting positions.

scipy.stats.mstats.meppf

`scipy.stats.mstats.`**`meppf`**(*data*, *alpha=0.4*, *beta=0.4*)

Returns plotting positions (or empirical percentile points) for the data.

Plotting positions are defined as `(i-alpha)/(n+1-alpha-beta)`, where:

- i is the rank order statistics
- n is the number of unmasked values along the given axis
- *alpha* and *beta* are two parameters.

Typical values for* alpha *and* beta *are:

- (0,1) : `p(k) = k/n`, linear interpolation of cdf (R, type 4)
- (.5,.5) : `p(k) = (k-1/2.)/n`, piecewise linear function (R, type 5)
- (0,0) : `p(k) = k/(n+1)`, Weibull (R type 6)
- (1,1) : `p(k) = (k-1)/(n-1)`, in this case, `p(k) = mode[F(x[k])]`. That's R default (R type 7)
- (1/3,1/3): `p(k) = (k-1/3)/(n+1/3)`, then `p(k) ~ median[F(x[k])]`. The resulting quantile estimates are approximately median-unbiased regardless of the distribution of x. (R type 8)
- (3/8,3/8): `p(k) = (k-3/8)/(n+1/4)`, Blom. The resulting quantile estimates are approximately unbiased if x is normally distributed (R type 9)
- (.4,.4) : approximately quantile unbiased (Cunnane)
- (.35,.35): APL, used with PWM
- (.3175, .3175): used in scipy.stats.probplot

Parameters

data [array_like] Input data, as a sequence or array of dimension at most 2.
alpha [float, optional] Plotting positions parameter. Default is 0.4.
beta [float, optional] Plotting positions parameter. Default is 0.4.

Returns

positions [MaskedArray] The calculated plotting positions.

scipy.stats.mstats.moment

scipy.stats.mstats.**moment**(*a*, *moment=1*, *axis=0*)

Calculates the nth moment about the mean for a sample.

Parameters

a [array_like] data
moment [int, optional] order of central moment that is returned
axis [int or None, optional] Axis along which the central moment is computed. Default is 0. If None, compute over the whole array *a*.

Returns

n-th central moment
[ndarray or float] The appropriate moment along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

Notes

For more details about `moment`, see *stats.moment*.

scipy.stats.mstats.skew

scipy.stats.mstats.**skew**(*a*, *axis=0*, *bias=True*)

Computes the skewness of a data set.

Parameters

a [ndarray] data
axis [int or None, optional] Axis along which skewness is calculated. Default is 0. If None, compute over the whole array *a*.
bias [bool, optional] If False, then the calculations are corrected for statistical bias.

Returns

skewness [ndarray] The skewness of values along an axis, returning 0 where all values are equal.

Notes

For more details about `skew`, see *stats.skew*.

scipy.stats.mstats.tmean

scipy.stats.mstats.**tmean**(*a*, *limits=None*, *inclusive=(True, True)*, *axis=None*)

Compute the trimmed mean.

Parameters

a	[array_like] Array of values.
limits	[None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None (default), then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval.
inclusive	[(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
axis	[int or None, optional] Axis along which to operate. If None, compute over the whole array. Default is None.

Returns

tmean	[float]

Notes

For more details on `tmean`, see *stats.tmean*.

Examples

```
>>> from scipy.stats import mstats
>>> a = np.array([[6, 8, 3, 0],
...               [3, 9, 1, 2],
...               [8, 7, 8, 2],
...               [5, 6, 0, 2],
...               [4, 5, 5, 2]])
...
...
>>> mstats.tmean(a, (2,5))
3.3
>>> mstats.tmean(a, (2,5), axis=0)
masked_array(data=[4.0, 5.0, 4.0, 2.0],
             mask=[False, False, False, False],
       fill_value=1e+20)
```

scipy.stats.mstats.tvar

scipy.stats.mstats.**tvar**(*a*, *limits=None*, *inclusive=(True, True)*, *axis=0*, *ddof=1*)

Compute the trimmed variance

This function computes the sample variance of an array of values, while ignoring values which are outside of given *limits*.

Parameters

a	[array_like] Array of values.
limits	[None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.
inclusive	[(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
axis	[int or None, optional] Axis along which to operate. If None, compute over the whole array. Default is zero.
ddof	[int, optional] Delta degrees of freedom. Default is 1.

Returns

tvar	[float] Trimmed variance.

Notes

For more details on `tvar`, see *stats.tvar*.

scipy.stats.mstats.tmin

scipy.stats.mstats.**tmin**(*a*, *lowerlimit=None*, *axis=0*, *inclusive=True*)

Compute the trimmed minimum

Parameters

a	[array_like] array of values
lowerlimit	[None or float, optional] Values in the input array less than the given limit will be ignored. When lowerlimit is None, then all values are used. The default value is None.
axis	[int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.
inclusive	[{True, False}, optional] This flag determines whether values exactly equal to the lower limit are included. The default value is True.

Returns

tmin	[float, int or ndarray]

Notes

For more details on `tmin`, see *stats.tmin*.

Examples

```
>>> from scipy.stats import mstats
>>> a = np.array([[6, 8, 3, 0],
...               [3, 2, 1, 2],
...               [8, 1, 8, 2],
...               [5, 3, 0, 2],
...               [4, 7, 5, 2]])
...
>>> mstats.tmin(a, 5)
masked_array(data=[5, 7, 5, --],
             mask=[False, False, False,  True],
       fill_value=999999)
```

scipy.stats.mstats.tmax

scipy.stats.mstats.**tmax**(*a*, *upperlimit=None*, *axis=0*, *inclusive=True*)

Compute the trimmed maximum

This function computes the maximum value of an array along a given axis, while ignoring values larger than a specified upper limit.

Parameters

a [array_like] array of values

upperlimit [None or float, optional] Values in the input array greater than the given limit will be ignored. When upperlimit is None, then all values are used. The default value is None.

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

inclusive [{True, False}, optional] This flag determines whether values exactly equal to the upper limit are included. The default value is True.

Returns

tmax [float, int or ndarray]

Notes

For more details on `tmax`, see *stats.tmax*.

Examples

```
>>> from scipy.stats import mstats
>>> a = np.array([[6, 8, 3, 0],
...               [3, 9, 1, 2],
...               [8, 7, 8, 2],
...               [5, 6, 0, 2],
...               [4, 5, 5, 2]])
...
...
>>> mstats.tmax(a, 4)
masked_array(data=[4, --, 3, 2],
             mask=[False,  True, False, False],
       fill_value=999999)
```

scipy.stats.mstats.tsem

scipy.stats.mstats.**tsem**(*a*, *limits=None*, *inclusive=(True, True)*, *axis=0*, *ddof=1*)

Compute the trimmed standard error of the mean.

This function finds the standard error of the mean for given values, ignoring values outside the given *limits*.

Parameters

a	[array_like] array of values
limits	[None or (lower limit, upper limit), optional] Values in the input array less than the lower limit or greater than the upper limit will be ignored. When limits is None, then all values are used. Either of the limit values in the tuple can also be None representing a half-open interval. The default value is None.
inclusive	[(bool, bool), optional] A tuple consisting of the (lower flag, upper flag). These flags determine whether values exactly equal to the lower or upper limits are included. The default value is (True, True).
axis	[int or None, optional] Axis along which to operate. If None, compute over the whole array. Default is zero.
ddof	[int, optional] Delta degrees of freedom. Default is 1.

Returns

tsem	[float]

Notes

For more details on `tsem`, see *stats.tsem*.

scipy.stats.mstats.variation

scipy.stats.mstats.**variation**(*a*, *axis=0*, *ddof=0*)

Compute the coefficient of variation.

The coefficient of variation is the standard deviation divided by the mean. This function is equivalent to:

```
np.std(x, axis=axis, ddof=ddof) / np.mean(x)
```

The default for `ddof` is 0, but many definitions of the coefficient of variation use the square root of the unbiased sample variance for the sample standard deviation, which corresponds to `ddof=1`.

Parameters

a	[array_like] Input array.
axis	[int or None, optional] Axis along which to calculate the coefficient of variation. Default is 0. If None, compute over the whole array *a*.
ddof	[int, optional] Delta degrees of freedom. Default is 0.

Returns

variation	[ndarray] The calculated variation along the requested axis.

Notes

For more details about *variation*, see *stats.variation*.

Examples

```
>>> from scipy.stats.mstats import variation
>>> a = np.array([2,8,4])
>>> variation(a)
0.5345224838248487
>>> b = np.array([2,8,3,4])
>>> c = np.ma.masked_array(b, mask=[0,0,1,0])
>>> variation(c)
0.5345224838248487
```

In the example above, it can be seen that this works the same as *stats.variation* except 'stats.mstats.variation' ignores masked array elements.

scipy.stats.mstats.find_repeats

scipy.stats.mstats.**find_repeats**(*arr*)

Find repeats in arr and return a tuple (repeats, repeat_count).

The input is cast to float64. Masked values are discarded.

Parameters

arr	[sequence] Input array. The array is flattened if it is not 1D.

Returns

repeats	[ndarray] Array of repeated values.
counts	[ndarray] Array of counts.

scipy.stats.mstats.sem

scipy.stats.mstats.**sem**(*a*, *axis=0*, *ddof=1*)

Calculates the standard error of the mean of the input array.

Also sometimes called standard error of measurement.

Parameters

a	[array_like] An array containing the values for which the standard error is returned.
axis	[int or None, optional] If axis is None, ravel *a* first. If axis is an integer, this will be the axis over which to operate. Defaults to 0.
ddof	[int, optional] Delta degrees-of-freedom. How many degrees of freedom to adjust for bias in limited samples relative to the population estimate of variance. Defaults to 1.

Returns

s	[ndarray or float] The standard error of the mean in the sample(s), along the input axis.

Notes

The default value for *ddof* changed in scipy 0.15.0 to be consistent with *stats.sem* as well as with the most common definition used (like in the R documentation).

Examples

Find standard error along the first axis:

```
>>> from scipy import stats
>>> a = np.arange(20).reshape(5,4)
>>> print(stats.mstats.sem(a))
[2.8284271247461903 2.8284271247461903 2.8284271247461903
 2.8284271247461903]
```

Find standard error across the whole array, using n degrees of freedom:

```
>>> print(stats.mstats.sem(a, axis=None, ddof=0))
1.2893796958227628
```

scipy.stats.mstats.trimmed_mean

scipy.stats.mstats.**trimmed_mean**(*a*, *limits=(0.1, 0.1)*, *inclusive=(1, 1)*, *relative=True*, *axis=None*)

Returns the trimmed mean of the data along the given axis.

Parameters

a	[sequence] Input array
limits	[{None, tuple}, optional] If *relative* is False, tuple (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit are masked. If *relative* is True, tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after

trimming is n*(1.-sum(limits)) In each case, the value of one limit can be set to None to indicate an open interval.
If limits is None, no trimming is performed

inclusive [{(bool, bool) tuple}, optional] If *relative* is False, tuple indicating whether values exactly equal to the absolute limits are allowed. If *relative* is True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

relative [bool, optional] Whether to consider the limits as absolute values (False) or proportions to cut (True).

axis [int, optional] Axis along which to trim.

scipy.stats.mstats.trimmed_mean_ci

scipy.stats.mstats.**trimmed_mean_ci**(*data*, *limits=(0.2, 0.2)*, *inclusive=(True, True)*, *alpha=0.05*, *axis=None*)

Selected confidence interval of the trimmed mean along the given axis.

Parameters

data [array_like] Input data.

limits [{None, tuple}, optional] None or a two item tuple. Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. If `n` is the number of unmasked data before trimming, then (`n * limits[0]`)th smallest data and (`n * limits[1]`)th largest data are masked. The total number of unmasked data after trimming is `n * (1. - sum(limits))`. The value of one limit can be set to None to indicate an open interval.
Defaults to (0.2, 0.2).

inclusive [(2,) tuple of boolean, optional] If relative==False, tuple indicating whether values exactly equal to the absolute limits are allowed. If relative==True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).
Defaults to (True, True).

alpha [float, optional] Confidence level of the intervals.
Defaults to 0.05.

axis [int, optional] Axis along which to cut. If None, uses a flattened version of *data*.
Defaults to None.

Returns

trimmed_mean_ci
[(2,) ndarray] The lower and upper confidence intervals of the trimmed data.

scipy.stats.mstats.trimmed_std

scipy.stats.mstats.**trimmed_std**(*a*, *limits=(0.1, 0.1)*, *inclusive=(1, 1)*, *relative=True*, *axis=None*, *ddof=0*)

Returns the trimmed standard deviation of the data along the given axis.

Parameters

a [sequence] Input array

limits [{None, tuple}, optional] If *relative* is False, tuple (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit are masked.
If *relative* is True, tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.
Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after

trimming is n*(1.-sum(limits)) In each case, the value of one limit can be set to None to indicate an open interval.
If limits is None, no trimming is performed

inclusive [{(bool, bool) tuple}, optional] If *relative* is False, tuple indicating whether values exactly equal to the absolute limits are allowed. If *relative* is True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

relative [bool, optional] Whether to consider the limits as absolute values (False) or proportions to cut (True).

axis [int, optional] Axis along which to trim.

ddof [{0,integer}, optional] Means Delta Degrees of Freedom. The denominator used during computations is (n-ddof). DDOF=0 corresponds to a biased estimate, DDOF=1 to an unbiased estimate of the variance.

scipy.stats.mstats.trimmed_var

scipy.stats.mstats.**trimmed_var**(*a*, *limits=(0.1, 0.1)*, *inclusive=(1, 1)*, *relative=True*, *axis=None*, *ddof=0*)

Returns the trimmed variance of the data along the given axis.

Parameters

a [sequence] Input array

limits [{None, tuple}, optional] If *relative* is False, tuple (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit are masked.
If *relative* is True, tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.
Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) In each case, the value of one limit can be set to None to indicate an open interval.
If limits is None, no trimming is performed

inclusive [{(bool, bool) tuple}, optional] If *relative* is False, tuple indicating whether values exactly equal to the absolute limits are allowed. If *relative* is True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

relative [bool, optional] Whether to consider the limits as absolute values (False) or proportions to cut (True).

axis [int, optional] Axis along which to trim.

ddof [{0,integer}, optional] Means Delta Degrees of Freedom. The denominator used during computations is (n-ddof). DDOF=0 corresponds to a biased estimate, DDOF=1 to an unbiased estimate of the variance.

Frequency statistics

scoreatpercentile(data, per[, limit, …])	Calculate the score at the given 'per' percentile of the sequence a.

scipy.stats.mstats.scoreatpercentile

scipy.stats.mstats.**scoreatpercentile**(*data*, *per*, *limit=()*, *alphap=0.4*, *betap=0.4*)

Calculate the score at the given 'per' percentile of the sequence a. For example, the score at per=50 is the median.

This function is a shortcut to mquantile

Correlation functions

f_oneway(*args)	Performs a 1-way ANOVA, returning an F-value and probability given any number of groups.
pearsonr(x, y)	Calculates a Pearson correlation coefficient and the p-value for testing non-correlation.
spearmanr(x[, y, use_ties, axis, …])	Calculates a Spearman rank-order correlation coefficient and the p-value to test for non-correlation.
pointbiserialr(x, y)	Calculates a point biserial correlation coefficient and its p-value.
kendalltau(x, y[, use_ties, use_missing, method])	Computes Kendall's rank correlation tau on two variables *x* and *y*.
kendalltau_seasonal(x)	Computes a multivariate Kendall's rank correlation tau, for seasonal data.
linregress(x[, y])	Linear regression calculation
siegelslopes(y[, x, method])	Computes the Siegel estimator for a set of points (x, y).
theilslopes(y[, x, alpha])	Computes the Theil-Sen estimator for a set of points (x, y).
sen_seasonal_slopes(x)	

scipy.stats.mstats.f_oneway

scipy.stats.mstats.**f_oneway**(**args*)

Performs a 1-way ANOVA, returning an F-value and probability given any number of groups. From Heiman, pp.394-7.

Usage: `f_oneway(*args)`, where `*args` is 2 or more arrays, one per treatment group.

Returns

statistic [float] The computed F-value of the test.
pvalue [float] The associated p-value from the F-distribution.

scipy.stats.mstats.pearsonr

scipy.stats.mstats.**pearsonr**(*x*, *y*)

Calculates a Pearson correlation coefficient and the p-value for testing non-correlation.

The Pearson correlation coefficient measures the linear relationship between two datasets. Strictly speaking, Pearson's correlation requires that each dataset be normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply an exact linear relationship. Positive correlations imply that as *x* increases, so does *y*. Negative correlations imply that as *x* increases, *y* decreases.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Pearson correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters

x [1-D array_like] Input
y [1-D array_like] Input

Returns

pearsonr [float] Pearson's correlation coefficient, 2-tailed p-value.

References

http://www.statsoft.com/textbook/glosp.html#Pearson%20Correlation

scipy.stats.mstats.spearmanr

`scipy.stats.mstats.`**`spearmanr`**(*x*, *y=None*, *use_ties=True*, *axis=None*, *nan_policy='propagate'*, *alternative='two-sided'*)

Calculates a Spearman rank-order correlation coefficient and the p-value to test for non-correlation.

The Spearman correlation is a nonparametric measure of the linear relationship between two datasets. Unlike the Pearson correlation, the Spearman correlation does not assume that both datasets are normally distributed. Like other correlation coefficients, this one varies between -1 and +1 with 0 implying no correlation. Correlations of -1 or +1 imply a monotonic relationship. Positive correlations imply that as *x* increases, so does *y*. Negative correlations imply that as *x* increases, *y* decreases.

Missing values are discarded pair-wise: if a value is missing in *x*, the corresponding value in *y* is masked.

The p-value roughly indicates the probability of an uncorrelated system producing datasets that have a Spearman correlation at least as extreme as the one computed from these datasets. The p-values are not entirely reliable but are probably reasonable for datasets larger than 500 or so.

Parameters

x, y [1D or 2D array_like, y is optional] One or two 1-D or 2-D arrays containing multiple variables and observations. When these are 1-D, each represents a vector of observations of a single variable. For the behavior in the 2-D case, see under `axis`, below.

use_ties [bool, optional] DO NOT USE. Does not do anything, keyword is only left in place for backwards compatibility reasons.

axis [int or None, optional] If axis=0 (default), then each column represents a variable, with observations in the rows. If axis=1, the relationship is transposed: each row represents a variable, while the columns contain observations. If axis=None, then both arrays will be raveled.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. Default is 'two-sided'. The following options are available:

- 'two-sided': the correlation is nonzero
- 'less': the correlation is negative (less than zero)
- 'greater': the correlation is positive (greater than zero)

New in version 1.7.0.

Returns

correlation
: [float] Spearman correlation coefficient

pvalue [float] 2-tailed p-value.

References

[CRCProbStat2000] section 14.7

scipy.stats.mstats.pointbiserialr

scipy.stats.mstats.**pointbiserialr**(*x*, *y*)

Calculates a point biserial correlation coefficient and its p-value.

Parameters

x [array_like of bools] Input array.

y [array_like] Input array.

Returns

correlation
: [float] R value

pvalue [float] 2-tailed p-value

Notes

Missing values are considered pair-wise: if a value is missing in x, the corresponding value in y is masked.

For more details on `pointbiserialr`, see *stats.pointbiserialr*.

scipy.stats.mstats.kendalltau

scipy.stats.mstats.**kendalltau**(*x*, *y*, *use_ties=True*, *use_missing=False*, *method='auto'*)

Computes Kendall's rank correlation tau on two variables *x* and *y*.

Parameters

x [sequence] First data list (for example, time).

y [sequence] Second data list.

use_ties [{True, False}, optional] Whether ties correction should be performed.

use_missing
: [{False, True}, optional] Whether missing data should be allocated a rank of 0 (False) or the average rank (True)

method: {'auto', 'asymptotic', 'exact'}, optional
: Defines which method is used to calculate the p-value [1]. 'asymptotic' uses a normal approximation valid for large samples. 'exact' computes the exact p-value, but can only be used if no ties are present. As the sample size increases, the 'exact' computation time may grow and the result may lose some precision. 'auto' is the default and selects the appropriate method based on a trade-off between speed and accuracy.

Returns

correlation
: [float] Kendall tau

pvalue [float] Approximate 2-side p-value.

References

[1]

scipy.stats.mstats.kendalltau_seasonal

scipy.stats.mstats.**kendalltau_seasonal**(*x*)

Computes a multivariate Kendall's rank correlation tau, for seasonal data.

Parameters

x [2-D ndarray] Array of seasonal data, with seasons in columns.

scipy.stats.mstats.linregress

scipy.stats.mstats.**linregress**(*x*, *y=None*)

Linear regression calculation

Note that the non-masked version is used, and that this docstring is replaced by the non-masked docstring + some info on missing data.

scipy.stats.mstats.siegelslopes

scipy.stats.mstats.**siegelslopes**(*y*, *x=None*, *method='hierarchical'*)

Computes the Siegel estimator for a set of points (x, y).

siegelslopes implements a method for robust linear regression using repeated medians to fit a line to the points (x, y). The method is robust to outliers with an asymptotic breakdown point of 50%.

Parameters

y [array_like] Dependent variable.

x [array_like or None, optional] Independent variable. If None, use `arange(len(y))` instead.

method [{'hierarchical', 'separate'}] If 'hierarchical', estimate the intercept using the estimated slope `medslope` (default option). If 'separate', estimate the intercept independent of the estimated slope. See Notes for details.

Returns

medslope [float] Estimate of the slope of the regression line.

medintercept
: [float] Estimate of the intercept of the regression line.

See also:

theilslopes

a similar technique without repeated medians

Notes

For more details on *siegelslopes*, see *scipy.stats.siegelslopes*.

scipy.stats.mstats.theilslopes

scipy.stats.mstats.**theilslopes**(*y*, *x=None*, *alpha=0.95*)

Computes the Theil-Sen estimator for a set of points (x, y).

theilslopes implements a method for robust linear regression. It computes the slope as the median of all slopes between paired values.

Parameters

y	[array_like] Dependent variable.
x	[array_like or None, optional] Independent variable. If None, use `arange(len(y))` instead.
alpha	[float, optional] Confidence degree between 0 and 1. Default is 95% confidence. Note that *alpha* is symmetric around 0.5, i.e. both 0.1 and 0.9 are interpreted as "find the 90% confidence interval".

Returns

medslope	[float] Theil slope.
medintercept	[float] Intercept of the Theil line, as `median(y) - medslope*median(x)`.
lo_slope	[float] Lower bound of the confidence interval on *medslope*.
up_slope	[float] Upper bound of the confidence interval on *medslope*.

See also:

siegelslopes

a similar technique with repeated medians

Notes

For more details on *theilslopes*, see *stats.theilslopes*.

scipy.stats.mstats.sen_seasonal_slopes

scipy.stats.mstats.**sen_seasonal_slopes**(*x*)

Statistical tests

ttest_1samp(a, popmean[, axis])	Calculates the T-test for the mean of ONE group of scores.
ttest_onesamp(a, popmean[, axis])	Calculates the T-test for the mean of ONE group of scores.
ttest_ind(a, b[, axis, equal_var])	Calculates the T-test for the means of TWO INDEPENDENT samples of scores.

continues on next page

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ttest_rel(a, b[, axis])	Calculates the T-test on TWO RELATED samples of scores, a and b.
chisquare(f_obs[, f_exp, ddof, axis])	Calculate a one-way chi-square test.
kstest(data1, data2[, args, alternative, mode])	***Parameters***
ks_2samp(data1, data2[, alternative, mode])	Computes the Kolmogorov-Smirnov test on two samples.
ks_1samp(x, cdf[, args, alternative, mode])	Computes the Kolmogorov-Smirnov test on one sample of masked values.
ks_twosamp(data1, data2[, alternative, mode])	Computes the Kolmogorov-Smirnov test on two samples.
mannwhitneyu(x, y[, use_continuity])	Computes the Mann-Whitney statistic
rankdata(data[, axis, use_missing])	Returns the rank (also known as order statistics) of each data point along the given axis.
kruskal(*args)	Compute the Kruskal-Wallis H-test for independent samples
kruskalwallis(*args)	Compute the Kruskal-Wallis H-test for independent samples
friedmanchisquare(*args)	Friedman Chi-Square is a non-parametric, one-way within-subjects ANOVA.
brunnermunzel(x, y[, alternative, distribution])	Computes the Brunner-Munzel test on samples x and y
skewtest(a[, axis])	Tests whether the skew is different from the normal distribution.
kurtosistest(a[, axis])	Tests whether a dataset has normal kurtosis
normaltest(a[, axis])	Tests whether a sample differs from a normal distribution.

scipy.stats.mstats.ttest_1samp

scipy.stats.mstats.**ttest_1samp**(*a*, *popmean*, *axis=0*)

Calculates the T-test for the mean of ONE group of scores.

Parameters

a [array_like] sample observation

popmean [float or array_like] expected value in null hypothesis, if array_like than it must have the same shape as *a* excluding the axis dimension

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole array *a*.

Returns

statistic [float or array] t-statistic

pvalue [float or array] two-tailed p-value

Notes

For more details on `ttest_1samp`, see *stats.ttest_1samp*.

scipy.stats.mstats.ttest_onesamp

scipy.stats.mstats.**ttest_onesamp**(*a*, *popmean*, *axis=0*)

Calculates the T-test for the mean of ONE group of scores.

Parameters

a	[array_like] sample observation
popmean	[float or array_like] expected value in null hypothesis, if array_like than it must have the same shape as *a* excluding the axis dimension
axis	[int or None, optional] Axis along which to compute test. If None, compute over the whole array *a*.

Returns

statistic	[float or array] t-statistic
pvalue	[float or array] two-tailed p-value

Notes

For more details on `ttest_1samp`, see *stats.ttest_1samp*.

scipy.stats.mstats.ttest_ind

scipy.stats.mstats.**ttest_ind**(*a*, *b*, *axis=0*, *equal_var=True*)

Calculates the T-test for the means of TWO INDEPENDENT samples of scores.

Parameters

a, b	[array_like] The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).
axis	[int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.
equal_var	[bool, optional] If True, perform a standard independent 2 sample test that assumes equal population variances. If False, perform Welch's t-test, which does not assume equal population variance. New in version 0.17.0.

Returns

statistic	[float or array] The calculated t-statistic.
pvalue	[float or array] The two-tailed p-value.

Notes

For more details on `ttest_ind`, see *stats.ttest_ind*.

scipy.stats.mstats.ttest_rel

scipy.stats.mstats.**ttest_rel**(*a*, *b*, *axis=0*)

Calculates the T-test on TWO RELATED samples of scores, a and b.

Parameters

a, b [array_like] The arrays must have the same shape.

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

Returns

statistic [float or array] t-statistic

pvalue [float or array] two-tailed p-value

Notes

For more details on `ttest_rel`, see *stats.ttest_rel*.

scipy.stats.mstats.chisquare

scipy.stats.mstats.**chisquare**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*)

Calculate a one-way chi-square test.

The chi-square test tests the null hypothesis that the categorical data has the given frequencies.

Parameters

f_obs [array_like] Observed frequencies in each category.

f_exp [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof [int, optional] "Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis [int or None, optional] The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

Returns

chisq [float or ndarray] The chi-squared test statistic. The value is a float if *axis* is None or *f_obs* and *f_exp* are 1-D.

p [float or ndarray] The p-value of the test. The value is a float if *ddof* and the return value *chisq* are scalars.

See also:

scipy.stats.power_divergence

scipy.stats.fisher_exact

Fisher exact test on a 2x2 contingency table.

scipy.stats.barnard_exact

An unconditional exact test. An alternative to chi-squared test for small sample sizes.

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5. According to [3], the total number of samples is recommended to be greater than 13, otherwise exact tests (such as Barnard's Exact test) should be used because they do not overreject.

Also, the sum of the observed and expected frequencies must be the same for the test to be valid; *chisquare* raises an error if the sums do not agree within a relative tolerance of `1e-8`.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not chi-square, in which case this test is not appropriate.

References

[1], [2], [3]

Examples

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```
>>> from scipy.stats import chisquare
>>> chisquare([16, 18, 16, 14, 12, 12])
(2.0, 0.84914503608460956)
```

With *f_exp* the expected frequencies can be given.

```
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])
(3.5, 0.62338762774958223)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T
>>> obs.shape
(6, 2)
>>> chisquare(obs)
(array([ 2.        ,  6.66666667]), array([ 0.84914504,  0.24663415]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> chisquare(obs, axis=None)
(23.31034482758621, 0.015975692534127565)
>>> chisquare(obs.ravel())
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)
(2.0, 0.7357588823428847)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with *ddof*.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we use `axis=1`:

```
>>> chisquare([16, 18, 16, 14, 12, 12],
...           f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
...           axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

scipy.stats.mstats.kstest

scipy.stats.mstats.**kstest**(*data1*, *data2*, *args=()*, *alternative='two-sided'*, *mode='auto'*)

Parameters

data1 [array_like]
data2 [str, callable or array_like]
args [tuple, sequence, optional] Distribution parameters, used if *data1* or *data2* are strings.
alternative [str, as documented in stats.kstest]
mode [str, as documented in stats.kstest]

Returns

tuple of (K-S statistic, probability)

scipy.stats.mstats.ks_2samp

scipy.stats.mstats.**ks_2samp**(*data1*, *data2*, *alternative='two-sided'*, *mode='auto'*)

Computes the Kolmogorov-Smirnov test on two samples.

Missing values in *x* and/or *y* are discarded.

Parameters

data1 [array_like] First data set
data2 [array_like] Second data set
alternative [{'two-sided', 'less', 'greater'}, optional] Indicates the alternative hypothesis. Default is 'two-sided'.

mode [{'auto', 'exact', 'asymp'}, optional] Defines the method used for calculating the p-value. The following options are available (default is 'auto'):
- 'auto' : use 'exact' for small size arrays, 'asymp' for large
- 'exact' : use approximation to exact distribution of test statistic
- 'asymp' : use asymptotic distribution of test statistic

Returns

d [float] Value of the Kolmogorov Smirnov test
p [float] Corresponding p-value.

scipy.stats.mstats.ks_1samp

scipy.stats.mstats.**ks_1samp**(*x*, *cdf*, *args=()*, *alternative='two-sided'*, *mode='auto'*)

Computes the Kolmogorov-Smirnov test on one sample of masked values.

Missing values in *x* are discarded.

Parameters

x [array_like] a 1-D array of observations of random variables.
cdf [str or callable] If a string, it should be the name of a distribution in *scipy.stats*. If a callable, that callable is used to calculate the cdf.
args [tuple, sequence, optional] Distribution parameters, used if *cdf* is a string.
alternative [{'two-sided', 'less', 'greater'}, optional] Indicates the alternative hypothesis. Default is 'two-sided'.
mode [{'auto', 'exact', 'asymp'}, optional] Defines the method used for calculating the p-value. The following options are available (default is 'auto'):
- 'auto' : use 'exact' for small size arrays, 'asymp' for large
- 'exact' : use approximation to exact distribution of test statistic
- 'asymp' : use asymptotic distribution of test statistic

Returns

d [float] Value of the Kolmogorov Smirnov test
p [float] Corresponding p-value.

scipy.stats.mstats.ks_twosamp

scipy.stats.mstats.**ks_twosamp**(*data1*, *data2*, *alternative='two-sided'*, *mode='auto'*)

Computes the Kolmogorov-Smirnov test on two samples.

Missing values in *x* and/or *y* are discarded.

Parameters

data1 [array_like] First data set
data2 [array_like] Second data set
alternative [{'two-sided', 'less', 'greater'}, optional] Indicates the alternative hypothesis. Default is 'two-sided'.
mode [{'auto', 'exact', 'asymp'}, optional] Defines the method used for calculating the p-value. The following options are available (default is 'auto'):
- 'auto' : use 'exact' for small size arrays, 'asymp' for large
- 'exact' : use approximation to exact distribution of test statistic
- 'asymp' : use asymptotic distribution of test statistic

Returns

d [float] Value of the Kolmogorov Smirnov test
p [float] Corresponding p-value.

scipy.stats.mstats.mannwhitneyu

scipy.stats.mstats.**mannwhitneyu**(*x*, *y*, *use_continuity=True*)

Computes the Mann-Whitney statistic

Missing values in *x* and/or *y* are discarded.

Parameters

x [sequence] Input
y [sequence] Input
use_continuity
[{True, False}, optional] Whether a continuity correction (1/2.) should be taken into account.

Returns

statistic [float] The minimum of the Mann-Whitney statistics
pvalue [float] Approximate two-sided p-value assuming a normal distribution.

scipy.stats.mstats.rankdata

scipy.stats.mstats.**rankdata**(*data*, *axis=None*, *use_missing=False*)

Returns the rank (also known as order statistics) of each data point along the given axis.

If some values are tied, their rank is averaged. If some values are masked, their rank is set to 0 if use_missing is False, or set to the average rank of the unmasked values if use_missing is True.

Parameters

data [sequence] Input data. The data is transformed to a masked array
axis [{None,int}, optional] Axis along which to perform the ranking. If None, the array is first flattened. An exception is raised if the axis is specified for arrays with a dimension larger than 2
use_missing
[bool, optional] Whether the masked values have a rank of 0 (False) or equal to the average rank of the unmasked values (True).

scipy.stats.mstats.kruskal

scipy.stats.mstats.**kruskal**(**args*)

Compute the Kruskal-Wallis H-test for independent samples

Parameters

sample1, sample2, …
[array_like] Two or more arrays with the sample measurements can be given as arguments.

Returns

statistic [float] The Kruskal-Wallis H statistic, corrected for ties
pvalue [float] The p-value for the test using the assumption that H has a chi square distribution

Notes

For more details on `kruskal`, see *stats.kruskal*.

Examples

```
>>> from scipy.stats.mstats import kruskal
```

Random samples from three different brands of batteries were tested to see how long the charge lasted. Results were as follows:

```
>>> a = [6.3, 5.4, 5.7, 5.2, 5.0]
>>> b = [6.9, 7.0, 6.1, 7.9]
>>> c = [7.2, 6.9, 6.1, 6.5]
```

Test the hypotesis that the distribution functions for all of the brands' durations are identical. Use 5% level of significance.

```
>>> kruskal(a, b, c)
KruskalResult(statistic=7.113812154696133, pvalue=0.028526948491942164)
```

The null hypothesis is rejected at the 5% level of significance because the returned p-value is less than the critical value of 5%.

scipy.stats.mstats.kruskalwallis

scipy.stats.mstats.**kruskalwallis**(**args*)

Compute the Kruskal-Wallis H-test for independent samples

Parameters

sample1, sample2, …
: [array_like] Two or more arrays with the sample measurements can be given as arguments.

Returns

statistic [float] The Kruskal-Wallis H statistic, corrected for ties
pvalue [float] The p-value for the test using the assumption that H has a chi square distribution

Notes

For more details on `kruskal`, see *stats.kruskal*.

Examples

```
>>> from scipy.stats.mstats import kruskal
```

Random samples from three different brands of batteries were tested to see how long the charge lasted. Results were as follows:

```
>>> a = [6.3, 5.4, 5.7, 5.2, 5.0]
>>> b = [6.9, 7.0, 6.1, 7.9]
>>> c = [7.2, 6.9, 6.1, 6.5]
```

Test the hypotesis that the distribution functions for all of the brands' durations are identical. Use 5% level of significance.

```
>>> kruskal(a, b, c)
KruskalResult(statistic=7.113812154696133, pvalue=0.028526948491942164)
```

The null hypothesis is rejected at the 5% level of significance because the returned p-value is less than the critical value of 5%.

scipy.stats.mstats.friedmanchisquare

scipy.stats.mstats.**friedmanchisquare**(**args*)

Friedman Chi-Square is a non-parametric, one-way within-subjects ANOVA. This function calculates the Friedman Chi-square test for repeated measures and returns the result, along with the associated probability value.

Each input is considered a given group. Ideally, the number of treatments among each group should be equal. If this is not the case, only the first n treatments are taken into account, where n is the number of treatments of the smallest group. If a group has some missing values, the corresponding treatments are masked in the other groups. The test statistic is corrected for ties.

Masked values in one group are propagated to the other groups.

Returns

statistic [float] the test statistic.
pvalue [float] the associated p-value.

scipy.stats.mstats.brunnermunzel

scipy.stats.mstats.**brunnermunzel**(*x*, *y*, *alternative='two-sided'*, *distribution='t'*)

Computes the Brunner-Munzel test on samples x and y

Missing values in *x* and/or *y* are discarded.

Parameters

x, y [array_like] Array of samples, should be one-dimensional.
alternative
['less', 'two-sided', or 'greater', optional] Whether to get the p-value for the one-sided hypothesis ('less' or 'greater') or for the two-sided hypothesis ('two-sided'). Defaults value is 'two-sided' .
distribution: 't' or 'normal', optional
Whether to get the p-value by t-distribution or by standard normal distribution. Defaults value is 't' .

Returns

statistic [float] The Brunner-Munzer W statistic.
pvalue [float] p-value assuming an t distribution. One-sided or two-sided, depending on the choice of *alternative* and *distribution*.

See also:

mannwhitneyu

Mann-Whitney rank test on two samples.

Notes

For more details on *brunnermunzel*, see *stats.brunnermunzel*.

scipy.stats.mstats.skewtest

scipy.stats.mstats.**skewtest**(*a*, *axis=0*)

Tests whether the skew is different from the normal distribution.

Parameters

a	[array] The data to be tested
axis	[int or None, optional] Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.

Returns

statistic	[float] The computed z-score for this test.
pvalue	[float] a 2-sided p-value for the hypothesis test

Notes

For more details about *skewtest*, see *stats.skewtest*.

scipy.stats.mstats.kurtosistest

scipy.stats.mstats.**kurtosistest**(*a*, *axis=0*)

Tests whether a dataset has normal kurtosis

Parameters

a	[array] array of the sample data
axis	[int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

Returns

statistic	[float] The computed z-score for this test.
pvalue	[float] The 2-sided p-value for the hypothesis test

Notes

For more details about *kurtosistest*, see *stats.kurtosistest*.

scipy.stats.mstats.normaltest

scipy.stats.mstats.**normaltest**(*a*, *axis=0*)

Tests whether a sample differs from a normal distribution.

Parameters

a [array_like] The array containing the data to be tested.

axis [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

Returns

statistic [float or array] `s^2 + k^2`, where `s` is the z-score returned by *skewtest* and `k` is the z-score returned by *kurtosistest*.

pvalue [float or array] A 2-sided chi squared probability for the hypothesis test.

Notes

For more details about *normaltest*, see *stats.normaltest*.

Transformations

obrientransform(*args)	Computes a transform on input data (any number of columns).
trim(a[, limits, inclusive, relative, axis])	Trims an array by masking the data outside some given limits.
trima(a[, limits, inclusive])	Trims an array by masking the data outside some given limits.
trimmed_stde(a[, limits, inclusive, axis])	Returns the standard error of the trimmed mean along the given axis.
trimr(a[, limits, inclusive, axis])	Trims an array by masking some proportion of the data on each end.
trimtail(data[, proportiontocut, tail, …])	Trims the data by masking values from one tail.
trimboth(data[, proportiontocut, inclusive, …])	Trims the smallest and largest data values.
winsorize(a[, limits, inclusive, inplace, …])	Returns a Winsorized version of the input array.
zmap(scores, compare[, axis, ddof, nan_policy])	Calculate the relative z-scores.
zscore(a[, axis, ddof, nan_policy])	Compute the z score.

scipy.stats.mstats.obrientransform

scipy.stats.mstats.**obrientransform**(**args*)

Computes a transform on input data (any number of columns). Used to test for homogeneity of variance prior to running one-way stats. Each array in `*args` is one level of a factor. If an *f_oneway()* run on the transformed data and found significant, variances are unequal. From Maxwell and Delaney, p.112.

Returns: transformed data for use in an ANOVA

scipy.stats.mstats.trim

scipy.stats.mstats.**trim**(*a*, *limits=None*, *inclusive=(True, True)*, *relative=False*, *axis=None*)

Trims an array by masking the data outside some given limits.

Returns a masked version of the input array.

Parameters

a [sequence] Input array

limits [{None, tuple}, optional] If *relative* is False, tuple (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit are masked.
If *relative* is True, tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.
Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) In each case, the value of one limit can be set to None to indicate an open interval.
If limits is None, no trimming is performed

inclusive [{(bool, bool) tuple}, optional] If *relative* is False, tuple indicating whether values exactly equal to the absolute limits are allowed. If *relative* is True, tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

relative [bool, optional] Whether to consider the limits as absolute values (False) or proportions to cut (True).

axis [int, optional] Axis along which to trim.

Examples

```
>>> from scipy.stats.mstats import trim
>>> z = [ 1, 2, 3, 4, 5, 6, 7, 8, 9,10]
>>> print(trim(z,(3,8)))
[-- -- 3 4 5 6 7 8 -- --]
>>> print(trim(z,(0.1,0.2),relative=True))
[-- 2 3 4 5 6 7 8 -- --]
```

scipy.stats.mstats.trima

scipy.stats.mstats.**trima**(*a*, *limits=None*, *inclusive=(True, True)*)

Trims an array by masking the data outside some given limits.

Returns a masked version of the input array.

Parameters

a [array_like] Input array.

limits [{None, tuple}, optional] Tuple of (lower limit, upper limit) in absolute values. Values of the input array lower (greater) than the lower (upper) limit will be masked. A limit is None indicates an open interval.

inclusive [(bool, bool) tuple, optional] Tuple of (lower flag, upper flag), indicating whether values exactly equal to the lower (upper) limit are allowed.

Examples

```
>>> from scipy.stats.mstats import trima
```

```
>>> a = np.arange(10)
```

The interval is left-closed and right-open, i.e., *[2, 8)*. Trim the array by keeping only values in the interval.

```
>>> trima(a, limits=(2, 8), inclusive=(True, False))
masked_array(data=[--, --, 2, 3, 4, 5, 6, 7, --, --],
             mask=[ True,  True, False, False, False, False, False, False,
                    True,  True],
       fill_value=999999)
```

scipy.stats.mstats.trimmed_stde

scipy.stats.mstats.**trimmed_stde**(*a*, *limits=(0.1, 0.1)*, *inclusive=(1, 1)*, *axis=None*)

Returns the standard error of the trimmed mean along the given axis.

Parameters

a [sequence] Input array

limits [{(0.1,0.1), tuple of float}, optional] tuple (lower percentage, upper percentage) to cut on each side of the array, with respect to the number of unmasked data.
If n is the number of unmasked data before trimming, the values smaller than `n * limits[0]` and the values larger than `n * `limits[1]` are masked, and the total number of unmasked data after trimming is `n * (1.-sum(limits))`. In each case, the value of one limit can be set to None to indicate an open interval. If *limits* is None, no trimming is performed.

inclusive [{(bool, bool) tuple} optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis [int, optional] Axis along which to trim.

Returns

trimmed_stde
[scalar or ndarray]

scipy.stats.mstats.trimr

scipy.stats.mstats.**trimr**(*a*, *limits=None*, *inclusive=(True, True)*, *axis=None*)

Trims an array by masking some proportion of the data on each end. Returns a masked version of the input array.

Parameters

a [sequence] Input array.

limits [{None, tuple}, optional] Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)). The value of one limit can be set to None to indicate an open interval.

inclusive [{(True,True) tuple}, optional] Tuple of flags indicating whether the number of data being masked on the left (right) end should be truncated (True) or rounded (False) to integers.

axis [{None,int}, optional] Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

scipy.stats.mstats.trimtail

scipy.stats.mstats.**trimtail**(*data*, *proportiontocut=0.2*, *tail='left'*, *inclusive=(True, True)*, *axis=None*)

Trims the data by masking values from one tail.

Parameters

data [array_like] Data to trim.

proportiontocut [float, optional] Percentage of trimming. If n is the number of unmasked values before trimming, the number of values after trimming is `(1 - proportiontocut) * n`. Default is 0.2.

tail [{'left','right'}, optional] If 'left' the *proportiontocut* lowest values will be masked. If 'right' the *proportiontocut* highest values will be masked. Default is 'left'.

inclusive [{(bool, bool) tuple}, optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False). Default is (True, True).

axis [int, optional] Axis along which to perform the trimming. If None, the input array is first flattened. Default is None.

Returns

trimtail [ndarray] Returned array of same shape as *data* with masked tail values.

scipy.stats.mstats.trimboth

scipy.stats.mstats.**trimboth**(*data*, *proportiontocut=0.2*, *inclusive=(True, True)*, *axis=None*)

Trims the smallest and largest data values.

Trims the *data* by masking the `int(proportiontocut * n)` smallest and `int(proportiontocut * n)` largest values of data along the given axis, where n is the number of unmasked values before trimming.

Parameters

data [ndarray] Data to trim.

proportiontocut [float, optional] Percentage of trimming (as a float between 0 and 1). If n is the number of unmasked values before trimming, the number of values after trimming is `(1 - 2*proportiontocut) * n`. Default is 0.2.

inclusive [{(bool, bool) tuple}, optional] Tuple indicating whether the number of data being masked on each side should be rounded (True) or truncated (False).

axis [int, optional] Axis along which to perform the trimming. If None, the input array is first flattened.

scipy.stats.mstats.winsorize

scipy.stats.mstats.**winsorize**(*a*, *limits=None*, *inclusive=(True, True)*, *inplace=False*, *axis=None*, *nan_policy='propagate'*)

Returns a Winsorized version of the input array.

The (limits[0])th lowest values are set to the (limits[0])th percentile, and the (limits[1])th highest values are set to the (1 - limits[1])th percentile. Masked values are skipped.

Parameters

a [sequence] Input array.

limits [{None, tuple of float}, optional] Tuple of the percentages to cut on each side of the array, with respect to the number of unmasked data, as floats between 0. and 1. Noting n the number of unmasked data before trimming, the (n*limits[0])th smallest data and the (n*limits[1])th largest data are masked, and the total number of unmasked data after trimming is n*(1.-sum(limits)) The value of one limit can be set to None to indicate an open interval.

inclusive [{(True, True) tuple}, optional] Tuple indicating whether the number of data being masked on each side should be truncated (True) or rounded (False).

inplace [{False, True}, optional] Whether to winsorize in place (True) or to use a copy (False)

axis [{None, int}, optional] Axis along which to trim. If None, the whole array is trimmed, but its shape is maintained.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. The following options are available (default is 'propagate'):

- 'propagate': allows nan values and may overwrite or propagate them
- 'raise': throws an error
- 'omit': performs the calculations ignoring nan values

Notes

This function is applied to reduce the effect of possibly spurious outliers by limiting the extreme values.

Examples

```
>>> from scipy.stats.mstats import winsorize
```

A shuffled array contains integers from 1 to 10.

```
>>> a = np.array([10, 4, 9, 8, 5, 3, 7, 2, 1, 6])
```

The 10% of the lowest value (i.e., *1*) and the 20% of the highest values (i.e., *9* and *10*) are replaced.

```
>>> winsorize(a, limits=[0.1, 0.2])
masked_array(data=[8, 4, 8, 8, 5, 3, 7, 2, 2, 6],
             mask=False,
       fill_value=999999)
```

scipy.stats.mstats.zmap

scipy.stats.mstats.**zmap**(*scores*, *compare*, *axis=0*, *ddof=0*, *nan_policy='propagate'*)

Calculate the relative z-scores.

Return an array of z-scores, i.e., scores that are standardized to zero mean and unit variance, where mean and variance are calculated from the comparison array.

Parameters

scores [array_like] The input for which z-scores are calculated.

compare [array_like] The input from which the mean and standard deviation of the normalization are taken; assumed to have the same dimension as *scores*.

axis [int or None, optional] Axis over which mean and variance of *compare* are calculated. Default is 0. If None, compute over the whole array *scores*.

ddof [int, optional] Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle the occurrence of nans in *compare*. 'propagate' returns nan, 'raise' raises an exception, 'omit' performs the calculations ignoring nan values. Default is 'propagate'. Note that when the value is 'omit', nans in *scores* also propagate to the output, but they do not affect the z-scores computed for the non-nan values.

Returns

zscore [array_like] Z-scores, in the same shape as *scores*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> from scipy.stats import zmap
>>> a = [0.5, 2.0, 2.5, 3]
>>> b = [0, 1, 2, 3, 4]
>>> zmap(a, b)
array([-1.06066017,  0.        ,  0.35355339,  0.70710678])
```

scipy.stats.mstats.zscore

scipy.stats.mstats.**zscore**(*a*, *axis=0*, *ddof=0*, *nan_policy='propagate'*)

Compute the z score.

Compute the z score of each value in the sample, relative to the sample mean and standard deviation.

Parameters

a [array_like] An array like object containing the sample data.

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof [int, optional] Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

nan_policy

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'. Note that when the value is 'omit', nans in the input also propagate to the output, but they do not affect the z-scores computed for the non-nan values.

Returns

zscore [array_like] The z-scores, standardized by mean and standard deviation of input array *a*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> a = np.array([ 0.7972,  0.0767,  0.4383,  0.7866,  0.8091,
...                0.1954,  0.6307,  0.6599,  0.1065,  0.0508])
>>> from scipy import stats
>>> stats.zscore(a)
array([ 1.1273, -1.247 , -0.0552,  1.0923,  1.1664, -0.8559,  0.5786,
        0.6748, -1.1488, -1.3324])
```

Computing along a specified axis, using n-1 degrees of freedom (`ddof=1`) to calculate the standard deviation:

```
>>> b = np.array([[ 0.3148,  0.0478,  0.6243,  0.4608],
...               [ 0.7149,  0.0775,  0.6072,  0.9656],
...               [ 0.6341,  0.1403,  0.9759,  0.4064],
...               [ 0.5918,  0.6948,  0.904 ,  0.3721],
...               [ 0.0921,  0.2481,  0.1188,  0.1366]])
>>> stats.zscore(b, axis=1, ddof=1)
array([[-0.19264823, -1.28415119,  1.07259584,  0.40420358],
       [ 0.33048416, -1.37380874,  0.04251374,  1.00081084],
       [ 0.26796377, -1.12598418,  1.23283094, -0.37481053],
       [-0.22095197,  0.24468594,  1.19042819, -1.21416216],
       [-0.82780366,  1.4457416 , -0.43867764, -0.1792603 ]])
```

An example with *nan_policy='omit'*:

```
>>> x = np.array([[25.11, 30.10, np.nan, 32.02, 43.15],
...               [14.95, 16.06, 121.25, 94.35, 29.81]])
>>> stats.zscore(x, axis=1, nan_policy='omit')
array([[-1.13490897, -0.37830299,         nan, -0.08718406,  1.60039602],
       [-0.91611681, -0.89090508,  1.4983032 ,  0.88731639, -0.5785977 ]])
```

Other

argstoarray(*args)	Constructs a 2D array from a group of sequences.
count_tied_groups(x[, use_missing])	Counts the number of tied values.
msign(x)	Returns the sign of x, or 0 if x is masked.
compare_medians_ms(group_1, group_2[, axis])	Compares the medians from two independent groups along the given axis.
median_cihs(data[, alpha, axis])	Computes the alpha-level confidence interval for the median of the data.
mjci(data[, prob, axis])	Returns the Maritz-Jarrett estimators of the standard error of selected experimental quantiles of the data.
mquantiles_cimj(data[, prob, alpha, axis])	Computes the alpha confidence interval for the selected quantiles of the data, with Maritz-Jarrett estimators.
rsh(data[, points])	Evaluates Rosenblatt's shifted histogram estimators for each data point.

scipy.stats.mstats.argstoarray

scipy.stats.mstats.**argstoarray**(**args*)

Constructs a 2D array from a group of sequences.

Sequences are filled with missing values to match the length of the longest sequence.

Parameters

args [sequences] Group of sequences.

Returns

argstoarray

[MaskedArray] A (*m* x *n*) masked array, where *m* is the number of arguments and *n* the length of the longest argument.

Notes

`numpy.ma.row_stack` has identical behavior, but is called with a sequence of sequences.

Examples

A 2D masked array constructed from a group of sequences is returned.

```
>>> from scipy.stats.mstats import argstoarray
>>> argstoarray([1, 2, 3], [4, 5, 6])
masked_array(
 data=[[1.0, 2.0, 3.0],
       [4.0, 5.0, 6.0]],
 mask=[[False, False, False],
       [False, False, False]],
 fill_value=1e+20)
```

The returned masked array filled with missing values when the lengths of sequences are different.

```
>>> argstoarray([1, 3], [4, 5, 6])
masked_array(
 data=[[1.0, 3.0, --],
       [4.0, 5.0, 6.0]],
 mask=[[False, False,  True],
       [False, False, False]],
 fill_value=1e+20)
```

scipy.stats.mstats.count_tied_groups

scipy.stats.mstats.**count_tied_groups**(*x*, *use_missing=False*)

Counts the number of tied values.

Parameters

x [sequence] Sequence of data on which to counts the ties

use_missing

[bool, optional] Whether to consider missing values as tied.

Returns

count_tied_groups

[dict] Returns a dictionary (nb of ties: nb of groups).

Examples

```
>>> from scipy.stats import mstats
>>> z = [0, 0, 0, 2, 2, 2, 3, 3, 4, 5, 6]
>>> mstats.count_tied_groups(z)
{2: 1, 3: 2}
```

In the above example, the ties were 0 (3x), 2 (3x) and 3 (2x).

```
>>> z = np.ma.array([0, 0, 1, 2, 2, 2, 3, 3, 4, 5, 6])
>>> mstats.count_tied_groups(z)
{2: 2, 3: 1}
>>> z[[1,-1]] = np.ma.masked
>>> mstats.count_tied_groups(z, use_missing=True)
{2: 2, 3: 1}
```

scipy.stats.mstats.msign

scipy.stats.mstats.**msign**(*x*)

Returns the sign of x, or 0 if x is masked.

scipy.stats.mstats.compare_medians_ms

scipy.stats.mstats.**compare_medians_ms**(*group_1*, *group_2*, *axis=None*)

Compares the medians from two independent groups along the given axis.

The comparison is performed using the McKean-Schrader estimate of the standard error of the medians.

Parameters

group_1 [array_like] First dataset. Has to be of size >=7.
group_2 [array_like] Second dataset. Has to be of size >=7.
axis [int, optional] Axis along which the medians are estimated. If None, the arrays are flattened. If *axis* is not None, then *group_1* and *group_2* should have the same shape.

Returns

compare_medians_ms
[{float, ndarray}] If *axis* is None, then returns a float, otherwise returns a 1-D ndarray of floats with a length equal to the length of *group_1* along *axis*.

scipy.stats.mstats.median_cihs

scipy.stats.mstats.**median_cihs**(*data*, *alpha=0.05*, *axis=None*)

Computes the alpha-level confidence interval for the median of the data.

Uses the Hettmasperger-Sheather method.

Parameters

data [array_like] Input data. Masked values are discarded. The input should be 1D only, or *axis* should be set to None.
alpha [float, optional] Confidence level of the intervals.
axis [int or None, optional] Axis along which to compute the quantiles. If None, use a flattened array.

Returns

median_cihs
Alpha level confidence interval.

scipy.stats.mstats.mjci

scipy.stats.mstats.**mjci**(*data*, *prob=[0.25, 0.5, 0.75]*, *axis=None*)

Returns the Maritz-Jarrett estimators of the standard error of selected experimental quantiles of the data.

Parameters

data [ndarray] Data array.
prob [sequence, optional] Sequence of quantiles to compute.
axis [int or None, optional] Axis along which to compute the quantiles. If None, use a flattened array.

scipy.stats.mstats.mquantiles_cimj

scipy.stats.mstats.**mquantiles_cimj**(*data*, *prob=[0.25, 0.5, 0.75]*, *alpha=0.05*, *axis=None*)

Computes the alpha confidence interval for the selected quantiles of the data, with Maritz-Jarrett estimators.

Parameters

data	[ndarray] Data array.
prob	[sequence, optional] Sequence of quantiles to compute.
alpha	[float, optional] Confidence level of the intervals.
axis	[int or None, optional] Axis along which to compute the quantiles. If None, use a flattened array.

Returns

ci_lower	[ndarray] The lower boundaries of the confidence interval. Of the same length as *prob*.
ci_upper	[ndarray] The upper boundaries of the confidence interval. Of the same length as *prob*.

scipy.stats.mstats.rsh

scipy.stats.mstats.**rsh**(*data*, *points=None*)

Evaluates Rosenblatt's shifted histogram estimators for each data point.

Rosenblatt's estimator is a centered finite-difference approximation to the derivative of the empirical cumulative distribution function.

Parameters

data	[sequence] Input data, should be 1-D. Masked values are ignored.
points	[sequence or None, optional] Sequence of points where to evaluate Rosenblatt shifted histogram. If None, use the data.

Other statistical functionality

Transformations

boxcox(x[, lmbda, alpha, optimizer])	Return a dataset transformed by a Box-Cox power transformation.
boxcox_normmax(x[, brack, method, optimizer])	Compute optimal Box-Cox transform parameter for input data.
boxcox_llf(lmb, data)	The boxcox log-likelihood function.
yeojohnson(x[, lmbda])	Return a dataset transformed by a Yeo-Johnson power transformation.
yeojohnson_normmax(x[, brack])	Compute optimal Yeo-Johnson transform parameter.
yeojohnson_llf(lmb, data)	The yeojohnson log-likelihood function.
obrientransform(*args)	Compute the O'Brien transform on input data (any number of arrays).
sigmaclip(a[, low, high])	Perform iterative sigma-clipping of array elements.
trimboth(a, proportiontocut[, axis])	Slice off a proportion of items from both ends of an array.
trim1(a, proportiontocut[, tail, axis])	Slice off a proportion from ONE end of the passed array distribution.
zmap(scores, compare[, axis, ddof, nan_policy])	Calculate the relative z-scores.
zscore(a[, axis, ddof, nan_policy])	Compute the z score.

scipy.stats.boxcox

scipy.stats.**boxcox**(*x*, *lmbda=None*, *alpha=None*, *optimizer=None*)

Return a dataset transformed by a Box-Cox power transformation.

Parameters

x [ndarray] Input array. Must be positive 1-dimensional. Must not be constant.

lmbda [{None, scalar}, optional] If *lmbda* is not None, do the transformation for that value. If *lmbda* is None, find the lambda that maximizes the log-likelihood function and return it as the second output argument.

alpha [{None, float}, optional] If `alpha` is not None, return the `100 * (1-alpha)%` confidence interval for *lmbda* as the third output argument. Must be between 0.0 and 1.0.

optimizer [callable, optional] If *lmbda* is None, *optimizer* is the scalar optimizer used to find the value of *lmbda* that minimizes the negative log-likelihood function. *optimizer* is a callable that accepts one argument:

fun [callable] The objective function, which evaluates the negative log-likelihood function at a provided value of *lmbda*

and returns an object, such as an instance of *scipy.optimize.OptimizeResult*, which holds the optimal value of *lmbda* in an attribute *x*.

See the example in *boxcox_normmax* or the documentation of *scipy.optimize.minimize_scalar* for more information.

If *lmbda* is not None, *optimizer* is ignored.

Returns

boxcox [ndarray] Box-Cox power transformed array.

maxlog [float, optional] If the *lmbda* parameter is None, the second returned argument is the lambda that maximizes the log-likelihood function.

(min_ci, max_ci) [tuple of float, optional] If *lmbda* parameter is None and `alpha` is not None, this returned tuple of floats represents the minimum and maximum confidence limits given `alpha`.

See also:

probplot, **boxcox_normplot**, **boxcox_normmax**, **boxcox_llf**

Notes

The Box-Cox transform is given by:

```
y = (x**lmbda - 1) / lmbda,  for lmbda != 0
    log(x),                  for lmbda = 0
```

boxcox requires the input data to be positive. Sometimes a Box-Cox transformation provides a shift parameter to achieve this; *boxcox* does not. Such a shift parameter is equivalent to adding a positive constant to *x* before calling *boxcox*.

The confidence limits returned when `alpha` is provided give the interval where:

$$llf(\hat{\lambda}) - llf(\lambda) < \frac{1}{2}\chi^2(1-\alpha, 1),$$

with `llf` the log-likelihood function and χ^2 the chi-squared function.

References

G.E.P. Box and D.R. Cox, “An Analysis of Transformations”, Journal of the Royal Statistical Society B, 26, 211-252 (1964).

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

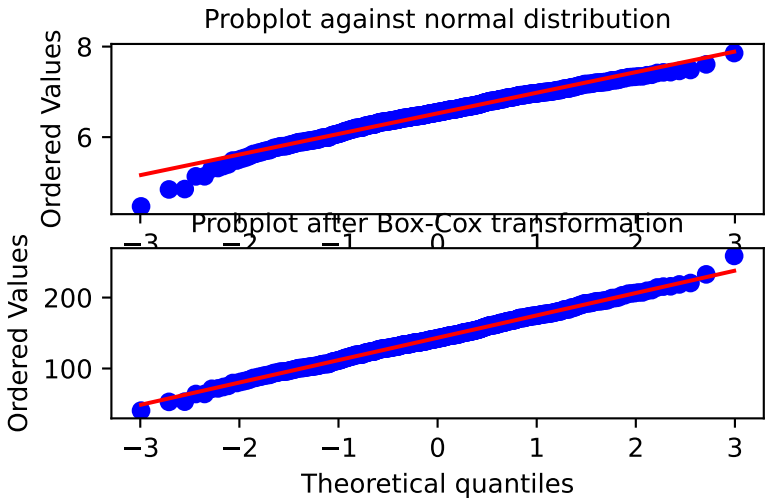
We generate some random variates from a non-normal distribution and make a probability plot for it, to show it is non-normal in the tails:

```
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(211)
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> prob = stats.probplot(x, dist=stats.norm, plot=ax1)
>>> ax1.set_xlabel('')
>>> ax1.set_title('Probplot against normal distribution')
```

We now use *boxcox* to transform the data so it’s closest to normal:

```
>>> ax2 = fig.add_subplot(212)
>>> xt, _ = stats.boxcox(x)
>>> prob = stats.probplot(xt, dist=stats.norm, plot=ax2)
>>> ax2.set_title('Probplot after Box-Cox transformation')
```

```
>>> plt.show()
```



scipy.stats.boxcox_normmax

scipy.stats.**boxcox_normmax**(*x*, *brack=None*, *method='pearsonr'*, *optimizer=None*)

Compute optimal Box-Cox transform parameter for input data.

Parameters

x [array_like] Input array.

brack [2-tuple, optional, default (-2.0, 2.0)] The starting interval for a downhill bracket search for the default *optimize.brent* solver. Note that this is in most cases not critical; the final result is allowed to be outside this bracket. If *optimizer* is passed, *brack* must be None.

method [str, optional] The method to determine the optimal transform parameter (*boxcox* `lmbda` parameter). Options are:

'pearsonr' (default)
Maximizes the Pearson correlation coefficient between `y = boxcox(x)` and the expected values for `y` if *x* would be normally-distributed.

'mle' Minimizes the log-likelihood *boxcox_llf*. This is the method used in *boxcox*.

'all' Use all optimization methods available, and return all results. Useful to compare different methods.

optimizer [callable, optional] *optimizer* is a callable that accepts one argument:

fun [callable] The objective function to be optimized. *fun* accepts one argument, the Box-Cox transform parameter *lmbda*, and returns the negative log-likelihood function at the provided value. The job of *optimizer* is to find the value of *lmbda* that minimizes *fun*.

and returns an object, such as an instance of *scipy.optimize.OptimizeResult*, which holds the optimal value of *lmbda* in an attribute *x*.

See the example below or the documentation of *scipy.optimize.minimize_scalar* for more information.

Returns

maxlog [float or ndarray] The optimal transform parameter found. An array instead of a scalar for `method='all'`.

See also:

boxcox, **boxcox_llf**, **boxcox_normplot**, **scipy.optimize.minimize_scalar**

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

We can generate some data and determine the optimal `lmbda` in various ways:

```
>>> rng = np.random.default_rng()
>>> x = stats.loggamma.rvs(5, size=30, random_state=rng) + 5
>>> y, lmax_mle = stats.boxcox(x)
>>> lmax_pearsonr = stats.boxcox_normmax(x)
```

```
>>> lmax_mle
1.4613865614008015
>>> lmax_pearsonr
```

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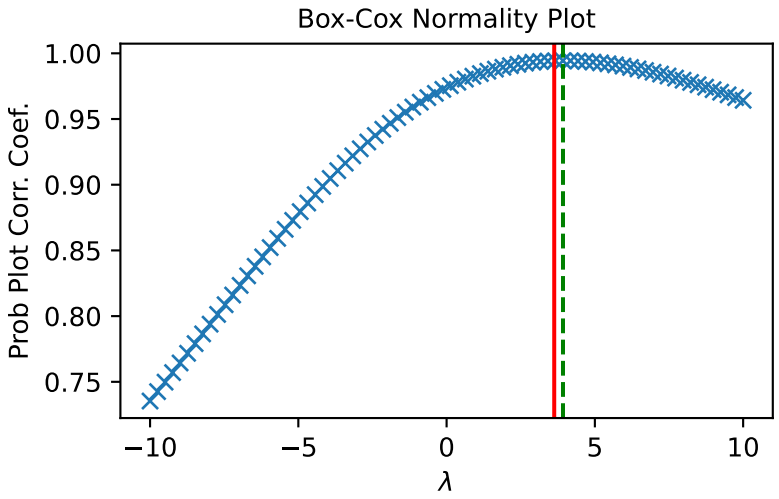
```
1.6685004886804342
>>> stats.boxcox_normmax(x, method='all')
array([1.66850049, 1.46138656])
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> prob = stats.boxcox_normplot(x, -10, 10, plot=ax)
>>> ax.axvline(lmax_mle, color='r')
>>> ax.axvline(lmax_pearsonr, color='g', ls='--')
```

```
>>> plt.show()
```



Alternatively, we can define our own *optimizer* function. Suppose we are only interested in values of *lmbda* on the interval [6, 7], we want to use *scipy.optimize.minimize_scalar* with `method='bounded'`, and we want to use tighter tolerances when optimizing the log-likelihood function. To do this, we define a function that accepts positional argument *fun* and uses *scipy.optimize.minimize_scalar* to minimize *fun* subject to the provided bounds and tolerances:

```
>>> from scipy import optimize
>>> options = {'xatol': 1e-12}  # absolute tolerance on `x`
>>> def optimizer(fun):
...     return optimize.minimize_scalar(fun, bounds=(6, 7),
...                                     method="bounded", options=options)
>>> stats.boxcox_normmax(x, optimizer=optimizer)
6.000...
```

scipy.stats.boxcox_llf

scipy.stats.**boxcox_llf**(*lmb*, *data*)

The boxcox log-likelihood function.

Parameters

lmb	[scalar] Parameter for Box-Cox transformation. See *boxcox* for details.
data	[array_like] Data to calculate Box-Cox log-likelihood for. If *data* is multi-dimensional, the log-likelihood is calculated along the first axis.

Returns

llf	[float or ndarray] Box-Cox log-likelihood of *data* given *lmb*. A float for 1-D *data*, an array otherwise.

See also:

boxcox, **probplot**, **boxcox_normplot**, **boxcox_normmax**

Notes

The Box-Cox log-likelihood function is defined here as

$$llf = (\lambda - 1)\sum_i(\log(x_i)) - N/2\log(\sum_i(y_i - \bar{y})^2/N),$$

where `y` is the Box-Cox transformed input data `x`.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.axes_grid1.inset_locator import inset_axes
```

Generate some random variates and calculate Box-Cox log-likelihood values for them for a range of `lmbda` values:

```
>>> rng = np.random.default_rng()
>>> x = stats.loggamma.rvs(5, loc=10, size=1000, random_state=rng)
>>> lmbdas = np.linspace(-2, 10)
>>> llf = np.zeros(lmbdas.shape, dtype=float)
>>> for ii, lmbda in enumerate(lmbdas):
...     llf[ii] = stats.boxcox_llf(lmbda, x)
```

Also find the optimal lmbda value with *boxcox*:

```
>>> x_most_normal, lmbda_optimal = stats.boxcox(x)
```

Plot the log-likelihood as function of lmbda. Add the optimal lmbda as a horizontal line to check that that's really the optimum:

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(lmbdas, llf, 'b.-')
>>> ax.axhline(stats.boxcox_llf(lmbda_optimal, x), color='r')
```

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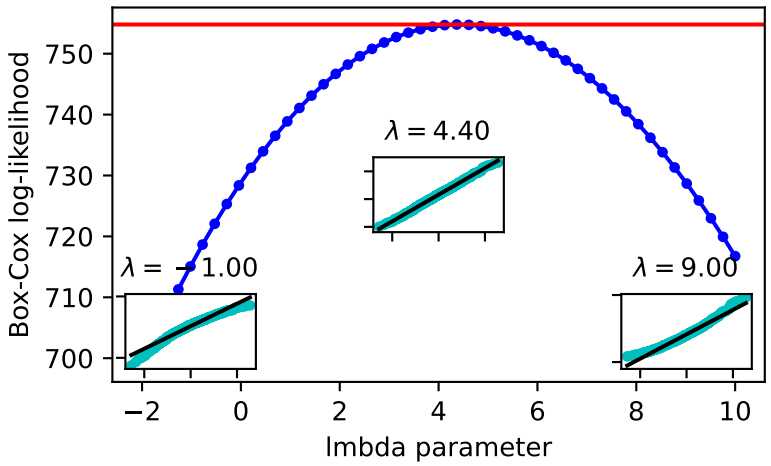
```
>>> ax.set_xlabel('lmbda parameter')
>>> ax.set_ylabel('Box-Cox log-likelihood')
```

Now add some probability plots to show that where the log-likelihood is maximized the data transformed with *boxcox* looks closest to normal:

```
>>> locs = [3, 10, 4]  # 'lower left', 'center', 'lower right'
>>> for lmbda, loc in zip([-1, lmbda_optimal, 9], locs):
...     xt = stats.boxcox(x, lmbda=lmbda)
...     (osm, osr), (slope, intercept, r_sq) = stats.probplot(xt)
...     ax_inset = inset_axes(ax, width="20%", height="20%", loc=loc)
...     ax_inset.plot(osm, osr, 'c.', osm, slope*osm + intercept, 'k-')
...     ax_inset.set_xticklabels([])
...     ax_inset.set_yticklabels([])
...     ax_inset.set_title(r'$\lambda=%1.2f$' % lmbda)
```

```
>>> plt.show()
```



scipy.stats.yeojohnson

`scipy.stats.`**`yeojohnson`**(*x*, *lmbda=None*)

Return a dataset transformed by a Yeo-Johnson power transformation.

Parameters

x [ndarray] Input array. Should be 1-dimensional.

lmbda [float, optional] If `lmbda` is `None`, find the lambda that maximizes the log-likelihood function and return it as the second output argument. Otherwise the transformation is done for the given value.

Returns

yeojohnson: ndarray

Yeo-Johnson power transformed array.

maxlog [float, optional] If the *lmbda* parameter is None, the second returned argument is the lambda that maximizes the log-likelihood function.

See also:

probplot, **yeojohnson_normplot**, **yeojohnson_normmax**, **yeojohnson_llf**, **boxcox**

Notes

The Yeo-Johnson transform is given by:

```
y = ((x + 1)**lmbda - 1) / lmbda,                for x >= 0, lmbda != 0
    log(x + 1),                                  for x >= 0, lmbda = 0
    -((-x + 1)**(2 - lmbda) - 1) / (2 - lmbda),  for x < 0, lmbda != 2
    -log(-x + 1),                                for x < 0, lmbda = 2
```

Unlike *boxcox*, *yeojohnson* does not require the input data to be positive.

New in version 1.2.0.

References

I. Yeo and R.A. Johnson, "A New Family of Power Transformations to Improve Normality or Symmetry", Biometrika 87.4 (2000):

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

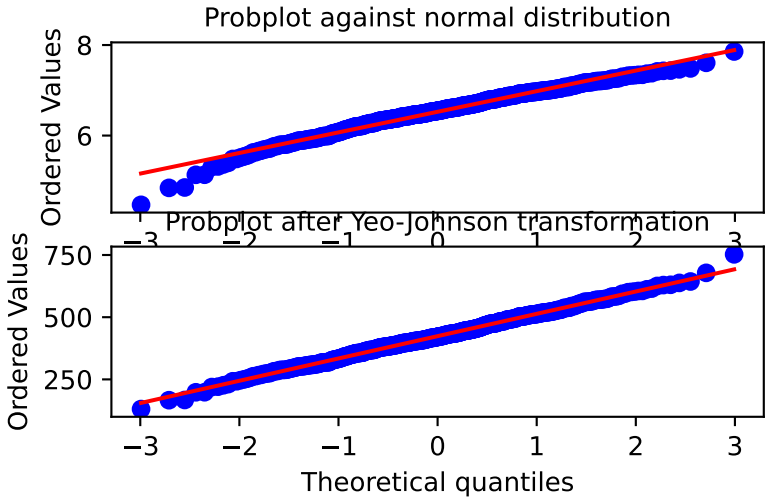
We generate some random variates from a non-normal distribution and make a probability plot for it, to show it is non-normal in the tails:

```
>>> fig = plt.figure()
>>> ax1 = fig.add_subplot(211)
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> prob = stats.probplot(x, dist=stats.norm, plot=ax1)
>>> ax1.set_xlabel('')
>>> ax1.set_title('Probplot against normal distribution')
```

We now use *yeojohnson* to transform the data so it's closest to normal:

```
>>> ax2 = fig.add_subplot(212)
>>> xt, lmbda = stats.yeojohnson(x)
>>> prob = stats.probplot(xt, dist=stats.norm, plot=ax2)
>>> ax2.set_title('Probplot after Yeo-Johnson transformation')
```

```
>>> plt.show()
```



scipy.stats.yeojohnson_normmax

scipy.stats.**yeojohnson_normmax**(*x*, *brack=(- 2, 2)*)

Compute optimal Yeo-Johnson transform parameter.

Compute optimal Yeo-Johnson transform parameter for input data, using maximum likelihood estimation.

Parameters

x [array_like] Input array.

brack [2-tuple, optional] The starting interval for a downhill bracket search with *optimize.brent*. Note that this is in most cases not critical; the final result is allowed to be outside this bracket.

Returns

maxlog [float] The optimal transform parameter found.

See also:

yeojohnson, **yeojohnson_llf**, **yeojohnson_normplot**

Notes

New in version 1.2.0.

Examples

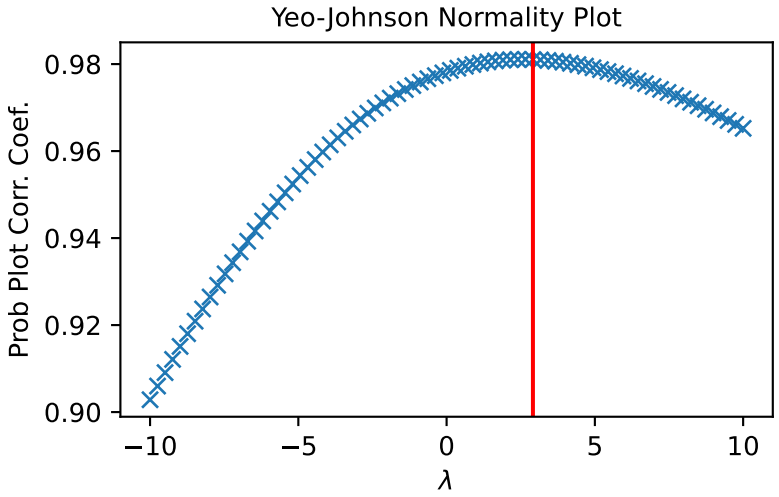
```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

Generate some data and determine optimal `lmbda`

```
>>> rng = np.random.default_rng()
>>> x = stats.loggamma.rvs(5, size=30, random_state=rng) + 5
>>> lmax = stats.yeojohnson_normmax(x)
```

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> prob = stats.yeojohnson_normplot(x, -10, 10, plot=ax)
>>> ax.axvline(lmax, color='r')
```

```
>>> plt.show()
```



scipy.stats.yeojohnson_llf

scipy.stats.**yeojohnson_llf**(*lmb*, *data*)

The yeojohnson log-likelihood function.

Parameters

lmb [scalar] Parameter for Yeo-Johnson transformation. See *yeojohnson* for details.

data [array_like] Data to calculate Yeo-Johnson log-likelihood for. If *data* is multi-dimensional, the log-likelihood is calculated along the first axis.

Returns

llf [float] Yeo-Johnson log-likelihood of *data* given *lmb*.

See also:

yeojohnson, **probplot**, **yeojohnson_normplot**, **yeojohnson_normmax**

Notes

The Yeo-Johnson log-likelihood function is defined here as

$$llf = -N/2 \log(\hat{\sigma}^2) + (\lambda - 1) \sum_i \text{sign}\,(x_i) \log(|x_i| + 1)$$

where $\hat{\sigma}^2$ is estimated variance of the the Yeo-Johnson transformed input data `x`.

New in version 1.2.0.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> from mpl_toolkits.axes_grid1.inset_locator import inset_axes
```

Generate some random variates and calculate Yeo-Johnson log-likelihood values for them for a range of `lmbda` values:

```
>>> x = stats.loggamma.rvs(5, loc=10, size=1000)
>>> lmbdas = np.linspace(-2, 10)
>>> llf = np.zeros(lmbdas.shape, dtype=float)
>>> for ii, lmbda in enumerate(lmbdas):
...     llf[ii] = stats.yeojohnson_llf(lmbda, x)
```

Also find the optimal lmbda value with *yeojohnson*:

```
>>> x_most_normal, lmbda_optimal = stats.yeojohnson(x)
```

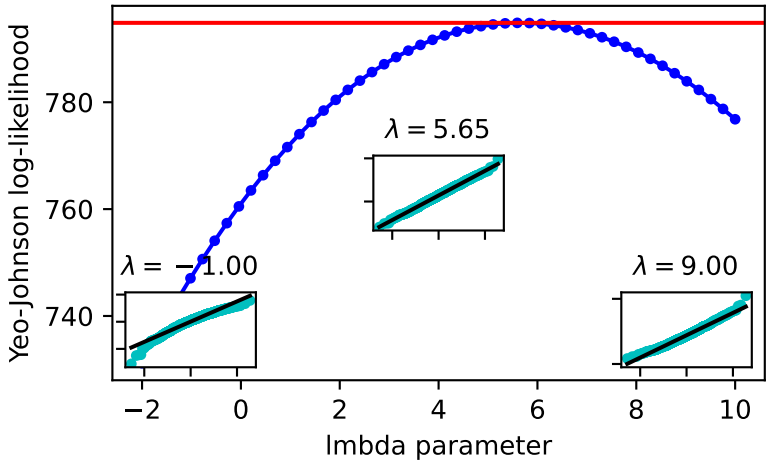
Plot the log-likelihood as function of lmbda. Add the optimal lmbda as a horizontal line to check that that's really the optimum:

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> ax.plot(lmbdas, llf, 'b.-')
>>> ax.axhline(stats.yeojohnson_llf(lmbda_optimal, x), color='r')
>>> ax.set_xlabel('lmbda parameter')
>>> ax.set_ylabel('Yeo-Johnson log-likelihood')
```

Now add some probability plots to show that where the log-likelihood is maximized the data transformed with *yeojohnson* looks closest to normal:

```
>>> locs = [3, 10, 4]  # 'lower left', 'center', 'lower right'
>>> for lmbda, loc in zip([-1, lmbda_optimal, 9], locs):
...     xt = stats.yeojohnson(x, lmbda=lmbda)
...     (osm, osr), (slope, intercept, r_sq) = stats.probplot(xt)
...     ax_inset = inset_axes(ax, width="20%", height="20%", loc=loc)
...     ax_inset.plot(osm, osr, 'c.', osm, slope*osm + intercept, 'k-')
...     ax_inset.set_xticklabels([])
...     ax_inset.set_yticklabels([])
...     ax_inset.set_title(r'$\lambda=%1.2f$' % lmbda)
```

```
>>> plt.show()
```



scipy.stats.obrientransform

scipy.stats.**obrientransform**(**args*)

Compute the O'Brien transform on input data (any number of arrays).

Used to test for homogeneity of variance prior to running one-way stats. Each array in `*args` is one level of a factor. If *f_oneway* is run on the transformed data and found significant, the variances are unequal. From Maxwell and Delaney [1], p.112.

Parameters

args [tuple of array_like] Any number of arrays.

Returns

obrientransform

[ndarray] Transformed data for use in an ANOVA. The first dimension of the result corresponds to the sequence of transformed arrays. If the arrays given are all 1-D of the same length, the return value is a 2-D array; otherwise it is a 1-D array of type object, with each element being an ndarray.

References

[1]

Examples

We'll test the following data sets for differences in their variance.

```
>>> x = [10, 11, 13, 9, 7, 12, 12, 9, 10]
>>> y = [13, 21, 5, 10, 8, 14, 10, 12, 7, 15]
```

Apply the O'Brien transform to the data.

```
>>> from scipy.stats import obrientransform
>>> tx, ty = obrientransform(x, y)
```

Use *scipy.stats.f_oneway* to apply a one-way ANOVA test to the transformed data.

```
>>> from scipy.stats import f_oneway
>>> F, p = f_oneway(tx, ty)
>>> p
0.1314139477040335
```

If we require that `p < 0.05` for significance, we cannot conclude that the variances are different.

scipy.stats.sigmaclip

scipy.stats.**sigmaclip**(*a*, *low=4.0*, *high=4.0*)

Perform iterative sigma-clipping of array elements.

Starting from the full sample, all elements outside the critical range are removed, i.e. all elements of the input array *c* that satisfy either of the following conditions:

```
c < mean(c) - std(c)*low
c > mean(c) + std(c)*high
```

The iteration continues with the updated sample until no elements are outside the (updated) range.

Parameters

a	[array_like] Data array, will be raveled if not 1-D.
low	[float, optional] Lower bound factor of sigma clipping. Default is 4.
high	[float, optional] Upper bound factor of sigma clipping. Default is 4.

Returns

clipped	[ndarray] Input array with clipped elements removed.
lower	[float] Lower threshold value use for clipping.
upper	[float] Upper threshold value use for clipping.

Examples

```
>>> from scipy.stats import sigmaclip
>>> a = np.concatenate((np.linspace(9.5, 10.5, 31),
...                     np.linspace(0, 20, 5)))
>>> fact = 1.5
>>> c, low, upp = sigmaclip(a, fact, fact)
>>> c
array([  9.96666667,  10.        ,  10.03333333,  10.        ])
>>> c.var(), c.std()
(0.00055555555555555165, 0.023570226039551501)
>>> low, c.mean() - fact*c.std(), c.min()
(9.9646446609406727, 9.9646446609406727, 9.9666666666666668)
>>> upp, c.mean() + fact*c.std(), c.max()
(10.035355339059327, 10.035355339059327, 10.033333333333333)
```

```
>>> a = np.concatenate((np.linspace(9.5, 10.5, 11),
...                     np.linspace(-100, -50, 3)))
>>> c, low, upp = sigmaclip(a, 1.8, 1.8)
>>> (c == np.linspace(9.5, 10.5, 11)).all()
True
```

scipy.stats.trimboth

scipy.stats.**trimboth**(*a*, *proportiontocut*, *axis=0*)

Slice off a proportion of items from both ends of an array.

Slice off the passed proportion of items from both ends of the passed array (i.e., with *proportiontocut* = 0.1, slices leftmost 10% **and** rightmost 10% of scores). The trimmed values are the lowest and highest ones. Slice off less if proportion results in a non-integer slice index (i.e. conservatively slices off *proportiontocut*).

Parameters

a [array_like] Data to trim.

proportiontocut [float] Proportion (in range 0-1) of total data set to trim of each end.

axis [int or None, optional] Axis along which to trim data. Default is 0. If None, compute over the whole array *a*.

Returns

out [ndarray] Trimmed version of array *a*. The order of the trimmed content is undefined.

See also:

trim_mean

Examples

```
>>> from scipy import stats
>>> a = np.arange(20)
>>> b = stats.trimboth(a, 0.1)
>>> b.shape
(16,)
```

scipy.stats.trim1

scipy.stats.**trim1**(*a*, *proportiontocut*, *tail='right'*, *axis=0*)

Slice off a proportion from ONE end of the passed array distribution.

If *proportiontocut* = 0.1, slices off 'leftmost' or 'rightmost' 10% of scores. The lowest or highest values are trimmed (depending on the tail). Slice off less if proportion results in a non-integer slice index (i.e. conservatively slices off *proportiontocut*).

Parameters

a [array_like] Input array.

proportiontocut [float] Fraction to cut off of 'left' or 'right' of distribution.

tail [{'left', 'right'}, optional] Defaults to 'right'.

axis [int or None, optional] Axis along which to trim data. Default is 0. If None, compute over the whole array *a*.

Returns

trim1 [ndarray] Trimmed version of array *a*. The order of the trimmed content is undefined.

Examples

```
>>> from scipy import stats
>>> a = np.arange(20)
>>> b = stats.trim1(a, 0.5, 'left')
>>> b
array([10, 11, 12, 13, 14, 16, 15, 17, 18, 19])
```

scipy.stats.zmap

scipy.stats.**zmap**(*scores*, *compare*, *axis=0*, *ddof=0*, *nan_policy='propagate'*)

Calculate the relative z-scores.

Return an array of z-scores, i.e., scores that are standardized to zero mean and unit variance, where mean and variance are calculated from the comparison array.

Parameters

scores [array_like] The input for which z-scores are calculated.

compare [array_like] The input from which the mean and standard deviation of the normalization are taken; assumed to have the same dimension as *scores*.

axis [int or None, optional] Axis over which mean and variance of *compare* are calculated. Default is 0. If None, compute over the whole array *scores*.

ddof [int, optional] Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle the occurrence of nans in *compare*. 'propagate' returns nan, 'raise' raises an exception, 'omit' performs the calculations ignoring nan values. Default is 'propagate'. Note that when the value is 'omit', nans in *scores* also propagate to the output, but they do not affect the z-scores computed for the non-nan values.

Returns

zscore [array_like] Z-scores, in the same shape as *scores*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> from scipy.stats import zmap
>>> a = [0.5, 2.0, 2.5, 3]
>>> b = [0, 1, 2, 3, 4]
>>> zmap(a, b)
array([-1.06066017,  0.        ,  0.35355339,  0.70710678])
```

scipy.stats.zscore

scipy.stats.**zscore**(*a*, *axis=0*, *ddof=0*, *nan_policy='propagate'*)

Compute the z score.

Compute the z score of each value in the sample, relative to the sample mean and standard deviation.

Parameters

a [array_like] An array like object containing the sample data.

axis [int or None, optional] Axis along which to operate. Default is 0. If None, compute over the whole array *a*.

ddof [int, optional] Degrees of freedom correction in the calculation of the standard deviation. Default is 0.

nan_policy
[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'. Note that when the value is 'omit', nans in the input also propagate to the output, but they do not affect the z-scores computed for the non-nan values.

Returns

zscore [array_like] The z-scores, standardized by mean and standard deviation of input array *a*.

Notes

This function preserves ndarray subclasses, and works also with matrices and masked arrays (it uses *asanyarray* instead of *asarray* for parameters).

Examples

```
>>> a = np.array([ 0.7972,  0.0767,  0.4383,  0.7866,  0.8091,
...                0.1954,  0.6307,  0.6599,  0.1065,  0.0508])
>>> from scipy import stats
>>> stats.zscore(a)
array([ 1.1273, -1.247 , -0.0552,  1.0923,  1.1664, -0.8559,  0.5786,
        0.6748, -1.1488, -1.3324])
```

Computing along a specified axis, using n-1 degrees of freedom (`ddof=1`) to calculate the standard deviation:

```
>>> b = np.array([[ 0.3148,  0.0478,  0.6243,  0.4608],
...               [ 0.7149,  0.0775,  0.6072,  0.9656],
...               [ 0.6341,  0.1403,  0.9759,  0.4064],
...               [ 0.5918,  0.6948,  0.904 ,  0.3721],
...               [ 0.0921,  0.2481,  0.1188,  0.1366]])
>>> stats.zscore(b, axis=1, ddof=1)
array([[-0.19264823, -1.28415119,  1.07259584,  0.40420358],
       [ 0.33048416, -1.37380874,  0.04251374,  1.00081084],
       [ 0.26796377, -1.12598418,  1.23283094, -0.37481053],
       [-0.22095197,  0.24468594,  1.19042819, -1.21416216],
       [-0.82780366,  1.4457416 , -0.43867764, -0.1792603 ]])
```

An example with *nan_policy='omit'*:

```
>>> x = np.array([[25.11, 30.10, np.nan, 32.02, 43.15],
...               [14.95, 16.06, 121.25, 94.35, 29.81]])
>>> stats.zscore(x, axis=1, nan_policy='omit')
array([[-1.13490897, -0.37830299,         nan, -0.08718406,  1.60039602],
       [-0.91611681, -0.89090508,  1.4983032 ,  0.88731639, -0.5785977 ]])
```

Statistical distances

wasserstein_distance(u_values, v_values[, …])	Compute the first Wasserstein distance between two 1D distributions.
energy_distance(u_values, v_values[, …])	Compute the energy distance between two 1D distributions.

scipy.stats.wasserstein_distance

scipy.stats.**wasserstein_distance**(*u_values*, *v_values*, *u_weights=None*, *v_weights=None*)

Compute the first Wasserstein distance between two 1D distributions.

This distance is also known as the earth mover's distance, since it can be seen as the minimum amount of "work" required to transform u into v, where "work" is measured as the amount of distribution weight that must be moved, multiplied by the distance it has to be moved.

New in version 1.0.0.

Parameters

u_values, v_values
: [array_like] Values observed in the (empirical) distribution.

u_weights, v_weights
: [array_like, optional] Weight for each value. If unspecified, each value is assigned the same weight. *u_weights* (resp. *v_weights*) must have the same length as *u_values* (resp. *v_values*). If the weight sum differs from 1, it must still be positive and finite so that the weights can be normalized to sum to 1.

Returns

distance
: [float] The computed distance between the distributions.

Notes

The first Wasserstein distance between the distributions u and v is:

$$l_1(u, v) = \inf_{\pi \in \Gamma(u,v)} \int_{\mathbb{R}\times\mathbb{R}} |x - y| \mathrm{d}\pi(x, y)$$

where $\Gamma(u, v)$ is the set of (probability) distributions on $\mathbb{R} \times \mathbb{R}$ whose marginals are u and v on the first and second factors respectively.

If U and V are the respective CDFs of u and v, this distance also equals to:

$$l_1(u, v) = \int_{-\infty}^{+\infty} |U - V|$$

See [2] for a proof of the equivalence of both definitions.

The input distributions can be empirical, therefore coming from samples whose values are effectively inputs of the function, or they can be seen as generalized functions, in which case they are weighted sums of Dirac delta functions located at the specified values.

References

[1], [2]

Examples

```
>>> from scipy.stats import wasserstein_distance
>>> wasserstein_distance([0, 1, 3], [5, 6, 8])
5.0
>>> wasserstein_distance([0, 1], [0, 1], [3, 1], [2, 2])
0.25
>>> wasserstein_distance([3.4, 3.9, 7.5, 7.8], [4.5, 1.4],
...                      [1.4, 0.9, 3.1, 7.2], [3.2, 3.5])
4.0781331438047861
```

scipy.stats.energy_distance

scipy.stats.**energy_distance**(*u_values*, *v_values*, *u_weights=None*, *v_weights=None*)

Compute the energy distance between two 1D distributions.

New in version 1.0.0.

Parameters

u_values, v_values
: [array_like] Values observed in the (empirical) distribution.

u_weights, v_weights
: [array_like, optional] Weight for each value. If unspecified, each value is assigned the same weight. *u_weights* (resp. *v_weights*) must have the same length as *u_values* (resp. *v_values*). If the weight sum differs from 1, it must still be positive and finite so that the weights can be normalized to sum to 1.

Returns

distance
: [float] The computed distance between the distributions.

Notes

The energy distance between two distributions u and v, whose respective CDFs are U and V, equals to:

$$D(u,v) = (2\mathbb{E}|X-Y| - \mathbb{E}|X-X'| - \mathbb{E}|Y-Y'|)^{1/2}$$

where X and X' (resp. Y and Y') are independent random variables whose probability distribution is u (resp. v).

As shown in [2], for one-dimensional real-valued variables, the energy distance is linked to the non-distribution-free version of the Cramér-von Mises distance:

$$D(u,v) = \sqrt{2} l_2(u,v) = \left(2 \int_{-\infty}^{+\infty} (U-V)^2\right)^{1/2}$$

Note that the common Cramér-von Mises criterion uses the distribution-free version of the distance. See [2] (section 2), for more details about both versions of the distance.

The input distributions can be empirical, therefore coming from samples whose values are effectively inputs of the function, or they can be seen as generalized functions, in which case they are weighted sums of Dirac delta functions located at the specified values.

References

[1], [2], [3], [4]

Examples

```
>>> from scipy.stats import energy_distance
>>> energy_distance([0], [2])
2.0000000000000004
>>> energy_distance([0, 8], [0, 8], [3, 1], [2, 2])
1.0000000000000002
>>> energy_distance([0.7, 7.4, 2.4, 6.8], [1.4, 8. ],
...                 [2.1, 4.2, 7.4, 8. ], [7.6, 8.8])
0.88003340976158217
```

Random variate generation / CDF Inversion

rvs_ratio_uniforms(pdf, umax, vmin, vmax[, …])	Generate random samples from a probability density function using the ratio-of-uniforms method.
NumericalInverseHermite(dist, *[, tol, …])	A Hermite spline fast numerical inverse of a probability distribution.

scipy.stats.rvs_ratio_uniforms

scipy.stats.**rvs_ratio_uniforms**(*pdf*, *umax*, *vmin*, *vmax*, *size=1*, *c=0*, *random_state=None*)

Generate random samples from a probability density function using the ratio-of-uniforms method.

Parameters

pdf [callable] A function with signature *pdf(x)* that is proportional to the probability density function of the distribution.

umax [float] The upper bound of the bounding rectangle in the u-direction.

vmin [float] The lower bound of the bounding rectangle in the v-direction.

vmax [float] The upper bound of the bounding rectangle in the v-direction.

size [int or tuple of ints, optional] Defining number of random variates (default is 1).

c [float, optional.] Shift parameter of ratio-of-uniforms method, see Notes. Default is 0.

random_state

[{None, int, numpy.random.Generator,] numpy.random.RandomState}, optional

If *seed* is None (or *np.random*), the numpy.random.RandomState singleton is used. If *seed* is an int, a new RandomState instance is used, seeded with *seed*. If *seed* is already a Generator or RandomState instance then that instance is used.

Returns

rvs [ndarray] The random variates distributed according to the probability distribution defined by the pdf.

Notes

Given a univariate probability density function *pdf* and a constant *c*, define the set `A = {(u, v) : 0 < u <= sqrt(pdf(v/u + c))}`. If *(U, V)* is a random vector uniformly distributed over *A*, then *V/U + c* follows a distribution according to *pdf*.

The above result (see [1], [2]) can be used to sample random variables using only the pdf, i.e. no inversion of the cdf is required. Typical choices of *c* are zero or the mode of *pdf*. The set *A* is a subset of the rectangle `R = [0, umax] x [vmin, vmax]` where

- `umax = sup sqrt(pdf(x))`
- `vmin = inf (x - c) sqrt(pdf(x))`
- `vmax = sup (x - c) sqrt(pdf(x))`

In particular, these values are finite if *pdf* is bounded and `x**2 * pdf(x)` is bounded (i.e. subquadratic tails). One can generate *(U, V)* uniformly on *R* and return *V/U + c* if *(U, V)* are also in *A* which can be directly verified.

The algorithm is not changed if one replaces *pdf* by k * *pdf* for any constant k > 0. Thus, it is often convenient to work with a function that is proportional to the probability density function by dropping unneccessary normalization factors.

Intuitively, the method works well if *A* fills up most of the enclosing rectangle such that the probability is high that *(U, V)* lies in *A* whenever it lies in *R* as the number of required iterations becomes too large otherwise. To be more precise, note that the expected number of iterations to draw *(U, V)* uniformly distributed on *R* such that *(U, V)* is also in *A* is given by the ratio `area(R) / area(A) = 2 * umax * (vmax - vmin) / area(pdf)`, where *area(pdf)* is the integral of *pdf* (which is equal to one if the probability density function is used but can take on other values if a function proportional to the density is used). The equality holds since the area of *A* is equal to 0.5 * area(pdf) (Theorem 7.1 in [1]). If the sampling fails to generate a single random variate after 50000 iterations (i.e. not a single draw is in *A*), an exception is raised.

If the bounding rectangle is not correctly specified (i.e. if it does not contain *A*), the algorithm samples from a distribution different from the one given by *pdf*. It is therefore recommended to perform a test such as *kstest* as a check.

References

[1], [2], [3]

Examples

```
>>> from scipy import stats
>>> rng = np.random.default_rng()
```

Simulate normally distributed random variables. It is easy to compute the bounding rectangle explicitly in that case. For simplicity, we drop the normalization factor of the density.

```
>>> f = lambda x: np.exp(-x**2 / 2)
>>> v_bound = np.sqrt(f(np.sqrt(2))) * np.sqrt(2)
>>> umax, vmin, vmax = np.sqrt(f(0)), -v_bound, v_bound
>>> rvs = stats.rvs_ratio_uniforms(f, umax, vmin, vmax, size=2500,
...                                random_state=rng)
```

The K-S test confirms that the random variates are indeed normally distributed (normality is not rejected at 5% significance level):

```
>>> stats.kstest(rvs, 'norm')[1]
0.250634764150542
```

The exponential distribution provides another example where the bounding rectangle can be determined explicitly.

```
>>> rvs = stats.rvs_ratio_uniforms(lambda x: np.exp(-x), umax=1,
...                                vmin=0, vmax=2*np.exp(-1), size=1000,
...                                random_state=rng)
>>> stats.kstest(rvs, 'expon')[1]
0.21121052054580314
```

scipy.stats.NumericalInverseHermite

class scipy.stats.**NumericalInverseHermite**(*dist*, ***, *tol=1e-12*, *max_intervals=100000*)

A Hermite spline fast numerical inverse of a probability distribution.

The initializer of *NumericalInverseHermite* accepts *dist*, an object representing a continuous distribution, and provides an object with methods that approximate *dist.ppf* and *dist.rvs*. For most distributions, these methods are faster than those of *dist* itself.

Parameters

dist [object] Object representing the distribution for which a fast numerical inverse is desired; for instance, a frozen instance of a *scipy.stats* continuous distribution. See Notes and Examples for details.

tol [float, optional] u-error tolerance (see Notes). The default is 1e-12.

max_intervals [int, optional] Maximum number of intervals in the cubic Hermite spline used to approximate the percent point function. The default is 100000.

Notes

NumericalInverseHermite approximates the inverse of a continuous statistical distribution's CDF with a cubic Hermite spline.

As described in [1], it begins by evaluating the distribution's PDF and CDF at a mesh of quantiles `x` within the distribution's support. It uses the results to fit a cubic Hermite spline `H` such that `H(p) == x`, where `p` is the array of percentiles corresponding with the quantiles `x`. Therefore, the spline approximates the inverse of the distribution's CDF to machine precision at the percentiles `p`, but typically, the spline will not be as accurate at the midpoints between the percentile points:

```
p_mid = (p[:-1] + p[1:])/2
```

so the mesh of quantiles is refined as needed to reduce the maximum "u-error":

```
u_error = np.max(np.abs(dist.cdf(H(p_mid)) - p_mid))
```

below the specified tolerance *tol*. Refinement stops when the required tolerance is achieved or when the number of mesh intervals after the next refinement could exceed the maximum allowed number *max_intervals*.

The object *dist* must have methods `pdf`, `cdf`, and `ppf` that behave like those of a *frozen* instance of *scipy.stats.rv_continuous*. Specifically, it must have methods `pdf` and `cdf` that accept exactly one ndarray argument `x` and return the probability density function and cumulative density function (respectively) at `x`. The object must also have a method `ppf` that accepts a float `p` and returns the percentile point function at `p`. The object may also have a method `isf` that accepts a float `p` and returns the inverse survival function at `p`; if it does not, it will be assigned an attribute `isf` that calculates the inverse survival function using `ppf`. The `ppf` and `isf`

methods will each be evaluated at a small positive float ``p (e.g. p = utol/10), and the domain over which the approximate numerical inverse is defined will be ppf(p) to isf(p). The approximation will not be accurate in the extreme tails beyond this domain.

References

[1]

Examples

For some distributions, dist.ppf and dist.rvs are quite slow. For instance, consider *scipy.stats.genexpon*. We freeze the distribution by passing all shape parameters into its initializer and time the resulting object's ppf and rvs functions.

```
>>> import numpy as np
>>> from scipy import stats
>>> from timeit import timeit
>>> time_once = lambda f: f"{timeit(f, number=1)*1000:.6} ms"
>>> dist = stats.genexpon(9, 16, 3)  # freeze the distribution
>>> p = np.linspace(0.01, 0.99, 99)  # percentiles from 1% to 99%
>>> time_once(lambda: dist.ppf(p))
'154.565 ms'  # may vary
```

```
>>> time_once(lambda: dist.rvs(size=100))
'148.979 ms'  # may vary
```

The *NumericalInverseHermite* has a method that approximates dist.ppf.

```
>>> from scipy.stats import NumericalInverseHermite
>>> fni = NumericalInverseHermite(dist)
>>> np.allclose(fni.ppf(p), dist.ppf(p))
True
```

In some cases, it is faster to both generate the fast numerical inverse and use it than to call dist.ppf.

```
>>> def time_me():
...     fni = NumericalInverseHermite(dist)
...     fni.ppf(p)
>>> time_once(time_me)
'11.9222 ms'  # may vary
```

After generating the fast numerical inverse, subsequent calls to its methods are much faster. >>> time_once(lambda: fni.ppf(p)) '0.0819 ms' # may vary

The fast numerical inverse can also be used to generate random variates using inverse transform sampling.

```
>>> time_once(lambda: fni.rvs(size=100))
'0.0911 ms'  # may vary
```

Depending on the implementation of the distribution's random sampling method, the random variates generated may be nearly identical, given the same random state.

```
>>> # `seed` ensures identical random streams are used by each `rvs`␣
↪method
>>> seed = 500072020
>>> rvs1 = dist.rvs(size=100, random_state=np.random.default_rng(seed))
>>> rvs2 = fni.rvs(size=100, random_state=np.random.default_rng(seed))
>>> np.allclose(rvs1, rvs2)
True
```

To use *NumericalInverseHermite* with a custom distribution, users may subclass *scipy.stats.rv_continuous* and initialize a frozen instance or create an object with equivalent `pdf`, `cdf`, and `ppf` methods. For instance, the following object represents the standard normal distribution. For simplicity, we use *scipy.special.ndtr* and *scipy.special.ndtri* to compute the `cdf` and `ppf`, respectively.

```
>>> from scipy.special import ndtr, ndtri
>>>
>>> class MyNormal:
...
...     def pdf(self, x):
...         return 1/np.sqrt(2*np.pi) * np.exp(-x**2 / 2)
...
...     def cdf(self, x):
...         return ndtr(x)
...
...     def ppf(self, x):
...         return ndtri(x)
...
>>> dist1 = MyNormal()
>>> fni1 = NumericalInverseHermite(dist1)
>>>
>>> dist2 = stats.norm()
>>> fni2 = NumericalInverseHermite(dist2)
>>>
>>> print(fni1.rvs(random_state=seed), fni2.rvs(random_state=seed))
-1.9603810921759424 -1.9603810921747074
```

Attributes

intervals [int] The number of intervals of the interpolant.

midpoint_error
[float] The maximum u-error at an interpolant interval midpoint.

Methods

ppf(q)	Approximate percent point function (inverse *cdf*) of the given RV.
qrvs([size, d, qmc_engine])	Quasi-random variates of the given RV.
rvs([size, random_state])	Random variates of the given RV.

scipy.stats.NumericalInverseHermite.ppf

NumericalInverseHermite.**ppf**(*q*)

Approximate percent point function (inverse *cdf*) of the given RV.

Parameters

q [array_like] lower tail probability.

Returns

x [array_like] quantile corresponding to the lower tail probability *q*.

scipy.stats.NumericalInverseHermite.qrvs

NumericalInverseHermite.**qrvs**(*size=None*, *d=None*, *qmc_engine=None*)

Quasi-random variates of the given RV.

The *qmc_engine* is used to draw uniform quasi-random variates, and these are converted to quasi-random variates of the given RV using inverse transform sampling.

Parameters

size [int, tuple of ints, or None; optional] Defines shape of random variates array. Default is `None`.

d [int or None, optional] Defines dimension of uniform quasi-random variates to be transformed. Default is `None`.

qmc_engine [scipy.stats.qmc.QMCEngine(d=1), optional] Defines the object to use for drawing quasi-random variates. Default is `None`, which uses *scipy.stats.qmc.Halton(1)*.

Returns

rvs [ndarray or scalar] Quasi-random variates. See Notes for shape information.

Notes

The shape of the output array depends on *size*, *d*, and *qmc_engine*. The intent is for the interface to be natural, but the detailed rules to achieve this are complicated.

- If *qmc_engine* is `None`, a *scipy.stats.qmc.Halton* instance is created with dimension *d*. If *d* is not provided, `d=1`.
- If *qmc_engine* is not `None` and *d* is `None`, *d* is determined from the dimension of the *qmc_engine*.
- If *qmc_engine* is not `None` and *d* is not `None` but the dimensions are inconsistent, a `ValueError` is raised.
- After *d* is determined according to the rules above, the output shape is `tuple_shape + d_shape`, where:
  - `tuple_shape = tuple()` if *size* is `None`,
  - `tuple_shape = (size,)` if *size* is an `int`,
  - `tuple_shape = size` if *size* is a sequence,
  - `d_shape = tuple()` if *d* is `None` or *d* is 1, and
  - `d_shape = (d,)` if *d* is greater than 1.

The elements of the returned array are part of a low-discrepancy sequence. If d is 1, this means that none of the samples are truly independent. If $d > 1$, each slice `rvs[..., i]` will be of a quasi-independent sequence; see *scipy.stats.qmc.QMCEngine* for details. Note that when $d > 1$, the samples returned are still those of the provided univariate distribution, not a multivariate generalization of that distribution.

scipy.stats.NumericalInverseHermite.rvs

`NumericalInverseHermite.`**`rvs`**(*size=None*, *random_state=None*)

Random variates of the given RV.

The *random_state* is used to draw uniform pseudo-random variates, and these are converted to pseudo-random variates of the given RV using inverse transform sampling.

Parameters

size [int, tuple of ints, or None; optional] Defines shape of array of random variates. Default is `None`.

random_state [{None, int, `numpy.random.Generator`,] `numpy.random.RandomState`}, optional
Defines the object to use for drawing pseudorandom variates. If *random_state* is `None` the *np.random.RandomState* singleton is used. If *random_state* is an `int`, a new `RandomState` instance is used, seeded with *random_state*. If *random_state* is already a `RandomState` or `Generator` instance, then that object is used. Default is None.

Returns

rvs [ndarray or scalar] Random variates of given *size*. If *size* is `None`, a scalar is returned.

Circular statistical functions

circmean(samples[, high, low, axis, nan_policy])	Compute the circular mean for samples in a range.
circvar(samples[, high, low, axis, nan_policy])	Compute the circular variance for samples assumed to be in a range.
circstd(samples[, high, low, axis, nan_policy])	Compute the circular standard deviation for samples assumed to be in the range [low to high].

scipy.stats.circmean

`scipy.stats.`**`circmean`**(*samples*, *high=6.283185307179586*, *low=0*, *axis=None*, *nan_policy='propagate'*)

Compute the circular mean for samples in a range.

Parameters

samples [array_like] Input array.

high [float or int, optional] High boundary for circular mean range. Default is `2*pi`.

low [float or int, optional] Low boundary for circular mean range. Default is 0.

axis [int, optional] Axis along which means are computed. The default is to compute the mean of the flattened array.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

circmean [float] Circular mean.

Examples

```
>>> from scipy.stats import circmean
>>> circmean([0.1, 2*np.pi+0.2, 6*np.pi+0.3])
0.2
```

```
>>> from scipy.stats import circmean
>>> circmean([0.2, 1.4, 2.6], high = 1, low = 0)
0.4
```

scipy.stats.circvar

`scipy.stats.`**`circvar`**(*samples*, *high=6.283185307179586*, *low=0*, *axis=None*, *nan_policy='propagate'*)

Compute the circular variance for samples assumed to be in a range.

Parameters

samples [array_like] Input array.
high [float or int, optional] High boundary for circular variance range. Default is `2*pi`.
low [float or int, optional] Low boundary for circular variance range. Default is 0.
axis [int, optional] Axis along which variances are computed. The default is to compute the variance of the flattened array.
nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

circvar [float] Circular variance.

Notes

This uses a definition of circular variance that in the limit of small angles returns a number close to the 'linear' variance.

Examples

```
>>> from scipy.stats import circvar
>>> circvar([0, 2*np.pi/3, 5*np.pi/3])
2.19722457734
```

scipy.stats.circstd

scipy.stats.**circstd**(*samples*, *high=6.283185307179586*, *low=0*, *axis=None*, *nan_policy='propagate'*)

Compute the circular standard deviation for samples assumed to be in the range [low to high].

Parameters

samples [array_like] Input array.

high [float or int, optional] High boundary for circular standard deviation range. Default is `2*pi`.

low [float or int, optional] Low boundary for circular standard deviation range. Default is 0.

axis [int, optional] Axis along which standard deviations are computed. The default is to compute the standard deviation of the flattened array.

nan_policy

[{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

circstd [float] Circular standard deviation.

Notes

This uses a definition of circular standard deviation that in the limit of small angles returns a number close to the 'linear' standard deviation.

Examples

```
>>> from scipy.stats import circstd
>>> circstd([0, 0.1*np.pi/2, 0.001*np.pi, 0.03*np.pi/2])
0.063564063306
```

Contingency table functions

chi2_contingency(observed[, correction, lambda_])	Chi-square test of independence of variables in a contingency table.
contingency.crosstab(*args[, levels, sparse])	Return table of counts for each possible unique combination in `*args`.
contingency.expected_freq(observed)	Compute the expected frequencies from a contingency table.
contingency.margins(a)	Return a list of the marginal sums of the array *a*.
contingency.relative_risk(exposed_cases, …)	Compute the relative risk (also known as the risk ratio).
contingency.association(observed[, method, …])	Calculates degree of association between two nominal variables.
fisher_exact(table[, alternative])	Perform a Fisher exact test on a 2x2 contingency table.
barnard_exact(table[, alternative, pooled, n])	Perform a Barnard exact test on a 2x2 contingency table.
boschloo_exact(table[, alternative, n])	Perform Boschloo's exact test on a 2x2 contingency table.

scipy.stats.chi2_contingency

scipy.stats.**chi2_contingency**(*observed*, *correction=True*, *lambda_=None*)

Chi-square test of independence of variables in a contingency table.

This function computes the chi-square statistic and p-value for the hypothesis test of independence of the observed frequencies in the contingency table [1] *observed*. The expected frequencies are computed based on the marginal sums under the assumption of independence; see *scipy.stats.contingency.expected_freq*. The number of degrees of freedom is (expressed using numpy functions and attributes):

```
dof = observed.size - sum(observed.shape) + observed.ndim - 1
```

Parameters

observed [array_like] The contingency table. The table contains the observed frequencies (i.e. number of occurrences) in each category. In the two-dimensional case, the table is often described as an "R x C table".

correction [bool, optional] If True, *and* the degrees of freedom is 1, apply Yates' correction for continuity. The effect of the correction is to adjust each observed value by 0.5 towards the corresponding expected value.

lambda_ [float or str, optional] By default, the statistic computed in this test is Pearson's chi-squared statistic [2]. *lambda_* allows a statistic from the Cressie-Read power divergence family [3] to be used instead. See *power_divergence* for details.

Returns

chi2 [float] The test statistic.

p [float] The p-value of the test

dof [int] Degrees of freedom

expected [ndarray, same shape as *observed*] The expected frequencies, based on the marginal sums of the table.

See also:

contingency.expected_freq

fisher_exact

chisquare

power_divergence

barnard_exact

boschloo_exact

Notes

An often quoted guideline for the validity of this calculation is that the test should be used only if the observed and expected frequencies in each cell are at least 5.

This is a test for the independence of different categories of a population. The test is only meaningful when the dimension of *observed* is two or more. Applying the test to a one-dimensional table will always result in *expected* equal to *observed* and a chi-square statistic equal to 0.

This function does not handle masked arrays, because the calculation does not make sense with missing values.

Like stats.chisquare, this function computes a chi-square statistic; the convenience this function provides is to figure out the expected frequencies and degrees of freedom from the given contingency table. If these were already known, and if the Yates' correction was not required, one could use stats.chisquare. That is, if one calls:

```
chi2, p, dof, ex = chi2_contingency(obs, correction=False)
```

then the following is true:

```
(chi2, p) == stats.chisquare(obs.ravel(), f_exp=ex.ravel(),
                             ddof=obs.size - 1 - dof)
```

The *lambda_* argument was added in version 0.13.0 of scipy.

References

[1], [2], [3]

Examples

A two-way example (2 x 3):

```
>>> from scipy.stats import chi2_contingency
>>> obs = np.array([[10, 10, 20], [20, 20, 20]])
>>> chi2_contingency(obs)
(2.7777777777777777,
 0.24935220877729619,
 2,
 array([[ 12.,  12.,  16.],
        [ 18.,  18.,  24.]]))
```

Perform the test using the log-likelihood ratio (i.e. the "G-test") instead of Pearson's chi-squared statistic.

```
>>> g, p, dof, expctd = chi2_contingency(obs, lambda_="log-likelihood")
>>> g, p
(2.7688587616781319, 0.25046668010954165)
```

A four-way example (2 x 2 x 2 x 2):

```
>>> obs = np.array(
...     [[[[12, 17],
...        [11, 16]],
...       [[11, 12],
...        [15, 16]]],
...      [[[23, 15],
...        [30, 22]],
...       [[14, 17],
...        [15, 16]]]])
>>> chi2_contingency(obs)
(8.7584514426741897,
 0.64417725029295503,
 11,
 array([[[[ 14.15462386,  14.15462386],
          [ 16.49423111,  16.49423111]],
```

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```
          [[ 11.2461395 ,  11.2461395 ],
           [ 13.10500554,  13.10500554]]],
         [[[ 19.5591166 ,  19.5591166 ],
           [ 22.79202844,  22.79202844]],
          [[ 15.54012004,  15.54012004],
           [ 18.10873492,  18.10873492]]]]))
```

scipy.stats.contingency.crosstab

scipy.stats.contingency.**crosstab**(**args*, *levels=None*, *sparse=False*)

Return table of counts for each possible unique combination in `*args`.

When `len(args) > 1`, the array computed by this function is often referred to as a *contingency table* [1].

The arguments must be sequences with the same length. The second return value, *count*, is an integer array with `len(args)` dimensions. If *levels* is None, the shape of *count* is `(n0, n1, ...)`, where `nk` is the number of unique elements in `args[k]`.

Parameters

args [sequences] A sequence of sequences whose unique aligned elements are to be counted. The sequences in args must all be the same length.

levels [sequence, optional] If *levels* is given, it must be a sequence that is the same length as *args*. Each element in *levels* is either a sequence or None. If it is a sequence, it gives the values in the corresponding sequence in *args* that are to be counted. If any value in the sequences in *args* does not occur in the corresponding sequence in *levels*, that value is ignored and not counted in the returned array *count*. The default value of *levels* for `args[i]` is `np.unique(args[i])`

sparse [bool, optional] If True, return a sparse matrix. The matrix will be an instance of the *scipy.sparse.coo_matrix* class. Because SciPy's sparse matrices must be 2-d, only two input sequences are allowed when *sparse* is True. Default is False.

Returns

elements [tuple of numpy.ndarrays.] Tuple of length `len(args)` containing the arrays of elements that are counted in *count*. These can be interpreted as the labels of the corresponding dimensions of *count*. If *levels* was given, then if `levels[i]` is not None, `elements[i]` will hold the values given in `levels[i]`.

count [numpy.ndarray or scipy.sparse.coo_matrix] Counts of the unique elements in `zip(*args)`, stored in an array. Also known as a *contingency table* when `len(args) > 1`.

See also:

numpy.unique

Notes

New in version 1.7.0.

References

[1]

Examples

```
>>> from scipy.stats.contingency import crosstab
```

Given the lists *a* and *x*, create a contingency table that counts the frequencies of the corresponding pairs.

```
>>> a = ['A', 'B', 'A', 'A', 'B', 'B', 'A', 'A', 'B', 'B']
>>> x = ['X', 'X', 'X', 'Y', 'Z', 'Z', 'Y', 'Y', 'Z', 'Z']
>>> (avals, xvals), count = crosstab(a, x)
>>> avals
array(['A', 'B'], dtype='<U1')
>>> xvals
array(['X', 'Y', 'Z'], dtype='<U1')
>>> count
array([[2, 3, 0],
       [1, 0, 4]])
```

So *('A', 'X')* occurs twice, *('A', 'Y')* occurs three times, etc.

Higher dimensional contingency tables can be created.

```
>>> p = [0, 0, 0, 0, 1, 1, 1, 0, 0, 1]
>>> (avals, xvals, pvals), count = crosstab(a, x, p)
>>> count
array([[[2, 0],
        [2, 1],
        [0, 0]],
       [[1, 0],
        [0, 0],
        [1, 3]]])
>>> count.shape
(2, 3, 2)
```

The values to be counted can be set by using the *levels* argument. It allows the elements of interest in each input sequence to be given explicitly instead finding the unique elements of the sequence.

For example, suppose one of the arguments is an array containing the answers to a survey question, with integer values 1 to 4. Even if the value 1 does not occur in the data, we want an entry for it in the table.

```
>>> q1 = [2, 3, 3, 2, 4, 4, 2, 3, 4, 4, 4, 3, 3, 3, 4]  # 1 does not␣
↪occur.
>>> q2 = [4, 4, 2, 2, 2, 4, 1, 1, 2, 2, 4, 2, 2, 2, 4]  # 3 does not␣
↪occur.
>>> options = [1, 2, 3, 4]
>>> vals, count = crosstab(q1, q2, levels=(options, options))
```

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```
>>> count
array([[0, 0, 0, 0],
       [1, 1, 0, 1],
       [1, 4, 0, 1],
       [0, 3, 0, 3]])
```

If *levels* is given, but an element of *levels* is None, the unique values of the corresponding argument are used. For example,

```
>>> vals, count = crosstab(q1, q2, levels=(None, options))
>>> vals
[array([2, 3, 4]), [1, 2, 3, 4]]
>>> count
array([[1, 1, 0, 1],
       [1, 4, 0, 1],
       [0, 3, 0, 3]])
```

If we want to ignore the pairs where 4 occurs in `q2`, we can give just the values [1, 2] to *levels*, and the 4 will be ignored:

```
>>> vals, count = crosstab(q1, q2, levels=(None, [1, 2]))
>>> vals
[array([2, 3, 4]), [1, 2]]
>>> count
array([[1, 1],
       [1, 4],
       [0, 3]])
```

Finally, let's repeat the first example, but return a sparse matrix:

```
>>> (avals, xvals), count = crosstab(a, x, sparse=True)
>>> count
<2x3 sparse matrix of type '<class 'numpy.int64'>'
        with 4 stored elements in COOrdinate format>
>>> count.A
array([[2, 3, 0],
       [1, 0, 4]])
```

scipy.stats.contingency.expected_freq

`scipy.stats.contingency.`**`expected_freq`**(*observed*)

Compute the expected frequencies from a contingency table.

Given an n-dimensional contingency table of observed frequencies, compute the expected frequencies for the table based on the marginal sums under the assumption that the groups associated with each dimension are independent.

Parameters

observed [array_like] The table of observed frequencies. (While this function can handle a 1-D array, that case is trivial. Generally *observed* is at least 2-D.)

Returns

expected [ndarray of float64] The expected frequencies, based on the marginal sums of the table. Same shape as *observed*.

Examples

```
>>> from scipy.stats.contingency import expected_freq
>>> observed = np.array([[10, 10, 20],[20, 20, 20]])
>>> expected_freq(observed)
array([[ 12.,  12.,  16.],
       [ 18.,  18.,  24.]])
```

scipy.stats.contingency.margins

scipy.stats.contingency.**margins**(*a*)

Return a list of the marginal sums of the array *a*.

Parameters

a [ndarray] The array for which to compute the marginal sums.

Returns

margsums [list of ndarrays] A list of length *a.ndim*. *margsums[k]* is the result of summing *a* over all axes except *k*; it has the same number of dimensions as *a*, but the length of each axis except axis *k* will be 1.

Examples

```
>>> a = np.arange(12).reshape(2, 6)
>>> a
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11]])
>>> from scipy.stats.contingency import margins
>>> m0, m1 = margins(a)
>>> m0
array([[15],
       [51]])
>>> m1
array([[ 6,  8, 10, 12, 14, 16]])
```

```
>>> b = np.arange(24).reshape(2,3,4)
>>> m0, m1, m2 = margins(b)
>>> m0
array([[[ 66]],
       [[210]]])
>>> m1
array([[[ 60],
        [ 92],
        [124]]])
>>> m2
array([[[60, 66, 72, 78]]])
```

scipy.stats.contingency.relative_risk

scipy.stats.contingency.**relative_risk**(*exposed_cases*, *exposed_total*, *control_cases*, *control_total*)

Compute the relative risk (also known as the risk ratio).

This function computes the relative risk associated with a 2x2 contingency table ([1], section 2.2.3; [2], section 3.1.2). Instead of accepting a table as an argument, the individual numbers that are used to compute the relative risk are given as separate parameters. This is to avoid the ambiguity of which row or column of the contingency table corresponds to the "exposed" cases and which corresponds to the "control" cases. Unlike, say, the odds ratio, the relative risk is not invariant under an interchange of the rows or columns.

Parameters

exposed_cases
: [nonnegative int] The number of "cases" (i.e. occurrence of disease or other event of interest) among the sample of "exposed" individuals.

exposed_total
: [positive int] The total number of "exposed" individuals in the sample.

control_cases
: [nonnegative int] The number of "cases" among the sample of "control" or non-exposed individuals.

control_total
: [positive int] The total number of "control" individuals in the sample.

Returns

result
: [instance of *RelativeRiskResult*] The object has the float attribute `relative_risk`, which is:

```
rr = (exposed_cases/exposed_total) / (control_cases/
↪control_total)
```

The object also has the method `confidence_interval` to compute the confidence interval of the relative risk for a given confidence level.

Notes

The R package epitools has the function *riskratio*, which accepts a table with the following layout:

```
                disease=0   disease=1
exposed=0 (ref)    n00         n01
exposed=1          n10         n11
```

With a 2x2 table in the above format, the estimate of the CI is computed by *riskratio* when the argument method="wald" is given, or with the function *riskratio.wald*.

For example, in a test of the incidence of lung cancer among a sample of smokers and nonsmokers, the "exposed" category would correspond to "is a smoker" and the "disease" category would correspond to "has or had lung cancer".

To pass the same data to `relative_risk`, use:

```
relative_risk(n11, n10 + n11, n01, n00 + n01)
```

New in version 1.7.0.

References

[1], [2]

Examples

```
>>> from scipy.stats.contingency import relative_risk
```

This example is from Example 3.1 of [2]. The results of a heart disease study are summarized in the following table:

```
          High CAT   Low CAT    Total
          --------   -------    -----
CHD          27          44        71
No CHD       95         443       538

Total       122         487       609
```

CHD is coronary heart disease, and CAT refers to the level of circulating catecholamine. CAT is the "exposure" variable, and high CAT is the "exposed" category. So the data from the table to be passed to `relative_risk` is:

```
exposed_cases = 27
exposed_total = 122
control_cases = 44
control_total = 487
```

```
>>> result = relative_risk(27, 122, 44, 487)
>>> result.relative_risk
2.4495156482861398
```

Find the confidence interval for the relative risk.

```
>>> result.confidence_interval(confidence_level=0.95)
ConfidenceInterval(low=1.5836990926700116, high=3.7886786315466354)
```

The interval does not contain 1, so the data supports the statement that high CAT is associated with greater risk of CHD.

scipy.stats.contingency.association

scipy.stats.contingency.**association**(*observed*, *method='cramer'*, *correction=False*, *lambda_=None*)

Calculates degree of association between two nominal variables.

The function provides the option for computing one of three measures of association between two nominal variables from the data given in a 2d contingency table: Tschuprow's T, Pearson's Contingency Coefficient and Cramer's V.

Parameters

observed [array-like] The array of observed values
method [{"cramer", "tschuprow", "pearson"} (default = "cramer")] The association test statistic.
correction [bool, optional] Inherited from *scipy.stats.contingency.chi2_contingency()*
lambda_ [float or str, optional] Inherited from *scipy.stats.contingency.chi2_contingency()*

Returns

statistic [float] Value of the test statistic

Notes

Cramer's V, Tschuprow's T and Pearson's Contingency Coefficient, all measure the degree to which two nominal or ordinal variables are related, or the level of their association. This differs from correlation, although many often mistakenly consider them equivalent. Correlation measures in what way two variables are related, whereas, association measures how related the variables are. As such, association does not subsume independent variables, and is rather a test of independence. A value of 1.0 indicates perfect association, and 0.0 means the variables have no association.

Both the Cramer's V and Tschuprow's T are extensions of the phi coefficient. Moreover, due to the close relationship between the Cramer's V and Tschuprow's T the returned values can often be similar or even equivalent. They are likely to diverge more as the array shape diverges from a 2x2.

References

[1], [2], [3], [4], [5]

Examples

An example with a 4x2 contingency table:

```
>>> from scipy.stats.contingency import association
>>> obs4x2 = np.array([[100, 150], [203, 322], [420, 700], [320, 210]])
```

Pearson's contingency coefficient >>> association(obs4x2, method="pearson") 0.18303298140595667

Cramer's V

```
>>> association(obs4x2, method="cramer")
0.18617813077483678
```

Tschuprow's T

```
>>> association(obs4x2, method="tschuprow")
0.14146478765062995
```

scipy.stats.fisher_exact

scipy.stats.**fisher_exact**(*table*, *alternative='two-sided'*)

Perform a Fisher exact test on a 2x2 contingency table.

Parameters

table [array_like of ints] A 2x2 contingency table. Elements must be non-negative integers.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the alternative hypothesis. The following options are available (default is 'two-sided'):

- 'two-sided'
- 'less': one-sided

- 'greater': one-sided

See the Notes for more details.

Returns

oddsratio [float] This is prior odds ratio and not a posterior estimate.

p_value [float] P-value, the probability of obtaining a distribution at least as extreme as the one that was actually observed, assuming that the null hypothesis is true.

See also:

chi2_contingency

Chi-square test of independence of variables in a contingency table. This can be used as an alternative to *fisher_exact* when the numbers in the table are large.

barnard_exact

Barnard's exact test, which is a more powerful alternative than Fisher's exact test for 2x2 contingency tables.

boschloo_exact

Boschloo's exact test, which is a more powerful alternative than Fisher's exact test for 2x2 contingency tables.

Notes

Null hypothesis and p-values

The null hypothesis is that the input table is from the hypergeometric distribution with parameters (as used in *hypergeom*) `M = a + b + c + d`, `n = a + b` and `N = a + c`, where the input table is `[[a, b], [c, d]]`. This distribution has support `max(0, N + n - M) <= x <= min(N, n)`, or, in terms of the values in the input table, `min(0, a - d) <= x <= a + min(b, c)`. `x` can be interpreted as the upper-left element of a 2x2 table, so the tables in the distribution have form:

```
[  x           n - x     ]
[N - x    M - (n + N) + x]
```

For example, if:

```
table = [6  2]
        [1  4]
```

then the support is `2 <= x <= 7`, and the tables in the distribution are:

```
[2 6]   [3 5]   [4 4]   [5 3]   [6 2]  [7 1]
[5 0]   [4 1]   [3 2]   [2 3]   [1 4]  [0 5]
```

The probability of each table is given by the hypergeometric distribution `hypergeom.pmf(x, M, n, N)`. For this example, these are (rounded to three significant digits):

```
x       2      3      4      5       6        7
p  0.0163  0.163  0.408  0.326  0.0816  0.00466
```

These can be computed with:

```
>>> from scipy.stats import hypergeom
>>> table = np.array([[6, 2], [1, 4]])
>>> M = table.sum()
```

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```
>>> n = table[0].sum()
>>> N = table[:, 0].sum()
>>> start, end = hypergeom.support(M, n, N)
>>> hypergeom.pmf(np.arange(start, end+1), M, n, N)
array([0.01631702, 0.16317016, 0.40792541, 0.32634033, 0.08158508,
       0.004662  ])
```

The two-sided p-value is the probability that, under the null hypothesis, a random table would have a probability equal to or less than the probability of the input table. For our example, the probability of the input table (where `x = 6`) is 0.0816. The x values where the probability does not exceed this are 2, 6 and 7, so the two-sided p-value is `0.0163 + 0.0816 + 0.00466 ~= 0.10256`:

```
>>> from scipy.stats import fisher_exact
>>> oddsr, p = fisher_exact(table, alternative='two-sided')
>>> p
0.10256410256410257
```

The one-sided p-value for `alternative='greater'` is the probability that a random table has `x >= a`, which in our example is `x >= 6`, or `0.0816 + 0.00466 ~= 0.08626`:

```
>>> oddsr, p = fisher_exact(table, alternative='greater')
>>> p
0.08624708624708627
```

This is equivalent to computing the survival function of the distribution at `x = 5` (one less than `x` from the input table, because we want to include the probability of `x = 6` in the sum):

```
>>> hypergeom.sf(5, M, n, N)
0.08624708624708627
```

For `alternative='less'`, the one-sided p-value is the probability that a random table has `x <= a`, (i.e. `x <= 6` in our example), or `0.0163 + 0.163 + 0.408 + 0.326 + 0.0816 ~= 0.9949`:

```
>>> oddsr, p = fisher_exact(table, alternative='less')
>>> p
0.9953379953379957
```

This is equivalent to computing the cumulative distribution function of the distribution at `x = 6`:

```
>>> hypergeom.cdf(6, M, n, N)
0.9953379953379957
```

Odds ratio

The calculated odds ratio is different from the one R uses. This SciPy implementation returns the (more common) "unconditional Maximum Likelihood Estimate", while R uses the "conditional Maximum Likelihood Estimate".

Examples

Say we spend a few days counting whales and sharks in the Atlantic and Indian oceans. In the Atlantic ocean we find 8 whales and 1 shark, in the Indian ocean 2 whales and 5 sharks. Then our contingency table is:

```
        Atlantic  Indian
whales     8         2
sharks     1         5
```

We use this table to find the p-value:

```
>>> from scipy.stats import fisher_exact
>>> oddsratio, pvalue = fisher_exact([[8, 2], [1, 5]])
>>> pvalue
0.0349...
```

The probability that we would observe this or an even more imbalanced ratio by chance is about 3.5%. A commonly used significance level is 5%–if we adopt that, we can therefore conclude that our observed imbalance is statistically significant; whales prefer the Atlantic while sharks prefer the Indian ocean.

scipy.stats.barnard_exact

scipy.stats.**barnard_exact**(*table*, *alternative='two-sided'*, *pooled=True*, *n=32*)

Perform a Barnard exact test on a 2x2 contingency table.

Parameters

table [array_like of ints] A 2x2 contingency table. Elements should be non-negative integers.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the null and alternative hypotheses. Default is 'two-sided'. Please see explanations in the Notes section below.

pooled [bool, optional] Whether to compute score statistic with pooled variance (as in Student's t-test, for example) or unpooled variance (as in Welch's t-test). Default is `True`.

n [int, optional] Number of sampling points used in the construction of the sampling method. Note that this argument will automatically be converted to the next higher power of 2 since *scipy.stats.qmc.Sobol* is used to select sample points. Default is 32. Must be positive. In most cases, 32 points is enough to reach good precision. More points comes at performance cost.

Returns

ber [BarnardExactResult] A result object with the following attributes.

statistic [float] The Wald statistic with pooled or unpooled variance, depending on the user choice of *pooled*.

pvalue [float] P-value, the probability of obtaining a distribution at least as extreme as the one that was actually observed, assuming that the null hypothesis is true.

See also:

chi2_contingency

Chi-square test of independence of variables in a contingency table.

fisher_exact

Fisher exact test on a 2x2 contingency table.

boschloo_exact

Boschloo's exact test on a 2x2 contingency table, which is an uniformly more powerful alternative to Fisher's exact test.

Notes

Barnard's test is an exact test used in the analysis of contingency tables. It examines the association of two categorical variables, and is a more powerful alternative than Fisher's exact test for 2x2 contingency tables.

Let's define X_0 a 2x2 matrix representing the observed sample, where each column stores the binomial experiment, as in the example below. Let's also define p_1, p_2 the theoretical binomial probabilities for x_{11} and x_{12}. When using Barnard exact test, we can assert three different null hypotheses :

- $H_0 : p_1 \geq p_2$ versus $H_1 : p_1 < p_2$, with *alternative* = "less"
- $H_0 : p_1 \leq p_2$ versus $H_1 : p_1 > p_2$, with *alternative* = "greater"
- $H_0 : p_1 = p_2$ versus $H_1 : p_1 \neq p_2$, with *alternative* = "two-sided" (default one)

In order to compute Barnard's exact test, we are using the Wald statistic [3] with pooled or unpooled variance. Under the default assumption that both variances are equal (`pooled = True`), the statistic is computed as:

$$T(X) = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\hat{p}(1-\hat{p})(\frac{1}{c_1} + \frac{1}{c_2})}}$$

with $\hat{p}_1, \hat{p}_2$ and $\hat{p}$ the estimator of p_1, p_2 and p, the latter being the combined probability, given the assumption that $p_1 = p_2$.

If this assumption is invalid (`pooled = False`), the statistic is:

$$T(X) = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{c_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{c_2}}}$$

The p-value is then computed as:

$$\sum \binom{c_1}{x_{11}} \binom{c_2}{x_{12}} \pi^{x_{11}+x_{12}} (1-\pi)^{t-x_{11}-x_{12}}$$

where the sum is over all 2x2 contingency tables X such that: * $T(X) \leq T(X_0)$ when *alternative* = "less", * $T(X) \geq T(X_0)$ when *alternative* = "greater", or * $T(X) \geq |T(X_0)|$ when *alternative* = "two-sided". Above, c_1, c_2 are the sum of the columns 1 and 2, and t the total (sum of the 4 sample's element).

The returned p-value is the maximum p-value taken over the nuisance parameter π, where $0 \leq \pi \leq 1$.

This function's complexity is $O(nc_1c_2)$, where *n* is the number of sample points.

References

[1], [2], [3]

Examples

An example use of Barnard's test is presented in [2].

> Consider the following example of a vaccine efficacy study (Chan, 1998). In a randomized clinical trial of 30 subjects, 15 were inoculated with a recombinant DNA influenza vaccine and the 15 were inoculated with a placebo. Twelve of the 15 subjects in the placebo group (80%) eventually became infected with influenza whereas for the vaccine group, only 7 of the 15 subjects (47%) became infected. The data are tabulated as a 2 x 2 table:

```
    Vaccine  Placebo
Yes      7        12
No       8        3
```

When working with statistical hypothesis testing, we usually use a threshold probability or significance level upon which we decide to reject the null hypothesis H_0. Suppose we choose the common significance level of 5%.

Our alternative hypothesis is that the vaccine will lower the chance of becoming infected with the virus; that is, the probability p_1 of catching the virus with the vaccine will be *less than* the probability p_2 of catching the virus without the vaccine. Therefore, we call *barnard_exact* with the `alternative="less"` option:

```
>>> import scipy.stats as stats
>>> res = stats.barnard_exact([[7, 12], [8, 3]], alternative="less")
>>> res.statistic
-1.894...
>>> res.pvalue
0.03407...
```

Under the null hypothesis that the vaccine will not lower the chance of becoming infected, the probability of obtaining test results at least as extreme as the observed data is approximately 3.4%. Since this p-value is less than our chosen significance level, we have evidence to reject H_0 in favor of the alternative.

Suppose we had used Fisher's exact test instead:

```
>>> _, pvalue = stats.fisher_exact([[7, 12], [8, 3]], alternative="less")
>>> pvalue
0.0640...
```

With the same threshold significance of 5%, we would not have been able to reject the null hypothesis in favor of the alternative. As stated in [2], Barnard's test is uniformly more powerful than Fisher's exact test because Barnard's test does not condition on any margin. Fisher's test should only be used when both sets of marginals are fixed.

scipy.stats.boschloo_exact

scipy.stats.**boschloo_exact**(*table*, *alternative='two-sided'*, *n=32*)

Perform Boschloo's exact test on a 2x2 contingency table.

Parameters

table [array_like of ints] A 2x2 contingency table. Elements should be non-negative integers.

alternative [{'two-sided', 'less', 'greater'}, optional] Defines the null and alternative hypotheses. Default is 'two-sided'. Please see explanations in the Notes section below.

n [int, optional] Number of sampling points used in the construction of the sampling method. Note that this argument will automatically be converted to the next higher power of 2 since *scipy.stats.qmc.Sobol* is used to select sample points. Default is 32. Must be

positive. In most cases, 32 points is enough to reach good precision. More points comes at performance cost.

Returns

ber [BoschlooExactResult] A result object with the following attributes.

statistic [float] The statistic used in Boschloo's test; that is, the p-value from Fisher's exact test.

pvalue [float] P-value, the probability of obtaining a distribution at least as extreme as the one that was actually observed, assuming that the null hypothesis is true.

See also:

`chi2_contingency`

Chi-square test of independence of variables in a contingency table.

`fisher_exact`

Fisher exact test on a 2x2 contingency table.

`barnard_exact`

Barnard's exact test, which is a more powerful alternative than Fisher's exact test for 2x2 contingency tables.

Notes

Boschloo's test is an exact test used in the analysis of contingency tables. It examines the association of two categorical variables, and is a uniformly more powerful alternative to Fisher's exact test for 2x2 contingency tables.

Let's define X_0 a 2x2 matrix representing the observed sample, where each column stores the binomial experiment, as in the example below. Let's also define p_1, p_2 the theoretical binomial probabilities for x_{11} and x_{12}. When using Boschloo exact test, we can assert three different null hypotheses :

- $H_0 : p_1 \geq p_2$ versus $H_1 : p_1 < p_2$, with *alternative* = "less"
- $H_0 : p_1 \leq p_2$ versus $H_1 : p_1 > p_2$, with *alternative* = "greater"
- $H_0 : p_1 = p_2$ versus $H_1 : p_1 \neq p_2$, with *alternative* = "two-sided" (default one)

Boschloo's exact test uses the p-value of Fisher's exact test as a statistic, and Boschloo's p-value is the probability under the null hypothesis of observing such an extreme value of this statistic.

Boschloo's and Barnard's are both more powerful than Fisher's exact test.

New in version 1.7.0.

References

[1], [2], [3]

Examples

In the following example, we consider the article "Employee attitudes and job satisfaction" [3] which reports the results of a survey from 63 scientists and 117 college professors. Of the 63 scientists, 31 said they were very satisfied with their jobs, whereas 74 of the college professors were very satisfied with their work. Is this significant evidence that college professors are happier with their work than scientists? The following table summarizes the data mentioned above:

```
                 college professors   scientists
Very Satisfied   74                     31
Dissatisfied     43                     32
```

When working with statistical hypothesis testing, we usually use a threshold probability or significance level upon which we decide to reject the null hypothesis H_0. Suppose we choose the common significance level of 5%.

Our alternative hypothesis is that college professors are truly more satisfied with their work than scientists. Therefore, we expect p_1 the proportion of very satisfied college professors to be greater than p_2, the proportion of very satisfied scientists. We thus call *boschloo_exact* with the `alternative="greater"` option:

```
>>> import scipy.stats as stats
>>> res = stats.boschloo_exact([[74, 31], [43, 32]], alternative="greater
↪")
>>> res.statistic
0.0483...
>>> res.pvalue
0.0355...
```

Under the null hypothesis that scientists are happier in their work than college professors, the probability of obtaining test results at least as extreme as the observed data is approximately 3.55%. Since this p-value is less than our chosen significance level, we have evidence to reject H_0 in favor of the alternative hypothesis.

Plot-tests

ppcc_max(x[, brack, dist])	Calculate the shape parameter that maximizes the PPCC.
ppcc_plot(x, a, b[, dist, plot, N])	Calculate and optionally plot probability plot correlation coefficient.
probplot(x[, sparams, dist, fit, plot, rvalue])	Calculate quantiles for a probability plot, and optionally show the plot.
boxcox_normplot(x, la, lb[, plot, N])	Compute parameters for a Box-Cox normality plot, optionally show it.
yeojohnson_normplot(x, la, lb[, plot, N])	Compute parameters for a Yeo-Johnson normality plot, optionally show it.

scipy.stats.ppcc_max

scipy.stats.**ppcc_max**(*x*, *brack=(0.0, 1.0)*, *dist='tukeylambda'*)

Calculate the shape parameter that maximizes the PPCC.

The probability plot correlation coefficient (PPCC) plot can be used to determine the optimal shape parameter for a one-parameter family of distributions. ppcc_max returns the shape parameter that would maximize the probability plot correlation coefficient for the given data to a one-parameter family of distributions.

Parameters

x [array_like] Input array.

brack [tuple, optional] Triple (a,b,c) where (a<b<c). If bracket consists of two numbers (a, c) then they are assumed to be a starting interval for a downhill bracket search (see *scipy.optimize.brent*).

dist [str or stats.distributions instance, optional] Distribution or distribution function name. Objects that look enough like a stats.distributions instance (i.e. they have a `ppf` method) are also accepted. The default is `'tukeylambda'`.

Returns

shape_value
[float] The shape parameter at which the probability plot correlation coefficient reaches its max value.

See also:

ppcc_plot, **probplot**, **boxcox**

Notes

The brack keyword serves as a starting point which is useful in corner cases. One can use a plot to obtain a rough visual estimate of the location for the maximum to start the search near it.

References

[1], [2]

Examples

First we generate some random data from a Weibull distribution with shape parameter 2.5:

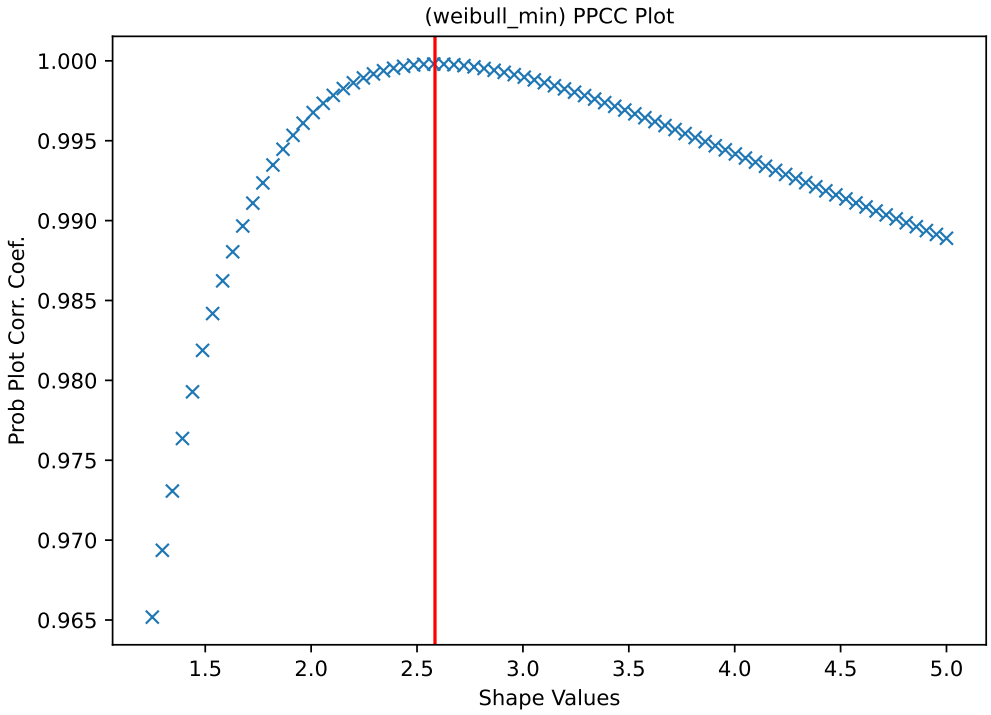
```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> c = 2.5
>>> x = stats.weibull_min.rvs(c, scale=4, size=2000, random_state=rng)
```

Generate the PPCC plot for this data with the Weibull distribution.

```
>>> fig, ax = plt.subplots(figsize=(8, 6))
>>> res = stats.ppcc_plot(x, c/2, 2*c, dist='weibull_min', plot=ax)
```

We calculate the value where the shape should reach its maximum and a red line is drawn there. The line should coincide with the highest point in the PPCC graph.

```
>>> cmax = stats.ppcc_max(x, brack=(c/2, 2*c), dist='weibull_min')
>>> ax.axvline(cmax, color='r')
>>> plt.show()
```


(weibull_min) PPCC Plot
Prob Plot Corr. Coef.
1.000
0.995
0.990
0.985
0.980
0.975
0.970
0.965
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
Shape Values

scipy.stats.ppcc_plot

scipy.stats.**ppcc_plot**(*x*, *a*, *b*, *dist='tukeylambda'*, *plot=None*, *N=80*)

Calculate and optionally plot probability plot correlation coefficient.

The probability plot correlation coefficient (PPCC) plot can be used to determine the optimal shape parameter for a one-parameter family of distributions. It cannot be used for distributions without shape parameters (like the normal distribution) or with multiple shape parameters.

By default a Tukey-Lambda distribution (*stats.tukeylambda*) is used. A Tukey-Lambda PPCC plot interpolates from long-tailed to short-tailed distributions via an approximately normal one, and is therefore particularly useful in practice.

Parameters

x	[array_like] Input array.
a, b	[scalar] Lower and upper bounds of the shape parameter to use.
dist	[str or stats.distributions instance, optional] Distribution or distribution function name. Objects that look enough like a stats.distributions instance (i.e. they have a `ppf` method) are also accepted. The default is `'tukeylambda'`.
plot	[object, optional] If given, plots PPCC against the shape parameter. *plot* is an object that has to have methods "plot" and "text". The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.
N	[int, optional] Number of points on the horizontal axis (equally distributed from *a* to *b*).

Returns

svals	[ndarray] The shape values for which *ppcc* was calculated.
ppcc	[ndarray] The calculated probability plot correlation coefficient values.

See also:

ppcc_max, **probplot**, **boxcox_normplot**, **tukeylambda**

References

J.J. Filliben, "The Probability Plot Correlation Coefficient Test for Normality", Technometrics, Vol. 17, pp. 111-117, 1975.

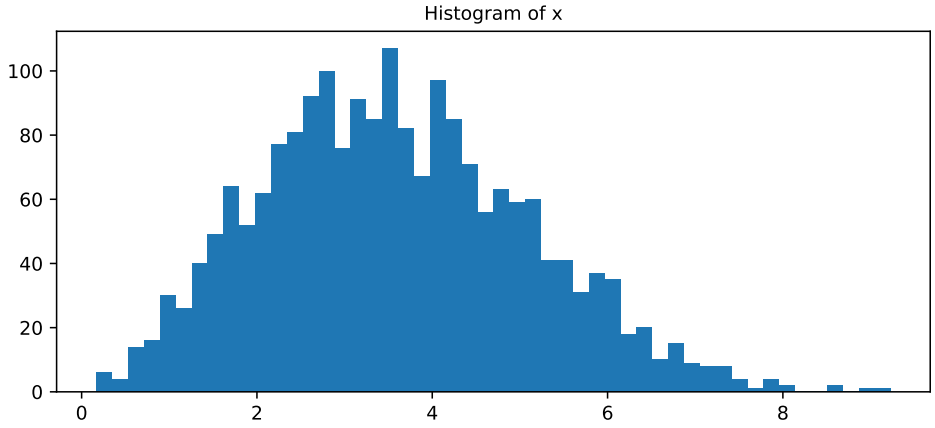
Examples

First we generate some random data from a Weibull distribution with shape parameter 2.5, and plot the histogram of the data:

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> rng = np.random.default_rng()
>>> c = 2.5
>>> x = stats.weibull_min.rvs(c, scale=4, size=2000, random_state=rng)
```

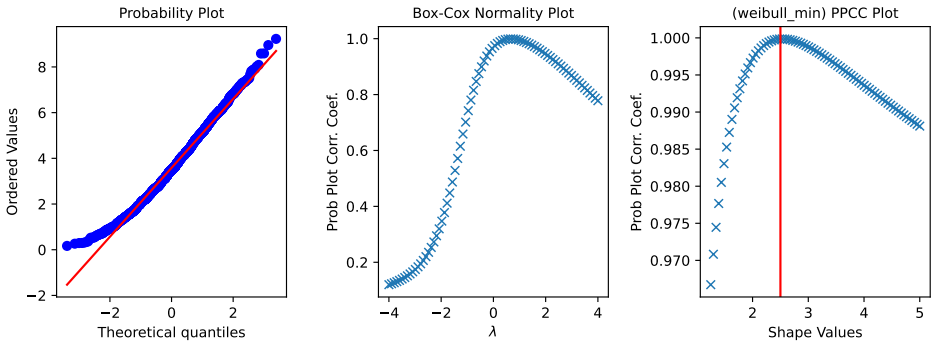
Take a look at the histogram of the data.

```
>>> fig1, ax = plt.subplots(figsize=(9, 4))
>>> ax.hist(x, bins=50)
>>> ax.set_title('Histogram of x')
>>> plt.show()
```



Now we explore this data with a PPCC plot as well as the related probability plot and Box-Cox normplot. A red line is drawn where we expect the PPCC value to be maximal (at the shape parameter `c` used above):

```
>>> fig2 = plt.figure(figsize=(12, 4))
>>> ax1 = fig2.add_subplot(1, 3, 1)
>>> ax2 = fig2.add_subplot(1, 3, 2)
>>> ax3 = fig2.add_subplot(1, 3, 3)
>>> res = stats.probplot(x, plot=ax1)
>>> res = stats.boxcox_normplot(x, -4, 4, plot=ax2)
>>> res = stats.ppcc_plot(x, c/2, 2*c, dist='weibull_min', plot=ax3)
>>> ax3.axvline(c, color='r')
>>> plt.show()
```



scipy.stats.probplot

scipy.stats.**probplot**(*x*, *sparams=()*, *dist='norm'*, *fit=True*, *plot=None*, *rvalue=False*)

Calculate quantiles for a probability plot, and optionally show the plot.

Generates a probability plot of sample data against the quantiles of a specified theoretical distribution (the normal distribution by default). *probplot* optionally calculates a best-fit line for the data and plots the results using Matplotlib or a given plot function.

Parameters

x [array_like] Sample/response data from which *probplot* creates the plot.

sparams [tuple, optional] Distribution-specific shape parameters (shape parameters plus location and scale).

dist [str or stats.distributions instance, optional] Distribution or distribution function name. The default is 'norm' for a normal probability plot. Objects that look enough like a stats.distributions instance (i.e. they have a `ppf` method) are also accepted.

fit [bool, optional] Fit a least-squares regression (best-fit) line to the sample data if True (default).

plot [object, optional] If given, plots the quantiles. If given and *fit* is True, also plots the least squares fit. *plot* is an object that has to have methods "plot" and "text". The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.

Returns

(osm, osr) [tuple of ndarrays] Tuple of theoretical quantiles (osm, or order statistic medians) and ordered responses (osr). *osr* is simply sorted input *x*. For details on how *osm* is calculated see the Notes section.

(slope, intercept, r) [tuple of floats, optional] Tuple containing the result of the least-squares fit, if that is performed by *probplot*. *r* is the square root of the coefficient of determination. If `fit=False` and `plot=None`, this tuple is not returned.

Notes

Even if *plot* is given, the figure is not shown or saved by *probplot*; `plt.show()` or `plt.savefig('figname.png')` should be used after calling *probplot*.

probplot generates a probability plot, which should not be confused with a Q-Q or a P-P plot. Statsmodels has more extensive functionality of this type, see `statsmodels.api.ProbPlot`.

The formula used for the theoretical quantiles (horizontal axis of the probability plot) is Filliben's estimate:

```
quantiles = dist.ppf(val), for

        0.5**(1/n),                    for i = n
  val = (i - 0.3175) / (n + 0.365),    for i = 2, ..., n-1
        1 - 0.5**(1/n),                for i = 1
```

where `i` indicates the i-th ordered value and `n` is the total number of values.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
>>> nsample = 100
>>> rng = np.random.default_rng()
```

A t distribution with small degrees of freedom:

```
>>> ax1 = plt.subplot(221)
>>> x = stats.t.rvs(3, size=nsample, random_state=rng)
>>> res = stats.probplot(x, plot=plt)
```

A t distribution with larger degrees of freedom:

```
>>> ax2 = plt.subplot(222)
>>> x = stats.t.rvs(25, size=nsample, random_state=rng)
>>> res = stats.probplot(x, plot=plt)
```

A mixture of two normal distributions with broadcasting:

```
>>> ax3 = plt.subplot(223)
>>> x = stats.norm.rvs(loc=[0,5], scale=[1,1.5],
...                    size=(nsample//2,2), random_state=rng).ravel()
>>> res = stats.probplot(x, plot=plt)
```

A standard normal distribution:

```
>>> ax4 = plt.subplot(224)
>>> x = stats.norm.rvs(loc=0, scale=1, size=nsample, random_state=rng)
>>> res = stats.probplot(x, plot=plt)
```

Produce a new figure with a loggamma distribution, using the `dist` and `sparams` keywords:

```
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> x = stats.loggamma.rvs(c=2.5, size=500, random_state=rng)
>>> res = stats.probplot(x, dist=stats.loggamma, sparams=(2.5,), plot=ax)
>>> ax.set_title("Probplot for loggamma dist with shape parameter 2.5")
```

Show the results with Matplotlib:

```
>>> plt.show()
```

scipy.stats.boxcox_normplot

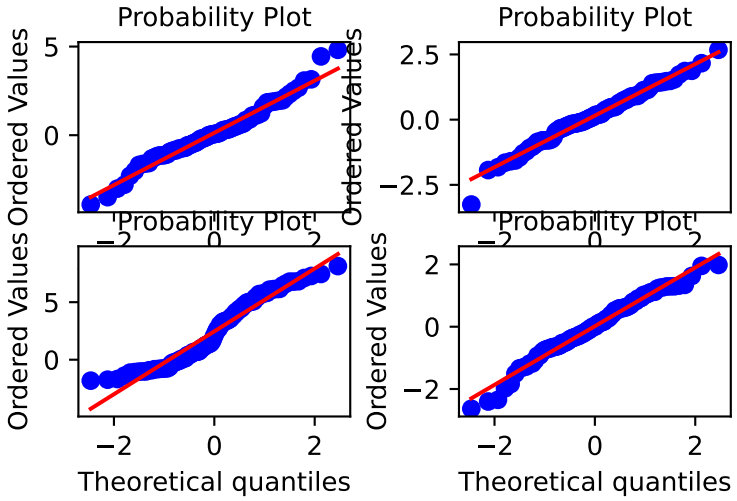
scipy.stats.**boxcox_normplot**(*x*, *la*, *lb*, *plot=None*, *N=80*)

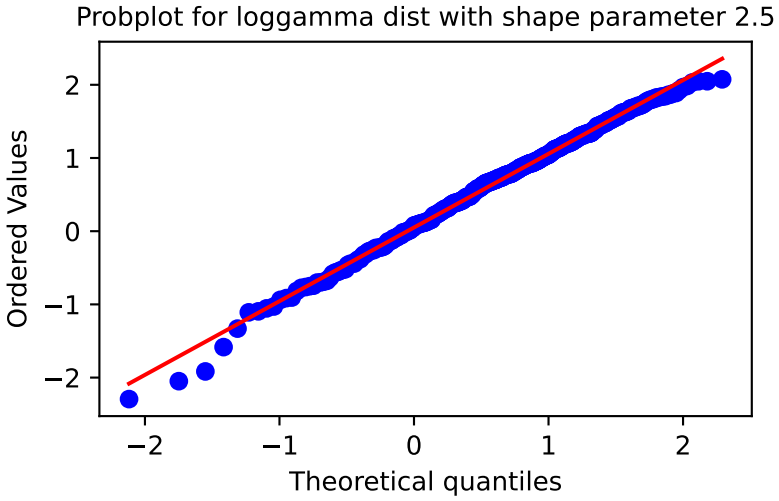
Compute parameters for a Box-Cox normality plot, optionally show it.

A Box-Cox normality plot shows graphically what the best transformation parameter is to use in *boxcox* to obtain a distribution that is close to normal.

Parameters

x [array_like] Input array.


Probability Plot
Probability Plot
Probability Plot
Probability Plot
Ordered Values
Ordered Values
Ordered Values
Ordered Values
Theoretical quantiles
Theoretical quantiles


Probplot for loggamma dist with shape parameter 2.5
Ordered Values
Theoretical quantiles

la, lb [scalar] The lower and upper bounds for the `lmbda` values to pass to *boxcox* for Box-Cox transformations. These are also the limits of the horizontal axis of the plot if that is generated.

plot [object, optional] If given, plots the quantiles and least squares fit. *plot* is an object that has to have methods "plot" and "text". The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.

N [int, optional] Number of points on the horizontal axis (equally distributed from *la* to *lb*).

Returns

lmbdas [ndarray] The `lmbda` values for which a Box-Cox transform was done.

ppcc [ndarray] Probability Plot Correlelation Coefficient, as obtained from *probplot* when fitting the Box-Cox transformed input *x* against a normal distribution.

See also:

probplot, **boxcox**, **boxcox_normmax**, **boxcox_llf**, **ppcc_max**

Notes

Even if *plot* is given, the figure is not shown or saved by *boxcox_normplot*; `plt.show()` or `plt.savefig('figname.png')` should be used after calling *probplot*.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

Generate some non-normally distributed data, and create a Box-Cox plot:

```
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> prob = stats.boxcox_normplot(x, -20, 20, plot=ax)
```

Determine and plot the optimal `lmbda` to transform `x` and plot it in the same plot:

```
>>> _, maxlog = stats.boxcox(x)
>>> ax.axvline(maxlog, color='r')
```

```
>>> plt.show()
```

scipy.stats.yeojohnson_normplot

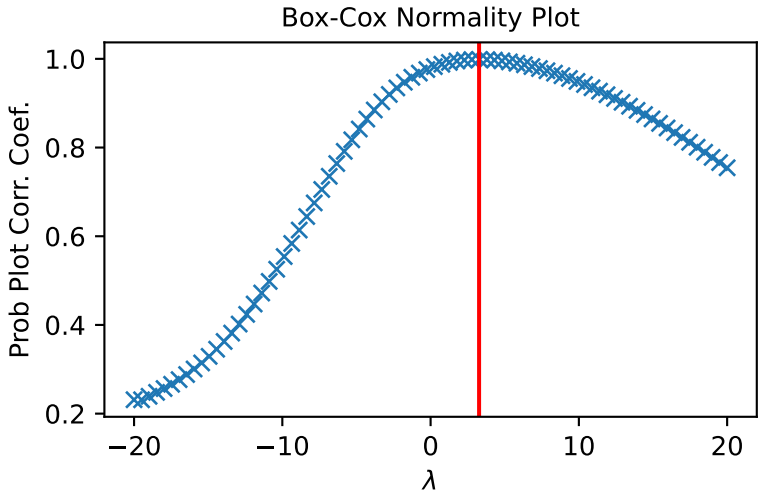
`scipy.stats.`**`yeojohnson_normplot`**(*x*, *la*, *lb*, *plot=None*, *N=80*)

Compute parameters for a Yeo-Johnson normality plot, optionally show it.

A Yeo-Johnson normality plot shows graphically what the best transformation parameter is to use in *yeojohnson* to obtain a distribution that is close to normal.

Parameters

x [array_like] Input array.



la, lb [scalar] The lower and upper bounds for the `lmbda` values to pass to *`yeojohnson`* for Yeo-Johnson transformations. These are also the limits of the horizontal axis of the plot if that is generated.

plot [object, optional] If given, plots the quantiles and least squares fit. *plot* is an object that has to have methods "plot" and "text". The `matplotlib.pyplot` module or a Matplotlib Axes object can be used, or a custom object with the same methods. Default is None, which means that no plot is created.

N [int, optional] Number of points on the horizontal axis (equally distributed from *la* to *lb*).

Returns

lmbdas [ndarray] The `lmbda` values for which a Yeo-Johnson transform was done.

ppcc [ndarray] Probability Plot Correlelation Coefficient, as obtained from *`probplot`* when fitting the Box-Cox transformed input *x* against a normal distribution.

See also:

`probplot`, **`yeojohnson`**, **`yeojohnson_normmax`**, **`yeojohnson_llf`**, **`ppcc_max`**

Notes

Even if *plot* is given, the figure is not shown or saved by *boxcox_normplot*; `plt.show()` or `plt.savefig('figname.png')` should be used after calling *probplot*.

New in version 1.2.0.

Examples

```
>>> from scipy import stats
>>> import matplotlib.pyplot as plt
```

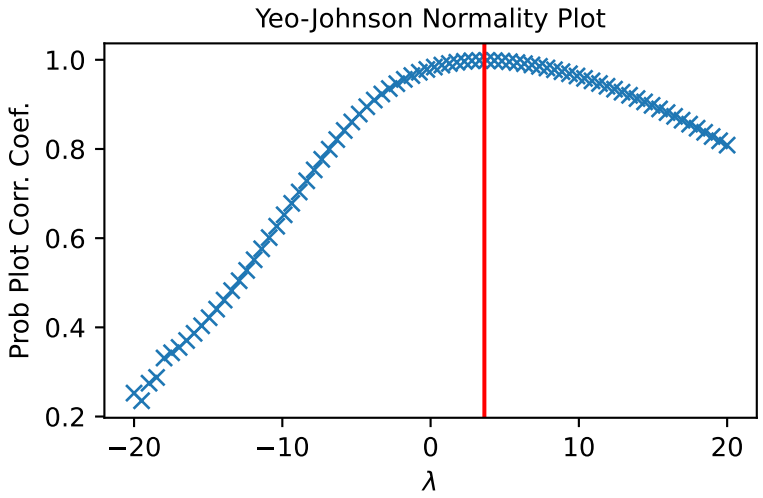
Generate some non-normally distributed data, and create a Yeo-Johnson plot:

```
>>> x = stats.loggamma.rvs(5, size=500) + 5
>>> fig = plt.figure()
>>> ax = fig.add_subplot(111)
>>> prob = stats.yeojohnson_normplot(x, -20, 20, plot=ax)
```

Determine and plot the optimal `lmbda` to transform `x` and plot it in the same plot:

```
>>> _, maxlog = stats.yeojohnson(x)
>>> ax.axvline(maxlog, color='r')
```

```
>>> plt.show()
```



Univariate and multivariate kernel density estimation

gaussian_kde(dataset[, bw_method, weights])	Representation of a kernel-density estimate using Gaussian kernels.

scipy.stats.gaussian_kde

class scipy.stats.**gaussian_kde**(*dataset*, *bw_method=None*, *weights=None*)

Representation of a kernel-density estimate using Gaussian kernels.

Kernel density estimation is a way to estimate the probability density function (PDF) of a random variable in a non-parametric way. *gaussian_kde* works for both uni-variate and multi-variate data. It includes automatic bandwidth determination. The estimation works best for a unimodal distribution; bimodal or multi-modal distributions tend to be oversmoothed.

Parameters

dataset [array_like] Datapoints to estimate from. In case of univariate data this is a 1-D array, otherwise a 2-D array with shape (# of dims, # of data).

bw_method

[str, scalar or callable, optional] The method used to calculate the estimator bandwidth. This can be 'scott', 'silverman', a scalar constant or a callable. If a scalar, this will be used directly as *kde.factor*. If a callable, it should take a *gaussian_kde* instance as only parameter and return a scalar. If None (default), 'scott' is used. See Notes for more details.

weights [array_like, optional] weights of datapoints. This must be the same shape as dataset. If None (default), the samples are assumed to be equally weighted

Notes

Bandwidth selection strongly influences the estimate obtained from the KDE (much more so than the actual shape of the kernel). Bandwidth selection can be done by a "rule of thumb", by cross-validation, by "plug-in methods" or by other means; see [3], [4] for reviews. *gaussian_kde* uses a rule of thumb, the default is Scott's Rule.

Scott's Rule [1], implemented as `scotts_factor`, is:

```
n**(-1./(d+4)),
```

with `n` the number of data points and `d` the number of dimensions. In the case of unequally weighted points, `scotts_factor` becomes:

```
neff**(-1./(d+4)),
```

with `neff` the effective number of datapoints. Silverman's Rule [2], implemented as `silverman_factor`, is:

```
(n * (d + 2) / 4.)**(-1. / (d + 4)).
```

or in the case of unequally weighted points:

```
(neff * (d + 2) / 4.)**(-1. / (d + 4)).
```

Good general descriptions of kernel density estimation can be found in [1] and [2], the mathematics for this multi-dimensional implementation can be found in [1].

With a set of weighted samples, the effective number of datapoints `neff` is defined by:

```
neff = sum(weights)^2 / sum(weights^2)
```

as detailed in [5].

References

[1], [2], [3], [4], [5]

Examples

Generate some random two-dimensional data:

```
>>> from scipy import stats
>>> def measure(n):
...     "Measurement model, return two coupled measurements."
...     m1 = np.random.normal(size=n)
...     m2 = np.random.normal(scale=0.5, size=n)
...     return m1+m2, m1-m2
```

```
>>> m1, m2 = measure(2000)
>>> xmin = m1.min()
>>> xmax = m1.max()
>>> ymin = m2.min()
>>> ymax = m2.max()
```

Perform a kernel density estimate on the data:

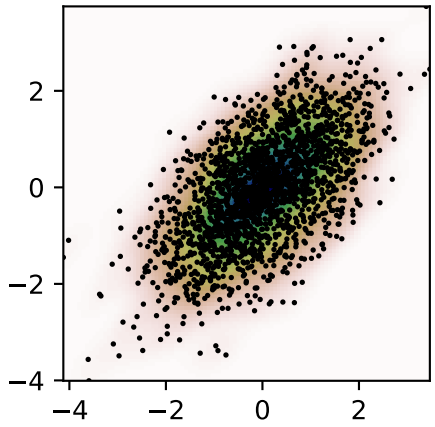
```
>>> X, Y = np.mgrid[xmin:xmax:100j, ymin:ymax:100j]
>>> positions = np.vstack([X.ravel(), Y.ravel()])
>>> values = np.vstack([m1, m2])
>>> kernel = stats.gaussian_kde(values)
>>> Z = np.reshape(kernel(positions).T, X.shape)
```

Plot the results:

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.imshow(np.rot90(Z), cmap=plt.cm.gist_earth_r,
...           extent=[xmin, xmax, ymin, ymax])
>>> ax.plot(m1, m2, 'k.', markersize=2)
>>> ax.set_xlim([xmin, xmax])
>>> ax.set_ylim([ymin, ymax])
>>> plt.show()
```

Attributes

dataset	[ndarray] The dataset with which *gaussian_kde* was initialized.
d	[int] Number of dimensions.
n	[int] Number of datapoints.
neff	[int] Effective number of datapoints. New in version 1.2.0.



factor [float] The bandwidth factor, obtained from *kde.covariance_factor*, with which the covariance matrix is multiplied.
covariance [ndarray] The covariance matrix of *dataset*, scaled by the calculated bandwidth (*kde.factor*).
inv_cov [ndarray] The inverse of *covariance*.

Methods

evaluate(points)	Evaluate the estimated pdf on a set of points.
__call__(points)	Evaluate the estimated pdf on a set of points.
integrate_gaussian(mean, cov)	Multiply estimated density by a multivariate Gaussian and integrate over the whole space.
integrate_box_1d(low, high)	Computes the integral of a 1D pdf between two bounds.
integrate_box(low_bounds, high_bounds[, maxpts])	Computes the integral of a pdf over a rectangular interval.
integrate_kde(other)	Computes the integral of the product of this kernel density estimate with another.
pdf(x)	Evaluate the estimated pdf on a provided set of points.
logpdf(x)	Evaluate the log of the estimated pdf on a provided set of points.
resample([size, seed])	Randomly sample a dataset from the estimated pdf.
set_bandwidth([bw_method])	Compute the estimator bandwidth with given method.
covariance_factor()	Computes the coefficient (*kde.factor*) that multiplies the data covariance matrix to obtain the kernel covariance matrix.

scipy.stats.gaussian_kde.evaluate

gaussian_kde.**evaluate**(*points*)
Evaluate the estimated pdf on a set of points.

Parameters

points [(# of dimensions, # of points)-array] Alternatively, a (# of dimensions,) vector can be passed in and treated as a single point.

Returns

values [(# of points,)-array] The values at each point.

scipy.stats.gaussian_kde.__call__

gaussian_kde.**__call__**(*points*)

Evaluate the estimated pdf on a set of points.

Parameters

points [(# of dimensions, # of points)-array] Alternatively, a (# of dimensions,) vector can be passed in and treated as a single point.

Returns

values [(# of points,)-array] The values at each point.

Raises

ValueError [if the dimensionality of the input points is different than] the dimensionality of the KDE.

scipy.stats.gaussian_kde.integrate_gaussian

gaussian_kde.**integrate_gaussian**(*mean*, *cov*)

Multiply estimated density by a multivariate Gaussian and integrate over the whole space.

Parameters

mean [aray_like] A 1-D array, specifying the mean of the Gaussian.
cov [array_like] A 2-D array, specifying the covariance matrix of the Gaussian.

Returns

result [scalar] The value of the integral.

Raises

ValueError If the mean or covariance of the input Gaussian differs from the KDE's dimensionality.

scipy.stats.gaussian_kde.integrate_box_1d

gaussian_kde.**integrate_box_1d**(*low*, *high*)

Computes the integral of a 1D pdf between two bounds.

Parameters

low [scalar] Lower bound of integration.
high [scalar] Upper bound of integration.

Returns

value [scalar] The result of the integral.

Raises

ValueError If the KDE is over more than one dimension.

scipy.stats.gaussian_kde.integrate_box

gaussian_kde.**integrate_box**(*low_bounds*, *high_bounds*, *maxpts=None*)

Computes the integral of a pdf over a rectangular interval.

Parameters

low_bounds
: [array_like] A 1-D array containing the lower bounds of integration.

high_bounds
: [array_like] A 1-D array containing the upper bounds of integration.

maxpts : [int, optional] The maximum number of points to use for integration.

Returns

value : [scalar] The result of the integral.

scipy.stats.gaussian_kde.integrate_kde

gaussian_kde.**integrate_kde**(*other*)

Computes the integral of the product of this kernel density estimate with another.

Parameters

other : [gaussian_kde instance] The other kde.

Returns

value : [scalar] The result of the integral.

Raises

ValueError
: If the KDEs have different dimensionality.

scipy.stats.gaussian_kde.pdf

gaussian_kde.**pdf**(*x*)

Evaluate the estimated pdf on a provided set of points.

Notes

This is an alias for *gaussian_kde.evaluate*. See the `evaluate` docstring for more details.

scipy.stats.gaussian_kde.logpdf

gaussian_kde.**logpdf**(*x*)

Evaluate the log of the estimated pdf on a provided set of points.

scipy.stats.gaussian_kde.resample

gaussian_kde.**resample**(*size=None*, *seed=None*)

Randomly sample a dataset from the estimated pdf.

Parameters

size [int, optional] The number of samples to draw. If not provided, then the size is the same as the effective number of samples in the underlying dataset.

seed [{None, int, numpy.random.Generator,] numpy.random.RandomState}, optional
If *seed* is None (or *np.random*), the numpy.random.RandomState singleton is used. If *seed* is an int, a new RandomState instance is used, seeded with *seed*. If *seed* is already a Generator or RandomState instance then that instance is used.

Returns

resample [(self.d, *size*) ndarray] The sampled dataset.

scipy.stats.gaussian_kde.set_bandwidth

gaussian_kde.**set_bandwidth**(*bw_method=None*)

Compute the estimator bandwidth with given method.

The new bandwidth calculated after a call to *set_bandwidth* is used for subsequent evaluations of the estimated density.

Parameters

bw_method
[str, scalar or callable, optional] The method used to calculate the estimator bandwidth. This can be 'scott', 'silverman', a scalar constant or a callable. If a scalar, this will be used directly as *kde.factor*. If a callable, it should take a *gaussian_kde* instance as only parameter and return a scalar. If None (default), nothing happens; the current *kde.covariance_factor* method is kept.

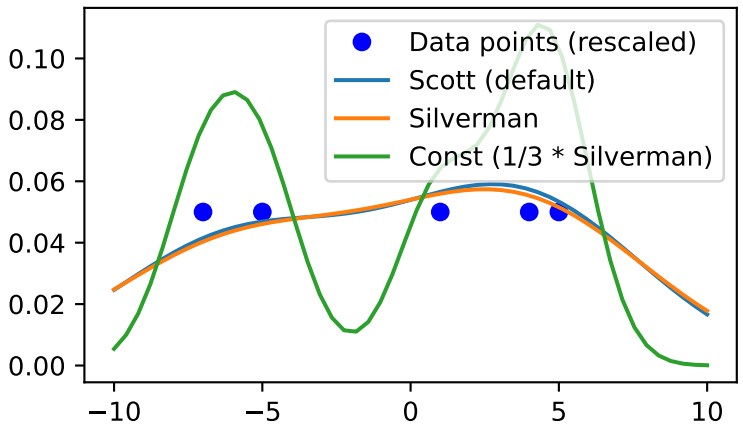
Notes

New in version 0.11.

Examples

```
>>> import scipy.stats as stats
>>> x1 = np.array([-7, -5, 1, 4, 5.])
>>> kde = stats.gaussian_kde(x1)
>>> xs = np.linspace(-10, 10, num=50)
>>> y1 = kde(xs)
>>> kde.set_bandwidth(bw_method='silverman')
>>> y2 = kde(xs)
>>> kde.set_bandwidth(bw_method=kde.factor / 3.)
>>> y3 = kde(xs)
```

```
>>> import matplotlib.pyplot as plt
>>> fig, ax = plt.subplots()
>>> ax.plot(x1, np.full(x1.shape, 1 / (4. * x1.size)), 'bo',
...         label='Data points (rescaled)')
>>> ax.plot(xs, y1, label='Scott (default)')
>>> ax.plot(xs, y2, label='Silverman')
>>> ax.plot(xs, y3, label='Const (1/3 * Silverman)')
>>> ax.legend()
>>> plt.show()
```



scipy.stats.gaussian_kde.covariance_factor

gaussian_kde.**covariance_factor**()

Computes the coefficient (*kde.factor*) that multiplies the data covariance matrix to obtain the kernel covariance matrix. The default is `scotts_factor`. A subclass can overwrite this method to provide a different method, or set it through a call to *kde.set_bandwidth*.

Warnings used in `scipy.stats`

F_onewayConstantInputWarning([msg])	Warning generated by *f_oneway* when an input is constant, e.g.
F_onewayBadInputSizesWarning	Warning generated by *f_oneway* when an input has length 0, or if all the inputs have length 1.
PearsonRConstantInputWarning([msg])	Warning generated by *pearsonr* when an input is constant.
PearsonRNearConstantInputWarning([msg])	Warning generated by *pearsonr* when an input is nearly constant.
SpearmanRConstantInputWarning([msg])	Warning generated by *spearmanr* when an input is constant.

scipy.stats.F_onewayConstantInputWarning

exception scipy.stats.**F_onewayConstantInputWarning**(*msg=None*)
Warning generated by *f_oneway* when an input is constant, e.g. each of the samples provided is a constant array.

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.stats.F_onewayBadInputSizesWarning

exception scipy.stats.**F_onewayBadInputSizesWarning**
Warning generated by *f_oneway* when an input has length 0, or if all the inputs have length 1.

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.stats.PearsonRConstantInputWarning

exception scipy.stats.**PearsonRConstantInputWarning**(*msg=None*)
Warning generated by *pearsonr* when an input is constant.

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.stats.PearsonRNearConstantInputWarning

exception scipy.stats.**PearsonRNearConstantInputWarning**(*msg=None*)
Warning generated by *pearsonr* when an input is nearly constant.

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

scipy.stats.SpearmanRConstantInputWarning

exception scipy.stats.**SpearmanRConstantInputWarning**(*msg=None*)
Warning generated by *spearmanr* when an input is constant.

with_traceback()
Exception.with_traceback(tb) – set self.__traceback__ to tb and return self.

3.3.30 Result classes

RelativeRiskResult(relative_risk, …)	Result of *scipy.stats.contingency.relative_risk*.
BinomTestResult(k, n, alternative, pvalue, …)	Result of *scipy.stats.binomtest*.

scipy.stats._result_classes.RelativeRiskResult

class scipy.stats._result_classes.**RelativeRiskResult**(*relative_risk*, *exposed_cases*, *exposed_total*, *control_cases*, *control_total*)

Result of *scipy.stats.contingency.relative_risk*.

Attributes

relative_risk
: [float] This is:

```
(exposed_cases/exposed_total) / (control_cases/control_
↪total)
```

exposed_cases
: [int] The number of "cases" (i.e. occurrence of disease or other event of interest) among the sample of "exposed" individuals.

exposed_total
: [int] The total number of "exposed" individuals in the sample.

control_cases
: [int] The number of "cases" among the sample of "control" or non-exposed individuals.

control_total
: [int] The total number of "control" individuals in the sample.

Methods

confidence_interval :	Compute the confidence interval for the relative risk estimate.

scipy.stats._result_classes.BinomTestResult

class scipy.stats._result_classes.**BinomTestResult**(*k*, *n*, *alternative*, *pvalue*, *proportion_estimate*)

Result of *scipy.stats.binomtest*.

Attributes

k [int] The number of successes (copied from *binomtest* input).

n [int] The number of trials (copied from *binomtest* input).

alternative
: [str] Indicates the alternative hypothesis specified in the input to *binomtest*. It will be one of `'two-sided'`, `'greater'`, or `'less'`.

pvalue [float] The p-value of the hypothesis test.

proportion_estimate
: [float] The estimate of the proportion of successes.

Methods

proportion_ci :	Compute the confidence interval for the estimate of the proportion.

3.3.31 Low-level callback functions

Some functions in SciPy take as arguments callback functions, which can either be python callables or low-level compiled functions. Using compiled callback functions can improve performance somewhat by avoiding wrapping data in Python objects.

Such low-level functions in SciPy are wrapped in `LowLevelCallable` objects, which can be constructed from function pointers obtained from ctypes, cffi, Cython, or contained in Python *PyCapsule* objects.

`LowLevelCallable`(function[, user_data, …])	Low-level callback function.

scipy.LowLevelCallable

class scipy.**LowLevelCallable**(*function*, *user_data=None*, *signature=None*)

Low-level callback function.

Parameters

function [{PyCapsule, ctypes function pointer, cffi function pointer}] Low-level callback function.

user_data [{PyCapsule, ctypes void pointer, cffi void pointer}] User data to pass on to the callback function.

signature [str, optional] Signature of the function. If omitted, determined from *function*, if possible.

Notes

The argument `function` can be one of:

- PyCapsule, whose name contains the C function signature
- ctypes function pointer
- cffi function pointer

The signature of the low-level callback must match one of those expected by the routine it is passed to.

If constructing low-level functions from a PyCapsule, the name of the capsule must be the corresponding signature, in the format:

```
return_type (arg1_type, arg2_type, ...)
```

For example:

```
"void (double)"
"double (double, int *, void *)"
```

The context of a PyCapsule passed in as `function` is used as `user_data`, if an explicit value for `user_data` was not given.

Attributes

function Callback function given.

user_data User data given.
signature Signature of the function.

Methods

from_cython(module, name[, user_data, signature])	Create a low-level callback function from an exported Cython function.

scipy.LowLevelCallable.from_cython

classmethod LowLevelCallable.**from_cython**(*module*, *name*, *user_data=None*, *signature=None*)

Create a low-level callback function from an exported Cython function.

Parameters

module [module] Cython module where the exported function resides
name [str] Name of the exported function
user_data [{PyCapsule, ctypes void pointer, cffi void pointer}, optional] User data to pass on to the callback function.
signature [str, optional] Signature of the function. If omitted, determined from *function*.

See also:

Functions accepting low-level callables:

scipy.integrate.quad, *scipy.ndimage.generic_filter*, *scipy.ndimage.generic_filter1d*, *scipy.ndimage.geometric_transform*

Usage examples:

Extending scipy.ndimage in C, *Faster integration using low-level callback functions*

3.4 SciPy structure

All SciPy modules should follow the following conventions. In the following, a *SciPy module* is defined as a Python package, say `yyy`, that is located in the scipy/ directory.

- Ideally, each SciPy module should be as self-contained as possible. That is, it should have minimal dependencies on other packages or modules. Even dependencies on other SciPy modules should be kept to a minimum. A dependency on NumPy is of course assumed.
- Directory `yyy/` contains:
  - A file `setup.py` that defines `configuration(parent_package='',top_path=None)` function for `numpy.distutils`.
  - A directory `tests/` that contains files `test_<name>.py` corresponding to modules `yyy/<name>{.py,.so,/}`.
- Private modules should be prefixed with an underscore _, for instance `yyy/_somemodule.py`.
- User-visible functions should have good documentation following the NumPy documentation style.
- The `__init__.py` of the module should contain the main reference documentation in its docstring. This is connected to the Sphinx documentation under `doc/` via Sphinx's automodule directive.

The reference documentation should first give a categorized list of the contents of the module using `autosummary::` directives, and after that explain points essential for understanding the use of the module.

Tutorial-style documentation with extensive examples should be separate and put under `doc/source/tutorial/`.

See the existing SciPy submodules for guidance.

For further details on NumPy distutils, see NumPy Distutils - User's Guide.

CHAPTER

FOUR

DEVELOPER DOCUMENTATION

Bellow you will find general information about contributing. For an overview of where help or new features are desired or planned, see the roadmap. And for a more detailed look at how the SciPy project works, see the organization section.

4.1 SciPy Code of Conduct

4.1.1 Introduction

This code of conduct applies to all spaces managed by the SciPy project, including all public and private mailing lists, issue trackers, wikis, blogs, Twitter, and any other communication channel used by our community. The SciPy project does not organize in-person events, however, events related to our community should have a code of conduct similar in spirit to this one.

This code of conduct should be honored by everyone who participates in the SciPy community formally or informally, or claims any affiliation with the project, in any project-related activities, and, especially, when representing the project, in any role.

This code is neither exhaustive nor complete. It serves to distill our common understanding of a collaborative, shared environment and goals. Please try to follow this code in spirit as much as in letter, to create a friendly and productive environment that enriches the surrounding community.

4.1.2 Specific guidelines

We strive to:

1. Be open. We invite anyone to participate in our community. We prefer to use public methods of communication for project-related messages, unless discussing something sensitive. This applies to messages for help or project-related support, too; not only is a public-support request much more likely to result in an answer to a question, it also ensures that any inadvertent mistakes in answering are more easily detected and corrected.
2. Be empathetic, welcoming, friendly, and patient. We work together to resolve conflict, and assume good intentions. We may all experience some frustration from time to time, but we do not allow frustration to turn into a personal attack. A community where people feel uncomfortable or threatened is not a productive one.
3. Be collaborative. Our work will be used by other people, and in turn we will depend on the work of others. When we make something for the benefit of the project, we are willing to explain to others how it works, so that they can build on the work to make it even better. Any decision we make will affect users and colleagues, and we take those consequences seriously when making decisions.
4. Be inquisitive. Nobody knows everything! Asking questions early avoids many problems later, so we encourage questions, although we may direct them to the appropriate forum. We will try hard to be responsive and helpful.

5. Be careful in the words that we choose. We are careful and respectful in our communication and we take responsibility for our own speech. Be kind to others. Do not insult or put down other participants. We will not accept harassment or other exclusionary behavior, such as:

- Violent threats or language directed against another person.
- Sexist, racist, or otherwise discriminatory jokes and language.
- Posting sexually explicit or violent material.
- Posting (or threatening to post) other people's personally identifying information ("doxing").
- Sharing private content, such as emails sent privately or non-publicly, or unlogged forums, such as IRC channel history, without the sender's consent.
- Personal insults, especially those using racist or sexist terms.
- Unwelcome sexual attention.
- Excessive profanity. Please avoid swearwords; people differ greatly in their sensitivity to swearing.
- Repeated harassment of others. In general, if someone asks you to stop, then stop.
- Advocating for, or encouraging, any of the above behavior.

4.1.3 Diversity statement

The SciPy project welcomes and encourages participation by everyone. We are committed to being a community that everyone enjoys being part of. Although we may not always be able to accommodate each individual's preferences, we try our best to treat everyone kindly.

No matter how you identify yourself or how others perceive you: we welcome you. Though no list can hope to be comprehensive, we explicitly honor diversity in: age, culture, ethnicity, genotype, gender identity or expression, language, national origin, neurotype, phenotype, political beliefs, profession, race, religion, sexual orientation, socioeconomic status, subculture and technical ability, to the extent that these do not conflict with this code of conduct.

Though we welcome people fluent in all languages, SciPy development is conducted in English.

Standards for behavior in the SciPy community are detailed in the Code of Conduct above. Participants in our community should uphold these standards in all their interactions and help others to do so as well (see next section).

4.1.4 Reporting guidelines

We know that it is painfully common for internet communication to start at or devolve into obvious and flagrant abuse. We also recognize that sometimes people may have a bad day, or be unaware of some of the guidelines in this Code of Conduct. Please keep this in mind when deciding on how to respond to a breach of this Code.

For clearly intentional breaches, report those to the Code of Conduct committee (see below). For possibly unintentional breaches, you may reply to the person and point out this Code of Conduct (either in public or in private, whatever is most appropriate). If you would prefer not to do that, please feel free to report to the Code of Conduct committee directly, or ask the committee for advice, in confidence.

You can report issues to the SciPy Code of Conduct Committee, at scipy-conduct@googlegroups.com. Currently, the committee consists of:

- Stefan van der Walt
- Nathaniel J. Smith
- Ralf Gommers

If your report involves any members of the committee, or if they feel they have a conflict of interest in handling it, then they will recuse themselves from considering your report. Alternatively, if, for any reason, you feel uncomfortable making a report to the committee, then you can also contact:

- Chair of the SciPy Steering Committee: Ralf Gommers, or
- Senior NumFOCUS staff: conduct@numfocus.org

4.1.5 Incident reporting resolution & Code of Conduct enforcement

This section summarizes the most important points, more details can be found in CoC_reporting_manual.

We will investigate and respond to all complaints. The SciPy Code of Conduct Committee and the SciPy Steering Committee (if involved) will protect the identity of the reporter, and treat the content of complaints as confidential (unless the reporter agrees otherwise).

In case of severe and obvious breaches, e.g., personal threat or violent, sexist or racist language, we will immediately disconnect the originator from SciPy communication channels; please see the manual for details.

In cases not involving clear severe and obvious breaches of this code of conduct, the process for acting on any received code of conduct violation report will be:

1. acknowledgement that the report has been received
2. reasonable discussion/feedback
3. mediation (if feedback didn't help, and only if both reporter and reportee agree to this)
4. enforcement via transparent decision (see CoC_resolutions) by the Code of Conduct Committee

The committee will respond to any report as soon as possible, and at most within 72 hours.

4.1.6 Endnotes

We are thankful to the groups behind the following documents, from which we drew content and inspiration:

- The Apache Foundation Code of Conduct
- The Contributor Covenant
- Jupyter Code of Conduct
- Open Source Guides - Code of Conduct

4.2 Ways to Contribute

This document aims to give an overview of the ways to contribute to SciPy. It tries to answer commonly asked questions and provide some insight into how the community process works in practice. Readers who are familiar with the SciPy community and are experienced Python coders may want to jump straight to the *SciPy contributor guide*.

There are a lot of ways you can contribute:

- Contributing new code
- Fixing bugs, improving documentation, and other maintenance work
- Reviewing open pull requests
- Triaging issues

- Working on the scipy.org website
- Answering questions and participating on the scipy-dev and scipy-user mailing lists.

4.2.1 Contributing new code

If you have been working with the scientific Python toolstack for a while, you probably have some code lying around of which you think "this could be useful for others too". Perhaps it's a good idea then to contribute it to SciPy or another open source project. The first question to ask is then, where does this code belong? That question is hard to answer here, so we start with a more specific one: *what code is suitable for putting into SciPy?* Almost all of the new code added to SciPy has in common that it's potentially useful in multiple scientific domains and it fits in the scope of existing SciPy subpackages (see *Deciding on new features*). In principle new subpackages can be added too, but this is far less common. For code that is specific to a single application, there may be an existing project that can use the code. Some SciKits (scikit-learn, scikit-image, statsmodels, etc.) are good examples here; they have a narrower focus and because of that more domain-specific code than SciPy.

Now if you have code that you would like to see included in SciPy, how do you go about it? After checking that your code can be distributed in SciPy under a compatible license (see *License Considerations*), the first step is to discuss on the scipy-dev mailing list. All new features, as well as changes to existing code, are discussed and decided on there. You can, and probably should, already start this discussion before your code is finished. Remember that in order to be added to SciPy your code will need to be reviewed by someone else, so try to find someone willing to review your work while you're at it.

Assuming the outcome of the discussion on the mailing list is positive and you have a function or piece of code that does what you need it to do, what next? Before code is added to SciPy, it at least has to have good documentation, unit tests, benchmarks, and correct code style.

1. ***Unit tests***

   In principle you should aim to create unit tests that exercise all the code that you are adding. This gives some degree of confidence that your code runs correctly, also on Python versions and hardware or OSes that you don't have available yourself. An extensive description of how to write unit tests is given in Testing Guidelines, and *Running SciPy Tests Locally* documents how to run them.

2. ***Benchmarks***

   Unit tests check for correct functionality; benchmarks measure code performance. Not all existing SciPy code has benchmarks, but it should: as SciPy grows it is increasingly important to monitor execution times in order to catch unexpected regressions. More information about writing and running benchmarks is available in *Benchmarking SciPy with airspeed velocity*.

3. ***Documentation***

   Clear and complete documentation is essential in order for users to be able to find and understand the code. Documentation for individual functions and classes – which includes at least a basic description, type and meaning of all parameters and returns values, and usage examples in doctest format – is put in docstrings. Those docstrings can be read within the interpreter, and are compiled into a reference guide in html and pdf format. Higher-level documentation for key (areas of) functionality is provided in tutorial format and/or in module docstrings. A guide on how to write documentation is given in A Guide to NumPy Documentation, and *Rendering Documentation with Sphinx* explains how to preview the documentation as it will appear online.

4. ***Code style***

   Uniformity of style in which code is written is important to others trying to understand the code. SciPy follows the standard Python guidelines for code style, PEP8. In order to check that your code conforms to PEP8, you can use the pep8 package style checker. Most IDEs and text editors have settings that can help you follow PEP8, for example by translating tabs by four spaces. Using pyflakes to check your code is also a good idea. More information is available in *PEP8 and SciPy*.

A *checklist*, including these and other requirements, is available at the end of the example *Development workflow*.

Another question you may have is: *where exactly do I put my code*? To answer this, it is useful to understand how the SciPy public API (application programming interface) is defined. For most modules the API is two levels deep, which means your new function should appear as `scipy.subpackage.my_new_func`. `my_new_func` can be put in an existing or new file under `/scipy/<subpackage>/`, its name is added to the `__all__` list in that file (which lists all public functions in the file), and those public functions are then imported in `/scipy/<subpackage>/__init__.py`. Any private functions/classes should have a leading underscore (_) in their name. A more detailed description of what the public API of SciPy is, is given in *SciPy API*.

Once you think your code is ready for inclusion in SciPy, you can send a pull request (PR) on Github. We won't go into the details of how to work with git here, this is described well in git-development and on the Github help pages. When you send the PR for a new feature, be sure to also mention this on the scipy-dev mailing list. This can prompt interested people to help review your PR. Assuming that you already got positive feedback before on the general idea of your code/feature, the purpose of the code review is to ensure that the code is correct, efficient and meets the requirements outlined above. In many cases the code review happens relatively quickly, but it's possible that it stalls. If you have addressed all feedback already given, it's perfectly fine to ask on the mailing list again for review (after a reasonable amount of time, say a couple of weeks, has passed). Once the review is completed, the PR is merged into the "master" branch of SciPy.

The above describes the requirements and process for adding code to SciPy. It doesn't yet answer the question though how decisions are made exactly. The basic answer is: decisions are made by consensus, by everyone who chooses to participate in the discussion on the mailing list. This includes developers, other users and yourself. Aiming for consensus in the discussion is important – SciPy is a project by and for the scientific Python community. In those rare cases that agreement cannot be reached, the maintainers of the module in question can decide the issue.

License Considerations

I based my code on existing Matlab/R/... code I found online, is this OK?

It depends. SciPy is distributed under a BSD license, so if the code that you based your code on is also BSD licensed or has a BSD-compatible license (e.g. MIT, PSF) then it's OK. Code which is GPL or Apache licensed, has no clear license, requires citation or is free for academic use only can't be included in SciPy. Therefore if you copied existing code with such a license or made a direct translation to Python of it, your code can't be included. If you're unsure, please ask on the scipy-dev mailing list.

Why is SciPy under the BSD license and not, say, the GPL?

Like Python, SciPy uses a "permissive" open source license, which allows proprietary re-use. While this allows companies to use and modify the software without giving anything back, it is felt that the larger user base results in more contributions overall, and companies often publish their modifications anyway, without being required to. See John Hunter's BSD pitch.

For more information about SciPy's license, see *Licensing*.

4.2.2 Maintaining existing code

The previous section talked specifically about adding new functionality to SciPy. A large part of that discussion also applies to maintenance of existing code. Maintenance means fixing bugs, improving code quality, documenting existing functionality better, adding missing unit tests, adding performance benchmarks, keeping build scripts up-to-date, etc. The SciPy issue list contains all reported bugs, build/documentation issues, etc. Fixing issues helps improve the overall quality of SciPy, and is also a good way of getting familiar with the project. You may also want to fix a bug because you ran into it and need the function in question to work correctly.

The discussion on code style and unit testing above applies equally to bug fixes. It is usually best to start by writing a unit test that shows the problem, i.e. it should pass but doesn't. Once you have that, you can fix the code so that the test does pass. That should be enough to send a PR for this issue. Unlike when adding new code, discussing this on the mailing list may not be necessary - if the old behavior of the code is clearly incorrect, no one will object to having it fixed. It may

be necessary to add some warning or deprecation message for the changed behavior. This should be part of the review process.

Note: Pull requests that *only* change code style, e.g. fixing some PEP8 issues in a file, are discouraged. Such PRs are often not worth cluttering the git annotate history, and take reviewer time that may be better spent in other ways. Code style cleanups of code that is touched as part of a functional change are fine however.

4.2.3 Reviewing pull requests

Reviewing open pull requests (PRs) is very welcome, and a valuable way to help increase the speed at which the project moves forward. If you have specific knowledge/experience in a particular area (say "optimization algorithms" or "special functions") then reviewing PRs in that area is especially valuable - sometimes PRs with technical code have to wait for a long time to get merged due to a shortage of appropriate reviewers.

We encourage everyone to get involved in the review process; it's also a great way to get familiar with the code base. Reviewers should ask themselves some or all of the following questions:

- Was this change adequately discussed (relevant for new features and changes in existing behavior)?
- Is the feature scientifically sound? Algorithms may be known to work based on literature; otherwise, closer look at correctness is valuable.
- Is the intended behavior clear under all conditions (e.g. unexpected inputs like empty arrays or nan/inf values)?
- Does the code meet the quality, test and documentation expectation outline under *Contributing new code*?

If we do not know you yet, consider introducing yourself.

4.2.4 Other ways to contribute

There are many ways to contribute other than writing code.

Triaging issues (investigating bug reports for validity and possible actions to take) is also a useful activity. SciPy has many hundreds of open issues; closing invalid ones and correctly labeling valid ones (ideally with some first thoughts in a comment) allows prioritizing maintenance work and finding related issues easily when working on an existing function or subpackage.

Participating in discussions on the scipy-user and scipy-dev mailing lists is a contribution in itself. Everyone who writes to those lists with a problem or an idea would like to get responses, and writing such responses makes the project and community function better and appear more welcoming.

The scipy.org website contains a lot of information on both SciPy the project and SciPy the community, and it can always use a new pair of hands. The sources for the website live in their own separate repo: https://github.com/scipy/scipy.org

4.2.5 Getting started

Thanks for your interest in contributing to SciPy! If you're interested in contributing code, we hope you'll continue on to the *SciPy contributor guide* for details on how to set up your development environment, implement your improvements, and submit your first PR!

4.3 Development environment quickerstart guide (Linux and Mac)

With conda installed (through Miniforge or Mambaforge, Miniconda or Anaconda), execute the following commands at the terminal from the base directory of your SciPy clone:

```
# Create an environment with all development dependencies
conda env create -f environment.yml  # works with `mamba` too
conda activate scipy-dev

# Initialize git submodules
git submodule update --init

# Build SciPy for development work plus run tests
python runtests.py    # Alternatively, it's fine to use `python setup.py
↪develop`

# Install SciPy in develop mode in conda
conda develop .
```

For more detailed instructions, see the other *Development environment* guides.

4.4 SciPy contributor guide

This guide is designed to help you quickly find the information you need about SciPy development after you've reviewed the introductory material in *Ways to Contribute*. If you're new to this and want to start coding ASAP, you've found the right place.

- *Development environment* - how to set up and maintain a development environment, including installing compilers and SciPy dependencies, creating a personal fork of the SciPy repository on GitHub, using git to manage a local repository with development branches, performing an in-place build of SciPy, and creating a virtual environment that adds this development version of SciPy to the Python path
- *Editing SciPy* - how to edit SciPy Python code, with tips on finding which module contains SciPy functionality to be edited, adding new modules to SciPy, and complying with PEP8 style standards
- *Unit tests* - how to write and run unit tests for SciPy with the pytest framework
- *Documentation* - how to write reStructuredText documentation that complies with docstring standards, build documentation locally with Sphinx, and view documentation built during continuous integration checks
- *Benchmarks* - how to benchmark code with airspeed velocity
- *Compiled code* - how to add fast, compiled code to SciPy
- *Continuous Integration* - how does our continuous integration system works and how to debug your PR

4.4.1 Development environment

- *Development environment quickerstart guide (Linux and Mac)* contains just the commands you need to get started on Mac and Linux
- quickstart-pip presents an overview of setting up the development environment using pip on Linux
- *Development environment quickstart guide (macOS)* presents a step-by-step process for setting up a convenient SciPy development environment in macOS
- *Development environment quickstart guide (Ubuntu)* presents a step-by-step process for setting up a convenient SciPy development environment in Ubuntu
- build-windows presents a step-by-step process for building SciPy on Windows
- quickstart-docker presents a step-by-step process for building SciPy using Docker; if you have trouble with the instructions above, this may be your best option
- quickstart-gitpod presents a step-by-step process for using Gitpod for SciPy development; this process requires minimal setup and is newcomer friendly
- building may have some helpful hints if you need to deviate from the guides above
- recommended-development-setup includes additional notes about the development setup; all of this information is contained elsewhere, but it is retained as a legacy document

4.4.2 Editing SciPy

- *Development workflow* lays out what to do after your development environment is set up
- SciPy Development Workflow is a five-minute video example of fixing a bug and submitting a pull request
- *PEP8 and SciPy* gives some tips for ensuring that your code is PEP8 compliant
- git-development is a guide to using `git`, the distributed version-control system used to manage the changes made to SciPy code from around the world
- *SciPy API* contains some important notes about how SciPy code is organized and documents the structure of the SciPy API; if you are going to import other SciPy code, read this first
- reviewing-prs explains how to review another author's SciPy code locally
- NumPy Distutils - Users Guide - check this out before adding any new files to SciPy
- *Adding New Methods, Functions, and Classes* has information on how to add new methods, functions and classes
- *SciPy Core Developer Guide* has background information including how decisions are made and how a release is prepared; it's geared toward *Core Developers*, but contains useful information for all contributors

4.4.3 Unit tests

- Testing Guidelines is the definitive guide to writing unit tests of SciPy code
- *Running SciPy Tests Locally* documents `runtests.py`, a convenient script for building SciPy and running tests locally

4.4.4 Documentation

- A Guide to NumPy Documentation contains everything you need to know about writing docstrings, which are rendered to produce HTML documentation using Sphinx
- *Rendering Documentation with Sphinx* it's important to check how changes to the documentation render before merging a PR; this document explains how you can do that

4.4.5 Benchmarks

- *Benchmarking SciPy with airspeed velocity* explains how to add benchmarks to SciPy using airspeed velocity

4.4.6 Compiled code

- *Adding Cython to SciPy* extending and compiling Python code with Cython can significantly improve its performance; this document helps you get started
- other-languages discusses the use of C, C++, and Fortran code in SciPy
- *Public Cython APIs* on guidelines on exposing public Cython APIs

4.5 SciPy Roadmap

This roadmap page contains only the most important ideas and needs for SciPy going forward. For a more detailed roadmap, including per-subpackage status, many more ideas, API stability and more, see *Detailed SciPy Roadmap*.

4.5.1 Support for distributed arrays and GPU arrays

NumPy has split its API from its execution engine with `__array_function__` and `__array_ufunc__`. This will enable parts of SciPy to accept distributed arrays (e.g. `dask.array.Array`) and GPU arrays (e.g. `cupy.ndarray`) that implement the `ndarray` interface. At the moment it is not yet clear which algorithms will work out of the box, and if there are significant performance gains when they do. We want to create a map of which parts of the SciPy API work, and improve support over time.

In addition to making use of NumPy protocols like `__array_function__`, we can make use of these protocols in SciPy as well. That will make it possible to (re)implement SciPy functions like, e.g., those in `scipy.signal` for Dask or GPU arrays (see NEP 18 - use outside of NumPy). NumPy's features in this areas are still evolving, see e.g. NEP 37 - A dispatch protocol for NumPy-like modules, and SciPy is an important "client" for those features.

4.5.2 Performance improvements

Speed improvements, lower memory usage and the ability to parallelize algorithms are beneficial to most science domains and use cases. We have established an API design pattern for multiprocessing - using the `workers` keyword - that can be adopted in many more functions.

Enabling the use of an accelerator like Pythran, possibly via Transonic, and making it easier for users to use Numba's `@njit` in their code that relies on SciPy functionality would unlock a lot of performance gain. That needs a strategy though, all solutions are still maturing (see for example this overview).

Finally, many individual functions can be optimized for performance. `scipy.optimize` and `scipy.interpolate` functions are particularly often requested in this respect.

4.5.3 Statistics enhancements

The `scipy.stats` enhancements listed in the *Detailed SciPy Roadmap* are of particularly high importance to the project.

- Improve the options for fitting a probability distribution to data.
- Expand the set of hypothesis tests. In particular, include all the basic variations of analysis of variance.
- Add confidence intervals for all statistical tests.

4.5.4 Support for more hardware platforms

SciPy now has continuous integration for ARM64 (or `aarch64`) and POWER8/9 (or `ppc64le`), and binaries are available via Miniforge. Wheels on PyPI for these platforms are now also possible (with the `manylinux2014` standard), and requests for those are becoming more frequent.

Additionally, having IBM Z (or `s390x`) in CI is now possible with TravisCI but not yet done - and `manylinux2014` wheels for that platform are also possible then. Finally, resolving open AIX build issues would help users.

4.5.5 Implement sparse arrays in addition to sparse matrices

The sparse matrix formats are mostly feature-complete, however the main issue is that they act like `numpy.matrix` (which will be deprecated in NumPy at some point). What we want is sparse *arrays* that act like `numpy.ndarray`. This is being worked on in https://github.com/pydata/sparse, which is quite far along. The tentative plan is:

- Start depending on `pydata/sparse` once it's feature-complete enough (it still needs a CSC/CSR equivalent) and okay performance-wise.
- Indicate in the documentation that for new code users should prefer `pydata/sparse` over sparse matrices.
- When NumPy deprecates `numpy.matrix`, vendor that or maintain it as a stand-alone package.

4.6 Detailed SciPy Roadmap

Most of this roadmap is intended to provide a high-level view on what is most needed per SciPy submodule in terms of new functionality, bug fixes, etc. Besides important "business as usual" changes, it contains ideas for major new features - those are marked as such, and are expected to take significant dedicated effort. Things not mentioned in this roadmap are not necessarily unimportant or out of scope, however we (the SciPy developers) want to provide to our users and contributors a clear picture of where SciPy is going and where help is needed most.

Note: This is the detailed roadmap. A very high-level overview with only the most important ideas is *SciPy Roadmap*.

4.6.1 General

This roadmap will be evolving together with SciPy. Updates can be submitted as pull requests. For large or disruptive changes you may want to discuss those first on the scipy-dev mailing list.

API changes

In general, we want to evolve the API to remove known warts as much as possible, *however as much as possible without breaking backwards compatibility*.

Also, it should be made (even) more clear what is public and what is private in SciPy. Everything private should be named starting with an underscore as much as possible.

Test coverage

Test coverage of code added in the last few years is quite good, and we aim for a high coverage for all new code that is added. However, there is still a significant amount of old code for which coverage is poor. Bringing that up to the current standard is probably not realistic, but we should plug the biggest holes.

Besides coverage there is also the issue of correctness - older code may have a few tests that provide decent statement coverage, but that doesn't necessarily say much about whether the code does what it says on the box. Therefore code review of some parts of the code (`stats`, `signal` and `ndimage` in particular) is necessary.

Documentation

The main website, scipy.org, needs to be rewritten. As discussed in the mail list, the SciPy stack is not relevant anymore and this website should be made about SciPy only following the example of numpy.org. There is a lot of new content to write

Otherwise, the documentation is in good shape. Expanding of current docstrings and putting them in the standard NumPy format should continue, so the number of reST errors and glitches in the html docs decreases. Most modules also have a tutorial in the reference guide that is a good introduction, however there are a few missing or incomplete tutorials - this should be fixed.

Benchmarks

The `asv`-based benchmark system is in reasonable shape. It is quite easy to add new benchmarks, however running the benchmarks is not very intuitive. Making this easier is a priority. In addition, we should run them in our CI (gh-8779 is an ongoing attempt at this).

Use of Cython

Regarding Cython code:

- It's not clear how much functionality can be Cythonized without making the .so files too large. This needs measuring.
- Cython's old syntax for using NumPy arrays should be removed and replaced with Cython memoryviews.

Windows build issues

SciPy critically relies on Fortran code. This is still problematic on Windows. There are currently only two options: using Intel Fortran, or using MSVC + gfortran. The former is expensive, while the latter works (it's what we use for releases) but is quite hard to do correctly. For allowing contributors and end users to reliably build SciPy on Windows, using the Flang compiler looks like the best way forward long-term.

Continuous integration

Continuous integration is in good shape, it currently covers the Windows, macOS and Linux, ARM64 and ppc64le platforms, as well as a range of versions of our dependencies and building release quality wheels.

Size of binaries

SciPy binaries are quite large (e.g. an unzipped manylinux wheel for 1.4.1 is 91 MB), and this can be problematic - for example for use in AWS Lambda, which has a 250 MB size limit. We aim to keep binary size as low as possible; when adding new compiled extensions, this needs checking. Stripping of debug symbols in `multibuild` can likely be improved (see this issue).

4.6.2 Modules

cluster

This module is in good shape.

constants

This module is basically done, low-maintenance and without open issues.

fft

This module is in good shape.

integrate

Needed for ODE solvers:

- Documentation is pretty bad, needs fixing
- A new ODE solver interface (`solve_ivp`) was added in SciPy 1.0.0. In the future we can consider (soft-)deprecating the older API.

The numerical integration functions are in good shape. Support for integrating complex-valued functions and integrating multiple intervals (see gh-3325) could be added.

interpolate

Ideas for new features:

- Spline fitting routines with better user control.
- Transparent tensor-product splines.
- NURBS support.
- Mesh refinement and coarsening of B-splines and corresponding tensor products.

io

wavfile:

- PCM float will be supported, for anything else use `audiolab` or other specialized libraries.
- Raise errors instead of warnings if data not understood.

Other sub-modules (matlab, netcdf, idl, harwell-boeing, arff, matrix market) are in good shape.

linalg

`scipy.linalg` is in good shape.

Needed:

- Reduce duplication of functions with `numpy.linalg`, make APIs consistent.
- `get_lapack_funcs` should always use `flapack`
- Wrap more LAPACK functions
- One too many funcs for LU decomposition, remove one

Ideas for new features:

- Add type-generic wrappers in the Cython BLAS and LAPACK
- Make many of the linear algebra routines into gufuncs

BLAS and LAPACK

The Python and Cython interfaces to BLAS and LAPACK in `scipy.linalg` are one of the most important things that SciPy provides. In general `scipy.linalg` is in good shape, however we can make a number of improvements:

1. Library support. Our released wheels now ship with OpenBLAS, which is currently the only feasible performant option (ATLAS is too slow, MKL cannot be the default due to licensing issues, Accelerate support is dropped because Apple doesn't update Accelerate anymore). OpenBLAS isn't very stable though, sometimes its releases break things and it has issues with threading (currently the only issue for using SciPy with PyPy3). We need at the very least better support for debugging OpenBLAS issues, and better documentation on how to build SciPy with it. An option is to use BLIS for a BLAS interface (see numpy gh-7372).
2. Support for newer LAPACK features. In SciPy 1.2.0 we increased the minimum supported version of LAPACK to 3.4.0. Now that we dropped Python 2.7, we can increase that version further (MKL + Python 2.7 was the blocker for >3.4.0 previously) and start adding support for new features in LAPACK.

misc

`scipy.misc` will be removed as a public module. Most functions in it have been moved to another submodule or deprecated. The few that are left:

- `info`, `who` : these are NumPy functions
- `derivative`, `central_diff_weight` : remove, possibly replacing them with more extensive functionality for numerical differentiation.

ndimage

Underlying `ndimage` is a powerful interpolation engine. Users come with an expectation of one of two models: a pixel model with `(1, 1)` elements having centers `(0.5, 0.5)`, or a data point model, where values are defined at points on a grid. Over time, we've become convinced that the data point model is better defined and easier to implement, but this should be clearly communicated in the documentation.

More importantly, still, SciPy implements one *variant* of this data point model, where datapoints at any two extremes of an axis share a spatial location under *periodic wrapping* mode. E.g., in a 1D array, you would have `x[0]` and `x[-1]` co-located. A very common use-case, however, is for signals to be periodic, with equal spacing between the first and last element along an axis (instead of zero spacing). Wrapping modes for this use-case were added in gh-8537, next the interpolation routines should be updated to use those modes. This should address several issues, including gh-1323, gh-1903, gh-2045 and gh-2640.

The morphology interface needs to be standardized:

- binary dilation/erosion/opening/closing take a "structure" argument, whereas their grey equivalent take size (has to be a tuple, not a scalar), footprint, or structure.
- a scalar should be acceptable for size, equivalent to providing that same value for each axis.
- for binary dilation/erosion/opening/closing, the structuring element is optional, whereas it's mandatory for grey. Grey morphology operations should get the same default.
- other filters should also take that default value where possible.

odr

This module is in reasonable shape, although it could use a bit more maintenance. No major plans or wishes here.

optimize

Overall this module is in good shape. Two good global optimizers were added in 1.2.0; large-scale optimizers is still a gap that could be filled. Other things that are needed:

- Many ideas for additional functionality (e.g. integer constraints, sparse matrix support, performance improvements) in `linprog`, see gh-9269.
- Add functionality to the benchmark suite to compare results more easily (e.g. with summary plots).
- deprecate the `fmin_*` functions in the documentation, `minimize` is preferred.
- `scipy.optimize` has an extensive set of benchmarks for accuracy and speed of the global optimizers. That has allowed adding new optimizers (`shgo` and `dual_annealing`) with significantly better performance than the existing ones. The `optimize` benchmark system itself is slow and hard to use however; we need to make it faster and make it easier to compare performance of optimizers via plotting performance profiles.

signal

Convolution and correlation: (Relevant functions are convolve, correlate, fftconvolve, convolve2d, correlate2d, and sepfir2d.) Eliminate the overlap with *ndimage* (and elsewhere). From `numpy`, `scipy.signal` and `scipy.ndimage` (and anywhere else we find them), pick the "best of class" for 1-D, 2-D and n-d convolution and correlation, put the implementation somewhere, and use that consistently throughout SciPy.

B-splines: (Relevant functions are bspline, cubic, quadratic, gauss_spline, cspline1d, qspline1d, cspline2d, qspline2d, cspline1d_eval, and spline_filter.) Move the good stuff to *interpolate* (with appropriate API changes to match how things are done in *interpolate*), and eliminate any duplication.

Filter design: merge *firwin* and *firwin2* so *firwin2* can be removed.

Continuous-Time Linear Systems: remove *lsim2*, *impulse2*, *step2*. The *lsim*, *impulse* and *step* functions now "just work" for any input system. Further improve the performance of `ltisys` (fewer internal transformations between different representations). Fill gaps in lti system conversion functions.

Second Order Sections: Make SOS filtering equally capable as existing methods. This includes ltisys objects, an *lfiltic* equivalent, and numerically stable conversions to and from other filter representations. SOS filters could be considered as the default filtering method for ltisys objects, for their numerical stability.

Wavelets: what's there now doesn't make much sense. Continuous wavelets only at the moment - decide whether to completely rewrite or remove them. Discrete wavelet transforms are out of scope (PyWavelets does a good job for those).

sparse

The sparse matrix formats are mostly feature-complete, however the main issue is that they act like `numpy.matrix` (which will be deprecated in NumPy at some point). What we want is sparse arrays, that act like `numpy.ndarray`. This is being worked on in https://github.com/pydata/sparse, which is quite far along. The tentative plan is:

- Start depending on `pydata/sparse` once it's feature-complete enough (it still needs a CSC/CSR equivalent) and okay performance-wise.
- Add support for `pydata/sparse` to `scipy.sparse.linalg` (and perhaps to `scipy.sparse.csgraph` after that).
- Indicate in the documentation that for new code users should prefer `pydata/sparse` over sparse matrices.
- When NumPy deprecates `numpy.matrix`, vendor that or maintain it as a stand-alone package.

Regarding the different sparse matrix formats: there are a lot of them. These should be kept, but improvements/optimizations should go into CSR/CSC, which are the preferred formats. LIL may be the exception, it's inherently inefficient. It could be dropped if DOK is extended to support all the operations LIL currently provides.

sparse.csgraph

This module is in good shape.

sparse.linalg

Arpack is in good shape.

isolve:

- callback keyword is inconsistent
- tol keyword is broken, should be relative tol
- Fortran code not re-entrant (but we don't solve, maybe re-use from PyKrilov)

dsolve:

- add sparse Cholesky or incomplete Cholesky
- add sparse QR
- improve interface to SuiteSparse UMFPACK
- add interfaces to SuiteSparse CHOLMOD and SPQR

Ideas for new features:

- Wrappers for PROPACK for faster sparse SVD computation.

spatial

QHull wrappers are in good shape, as is `cKDTree`.

Needed:

- `KDTree` will be removed, and `cKDTree` will be renamed to `KDTree` in a backwards-compatible way.
- `distance_wrap.c` needs to be cleaned up (maybe rewrite in Cython).

special

Though there are still a lot of functions that need improvements in precision, probably the only show-stoppers are hypergeometric functions, parabolic cylinder functions, and spheroidal wave functions. Three possible ways to handle this:

1. Get good double-precision implementations. This is doable for parabolic cylinder functions (in progress). I think it's possible for hypergeometric functions, though maybe not in time. For spheroidal wavefunctions this is not possible with current theory.
2. Port Boost's arbitrary precision library and use it under the hood to get double precision accuracy. This might be necessary as a stopgap measure for hypergeometric functions; the idea of using arbitrary precision has been suggested before by @nmayorov and in gh-5349. Likely necessary for spheroidal wave functions, this could be reused: https://github.com/radelman/scattering.
3. Add clear warnings to the documentation about the limits of the existing implementations.

stats

The `scipy.stats` subpackage aims to provide fundamental statistical methods as might be covered in standard statistics texts such as Johnson's "Miller & Freund's Probability and Statistics for Engineers", Sokal & Rohlf's "Biometry", or Zar's "Biostatistical Analysis". It does not seek to duplicate the advanced functionality of downstream packages (e.g. StatsModels, LinearModels, PyMC3); instead, it can provide a solid foundation on which they can build. (Note that these are rough guidelines, not strict rules. "Advanced" is an ill-defined and subjective term, and "advanced" methods may also be included in SciPy, especially if no other widely used and well-supported package covers the topic. Also note that *some* duplication with downstream projects is inevitable and not necessarily a bad thing.)

The following improvements will help SciPy better serve this role.

- Add fundamental and widely used hypothesis tests:
  - Tukey-Kramer test
  - Dunnett's test
  - the various types of analysis of variance (ANOVA):
    - two-way ANOVA (single replicate, uniform number of replicates, variable number of replicates)
    - multiway ANOVA (i.e. generalize two-way ANOVA)
    - nested ANOVA
    - analysis of covariance (ANCOVA)
- Add additional tools for meta-analysis; currently we have just *combine_pvalues*.
- Enhance the *fit* method of the continuous probability distributions:
  - Expand the options for fitting to include:
    - maximal product spacings
    - method of L-moments / probability weighted moments
  - Include measures of goodness-of-fit in the results
  - Handle censored data (e.g. merge gh-13699)
- Implement additional widely used continuous and discrete probability distributions:
  - multivariate t distribution
  - mixture distributions
- Improve the core calculations provided by SciPy's probability distributions so they can robustly handle wide ranges of parameter values. Specifically, replace many of the PDF and CDF methods from the Fortran library CDFLIB used in scipy.special with Boost implementations as in gh-13328.

In addition, we should:

- Continue work on making the function signatures of `stats` and `stats.mstats` more consistent, and add tests to ensure that that remains the case.
- Improve statistical tests: consistently provide options for one- and two-sided alternative hypotheses where applicable, return confidence intervals for the test statistic, and implement exact p-value calculations - considering the possibility of ties - where computationally feasible.

4.7 Toolchain Roadmap

The use of the SciPy library requires (or optionally depends upon) several other libraries in order to operate, the main dependencies being Python and NumPy. It requires a larger collection of libraries and tools in order to build the library or to build the documentation.

Of course, the tooling and libraries are themselves not static. This document aims to provide a guide as to how SciPy's use of these dynamic dependencies will proceed over time.

SciPy aims to be compatible with a number of releases of its dependent libraries and tools. Forcing the user base to other components for upgrade for every release would greatly diminish the value of SciPy. However, maintaining backwards compatibility with very old tooling/libraries imposes limitations on which newer functionalities and capabilities can be incorporated. SciPy takes a somewhat conservative approach, maintaining compatibility with several major releases of Python and NumPy on the major platforms. (That may in and of itself impose further restrictions. See the C Compilers section for an example.)

- First and foremost, SciPy is a Python project, hence it requires a Python environment.
- BLAS and LAPACK numerical libraries need to be installed.
- Compilers for C, C++, Fortran code are needed, as well as for Cython & Pythran (the latter is opt-out currently)
- The Python environment needs the `NumPy` package to be installed.
- Testing requires the `pytest` Python package.
- Building the documentation requires the `matplotlib`, Sphinx packages along with PyData theme, as well as a LaTeX installation.

The tooling used to build CPython has some implications for the tooling used in building SciPy. It also has implications for the examples used in the documentation (e.g., docstrings for functions), as these examples can only use functionality present in all supported configurations.

4.7.1 Building SciPy

Python Versions

SciPy is compatible with several versions of Python. When dropping support for older Python versions, SciPy takes guidance from NEP 29[10]. Python 2.7 support was dropped for SciPy releases numbered 1.3 and above but is still available in release 1.2.x, which is a long-term support release[1],[2].

Date	Pythons supported
2018	Py2.7, Py3.4+ (SciPy 1.2.x is the last release to support Python 2.7)
2019	Py3.5+ (but Py2.7-specific code not removed)
2020	Py3.6+ (removal of Py2.7-specific code permitted)
2021	Py3.7+

[10] https://numpy.org/neps/nep-0029-deprecation_policy.html
[1] https://docs.scipy.org/doc/scipy/reference/release.1.2.0.html
[2] https://python3statement.org

NumPy

SciPy depends on NumPy but releases of SciPy are not tied to releases of NumPy. SciPy attempts to be compatible with at least the 4 previous releases of NumPy. In particular, SciPy cannot rely on features of just the latest NumPy, but needs to be written using what is common in all of those 4 releases.[?],[3].

The table shows the NumPy versions suitable for each major Python version (for SciPy 1.3.x unless otherwise stated).

Python	Minimum NumPy version	Maximum NumPy version
2.7 (SciPy 1.2)	1.8.2	1.16.x
3.5 (SciPy 1.4)	1.13.3	1.18.x
3.6 (SciPy 1.5)	1.14.5	1.19.x
3.7	1.16.5	>= 1.20.x
3.8	1.17.3	>= 1.20.x
3.9	1.19.3	>= 1.20.x

Compilers

Building SciPy requires compilers for C, C++, Fortran, as well as the python transpilers Cython and Pythran (the latter is an opt-out dependency as of version 1.7.0).

To maintain compatibility with a large number of platforms & setups, especially where using the official wheels (or other distribution channels like Anaconda or conda-forge) is not possible, SciPy keeps compatibility with old compilers.

Official Builds

Currently, SciPy wheels are being built as follows:

Platform	Azure Base Image[14]	Compilers	Comment
Linux (nightly)	`ubuntu-18.04`	GCC 4.8	See `azure-pipelines.yml`
Linux (release)	`ubuntu-18.04`	GCC 7.5	Built in separate repo[15]
OSX	`macOS-10.14`	LLVM 11.0	Built in separate repo[15]
Windows	`VS2017-Win2016`	Visual Studio 2017 (15.9)	See `azure-pipelines.yml`

Note that the OSX wheels additionally vendor gfortran 4.8, see[15].

C Compilers

SciPy is compatible with most modern C compilers (in particular `clang`). In addition to concerns about compatibility with non-standard platforms, there was a long-standing restriction that Windows builds of SciPy had to use the same version of the Microsoft Visual C++ compiler as were used for CPython itself, for reasons of ABI-compatibility[6],[7],[8],[9].

With the introduction of the "Universal C Runtime"[16] since the release of Visual Studio 2015, this restriction has been lifted. For more context, see the explanations by Steve Dower (member of the CPython-on-Windows core developers) on this topic[17].

[3] https://docs.scipy.org/doc/numpy/release.html
[14] https://docs.microsoft.com/en-us/azure/devops/pipelines/agents/hosted
[15] https://github.com/MacPython/scipy-wheels
[6] https://blogs.msdn.microsoft.com/vcblog/2013/07/19/c99-library-support-in-visual-studio-2013/
[7] https://pythondev.readthedocs.io/windows.html#python-and-visual-studio-version-matrix
[8] https://en.wikipedia.org/wiki/Microsoft_Visual_C%2B%2B#Internal_version_numbering
[9] https://wiki.python.org/moin/WindowsCompilers
[16] https://docs.microsoft.com/en-gb/cpp/windows/universal-crt-deployment
[17] https://discuss.python.org/t/toolchain-upgrade-on-windows/6377/4

The use of MS Visual Studio 9.0 (which doesn't have support C99) to build Python 2.7 has meant that C code in SciPy has had to conform to the earlier C90 standard for the language and standard library. With the dropping of Python 2.7 for SciPy 1.3.x, the C90 restriction is no longer imposed by compilers. For GCC version < 5, an explicit `-std=c99` may have to be added by the user if C99 features are used in SciPy code.

In terms of C language standards, it's relevant to note that C11 has optional features[12] (e.g. atomics, threading), some of which (VLAs & complex types) were mandatory in the C99 standard. C17 (occasionally called C18) can be considered a bug fix for C11, so generally, C11 may be skipped entirely.

SciPy has been restricted in the use of more advanced language features by the available compiler support, and Microsoft in particular has taken very long to achieve conformance to C99/C11/C17, however starting from MS Visual Studio 16.8, C11/C17 is supported[11] (though without the C11 optional features).

Therefore, using C features beyond C90 is contingent upon updating the windows toolchain for SciPy, as well as checking compiler support for the desired feature across all minimally supported compiler versions. In short:

CPython	MS Visual C++	C Standard
2.7, 3.0, 3.1, 3.2	9.0	C90
3.3, 3.4	10.0	C90 & some of C99
3.5, 3.6	14.0	C90 & most of C99
3.7, 3.8, 3.9	15.7	Dependent on MSVC version used to build SciPy

C and C++ Language Standards

C and C++ language standards for SciPy are generally guidelines rather than official decisions. This is particularly true of attempting to predict adoption timelines for newer standards.

Date	C/C++ Standard
<= 2018	C90
2019	C90 for old code, may consider C99 for new
2020	C99
2020	C++11
2021	C++14
?	C11, C17, C++17, C++20

For C, C11/C17 support will be available as soon as the `vmImage` for building SciPy is upgraded to `windows-2019` (which is compatible with currently supported CPython versions and "just" needs to be executed). This is because GCC & LLVM support all relevant C11 features with the oldest currently used versions, and C17 is just a bugfix for C11, as mentioned above.

On the C++ side, since dropping support for Python 2.7, C++11 can be used universally. For C++14, Windows is not a restriction anymore since Visual Studio 15.9 (<-> _MSC_VER 19.16, see[?]), has full support (same for C++17), see[4]. However, using C++14 still requires bumping the GCC minimal requirement to 5.x and C++17 will require GCC >= 7[4]. Compiler support for C++20 is still under heavy development.

Note: Developer Note: Some C99 features would be useful for scientific programming, in particular better support of IEEE 754[5]. SciPy has a small include file `scipy/_lib/_c99compat.h` which provides access to a few functions. Use in conjunction with `<numpy/npy_math.h>`.

[12] https://en.wikipedia.org/wiki/C11_%28C_standard_revision%29#Optional_features
[11] https://devblogs.microsoft.com/cppblog/c11-and-c17-standard-support-arriving-in-msvc/
[4] https://en.cppreference.com/w/cpp/compiler_support
[5] https://en.wikipedia.org/wiki/IEEE_754-1985

Feature	Workaround
`isnan()`, `isinf()`, `isfinite()`	Use `sc_isnan()`, `sc_isinf()`, `sc_isfinite()`
`NAN`	Use `NPY_NAN` (it is *almost* equivalent)
inline functions	Make static functions and place in an include .h file
mid-block variable declarations	Declare variables at the top of the block

Fortran Compilers

Generally, any well-maintained compiler is likely suitable and can be used to build SciPy.

Tool	Version
gfortran	>= 4.8.0
ifort	A recent version
flang	A recent version

Cython Compiler

SciPy always requires a recent Cython compiler.

Tool	Tool Version	SciPy version
Cython	>= 0.29.13	1.4.1
Cython	>= 0.29.18	1.5.0

OpenMP support

For various reasons[13], SciPy cannot be distributed with built-in OpenMP support. When using the optional Pythran support, OpenMP-enabled parallel code can be generated when building from source.

Other Libraries

Any library conforming to the BLAS/LAPACK interface may be used. OpenBLAS, ATLAS, MKL, BLIS, and reference Netlib libraries are known to work.

Library	Minimum version
LAPACK	3.4.1
BLAS	A recent version of OpenBLAS, MKL or ATLAS. The Accelerate BLAS is no longer supported.

There are some additional optional dependencies.

Library	Version	URL
mpmath	Recent	http://mpmath.org/
scikit-umfpack	Recent	https://pypi.org/project/scikit-umfpack/

Moreover, Scipy supports interaction with other libraries. The test suite has additional compatibility tests that are run when these are installed:

[13] https://github.com/scipy/scipy/issues/10239

Tool	Version	URL
pydata/sparse	Recent	https://github.com/pydata/sparse/

4.7.2 Testing and Benchmarking

Testing and benchmarking require recent versions of:

Tool	Version	URL
pytest	Recent	https://docs.pytest.org/en/latest/
asv (airspeed velocity)	Recent	https://asv.readthedocs.io/

4.7.3 Building the Documentation

Tool	Version
Sphinx	Whatever recent versions work. >= 2.0.
PyData Sphinx theme	Whatever recent versions work. >= 0.6.1.
Sphinx-Panels	Whatever recent versions work. >= 0.5.2.
numpydoc	Whatever recent versions work. >= 0.8.0.
matplotlib	Generally suggest >= 2.0.
LaTeX	A recent distribution, such as `TeX Live 2016`.

[The `numpydoc` package is also used, but that is currently packaged in `doc/sphinxext`.]

Note: Developer Note: The versions of `numpy` and `matplotlib` required have implications for the examples in Python docstrings. Examples must be able to be executed both in the environment used to build the documentation, as well as with any supported versions of `numpy/matplotlib` that a user may use with this release of SciPy.

4.7.4 Packaging

A Recent version of:

Tool	Version	URL
setuptools	Recent	https://pypi.org/project/setuptools/
wheel	Recent	https://pythonwheels.com
multibuild	Recent	https://github.com/matthew-brett/multibuild

Making a SciPy release and *Distributing* contain information on making and distributing a SciPy release.

4.7.5 References

4.8 SciPy Core Developer Guide

4.8.1 Decision making process

SciPy has a formal governance model, documented in *SciPy Project Governance*. The section below documents in an informal way what happens in practice for decision making about code and commit rights. The formal governance model is leading, the below is only provided for context.

Code

Any significant decisions on adding (or not adding) new features, breaking backwards compatibility or making other significant changes to the codebase should be made on the scipy-dev mailing list after a discussion (preferably with full consensus).

Any non-trivial change (where trivial means a typo, or a one-liner maintenance commit) has to go in through a pull request (PR). It has to be reviewed by another developer. In case review doesn't happen quickly enough and it is important that the PR is merged quickly, the submitter of the PR should send a message to mailing list saying he/she intends to merge that PR without review at time X for reason Y unless someone reviews it before then.

Changes and new additions should be tested. Untested code is broken code.

Commit rights

Who gets commit rights is decided by the SciPy Steering Council; changes in commit rights will then be announced on the scipy-dev mailing list.

4.9 Deciding on new features

The general decision rule to accept a proposed new feature has so far been conditional on:

1. The method is applicable in many fields and "generally agreed" to be useful,
2. It fits the topic of the submodule, and does not require extensive support frameworks to operate,
3. The implementation looks sound and unlikely to need much tweaking in the future (e.g., limited expected maintenance burden),
4. Someone wants to contribute it, and
5. Someone wants to review it.

The last criterion is often a sticking point for proposed features. Code cannot be merged until it has been thoroughly reviewed, and there is always a backlog of maintenance tasks that compete for reviewers' time. Ideally, contributors should line up a reviewer with suitable domain expertise before beginning work.

Although it's difficult to give hard rules on what "generally useful and generally agreed to work" means, it may help to weigh the following against each other:

- Is the method used/useful in different domains in practice? How much domain-specific background knowledge is needed to use it properly?
- Consider the code already in the module. Is what you are adding an omission? Does it solve a problem that you'd expect the module be able to solve? Does it supplement an existing feature in a significant way?

- Consider the equivalence class of similar methods / features usually expected. Among them, what would in principle be the minimal set so that there's not a glaring omission in the offered features remaining? How much stuff would that be? Does including a representative one of them cover most use cases? Would it in principle sound reasonable to include everything from the minimal set in the module?
- Is what you are adding something that is well understood in the literature? If not, how sure are you that it will turn out well? Does the method perform well compared to other similar ones?
- Note that the twice-a-year release cycle and backward-compatibility policy makes correcting things later on more difficult.

The scopes of the submodules also vary, so it's probably best to consider each as if it's a separate project - "numerical evaluation of special functions" is relatively well-defined, but "commonly needed optimization algorithms" less so.

4.9.1 Development on GitHub

SciPy development largely takes place on GitHub; this section describes the expected way of working for issues, pull requests and managing the main `scipy` repository.

Labels and Milestones

Each issue and pull request normally gets at least two labels: one for the topic or component (`scipy.stats`, `Documentation`, etc.), and one for the nature of the issue or pull request (`enhancement`, `maintenance`, `defect`, etc.). Other labels that may be added depending on the situation:

- `easy-fix`: for issues suitable to be tackled by new contributors.
- `needs-work`: for pull requests that have review comments that haven't been addressed.
- `needs-decision`: for issues or pull requests that need a decision.
- `needs-champion`: for pull requests that were not finished by the original author, but are worth resurrecting.
- `backport-candidate`: bugfixes that should be considered for backporting by the release manager.

A milestone is created for each version number for which a release is planned. Issues that need to be addressed and pull requests that need to be merged for a particular release should be set to the corresponding milestone. After a pull request is merged, its milestone (and that of the issue it closes) should be set to the next upcoming release - this makes it easy to get an overview of changes and to add a complete list of those to the release notes.

Pull request review workflow

When reviewing pull requests, please make use of pull request workflow features, see pull-request-workflow-features.

Dealing with pull requests

- When merging contributions, a committer is responsible for ensuring that those meet the requirements outlined in Contributing to SciPy. Also check that new features and backwards compatibility breaks were discussed on the scipy-dev mailing list.
- New code goes in via a pull request (PR).
- Merge new code with the green button. In case of merge conflicts, ask the PR submitter to rebase (this may require providing some git instructions).
- Backports and trivial additions to finish a PR (really trivial, like a typo or PEP8 fix) can be pushed directly.

- For PRs that add new features or are in some way complex, wait at least a day or two before merging it. That way, others get a chance to comment before the code goes in.
- Squashing commits or cleaning up commit messages of a PR that you consider too messy is OK. Make sure though to retain the original author name when doing this.
- Make sure that the labels and milestone on a merged PR are set correctly.
- When you want to reject a PR: if it's very obvious you can just close it and explain why, if not obvious then it's a good idea to first explain why you think the PR is not suitable for inclusion in SciPy and then let a second committer comment or close.

Backporting

All pull requests (whether they contain enhancements, bug fixes or something else), should be made against master. Only bug fixes are candidates for backporting to a maintenance branch. The backport strategy for SciPy is to (a) only backport fixes that are important, and (b) to only backport when it's reasonably sure that a new bugfix release on the relevant maintenance branch will be made. Typically, the developer who merges an important bugfix adds the `backport-candidate` label and pings the release manager, who decides on whether and when the backport is done. After the backport is completed, the `backport-candidate` label has to be removed again.

A good strategy for a backport pull request is to combine several master branch pull requests, to reduce the burden on continuous integration tests and to reduce the merge commit cluttering of maintenance branch history. It is generally best to have a single commit for each of the master branch pull requests represented in the backport pull request. This way, history is clear and can be reverted in a straightforward manner if needed.

Release notes

When a PR gets merged, consider if the changes need to be mentioned in the release notes. What needs mentioning: new features, backwards incompatible changes, deprecations, and "other changes" (anything else noteworthy enough, see older release notes for the kinds of things worth mentioning).

Release note entries are maintained on the wiki, (e.g. https://github.com/scipy/scipy/wiki/Release-note-entries-for-SciPy-1.2.0). The release manager will gather content from there and integrate it into the html docs. We use this mechanism to avoid merge conflicts that would happen if every PR touched the same file under `doc/release/` directly.

Changes can be monitored (Atom feed) and pulled (the wiki is a git repo: `https://github.com/scipy/scipy.wiki.git`).

Other

PR status page: When new commits get added to a pull request, GitHub doesn't send out any notifications. The `needs-work` label may not be justified anymore though. This page gives an overview of PRs that were updated, need review, need a decision, etc.

Cross-referencing: Cross-referencing issues and pull requests on GitHub is often useful. GitHub allows doing that by using `gh-xxxx` or `#xxxx` with `xxxx` the issue/PR number. The `gh-xxxx` format is strongly preferred, because it's clear that that is a GitHub link. Older issues contain `#xxxx` which is about Trac (what we used pre-GitHub) tickets.

PR naming convention: Pull requests, issues and commit messages usually start with a three-letter abbreviation like `ENH:` or `BUG:`. This is useful to quickly see what the nature of the commit/PR/issue is. For the full list of abbreviations, see writing the commit message.

4.9.2 Licensing

SciPy is distributed under the modified (3-clause) BSD license. All code, documentation and other files added to SciPy by contributors is licensed under this license, unless another license is explicitly specified in the source code. Contributors keep the copyright for code they wrote and submit for inclusion to SciPy.

Other licenses that are compatible with the modified BSD license that SciPy uses are 2-clause BSD, MIT and PSF. Incompatible licenses are GPL, Apache and custom licenses that require attribution/citation or prohibit use for commercial purposes.

PRs are often submitted with content copied or derived from unlicensed code or code from a default license that is not compatible with SciPy's license. For instance, code published on StackOverflow is covered by a CC-BY-SA license, which is not compatible due to the share-alike clause. These contributions cannot be accepted for inclusion in SciPy unless the original code author is willing to (re)license his/her code under the modified BSD (or compatible) license. If the original author agrees, add a comment saying so to the source files and forward the relevant communication to the scipy-dev mailing list.

Another common occurrence is for code to be translated or derived from code in R, Octave (both GPL-licensed) or a commercial application. Such code also cannot be included in SciPy. Simply implementing functionality with the same API as found in R/Octave/… is fine though, as long as the author doesn't look at the original incompatibly-licensed source code.

4.9.3 Version numbering

SciPy version numbering complies to PEP 440. Released final versions, which are the only versions appearing on PyPI, are numbered `MAJOR.MINOR.MICRO` where:

- `MAJOR` is an integer indicating the major version. It changes very rarely; a change in `MAJOR` indicates large (possibly backwards-incompatible) changes.
- `MINOR` is an integer indicating the minor version. Minor versions are typically released twice a year and can contain new features, deprecations and bug-fixes.
- `MICRO` is an integer indicating a bug-fix version. Bug-fix versions are released when needed, typically one or two per minor version. They cannot contain new features or deprecations.

Released alpha, beta and rc (release candidate) versions are numbered like final versions but with postfixes `a#`, `b#` and `rc#` respectively, with `#` an integer. Development versions are postfixed with `.dev0+<git-commit-hash>`.

Examples of valid SciPy version strings are:

```
0.16.0
0.15.1
0.14.0a1
0.14.0b2
0.14.0rc1
0.17.0.dev0+ac53f09
```

An installed SciPy version contains these version identifiers:

```
scipy.__version__            # complete version string, including git commit␣
↪hash for dev versions
scipy.version.short_version  # string, only major.minor.micro
scipy.version.version        # string, same as scipy.__version__
scipy.version.full_version   # string, same as scipy.__version__
```

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```
scipy.version.release         # bool, development or (alpha/beta/rc/final)␣
↪released version
scipy.version.git_revision    # string, git commit hash from which scipy was␣
↪built
```

4.9.4 Deprecations

There are various reasons for wanting to remove existing functionality: it's buggy, the API isn't understandable, it's superseded by functionality with better performance, it needs to be moved to another SciPy submodule, etc.

In general it's not a good idea to remove something without warning users about that removal first. Therefore this is what should be done before removing something from the public API:

1. Propose to deprecate the functionality on the scipy-dev mailing list and get agreement that that's OK.
2. Add a `DeprecationWarning` for it, which states that the functionality was deprecated, and in which release. For Cython APIs, see *Deprecating public Cython APIs* for the practical steps.
3. Mention the deprecation in the release notes for that release.
4. Wait till at least 6 months after the release date of the release that introduced the `DeprecationWarning` before removing the functionality.
5. Mention the removal of the functionality in the release notes.

The 6 months waiting period in practice usually means waiting two releases. When introducing the warning, also ensure that those warnings are filtered out when running the test suite so they don't pollute the output.

It's possible that there is reason to want to ignore this deprecation policy for a particular deprecation; this can always be discussed on the scipy-dev mailing list.

4.9.5 Distributing

Distributing Python packages is nontrivial - especially for a package with complex build requirements like SciPy - and subject to change. For an up-to-date overview of recommended tools and techniques, see the Python Packaging User Guide. This document discusses some of the main issues and considerations for SciPy.

Dependencies

Dependencies are things that a user has to install in order to use (or build/test) a package. They usually cause trouble, especially if they're not optional. SciPy tries to keep its dependencies to a minimum; currently they are:

Unconditional run-time dependencies:

- Numpy

Conditional run-time dependencies:

- pytest (to run the test suite)
- asv (to run the benchmarks)
- matplotlib (for some functions that can produce plots)
- Pillow (for image loading/saving)
- scikits.umfpack (optionally used in `sparse.linalg`)

- mpmath (for more extended tests in `special`)
- pydata/sparse (compatibility support in `scipy.sparse`)

Unconditional build-time dependencies:

- Numpy
- A BLAS and LAPACK implementation (reference BLAS/LAPACK, ATLAS, OpenBLAS, MKL are all known to work)
- Cython
- setuptools
- pybind11

Conditional build-time dependencies:

- wheel (`python setup.py bdist_wheel`)
- Sphinx (docs)
- PyData Sphinx theme (docs)
- Sphinx-Panels (docs)
- matplotlib (docs)
- LaTeX (pdf docs)
- Pillow (docs)

Furthermore of course one needs C, C++ and Fortran compilers to build SciPy, but those we don't consider to be dependencies and are therefore not discussed here. For details, see https://scipy.github.io/devdocs/building/.

When a package provides useful functionality and it's proposed as a new dependency, consider also if it makes sense to vendor (i.e. ship a copy of it with scipy) the package instead. For example, decorator is vendored in `scipy._lib`.

The only dependency that is reported to pip is Numpy, see `install_requires` in SciPy's main `setup.py`. The other dependencies aren't needed for SciPy to function correctly

Issues with dependency handling

There are some issues with how Python packaging tools handle dependencies reported by projects. Because SciPy gets regular bug reports about this, we go in a bit of detail here.

SciPy only reports its dependency on NumPy via `install_requires` if NumPy isn't installed at all on a system, or when building wheels with `bdist_wheel`. SciPy no longer uses `setup_requires` (which in the past invoked `easy_install`); build dependencies are now handled only via `pyproject.toml`. `pyproject.toml` relies on PEP 517; `pip` has `--no-use-pep517` and `--no-build-isolation` flags that may ignore `pyproject.toml` or treat it differently - if users use those flags, they are responsible for installing the correct build dependencies themselves.

Version ranges for NumPy and other dependencies

For dependencies it's important to set lower and upper bounds on their versions. For *build-time* dependencies, they are specified in `pyproject.toml` and the versions will *only* apply to the SciPy build itself. It's fine to specify either a range or a specific version for a dependency like `wheel` or `setuptools`. For NumPy we have to worry about ABI compatibility too, hence we specify the version with == to the lowest supported version (because NumPy's ABI is backward but not forward compatible).

For *run-time dependencies* (currently only `numpy`), we specify the range of versions in `pyproject.toml` and in `install_requires` in `setup.py`. Getting the upper bound right is slightly tricky. If we don't set any bound, a too-new version will be pulled in a few years down the line, and NumPy may have deprecated and removed some API that SciPy depended on by then. On the other hand if we set the upper bound to the newest already-released version,

then as soon as a new NumPy version is released there will be no matching SciPy version that works with it. Given that NumPy and SciPy both release in a 6-monthly cadence and that features that get deprecated in NumPy should stay around for another two releases, we specify the upper bound as `<1.xx+3.0` (where `xx` is the minor version of the latest already-released NumPy.

Supported Python and NumPy versions

The Python versions that SciPy supports are listed in the list of PyPI classifiers in `setup.py`, and mentioned in the release notes for each release. All newly released Python versions will be supported as soon as possible. For the general policy on dropping support for a Python or NumPy version, see NEP 29. The final decision on dropping support is always taken on the scipy-dev mailing list.

The lowest supported Numpy version for a SciPy version is mentioned in the release notes and is encoded in `pyproject.toml`, `scipy/__init__.py` and the `install_requires` field of `setup.py`. Typically the latest SciPy release supports ~5-7 minor versions of NumPy: up to 2.5 years' old NumPy versions, (given that the frequency of NumPy releases is about 2x/year at the time of writing) plus two versions into the future.

Supported versions of optional dependencies and compilers is documented in *Toolchain Roadmap*. Note that not all versions of optional dependencies that are supported are tested well or at all by SciPy's Continuous Integration setup. Issues regarding this are dealt with as they come up in the issue tracker or mailing list.

Building binary installers

Note: This section is only about building SciPy binary installers to *distribute*. For info on building SciPy on the same machine as where it will be used, see this scipy.org page.

There are a number of things to take into consideration when building binaries and distributing them on PyPI or elsewhere.

General

- A binary is specific for a single Python version (because different Python versions aren't ABI-compatible, at least up to Python 3.4).
- Build against the lowest NumPy version that you need to support, then it will work for all NumPy versions with the same major version number (NumPy does maintain backwards ABI compatibility).

Windows

- The currently most easily available toolchain for building Python.org compatible binaries for SciPy is installing MSVC (see https://wiki.python.org/moin/WindowsCompilers) and mingw64-gfortran. Support for this configuration requires numpy.distutils from NumPy >= 1.14.dev and a gcc/gfortran-compiled static `openblas.a`. This configuration is currently used in the Appveyor configuration for https://github.com/MacPython/scipy-wheels
- For 64-bit Windows installers built with a free toolchain, use the method documented at https://github.com/numpy/numpy/wiki/Mingw-static-toolchain. That method will likely be used for SciPy itself once it's clear that the maintenance of that toolchain is sustainable long-term. See the MingwPy project and this thread for details.
- The other way to produce 64-bit Windows installers is with `icc`, `ifort` plus `MKL` (or `MSVC` instead of `icc`). For Intel toolchain instructions see this article and for (partial) MSVC instructions see this wiki page.
- Older SciPy releases contained a .exe "superpack" installer. Those contain 3 complete builds (no SSE, SSE2, SSE3), and were built with https://github.com/numpy/numpy-vendor. That build setup is known to not work well anymore and is no longer supported. It used g77 instead of gfortran, due to complex DLL distribution issues (see gh-2829). Because the toolchain is no longer supported, g77 support isn't needed anymore and SciPy can now include Fortran 90/95 code.

OS X

- To produce OS X wheels that work with various Python versions (from python.org, Homebrew, MacPython), use the build method provided by https://github.com/MacPython/scipy-wheels.
- DMG installers for the Python from python.org on OS X can still be produced by `tools/scipy-macosx-installer/`. SciPy doesn't distribute those installers anymore though, now that there are binary wheels on PyPi.

Linux

- PyPi-compatible Linux wheels can be produced via the manylinux project. The corresponding build setup for TravisCI for SciPy is set up in https://github.com/MacPython/scipy-wheels.

Other Linux build-setups result to PyPi incompatible wheels, which would need to be distributed via custom channels, e.g. in a Wheelhouse, see at the wheel and Wheelhouse docs.

4.9.6 Making a SciPy release

At the highest level, this is what the release manager does to release a new SciPy version:

1. Propose a release schedule on the scipy-dev mailing list.
2. Create the maintenance branch for the release.
3. Tag the release.
4. Build all release artifacts (sources, installers, docs).
5. Upload the release artifacts.
6. Announce the release.
7. Port relevant changes to release notes and build scripts to master.

In this guide we attempt to describe in detail how to perform each of the above steps. In addition to those steps, which have to be performed by the release manager, here are descriptions of release-related activities and conventions of interest:

- *Backporting*
- *Labels and Milestones*
- *Version numbering*
- *Supported Python and NumPy versions*
- *Deprecations*

Proposing a release schedule

A typical release cycle looks like:

- Create the maintenance branch
- Release a beta version
- Release a "release candidate" (RC)
- If needed, release one or more new RCs
- Release the final version once there are no issues with the last release candidate

There's usually at least one week between each of the above steps. Experience shows that a cycle takes between 4 and 8 weeks for a new minor version. Bug-fix versions don't need a beta or RC, and can be done much quicker.

Ideally the final release is identical to the last RC, however there may be minor difference - it's up to the release manager to judge the risk of that. Typically, if compiled code or complex pure Python code changes then a new RC is needed, while a simple bug-fix that's backported from master doesn't require a new RC.

To propose a schedule, send a list with estimated dates for branching and beta/rc/final releases to scipy-dev. In the same email, ask everyone to check if there are important issues/PRs that need to be included and aren't tagged with the Milestone for the release or the "backport-candidate" label.

Creating the maintenance branch

Before branching, ensure that the release notes are updated as far as possible. Include the output of `tools/gh_lists.py` and `tools/authors.py` in the release notes.

Maintenance branches are named `maintenance/<major>.<minor>.x` (e.g. 0.19.x). To create one, simply push a branch with the correct name to the scipy repo. Immediately after, push a commit where you increment the version number on the master branch and add release notes for that new version. Send an email to scipy-dev to let people know that you've done this.

Updating upper bounds of dependencies

In master we do not set upper bounds, because we want to test new releases or development versions of dependencies there. In a maintenance branch however, the goal is to be able to create releases that stay working for years. Hence correct upper bounds must be set. The following places must be updated after creating a maintenance branch:

- ***`pyproject.toml`: all build-time dependencies, as well as supported Python***

  and NumPy versions
- `setup.py`: supported Python and NumPy versions
- `scipy/__init__.py`: for NumPy version check

Each file has comments describing how to set the correct upper bounds.

Tagging a release

First ensure that you have set up GPG correctly. See https://github.com/scipy/scipy/issues/4919 for a discussion of signing release tags, and https://keyring.debian.org/creating-key.html for instructions on creating a GPG key if you do not have one. Note that on some platforms it may be more suitable to use `gpg2` instead of `gpg` so that passwords may be stored by `gpg-agent` as discussed in https://github.com/scipy/scipy/issues/10189. When preparing a release remotely, it may be necessary to set `pinentry-mode loopback` in `~/.gnupg/gpg-agent.conf` because use of `gpg2` will otherwise proceed via an inaccessible graphical password prompt.

To make your key more readily identifiable as you, consider sending your key to public keyservers, with a command such as:

```
gpg --send-keys <yourkeyid>
```

Check that all relevant commits are in the branch. In particular, check issues and PRs under the Milestone for the release (https://github.com/scipy/scipy/milestones), PRs labeled "backport-candidate", and that the release notes are up-to-date and included in the html docs.

Then edit `setup.py` to get the correct version number (set `ISRELEASED = True`) and commit it with a message like `REL: set version to <version-number>`. Don't push this commit to the SciPy repo yet.

Finally tag the release locally with `git tag -s <v1.x.y>` (the `-s` ensures the tag is signed). If `gpg2` is preferred, then `git config --global gpg.program gpg2` may be appropriate. Continue with building release artifacts (next section). Only push the release commit to the scipy repo once you have built the sdists and docs successfully. Then continue with building wheels. Only push the release tag to the repo once all wheels have been built successfully on TravisCI and Appveyor (if it fails, you have to move the tag otherwise - which is bad practice). Finally, after pushing the tag, also push a second commit which increments the version number and sets `ISRELEASED` to False again. This also applies with new release candidates, and for removing the `rc` affix when switching from release candidate to release proper.

Building release artifacts

Here is a complete list of artifacts created for a release:

- source archives (`.tar.gz`, `.zip` and `.tar.xz` for GitHub Releases, only `.tar.gz` is uploaded to PyPI)
- Binary wheels for Windows, Linx and OS X
- Documentation (`html`, `pdf`)
- A `README` file
- A `Changelog` file

Source archives, Changelog and README are built by running `paver release` in the repo root, and end up in `REPO_ROOT/release/`. Do this after you've created the signed tag locally. `paver release` will be sensitive to the version of Cython available in your build environment, so make sure your version matches the minimum requirements for the release. If this completes without issues, push the release commit (not the tag, see section above) to the scipy repo. If `pavement.py` is causing issues, it is also possible to simply use `python setup.py sdist` and perform the release notes task from `pavement.py` by hand.

To build wheels, push a commit to a branch used for the current release at https://github.com/MacPython/scipy-wheels . This triggers builds for all needed Python versions on TravisCI. Update and check the `.travis.yml` and `appveyor.yml` config files what commit to build, and what Python and NumPy are used for the builds (it needs to be the lowest supported NumPy version for each Python version). See the README file in the scipy-wheels repo for more details. Note that because several months may pass between `SciPy` releases, it is sometimes necessary to update the versions of the `gfortran-install` and `multibuild` submodules used for wheel builds. If the wheels builds reveal issues that need to be fixed with backports on the maintenance branch, you may remove the local tags (for example `git tag -d v1.2.0rc1`) and restart with tagging above on the new candidate commit.

The TravisCI and Appveyor builds run the tests from the built wheels and if they pass, upload the wheels to a container pointed to at https://github.com/MacPython/scipy-wheels Once there are successful wheel builds, it is recommended to create a versioned branch in the `scipy-wheels` repo, which will for example be adjusted to point to different maintenance branch commits if there are multiple release candidates.

From there you can download them for uploading to PyPI. This can be done in an automated fashion using `tools/download-wheels.py`:

```
$ python tools/download-wheels.py 1.5.0rc1 -w REPO_ROOT/release/installers
```

The correct URL to use is shown in https://github.com/MacPython/scipy-wheels and should agree with the above one.

After this, we want to regenerate the README file, in order to have the MD5 and SHA256 checksums of the just downloaded wheels in it. Run:

```
$ paver write_release_and_log
```

Uploading release artifacts

For a release there are currently five places on the web to upload things to:

- PyPI (tarballs, wheels)
- Github releases (tarballs, release notes, Changelog)
- scipy.org (an announcement of the release)
- docs.scipy.org (html/pdf docs)

PyPI:

Upload first the wheels and then the sdist:

```
twine upload -s REPO_ROOT/release/installers/*.whl
twine upload -s REPO_ROOT/release/installers/scipy-1.x.y.tar.gz
```

If `gpg2` is preferred, then the above commands may also include `--sign-with gpg2`

Github Releases:

Use GUI on https://github.com/scipy/scipy/releases to create release and upload all release artifacts. At this stage, it is appropriate to push the tag and associate the new release (candidate) with this tag in the GUI. For example, `git push upstream v1.2.0rc1`, where `upstream` represents `scipy/scipy`. It is useful to check a previous release to determine exactly which artifacts should be included in the GUI upload process. Also, note that the release notes are not automatically populated into the release description on GitHub, and some manual reformatting to markdown can be quite helpful to match the formatting of previous releases on the site. We generally do not include Issue and Pull Request lists in these GUI descriptions.

scipy.org:

Sources for the site are in https://github.com/scipy/scipy.org. Update the News section in `www/index.rst` and then do `make upload USERNAME=yourusername`. This is only for proper releases, not release candidates.

docs.scipy.org:

First build the scipy docs, by running `make dist` in `scipy/doc/`. Verify that they look OK, then upload them to the doc server with `make upload USERNAME=rgommers RELEASE=0.19.0`. Note that SSH access to the doc server is needed; ask @pv (server admin) or @rgommers (can upload) if you don't have that.

The sources for the website itself are maintained in https://github.com/scipy/docs.scipy.org/. Add the new SciPy version in the table of releases in `index.rst`. Push that commit, then do `make upload USERNAME=yourusername`. This is only for proper releases, not release candidates.

Wrapping up

Send an email announcing the release to the following mailing lists:

- scipy-dev
- numpy-discussion
- python-announce (not for beta/rc releases)

For beta and rc versions, ask people in the email to test (run the scipy tests and test against their own code) and report issues on Github or scipy-dev.

After the final release is done, port relevant changes to release notes, build scripts, author name mapping in `tools/authors.py` and any other changes that were only made on the maintenance branch to master.

4.10 SciPy API Development Guide

4.10.1 A Design Specification for `nan_policy`

Many functions in *scipy.stats* have a parameter called `nan_policy` that determines how the function handles data that contains `nan`. In this section, we provide SciPy developer guidelines for how `nan_policy` is intended to be used, to ensure that as this parameter is added to new functions, we maintain a consistent API.

The basic API

The parameter `nan_policy` accepts three possible strings: `'omit'`, `'raise'` and `'propagate'`. The meanings are:

- `nan_policy='omit'`: Ignore occurrences of `nan` in the input. Do not generate a warning if the input contains `nan` (unless the equivalent input with the `nan` values removed would generate a warning). For example, for the simple case of a function that accepts a single array and returns a scalar (and ignoring the possible use of `axis` for the moment):

```
func([1.0, 3.0, np.nan, 5.0], nan_policy='omit')
```

should behave the same as:

```
func([1.0, 3.0, 5.0])
```

More generally, for functions that return a scalar, `func(a, nan_policy='omit')` should behave the same as `func(a[~np.isnan(a)])`.

For functions that transform a vector to a new vector of the same size and for which each entry in the output array depends on more than just the corresponding value in the input array[1] (e.g. *scipy.stats.zscore*, *scipy.stats.boxcox* *when* `lmbda` *is None*),:

```
y = func(a, nan_policy='omit')
```

should behave the same as:

```
nan_mask = np.isnan(a)
y = np.empty(a.shape, dtype=np.float64)
y[~nan_mask] = func(a[~nan_mask])
y[nan_mask] = np.nan
```

(In general, the dtype of `y` might depend on `a` and on the expected behavior of `func`). In other words, a *nan* in the input gives a corresponding *nan* in the output, but the presence of that *nan* does not affect the calculation of the non-*nan* values.

Unit tests for this property should be used to test functions that handle `nan_policy`.

For functions that return a scalar and that accept two or more arguments but whose values are not related (e.g. *scipy.stats.ansari*, *scipy.stats.f_oneway*), the same idea applies to each input array. So:

```
func(a, b, nan_policy='omit')
```

should behave the same as:

[1] If an element of the output depends only on the corresponding element of the input (e.g. `numpy.sin`, *scipy.special.gamma*), then there is no need for a `nan_policy` parameter.

```
func(a[~np.isnan(a)], b[~np.isnan(b)])
```

For inputs with *related* or *paired* values (e.g. *scipy.stats.pearsonr*, *scipy.stats.ttest_rel*) the recommended behavior is to omit all the values for which any of the related values are `nan`. For a function with two related array inputs, this means:

```
y = func(a, b, nan_policy='omit')
```

should behave the same as:

```
hasnan = np.isnan(a) | np.isnan(b)  # Union of the isnan masks.
y = func(a[~hasnan], b[~hasnan])
```

The docstring for such a function should clearly state this behavior.

- `nan_policy='raise'`: Raise a `ValueError`.
- `nan_policy='propagate'`: Propagate the `nan` value to the output. Typically, this means just execute the function without checking for `nan`, but see

  https://github.com/scipy/scipy/issues/7818

  for an example where that might lead to unexpected output.

`nan_policy` combined with an `axis` parameter

There is nothing surprising here–the principle mentioned above still applies when the function has an `axis` parameter. Suppose, for example, `func` reduces a 1-d array to a scalar, and handles n-d arrays as a collection of 1-d arrays, with the `axis` parameter specifying the axis along which the reduction is to be applied. If, say:

```
func([1, 3, 4])      -> 10.0
func([2, -3, 8, 2]) ->  4.2
func([7, 8])         ->  9.5
func([])             -> -inf
```

then:

```
func([[  1, nan,   3,   4],
      [  2,  -3,   8,   2],
      [nan,   7, nan,   8],
      [nan, nan, nan, nan]], nan_policy='omit', axis=-1)
```

must give the result:

```
np.array([10.0, 4.2, 9.5, -inf])
```

Edge cases

A function that implements the `nan_policy` parameter should gracefully handle the case where *all* the values in the input array(s) are `nan`. The basic principle described above still applies:

```
func([nan, nan, nan], nan_policy='omit')
```

should behave the same as:

```
func([])
```

In practice, when adding `nan_policy` to an existing function, it is not unusual to find that the function doesn't already handle this case in a well-defined manner, and some thought and design may have to be applied to ensure that it works. The correct behavior (whether that be to return `nan`, return some other value, raise an exception, or something else) will be determined on a case-by-case basis.

Why doesn't `nan_policy` also apply to `inf`?

Although we learn in grade school that "infinity is not a number", the floating point values `nan` and `inf` are qualitatively different. The values `inf` and `-inf` act much more like regular floating point values than `nan`.

- One can compare `inf` to other floating point values and it behaves as expected, e.g. `3 < inf` is True.
- For the most part, arithmetic works "as expected" with `inf`, e.g. `inf + inf = inf`, `-2*inf = -inf`, `1/inf = 0`, etc.
- Many existing functions work "as expected" with `inf`: `np.log(inf) = inf`, `np.exp(-inf) = 0`, `np.array([1.0, -1.0, np.inf]).min() = -1.0`, etc.

So while `nan` almost always means "something went wrong" or "something is missing", `inf` can in many cases be treated as a useful floating point value.

It is also consistent with the NumPy `nan` functions to not ignore `inf`:

```
>>> np.nanmax([1, 2, 3, np.inf, np.nan])
inf
>>> np.nansum([1, 2, 3, np.inf, np.nan])
inf
>>> np.nanmean([8, -np.inf, 9, 1, np.nan])
-inf
```

How *not* to implement `nan_policy`

In the past (and possibly currently), some `stats` functions handled `nan_policy` by using a masked array to mask the `nan` values, and then computing the result using the functions in the `mstats` subpackage. The problem with this approach is that the masked array code might convert `inf` to a masked value, which we don't want to do (see above). It also means that, if care is not taken, the return value will be a masked array, which will likely be a surprise to the user if they passed in regular arrays.

4.10.2 Adding vectorized ufuncs in `scipy.special`

Many of the functions in `special` are vectorized versions of scalar functions. The scalar functions are written by hand and the necessary loops for vectorization are generated automatically. This section discusses the steps necessary to add a new vectorized special function.

The first step in adding a new vectorized function is writing the corresponding scalar function. This can be done in Cython, C, C++, or Fortran. If starting from scratch then Cython should be preferred because the code is easier to maintain for developers only familiar with Python. If the primary code is in Fortran then it is necessary to write a C wrapper around the code; for examples of such wrappers see `specfun_wrappers.c`.

After implementing the scalar function, register the new function by adding an entry to `functions.json`. The docstring in `generate_ufuncs.py` explains the format. Also add documentation for the new function by adding an entry to `add_newdocs.py`; look in the file for examples.

When writing the parameters section of the documentation for ufuncs, the type of an argument should be `array_like`. Discussion of whether an argument can be e.g. real or complex-valued should be saved for the description. So for example, if we were to document the parameters for the Gamma function then it should look like this:

```
Parameters
----------
z : array_like
    Real or complex valued argument
```

When documenting the returns section, the type of the returned value should be `scalar or ndarray` since ufuncs return scalars when given scalars as arguments. Also keep in mind that providing a `name` for the return value is optional, and indeed is often not helpful for special functions. So for the Gamma function we might have something like this:

```
Returns
-------
scalar or ndarray
    Values of the Gamma function
```

4.11 SciPy Project Governance

The purpose of this document is to formalize the governance process used by the SciPy project in both ordinary and extraordinary situations, and to clarify how decisions are made and how the various elements of our community interact, including the relationship between open source collaborative development and work that may be funded by for-profit or non-profit entities.

4.11.1 The Project

The SciPy Project (The Project) is an open source software project. The goal of The Project is to develop open source software for scientific computing in Python, and, in particular, the `scipy` package. The Software developed by The Project is released under the BSD (or similar) open source license, developed openly and hosted on public GitHub repositories under the `scipy` GitHub organization.

The Project is developed by a team of distributed developers, called Contributors. Contributors are individuals who have contributed code, documentation, designs, or other work to the Project. Anyone can be a Contributor. Contributors can be affiliated with any legal entity or none. Contributors participate in the project by submitting, reviewing, and discussing GitHub Pull Requests and Issues and participating in open and public Project discussions on GitHub, mailing lists, and other channels. The foundation of Project participation is openness and transparency.

The Project Community consists of all Contributors and Users of the Project. Contributors work on behalf of and are responsible to the larger Project Community and we strive to keep the barrier between Contributors and Users as low as possible.

The Project is not a legal entity, nor does it currently have any formal relationships with legal entities.

4.11.2 Governance

This section describes the governance and leadership model of The Project.

The foundations of Project governance are:

- openness and transparency
- active contribution
- institutional neutrality

Traditionally, Project leadership was provided by a subset of Contributors, called Core Developers, whose active and consistent contributions have been recognized by their receiving "commit rights" to the Project GitHub repositories. In general, all Project decisions are made through consensus among the Core Developers with input from the Community.

While this approach has served us well, as the Project grows, we see a need for a more formal governance model. The SciPy Core Developers expressed a preference for a leadership model which includes a BDFL (Benevolent Dictator for Life). Therefore, moving forward The Project leadership will consist of a BDFL and Steering Council.

BDFL

The Project will have a BDFL (Benevolent Dictator for Life), who is currently Pauli Virtanen. As Dictator, the BDFL has the authority to make all final decisions for The Project. As Benevolent, the BDFL, in practice, chooses to defer that authority to the consensus of the community discussion channels and the Steering Council (see below). It is expected, and in the past has been the case, that the BDFL will only rarely assert his/her final authority. Because rarely used, we refer to BDFL's final authority as a "special" or "overriding" vote. When it does occur, the BDFL override typically happens in situations where there is a deadlock in the Steering Council or if the Steering Council asks the BDFL to make a decision on a specific matter. To ensure the benevolence of the BDFL, The Project encourages others to fork the project if they disagree with the overall direction the BDFL is taking. The BDFL may delegate his/her authority on a particular decision or set of decisions to any other Council member at his/her discretion.

The BDFL can appoint his/her successor, but it is expected that the Steering Council would be consulted on this decision. If the BDFL is unable to appoint a successor, the Steering Council will make this decision - preferably by consensus, but if needed, by a majority vote.

Note that the BDFL can step down at any time, and acting in good faith, will also listen to serious calls to do so. Also note that the BDFL is more a role for fallback decision making rather than that of a director/CEO.

Steering Council

The Project will have a Steering Council that consists of Project Contributors who have produced contributions that are substantial in quality and quantity, and sustained over at least one year. The overall role of the Council is to ensure, through working with the BDFL and taking input from the Community, the long-term well-being of the project, both technically and as a community.

The Council will have a Chair, who is tasked with keeping the organizational aspects of the functioning of the Council and the Project on track. The Council will also appoint a Release Manager for the Project, who has final responsibility for one or more releases.

During the everyday project activities, Council Members participate in all discussions, code review, and other project activities as peers with all other Contributors and the Community. In these everyday activities, Council Members do not have any special power or privilege through their membership on the Council. However, it is expected that because of the quality and quantity of their contributions and their expert knowledge of the Project Software and Services, Council Members will provide useful guidance, both technical and in terms of project direction, to potentially less experienced contributors.

The Steering Council and its Members play a special role in certain situations. In particular, the Council may:

- Make decisions about the overall scope, vision, and direction of the project.
- Make decisions about strategic collaborations with other organizations or individuals.
- Make decisions about specific technical issues, features, bugs, and pull requests. They are the primary mechanism of guiding the code review process and merging pull requests.
- Make decisions about the Services that are run by The Project and manage those Services for the benefit of the Project and Community.
- Make decisions when regular community discussion does not produce consensus on an issue in a reasonable time frame.
- Update policy documents, such as this one.

Council membership

To become eligible for being a Steering Council Member, an individual must be a Project Contributor who has produced contributions that are substantial in quality and quantity, and sustained over at least one year. Potential Council Members are nominated by existing Council members and voted upon by the existing Council after asking if the potential Member is interested and willing to serve in that capacity. The Council will be initially formed from the set of existing Core Developers who, as of January 2017, have been significantly active over the last two years.

When considering potential Members, the Council will look at candidates with a comprehensive view of their contributions. This will include, but is not limited to, code, code review, infrastructure work, mailing list and chat participation, community help/building, education and outreach, design work, etc. We are deliberately not setting arbitrary quantitative metrics (like "100 commits in this repo") to avoid encouraging behavior that plays to the metrics rather than the project's overall well-being. We want to encourage a diverse array of backgrounds, viewpoints, and talents in our team, which is why we explicitly do not define code as the sole metric on which council membership will be evaluated.

If a Council Member becomes inactive in the project for a period of one year, they will be considered for removal from the Council. Before removal, inactive Member will be approached to see if they plan on returning to active participation. If not, they will be removed immediately upon a Council vote. If they plan on returning to active participation soon, they will be given a grace period of one year. If they don't return to active participation within that time period they will be removed by vote of the Council without further grace period. All former Council Members can be considered for membership again at any time in the future, like any other Project Contributor. Retired Council Members will be listed on the project website, acknowledging the period during which they were active in the Council.

The Council reserves the right to eject current Members, other than the BDFL, if they are deemed to be actively harmful to the project's well-being, and attempts at communication and conflict resolution have failed.

A list of current Steering Council Members is maintained at the page governance-people.

Council Chair

The Chair will be appointed by the Steering Council. The Chair can stay on as long as he/she wants, but may step down at any time and will listen to serious calls to do so (similar to the BDFL role). The Chair will be responsible for:

- Starting a review of the technical direction of the project (as captured by the *SciPy Roadmap*) bi-yearly, around mid-April and mid-October.
- At the same times of the year, summarizing any relevant organizational updates and issues in the preceding period, and asking for feedback/suggestions on the mailing list.
- Ensuring the composition of the Steering Council stays current.
- Ensuring matters discussed in private by the Steering Council get summarized on the mailing list to keep the Community informed.
- Ensuring other important organizational documents (e.g., Code of Conduct, Fiscal Sponsorship Agreement) stay current after they are added.

Release Manager

The Release Manager has final responsibility for making a release. This includes:

- Proposing of and deciding on the timing of a release.
- Determining the content of a release in case there is no consensus on a particular change or feature.
- Creating the release and announcing it on the relevant public channels.

For more details on what those responsibilities look like in practice, see *Making a SciPy release*.

Conflict of interest

It is expected that the BDFL and Council Members will be employed at a wide range of companies, universities, and non-profit organizations. Because of this, it is possible that Members will have a conflict of interest. Such conflicts of interest include, but are not limited to:

- Financial interest, such as investments, employment or contracting work, outside of The Project that may influence their work on The Project.
- Access to proprietary information of their employer that could potentially leak into their work with the Project.

All members of the Council, BDFL included, shall disclose to the rest of the Council any conflict of interest they may have. Members with a conflict of interest in a particular issue may participate in Council discussions on that issue, but must recuse themselves from voting on the issue. If the BDFL has recused his/herself for a particular decision, the Council will appoint a substitute BDFL for that decision.

Private communications of the Council

Unless specifically required, all Council discussions and activities will be public and done in collaboration and discussion with the Project Contributors and Community. The Council will have a private mailing list that will be used sparingly and only when a specific matter requires privacy. When private communications and decisions are needed, the Council will do its best to summarize those to the Community after removing personal/private/sensitive information that should not be posted to the public internet.

Council decision making

If it becomes necessary for the Steering Council to produce a formal decision, then they will use a form of the Apache Foundation voting process. This is a formalized version of consensus, in which +1 votes indicate agreement, -1 votes are vetoes (and must be accompanied with a rationale, as above), and one can also vote fractionally (e.g. -0.5, +0.5) if one wishes to express an opinion without registering a full veto. These numeric votes are also often used informally as a way of getting a general sense of people's feelings on some issue, and should not normally be taken as formal votes. A formal vote only occurs if explicitly declared, and if this does occur, then the vote should be held open for long enough to give all interested Council Members a chance to respond – at least one week.

In practice, we anticipate that for most Steering Council decisions (e.g., voting in new members) a more informal process will suffice.

4.11.3 Institutional Partners and funding

The Steering Council is the primary leadership for the project. No outside institution, individual, or legal entity has the ability to own, control, usurp, or influence the project other than by participating in the Project as Contributors and Council Members. However, because institutions can be an important funding mechanism for the project, it is important to formally acknowledge institutional participation in the project. These are Institutional Partners.

An Institutional Contributor is any individual Project Contributor who contributes to the project as part of their official duties at an Institutional Partner. Likewise, an Institutional Council Member is any Project Steering Council Member who contributes to the project as part of their official duties at an Institutional Partner.

With these definitions, an Institutional Partner is any recognized legal entity in any country that employs at least 1 Institutional Contributor or Institutional Council Member. Institutional Partners can be for-profit or non-profit entities.

Institutions become eligible to become an Institutional Partner by employing individuals who actively contribute to The Project as part of their official duties. To state this another way, the only way for a Partner to influence the project is by actively contributing to the open development of the project, in equal terms to any other member of the community of Contributors and Council Members. Merely using Project Software in institutional context does not allow an entity to become an Institutional Partner. Financial gifts do not enable an entity to become an Institutional Partner. Once an institution becomes eligible for Institutional Partnership, the Steering Council must nominate and approve the Partnership.

If, at some point, an existing Institutional Partner stops having any contributing employees, then a one year grace period commences. If, at the end of this one-year period, they continue not to have any contributing employees, then their Institutional Partnership will lapse, and resuming it will require going through the normal process for new Partnerships.

An Institutional Partner is free to pursue funding for their work on The Project through any legal means. This could involve a non-profit organization raising money from private foundations and donors or a for-profit company building proprietary products and services that leverage Project Software and Services. Funding acquired by Institutional Partners to work on The Project is called Institutional Funding. However, no funding obtained by an Institutional Partner can override the Steering Council. If a Partner has funding to do SciPy work and the Council decides to not pursue that work as a project, the Partner is free to pursue it on their own. However, in this situation, that part of the Partner's work will not be under the SciPy umbrella and cannot use the Project trademarks in any way that suggests a formal relationship.

Institutional Partner benefits are:

- acknowledgement on the SciPy website and in talks
- ability to acknowledge their own funding sources on the SciPy website and in talks
- ability to influence the project through the participation of their Council Member
- invitation of the Council Members to SciPy Developer Meetings

A list of current Institutional Partners is maintained at the page governance-people.

4.11.4 Document history

https://github.com/scipy/scipy/commits/master/doc/source/dev/governance/governance.rst

4.11.5 Acknowledgements

Substantial portions of this document were adapted from the Jupyter/IPython project's governance document and NumPy's governance document.

4.11.6 License

To the extent possible under law, the authors have waived all copyright and related or neighboring rights to the SciPy project governance document, as per the CC-0 public domain dedication / license.

4.12 Development environment quickstart guide (macOS)

This quickstart guide will cover:

- setting up and maintaining a development environment, including installing compilers and SciPy build dependencies;
- creating a personal fork of the SciPy repository on GitHub;
- using git to manage a local repository with development branches;
- performing an in-place build of SciPy; and
- creating a virtual environment that adds this development version of SciPy to the Python path

in macOS (Tested on 11.1).

Note: This guide does not present the only way to set up a development environment; there are many valid choices of Python distribution, C/Fortran compiler, and installation options. The steps here can often be adapted for other choices, but we cannot provide documentation tailored for them.

This guide assumes that you are starting without an existing Python 3 installation. If you already have Python 3, you might want to uninstall it first to avoid ambiguity over which Python version is being used at the command line.

4.12.1 Building SciPy

1. Install Apple Developer Tools. An easy way to do this is to open a terminal window, enter the command `xcode-select --install`, and follow the prompts. Apple Developer Tools includes git, the software we need to download and manage the SciPy source code.
2. Download, install, and test the latest release of the Anaconda Distribution of Python. In addition to the latest version of Python 3, the Anaconda Distribution includes dozens of the most popular Python packages for scientific computing, the `conda` package manager, and tools for managing virtual environments.

   If you're installing using the terminal, be sure to follow the "Next Steps" listed after the installer finishes. You might also need to restart your terminal window or enter `source ~/.bash_profile` for all the changes to take effect.

3. (Optional) In a terminal window, enter `conda list`. This shows a list of all the Python packages that came with the Anaconda Distribution of Python. Note the latest released version of SciPy is among them; this is not the development version you are going to build and will be able to modify.

   Ideally, we'd like to have both versions, and we'd like to be able to switch between the two as needed. Virtual environments can do just that. With a few keystrokes in the terminal or even the click of an icon, we can enable or disable our development version. Let's set that up.

   Note: If `conda` is not a recognized command, try restarting your terminal. If it is still not recognized, please see "Should I add Anaconda to the macOS or Linux PATH?" in the Anaconda FAQ.

   ---

4. Enter `conda create --name scipydev` to create an empty virtual environment named `scipydev` (or another name that you prefer). This tells `conda` to create a new, empty environment for our packages. Activate the environment with `conda activate scipydev`. Note that you'll need to have this virtual environment active whenever you want to work with the development version of SciPy.

5. Enter `conda config --env --add channels conda-forge` to tell Anaconda the source we want for our packages. Then enter `conda install python=3.8 numpy pybind11 cython pythran pytest compilers sphinx pydata-sphinx-theme sphinx-panels matplotlib mypy` to install the following packages:

   - `numpy pybind11 cython pythran` are four packages that SciPy depends on.
   - `compilers` holds compilers used to build SciPy's Fortran, C, and C++ source code.
   - `pytest` is needed for running the test suite.
   - `sphinx`, `pydata-sphinx-theme`, `sphinx-panels` and `matplotlib` are required to render the SciPy documentation.
   - `mypy` is a static type checker for Python. Consider using it.

   Note that we're installing SciPy's build dependencies and some other software, but not SciPy itself.

6. Browse to the SciPy repository on GitHub and create your own fork. You'll need to create a GitHub account if you don't already have one.

7. Browse to your fork. Your fork will have a URL like https://github.com/mdhaber/scipy, except with your GitHub username in place of "mdhaber".

8. Click the big, green "Clone or download" button, and copy the ".git" URL to the clipboard. The URL will be the same as your fork's URL, except it will end in ".git".

9. Create a folder for the SciPy source code in a convenient place on your computer. Navigate to it in the terminal.

10. Enter the command `git clone` followed by your fork's .git URL. Note that this creates in the terminal's working directory a `scipy` folder containing the SciPy source code.

11. In the terminal, navigate into the `scipy` root directory (e.g. `cd scipy`).

12. Initialize git submodules: `git submodule update --init`.

13. Do an in-place build: enter `python3 setup.py build_ext --inplace`. This will compile the C, C++, and Fortran code that comes with SciPy. We installed `python3` with Anaconda. `setup.py` is a script in the root directory of SciPy, which is why you have to be in the SciPy root directory to call it. `build_ext` is a command defined in `setup.py`, and `--inplace` is an option we'll use to ensure that the compiling happens in the SciPy directory you already have rather than the default location for Python packages. By building in-place, you avoid having to re-build SciPy before you can test changes to the Python code.

14. Test the build: enter `python3 runtests.py -v`. `runtests.py` is another script in the SciPy root directory. It runs a suite of tests that make sure SciPy is working as it should, and `-v` activates the `--verbose` option

to show all the test output. If the tests are successful, you now have a working development build of SciPy! You could stop here, but you would only be able to use this development build when the Python working directory is the SciPy root directory.

15. Enter `conda develop .`, where `.` refers to the present directory. This will allow us to `import` the development version of SciPy in Python regardless of Python's working directory.

16. In a new terminal window, test your setup. If you activate your virtual environment (e.g. `conda activate scipydev`) and run Python code that imports from SciPy, any changes you make to the SciPy code should be reflected when the code runs. After deactivating the virtual environment (`conda deactivate`), Python imports from the version of SciPy installed by Anaconda. You can also check which version of SciPy you're using by executing in Python:

```
import scipy
print(scipy.__version__)
```

If you have successfully imported a development version of SciPy, the word `dev` will appear in the output, e.g.:

```
1.6.0.dev0+be97f1a
```

4.13 Development environment quickstart guide (Ubuntu)

This quickstart guide will cover:

- setting up and maintaining a development environment, including installing compilers and SciPy build dependencies;
- creating a personal fork of the SciPy repository on GitHub;
- using git to manage a local repository with development branches;
- performing an in-place build of SciPy; and
- creating a virtual environment that adds this development version of SciPy to the Python path

in Ubuntu. (Tested on 16.04, 18.04, and 20.04). *Users running Windows can follow these instructions after setting up* Windows Subsystem for Linux *or an Amazon EC2 instance with Ubuntu 20.04. However, the instructions for setting up a development environment with Docker may be more reliable.*

Note: This guide does not present the only way to set up a development environment; there are many valid choices of Python distribution, C/Fortran compiler, and installation options. The steps here can often be adapted for other choices, but we cannot provide documentation tailored for them.

This guide assumes that you are starting without an existing Python 3 installation. If you already have Python 3, you might want to uninstall it first to avoid ambiguity over which Python version is being used at the command line.

4.13.1 Building SciPy

1. Download, install, and test the latest release of the Anaconda Distribution of Python. In addition to the latest version of Python 3, the Anaconda Distribution includes dozens of the most popular Python packages for scientific computing, the `conda` package manager, and tools for managing virtual environments.

   If you're installing using the terminal, be sure to follow the "Next Steps" listed after the installer finishes. You might also need to restart your terminal window or enter `source ~/.bashrc` for all the changes to take effect.

2. (Optional) In a terminal window, enter `conda list`. This shows a list of all the Python packages that came with the Anaconda Distribution of Python. Note the latest released version of SciPy is among them; this is not the development version you are going to build and will be able to modify.

   Ideally, we'd like to have both versions, and we'd like to be able to switch between the two as needed. Virtual environments can do just that. With a few keystrokes in the terminal or even the click of an icon, we can enable or disable our development version. Let's set that up.

   Note: If `conda` is not a recognized command, try restarting your terminal. If it is still not recognized, please see "Should I add Anaconda to the macOS or Linux PATH?" in the Anaconda FAQ.

   ---

3. Enter `conda create --name scipydev python=3.8 numpy pybind11 cython pythran pytest gfortran_linux-64 gxx_linux-64 sphinx pydata-sphinx-theme sphinx-panels matplotlib mypy git`. This tells `conda` to create a virtual environment named `scipydev` (or another name that you prefer) with several packages.

   - `numpy pybind11 cython pythran` are four packages that SciPy depends on.
   - `gfortran_linux-64 gxx_linux-64` are compilers used to build SciPy's Fortran, C, and C++ source code.
   - `pytest` is needed for running the test suite.
   - `sphinx`, `pydata-sphinx-theme`, `sphinx-panels` and `matplotlib` are required to render the SciPy documentation.
   - `mypy` is a static type checker for Python. Consider using it.
   - `git` is a version control system used to download and manage the SciPy source code.

   Note that we're installing SciPy's build dependencies and some other software, but not SciPy itself.

   Note: You could `conda create` an empty virtual environment first, then `conda install` the packages, but creating the virtual environment with all the packages you need is preferable to installing packages individually because it makes it easier for `conda` to solve the package dependencies optimally.

   ---

4. You're still in the base environment. Activate your new virtual environment by entering `conda activate scipydev`. If you're working with an old version of `conda`, you might need to type `source activate scipydev` instead (see here). Note that you'll need to have this virtual environment active whenever you want to work with the development version of SciPy.

5. Browse to the SciPy repository on GitHub and create your own fork. You'll need to create a GitHub account if you don't already have one.

6. Browse to your fork. Your fork will have a URL like https://github.com/mdhaber/scipy, except with your GitHub username in place of "mdhaber".

7. Click the big, green "Clone or download" button, and copy the ".git" URL to the clipboard. The URL will be the same as your fork's URL, except it will end in ".git".

8. Create a folder for the SciPy source code in a convenient place on your computer. Navigate to it in the terminal.
9. Enter the command `git clone` followed by your fork's .git URL. Note that this creates in the terminal's working directory a `scipy` folder containing the SciPy source code.
10. In the terminal, navigate into the `scipy` root directory (e.g. `cd scipy`).
11. Initialize git submodules: `git submodule update --init`.
12. Do an in-place build: enter `python3 setup.py build_ext --inplace`. This will compile the C, C++, and Fortran code that comes with SciPy. We installed `python3` with Anaconda. `setup.py` is a script in the root directory of SciPy, which is why you have to be in the SciPy root directory to call it. `build_ext` is a command defined in `setup.py`, and `--inplace` is an option we'll use to ensure that the compiling happens in the SciPy directory you already have rather than the default location for Python packages. By building in-place, you avoid having to re-build SciPy before you can test changes to the Python code.
13. Test the build: enter `python3 runtests.py -v`. `runtests.py` is another script in the SciPy root directory. It runs a suite of tests that make sure SciPy is working as it should, and `-v` activates the `--verbose` option to show all the test output. If the tests are successful, you now have a working development build of SciPy! You could stop here, but you would only be able to use this development build when the Python working directory is the SciPy root directory.
14. Enter `conda develop .`, where `.` refers to the present directory. This will allow us to `import` the development version of SciPy in Python regardless of Python's working directory.
15. In a new terminal window, test your setup. If you activate your virtual environment (e.g. `conda activate scipydev`) and run Python code that imports from SciPy, any changes you make to the SciPy code should be reflected when the code runs. After deactivating the virtual environment (`conda deactivate`), Python imports from the version of SciPy installed by Anaconda. You can also check which version of SciPy you're using by executing in Python:

```
import scipy
print(scipy.__version__)
```

If you have successfully imported a development version of SciPy, the word `dev` will appear in the output, e.g.:

```
1.6.0.dev0+be97f1a
```

4.14 Development workflow

Note: consider watching SciPy Development Workflow *before or after reading to see an example of fixing a bug and submitting a pull request.*

In *Development environment quickstart guide (macOS)* or *Development environment quickstart guide (Ubuntu)*, you created your own fork (copy) of the SciPy repository, cloned the repository on your own machine, and built SciPy from this source code. Before getting started here, there are two other things you need to do just once before you start modifying SciPy.

1. In a terminal, introduce yourself to Git:

```
git config --global user.email you@yourdomain.com
git config --global user.name "Your Name"
```

This information credits you for your work, but note that it will become publicly available if you "push" your work to GitHub. See Setting your commit email address in Git for more information.

2. Navigate to the root directory of your local SciPy repository and enter:

```
git remote add upstream https://github.com/scipy/scipy.git
```

This associates the name `upstream` with the official SciPy repository located at https://github.com/scipy/scipy.git. Note that when you cloned your fork of the SciPy repository, Git already associated the name `origin` with your fork. The reason you need both of these "remotes" is that you will typically start with the latest version of SciPy from the official repository `upstream`, make changes, "push" your changes to your fork of the repository `origin`, and then submit a "pull request" asking SciPy to "pull" your changes from your fork into the official repository.

3. Initialize git submodules:

```
git submodule update --init
```

This fetches and updates any submodules that SciPy needs (such as *Boost*).

4.14.1 Basic workflow

In short:

1. Start a new *feature branch* for each set of edits that you do. See *below*.
2. Hack away! See *below*.
3. When finished:
   - *Contributors*: push your feature branch to your own Github repo, and *create a pull request*.
   - *Core developers* If you want to push changes without further review, see the notes below.

This way of working helps to keep work well organized and the history as clear as possible.

See also:

There are many online tutorials to help you learn git. For discussions of specific git workflows, see these discussions on linux git workflow, and ipython git workflow.

Making a new feature branch

First, navigate to the SciPy root directory in your terminal and fetch new commits from the `upstream` repository:

```
git fetch upstream
```

Then, create a new branch based on the master branch of the upstream repository:

```
git checkout -b my-new-feature upstream/master
```

Equivalently, you might want to keep the master branch of your own repository up to date and create a new branch based on that:

```
git checkout master
git rebase upstream/master
git checkout -b my-new-feature
```

In order, these commands

1. ensure that the `master` branch of your local repository is checked out,

2. apply all the latest changes from the `upstream/master` (main SciPy repository master branch) to your local `master` branch, and
3. create and check out a new branch (`-b`) based on your local `master` branch.

In any case, it's important that your feature branch include the latest changes from the upstream master to help avoid merge conflicts when it's time to submit a pull request.

It's also a good idea to build this branch and run tests before continuing. Assuming you've followed *Development environment quickstart guide (macOS)* or *Development environment quickstart guide (Ubuntu)* to set up your development environment, you'll need to activate your development virtual environment, perform an in-place build, and run tests:

```
conda activate name-of-your-virtual-environment
python setup.py build_ext --inplace
python runtests.py -v
```

Otherwise, see building, *Running SciPy Tests Locally* for more information.

The editing workflow

Overview

```
# hack hack
git status # Optional
git diff # Optional
git add modified_file
git commit
# push the branch to your own Github repo
git push origin my-new-feature
```

In more detail

1. Make some changes. When you feel that you've made a complete, working set of related changes, move on to the next steps.
2. Optional: Check which files have changed with `git status` (see git status). You'll see a listing like this one:

```
# On branch my-new-feature
# Changed but not updated:
#   (use "git add <file>..." to update what will be committed)
#   (use "git checkout -- <file>..." to discard changes in working␣
↪directory)
#
#  modified:   README
#
# Untracked files:
#   (use "git add <file>..." to include in what will be committed)
#
#  INSTALL
no changes added to commit (use "git add" and/or "git commit -a")
```

3. Optional: Compare the changes with the previous version using with `git diff` (git diff). This brings up a simple text browser interface that highlights the difference between your files and the previous version.
4. Add any relevant modified or new files using `git add modified_file` (see git add). This puts the files into a staging area, which is a queue of files that will be added to your next commit. Only add files that have related, complete changes. Leave files with unfinished changes for later commits.

5. To commit the staged files into the local copy of your repo, do `git commit`. At this point, a text editor will open up to allow you to write a commit message. Read the *commit message section* to be sure that you are writing a properly formatted and sufficiently detailed commit message. After saving your message and closing the editor, your commit will be saved. For trivial commits, a short commit message can be passed in through the command line using the `-m` flag. For example, `git commit -am "ENH: Some message"`.

   In some cases, you will see this form of the commit command: `git commit -a`. The extra `-a` flag automatically commits all modified files and removes all deleted files. This can save you some typing of numerous `git add` commands; however, it can add unwanted changes to a commit if you're not careful. For more information, see why the -a flag? - and the helpful use-case description in the tangled working copy problem.

6. Push the changes to your forked repo on github:

   ```
   git push origin my-new-feature
   ```

   For more information, see git push.

Note: Assuming you have followed the instructions in these pages, git will create a default link to your github repo called `origin`. In git >= 1.7, you can ensure that the link to origin is permanently set by using the `--set-upstream` option:

```
git push --set-upstream origin my-new-feature
```

From now on, git will know that `my-new-feature` is related to the `my-new-feature` branch in your own github repo. Subsequent push calls are then simplified to the following:

```
git push
```

You have to use `--set-upstream` for each new branch that you create.

It may be the case that while you were working on your edits, new commits have been added to `upstream` that affect your work. In this case, follow the rebasing-on-master instructions to apply those changes to your branch.

Writing the commit message

Commit messages should be clear and follow a few basic rules. Example:

```
ENH: add functionality X to SciPy.<submodule>.

The first line of the commit message starts with a capitalized acronym
(options listed below) indicating what type of commit this is. Then a blank
line, then more text if needed.  Lines shouldn't be longer than 72
characters.  If the commit is related to a ticket, indicate that with
"See #3456", "See ticket 3456", "Closes #3456", or similar.
```

Describing the motivation for a change, the nature of a bug for bug fixes or some details on what an enhancement does are also good to include in a commit message. Messages should be understandable without looking at the code changes. A commit message like `MAINT: fixed another one` is an example of what not to do; the reader has to go look for context elsewhere.

Standard acronyms to start the commit message with are:

```
API: an (incompatible) API change
BENCH: changes to the benchmark suite
BLD: change related to building SciPy
BUG: bug fix
```

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```
DEP: deprecate something, or remove a deprecated object
DEV: development tool or utility
DOC: documentation
ENH: enhancement
MAINT: maintenance commit (refactoring, typos, etc.)
REV: revert an earlier commit
STY: style fix (whitespace, PEP8)
TST: addition or modification of tests
REL: related to releasing SciPy
```

Note: You can add some markers to skip part of the continuous integration. See *Continuous Integration*.

Asking for your changes to be merged with the main repo

When you feel your work is finished, you can create a pull request (PR). Github has a nice help page that outlines the process for filing pull requests.

If your changes involve modifications to the API or addition/modification of a function, you should initiate a code review. This involves sending an email to the SciPy mailing list with a link to your PR along with a description of and a motivation for your changes.

Checklist before submitting a PR

- Did you check that the code can be distributed under a BSD license? See *License Considerations*.
- Are there unit tests with good code coverage? See NumPy/SciPy Testing Guidelines.
- Do all unit tests pass locally? See *Running SciPy Tests Locally*.
- Do all public function have docstrings including examples? See the numpydoc docstring guide.
- Does the documentation render correctly? See *Rendering Documentation with Sphinx*.
- Is the code style correct? See *PEP8 and SciPy*.
- Are there benchmarks? See *Benchmarking SciPy with airspeed velocity*.
- Is the commit message formatted correctly?
- Is the docstring of the new functionality tagged with `.. versionadded:: X.Y.Z` (where `X.Y.Z` is the version number of the next release? See the `updating`, `workers`, and `constraints` documentation of `differential_evolution`, for example. You can get the next version number from the most recent release notes on the wiki or from the `MAJOR` and `MINOR` version number variables in `setup.py`.
- In case of larger additions, is there a tutorial or more extensive module-level description? Tutorial files are in `doc/source/tutorial`.
- If compiled code is added, is it integrated correctly via `setup.py`? See *Compiled code* for more information.

4.15 PEP8 and SciPy

All SciPy Python code should adhere to PEP8 style guidelines. It's so important that some continuous integration tests on GitHub will fail due to certain PEP8 violations. Here are a few tips for ensuring PEP8 compliance before pushing your code:

- Many integrated development environments (IDEs) have options that automatically check for PEP8 compliance. In Spyder, for example, enable Real-time code style analysis in Tools → Preferences → Editor → Code Introspection/Analysis and "Automatically remove trailing spaces when saving files" in in Tools → Preferences → Editor → Advanced Settings. This can help you fix PEP8 issues as you write your code.
- You can also perform checks using the `flake8` tool. After installing `flake8`, navigate to the SciPy root directory in a console window and try:

  ```
  flake8 scipy/optimize/linprog.py
  ```

  The absence of output indicates that there are no PEP8 issues with the file. Unfortunately, there is also no output if you get the file path wrong:

  ```
  flake8 scipy/optimize/linprog2.py
  ```

  (`linprog2.py` doesn't exist.) To make sure you have the path right, consider introducing (and then removing) a small PEP8 issue in the target file, such as a line that is over 79 characters long.
- If you have existing code with a lot of PEP8 issues, consider using `autopep8` to automatically fix most of them.

4.16 Rendering Documentation with Sphinx

SciPy docstrings are rendered to HTML using Sphinx and the PyData Sphinx theme. Writing docstrings is covered in the A Guide to NumPy Documentation; this document explains how to check that docstrings render properly.

For a video walkthrough, please see Rendering SciPy Documentation with Sphinx .

4.16.1 Rendering Documentation Locally

To render the documentation on your own machine:

0. Ensure that you have a working SciPy *Development environment* active. You need to be able to `import scipy` regardless of Python's working directory; the `python setup.py develop` and `conda develop` commands from the *quickstart* guides make this possible.
1. Install Sphinx, PyData Sphinx theme, Sphinx-Panels and matplotlib. For example, if you're using the Anaconda distribution of Python, enter in a terminal window `conda install sphinx pydata-sphinx-theme sphinx-panels matplotlib --channel conda-forge`. The list of requirements is in `scipy/doc_requirements.txt`.
2. In a terminal window, browse to the `scipy/doc` directory. Note the presence of the file `Makefile`.
3. Execute `git submodule update --init`. Some of the documentation theme files are not distributed with the main `scipy` repository; this keeps them up to date using git submodules.
4. Enter `make html-scipyorg`. If you have multiple version of Python on your path, you can choose which version to use by appending `PYTHON=python3.7` to this command, where `python3.7` is to be replaced with the name of the Python you use for SciPy development. This uses the Make build automation tool to execute the documentation build instructions from the `Makefile`. This can take a while the first time, but subsequent documentation builds are typically much faster.

5. View the documentation in `scipy/doc/build/html-scipyorg`. You can start with `index.html` and browse, or you can jump straight to the file you're interested in.

Note: Changes to certain documents do not take effect when Sphinx documentation is rebuilt. In this case, you can build from scratch by deleting the `scipy/doc/build` directory, then building again.

4.16.2 Checking Documentation on the Cloud

Once a PR is opened, you can check that documentation renders correctly on the cloud.

1. Log in to GitHub.
2. Log in CircleCI using your GitHub account.
3. Back in GitHub, at the bottom of the PR, select "Show all Checks".
4. Next to "ci/circleci: build_docs artifact", select "Details".

4.17 Running SciPy Tests Locally

Basic test writing and execution from within the Python interpreter is documented in the NumPy/SciPy Testing Guidelines. This page includes information about running tests from the command line using SciPy's `runtests.py`, which permits greater control. *Note: Before beginning, ensure that* `pytest` *is installed.*

To run all tests, navigate to the root SciPy directory at the command line and execute

```
python runtests.py -v
```

where `-v` activates the `--verbose` option. This builds SciPy (or updates an existing build) and runs the tests.

To run tests on a particular submodule, such as `optimize`, use the `--submodule` option:

```
python runtests.py -v -s optimize
```

To run a particular test module, use the `--test` option:

```
python runtests.py -v -t scipy.<module>.tests.<test_file>
```

Example for `scipy/optimize/tests/test_linprog.py` file tests, run:

```
python runtests.py -v -t scipy.optimize.tests.test_linprog
```

To run a test class:

```
python runtests.py -v -t scipy.<module>.tests.<test_file>::<TestClass>
```

Example for `TestLinprogRSCommon` class from `test_linprog.py`:

```
python runtests.py -v -t scipy.optimize.tests.test_
↪linprog::TestLinprogRSCommon
```

To run a particular test:

```
python runtests.py -v -t scipy.<module>.tests.<test_file>::<test_name>
```

Example for `test_unknown_solvers_and_options` from `test_linprog.py`:

```
python runtests.py -v -t scipy.optimize.tests.test_linprog::test_unknown_
↪solvers_and_options
```

For tests within a class, you need to specify the class name and the test name:

```
python runtests.py -v -t scipy.<module>.tests.<test_file>::<TestClass>::<test_
↪name>
```

Example:

```
python runtests.py -v -t scipy.optimize.tests.test_
↪linprog::TestLinprogRSCommon::test_nontrivial_problem_with_guess
```

Other useful options include:

- `--coverage` to generate a test coverage report in `scipy/build/coverage/index.html`. *Note:* `pytest-cov` *must be installed.*
- `--doc` to build the docs in `scipy/doc/build`. By default, docs are built only in the `html-scipyorg` format, but you can change this by appending the name of the desired format (e.g. `--doc latex`).
- `--bench` to run all benchmarks. See *Benchmarking SciPy with airspeed velocity*.
- `--pep8` to perform pep8 check.
- `--mypy` to run *mypy* on the codebase.
- `-n` or `--no-build` to prevent SciPy from updating the build before testing
- `-j` or `--parallel` *n* to engage *n* cores when building SciPy; e.g. `python runtests.py -j 4` engages four cores. As of #10172 this also runs the tests on four cores if `pytest-xdist` is installed.
- `-m` or `--mode full` to run the full test suite, including slow tests. For example, `python runtests.py -m full`.
- `--` to send remaining command line arguments to `pytest` instead of `runtest.py`. For instance, while `-n` sent to `pytest.py` activates the `--no-build` option, `-n` sent to `pytest` runs the tests on multiple cores; e.g. `python runtests.py -- -n 4` runs tests using four cores. *Note:* `pytest-xdist` *must be installed for testing on multiple cores.*

Other options not documented here are listed in the `main` function of the source code for `runtests.py`. For much more information about `pytest`, see the `pytest` documentation.

4.17.1 Tips:

If you built SciPy from source but are having trouble running tests after a change to the codebase, try deleting the `scipy/build` directory. This forces `runtest.py` to completely rebuild SciPy before performing tests.

There is an additional level of very slow tests (several minutes), which are disabled even when calling `python runtests.py -m full`. They can be enabled by setting the environment variable `SCIPY_XSLOW=1` before running the test suite.

4.18 Benchmarking SciPy with airspeed velocity

This document introduces benchmarking, including reviewing SciPy benchmark test results online, writing a benchmark test, and running it locally. For a video run-through of writing a test and running it locally, see Benchmarking SciPy.

As written in the airspeed velocity (asv) documentation:

> Airspeed velocity (asv) is a tool for benchmarking Python packages over their lifetime. Runtime, memory consumption, and even custom-computed values may be tracked. The results are displayed in an interactive web frontend that requires only a basic static webserver to host.

To see what this means, take a look at airspeed velocity of an unladen scipy. Each plot summarizes the execution time of a particular test over the commit history of the project; that is, as each commit is merged, the benchmark test is run, its execution time is measured, and the elapsed time is plotted. In addition to tracking the performance of the code, a commit is *intended* to affect, running *all* benchmarks for each commit is helpful for identifying unintentional regressions: significant increases in the execution time of one or more benchmark tests. As SciPy is a web of interconnected code, the repercussions of a small change may not be immediately obvious to a contributor, so this benchmark suite makes it easier to detect regressions and identify the commit that caused them. When you contribute a substantial new feature - or notice a feature that doesn't already have a benchmark test - please consider writing benchmarks.

4.18.1 Writing benchmarks

The Writing benchmarks *section of the airspeed velocity documentation is the definitive guide to writing benchmarks. Please see also the* SciPy benchmarks readme.

To see how benchmarks are written, take a look at `scipy/benchmarks/benchmarks/optimize_linprog.py`. Each subclass of `Benchmark` defines a benchmark test. For example, the `KleeMinty` class defines a benchmark test based on the Klee-Minty hypercube problem, a diabolical test of the simplex algorithm for linear programming. The class has four parts:

- `setup` prepares the benchmark to run. The execution time of this function is *not* counted in the benchmark results, so this is a good place to set up all variables that define the problem. In the `KleeMinty` example, this involves generating arrays `c`, `A_ub`, and `b_ub` corresponding with a Klee-Minty hypercube in `dims` dimensions and storing them as instance variables.
- `time_klee_minty` actually runs the benchmark test. This function executes after a `KleeMinty` object has been instantiated and `setup` has run, so it gets the arrays defining the problem from `self`. Note that the prefix `time` in the function name indicates to `asv` that the execution time of this function *is* to be counted in the benchmark results.
- `params` is a list of lists defining parameters of the test. Benchmarks are run for all possible combinations of these parameters. For example, the first time the benchmark is run, the first element of `methods` (`simplex`) is passed into `setup` and `time_klee_minty` as the first argument, `meth`, and the first element of `[3, 6, 9]` (`3`) is passed into `setup` and `time_klee_minty` as the second argument, `dims`. The next time the benchmark is run, `setup` and `time_klee_minty` are passed `revised simplex` and `6` as arguments, and so this continues until all combinations of parameters have been used.
- `param_names` is a list of human-readable names for each element of the `params` list. These are used for presenting results.

Results of this benchmark over the past few years are available by clicking on the KleeMinty.time_klee_minty link at airspeed velocity of an unladen scipy. Note that each trace of the plot corresponds with a combination of benchmark parameters and environment settings (e.g., the Cython version), and that the visibility of the traces can be toggled using the control panel on the left.

4.18.2 Running benchmarks locally

Before beginning, ensure that airspeed velocity *is installed.*

After contributing new benchmarks, you should test them locally before submitting a pull request.

To run all benchmarks, navigate to the root SciPy directory at the command line and execute:

```
python runtests.py --bench
```

where `--bench` activates the benchmark suite instead of the test suite. This builds SciPy and runs the benchmarks. (*Note: this could take a while. Benchmarks often take longer to run than unit tests, and each benchmark is run multiple times to measure the distribution in execution times.*)

To run benchmarks from a particular benchmark module, such as `optimize_linprog.py`, simply append the filename without the extension:

```
python runtests.py --bench optimize_linprog
```

To run a benchmark defined in a class, such as `KleeMinty` from `optimize_linprog.py`:

```
python runtests.py --bench optimize_linprog.KleeMinty
```

To compare benchmark results between the active branch and another, such as `master`:

```
python runtests.py --bench-compare master optimize_linprog.KleeMinty
```

All of the commands above display the results in plain text in the console, and the results are not saved for comparison with future commits. For greater control, a graphical view, and to have results saved for future comparison, you can use use the `asv` terminal command directly.

To use it, navigate to `scipy/benchmarks` in the console and then execute:

```
asv run
```

This command runs the whole benchmark suite and saves the results for comparison against future commits.

To run only a single benchmark, such as `KleeMinty` from `optimize_linprog.py`:

```
asv run --bench optimize_linprog.KleeMinty
```

One great feature of `asv` is that it can automatically run a benchmark not just for the current commit, but for every commit in a range. `linprog method='interior-point'` was merged into SciPy with commit `7fa17f2369e0e5ad055b23cc1a5ee079f9e8ca32`, so let's run the `KleeMinty` benchmark for 10 commits between then and now to track its performance over time:

```
asv run --bench optimize_linprog.KleeMinty --steps 10 7fa17f..
```

Note: This will take a while, because SciPy has to be rebuilt for each commit! For more information about specifying ranges of commits, see the git revisions documentation.

To "publish" the results (prepare them to be viewed) and "preview" them in an interactive console:

```
asv publish
asv preview
```

ASV will report that it is running a server. Using any browser, you can review the results by navigating to http://127.0.0.1:8080 (local machine, port 8080).

For much more information about the `asv` commands, see the airspeed velocity Commands documentation. (Tip: check out the `asv find` command and the `--quick`, `--skip-existing-commits`, and `--profile` options for `asv run`.)

4.19 Adding Cython to SciPy

As written on the Cython website:

> Cython is an optimising static compiler for both the Python programming language and the extended Cython programming language (based on Pyrex). It makes writing C extensions for Python as easy as Python itself.

If your code currently performs a lot of loops in Python, it might benefit from compilation with Cython. This document is intended to be a very brief introduction: just enough to see how to use Cython with SciPy. Once you have your code compiling, you can learn more about how to optimize it by reviewing the Cython documentation.

There are only two things you need to do in order for SciPy compile your code with Cython:

1. Include your code in a file with a `.pyx` extension rather than a `.py` extension. All files with a `.pyx` extension are automatically converted by Cython to `.c` files when SciPy is built.
2. Add an extension from this `.c` file to the configuration of the subpackage in which your code lives. Typically, this is very easy: add a single, formulaic line to the subpackage's `setup.py` file. Once added as an extension, the `.c` code will be compiled by your C compiler to machine code when SciPy is built.

4.19.1 Example

`scipy.optimize._linprog_rs.py` contains the implementation of the revised simplex method for `scipy.optimize.linprog`. The revised simplex method performs many elementary row operations on matrices, and so it was a natural candidate to be Cythonized.

Note that `scipy/optimize/_linprog_rs.py` imports the `BGLU` and `LU` classes from `._bglu_dense` exactly as if they were regular Python classes. But they're not. `BGLU` and `LU` are Cython classes defined in `/scipy/optimize/_bglu_dense.pyx`. There is nothing about the way they are imported or used that suggests that they are written in Cython; the only way so far that we can tell they are Cython classes is that they are defined in a file with a `.pyx` extension.

Even in `/scipy/optimize/_bglu_dense.pyx`, most of the code resembles Python. The most notable differences are the presence of `cimport`, `cdef`, and Cython decorators. None of these are strictly necessary. Without them, the pure Python code can still be compiled by Cython. The Cython language extensions are *just* tweaks to improve performance. This `.pyx` file is automatically converted to a `.c` file by Cython when SciPy is built.

The only thing left is to add an extension from this `.c` file using `numpy.distutils`. This takes just a single line in `scipy/optimize/setup.py`: `config.add_extension('_bglu_dense', sources=['_bglu_dense.c'])`, `_bglu_dense.c` is the source and `_bglu_dense` is the name of the extension (for consistency). When SciPy is built, `_bglu_dense.c` will be compiled to machine code, and we will be able to import the `LU` and `BGLU` classes from the extension `_bglu_dense`.

4.19.2 Exercise

See a video run-through of this exercise: Cythonizing SciPy Code

1. Update Cython and create a new branch (e.g., `git checkout -b cython_test`) in which to make some experimental changes to SciPy
2. Add some simple Python code in a `.py` file in the `/scipy/optimize` directory, say `/scipy/optimize/mypython.py`. For example:

```
def myfun():
    i = 1
    while i < 10000000:
        i += 1
    return i
```

3. Let's see how long this pure-Python loop takes so we can compare the performance of Cython. For example, in an IPython console in Spyder:

```
from scipy.optimize.mypython import myfun
%timeit myfun()
```

   I get something like:

```
715 ms ± 10.7 ms per loop
```

4. Save your `.py` file to a `.pyx` file, e.g. `mycython.pyx`.
5. Build SciPy. Note that a `.c` file has been added to the `/scipy/optimize` directory.
6. Somewhere near similar lines, add an extension from your `.c` file to `/scipy/optimize/setup.py`. e.g.:

```
config.add_extension('_group_columns', sources=['_group_columns.c'],)  #␣
↪was already here
config.add_extension('mycython', sources=['mycython.c'],)  # this was new
config.add_extension('_bglu_dense', sources=['_bglu_dense.c'])  # was␣
↪already there
```

7. Rebuild SciPy. Note that a `.so` file has been added to the `/scipy/optimize` directory.
8. Time it:

```
from scipy.optimize.mycython import myfun
%timeit myfun()
```

   I get something like:

```
359 ms ± 6.98 ms per loop
```

   Cython sped up the pure Python code by a factor of ~2.

9. That's not much of an improvement in the scheme of things. To see why, it helps to have Cython create an "annotated" version of our code to show bottlenecks. In a terminal window, call Cython on your `.pyx` file with the `-a` flag:

```
cython -a scipy/optimize/mycython.pyx
```

   Note that this creates a new `.html` file in the `/scipy/optimize` directory. Open the `.html` file in any browser.

10. The yellow-highlighted lines in the file indicate potential interaction between the compiled code and Python, which slows things down considerably. The intensity of the highlighting indicates the estimated severity of the interaction. In this case, much of the interaction can be avoided if we define the variable `i` as an integer so that Cython doesn't have to consider the possibility of it being a general Python object:

```
def myfun():
    cdef int i = 1  # our first line of Cython code
    while i < 10000000:
        i += 1
    return i
```

    Recreating the annotated `.html` file shows that most of the Python interaction has disappeared.

11. Rebuild SciPy, open an fresh IPython console, and `%timeit`:

```
from scipy.optimize.mycython import myfun
%timeit myfun()
```

I get something like: `68.6 ns ± 1.95 ns per loop`. The Cython code ran about 10 million times faster than the original Python code.

In this case, the compiler probably optimized away the loop, simply returning the final result. This sort of speedup is not typical for real code, but this exercise certainly illustrates the power of Cython when the alternative is many low-level operations in Python.

4.20 Public Cython APIs

As of Apr 2020, the following modules in SciPy expose functionality via a public `cdef` Cython API declarations:

- `scipy.linalg.cython_blas`
- `scipy.linalg.cython_lapack`
- `scipy.optimize.cython_optimize`
- `scipy.special.cython_special`

This uses Cython's declaration sharing features, where shared `cdef` items are declared in `*.pxd` files that are distributed together with the corresponding DLL/SO files in binary SciPy installations.

4.20.1 Application Binary Interface

Using these features in SciPy however requires SciPy contributors to take additional care with regard to maintaining Application Binary Interface (ABI) stability. This is similar to developing libraries in C, and different from how backward compatibility works in pure Python.

The main difference to Python originates from the fact that the declarations in the header `.pxd` files are used when code written by users is *compiled*, but they must also match with what is available in SciPy when the user code is *imported*.

User code may be compiled with one version of SciPy, and the compiled binary (which uses the binary interface declared in the `.pxd` files) can be used with a different SciPy version installed on the system. If the interfaces are not compatible, either an exception is raised or runtime memory corruption and crash ensue.

At import time, Cython checks that signatures of functions in the installed SciPy SO/DLL file match the one in the `.pxd` file used by the user during compilation, and raises a Python exception if there is a mismatch. If the SciPy code is structured correctly (see below), this check is performed only for functions that are actually imported in the user code.

We rely on this feature to provide a runtime safety check, which makes it easier for the users to detect incompatible SciPy versions via Python exceptions, instead of hard-to-trace runtime crashes.

4.20.2 ABI stability aim

SciPy aims to maintain ABI stability in Cython code, in the following sense:

> Binaries produced by compiling user source with one version of SciPy, are compatible with any other SciPy version with which the source code can be compiled.
> Trying to use an incompatible version of SciPy at runtime will result in a Python exception at user module import time.
> Trying to use an incompatible version of SciPy at compile time will result in a Cython error.

This means that users can use any compatible version of SciPy to compile binaries without having to pay attention to ABI, i.e.,

> ABI compatibility = API compatibility

Cython API backward/forward compatibility will be handled with a similar deprecation/removal policy as for the Python API, see *Deprecations*.

4.20.3 Implementing ABI stability in SciPy

The following rules in development of Cython APIs in SciPy are necessary to maintain the ABI stability aim above:

- Adding new `cdef` declarations (functions, structs, types, etc.) **is allowed**.
- Removing `cdef` declarations **is allowed**, but **should follow** general deprecation/removal policy.
- `cdef` declarations of functions **may be changed**.

  However, changes result in a backward incompatible API change which breaks any code using the changed signature, and **should follow** general deprecation/removal policy.
- `cdef` declarations of anything else (e.g. `struct`, `enum`, and types) are **final**. Once a declaration is exposed in the public Cython API in a released SciPy version, **it must not be changed**.

  If changes are necessary, they need to be carried out by adding new declarations with different names, and removing old ones.
- `cdef` classes are **not allowed** in the public APIs (TBD: backward compatibility of cdef classes needs more research, but must not be allowed when we are not sure)
- For each public API module (as in `scipy.linalg.cython_blas`), use a single interface `.pxd` declaration file.

  The public interface declaration file **should not** contain `cimport` statements. If it does, Cython's signature check will check all of the cimported functions, not only the ones that are used by user code, so that changing one of them breaks the whole API.
- If data structures are necessary, **prefer opaque structs** in the public API. The interface declarations should not contain any declarations of struct members. Allocation, freeing, and attribute access of data structures should be done with functions.

4.20.4 Deprecating public Cython APIs

To deprecate a public Cython API function, for example:

```
# scipy/something/foo.pxd
cdef public int somefunc()

# scipy/something/foo.pyx
cdef public int somefunc():
    return 42
```

you can add use the `scipy._lib.deprecation.deprecate_cython_api` function to do the deprecations at the end of the corresponding `.pyx` file:

```
# scipy/something/foo.pyx
cdef public int somefunc():
    return 42

from scipy._lib.deprecation import deprecate_cython_api
import scipy.something.foo as mod
deprecate_cython_api(mod, "somefunc", new_name="scipy.something.newfunc",
                     message="Deprecated in Scipy 1.5.0")
del deprecate_cython_api, mod
```

After this, Cython modules that `cimport somefunc`, will emit a *DeprecationWarning* at import time.

There is no way to deprecate Cython data structures and types. They can be however removed after all functions using them in the API are removed, having gone through the deprecation cycle.

Whole Cython modules can be deprecated similarly as Python modules, by emitting a *DeprecationWarning* on the top-level.

4.21 Adding New Methods, Functions, and Classes

While adding code to SciPy is in most cases quite straight forward, there are a few places where that is not the case. This document contains detailed information on some specific situations where it may not be clear from the outset what is involved in the task.

4.21.1 Adding A New Statistics Distribution

For hundreds of years statisticians, mathematicians and scientists have needed to understand, analyze and model data. This has led to a plethora of statisics distributions, many of which are related to others. Modeling of new types of data continues to give rise to new distributions, as does theoretical considerations being applied to new disciplines. SciPy models about a dozen discrete distributions *Discrete Statistical Distributions* and 100 continuous distributions *Continuous Statistical Distributions*.

To add a new distribution, a good reference is needed. Scipy typically uses [JKB] as its gold standard, with Wikipedia Distributions articles often providing some extra details and/or graphical plots.

How to create a new continuous distribution

There are a few steps to be done to add a continuous distribution to SciPy. (Adding a discrete distribution is similar). We'll use the fictitious "Squirrel" distribution in the instructions below.

Before Implementation

1. See if `Squirrel` has already been implemented–that saves a lot of effort!
   - It may have been implemented with a different name.
   - It may have been implemented with a different parameterization (shape parameters).
   - It may be a specialization of a more general family of distributions.

   It is very common for multiple disciplines to discover/rediscover a distribution (or a specialization or different parameterization). There are a few existing SciPy distributions which are specializations of other distributions. E.g. The *scipy.stats.arcsine* distribution is a specialization of the *scipy.stats.beta* distribution. These duplications exist for (very!) historical and widespread usage reasons. At this time, adding new specializations/reparametrizations of existing distributions to SciPy is not supported, mainly due to the increase in user confusion resulting from such additions.
2. Create a SciPy Issue on github, listing the distribution, references and reasons for its inclusion.

Implementation

1. Find an already existing distribution similar to `Squirrel`. Use its code as a template for `Squirrel`.
2. Read the docstring for class `rv_continuous` in scipy/stats/_distn_infrastructure.py.
3. Write the new code for class `squirrel_gen` and insert it into scipy/stats/_continuous_distns.py, which is in (mostly) alphabetical order by distribution name.
4. Does the distribution have infinite support? If not, left and/or right endpoints `a`, `b` need to be specified in the call to `squirrel_gen(name='squirrel', a=?, b=?)`.
5. If the support depends upon the shape parameters, `squirrel_gen._get_support()` needs to be implemented.
6. The default inherited `_argcheck()` implementation checks that the shape parameters are positive. Create a more appropriate implementation.
7. If `squirrel_gen.ppf()` is expensive to compute relative to `squirrel_gen.pdf()`, consider setting the `momtype` in the call to `squirrel_gen()`.
8. If `squirrel_gen.rvs()` is expensive to compute, consider implementing a specific `squirrel_gen._rvs()`.
9. Add the name to the listing in the docstring of scipy/stats/__init__.py.
10. Add the name and a good set of example shape parameters to the `distcont` list in scipy/stats/_distr_params.py. These shape parameters are used both for testing and automatic documentation generation.
11. Add the name and an _invalid_ set of example shape parameters to the list in `invdistcont`, also in _distr_params.py. These shape parameters are also used for testing.
12. Add a `TestSquirrel` class and any specific tests to scipy/stats/tests/test_distributions.py.
13. Run and pass(!) the tests.

After Implementation

1. Add a tutorial `doc/source/tutorial/stats/continuous_squirrel.rst`
2. Add it to the listing of continuous distributions in doc/source/tutorial/stats/continuous.rst.
3. Update the `number of continuous distributions` in the example code in doc/source/tutorial/stats.rst.
4. Build the documentation successfully.
5. Submit a PR.

References

4.22 Continuous Integration

Continuous integration is part of our development process and ensure that every piece of code or documentation which is contributed to SciPy is working and does not have unforeseen effects.

Note: Before submitting or updating your PR, please ensure that you tested your changes locally. See *Checklist before submitting a PR* and *Running SciPy Tests Locally*.

4.22.1 Workflows

We run more than 20 different workflows with different versions of the dependencies, different architectures, etc. A PR must pass all these checks before it can be merged as to ensure a sustainable state of the project.

Apart from the unit tests, the documentation and examples in the docstrings are also checked. These are common failing workflows as Sphinx and doctests have very strict rules. These aspects are very important as documentation and examples are user facing elements. Ensures that these elements are properly rendered.

The logs can be long, but you will always find out why your build/test did not pass a check. Simply click on `Details` to access the logs.

Following is a list of all the different workflows in use. They are grouped by CI resources providers.

GitHub Actions

- `Linux Tests`: test suite runs for Linux (`x86_64`)
- `macOS Tests`: test suite runs for macOS (`x86_64`)

Test suite runs on GitHub Actions and other platforms cover a range of test/environment conditions: Python and NumPy versions (lowest-supported to nightly builds), 32-bit vs. 64-bit, different compilers, and more - for details, see the `.yml` configuration files.

Azure

- `Lint`: PEP8 and code style
- `Windows Python`: test suite runs for Windows
- `Linux_Python_37_32bit_full`
- `wheel_optimized_gcc48`
- `source_distribution`: install via `sdist`, then run the test suite
- `refguide_asv_check`: doctests from examples and benchmarks

CircleCI

- `build_docs`: build the documentation
- `build_docs artifact`: live preview of the documentation
- `build_scipy`
- `run_benchmarks`: verify how the changes impact performance

Codecov

- `patch`: the impact on code coverage due to your changes
- `project`: the coverage of the whole project

4.22.2 Skipping

Being an open-source project, we have access to a quota of CI resources. Ultimately, resources are limited and we should use them with care. This is why we ask you to verify your changes locally before pushing them.

Depending on the proposed change, you might want to skip part of the checks. It will be at the discretion of a maintainer to re-run some tests before integration.

Skipping CI can be achieved by adding a special text in the commit message:

- `[skip azp]`: will skip Azure
- `[skip actions]`: will skip GitHub Actions
- `[skip ci]`: will skip *all* CI

Of course, you can combine these to skip multiple workflows.

This skip information should be placed on a new line. In this example, we just updated a `.rst` file in the documentation and ask to skip Azure and GitHub Actions' workflows:

```
DOC: improve QMCEngine examples.
[skip azp] [skip actions]
```

CHAPTER

FIVE

RELEASE NOTES

This is the list of changes to SciPy between each release. For full details, see the commit logs.

5.1 SciPy 1.7.0 Release Notes

Contents

- *SciPy 1.7.0 Release Notes*
  - *Highlights of this release*
  - *New features*
    - `scipy.cluster` *improvements*
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    - `scipy.linalg` *improvements*
    - `scipy.ndimage` *improvements*
    - `scipy.optimize` *improvements*
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    - `scipy.spatial` *improvements*
    - `scipy.special` *improvements*
    - `scipy.stats` *improvements*
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      - *Sample statistics*
      - *Statistical Distributions*
      - *Other*
      - *New* `scipy.stats.qmc` *module*
  - *Deprecated features*
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- *Backwards incompatible changes*
- *Other changes*
- *Authors*
- *Issues closed for 1.7.0*
- *Pull requests for 1.7.0*

SciPy 1.7.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning`s). Our development attention will now shift to bug-fix releases on the 1.7.x branch, and on adding new features on the master branch.

This release requires Python 3.7+ and NumPy 1.16.5 or greater.

For running on PyPy, PyPy3 6.0+ is required.

5.1.1 Highlights of this release

- A new submodule for quasi-Monte Carlo, *scipy.stats.qmc*, was added
- The documentation design was updated to use the same PyData-Sphinx theme as NumPy and other ecosystem libraries.
- We now vendor and leverage the Boost C++ library to enable numerous improvements for long-standing weaknesses in *scipy.stats*
- *scipy.stats* has six new distributions, eight new (or overhauled) hypothesis tests, a new function for bootstrapping, a class that enables fast random variate sampling and percentile point function evaluation, and many other enhancements.
- `cdist` and `pdist` distance calculations are faster for several metrics, especially weighted cases, thanks to a rewrite to a new C++ backend framework
- A new class for radial basis function interpolation, *RBFInterpolator*, was added to address issues with the *Rbf* class.

We gratefully acknowledge the Chan-Zuckerberg Initiative Essential Open Source Software for Science program for supporting many of the improvements to *scipy.stats*.

5.1.2 New features

`scipy.cluster` improvements

An optional argument, `seed`, has been added to `kmeans` and `kmeans2` to set the random generator and random state.

`scipy.interpolate` improvements

Improved input validation and error messages for `fitpack.bispev` and `fitpack.parder` for scenarios that previously caused substantial confusion for users.

The class *RBFInterpolator* was added to supersede the *Rbf* class. The new class has usage that more closely follows other interpolator classes, corrects sign errors that caused unexpected smoothing behavior, includes polynomial terms in the interpolant (which are necessary for some RBF choices), and supports interpolation using only the k-nearest neighbors for memory efficiency.

`scipy.linalg` improvements

An LAPACK wrapper was added for access to the `tgexc` subroutine.

`scipy.ndimage` improvements

`scipy.ndimage.affine_transform` is now able to infer the `output_shape` from the `out` array.

`scipy.optimize` improvements

The optional parameter `bounds` was added to `_minimize_neldermead` to support bounds constraints for the Nelder-Mead solver.

`trustregion` methods `trust-krylov`, `dogleg` and `trust-ncg` can now estimate `hess` by finite difference using one of `["2-point", "3-point", "cs"]`.

`halton` was added as a `sampling_method` in *`scipy.optimize.shgo`*. `sobol` was fixed and is now using *`scipy.stats.qmc.Sobol`*.

`halton` and `sobol` were added as `init` methods in *scipy.optimize.differential_evolution*.

`differential_evolution` now accepts an `x0` parameter to provide an initial guess for the minimization.

`least_squares` has a modest performance improvement when SciPy is built with Pythran transpiler enabled.

When `linprog` is used with `method 'highs'`, `'highs-ipm'`, or `'highs-ds'`, the result object now reports the marginals (AKA shadow prices, dual values) and residuals associated with each constraint.

`scipy.signal` improvements

`get_window` supports `general_cosine` and `general_hamming` window functions.

`scipy.signal.medfilt2d` now releases the GIL where appropriate to enable performance gains via multithreaded calculations.

`scipy.sparse` improvements

Addition of `dia_matrix` sparse matrices is now faster.

`scipy.spatial` improvements

`distance.cdist` and `distance.pdist` performance has greatly improved for certain weighted metrics. Namely: `minkowski`, `euclidean`, `chebyshev`, `canberra`, and `cityblock`.

Modest performance improvements for many of the unweighted `cdist` and `pdist` metrics noted above.

The parameter `seed` was added to *scipy.spatial.vq.kmeans* and *scipy.spatial.vq.kmeans2*.

The parameters `axis` and `keepdims` where added to *scipy.spatial.distance.jensenshannon*.

The `rotation` methods `from_rotvec` and `as_rotvec` now accept a `degrees` argument to specify usage of degrees instead of radians.

`scipy.special` improvements

Wright's generalized Bessel function for positive arguments was added as *scipy.special.wright_bessel*.

An implementation of the inverse of the Log CDF of the Normal Distribution is now available via *scipy.special.ndtri_exp*.

`scipy.stats` improvements

Hypothesis Tests

The Mann-Whitney-Wilcoxon test, `mannwhitneyu`, has been rewritten. It now supports n-dimensional input, an exact test method when there are no ties, and improved documentation. Please see "Other changes" for adjustments to default behavior.

The new function *scipy.stats.binomtest* replaces *scipy.stats.binom_test*. The new function returns an object that calculates a confidence intervals of the proportion parameter. Also, performance was improved from O(n) to O(log(n)) by using binary search.

The two-sample version of the Cramer-von Mises test is implemented in *scipy.stats.cramervonmises_2samp*.

The Alexander-Govern test is implemented in the new function *scipy.stats.alexandergovern*.

The new functions *scipy.stats.barnard_exact* and *scipy.stats. boschloo_exact* respectively perform Barnard's exact test and Boschloo's exact test for 2x2 contingency tables.

The new function *scipy.stats.page_trend_test* performs Page's test for ordered alternatives.

The new function *scipy.stats.somersd* performs Somers' D test for ordinal association between two variables.

An option, `permutations`, has been added in *scipy.stats.ttest_ind* to perform permutation t-tests. A `trim` option was also added to perform a trimmed (Yuen's) t-test.

The `alternative` parameter was added to the `skewtest`, `kurtosistest`, `ranksums`, `mood`, `ansari`, `linregress`, and `spearmanr` functions to allow one-sided hypothesis testing.

Sample statistics

The new function *scipy.stats.differential_entropy* estimates the differential entropy of a continuous distribution from a sample.

The `boxcox` and `boxcox_normmax` now allow the user to control the optimizer used to minimize the negative log-likelihood function.

A new function *scipy.stats.contingency.relative_risk* calculates the relative risk, or risk ratio, of a 2x2 contingency table. The object returned has a method to compute the confidence interval of the relative risk.

Performance improvements in the `skew` and `kurtosis` functions achieved by removal of repeated/redundant calculations.

Substantial performance improvements in *scipy.stats.mstats.hdquantiles_sd*.

The new function *scipy.stats.contingency.association* computes several measures of association for a contingency table: Pearsons contingency coefficient, Cramer's V, and Tschuprow's T.

The parameter `nan_policy` was added to *scipy.stats.zmap* to provide options for handling the occurrence of `nan` in the input data.

The parameter `ddof` was added to *scipy.stats.variation* and *scipy.stats.mstats.variation*.

The parameter `weights` was added to *scipy.stats.gmean*.

Statistical Distributions

We now vendor and leverage the Boost C++ library to address a number of previously reported issues in `stats`. Notably, `beta`, `binom`, `nbinom` now have Boost backends, and it is straightforward to leverage the backend for additional functions.

The skew Cauchy probability distribution has been implemented as *scipy.stats.skewcauchy*.

The Zipfian probability distribution has been implemented as *scipy.stats.zipfian*.

The new distributions `nchypergeom_fisher` and `nchypergeom_wallenius` implement the Fisher and Wallenius versions of the noncentral hypergeometric distribution, respectively.

The generalized hyperbolic distribution was added in *scipy.stats.genhyperbolic*.

The studentized range distribution was added in *scipy.stats.studentized_range*.

scipy.stats.argus now has improved handling for small parameter values.

Better argument handling/preparation has resulted in performance improvements for many distributions.

The `cosine` distribution has added ufuncs for `ppf`, `cdf`, `sf`, and `isf` methods including numerical precision improvements at the edges of the support of the distribution.

An option to fit the distribution to data by the method of moments has been added to the `fit` method of the univariate continuous distributions.

Other

scipy.stats.bootstrap has been added to allow estimation of the confidence interval and standard error of a statistic.

The new function *scipy.stats.contingency.crosstab* computes a contingency table (i.e. a table of counts of unique entries) for the given data.

scipy.stats.NumericalInverseHermite enables fast random variate sampling and percentile point function evaluation of an arbitrary univariate statistical distribution.

New `scipy.stats.qmc` module

This new module provides Quasi-Monte Carlo (QMC) generators and associated helper functions.

It provides a generic class *scipy.stats.qmc.QMCEngine* which defines a QMC engine/sampler. An engine is state aware: it can be continued, advanced and reset. 3 base samplers are available:

- *scipy.stats.qmc.Sobol* the well known Sobol low discrepancy sequence. Several warnings have been added to guide the user into properly using this sampler. The sequence is scrambled by default.
- *scipy.stats.qmc.Halton*: Halton low discrepancy sequence. The sequence is scrambled by default.
- *scipy.stats.qmc.LatinHypercube*: plain LHS design.

And 2 special samplers are available:

- *scipy.stats.qmc.MultinomialQMC*: sampling from a multinomial distribution using any of the base *scipy.stats.qmc.QMCEngine*.
- *scipy.stats.qmc.MultivariateNormalQMC*: sampling from a multivariate Normal using any of the base *scipy.stats.qmc.QMCEngine*.

The module also provide the following helpers:

- *scipy.stats.qmc.discrepancy*: assess the quality of a set of points in terms of space coverage.
- *scipy.stats.qmc.update_discrepancy*: can be used in an optimization loop to construct a good set of points.
- *scipy.stats.qmc.scale*: easily scale a set of points from (to) the unit interval to (from) a given range.

5.1.3 Deprecated features

`scipy.linalg` deprecations

- *scipy.linalg.pinv2* is deprecated and its functionality is completely subsumed into *scipy.linalg.pinv*
- Both `rcond`, `cond` keywords of *scipy.linalg.pinv* and *scipy.linalg.pinvh* were not working and now are deprecated. They are now replaced with functioning `atol` and `rtol` keywords with clear usage.

`scipy.spatial` deprecations

- *scipy.spatial.distance* metrics expect 1d input vectors but will call `np.squeeze` on their inputs to accept any extra length-1 dimensions. That behaviour is now deprecated.

5.1.4 Backwards incompatible changes

5.1.5 Other changes

We now accept and leverage performance improvements from the ahead-of-time Python-to-C++ transpiler, Pythran, which can be optionally disabled (via `export SCIPY_USE_PYTHRAN=0`) but is enabled by default at build time.

There are two changes to the default behavior of *scipy.stats.mannwhitenyu*:

- For years, use of the default `alternative=None` was deprecated; explicit `alternative` specification was required. Use of the new default value of `alternative`, "two-sided", is now permitted.

- Previously, all p-values were based on an asymptotic approximation. Now, for small samples without ties, the p-values returned are exact by default.

Support has been added for PEP 621 (project metadata in `pyproject.toml`)

We now support a Gitpod environment to reduce the barrier to entry for SciPy development; for more details see quickstart-gitpod.

5.1.6 Authors

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A total of 126 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

5.1.7 Issues closed for 1.7.0

- #636: Statistics Review: mannwhitneyu (Trac #109)
- #1346: signal.medfilt2d should fall back on signal.medfilt for types…
- #2118: Mann-Whitney statistic returns incorrect results (Trac #1593)
- #2158: special.chndtrix (ncx2.ppf) gives wrong results (Trac #1633)
- #3284: build_sphinx weirdness
- #3352: beta distribution sf
- #4067: Mannwhitneyu with arrays full of nan still reports significance

- #4080: entropy in Scipy
- #4641: mstats.mannwhitneyu and stats.mannwhitneyu return inconsistent…
- #5122: scipy.stats.binom.ppf Incorrect for p=0
- #5180: Rbf interpolation - use only K nearest neighbors
- #5258: affine_transform complains about output_shape when output array…
- #5562: Wishart degrees of freedom should be $v > p-1$ instead of $v…
- #5933: mstats_basic.py - mannwhitneyu [scipy/scipy/stats/mstats_basic.py]
- #6409: _unequal_var_ttest_denom causes ZeroDivisionError in early samples
- #6682: negative binomial survival function is imprecise
- #6897: scipy.stats.mannwhitneyu of empty sets gives p=0.0 and does not…
- #7303: stats.describe with nan_policy=omit returns matrix-wide minmax…
- #7406: scipy.stats.binom.ppf returns nan for q between 0 and 1 if n…
- #7437: ENH: add skewed Cauchy distribution to stats
- #7542: DOC: stats tutorials: Questions on arcsine and Student t formulae
- #7593: Meaning of `tol` argument in `scipy.optimize.minimize` is…
- #8565: Error in SmoothSphereBivariateSpline(): “ValueError: Error code…
- #8665: `scipy.ncx2.sf` should be monotone decreasing
- #8836: scipy.optimize.linprog(method='simplex') needs to return duals
- #9184: Mann-Whitney implementation wrong?
- #9450: allow seeding of init methods in vq.kmeans2
- #9704: RectSphereBivariateSpline fails for negative longitude
- #9836: scipy.stats.rice gives incorrect results when s is very low compared…
- #9904: Request/Proposal: Greatly improve scipy.interpolate.Rbf
- #9981: stats.kruskal : add a warning for an input with 2 or more columns
- #10358: DOC: linprog and linear_sum_assignment tutorials needed
- #10908: Nakami fitting doesn't converge (scipy.stats)
- #10933: Add scaled inverse chi2 distribution
- #11014: Barnard's Test for More Powerful Hypothesis Testing of 2x2 Contingency…
- #11050: Feature request: Nelder-Mead with bounds
- #11086: scipy.stats.skew doesn't work correctly for float point numbers
- #11113: inconsistent result from ttest_ind and mannwhitneyu when used…
- #11134: Wrong confidence interval for binomial distribution with p=0
- #11325: Add axis parameter for scipy.spatial.distance.jensenshannon
- #11474: scipy.stats.skellam.cdf(0) returns 0 for large mu1 = mu2
- #11523: scipy.stats.zipf doesn't implement zipf distribution
- #11848: How to get Lagrange / lambda multipliers out of 'linprog' optimize…

- #11909: Enable bounds for lambda in boxcox
- #12118: Docstring missing defaults
- #12132: Slow tests to be trimmed or moved to test('full')
- #12230: Dendrogram: enable leaves labelling with 'labels' when using…
- #12282: scipy.stats.chisquare test does not check that observed and expected…
- #12298: BUG: fmin_powell missing squeeze in 1.5.0rc
- #12403: Add nan_policy to stats.zmap
- #12518: Null hypothesis of Kolmogorov Smirnov test is not correctly described
- #12534: Feature request: scipy.linalg.norm to deal with 0-size array
- #12622: scipy.interpolate.interpn docstring example
- #12635: scipy.stats.beta.ppf gives unexpexted results
- #12669: Median-averaging of complex CSDs
- #12731: stats.ncx2.cdf fails for nc >> x >> 1
- #12778: Confusing documentation of scipy.stats.weightedtau
- #12794: [Bug] The result of stats.beta.isf is inconsistent with stats.beta.sf
- #12837: stats.mannwhitneyu could support arrays
- #12868: Vector-valued interpolation in `interp2d`
- #12922: Minimize with trust-constr method leads to TypeError if option…
- #12929: The use of starred expressions to create data detracts from understanding…
- #12965: domain of argument of scipy.interpolate.RectSphereBivariateSpline(u,…
- #13025: Generalized Hyperbolic Distribution
- #13090: Broken link in doc for signal.max_len_seq
- #13101: MAINT: Upgrade python version in docker file
- #13158: `signal.get_window()` has a missing doc link and cannot get…
- #13173: Uninformative error message from bisplev function
- #13234: BUG: stats: Wrong shape of burr.moment() and fisk.moment() when…
- #13242: Does kmeans "drop" clusters?
- #13243: tgsen uses an output argument for computing a default argument
- #13245: Kurtosis returning 1 for array of same elements
- #13257: GitHub Actions test failures for MacOS
- #13272: scipy.stats.yeojohnson_llf doc mistake
- #13280: Wrong results with hypergeom cdf
- #13285: description correction in scipy.stats.t
- #13287: Generate binomial CDF with mu instead of prob
- #13294: BUG: stats: wrong bounds returned by 'support' method for distributions…
- #13299: Typing for scipy.spatial

- #13300: Add a single individual to a latinhypercube initial population…
- #13311: MAINT: pavement.py PYVER is outdated
- #13339: savemat discards dimension information if any dimension is zero
- #13341: add scipy.stats.variation with an ddof parameter
- #13353: Documentation: in scipy.stats.johnsonsu, parameter `a` can…
- #13405: TST: add a few tests for sparse BSR ctor
- #13410: BUG: skew for empty array raises
- #13417: 10,000 times speedup for generating random numbers from the cosine…
- #13440: python runtest.py -t path-to-test.py failed
- #13454: Scipy cosine distance can be greater than 2
- #13459: Broken link in cramervonmises documentation
- #13494: One-word typo in the documentation of optimize.linprog_simplex
- #13501: minimize using Powell methods with Bounds leads to “TypeError:…
- #13509: signal.medfilt2d vs ndimage.median_filter
- #13511: DOC: error in description of “direc” parameter of “fmin_powell”
- #13526: TST: stats: intermittent `test_ttest_ind_randperm_alternative2…
- #13536: `_within_tolerance` seems an unnecessary repetition of `numpy.isclose`
- #13540: missing python 3.8 manylinux wheels on scipy-wheels-nightly
- #13559: shape error in linprog with revised simplex
- #13587: binned_statistic unreliable with single precision
- #13589: Better argument preparation for distributions in stats package.
- #13602: The crystallball distribution entropy is sometimes minus infinity
- #13606: MAINT: mypy: some typing errors while running mypy + adding mypy…
- #13608: Why does stats.binned_statistic_2d convert its values argument…
- #13609: BUG: SciPy pip install -e gets unusable version spec
- #13610: Highs solver did not provide a solution nor did it report a failure
- #13614: BUG: invgauss.cdf should return the correct value when `mu`…
- #13628: 1-letter typo in the definition of scipy.special.spence function…
- #13634: mmwrite fails on dense, skew-symmetric array
- #13646: Sparse matrix argmax() integer overflow on Windows 10
- #13647: `scipy.stats.qmc.LatinHypercube` cannot sample single sample…
- #13651: Documentation wrong in scipy.linalg.eigvalsh
- #13664: BUG: gamma distribution’s inverse survival function overflows…
- #13693: BUG: sokalmichener appears to incorrectly apply weights
- #13697: BUG: stats: Spurious warning generated by arcsine.pdf at the…
- #13704: Make it possible to pass a rank cut-off value relatively to the…

- #13707: Kullback Leibler Divergence broadcasting no longer works
- #13740: Scipy.optimize x0 out of bounds when it is within bounds.
- #13744: scipy.interpolate.interp1d has inconsistent behavior for non-unique…
- #13754: optimize.minimize 'trust' methods and finite difference Hessian…
- #13762: MAINT, TST: aarch64 stats test failures showing up in wheels…
- #13769: probplot draws fit line even when fit=False
- #13791: BUG: stats: wrapcauchy.cdf does not broadcast the shape parameter…
- #13793: CI: CircleCI doc build failure
- #13840: manylinux1 builds are failing because of C99 usage in `special/_cosine.c`
- #13850: CI: Homebrew is failing due to bintray
- #13875: BUG: chi2_contingency with Yates correction
- #13878: BUG: `signal.get_window` argument handling issue
- #13880: Remove all usages of numpy.compat
- #13896: Boschloo's Test for More Powerful Hypothesis Testing of 2x2 Contingency…
- #13923: Inverse of Log CDF of Normal Distribution
- #13933: `signal.get_window` does not support `general_cosine` and…
- #13950: DOC: scipy.spatial.KDTree.query
- #13969: N=4 must not exceed M=3
- #13970: Pearson's original paper on chi-square test could be referenced.
- #13984: Faster addition of sparse diagonal matrices
- #13988: An error occurred when using scipy.io.wavfile of scipy 1.6 version…
- #13997: BUG: sparse: Incorrect result from `dia_matrix.diagonal()`
- #14005: MAINT: optimize: `curve_fit` input error msg can be improved.
- #14038: MAINT: add type annotations for _sobol.pyx
- #14048: DOC: missing git submodule information
- #14055: linalg.solve: Unclear error when using assume_a='her' with real…
- #14093: DOC: Inconsistency in the definition of default values in the…
- #14158: TST, BUG: test_rbfinterp.py – test_interpolation_misfit_1d fails…
- #14170: TST: signal submodule test_filtfilt_gust failing on 32-bit amd64…
- #14194: MAINT: download-wheels.py missing import
- #14199: Generated sources for biasedurn extension are broken in 1.7.0rc1

5.1.8 Pull requests for 1.7.0

- #4824: Permutation Ttest (new PR)
- #4933: ENH: Update the Mann-Whitney-Wilcoxon test
- #7702: ENH: stats: Add Skewed Cauchy Distribution
- #8306: Optional Pythran support for scipy.signal.max_len_seq_inner
- #10170: MAINT: stats: Implement cdf and ppf as ufuncs for the cosine…
- #10454: ENH: Extend find_peaks_cwt to take numbers and iterables for…
- #10844: ENH: add stats.qmc module with quasi Monte Carlo functionality
- #11313: ENH: add Wright's generalized Bessel function
- #11352: ENH: stats: Add crosstab function.
- #11477: FIX: bounded parameter in cdfchn.f gives bad results
- #11695: ENH: stats: add method of moments to `rv_continuous.fit`
- #11911: ENH: Added bounds to boxcox and boxcox_normmax
- #12438: BUG: use ellipkm1 in elliptical filter design to prevent numerical…
- #12531: ENH: stats: add Page's L test
- #12603: ENH: stats: Add `binomtest` to replace `binom_test`.
- #12653: ENH: stats: add Somers' D test
- #12676: BUG: update median averaging in signal.csd
- #12760: BUG: special: erfinv(x<<1) loses precision
- #12801: ENH: Add single-sided p-values to remaining spearmanr and linregress
- #12873: ENH: Stats: add Alexander Govern Test
- #13008: ENH: Add 'alternative' to functions using normal CDF for p-value
- #13040: BUG: Allow RectSphereBivariateSpline to accept negative longitude
- #13048: ENH: stats: Add a function that computes the relative risk.
- #13067: ENH: Add weights parameter to stats.gmean
- #13084: ENH: fast Hankel transform
- #13104: MAINT: upgrade python version (drop python 3.6) for docker dev…
- #13153: ENH: added association measurements Pearsons Contingency Coefficient,…
- #13166: ENH: stats: Add nan_policy to zmap.
- #13175: MAINT: tests for tall cost matrices in `linear_sum_assignment`
- #13177: BUG: raise NotImplementedError in fourier_ellipsoid when ndim…
- #13184: BUG: stats: Fix min and max calculation of mstats.describe with…
- #13188: DOC: stats: make null and alternative hypotheses of kstest more…
- #13193: MAINT: stats: chisquare check sum of observed/expected frequencies
- #13197: ENH/MAINT: HiGHS upstream enhancements and bug fixes
- #13198: ENH: allow inference of output_shape from out array in affine_transform

- #13204: ENH: stats: add Zipfian (different from Zipf/zeta) distribution
- #13208: REL: set version to 1.7.0.dev0
- #13216: TST: stats: break up and mark slow tests
- #13224: Update docs for the weighted τ
- #13230: ENH: linalg: Add LAPACK wrapper for tgexc.
- #13232: MAINT: stats: raise error when input to kruskal has >1 dim
- #13233: DOC: stats: fix MGF of arcsine and entropy of t in tutorial
- #13236: MAINT: reorganize shared linear assignment tests
- #13237: BENCH: Refactor stats.Distribution to easily add new distributions
- #13238: BUG: stats: fix wrong shape output of burr and fisk distributions
- #13240: MAINT: add tests of trivial cost matrices for linear sum assignment
- #13252: DOC: optimize: add `optimize.linear_sum_assignment` tutorial.
- #13254: BUG: Fix precision issues for constant input in skew and kurtosis
- #13262: BUG: scipy.medfilt and .medfilt2d fixes
- #13263: ENH: add Cramer-von Mises test for two samples
- #13264: fix a minor typo in `stats.anderson` doc
- #13268: ENH: stats: Add implementation of _entropy for the t distr.
- #13273: DOC: stats: fix typo in Yeo-Johnson LL function documentation
- #13275: MAINT: stats: Correct a comment in the _fitstart method of gamma.
- #13283: BUG: stats: fix the cdf method of rv_discrete class
- #13286: DOC: stats: clairify rv_continuous/discrete.stats example
- #13288: DOC: stats: discrete distribution shape parameter restrictions
- #13289: MAINT: fix a build warning in sigtoolsmodule.c
- #13290: DOC: Expand the discussion of the nan_policy API.
- #13291: MAINT: signal, stats: Use keepdims where appropriate.
- #13292: DOC: stats: note another common parameterization of nbinom
- #13293: DOC: Change broken link for default values to archived link
- #13295: BUG: stats: fix the support method to return correct bounds
- #13296: DOC: stats: Fix latex markup in the kstwo docstring.
- #13297: TST: mark kde.logpdf overflow test as xslow
- #13298: Generalized Hyperbolic Distribution
- #13301: DOC: cluster: Add cluster number note to the docstring of cluster.vq.kmeans
- #13302: BUG: Fix ndimage.morphology.distance_transform_* argument handling
- #13303: CI: prevent Codecov giving false CI failures and wrong PR annotations
- #13313: ENH: static typing for qhull
- #13316: Pythran implementation of scipy.signal._spectral

- #13317: DOC: forward port 1.6.0 relnotes
- #13319: ENH: stats: add fast numerical inversion of distribution CDF
- #13320: ENH: x0 for differential_evolution
- #13324: DOC correct linprog highs versionadded to 1.6
- #13326: MAINT: update numpydoc to v1.1.0
- #13327: DOC: interpolate: improved docstring examples of `interpolate.interpn()`…
- #13328: ENH: Boost stats distributions
- #13330: ENH: stats: add noncentral hypergeometric distributions (Fisher's…
- #13331: MAINT/ENH: resolve mypy warnings/errors
- #13332: DOC: interpolate: improved docstring of `interpolate.interp2d`…
- #13333: ENH: stats: Some more _sf and _isf implementations.
- #13334: MAINT: stats: Clean up a few defunct comments in _continuous_distns.py
- #13336: Pythran version of scipy.optimize._group_columns
- #13337: DOC|ENH: type hinting in scipy.integrate.simpson
- #13346: ENH: stats: add 'ddof' parameter to the 'variation' function
- #13355: ENH: stats: implement _logpdf, _sf and _isf for loggamma.
- #13360: ENH|DOC: fix docstring and input validation in interpolate.RectSphereBivariateSpline
- #13366: BUG: stats: Don't raise ZeroDivisionError in _unequal_var_ttest_denom
- #13370: ENH: fix ARGUS distribution for small parameters in stats
- #13371: ENH: stats: add `bootstrap` for estimating confidence interval…
- #13373: BUG: io/matlab: preserve dimensions of empty >=2D arrays
- #13374: ENH: stats: add skewed Cauchy distribution
- #13379: BUG: sparse: fix verbosity in sparse lsqr
- #13383: TST: stats: mark many dimension permutation t-test slow
- #13384: MAINT: Make keywords array static
- #13388: PERF: Avoid duplicate mean calculations in skew and kurtosis
- #13389: DOC: Fix deprecated directive syntax
- #13390: DOC: Correct line length for Parameter Section underline
- #13393: MAINT: stats: allow wishart dim - 1 < df < dim
- #13395: DOC: fix typo in setup.py warning message
- #13396: BUG: Fix MLE for Nakagami `nakagami_gen.fit`
- #13397: MAINT:linalg: Fix tgsen family wrapper and ordqz
- #13406: TST: add error handling tests for sparse BSR ctor
- #13413: DOC: ultra-quickstart guide
- #13418: BUG: Fix moment returning inconsistent types and shapes
- #13423: DOC: Update example for leaf_label_func/dendrogram

- #13431: ENH: stats: override _rvs for nhypergeom
- #13432: Add indicator in NDInterpolator docstring that N must be > 1
- #13434: DOC: stats: note relationship between scaled-inv-chi2 and invgamma
- #13436: ENH: interpolate: add input validation to check input x-y is…
- #13441: ENH: add functionality `barnard_exact` test to scipy.stats.
- #13443: MAINT: stats: Updates for skewcauchy
- #13444: DOC: clarify range of `a` parameter fpr johnsonsu/johnsonsb
- #13445: DOC: fix runtests guidelines.
- #13446: MAINT: stats: Add _fitstart method to wrapcauchy.
- #13447: DEV: Update development Docker image
- #13448: ENH: Add annotations for `scipy.spatial.distance`
- #13451: DOC: minor formatting.
- #13458: DOC: indent see also.
- #13460: DOC: stats: Fix link to Cramer-von Mises wikipedia article.
- #13461: DOC: reorganize scipy.stats overview docs page
- #13463: DOC: misc formatting fixes
- #13466: DOC: Typo in see also s/SmoothUni/SmoothBi/g
- #13467: DOC: optimize: add description about `tol` argument for `minimize`.
- #13469: MAINT: Refactor optimization methods to use scipy.stats.qmc
- #13477: CI: pin numpy to 1.19.5 for the three macOS CI jobs
- #13478: DOC: fix typos where double :: for Sphinx directives were missing
- #13481: CI: pin numpy to 1.19.5 in the 4 parallel Windows builds on Azure
- #13482: CI: use numpy 1.20.0 again in macOS CI
- #13483: DOC: Multiple documentation syntax fixes.
- #13484: Move some pythran config from CI to setup
- #13487: DOC: add a tutorial about scipy.stats.qmc
- #13492: ENH: GH actions should not run on forks
- #13493: DEV: Enable gitpod for SciPy
- #13495: DOC One-word typo in the documentation of optimize.linprog_simplex
- #13499: DOC: describe LSAP implementation
- #13502: BUG: Bounds created with lists weren't working for Powell
- #13507: MAINT, TST: stats: centralize invalid parameters list for all…
- #13510: DOC: stats: fix small doc errors in 'multivariate_hypergeom'
- #13513: DOC: Added math notation in examples in ltisys.py
- #13514: ENH: simplify low_0_bit function for Sobol
- #13515: ENH: optimize: add bound constraint support for nelder-mead solver

- #13516: DOC: reduce LaTeX usage for johnsonb docstring
- #13519: BLD: remove build_sphinx support from setup.py
- #13527: TST: stats: xfail ttest_ind_randperm_alternative2 on 32 bit
- #13530: DOC: correct comparisons between median filter functions
- #13532: ENH: release the GIL inside medfilt2d
- #13538: DOC: optimize: fix minor doc error in 'fmin_powell' (#13511)
- #13546: DOC: fix list of "mode" options for ndimage
- #13549: ENH: stats: add 'alternative' keyword to some normality tests.
- #13551: MAINT: add git to docker env
- #13552: MAINT: stats: remove float_power shim
- #13553: DOC: use support rather than a/b in stats tutorial
- #13560: MAINT: optimize: improve linprog error message for sparse input…
- #13562: MAINT: optimize: using np.isclose instead of _within_tolerance.
- #13566: ENH: Speed up hdquantiles_sd()
- #13569: BENCH: optimize: benchmark only HiGHS methods; add bigger linprog…
- #13574: DOC: In description of cluster.hierarchy.dendrogram 'level' parameter,…
- #13576: ENH: improve discrepancy performance
- #13579: TST: Add pybind11 to tox environments
- #13583: BUG: Fix Dockerfile apt-get installs
- #13588: MAINT: forward port 1.6.1 relnotes.
- #13593: BUG: stats: preserve sample dtype for bin edges
- #13595: ENH: interpolate: add RBFInterpolator
- #13596: DOC: Fix indentation in new_stats_distribution.rst.inc
- #13601: Add dpss for get_window function
- #13604: DOC: Correct dual annealing visiting param range.
- #13605: Add Codecov badge to README
- #13607: MAINT: stats: fix crystalball entropy
- #13611: Better argument preparation for distributions in stats package.
- #13612: Add docker run command for Windows cmd
- #13613: MAINT, CI: mypy: fix typing errors + add mypy to CI
- #13616: FIX: Return correct output for invgauss.cdf when mu is very small
- #13617: MAINT: accept numbers and iterables for width in find_peaks_cwt
- #13620: CI: disable the mypy CI job (partial revert of gh-13613)
- #13621: DOC: signal: use array_like for input types
- #13622: MAINT: clean up some unused files, make `mypy scipy` pass
- #13623: CI: enable Mypy CI job again

- #13624: TST: test more values for `visiting_param` input to `dual_annealing`
- #13625: Rename integrate.simps to integrate.simpsons in documentation…
- #13631: ENH: add a `stats.differential_entropy` function
- #13633: BUG: stats.binned_statistic_2d user function expecting arrays
- #13641: ENH: Added degrees parameter to rotvec
- #13645: MAINT: mypy: don't install numpy-stubs
- #13649: BUG: sparse: csc_matrix.argmax() integer overflow
- #13650: ENH: stats: add 'alternative' parameter to ansari
- #13652: DOC: fix eigvalsh documentation (#13651)
- #13654: BUG: Fix LatinHypercubes
- #13656: DOC: Fix PCHIP references
- #13657: TST: remove IPython warning in debug session
- #13658: Remove spurious quotes in docstring
- #13661: ENH: stats: improve efficiency of / fix bug in exact permutation…
- #13667: MAINT: Make latest Docker image default
- #13668: MAINT: add .theia/ to .gitignore
- #13669: BLD: change SCIPY_USE_PYTHRAN default to `1`
- #13676: ENH Small improvements for LSQR with damp
- #13678: MAINT: add Pythran-generated files to .gitignore
- #13679: MAINT: move the `conda develop .` in the Gitpod config
- #13680: DOC: Add cKDTree note comparing it with KDTree
- #13681: DOC: build doc updates on Pythran, compiled code, and cleanups
- #13683: BUG: mmwrite correctly serializes non skew-symmetric arrays
- #13684: FIX: fix numerical overflow in gamma.isf method
- #13685: BUG: fix cosine distance range to 0-2
- #13694: MAINT: fix warning emitted when NumPy version is incorrect
- #13696: ENH: support trimming in ttest_ind
- #13698: BUG: stats: Fix spurious warnings generated by arcsine.pdf
- #13701: DEV: scipy.interpolate b-splines (periodic case)
- #13702: DEP: Clean up spent deprecations in spatial.distance
- #13703: MAINT: fix issues found by static code analysis
- #13706: ENH: stats: Implement sf and isf for the laplace distribution.
- #13711: MAINT: stats: fix broadcasting for scipy.stats.entropy
- #13712: BUG: stats: Override _fitstart for the invweibull distribution.
- #13713: DOC: update toolchain.rst to reflect windows universal C runtime
- #13714: MAINT: stats: Remove an unused list from test_continuous_basic.py.

- #13715: MAINT: stats: No need to suppress frechet deprecation warnings.
- #13716: MAINT: use super() as described by PEP 3135
- #13718: MAINT: new-style class, removing inheritance to object
- #13721: MAINT: add a type-ignore for mpmath (#13721)
- #13723: MAINT: mypy: ignore mpmath imports in mypy.ini
- #13724: DOC: pydata sphinx theme
- #13725: BENCH: add benchmark for Kendalltau
- #13727: CI: simplify Pythran configuration setup for Azure
- #13731: MAINT: stats: Some flake8-driven clean up.
- #13732: ENH: stats: Studentized Range Distribution
- #13735: DOC: correct Voronoi docstring
- #13738: DOC: add example to wright_bessel
- #13739: ENH: stats: Implement _sf and _isf for the chi distribution.
- #13741: MAINT: prevent overwriting of x in minimize
- #13747: DOC: Add note for interp1d for non-unique x-values
- #13749: MAINT: forward port 1.6.2 relnotes
- #13759: MAINT: simpson small performance speedups
- #13765: FIX: npymath missing causing npy_log1p to be unknown
- #13768: BENCH: Add missing pythran dependency
- #13770: ENH: stats.contingency: Add the sparse option to crosstab.
- #13774: DEP: Deprecate squeezing input vectors in spatial.distance
- #13775: Enable trust region methods to use a finite difference Hessian…
- #13777: DOC: Fix Ubuntu/Debian installation instructions
- #13778: DOC: remove references to RandomState
- #13782: MAINT: LBFGSB err msg on MAXLS changed closes #11718
- #13785: BENCH: Add benchmark for cdist/pdist with weights
- #13786: MAINT: Prepare cdist/pdist for C++ rework
- #13787: MAINT: stats: move entropy and differential_entropy functions…
- #13790: DOC: Add some dependencies for Dockerfile doc of scipy development.
- #13792: BUG: stats: Fix broadcasting in wrapcauchy.cdf
- #13795: MAINT: stats: add hypotests to __all__ in init.py, not stats.py
- #13797: MAINT: stats: probplot: don't plot least-squares fit line unless…
- #13798: MAINT: fix incorrect code comment in `hierarchy.to_tree`
- #13802: DEV: add environment.yml file for development with conda/mamba
- #13803: DOC: fix doc build warning about arxiv role already being registered
- #13804: DOC+MAINT: optimize: lb and ub in the Bounds constructor are…

- #13807: MAINT: Dont use parallel Sphinx
- #13808: MAINT: cluster.to_tree: more idiomatic looping over rows of matrix…
- #13810: MAINT: add a CODEOWNERS file
- #13811: MAINT: Add ci skip to azp
- #13814: ENH/DOC: pydata sphinx theme polishing
- #13817: DOC: Misc parameter typo and casing in scipy/linalg/_decomp_ldl.py
- #13818: MAINT: stats: keep `entropy` importable from `scipy.stats.distributions`
- #13820: BUG: update _kendall_p_exact ValueError to f-string
- #13831: FIX:DEP: Allow better tolerance control for pinv and pinvh and…
- #13832: BUG: stats: Fix rvs for levy_stable when alpha=1
- #13833: MAINT: Add inline type hintings for stats.qmc
- #13836: MAINT: Fix a couple compiler warnings.
- #13838: TST: relax test tolerances for BinomTest
- #13841: BLD: add `-std=c99` flag to scipy.special extensions using…
- #13845: ENH: stats: add `method` parameter to `differential_entropy`…
- #13847: TST: skip on optimize failure on macOS, mark one as xfail
- #13848: DOC: optimize: move Nelder Mead doc from Unconstrained minimization…
- #13849: DOC: Roadmap update
- #13852: CI: fix temporary wrong brew version from GitHub
- #13854: ENH: Update Scipy Gitpod
- #13859: TST: fix ultra-slow ttest permutations test
- #13860: MAINT: clean up LSAP error checking
- #13863: DOC: remove seed in examples
- #13865: DOC: optimize: The bounds param of differential_evolution is…
- #13866: MAINT: special: Remove an unused variable from _poly_approx in…
- #13867: DOC: stats: Explain meaning of alternatives for fisher_exact.
- #13868: CI: fix the failing job on linux.
- #13870: MAINT: move LSAP rectangular matrix handling into solver code
- #13871: DOC: Add Gitpod documentation
- #13876: Workflow : Add nightly release of NumPy in linux workflows
- #13877: DOC: Conform to numpydoc + uniformity.
- #13879: BUG: signal: fix get_window argument handling and add tests.
- #13881: CI: remove .travis.yml, remove codecov from CircleCI
- #13882: BLD: ensure incrementing dev version strings
- #13886: TST: optimize: skip test_network_flow_limited_capacity w/ UMFPACK…
- #13888: MAINT: Fix issues involving elif conditions

- #13891: Rename InivariateSpline to UnivariateSpline
- #13893: ENH: linprog HiGHS marginals/sensitivy analysis
- #13894: DOC: Add blank line before `Return` section.
- #13897: DOC: BLD: fix doc build version check, and improve build time
- #13903: MAINT: Gitpod fixes
- #13907: ENH: Rewrite minkowski metric in C++ with pybind11
- #13909: Revert "Workflow : Add nightly release of NumPy in linux workflows"
- #13910: DOC: update Readme
- #13911: MAINT: use dict built-in rather than OrderedDict
- #13920: BUG: Reactivate conda environment in init
- #13925: BUG: stats: magnitude of Yates' correction <= abs(observed-expected)…
- #13926: DOC: correct return type in disjoint_set.subsets docstring
- #13927: DOC/MAINT: Add copyright notice to qmc.primes_from_2_to
- #13928: BUG: DOC: signal: fix need argument config and add missing doc…
- #13929: REL: add PEP 621 (project metadata in pyproject.toml) support
- #13931: MAINT: special: get rid of _logit.c.src
- #13934: ENH: signal: make `get_window` supports `general_cosine`…
- #13940: MAINT: QMCEngine d input validation
- #13941: MAINT: forward port 1.6.3 relnotes
- #13944: BUG: spatial: fix weight handling of `distance.sokalmichener`.
- #13947: MAINT: Remove duplicate calculations in sokalmichener
- #13949: DOC: minor grammar fixes in minimize and KDTree.query
- #13951: ENH: Add Boschloo exact test to stats
- #13956: ENH: spatial: add `axis` and `keepdims` optional argument…
- #13963: MAINT: stats: Fix unused imports and a few other issues related…
- #13971: DOC: Add Karl Pearson's reference to chi-square test
- #13972: ENH: cluster: add an optional argument `seed` for `kmeans`…
- #13973: BLD: fix build warnings for causal/anticausal pointers in ndimage
- #13975: ENH: set empty array norm to zero.
- #13977: MAINT: signal: replace distutils templating with tempita
- #13978: MAINT: improve validations and keyword only arguments for some…
- #13979: ENH: Add Inverse of Log CDF of Normal Distribution
- #13983: Fixing `ndimage.watershed_ift` tutorial's documentation
- #13987: DOC: Adding examples to docstrings in morphology: white_tophat,…
- #13989: DOC: interpolate: improve examples of `RegularGridInterpolator`…
- #13990: MAINT, DOC: optimize: Make the input validation explanation clear…

- #13992: Workflow : Add nightly release of NumPy in linux workflows
- #13995: Doc: Continuous integration information
- #14000: BUG: sparse: Fix DIA.diagonal bug and add a regression test
- #14004: ENH: Fast addition dia matrix
- #14006: MAINT: optimize: add validation to check func parameter number…
- #14008: BUG: Raise exception for inconsistent WAV header
- #14009: DEP: Remove usage of numpy.compat
- #14010: MAINT: add support for wheel DL proxy
- #14012: DOC: Broaden Exact Test Reference
- #14015: MAINT: remove brew update
- #14017: BENCH: Add more formats for sparse arithmetic
- #14018: BENCH: add benchmark for f_oneway
- #14020: MAINT: modify np.int_ to np.int32 to make it the same for 32/64…
- #14023: MAINT: Fix clang build and remove some unicode characters
- #14025: BUG: sparse: fix DIA.setdiag issue
- #14026: TST: optimize: xfail part of test_powell
- #14029: CI: github macos fix
- #14030: MAINT: use 'yield from <expr>' (PEP 380)
- #14031: MAINT: new-style class, removing inheritance to object
- #14032: MAINT: CXXFLAGS for Pythran
- #14033: ENH: Port sqeuclidean and braycurtis to _distance_pybind
- #14034: MAINT: Clean-up 'next = __next__'
- #14045: MAINT: bump PYVER pavement.py
- #14047: DEV: initialize boost submodule in Gitpod Dockerfile
- #14051: BLD: if boost submodule content is missing, error out early
- #14052: DOC: missing submodule init information
- #14057: DOC: special: Add Examples to `psi` docstring
- #14058: BUG: fixed a dtype bug in linalg.solve.
- #14060: Doc: Fix typo in documentation of spence function.
- #14061: MAINT:stats: Type annotations for _sobol.pyx
- #14062: DOC: A few small fixes in quickstart_gitpod.rst
- #14063: DOC: signal: add Add Examples to `cont2discrete` docstring
- #14064: DOC: optimize: Add Examples to fmin_bfgs docstring
- #14065: Add example for scipy stats.trim1 under docstring
- #14066: DOC add example to scipy.special.hermite
- #14067: DOC add alpha docstring description, add example to docstring

- #14070: DOC add parameters, return, and example to docstring
- #14072: MAINT/TST: Fix tests failing with the nightly build of numpy.
- #14075: DOC Improve the code snippet in signal.hilbert docstring.
- #14076: DOC: Document Jensen-Shannon distance being accepted by cdist/pdist
- #14079: BLD: Avoid importing scipy.stats during cythonize stage
- #14082: MAINT: Remove old, commented extract_diagonal
- #14083: MAINT: sparse: Remove defunct function extract_diagonal
- #14085: ENH: Implement canberra distance in _distance_pybind
- #14086: MAINT: Clear scipy namespace of entries better imported from…
- #14088: Install Pythran from sources for python 3.10
- #14092: BUG: Fixes issue with clang.
- #14094: DOC: Correct the inconsistence definition of Default in class…
- #14105: TST: stats: mannwhitneyu: check that mstats and stats mannwhitneyu…
- #14106: DOC: stats.mstats: mannwhitneyu: the returned statistic is the…
- #14107: ENH: stats: bootstrap: add `vectorized` parameter; automatically…
- #14109: BUG: fix two issues in the fblas signature files
- #14110: DOC: mailmap update
- #14113: ENH: stats: bootstrap: add `paired` parameter
- #14116: MAINT: fix deprecated Python C API usage in odr
- #14118: DOC: 1.7.0 release notes
- #14125: DOC: fix typo
- #14126: ENH: stats: bootstrap: add `batch` parameter to control batch…
- #14127: CI: upgrade pip in benchmarks CI run
- #14130: BUG: Fix trust-constr report TypeError if verbose is set to 2…
- #14133: MAINT: interpolate: raise NotImplementedError not ValueError
- #14139: FIX/DOC: lsqr doctests print failure
- #14145: MAINT: 1.7.x version pins (“backport”)
- #14146: MAINT: commit count if no tag
- #14164: TST, BUG: fix rbf matrix value
- #14166: CI, MAINT: restrictions on pre-release CI
- #14171: TST: signal: Bump tolerances for a test of Gustafsson’s…
- #14175: TST: stats: Loosen tolerance in some binomtest tests.
- #14182: MAINT: stats: Update ppcc_plot and ppcc_max docstring.
- #14195: MAINT: download-wheels missing import
- #14230: REL: stop shipping generated Cython sources in sdist

5.2 SciPy 1.6.3 Release Notes

Contents

- *SciPy 1.6.3 Release Notes*
  - *Authors*
    - *Issues closed for 1.6.3*
    - *Pull requests for 1.6.3*

SciPy 1.6.3 is a bug-fix release with no new features compared to 1.6.2.

5.2.1 Authors

- Peter Bell
- Ralf Gommers
- Matt Haberland
- Peter Mahler Larsen
- Tirth Patel
- Tyler Reddy
- Pamphile ROY +
- Xingyu Liu +

A total of 8 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.6.3

- #13772: Divide by zero in distance.yule
- #13796: CI: prerelease_deps failures
- #13890: TST: spatial rotation failure in (1.6.3) wheels repo (ARM64)

Pull requests for 1.6.3

- #13755: CI: fix the matplotlib warning emitted during builing docs
- #13773: BUG: Divide by zero in yule dissimilarity of constant vectors
- #13799: CI/MAINT: deprecated np.typeDict
- #13819: substitute np.math.factorial with math.factorial
- #13895: TST: add random seeds in Rotation module

5.3 SciPy 1.6.2 Release Notes

Contents

- *SciPy 1.6.2 Release Notes*
  - *Authors*
    - *Issues closed for 1.6.2*
    - *Pull requests for 1.6.2*

SciPy 1.6.2 is a bug-fix release with no new features compared to 1.6.1. This is also the first SciPy release to place upper bounds on some dependencies to improve the long-term repeatability of source builds.

5.3.1 Authors

- Pradipta Ghosh +
- Tyler Reddy
- Ralf Gommers
- Martin K. Scherer +
- Robert Uhl
- Warren Weckesser

A total of 6 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.6.2

- #13512: `stats.gaussian_kde.evaluate` broken on S390X
- #13584: rotation._compute_euler_from_matrix() creates an array with negative…
- #13585: Behavior change in coo_matrix when dtype=None
- #13686: delta0 argument of scipy.odr.ODR() ignored

Pull requests for 1.6.2

- #12862: REL: put upper bounds on versions of dependencies
- #13575: BUG: fix `gaussian_kernel_estimate` on S390X
- #13586: BUG: sparse: Create a utility function `getdata`
- #13598: MAINT, BUG: enforce contiguous layout for output array in Rotation.as_euler
- #13687: BUG: fix scipy.odr to consider given delta0 argument

5.4 SciPy 1.6.1 Release Notes

Contents

- *SciPy 1.6.1 Release Notes*
  - *Authors*
    - *Issues closed for 1.6.1*
    - *Pull requests for 1.6.1*

SciPy 1.6.1 is a bug-fix release with no new features compared to 1.6.0.

Please note that for SciPy wheels to correctly install with Pip on macOS 11, Pip >= 20.3.3 is needed.

5.4.1 Authors

- Peter Bell
- Evgeni Burovski
- CJ Carey
- Ralf Gommers
- Peter Mahler Larsen
- Cheng H. Lee +
- Cong Ma
- Nicholas McKibben
- Nikola Forró
- Tyler Reddy
- Warren Weckesser

A total of 11 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.6.1

- #13072: BLD: Quadpack undefined references
- #13241: Not enough values to unpack when passing tuple to `blocksize`…
- #13329: Large sparse matrices of big integers lose information
- #13342: fftn crashes if shape arguments are supplied as ndarrays
- #13356: LSQBivariateSpline segmentation fault when quitting the Python…
- #13358: scipy.spatial.transform.Rotation object can not be deepcopied…
- #13408: Type of `has_sorted_indices` property
- #13412: Sorting spherical Voronoi vertices leads to crash in area calculation
- #13421: linear_sum_assignment - support for matrices with more than 2^31…

- #13428: `stats.exponnorm.cdf` returns `nan` for small values of `K`…
- #13465: KDTree.count_neighbors : 0xC0000005 error for tuple of different…
- #13468: directed_hausdorff issue with shuffle
- #13472: Failures on FutureWarnings with numpy 1.20.0 for lfilter, sosfilt…
- #13565: BUG: 32-bit wheels repo test failure in optimize

Pull requests for 1.6.1

- #13318: REL: prepare for SciPy 1.6.1
- #13344: BUG: fftpack doesn't work with ndarray shape argument
- #13345: MAINT: Replace scipy.take with numpy.take in FFT function docstrings.
- #13354: BUG: optimize: rename private functions to include leading underscore
- #13387: BUG: Support big-endian platforms and big-endian WAVs
- #13394: BUG: Fix Python crash by allocating larger array in LSQBivariateSpline
- #13400: BUG: sparse: Better validation for BSR ctor
- #13403: BUG: sparse: Propagate dtype through CSR/CSC constructors
- #13414: BUG: maintain dtype of SphericalVoronoi regions
- #13422: FIX: optimize: use npy_intp to store array dims for lsap
- #13425: BUG: spatial: make Rotation picklable
- #13426: BUG: `has_sorted_indices` and `has_canonical_format` should…
- #13430: BUG: stats: Fix exponnorm.cdf and exponnorm.sf for small K
- #13470: MAINT: silence warning generated by `spatial.directed_hausdorff`
- #13473: TST: fix failures due to new FutureWarnings in NumPy 1.21.dev0
- #13479: MAINT: update directed_hausdorff Cython code
- #13485: BUG: KDTree weighted count_neighbors doesn't work between two…
- #13503: TST: fix `test_fortranfile_read_mixed_record` on big-endian…
- #13518: DOC: document that pip >= 20.3.3 is needed for macOS 11
- #13520: BLD: update reqs based on oldest-supported-numpy in pyproject.toml
- #13567: TST, BUG: adjust tol on test_equivalence

5.5 SciPy 1.6.0 Release Notes

Contents

- *SciPy 1.6.0 Release Notes*
  - *Highlights of this release*
    - *New features*

- scipy.special *improvements*
- scipy.odr *improvements*
- scipy.integrate *improvements*
- scipy.cluster *improvements*
- scipy.interpolate *improvements*
- scipy.io *improvements*
- scipy.linalg *improvements*
- scipy.ndimage *improvements*
- scipy.optimize *improvements*
- scipy.signal *improvements*
- scipy.sparse *improvements*
- scipy.sparse.linalg *improvements*
- scipy.fft *improvements*
- scipy.spatial *improvements*
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- scipy *changes*
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- scipy.stats *changes*
  - *Other changes*
  - *Authors*
- *Issues closed for 1.6.0*
- *Pull requests for 1.6.0*

SciPy 1.6.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning`s). Our development attention will now shift to bug-fix releases on the 1.6.x branch, and on adding new features on the master branch.

This release requires Python 3.7+ and NumPy 1.16.5 or greater.

For running on PyPy, PyPy3 6.0+ is required.

5.5.1 Highlights of this release

- *scipy.ndimage* improvements: Fixes and ehancements to boundary extension modes for interpolation functions. Support for complex-valued inputs in many filtering and interpolation functions. New `grid_mode` option for *scipy.ndimage.zoom* to enable results consistent with scikit-image's `rescale`.
- *scipy.optimize.linprog* has fast, new methods for large, sparse problems from the `HiGHS` library.
- *scipy.stats* improvements including new distributions, a new test, and enhancements to existing distributions and tests

New features

5.5.2 `scipy.special` improvements

scipy.special now has improved support for 64-bit `LAPACK` backend

5.5.3 `scipy.odr` improvements

scipy.odr now has support for 64-bit integer `BLAS`

scipy.odr.ODR has gained an optional `overwrite` argument so that existing files may be overwritten.

5.5.4 `scipy.integrate` improvements

Some renames of functions with poor names were done, with the old names retained without being in the reference guide for backwards compatibility reasons: - `integrate.simps` was renamed to `integrate.simpson` - `integrate.trapz` was renamed to `integrate.trapezoid` - `integrate.cumtrapz` was renamed to `integrate.cumulative_trapezoid`

5.5.5 `scipy.cluster` improvements

scipy.cluster.hierarchy.DisjointSet has been added for incremental connectivity queries.

scipy.cluster.hierarchy.dendrogram return value now also includes leaf color information in *leaves_color_list*.

5.5.6 `scipy.interpolate` improvements

scipy.interpolate.interp1d has a new method `nearest-up`, similar to the existing method `nearest` but rounds half-integers up instead of down.

5.5.7 scipy.io improvements

Support has been added for reading arbitrary bit depth integer PCM WAV files from 1- to 32-bit, including the commonly-requested 24-bit depth.

5.5.8 scipy.linalg improvements

The new function *scipy.linalg.matmul_toeplitz* uses the FFT to compute the product of a Toeplitz matrix with another matrix.

scipy.linalg.sqrtm and *scipy.linalg.logm* have performance improvements thanks to additional Cython code.

Python LAPACK wrappers have been added for pptrf, pptrs, ppsv, pptri, and ppcon.

scipy.linalg.norm and the svd family of functions will now use 64-bit integer backends when available.

5.5.9 scipy.ndimage improvements

scipy.ndimage.convolve, *scipy.ndimage.correlate* and their 1d counterparts now accept both complex-valued images and/or complex-valued filter kernels. All convolution-based filters also now accept complex-valued inputs (e.g. gaussian_filter, uniform_filter, etc.).

Multiple fixes and enhancements to boundary handling were introduced to *scipy.ndimage* interpolation functions (i.e. affine_transform, geometric_transform, map_coordinates, rotate, shift, zoom).

A new boundary mode, grid-wrap was added which wraps images periodically, using a period equal to the shape of the input image grid. This is in contrast to the existing wrap mode which uses a period that is one sample smaller than the original signal extent along each dimension.

A long-standing bug in the reflect boundary condition has been fixed and the mode grid-mirror was introduced as a synonym for reflect.

A new boundary mode, grid-constant is now available. This is similar to the existing ndimage constant mode, but interpolation will still performed at coordinate values outside of the original image extent. This grid-constant mode is consistent with OpenCV's BORDER_CONSTANT mode and scikit-image's constant mode.

Spline pre-filtering (used internally by ndimage interpolation functions when order >= 2), now supports all boundary modes rather than always defaulting to mirror boundary conditions. The standalone functions spline_filter and spline_filter1d have analytical boundary conditions that match modes mirror, grid-wrap and reflect.

scipy.ndimage interpolation functions now accept complex-valued inputs. In this case, the interpolation is applied independently to the real and imaginary components.

The ndimage tutorials (https://docs.scipy.org/doc/scipy/reference/tutorial/ndimage.html) have been updated with new figures to better clarify the exact behavior of all of the interpolation boundary modes.

scipy.ndimage.zoom now has a grid_mode option that changes the coordinate of the center of the first pixel along an axis from 0 to 0.5. This allows resizing in a manner that is consistent with the behavior of scikit-image's resize and rescale functions (and OpenCV's cv2.resize).

5.5.10 `scipy.optimize` improvements

scipy.optimize.linprog has fast, new methods for large, sparse problems from the `HiGHS` C++ library. `method='highs-ds'` uses a high performance dual revised simplex implementation (HSOL), `method='highs-ipm'` uses an interior-point method with crossover, and `method='highs'` chooses between the two automatically. These methods are typically much faster and often exceed the accuracy of other `linprog` methods, so we recommend explicitly specifying one of these three method values when using `linprog`.

scipy.optimize.quadratic_assignment has been added for approximate solution of the quadratic assignment problem.

scipy.optimize.linear_sum_assignment now has a substantially reduced overhead for small cost matrix sizes

scipy.optimize.least_squares has improved performance when the user provides the jacobian as a sparse jacobian already in `csr_matrix` format

scipy.optimize.linprog now has an `rr_method` argument for specification of the method used for redundancy handling, and a new method for this purpose is available based on the interpolative decomposition approach.

5.5.11 `scipy.signal` improvements

scipy.signal.gammatone has been added to design FIR or IIR filters that model the human auditory system.

scipy.signal.iircomb has been added to design IIR peaking/notching comb filters that can boost/attenuate a frequency from a signal.

scipy.signal.sosfilt performance has been improved to avoid some previously- observed slowdowns

`scipy.signal.windows.taylor` has been added–the Taylor window function is commonly used in radar digital signal processing

scipy.signal.gauss_spline now supports `list` type input for consistency with other related SciPy functions

scipy.signal.correlation_lags has been added to allow calculation of the lag/ displacement indices array for 1D cross-correlation.

5.5.12 `scipy.sparse` improvements

A solver for the minimum weight full matching problem for bipartite graphs, also known as the linear assignment problem, has been added in *scipy.sparse.csgraph.min_weight_full_bipartite_matching*. In particular, this provides functionality analogous to that of *scipy.optimize.linear_sum_assignment*, but with improved performance for sparse inputs, and the ability to handle inputs whose dense representations would not fit in memory.

The time complexity of *scipy.sparse.block_diag* has been improved dramatically from quadratic to linear.

5.5.13 `scipy.sparse.linalg` improvements

The vendored version of `SuperLU` has been updated

5.5.14 `scipy.fft` improvements

The vendored `pocketfft` library now supports compiling with ARM neon vector extensions and has improved thread pool behavior.

5.5.15 `scipy.spatial` improvements

The python implementation of `KDTree` has been dropped and `KDTree` is now implemented in terms of `cKDTree`. You can now expect `cKDTree`-like performance by default. This also means `sys.setrecursionlimit` no longer needs to be increased for querying large trees.

`transform.Rotation` has been updated with support for Modified Rodrigues Parameters alongside the existing rotation representations (PR gh-12667).

`scipy.spatial.transform.Rotation` has been partially cythonized, with some performance improvements observed

scipy.spatial.distance.cdist has improved performance with the `minkowski` metric, especially for p-norm values of 1 or 2.

5.5.16 `scipy.stats` improvements

New distributions have been added to *scipy.stats*:

- The asymmetric Laplace continuous distribution has been added as *scipy.stats.laplace_asymmetric*.
- The negative hypergeometric distribution has been added as *scipy.stats.nhypergeom*.
- The multivariate t distribution has been added as *scipy.stats.multivariate_t*.
- The multivariate hypergeometric distribution has been added as *scipy.stats.multivariate_hypergeom*.

The `fit` method has been overridden for several distributions (`laplace`, `pareto`, `rayleigh`, `invgauss`, `logistic`, `gumbel_l`, `gumbel_r`); they now use analytical, distribution-specific maximum likelihood estimation results for greater speed and accuracy than the generic (numerical optimization) implementation.

The one-sample Cramér-von Mises test has been added as *scipy.stats.cramervonmises*.

An option to compute one-sided p-values was added to *scipy.stats.ttest_1samp*, *scipy.stats.ttest_ind_from_stats*, *scipy.stats.ttest_ind* and *scipy.stats.ttest_rel*.

The function *scipy.stats.kendalltau* now has an option to compute Kendall's tau-c (also known as Stuart's tau-c), and support has been added for exact p-value calculations for sample sizes `> 171`.

stats.trapz was renamed to *stats.trapezoid*, with the former name retained as an alias for backwards compatibility reasons.

The function *scipy.stats.linregress* now includes the standard error of the intercept in its return value.

The `_logpdf`, `_sf`, and `_isf` methods have been added to *scipy.stats.nakagami*; `_sf` and `_isf` methods also added to *scipy.stats.gumbel_r*

The `sf` method has been added to *scipy.stats.levy* and *scipy.stats.levy_l* for improved precision.

scipy.stats.binned_statistic_dd performance improvements for the following computed statistics: `max`, `min`, `median`, and `std`.

We gratefully acknowledge the Chan-Zuckerberg Initiative Essential Open Source Software for Science program for supporting many of these improvements to *scipy.stats*.

Deprecated features

5.5.17 `scipy.spatial` changes

Calling `KDTree.query` with `k=None` to find all neighbours is deprecated. Use `KDTree.query_ball_point` instead.

`distance.wminkowski` was deprecated; use `distance.minkowski` and supply weights with the `w` keyword instead.

Backwards incompatible changes

5.5.18 `scipy` changes

Using *`scipy.fft`* as a function aliasing `numpy.fft.fft` was removed after being deprecated in SciPy `1.4.0`. As a result, the *`scipy.fft`* submodule must be explicitly imported now, in line with other SciPy subpackages.

5.5.19 `scipy.interpolate` changes

5.5.20 `scipy.linalg` changes

5.5.21 `scipy.signal` changes

The output of `decimate`, `lfilter_zi`, `lfiltic`, `sos2tf`, and `sosfilt_zi` have been changed to match `numpy.result_type` of their inputs.

The window function `slepian` was removed. It had been deprecated since SciPy `1.1`.

5.5.22 `scipy.spatial` changes

`cKDTree.query` now returns 64-bit rather than 32-bit integers on Windows, making behaviour consistent between platforms (PR gh-12673).

5.5.23 `scipy.stats` changes

The `frechet_l` and `frechet_r` distributions were removed. They were deprecated since SciPy `1.0`.

Other changes

`setup_requires` was removed from `setup.py`. This means that users invoking `python setup.py install` without having numpy already installed will now get an error, rather than having numpy installed for them via `easy_install`. This install method was always fragile and problematic, users are encouraged to use `pip` when installing from source.

- Fixed a bug in *`scipy.optimize.dual_annealing`* `accept_reject` calculation that caused uphill jumps to be accepted less frequently.
- The time required for (un)pickling of *`scipy.stats.rv_continuous`*, *`scipy.stats.rv_discrete`*, and *scipy.stats.rv_frozen* has been significantly reduced (gh12550). Inheriting subclasses should note that `__setstate__` no longer calls `__init__` upon unpickling.

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A total of 122 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

5.5.24 Issues closed for 1.6.0

- #1323: ndimage.shift destroys data from edges (Trac #796)
- #1892: using rptfile= with an existing file causes a Fortran runtime…
- #1903: ndimage.rotate misses some values (Trac #1378)
- #1930: scipy.io.wavfile should be able to read 24 bit signed wave (Trac…
- #3158: Odd casting behaviour of signal.filtfilt
- #3203: interpolation.zoom incorrect output for certain cases
- #3645: BUG: stats: mstats.pearsonr calculation is wrong if the masks…
- #3665: Return Bunch objects from stats functions
- #4922: unexpected zero output values from zoom
- #5202: BUG: stats: Spurious warnings from the pdf method of several…
- #5223: Zoom does not return the same values when resizing a sub-array…
- #5396: scipy.spatial.distance.pdist documention bug
- #5489: ValueError: failed to create intent(cache|hide)|optional array–…
- #6096: loadmat drops dtype of empty arrays when squeeze_me=True
- #6713: sicpy.ndimage.zoom returns artefacts and boundaries in some cases
- #7125: Impossible to know number of dimensions in c function used by…
- #7324: scipy.ndimage.zoom bad interpolation when downsampling (zoom…

- #8131: BUG: geometric_transform wrap mode possible bug
- #8163: LSMR fails on some random values when providing an x0
- #8210: Why should I choose order > 1 for scipy.ndimage.zoom?
- #8465: Unexpected behavior with reflect mode of ndimage.rotate
- #8776: cdist behavior with Minkowsky and np.inf
- #9168: documentation of pearson3 in scipy.stats unclear
- #9223: Faster implementation of scipy.sparse.block_diag
- #9476: Invalid index in signal.medfilt2d's QUICK_SELECT
- #9857: scipy.odr.Output.sd_beta is not standard error
- #9865: Strange behavior of `ndimage.shift` and `ndimage.affine_transform`
- #10042: Consider support for multivariate student-t distribution?
- #10134: gausshyper distribution accepts invalid parameters
- #10179: str+bytes concatenation error in test_lapack.py
- #10216: cKDTree.query_ball_point speed regression
- #10463: ENH: vectorize scipy.fft for more CPU architectures
- #10593: Rename `sum` ndimage function
- #10595: scipy.stats.ttest_1samp should support alternative hypothesis
- #10610: ndimage.interpolation.spline_filter1d default value of mode
- #10620: ndimage.interpolation.zoom() option to work like skimage.transform.resize()
- #10711: Array Shapes Not Aligned Bug in scipy.optimize._lsq.lsq_linear.py
- #10782: BUG: optimize: methods unknown to `scipy.optimize.show_options`
- #10892: Possible typo in an equation of optimize/dual_annealing
- #11020: signal.fftconvolve return a tuple including lag information
- #11093: scipy.interpolate.interp1d can not handle datetime64
- #11170: Use manylinux2014 to get aarch64/ppc64le support
- #11186: BUG: stats: pearson3 CDF and SF functions incorrect when skew…
- #11366: DeprecationWarning due to invalid escape sequences
- #11403: Optimize raises "ValueError: `x0` violates bound constraints"…
- #11558: ENH: IIR comb filter
- #11559: BUG: iirdesign doesn't fail for frequencies above Nyquist
- #11567: scipy.signal.iirdesign doesn't check consistency of wp and ws…
- #11654: ENH: Add Negative Hypergeometric Distribution
- #11720: BUG: stats: wrong shape from median_absolute_deviation for arrays…
- #11746: BUG: stats: pearson3 returns size 1 arrays where other distributions…
- #11756: Improve and fix *Spline docstrings and code
- #11758: BUG: of scipy.interpolate.CubicSpline when `bc_type' is set…

- #11925: MAINT: remove character encoding check in CI?
- #11963: Test failures - TestLinprogIPSparseCholmod
- #12102: incorrect first moment of non central t-distribution
- #12113: scipy.stats.poisson docs for rate = 0
- #12152: ENH: signal.gauss_spline should accept a list
- #12157: BUG: Iteration index initialisation is wrong in scipy.optimize.linesearch.scalar_search_wolfe2
- #12162: Storing Rotation object in NumPy array returns an array with…
- #12176: cannot modify the slice of an array returned by `wavfile.read`
- #12190: retrieve leave colors from dendrogram
- #12196: PERF: scipy.linalg.pinv is very slow compared to numpy.linalg.pinv
- #12222: Interpolating categorical data (interp1d)
- #12231: Is the p-value of the Kruskal-Wallis test two-sided?
- #12249: ENH: least_squares: should not re-instanciate csr_matrix if already…
- #12264: DOC: optimize: linprog method-specific function signature
- #12290: DOC: Convex Hull areas are actually perimeters for 2-dimensional…
- #12308: integrate.solve_ivp with DOP853 method fails when yDot = 0
- #12326: BUG: stats.exponnorm.pdf returns 0 for small K
- #12337: scipy.sparse.linalg.eigsh documentation is misleading
- #12339: scipy.io.wavfile.write documentation has wrong example
- #12340: sparse.lil_matrix.tocsr() fails silently on matrices with nzn…
- #12350: Create a 2-parameter version of the gamma distribution
- #12369: scipy.signal.correlate has an error in the documentation, examples…
- #12373: interp1d returns incorrect values for step functions
- #12378: interpolate.NearestNDInterpolator.__call__ & LinearNDInterpolator.__call__…
- #12411: scipy.stats.spearmanr mishandles nan variables with “propogate”
- #12413: DOC: Remove the “Basic functions” section from the SciPy tutorial.
- #12415: scipy.stats.dirichlet documentation issue
- #12419: least_squares ValueError with ‘lm’ method - regression from 1.4.1…
- #12431: Request for Python wrapper for LAPACK’s ?pptrf (Cholesky factorization…
- #12458: spearmanr with entire NaN columns produces errors
- #12477: WIP: Addition of MLE for stats.invgauss/wald
- #12483: reading .wav fails when the file is too big on python 3.6.0
- #12490: BUG: stats: logistic and genlogistic logpdf overflow for large…
- #12499: LinearNDInterpolator raises ValueError when value array has writeable=False…
- #12523: Wrong key in __odrpack.c
- #12547: typo in scipy/cluster/_hierarchy.pyx

- #12549: DOC: least_squares return type is poorly formatted.
- #12578: TST: test_bounds_infeasible_2 failing on wheels repo cron jobs
- #12585: ENH: Add Multivariate Hypergeometric Distribution
- #12604: unintuitive conversion in `scipy.constants.lambda2nu`
- #12606: DOC: Invalid syntax in example.
- #12665: List of possible bugs found by automated code analysis
- #12696: scipy.optimize.fminbound, numpy depreciation warning Creating…
- #12699: TestProjections.test_iterative_refinements_dense failure
- #12701: TestDifferentialEvolutionSolver::test_L4 failing
- #12719: Misleading scipy.signal.get_window() docstring with 'exponential'…
- #12740: circstd doesn't handle R = hypot(S, C) > 1
- #12749: ENH: interp1d Matlab compatibility
- #12773: Meta-issue: ndimage spline boundary handling (NumFOCUS proposal)
- #12813: optimize.root(method="krylov") fails if options["tol_norm"] expects…
- #12815: stats.zscore inconsistent behavior when all values are the same
- #12840: scipy.signal.windows.dpss docstring typo
- #12874: Rotation.random vs stats.special_ortho_group
- #12881: FFT - documentation - examples - linspace construction
- #12904: BUG: parsing in loadarff()
- #12917: GitHub Actions nightly build triggered on forks
- #12919: BUG: numerical precision, use gammaln in nct.mean
- #12924: Rename Sample Based Integration Methods to Comply with Code of…
- #12940: Should the minimum numpy for AIX be bumped to 1.16.5
- #12951: A possible typo in scipy.stats.weightedtau
- #12952: [Documentation question] Would it be more precise to specify…
- #12970: Documentation presents second order sections as the correct choice…
- #12982: Calculate standard error of the intercept in linregress
- #12985: Possible wrong link in scipy.stats.wilcoxon doc
- #12991: least_squares broken with float32
- #13001: `OptimizeResult.message` from `L-BFGS-B` is a bytes, not…
- #13030: BUG: lint_diff.py still fails for backport PRs
- #13077: CI: codecov proper patch diffs
- #13085: Build failing on main branch after HiGHS solver merge
- #13088: BLD, BUG: wheel builds failure with HiGHS/optimize
- #13099: Wrong output format for empty sparse results of kron
- #13108: TST, CI: GitHub Actions MacOS Failures

- #13111: BUG, DOC: refguide check is failing
- #13127: ODR output file writing broken in conda env with system compilers
- #13134: FromTravis migration tracker
- #13140: BUG: signal: `ss2tf` incorrectly truncates output to integers.
- #13179: CI: lint is failing because of output to stderr
- #13182: Key appears twice in `test_optimize.test_show_options`
- #13191: `scipy.linalg.lapack.dgesjv` overwrites original arrays if…
- #13207: TST: Erratic test failure in test_cossin_separate
- #13221: BUG: pavement.py glitch
- #13239: Segmentation fault with `eigh(…, driver="evx")` for 10x10…
- #13248: ndimage: improper cval handling for complex-valued inputs

5.5.25 Pull requests for 1.6.0

- #8032: ENH: Add in taylor window common in Radar processing
- #8779: CI: Run benchmarks
- #9361: ENH: Add Kendall's tau-a and tau-c variants to scipy.stats.kendalltau()
- #11068: ENH: Adds correlation_lags function to scipy.signal
- #11119: ENH: add Cramer-von-Mises (one-sample) test to scipy.stats
- #11249: ENH: optimize: interpolative decomposition redundancy removal…
- #11346: ENH: add fast toeplitz matrix multiplication using FFT
- #11413: ENH: Multivariate t-distribution (stale)
- #11563: ENH: exact p-value in stats.kendalltau() for sample sizes > 171
- #11691: ENH: add a stack of reversal functions to linprog
- #12043: ENH: optimize: add HiGHS methods to linprog - continued
- #12061: Check parameter consistensy in signal.iirdesign
- #12067: MAINT: Cleanup OLDAPI in ndimage/src/_ctest.c
- #12069: DOC: Add developer guidelines for implementing the nan_policy…
- #12077: MAINT: malloc return value checks for cython
- #12080: MAINT: Remove suppress_warnings
- #12085: ENH: special: support ILP64 Lapack
- #12086: MAINT: Cleanup PyMODINIT_FUNC used during 2to3
- #12097: ENH: stats: override stats.rayleigh.fit with analytical MLE
- #12112: DOC: Improve integrate.nquad docstring
- #12125: TST: Add a test for stats.gmean with negative input
- #12139: TST: Reduce flakiness in lsmr test
- #12142: DOC: add a note in poisson distribution when mu=0 and k=0 in…

- #12144: DOC: Update ndimage.morphology.distance_transform*
- #12154: ENH: scipy.signal: allow lists in gauss_spline
- #12170: ENH: scipy.stats: add negative hypergeometric distribution
- #12177: MAINT: Correctly add input line to ValueError
- #12183: ENH: Use fromfile where possible
- #12186: MAINT: generalize tests in SphericalVoronoi
- #12198: TST: Fix str + bytes error
- #12199: ENH: match np.result_type behaviour in some scipy.signal functions
- #12200: ENH: add FIR and IIR gammatone filters to scipy.signal
- #12204: ENH: Add overwrite argument for odr.ODR() and its test.
- #12206: MAINT:lstsq: Switch to tranposed problem if the array is tall
- #12208: wavfile bugfixes and maintenance
- #12214: DOC: fix docstring of “sd_beta” of odr.Output.
- #12234: MAINT: prevent divide by zero warnings in scipy.optimize BFGS…
- #12235: REL: set version to 1.6.0.dev0
- #12237: BUG: Fix exit condition for QUICK_SELECT pivot
- #12242: ENH: Rename ndimage.sum to ndimage.sum_labels (keep sum as alias)
- #12243: EHN: Update SuperLU
- #12244: MAINT: stats: avoid spurious warnings in ncx2.pdf
- #12245: DOC: Fixed incorrect default for mode in scipy.ndimage.spline_filter1d
- #12248: MAINT: clean up pavement.py
- #12250: ENH: Replaced csr_matrix() by tocsr() and complemented docstring
- #12253: TST, CI: turn on codecov patch diffs
- #12259: MAINT: Remove duplicated test for import cycles
- #12263: ENH: Rename LocalSearchWrapper bounds
- #12265: BUG optimize: Accept np.matrix in lsq_linear
- #12266: BUG: Fix paren error in dual annealing accept_reject calculation
- #12269: MAINT: Included mismatched shapes in error messages.
- #12279: MAINT: `__array__` and array protocols cannot be used in sparse.
- #12281: DOC: update wheel DL docs
- #12283: ENH: odr: ILP64 Blas support in ODR
- #12284: ENH: linalg: support for ILP64 BLAS/LAPACK in f2py wrappers
- #12286: ENH: Cythonize scipy.spatial.transform.Rotation
- #12287: ENH: Read arbitrary bit depth (including 24-bit) WAVs
- #12292: BLD: fix musl compilation
- #12293: MAINT: Fix a DeprecationWarning in validate_runtests_log.py.

- #12296: DOC: Clarify area/volume in scipy.spatial.ConvexHull docstrings
- #12302: CI: Run travis builds on master to keep cache up to date
- #12305: TST: Cleanup print statements in tests
- #12323: ENH: Add a Bunch-like class to use as a backwards compatible…
- #12324: BUG: io: Fix an error that occurs when attempting to raise a…
- #12327: DOC: clarify docstrings of `query_ball_tree` and `query_pairs`
- #12334: PERF: Improve cKDTree.query_ball_point constant time cython overhead
- #12338: DOC: improve consistency and clarity of docs in linalg and sparse/linalg
- #12341: DOC: add Examples for KDTree query_ball_tree and query_pairs
- #12343: DOC: add examples for special.eval_legendre()
- #12349: BUG: avoid overflow in sum() for 32-bit systems
- #12351: DOC: Fix example wavfile to be 16bit
- #12352: [BUG] Consider 0/0 division in DOP853 error estimation
- #12353: Fix exception causes in vq.py
- #12354: MAINT: Cleanup unneeded void* cast in setlist.pxd
- #12355: TST: Remove hack for old win-amd64 bug
- #12356: ENH: Faster implementation of scipy.sparse.block_diag (#9411…
- #12357: MAINT,TST: update and run scipy/special/utils/convert.py
- #12358: TST: Check mstat.skewtest pvalue
- #12359: TST: Sparse matrix test with int64 indptr and indices
- #12363: DOC: ref. in CloughTocher2DInterpolator
- #12364: DOC: `sparse_distance_matrix` and `count_neighbors` examples
- #12371: MAINT, CI: bump to latest stable OpenBLAS
- #12372: MAINT: Minor cleanup of (c)KDTree tests
- #12374: DEP: Deprecate `distance.wminkowski`
- #12375: ENH: Add fast path for minkowski distance with p=1,2 and support…
- #12376: Fix exception causes in most of the codebase
- #12377: DOC: Quick fix - adds newline to correlation_lags docstring Examples…
- #12381: BENCH: remove obsolete goal_time param
- #12382: ENH: Replace KDTree with a thin wrapper over cKDTree
- #12385: DOC: improve docstrings of interpolate.NearestNDInterpolator.__call__…
- #12387: DOC/STY: add example to scipy.signal.correlate
- #12393: CI: Replace the existing check for non-ASCII characters with…
- #12394: CI: arm64 numpy now available
- #12395: ENH: improve stats.binned_statistic_dd performance
- #12396: DOC, MAINT: forward port 1.5.0 relnotes

- #12398: API: Disable len() and indexing of Rotation instances with single…
- #12399: MAINT: Replace some Unicode dash-like chars with an ASCII hyphen.
- #12402: update .mailmap
- #12404: MAINT: io: Change the encoding comment of test_mio.py to utf-8.
- #12416: CI: cache mingw, azure pipelines
- #12427: BUG: logic error in loop unrolling (cKDTree)
- #12432: DOC: Remove the "Basic functions" section from the SciPy tutorial.
- #12434: ENH:linalg: Add LAPACK wrappers pptrf/pptrs/ppsv/pptri/ppcon
- #12435: DOC: fix simplex math for scipy.stats.dirichlet documentation
- #12439: DOC: add API methods summary for NdPPoly
- #12443: BUG: stats: Improve calculation of exponnorm.pdf
- #12448: DOC: stats: Add "Examples" to the ansari docstring.
- #12450: ENH: add `leaves_color_list` for cluster.dendrogram dictionary.
- #12451: MAINT: remove "blacklist" terminology from code base
- #12452: DOC: clarify the meaning of whitening for cluster.vq.whiten()
- #12455: MAINT: clearer error message in setup.py
- #12457: ENH: stats: override stats.pareto.fit with analytical MLE
- #12460: check if column in spearman rho is entirely NaN or Inf
- #12463: DOC: improve and clean up *Spline docstrings in fitpack2.py
- #12474: ENH: linalg: speedup _sqrtm_triu by moving tight loop to Cython
- #12476: ENH: add IIR comb filter to scipy.signal
- #12484: Fix documentation for minimize
- #12486: DOC: add a note in poisson distribution when mu=0 and k=0 in…
- #12491: MAINT: forward port 1.5.1 release notes
- #12508: Fix exception causes all over the codebase
- #12514: ENH: stats: override stats.invgauss.fit with analytical MLE
- #12519: PERF: Avoid np.zeros when custom initialization is needed anyway
- #12520: DOC: Minor RST section renaming.
- #12521: MAINT: Remove unused imports
- #12522: PERF: Get rid of unnececssary allocation in VarReader5.cread_fieldnames
- #12524: DOC: special: Set Axes3D rect to avoid clipping labels in plot.
- #12525: Fix large sparse nnz
- #12526: DOC: Remove double section and too long header underline.
- #12527: Improve error message for wrong interpolation type
- #12530: Move redundant logic outside loop for conditional speedup in…
- #12532: ENH: Add norm={"forward", "backward"} to `scipy.fft`

- #12535: MAINT: Avoid sphinx deprecated aliases for SeeAlso and Only
- #12540: BUG: fix odr.output.work_ind key bug and add its test.
- #12541: ENH: add solver for minimum weight full bipartite matching
- #12550: PERF: pickling speed of rv*
- #12551: DOC: fix typo in cluster/_hierarchy.pyx
- #12552: CI: Cleanup travis pip installs
- #12556: BUG: Fix problem with Scipy.integrate.solve_bvp for big problems
- #12557: MAINT: Use extern templates to improve sparsetools compile time
- #12558: MAINT: Remove hack to allow scipy.fft to act like a function
- #12563: MAINT: Remove unused mu0 in special/orthogonal.py
- #12564: DOC: fix return type docstring for least_squares
- #12565: DOC: stats: respond to query about Kruskal-Wallis test being…
- #12566: BUG: Interpolate: use stable sort
- #12568: Updated documentation for as_quat
- #12571: DEP: remove deprecated slepian window
- #12573: DEP: remove `frechet_l` and `frechet_r`
- #12575: BUG: stats: fix multinomial.pmf NaNs when params sum > 1
- #12576: MAINT: remove warning from LSQSphereBivariateSpline
- #12582: ENH: Multivariate t-distribution
- #12587: ENH: speed up rvs of gengamma in scipy.stats
- #12588: DOC: add Examples add see also sections for LinearNDInterpolator,…
- #12597: ENH: Add single-sided p-values to t-tests
- #12599: Small update to scipy FFT tutorial
- #12600: ENH: disjoint set data structure
- #12602: BUG: add const for Read-only views in interpnd.pyx
- #12605: BUG: correct `np.asanyarray` use in `scipy.constants.lambda2nu`
- #12610: MAINT: forward port 1.5.2 release notes
- #12612: MAINT: stats: Use explicit keyword parameters instead of `**kwds`.
- #12616: DOC: make explicit docstring that interpolate.interp1d only accepts…
- #12618: DOC: Minor doc formatting.
- #12640: MAINT: stats: fix issues with scipy.stats.pearson3 docs, moment,…
- #12647: TST: Add Boost ellipr[cdfgj]_data test data
- #12648: DOC: Update special/utils/README with instructions
- #12649: DOC: simplified pip quickstart guide
- #12650: DOC: stats: Fix boxcox docstring: lambda can be negative.
- #12655: DOC: update Steering Council members listed in governance docs

- #12659: rv_sample expect bug
- #12663: DOC: optimize: try to fix linprog method-specific documentation
- #12664: BUG: stats: Fix logpdf with large negative values for logistic…
- #12666: MAINT: Fixes from static analysis
- #12667: ENH: Adding Modified Rodrigues Parameters to the Rotation class
- #12670: DOC: Update documentation for Gamma distribution
- #12673: API: Unconditionally return np.intp from cKDTree.query
- #12677: MAINT: Add Autogenerated notice to ufuncs.pyi
- #12682: MAINT: Remove _util._valarray
- #12688: MAINT: add f2py-generated scipy.integrate files to .gitignore
- #12689: BENCH: simplify benchmark setup, remove benchmarks/run.py
- #12694: scipy/stats: Add laplace_asymmetric continuous distribution
- #12695: DOC: update Ubuntu quickstart; conda compilers now work!
- #12698: MAINT: Replace np.max with np.maximum
- #12700: TST: bump test precision for constrained trustregion test
- #12702: TST: bump test tolerance for `DifferentialEvolutionSolver.test_L4`
- #12703: BUG: Improve input validation for sepfir2d
- #12708: MAINT: fix a typo in scipy.sparse
- #12709: BUG: bvls can fail catastrophically to converge
- #12711: MAINT: Use platform.python_implementation to determine IS_PYPY
- #12713: TST: Fix flaky test_lgmres
- #12716: DOC: add examples and tutorial links for interpolate functions…
- #12717: DOC: Fix Issue #5396
- #12725: ENH: Support complex-valued images and kernels for many ndimage…
- #12729: DEP: remove setup_requires
- #12732: BENCH: skip benchmarks instead of hiding them when SCIPY_XSLOW=0
- #12734: CI: Don't ignore line-length in the lint_diff check.
- #12736: DOC: Fix signal.windows.get_window() 'exponential' docstring
- #12737: ENH: stats: override stats.gumbel_r.fit and stats.gumbel_l.fit…
- #12738: ENH: stats: override stats.logistic.fit with system of equations…
- #12743: BUG: Avoid negative variances in circular statistics
- #12744: Prevent build error on GNU/Hurd
- #12746: TST: parameterize the test cases in test_ndimage.py
- #12752: DOC: Add examples for some root finding functions.
- #12754: MAINT, CI: Azure windows deps multiline
- #12756: ENH: stats: Add an sf method to levy for improved precision in…

- #12757: ENH: stats: Add an sf method to levy_l for improved precision.
- #12765: TST, MAINT: infeasible_2 context
- #12767: Fix spline interpolation boundary handling for modes reflect…
- #12769: DOC: syntax error in scipy.interpolate.bspl
- #12770: ENH: add nearest-up rounding to scipy.interpolate.interp1d
- #12771: TST: fix invalid input unit test for scipy.signal.gammatone
- #12775: ENH: Adds quadratic_assignment with two methods
- #12776: ENH: add grid-constant boundary handling in ndimage interpolation…
- #12777: Add Taylor Window function - Common in Radar DSP
- #12779: ENH: Improvements to pocketfft thread pool and ARM neon vectorization
- #12788: API: Rename cKDTree n_jobs argument to workers
- #12792: DOC: remove THANKS.txt file in favor of scipy.org
- #12793: Add new flag to authors tool
- #12802: BENCH: add scipy.ndimage.interpolation benchmarks
- #12803: Do not pin the version of numpy in unsupported python versions
- #12810: CI: fix 32-bit Linux build failure on Azure CI runs
- #12812: ENH: support interpolation of complex-valued images
- #12814: BUG: nonlin_solve shouldn't pass non-vector dx to tol_norm
- #12818: Update ckdtree.pyx
- #12822: MAINT: simplify directed_hausdorff
- #12827: DOC: Fix wrong name w being used instead of worN in docs.
- #12831: DOC: fix typo in sparse/base.py
- #12835: MAINT: stats: Improve vonmises PDF calculation.
- #12839: ENH: scipy.stats: add multivariate hypergeometric distribution
- #12843: changed M to N in windows.dpss
- #12846: MAINT: update minimum NumPy version to 1.16.5
- #12847: DOC: Unify the formula in docs of scipy.stats.pearsonr()
- #12849: DOC: polish QAP docs for consistency and readability
- #12852: ENH, MAINT: Bring KDTree interface to feature-parity with cKDTree
- #12858: DOC: use :doi: and :arxiv: directives for references
- #12872: lazily import multiprocessing.Pool in MapWrapper
- #12878: DOC: document ScalarFunction
- #12882: MAINT: stats: Change a test to use <= instead of strictly less…
- #12885: numpy.linspace calls edited to ensure correct spacing.
- #12886: DOC: stats: Add 'versionadded' to cramervonmises docstring.
- #12899: TST: make a couple of tests expected to fail on 32-bit architectures

- #12903: DOC: update Windows build guide and move into contributor guide
- #12907: DOC: clarify which array the precenter option applies to
- #12908: MAINT: spatial: Remove two occurrences of unused variables in…
- #12909: ENH: stats: Add methods gumbel_r._sf and gumbel_r._isf
- #12910: CI: travis: Remove some unnecessary code from .travis.yml.
- #12911: Minor fixes to dendrogram plotting
- #12921: CI: don't run GitHub Actions on fork or in cron job
- #12927: MAINT: rename integrate.simps to simpson
- #12934: MAINT: rename trapz and cumtrapz to (cumulative_)trapezoid
- #12936: MAINT: fix numerical precision in nct.stats
- #12938: MAINT: fix linter on master
- #12941: Update minimum AIX pinnings to match non AIX builds
- #12955: BUG: Fixed wrong NaNs check in scipy.stats.weightedtau
- #12958: ENH: stats: Implement _logpdf, _sf and _isf for nakagami.
- #12962: Correcting that p should be in [0,1] for a variety of discrete…
- #12964: BUG: added line.strip() to split_data_line()
- #12968: ENH: stats: Use only an analytical formula or scalar root-finding…
- #12971: MAINT: Declare support for Python 3.9
- #12972: MAINT: Remove redundant Python < 3.6 code
- #12980: DOC: Update documentation on optimize.rosen
- #12983: ENH: improvements to stats.linregress
- #12990: DOC: Clarify that using sos as output type for iirdesign can…
- #12992: DOC: capitalization and formatting in lsmr
- #12995: DOC: stats: Several documentation fixes.
- #12996: BUG: Improve error messages for `range` arg of binned_statistic_dd
- #12998: MAINT: approx_derivative with FP32 closes #12991
- #13004: TST: isinstance(OptimizeResult.message, str) closes #13001
- #13006: Keep correct dtype when loading empty mat arrays.
- #13009: MAINT: clip SLSQP step within bounds
- #13012: DOC: fix bilinear_zpk example labels
- #13013: ENH: Add `subset` and `subsets` methods to `DisjointSet`…
- #13029: MAINT: basinhopping callback for initial mininmisation
- #13032: DOC: fix docstring errors in in stats.wilcoxon
- #13036: BUG: forward port lint_diff shims
- #13041: MAINT: dogbox ensure x is within bounds closes #11403
- #13042: MAINT: forward port 1.5.4 release notes

- #13046: DOC: Update optimize.least_squares doc for all tolerance must…
- #13052: Typo fix for cluster documentation
- #13054: BUG: fix `scipy.optimize.show_options` for unknown methods….
- #13056: MAINT: fft: Fix a C++ compiler warning.
- #13057: Minor fixes on doc of function csr_tocsc
- #13058: DOC: stats: Replace np.float with np.float64 in a tutorial file.
- #13059: DOC: stats: Update the "Returns" section of the linregress docstring.
- #13060: MAINT: clip_x_for_func should be private
- #13061: DOC: signal.win -> signal.windows.win in Examples
- #13063: MAINT: Add suite-sparse and sksparse installation check
- #13070: MAINT: stats: Remove a couple obsolete comments.
- #13073: BUG: Fix scalar_search_wolfe2 to resolve #12157
- #13078: CI, MAINT: migrate Lint to Azure
- #13081: BLD: drop Python 3.6 support (NEP 29)
- #13082: MAINT: update minimum NumPy version to 1.16.5 in a couple more…
- #13083: DOC: update toolchain.rst
- #13086: DOC: Update the Parameters section of the correlation docstring
- #13087: ENH:signal: Speed-up Cython implementation of _sosfilt
- #13089: BLD, BUG: add c99 compiler flag to HiGHS basiclu library
- #13091: BUG: Fix GIL handling in _sosfilt
- #13094: DOC: clarify "location" in docstring of cKDTree.query
- #13095: Zoom resize update
- #13097: BUG: fix CubicSpline(…, bc_type="periodic") #11758
- #13100: BUG: sparse: Correct output format of kron
- #13107: ENH: faster linear_sum_assignment for small cost matrices
- #13110: CI, MAINT: refguide/asv checks to azure
- #13112: CI: fix MacOS CI
- #13113: CI: Install word list package for refguide-check
- #13115: BUG: add value range check for signal.iirdesign()
- #13116: CI: Don't report name errors after an exception in refguide-check
- #13117: CI: move sdist/pre-release test Azure
- #13119: Improve error message on friedmanchisquare function
- #13121: Fix factorial() for NaN on Python 3.10
- #13123: BLD: Specify file extension for language standard version tests
- #13128: TST: skip Fortran I/O test for ODR
- #13130: TST: skip factorial() float tests on Python 3.10

- #13136: CI:Add python dbg run to GH Actions
- #13138: CI: Port coverage, 64-bit BLAS, GCC 4.8 build to azure
- #13139: Fix edge case for mode='nearest' in ndimage.interpolation functions
- #13141: BUG: signal: Fix data type of the numerator returned by ss2tf.
- #13144: MAINT: stats: restrict gausshyper z > -1
- #13146: typo in csr.py
- #13148: BUG: stats: fix typo in stable rvs per gh-12870
- #13149: DOC: spatial/stats: cross-ref random rotation matrix functions
- #13151: MAINT: stats: Fix a test and a couple PEP-8 issues.
- #13152: MAINT: stats: Use np.take_along_axis in the private function…
- #13154: ENH: stats: Implement defined handling of constant inputs in…
- #13156: DOC: maintain equal display range for ndimage.zoom example
- #13159: CI: Azure: Don't run tests on merge commits, except for coverage
- #13160: DOC: stats: disambiguate location-shifted/noncentral
- #13161: BUG: DifferentialEvolutionSolver.__del__ can fail in garbage…
- #13163: BUG: stats: fix bug in spearmanr nan propagation
- #13167: MAINT: stats: Fix a test.
- #13169: BUG: stats: Fix handling of misaligned masks in mstats.pearsonr.
- #13178: CI: testing.yml –> macos.yml
- #13181: CI: fix lint
- #13190: BUG: optimize: fix a duplicate key bug for `test_show_options`
- #13192: BUG:linalg: Add overwrite option to gejsv wrapper
- #13194: BUG: slsqp should be able to use rel_step
- #13199: [skip travis] DOC: 1.6.0 release notes
- #13203: fix typos
- #13209: TST:linalg: set the seed for cossin test
- #13212: [DOC] Backtick and directive consistency.
- #13217: REL: add necessary setuptools and numpy version pins in pyproject.toml…
- #13226: BUG: pavement.py file handle fixes
- #13249: Handle cval correctly for ndimage functions with complex-valued…
- #13253: BUG,MAINT: Ensure all Pool objects are closed
- #13255: BUG:linalg: Fix heevx wrappers and add new tests
- #13260: CI: fix macOS testing
- #13269: CI: github actions: In the linux dbg tests, update apt before…
- #13279: MAINT: 1.6.0 rc2 backports

5.6 SciPy 1.5.4 Release Notes

Contents

- *SciPy 1.5.4 Release Notes*
  - *Authors*
    - *Issues closed for 1.5.4*
    - *Pull requests for 1.5.4*

SciPy 1.5.4 is a bug-fix release with no new features compared to 1.5.3. Importantly, wheels are now available for Python 3.9 and a more complete fix has been applied for issues building with XCode 12.

5.6.1 Authors

- Peter Bell
- CJ Carey
- Andrew McCluskey +
- Andrew Nelson
- Tyler Reddy
- Eli Rykoff +
- Ian Thomas +

A total of 7 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.5.4

- #12763: ndimage.fourier_ellipsoid segmentation fault
- #12789: TestConvolve2d.test_large_array failing on Windows ILP64 CI job
- #12857: sparse A[0,:] = ndarray is ok, A[:,0] = ndarray ValueError from…
- #12860: BUG: Build failure with Xcode 12
- #12935: Failure to build with Python 3.9.0 on macOS
- #12966: MAINT: lint_diff.py on some backport PRs
- #12988: BUG: Highly multi-dimensional `gaussian_kde` giving `-inf`…

Pull requests for 1.5.4

- #12790: TST: Skip TestConvolve2d.test_large_array if not enough memory
- #12851: BUG: sparse: fix inner indexed assignment of a 1d array
- #12875: BUG: segfault in ndimage.fourier_ellipsoid with length-1 dims
- #12937: CI: macOS3.9 testing
- #12957: MAINT: fixes XCode 12/ python 3.9.0 build for 1.5.x maint branch
- #12959: CI: add Windows Python 3.9 to CI
- #12974: MAINT: Run lint_diff.py against the merge target and only for…
- #12978: DOC: next_fast_len output doesn't match docstring
- #12979: BUG: fft.next_fast_len should accept keyword arguments
- #12989: BUG: improved the stability of kde for highly (1000s) multi-dimension…
- #13017: BUG: Add explicit cast to _tmp sum.
- #13022: TST: xfail test_maxiter_worsening()

5.7 SciPy 1.5.3 Release Notes

Contents

- *SciPy 1.5.3 Release Notes*
  - *Authors*
    - *Issues closed for 1.5.3*
    - *Pull requests for 1.5.3*

SciPy 1.5.3 is a bug-fix release with no new features compared to 1.5.2. In particular, Linux ARM64 wheels are now available and a compatibility issue with XCode 12 has been fixed.

5.7.1 Authors

- Peter Bell
- CJ Carey
- Thomas Duvernay +
- Gregory Lee
- Eric Moore
- odidev
- Dima Pasechnik
- Tyler Reddy
- Simon Segerblom Rex +

- Daniel B. Smith
- Will Tirone +
- Warren Weckesser

A total of 12 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.5.3

- #9611: Overflow error with new way of p-value calculation in kendall…
- #10069: scipy.ndimage.watershed_ift regression in 1.0.0
- #11260: BUG: DOP853 with complex data computes complex error norm, causing…
- #11479: RuntimeError: dictionary changed size during iteration on loading…
- #11972: BUG (solved): Error estimation in DOP853 ODE solver fails for…
- #12543: BUG: Picture rotated 180 degrees and rotated -180 degrees should…
- #12613: Travis X.4 and X.7 failures in master
- #12654: scipy.stats.combine_pvalues produces wrong results with method='mudholkar_george'
- #12819: BUG: Scipy Sparse slice indexing assignment Bug with zeros
- #12834: BUG: ValueError upon calling Scipy Interpolator objects
- #12836: ndimage.median can return incorrect values for integer inputs
- #12860: Build failure with Xcode 12

Pull requests for 1.5.3

- #12611: MAINT: prepare for SciPy 1.5.3
- #12614: MAINT: prevent reverse broadcasting
- #12617: MAINT: optimize: Handle nonscalar size 1 arrays in fmin_slsqp…
- #12623: MAINT: stats: Loosen some test tolerances.
- #12638: CI, MAINT: pin pytest for Azure win
- #12668: BUG: Ensure factorial is not too large in mstats.kendalltau
- #12705: MAINT: `openblas_support` added sha256 hash
- #12706: BUG: fix incorrect 1d case of the fourier_ellipsoid filter
- #12721: BUG: use special.sindg in ndimage.rotate
- #12724: BUG: per #12654 adjusted mudholkar_george method to combine p…
- #12726: BUG: Fix DOP853 error norm for complex problems
- #12730: CI: pin xdist for Azure windows
- #12786: BUG: stats: Fix formula in the `stats` method of the ARGUS…
- #12795: CI: Pin setuptools on windows CI
- #12830: [BUG] sparse: Avoid using size attribute in LIL __setitem__

- #12833: BUG: change list of globals items to list of a copy
- #12842: BUG: Use uint16 for cost in NI_WatershedElement
- #12845: BUG: avoid boolean or integer addition error in ndimage.measurements.median
- #12864: BLD: replace the #include of libqull_r.h with with this of qhull_ra.h…
- #12867: BUG: Fixes a ValueError yielded upon calling Scipy Interpolator…
- #12902: CI: Remove 'env' from pytest.ini
- #12913: MAINT: Ignore pytest's PytestConfigWarning

5.8 SciPy 1.5.2 Release Notes

Contents

- *SciPy 1.5.2 Release Notes*
  - *Authors*
    - *Issues closed for 1.5.2*
    - *Pull requests for 1.5.2*

SciPy 1.5.2 is a bug-fix release with no new features compared to 1.5.1.

5.8.1 Authors

- Peter Bell
- Tobias Biester +
- Evgeni Burovski
- Thomas A Caswell
- Ralf Gommers
- Sturla Molden
- Andrew Nelson
- ofirr +
- Sambit Panda
- Ilhan Polat
- Tyler Reddy
- Atsushi Sakai
- Pauli Virtanen

A total of 13 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.5.2

- #3847: Crash of interpolate.splprep(task=-1)
- #7395: splprep segfaults if fixed knots are specified
- #10761: scipy.signal.convolve2d produces incorrect values for large arrays
- #11971: DOC: search in devdocs returns wrong link
- #12155: BUG: Fix permutation of distance matrices in scipy.stats.multiscale_graphcorr
- #12203: Unable to install on PyPy 7.3.1 (Python 3.6.9)
- #12316: negative scipy.spatial.distance.correlation
- #12422: BUG: slsqp: ValueError: failed to initialize intent(inout) array…
- #12428: stats.truncnorm.rvs() never returns a scalar in 1.5
- #12441: eigvalsh inconsistent eigvals= subset_by_index=
- #12445: DOC: scipy.linalg.eigh
- #12449: Warnings are not filtered in csr_matrix.sum()
- #12469: SciPy 1.9 exception in LSQSphereBivariateSpline
- #12487: BUG: optimize: incorrect result from approx_fprime
- #12493: CI: GitHub Actions for maintenance branches
- #12533: eigh gives incorrect results
- #12579: BLD, MAINT: distutils issues in wheels repo

Pull requests for 1.5.2

- #12156: BUG: Fix permutation of distance matrices in scipy.stats.multiscale_graphcorr
- #12238: BUG: Use 64-bit indexing in convolve2d to avoid overflow
- #12256: BLD: Build lsap as a single extension instead of extension +…
- #12320: BUG: spatial: avoid returning negative correlation distance
- #12383: ENH: Make cKDTree.tree more efficient
- #12392: DOC: update scipy-sphinx-theme
- #12430: BUG: truncnorm and geninvgauss never return scalars from rvs
- #12437: BUG: optimize: cast bounds to floats in new_bounds_to_old/old_bounds_to_new
- #12442: MAINT:linalg: Fix for input args of eigvalsh
- #12461: MAINT: sparse: write matrix/asmatrix wrappers without warning…
- #12478: BUG: fix array_like input defects and add tests for all functions…
- #12488: BUG: fix approx_derivative step size. Closes #12487
- #12500: CI: actions branch trigger fix
- #12501: CI: actions branch trigger fix
- #12504: BUG: cKDTreeNode use after free
- #12529: MAINT: allow graceful docs re-upload

- #12538: BUG:linalg: eigh type parameter handling corrected
- #12560: MAINT: truncnorm.rvs compatibility for `Generator`
- #12562: redo gh-12188: fix segfaults in splprep with fixed knots
- #12586: BLD: Add -std=c99 to sigtools to compile with C99
- #12590: CI: Add GCC 4.8 entry to travis build matrix
- #12591: BLD: fix cython error on master-branch cython

5.9 SciPy 1.5.1 Release Notes

Contents

- *SciPy 1.5.1 Release Notes*
  - *Authors*
    - *Issues closed for 1.5.1*
    - *Pull requests for 1.5.1*

SciPy 1.5.1 is a bug-fix release with no new features compared to 1.5.0. In particular, an issue where DLL loading can fail for SciPy wheels on Windows with Python 3.6 has been fixed.

5.9.1 Authors

- Peter Bell
- Loïc Estève
- Philipp Thölke +
- Tyler Reddy
- Paul van Mulbregt
- Pauli Virtanen
- Warren Weckesser

A total of 7 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.5.1

- #9108: documentation: scipy.spatial.KDTree vs. scipy.spatial.cKDTree
- #12218: Type error in stats.ks_2samp when alternative != 'two-sided-
- #12406: DOC: Docstring in stats.anderson function not properly formatted
- #12418: Regression in hierarchy.dendogram

Pull requests for 1.5.1

- #12280: BUG: Fixes gh-12218, TypeError converting int to float inside…
- #12336: BUG: KDTree should reject complex input points
- #12344: MAINT: Don't use numpy's aliases of Python builtin objects.
- #12407: DOC: Fix docstring for dist param in anderson function
- #12410: CI: Run the Azure Windows Python36 32bit tests with mode 'fast'
- #12421: Fix regression in scipy 1.5.0 in dendogram when labels is a numpy…
- #12462: MAINT: move distributor_init import after __config__ import

5.10 SciPy 1.5.0 Release Notes

Contents

- *SciPy 1.5.0 Release Notes*
  - *Highlights of this release*
    - *New features*
  - `scipy.cluster` *improvements*
  - `scipy.fft` *improvements*
  - `scipy.integrate` *improvements*
  - `scipy.interpolate` *improvements*
  - `scipy.io` *improvements*
  - `scipy.linalg` *improvements*
  - `scipy.ndimage` *improvements*
  - `scipy.optimize` *improvements*
  - `scipy.signal` *improvements*
  - `scipy.sparse` *improvements*
  - `scipy.spatial` *improvements*
  - `scipy.special` *improvements*
  - `scipy.stats` *improvements*
    - *Deprecated features*
  - `scipy` *deprecations*
  - `scipy.special` *changes*
  - `scipy.stats` *changes*
    - *Backwards incompatible changes*
  - `scipy.interpolate` *changes*

- `scipy.linalg` *changes*
- `scipy.signal` *changes*
- `scipy.stats` *changes*
  - *Other changes*
  - *Authors*
- *Issues closed for 1.5.0*
- *Pull requests for 1.5.0*

SciPy 1.5.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning`s). Our development attention will now shift to bug-fix releases on the 1.5.x branch, and on adding new features on the master branch.

This release requires Python 3.6+ and NumPy 1.14.5 or greater.

For running on PyPy, PyPy3 6.0+ and NumPy 1.15.0 are required.

5.10.1 Highlights of this release

- wrappers for more than a dozen new `LAPACK` routines are now available in *`scipy.linalg.lapack`*
- Improved support for leveraging 64-bit integer size from linear algebra backends
- addition of the probability distribution for two-sided one-sample Kolmogorov-Smirnov tests

New features

5.10.2 `scipy.cluster` improvements

Initialization of *`scipy.cluster.vq.kmeans2`* using `minit="++"` had a quadratic complexity in the number of samples. It has been improved, resulting in a much faster initialization with quasi-linear complexity.

`scipy.cluster.hierarchy.dendrogram` now respects the `matplotlib` color palette

5.10.3 `scipy.fft` improvements

A new keyword-only argument `plan` is added to all FFT functions in this module. It is reserved for passing in a pre-computed plan from libraries providing a FFT backend (such as `PyFFTW` and `mkl-fft`), and it is currently not used in SciPy.

5.10.4 `scipy.integrate` improvements

5.10.5 `scipy.interpolate` improvements

5.10.6 `scipy.io` improvements

scipy.io.wavfile error messages are more explicit about what's wrong, and extraneous bytes at the ends of files are ignored instead of raising an error when the data has successfully been read.

scipy.io.loadmat gained a `simplify_cells` parameter, which if set to `True` simplifies the structure of the return value if the `.mat` file contains cell arrays.

`pathlib.Path` objects are now supported in *scipy.io* Matrix Market I/O functions

5.10.7 `scipy.linalg` improvements

scipy.linalg.eigh has been improved. Now various `LAPACK` drivers can be selected at will and also subsets of eigenvalues can be requested via `subset_by_value` keyword. Another keyword `subset_by_index` is introduced. Keywords `turbo` and `eigvals` are deprecated.

Similarly, standard and generalized Hermitian eigenvalue `LAPACK` routines `?<sy/he>evx` are added and existing ones now have full `_lwork` counterparts.

Wrappers for the following `LAPACK` routines have been added to *scipy.linalg.lapack*:

- ***?getc2: computes the LU factorization of a general matrix with complete***

  pivoting
- `?gesc2`: solves a linear system given an LU factorization from `?getc2`
- ***?gejsv: computes the singular value decomposition of a general matrix***

  with higher accuracy calculation of tiny singular values and their corresponding singular vectors
- ***?geqrfp: computes the QR factorization of a general matrix with***

  non-negative elements on the diagonal of R
- `?gtsvx`: solves a linear system with general tridiagonal matrix
- `?gttrf`: computes the LU factorization of a tridiagonal matrix
- `?gttrs`: solves a linear system given an LU factorization from `?gttrf`
- ***?ptsvx: solves a linear system with symmetric positive definite***

  tridiagonal matrix
- ***?pttrf: computes the LU factorization of a symmetric positive definite***

  tridiagonal matrix
- `?pttrs`: solves a linear system given an LU factorization from `?pttrf`
- ***?pteqr: computes the eigenvectors and eigenvalues of a positive definite***

  tridiagonal matrix
- `?tbtrs`: solves a linear system with a triangular banded matrix
- ***?csd: computes the Cosine Sine decomposition of an orthogonal/unitary***

  matrix

Generalized QR factorization routines (`?geqrf`) now have full `_lwork` counterparts.

scipy.linalg.cossin Cosine Sine decomposition of unitary matrices has been added.

The function *scipy.linalg.khatri_rao*, which computes the Khatri-Rao product, was added.

The new function *scipy.linalg.convolution_matrix* constructs the Toeplitz matrix representing one-dimensional convolution.

5.10.8 `scipy.ndimage` improvements

5.10.9 `scipy.optimize` improvements

The finite difference numerical differentiation used in various `minimize` methods that use gradients has several new features:

- 2-point, 3-point, or complex step finite differences can be used. Previously only a 2-step finite difference was available.
- There is now the possibility to use a relative step size, previously only an absolute step size was available.
- If the `minimize` method uses bounds the numerical differentiation strictly obeys those limits.
- The numerical differentiation machinery now makes use of a simple cache, which in some cases can reduce the number of function evaluations.
- `minimize`'s `method= 'powell'` now supports simple bound constraints

There have been several improvements to *scipy.optimize.linprog*:

- The `linprog` benchmark suite has been expanded considerably.
- `linprog`'s dense pivot-based redundancy removal routine and sparse presolve are faster
- When `scikit-sparse` is available, solving sparse problems with `method='interior-point'` is faster

The caching of values when optimizing a function returning both value and gradient together has been improved, avoiding repeated function evaluations when using a `HessianApproximation` such as `BFGS`.

`differential_evolution` can now use the modern `np.random.Generator` as well as the legacy `np.random.RandomState` as a seed.

5.10.10 `scipy.signal` improvements

A new optional argument `include_nyquist` is added to `freqz` functions in this module. It is used for including the last frequency (Nyquist frequency).

scipy.signal.find_peaks_cwt now accepts a `window_size` parameter for the size of the window used to calculate the noise floor.

5.10.11 `scipy.sparse` improvements

Outer indexing is now faster when using a 2d column vector to select column indices.

scipy.sparse.lil.tocsr is faster

Fixed/improved comparisons between pydata sparse arrays and sparse matrices

BSR format sparse multiplication performance has been improved.

scipy.sparse.linalg.LinearOperator has gained the new `ndim` class attribute

5.10.12 `scipy.spatial` improvements

scipy.spatial.geometric_slerp has been added to enable geometric spherical linear interpolation on an n-sphere

scipy.spatial.SphericalVoronoi now supports calculation of region areas in 2D and 3D cases

The tree building algorithm used by `cKDTree` has improved from quadratic worst case time complexity to loglinear. Benchmarks are also now available for building and querying of balanced/unbalanced kd-trees.

5.10.13 `scipy.special` improvements

The following functions now have Cython interfaces in *cython_special*:

- *scipy.special.erfinv*
- *scipy.special.erfcinv*
- *scipy.special.spherical_jn*
- *scipy.special.spherical_yn*
- *scipy.special.spherical_in*
- *scipy.special.spherical_kn*

scipy.special.log_softmax has been added to calculate the logarithm of softmax function. It provides better accuracy than `log(scipy.special.softmax(x))` for inputs that make softmax saturate.

5.10.14 `scipy.stats` improvements

The function for generating random samples in *scipy.stats.dlaplace* has been improved. The new function is approximately twice as fast with a memory footprint reduction between 25 % and 60 % (see gh-11069).

scipy.stats functions that accept a seed for reproducible calculations using random number generation (e.g. random variates from distributions) can now use the modern `np.random.Generator` as well as the legacy `np.random.RandomState` as a seed.

The `axis` parameter was added to *scipy.stats.rankdata*. This allows slices of an array along the given axis to be ranked independently.

The `axis` parameter was added to *scipy.stats.f_oneway*, allowing it to compute multiple one-way ANOVA tests for data stored in n-dimensional arrays. The performance of `f_oneway` was also improved for some cases.

The PDF and CDF methods for `stats.geninvgauss` are now significantly faster as the numerical integration to calculate the CDF uses a Cython based `LowLevelCallable`.

Moments of the normal distribution (*scipy.stats.norm*) are now calculated using analytical formulas instead of numerical integration for greater speed and accuracy

Moments and entropy trapezoidal distribution (`scipy.stats.trapz`) are now calculated using analytical formulas instead of numerical integration for greater speed and accuracy

Methods of the truncated normal distribution (*scipy.stats.truncnorm*), especially `_rvs`, are significantly faster after a complete rewrite.

The *fit* method of the Laplace distribution, *scipy.stats.laplace*, now uses the analytical formulas for the maximum likelihood estimates of the parameters.

Generation of random variates is now thread safe for all SciPy distributions. 3rd-party distributions may need to modify the signature of the `_rvs()` method to conform to `_rvs(self, ..., size=None, random_state=None)`. (A one-time VisibleDeprecationWarning is emitted when using non-conformant distributions.)

The Kolmogorov-Smirnov two-sided test statistic distribution (*scipy.stats.kstwo*) was added. Calculates the distribution of the K-S two-sided statistic `D_n` for a sample of size n, using a mixture of exact and asymptotic algorithms.

The new function `median_abs_deviation` replaces the deprecated `median_absolute_deviation`.

The `wilcoxon` function now computes the p-value for Wilcoxon's signed rank test using the exact distribution for inputs up to length 25. The function has a new `mode` parameter to specify how the p-value is to be computed. The default is `"auto"`, which uses the exact distribution for inputs up to length 25 and the normal approximation for larger inputs.

Added a new Cython-based implementation to evaluate guassian kernel estimates, which should improve the performance of `gaussian_kde`

The `winsorize` function now has a `nan_policy` argument for refined handling of `nan` input values.

The `binned_statistic_dd` function with `statistic="std"` performance was improved by ~4x.

`scipy.stats.kstest(rvs, cdf,...)` now handles both one-sample and two-sample testing. The one-sample variation uses *scipy.stats.ksone* (or *scipy.stats.kstwo* with back off to *scipy.stats.kstwobign*) to calculate the p-value. The two-sample variation, invoked if `cdf` is array_like, uses an algorithm described by Hodges to compute the probability directly, only backing off to *scipy.stats.kstwo* in case of overflow. The result in both cases is more accurate p-values, especially for two-sample testing with smaller (or quite different) sizes.

scipy.stats.maxwell performance improvements include a 20 % speed up for *fit()*` and 5 % for `pdf()`

scipy.stats.shapiro and *scipy.stats.jarque_bera* now return a named tuple for greater consistency with other `stats` functions

Deprecated features

5.10.15 `scipy` deprecations

5.10.16 `scipy.special` changes

The `bdtr`, `bdtrc`, and `bdtri` functions are deprecating non-negative non-integral `n` arguments.

5.10.17 `scipy.stats` changes

The function `median_absolute_deviation` is deprecated. Use `median_abs_deviation` instead.

The use of the string `"raw"` with the `scale` parameter of `iqr` is deprecated. Use `scale=1` instead.

Backwards incompatible changes

5.10.18 `scipy.interpolate` changes

5.10.19 `scipy.linalg` changes

The output signatures of `?syevr`, `?heevr` have been changed from `w, v, info` to `w, v, m, isuppz, info`

The order of output arguments `w`, `v` of `<sy/he>{gv, gvd, gvx}` is swapped.

5.10.20 `scipy.signal` changes

The output length of *`scipy.signal.upfirdn`* has been corrected, resulting outputs may now be shorter for some combinations of up/down ratios and input signal and filter lengths.

`scipy.signal.resample` now supports a `domain` keyword argument for specification of time or frequency domain input.

5.10.21 `scipy.stats` changes

Other changes

Improved support for leveraging 64-bit integer size from linear algebra backends in several parts of the SciPy codebase.

Shims designed to ensure the compatibility of SciPy with Python 2.7 have now been removed.

Many warnings due to unused imports and unused assignments have been addressed.

Many usage examples were added to function docstrings, and many input validations and intuitive exception messages have been added throughout the codebase.

Early stage adoption of type annotations in a few parts of the codebase

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A total of 129 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

5.10.22 Issues closed for 1.5.0

- #1455: ellipord does returns bogus values if gstop or gpass are negative…
- #1968: correlate2d's output does not agree with correlate's output in…
- #2744: BUG: optimize: '**kw' argument of 'newton_krylov' is not documented
- #4755: TypeError: data type "<i0" not understood
- #4921: scipy.optimize maxiter option not working as expected
- #5144: RuntimeWarning on csgraph.shortest_path when edge lengths are…
- #5309: Documentation of 'hybr' and 'lm' inconsistent in optimize.root
- #6026: Replace approx_grad with _numdiff.approx_derivative in scipy.optimize
- #6502: Computing Eigenvalues in an Interval with LAPACK
- #7058: Errors in special.bdtri and special.bdtr for non-integer k values
- #7700: SuperLU does not respect perm_c="NATURAL"
- #7895: Improvements to io.loadmat
- #8205: ValueError in scipy.linalg.eigvalsh for large matrix
- #8278: Memory limit for scipy.sparse.linalg.spsolve with scikit-umfpack
- #8327: scipy.stats.mstats.winsorize NaN handling
- #8341: scipy.stats.ks_2samp for masked and unmasked data give different…
- #8748: scipy.stats.kstest for same distribution: p-values nonuniform
- #9042: optimize: Incorrect statement about `jac` in the `minimize`…

- #9197: problem with scipy.signal.butter with 1000+ points array
- #9212: EIGH very very slow –> suggesting an easy fix
- #9553: ndimage routines behave badly when output has memory overlap…
- #9632: ndimage.maximum_filter undocumented behaviour using footprint…
- #9658: *scipy.optimize.minimize(method='COBYLA')* not threadsafe
- #9710: stats.weightedtau([1], [1.0]) SEGFAULTs
- #9797: Master Tracker for some Kolmogorov-Smirnov test Issues
- #9844: scipy.signal.upfirdn gives different length matrix versus MATLAB…
- #9872: scipy.signal.convolve is slower when vectorized
- #9913: BUG: No dt in StateSpace operations
- #10014: Distribution names `weibull_min`and `weibull_max` should…
- #10159: BUG: stats: chisquare returns incorrect results for arrays of…
- #10302: scipy.fft: Add a `plan` argument
- #10332: 'Incomplete wav chunk' inconsistent/reason unknown
- #10441: Remove uses of `numpy.dual`?
- #10558: Document implicit sum in csr_matrix() constructor
- #10788: LU with full pivoting
- #10841: Unexpected behavior in linalg.blas.dtrmm wrapper
- #10919: optimize._lbfgsb setulb() function violates parameter bounds
- #10963: kstest, ks_2samp: confusing `mode` argument descriptions
- #11022: Unexpected Result in factorial function with NaN input
- #11028: Documentation error in optimize.minimize
- #11058: Adding logsoftmax function
- #11076: ValueError: Unknown wave file format
- #11090: Misconception of the median absolute deviation in stats?
- #11095: BUG: find_peaks_cwt test failures in 32-bit Linux wheels
- #11107: scipy.io.mmread generated an error "TypeError: startswith first…
- #11123: Add wrapper for ?gttrf/?gttrs
- #11128: OverflowError in resample_poly (upfirdn)
- #11132: Possible bug: rv_discret.ppf for percentiles 0 and 100 and loc…
- #11163: Comparisons between scipy spmatrix and can sparse.SparseArray…
- #11168: Generalized Pareto variance inaccurate for concentrations near…
- #11169: Add wrapper for ?geqrfp
- #11184: 2-sided Kolmogorov Smirnov returns p-value of 1
- #11185: The .roots() or solve() function of scipy.interpolate.CubicHermiteSpline…
- #11190: Add wrapper for ?tbtrs

- #11200: Can no longer slice csr_matrix in 1.3.0
- #11207: _minimize_scalar_bounded: reference before assignment
- #11216: linprog: interior-point: Cholmod reordering can be reused
- #11223: Add wrappers for ?pttrf, ?pttrs
- #11224: Add wrapperfor ?pteqr
- #11235: MAINT: Missleading Error Message for IIR Filter
- #11244: Missing reference in `scipy.optimize.line_search`
- #11262: Hermitian Eigenvalue Problem eigh() API and wrapper change proposal
- #11266: Sparse matrix constructor data type detection changes on Numpy…
- #11270: CI failing: Travis CI Py36 refguide and Linux_Python_36_32bit_full…
- #11279: linalg.eigh checks whole array for finite values
- #11295: CI: azure does not auto-cancel old jobs on pushes
- #11299: stats.truncnorm.rvs 100x slower in v1.4.x than v1.3.3
- #11315: BUG: special: rgamma on negative integers smaller -34
- #11319: Missing `int64_t` declaration in rectangular_lsap.cpp
- #11323: Compilation failure due to missing symbol pthread_atfork
- #11332: BUG: directed_hausdorff distance on sets u and v when u is a…
- #11350: Khatri-Rao product
- #11354: ENH: Add wrapper for ?gejsv
- #11361: Dropped NaN in eval_genlaguerre function
- #11363: Dropped NaN in hyperu function
- #11365: scipy.stats.binned_statistic regressed in v1.4.0
- #11369: Dropped NaN in eval_hermite
- #11370: Dropped NaN in eval_gegenbauer
- #11373: Add wrapper for ?gtsvx
- #11374: Add wrapper for ?ptsvx
- #11391: csgraph.minimum_spanning_tree loses precision
- #11398: Update stats to cope with `np.random.Generator` machinery
- #11412: Array copying causes unwanted type casting from complex to float…
- #11415: Where is the Wiener Filter derived from?
- #11416: _lib._util.getargspec_no_self is missing KEYWORD_ONLY support
- #11428: Documentation on SHGO inequality constraints appears contradictory
- #11429: Add LAPACK's ZUNCSD cosine sine decomposition
- #11438: run_dualannealing passes bounds incorrectly in benchmarks/optimize.py
- #11441: Can't run optimize benchmarks
- #11442: Chebyshev weights

- #11448: Wrongly typed comparison in integrate.quad
- #11458: BUG: maximum_bipartite_matching produces infeasible solution
- #11460: CI failing: 2 Travis CI tests fail with numpy build or version…
- #11462: Bug on "++" initialization on "kmeans2"
- #11464: Shouldn't data type of KDE evaluation should be like in the input…
- #11468: performance of binned_statistics_2d 100x slowdown from 1.3.2…
- #11484: Callback function doesn't give the same value as the one being…
- #11492: Confusing dendrogram labelling
- #11493: scipy.optimize.least_squares fails if the return array of the…
- #11494: Error performing kronecker product between large sparse vectors
- #11503: medfilt produces 0 on input of length 1
- #11529: Pyflakes generates almost 700 warnings.
- #11566: irfft/irfft2/irfftn docs are slightly confusing re: input type.
- #11572: least_squares: too small tolerances not catched with method='lm'
- #11581: DOC: scipy.interpolate.RectSphereBivariateSpline
- #11586: Differential evolution breaks with LinearConstraints with sparse…
- #11595: scipy.spatial.cKDTree construction slow for some datasets
- #11598: output of special.voigt_profile when sigma=0
- #11601: linalg tests failing in runtests.py
- #11602: scipy.optimize.linear_sum_assignment returns reverse diagonal…
- #11610: Analytic formula for normal moments
- #11611: Build failure with gfortran 10
- #11613: TST, MAINT: test_quadpack TestCtypesQuad wasn't fully migrated…
- #11630: SmoothBivariateSpline bbox parameter
- #11635: typo in docstring of scipy.stats.norminvgauss
- #11637: BUG: core dumps when calling scipy.interpolate.interp1d with…
- #11638: better documentation for 'return_all' option in minimize(Nelder…
- #11652: TST, MAINT: CI failures for pre-release NumPy wheels
- #11659: optimize.fmin_l_bfgs_b needs bound check and appropiate error…
- #11660: BUG/ENH: distribution.ncf with nc=0 returns nan
- #11661: scipy.ndimage.convolve1d and correlate1d don't behave properly…
- #11669: p-value varies with the order of the data
- #11676: documentation of scipy.spatial.HalfspaceIntersection: wrong method…
- #11685: Rotation cannot be expressed as matrix
- #11686: MAINT: mypy imports of Cython "modules"
- #11693: TestDifferentialEvolutionSolver::test_L4 failing in CI

- #11696: DOC: incorrect compiler information for macOS in docs
- #11709: eigh() tests fail to pass, crash Python with seemingly ramdom…
- #11763: Small error in gamma continuous rv fit comments
- #11769: truncnorm.rvs Weird Behaviors
- #11770: crash in TestEigh::test_value_subsets
- #11795: trapz distribution mean computed using single precision
- #11800: Segmentation fault in scipy.odr for multidimensional independent…
- #11811: pyflakes silently failing on travis-ci
- #11826: Error with _fblas
- #11827: `fft.tests.test_numpy.test_multiprocess` hangs on Python3.8…
- #11835: tests with `multiprocessing` hang on Python 3.8 on macOS
- #11839: linalg.expm returns nans with RuntimeWarning: overflow encountered…
- #11856: Documentation of fit methods for `weibull_min` and `exponweib`…
- #11868: Function always evaluated twice when using HessianUpdateStrategy…
- #11875: Typo in the docstring of simps()
- #11877: kmeans2 '++' method is orders of magnitude slower than sklearn.cluster.KMeans()
- #11884: The upper code lines are dead code
- #11886: Array shape mismatch in scipy.optimize
- #11892: BUG: stats: Incorrect handling of edges cases by ttest_rel and…
- #11908: LinearOperator should have ndim attribute
- #11910: Documentation missing for what M is in init argument
- #11922: macOS actions CI has started failing in last couple of days.
- #11928: DOC: signal: Wrong description for sepfir2d, cspline2d, qspline2d
- #11944: curve_fit documentation unclear on default value of absolute_sigma
- #11945: Add a (potentially temporary) py.typed file?
- #11949: ValueError 'k exceeds matrix dimensions' for sparse.diagonal()…
- #11951: BUG: asv benchmark failed because of cython version
- #11967: BLD: Azure windows runs complain about drives
- #11973: oaconvolve(a,b,'same') differs in shape from convolve(a,b,'same')…
- #12002: pybind11 license
- #12003: MAINT: circular SphericalVoronoi input
- #12015: Reordering of CSC matrix breaks when you go above int32 limits
- #12031: Documentation Rendering Issues Visible in CircleCI Artifacts
- #12037: MAINT, CI: new Cython 3.0a4 issue
- #12087: DOC: some odr models are missing docs
- #12119: signal.fftconvolve no longer convolves types f8 and numpy.float64

- #12149: Documentation of Rosenbrock function
- #12173: Large memory usage when indexing sparse matrices with `np.ix_`
- #12178: BUG: stats: Some discrete distributions don't accept lists of…
- #12220: BUG, REL: gh_lists.py compromised scraping
- #12239: BUG: median absolute deviation handling of nan
- #12301: integer overflow in scipy.sparse.sputils.check_shape when matrix size > 2^32
- #12314: scipy.spatial.transform.Rotation multiplication does not normalize quaternion

5.10.23 Pull requests for 1.5.0

- #6510: Add Eigenvalue Range Functionality for Symmetric Eigenvalue Problems
- #9525: BUG: SuperLU 'NATURAL' order applies a column permutation
- #9634: Add the number of Jacobian evaluations to the output of L-BFGS-B.
- #9719: ENH: Added kstwo probability distribution for two-sided one-sample…
- #9783: WIP: optimize: added (dense) interpolative decomposition redundancy…
- #10053: Adding docstring to weibull_min and weibull_max based on issue…
- #10136: DEP: Add warning to linprog_verbose_callback
- #10380: ENH: add geometric_slerp
- #10602: MAINT: optimize: refactor common linprog arguments into namedtuple
- #10648: Bounds for the Powell minimization method
- #10673: ENH: approx_fprime –> approx_derivative
- #10759: ENH: calculation of region areas in spatial.SphericalVoronoi
- #10762: BENCH: optimize: more comprehensive linprog benchmarking
- #10796: ENH exact p-values of wilcoxon test in scipy.stats
- #10797: ENH: linalg: LU with full pivoting (wrappers for ?getc2/?gesc2)
- #10824: ENH: Fast gaussian kernel estimator
- #10942: BUG: prevent bound violation in L-BFGS-B optimize method
- #11003: ENH: add scipy.linalg.convolution_matrix
- #11023: improving error message for cubic-interpolate with duplicates
- #11045: MAINT: make bdt{r,rc,ri}() functions accept double n,k args +…
- #11063: Fix documentation error in optimize.minimize
- #11069: ENH: stats.dlaplace.rvs improvements
- #11071: DOC: Added examples to maximum_position in ndimage
- #11075: DOC: Update stylistic consistency in multiple files
- #11097: BUG: stats: fixing chisquare to return correct results for arrays…
- #11110: ENH: special: Cythonise erfinv, erfcinv
- #11112: BUG: special: Return NaN outside the domain of `eval_hermite`

- #11114: BUG: special: fix `hyp1f1` for nonnegative integral `a` and…
- #11115: DOC: special: add docstrings for `kei`, `ker`, `keip`,…
- #11130: ENH: support for circular input
- #11136: BUG: expm handling of empty input
- #11138: DOC: stylistic consistency, punctuation, etc.
- #11139: MAINT: cluster: use cython_blas, remove handwritten BLAS wrappers
- #11146: DOC: update docs on bp parameter for detrend
- #11151: DOC: special: add docstrings for `bei`, `ber`, `beip`,…
- #11156: ENH: add input validation for ellipord.
- #11157: DOC: stylistic revision, punctuation, consistency
- #11160: ignore warning on 0 * inf in basin hopping
- #11162: DOC: minor stylistic revision, undo changes
- #11164: ENH/ BUG: Pydata sparse equality
- #11171: Fix dtype validation of “seuclidean” metric V parameter
- #11177: BUG: stats: Improve genpareto stats calculations.
- #11180: MAINT: stats: Some clean up in test_distributions.py.
- #11187: ENH: add functionality log_softmax to SciPy.special.
- #11188: MAINT: add rvs method to argus in scipy.stats
- #11196: DOC: special: add to docstrings of Kelvin zeros functions
- #11202: BUG: fix edge counting in shortest_path
- #11218: BUG: scipy/interpolate: fix PPoly/Cubic*Spline roots() extrapolation…
- #11225: Add a warning to constant input for spearmanr() function
- #11226: Speed up of interior-point method for cholesky solver
- #11229: BUG: Explicit dtype specification in _upfirdn.py
- #11230: Additional citation for optimize tutorial
- #11231: Adds SLSQP test for duplicate f-evals (#10738)
- #11236: MAINT: Improved error message for Wn range in iirfilter.
- #11245: ENH: optimize: dense redundancy removal routine optimizations
- #11247: MAINT: Remove _lib/_numpy_compat.py
- #11248: BUG: rv_discrete.ppf() to handle loc
- #11251: DOC: add reference for linesearch zoom algorithm
- #11253: BUG: fix kendalltau issue where p-value becomes >1
- #11254: MAINT: make special.factorial handle nan correctly
- #11256: DOC: Updated documentation for scipy.linalg.qr
- #11265: Fix: Can no longer slice csr_matrix in 1.3.0
- #11267: BUG: Rework the scaling in the ks_2samp two-sided exact test.

- #11268: DOC: example of NonLinearConstraint
- #11269: Fix: Sparse matrix constructor data type detection changes on…
- #11276: BLD: update minimum Python, NumPy, Cython, Pybind11 versions
- #11277: MAINT: Cleanup conditionals for unsupported numpy verisons
- #11278: MAINT: Cleanup stats.iqr workarounds for unsupported NumPy versions
- #11282: TST/CI: improve traceback formatting for test failures
- #11284: fix docs & behavior for mode sequences in ndimage filters
- #11285: DOC: special: complete the docstrings of Chi-square functions
- #11286: BUG: make loadmat/savemat file opening close resources correctly
- #11287: CI: skip Azure and TravisCI builds on merges and direct pushes…
- #11288: DOC: Fix import in scipy.io.wavfile.read sample code
- #11289: BUG: Use context manager for open
- #11290: MAINT: Remove _lib._version in favour of _lib._pep440
- #11292: DOC: special: add docstrings for various convenience functions
- #11293: DOC: special: fix typo in `chdtri` docstring
- #11296: DOC: special: add to docstrings of Bessel zeros and derivatives
- #11297: DOC: special: add parameters/returns sections for Bessel integrals
- #11300: MAINT: Update vendored uarray version
- #11301: CI: azure conditions should require succeeded()
- #11302: ENH: build infrastructure for ILP64 BLAS + ARPACK conversion
- #11303: DOC: special: fix typo in `besselpoly` docstring
- #11304: ENH: MAINT: Rewrite of eigh() and relevant wrappers
- #11306: TST: skip test_aligned_mem linalg test that is crashing on ppcle64
- #11307: MAINT: Fix typo 'solutuion' -> 'solution'
- #11308: ENH: do not create 1d array out of a scalar
- #11310: MAINT: clean up object array creation, scalar/1d confusion
- #11311: DOC: Specify custom callable option for metric in cluster.hierarchy.fclusterdata
- #11316: BUG: special: fix behavior for `rgamma` zeros
- #11317: BUG: fix floating-point literal comparisons under C99
- #11318: TST: optimize: mark two linprog tests for skipping
- #11320: BUG: Include `int64_t` declaration to `rectangular_lsap.cpp`
- #11330: MAINT: Update vendored pypocketfft version
- #11333: BUG: directed_hausdorff subset fix
- #11335: [ENH] sparse: Loosen check for sparse outer indexing fast path
- #11337: Undefined name 'e' in pavement.py
- #11338: scipyoptdoc.py: Remove unused variable 'sixu'

- #11340: xrange() was removed in Python 3 in favor of range()
- #11342: range() was removed in Py3 in _binned_statistic.py
- #11343: BUG: constants: fix 'exact' values table
- #11347: ENH: add input validation function and apply it to needed functions
- #11348: MAINT: remove six.string_types usages
- #11349: MAINT: minor doc fix _minimize_trustregion_constr
- #11353: MAINT: py3 remove various six usages
- #11358: ENH: optimize: Use CSR format instead of LIL for speed
- #11362: MAINT: sys.version_info >= 3.5
- #11364: ENH: cache square of sums for f_oneway
- #11368: ENH: add optional argument, "include_nyquist", for freqz()
- #11372: BENCH: optimize: added linprog presolve benchmarks
- #11376: ENH: Add wrapper for ?gttrf/?gttrs
- #11377: MAINT: Remove Python 2 code from tools/authors.py
- #11378: ENH (WIP): Python wrapper for ?tbtrs
- #11379: MAINT: Remove six.with_metaclass from benchmarks/cython_special.py
- #11380: BUG: sparse/isolve: bicg and qmr don't treat x0 correctly
- #11382: MAINT: remove error throw in binned_statistic_dd() on non-finite…
- #11383: MAINT: _lib: remove py2 compat shims in getargspec
- #11384: MAINT: Use numpy scalar types directly
- #11385: ENH: special: add spherical Bessel functions to `cython_special`
- #11389: MAINT: line.startswith shouldn't be bytes
- #11393: ENH: Speed up truncnorm's ppf()and rvs() methods
- #11394: MAINT: Remove self._size (and self._random_state) from stats…
- #11395: correction in error message (%d->%g format)
- #11396: DOC: revert gh10540, removing mtrand
- #11397: MAINT: differential_evolution accepts np.random.Generator
- #11402: ENH: stats can use np.random.Generator
- #11404: ENH: add docstring of butter() for transfer function syntax problem
- #11405: DOC: Fix "see also" for SmoothBivariateSpline
- #11408: ENH: Add a `plan` argument to FFT functions in `scipy.fft`
- #11411: MAINT: check minimize duplicate evaluations
- #11418: ENH: Linalg: Python wrapper for ?geqrfp
- #11419: TST: Python 3.7 mac OS gcc multibuild fix
- #11423: ENH: Add tool to lint diffs
- #11425: FIX: _array_newton should preserve complex inputs

- #11426: MAINT: licence for global optimization benchmarks
- #11431: Make median_absolute_deviation scale argument aligned w/iqr
- #11432: Fix error message typo
- #11433: DOC: Remove L from longs
- #11434: MAINT: Python3 improvements to refguide_check.py
- #11435: DOC: Update runtest –parallel help
- #11436: MAINT: Remove checks for sys.version < 3.5
- #11437: DOC: Fix documentation issue
- #11439: Support path objects (PEP 519) in mmio functions
- #11440: correct bounds pass in run_dualannealing for benchmarks/optimize.py
- #11443: BENCH: optimize_linprog remove ImportError exception
- #11453: BUG: sparse: convert csc/csr indices to int64 as needed
- #11454: DOC: Remove caveat on `maximum_bipartite_matching`
- #11455: BUG: Fix _lib._util.getargspec_no_self lack of KEYWORD_ONLY support.
- #11456: Implementation of khatri_rao product
- #11459: BUG: fix augmentation being broken in maximum_bipartite_matching
- #11461: MAINT: minor spelling corrections in comments in SciPy.sparse.linalg.arpack
- #11467: [MRG] Make result data type of KDE evaluation like in the input…
- #11469: Update integrate.quad documentation
- #11472: Fixed result typo
- #11476: DOC: stats: Copy-edit the anderson docstring.
- #11478: ENH: avoid unnecessary array copies in matrix product
- #11481: BUG: Make special.hyperu return nan if any argument is nan
- #11483: BUG: Fixed `_kpp` initialization on `scipy.cluster.vq`, closing…
- #11485: ENH: Update docstring of class KrylovJacobian to fix #2744
- #11486: BUG: make special.eval_hermite return nan if second argument…
- #11487: ENH: improve docstring of correlate and correlate2d to fix #1968
- #11488: FIX: change “func -> fun” of scipy.optimize _root.py to solve…
- #11489: BUG: fixes typo introduced in PR #11253 in stats.mstats.kendalltau()
- #11490: DOC: fix typo in scipy/io/matlab/mio4.py
- #11495: MAINT: refactor slsqp to fix issue in callback function
- #11498: [DOC] mention graph cuts in maximum flow docstring
- #11499: DOC: Improve documentation of scipy.signal.signaltools.wiener
- #11506: DOC: Fix typo in documentation of scipy.stats.morestats
- #11508: ENH: avoid copy on sparse __init__ when dtype is given
- #11509: ENH: avoid unnecessary array copies in matrix product (again)

- #11510: [DOC] An ex. for creating arbitrary size tri-diagonal
- #11511: TST: pin numba for Travis/sparse
- #11513: TST: disable NumPy cache dir ppc64le
- #11514: BUG: make special.eval_genlaguerre return nan if passed nan
- #11517: ENH: improve sparse.lil.tocsr performance
- #11519: Fix fresnel documentation
- #11520: BUG: make special.eval_gegenbauer return nan if passed nan
- #11524: ENH: Cosine Sine Decomposition
- #11526: BUG: fix SLSQP max iteration setting to fix #4921
- #11527: ENH: improve docstring of weibull_min_gen and weibull_max_gen…
- #11530: MAINT: Removed 3 unused imports, 3 unused assignments from ndimage.
- #11531: DOC: fix typos in bdtr and bdtrc from gh PR 11045
- #11532: MAINT: Fixed several unused imports and unused assignments from…
- #11533: MAINT: Fixed about 100 unused imports, unused assignment warnings…
- #11534: FIX: Allow non-native byte order inputs to scipy.fft
- #11535: MAINT: Fixed several unused imports in _lib.
- #11536: MAINT: Fixed several unused imports and unused assignments in…
- #11537: MAINT: Removed an unused import in scipy/constants.
- #11538: MAINT: Fixed several unused imports in scipy/fft.
- #11539: MAINT: Fixed several unused imports and unused assignments in…
- #11540: MAINT: Fixed two unused imports in scipy/misc.
- #11541: MAINT: Fixed several unused imports and unused assignments in…
- #11542: MAINT: Fixed an unused import in scipy/odr.
- #11543: MAINT: Fixed several unused imports and unused assignments in…
- #11544: MAINT: Fixed unused imports and unused assignments in scipy/integrate.
- #11545: MAINT: Removed unused imports and fixed unused assignments in…
- #11546: MAINT: Removed unused imports; fixed unused assignments in scipy/signal.
- #11547: MAINT: Removed unused imports; fixed unused assignments in scipy/spatial
- #11548: MAINT: Removed unused imports; fixed unused assignments in scipy.sparse.
- #11549: MAINT: Replace xrange with range
- #11560: MAINT: stats: remove an _argcheck call
- #11573: MAINT: Removed unused imports; fixed unused assignments in scipy/stats.
- #11574: MAINT: Small change to `optimize.nnls` error messages.
- #11575: MAINT: Update sytrd/hetrd tests
- #11582: MAINT: fix typo in quadpack.py closes #11448
- #11585: TST: add openblas_support.py

- #11587: BUG: Differential evolution with LinearConstraint with sparse…
- #11588: MAINT: Fully display problem size in lsmr/lsqr.
- #11589: MAINT: Remove Python 2 workarounds
- #11590: MAINT: Remove Python2 module init
- #11605: Standardization of bounds in _linprog_util.py
- #11608: BUG: fix use of is in DE callback
- #11614: TST, MAINT: TestCtypesQuad skip with pytest
- #11619: ENH: add nan_policy argument and functionality to stats.mstats.winsorize
- #11621: MAINT: Cleanup uses of PY_VERSION_HEX, NPY_PY3K in ndimage
- #11622: MAINT: Cleanup uses of PY_VERSION_HEX, NPY_PY3K in sparse
- #11623: MAINT: Remove unnecessary 'from __future__ import …' statements
- #11626: MAINT: Cleanup uses of PY_VERSION_HEX
- #11627: ENH: add analytic formula for normal moments
- #11628: MAINT, TST: adjust azure for matplotlib release
- #11631: Revert to old behaviour for constant cost matrices in `linear_sum_assignment`
- #11632: MAINT: Define ARRAY_ANYORDER with DEF instead of cdef
- #11639: BUG: interpolate/interp1d: fail gracefully on all-nan inputs
- #11640: MAINT: Fix BLAS3 trmm wrapper for "side" arg
- #11642: TST, MAINT: remove dead code in Travis CI
- #11643: MAINT: fix conversion in binom_test
- #11645: MAINT: Assorted clean up.
- #11646: MAINT: Remove unnecessary 'from __future__ import …' statements
- #11647: DOC: document return_all arguments
- #11648: Perform geometric slerp in quaternion space
- #11651: DOC: Update paper URL in lambertw documentation
- #11653: PERF: Switch to C++ STL std::nth_element
- #11655: MAINT: Remove Python2 cStringStream
- #11657: ENH: Add wrapper for ?pttrf/?pttrs
- #11664: ENH: Add wrapper for ?gejsv
- #11665: ENH: Add wrapper for ?pteqr
- #11667: BUG: Non-central Fisher distribution (fix nan-values when nc=0)
- #11668: ENH: Add wrapper for ?gtsvx
- #11671: TST, CI: restore Azure temporarily
- #11672: Add warning to medfilt when array size < kernel_size
- #11674: TST: bump test precision for two np.dot related linalg tests.
- #11675: MAINT: pycodestyle clean-up

- #11677: ENH: Add wrapper for ?ptsvx
- #11679: BENCH: cKDTree benchmarks added: balanced/unbalanced tree (related…
- #11680: MAINT: rng_integers allows RandomState.randint or Generator.integers
- #11683: BUG: fix mode='mirror' on length 1 axes
- #11684: BUG: fix scipy.special.voigt_profile
- #11687: MAINT: sparse.linalg: avoid importing from `np.core`
- #11688: ENH: mypy: get specific about ignoring missing imports
- #11690: MAINT: mypy: fix errors about incompatible types in lists
- #11692: MAINT: mypy: fix remaining type errors
- #11694: TST, MAINT: bump to OpenBLAS 0.3.9 stable, raise tol for Win…
- #11697: DOC: fix pdf of norminvgauss in scipy.stats
- #11701: MAINT: special: add rudimentary types for `_ufuncs` extension…
- #11702: BUG: Fixed a post-merge bug for eigh()
- #11703: Improves docstring with consistent L2-norm
- #11705: DOC: Slerp the SphericalVoronoi docstring
- #11706: ENH: mypy: add `–mypy` option to `runtests.py`
- #11710: ENH: Modified stats.kstest() to use the exact stats.kstwo.sf()…
- #11715: DOC: add .. versionadded:: to as_matrix/from_matrix in spatial/transf…
- #11716: BENCH: fix benchmark imports for ``optimize_linprog.py``
- #11721: MAINT: io: Remove now-unnecessary `# type: ignore`
- #11722: MAINT: mypy: remove mpmath from the ratchet
- #11726: Handle constant input for scipy.stats.f_oneway
- #11729: BENCH: optimize: added infeasible benchmarks for linprog
- #11731: fix inaccurate information about Mac OS compiler (#11696)
- #11733: Fix inaccurate docstring example of HalfspaceIntersection
- #11734: Doc: fix inaccurate docstring of SmoothBivariateSpline.
- #11735: Bug: stats: fix wrong shape from median_absolute_deviation for…
- #11736: ENH: add input validations and its tests for FITPACK in fitpack2.py
- #11737: BUG: Prevent crashes due to MKL bug in ?heevr
- #11739: MAINT: special: add type stubs for `_test_round.pyx`
- #11740: MAINT: special: remove unused specfun f2py wrappers
- #11741: BUG: fix small tolerances handling for minpack and add a test.
- #11743: Doc: fix docstring of rfft, rfft2, rfftn, irfft, irfft2, irfftn…
- #11744: MAINT: Remove unused py3k.h code
- #11745: DOC: stats: Clean up ncf documentation.
- #11748: MAINT: special: type `cython_special` as `Any`

- #11750: MAINT: type hints for `_spherical_voronoi`
- #11752: DOC: fix docstring of scipy.optimize.least_squares
- #11753: ENH: add input validation for dendrogram and a test.
- #11755: MAINT: Replace uses of tostring with tobytes
- #11757: ENH: improve binned_statistics_2d performance.
- #11759: ENH: optimize: add HiGHS methods to linprog
- #11760: MAINT: Remove FileStream replaced by GenericStream
- #11761: MAINT: Replace npy_3kcompat.h shims
- #11765: TST: Speedup test_pascal which is VERY slow on Azure
- #11766: TST: speed up differential_evolution L8 test
- #11767: Change comment in continuous rv gamma fit function
- #11776: Add domain option for resample.
- #11784: BUG: Fixed calculation of nonzero elements in scipy.sparse.random
- #11786: ENH: stats: add axis keyword argument to scipy.stats.rankdata
- #11789: Doc: fix docstring of scipy.spatial.chebyshev
- #11792: DOC: dev: add guidelines for developing public Cython APIs
- #11794: MAINT: add comments explaining a problem in cython_optimize organization
- #11796: DOC: add a note about precision losing in csgraph.minimum_spanning_tree…
- #11797: ENH: Allow negative `axis` in `interpolate.BSpline`. Also…
- #11798: Add simplify_cells parameter to scipy.io.loadmat
- #11801: MAINT, DOC: minor changes of ratio-of-uniforms in scipy.stats
- #11802: BUG: fix scipy.odr to handle multidimensional independent and…
- #11803: scipy.stats.trapz: Use analytic formulas for stats and entropy.
- #11808: DOC: add Examples in the scipy.interpolate.interpn docstring.
- #11809: Duplicate entries are added together in csr_matrix constructor
- #11813: MAINT: bump pyflakes to version 2.1.1
- #11814: BUG: scipy.sparse.csr doctest failing with incorrect output value
- #11817: DOC: add Examples in the scipy.optimize.leastsq docstring
- #11820: ENH: Raise an error on incorrect bounds format in optimize.fmin_l_bfgs_b
- #11822: CI: add github actions for macOS
- #11824: DOC: add Examples in scipy.optimize.line_search docstring (line_search_wolfe2)
- #11830: TST: Always use fork for multiprocessing in fft tests
- #11831: DOC: add Examples and Returns in scipy.misc.central_diff_weights…
- #11832: DOC: stats: Some small corrections to a couple docstrings.
- #11833: BUG: Fix compiler_name when there are paths used in flags
- #11836: MAINT: re-introduce multiprocessing tests on Python3.8

- #11837: Doc: add Examples in scipy.optimize.fsolve docstring
- #11838: Doc: add Examples in scipy.sparse.linalg.minres docstring
- #11840: BUG: sparse.linalg: fix overflow in expm intermediate computation
- #11842: BLD: fix build with gfortran 10
- #11843: MAINT: Simplify floats in constants.py
- #11847: DOC: add a tutorial of scipy.optimize.linprog
- #11849: ENH: speed up geninvgauss by using cython
- #11852: CI: remove osx from travisCI
- #11857: BUG: Change parameter fc of gausspulse to float.
- #11861: order = degree + 1 for splines
- #11863: Make g77 ABI wrapper work with gfortran ABI lapack
- #11866: MAINT: add type ignores to sympy and matplotlib imports
- #11867: CI: Add arm64 in travis-ci
- #11869: DOC: signal: Add an example to the lsim2 docstring.
- #11870: DOC: signal: Use impulse instead of impulse2 in the impulse example…
- #11871: ENH: type ufuncs in special as ufuncs instead of Any
- #11872: BUG: avoid recomputing in scipy.optimize.optimize.MemoizeJac
- #11873: DOC: signal: Fix ODE in impulse and impulse2 docstrings.
- #11874: DOC: add Examples of docstring for scipy.interpolate.approximate_taylor_polynomial
- #11878: DOC: fixed a typo under scipy/integrate/quadrature.py
- #11879: BUG: Fix index arrays overflow in sparse.kron
- #11880: DOC: stats: Add Examples for bartlett, fligner, levene.
- #11881: MAINT: normalise numpy–>np in optimize.py
- #11882: DOC: add Examples for scipy.io.readsav docstring.
- #11883: DOC: add Returns and Examples for scipy.ndimage.correlate() docstring
- #11885: BUG: stats: Handle multidimensional arrays in f_oneway, and more.
- #11889: DOC: signal: Unify lsim and lsim2 examples.
- #11896: BUG: stats: Fix handling of size 0 inputs for ttest_rel and ttest_ind.
- #11897: DOC: Remove misleading default values from fit method
- #11898: MAINT: LinearVectorFunction.J is ndarray closes #11886
- #11902: BUG: linalg: test_heequb failure
- #11904: fix real-to-real transforms for complex inputs and overwrite_x=True
- #11906: DOC: stats: fix error caused by trapz docstring
- #11907: BUG: stats: fixed SEGFAULT from Issue #9710
- #11912: ENH: Respect matplotlib color palette with hierarchy/dendrogram.
- #11914: DOC: refine doc for spatial.distance.squareform

- #11915: ENH: Ndim linear operator
- #11919: ENH: expose “window_size” parameter in find_peaks_cwt()
- #11920: DOC: explain M, diffev
- #11923: CI: macOS install swig closes #11922
- #11924: DOC: add Examples for scipy.optimize.bracket() docstring
- #11930: DOC: add Examples and clean up for signal.qspline1d and signal.qspline_eval…
- #11931: DOC: add Examples for sparse.linalg.bicg docstring.
- #11933: DOC: Add original reference for Yao-Liu objective functions
- #11934: DOC, MAINT: mailmap update
- #11935: DOC: make scipy.stats.mode documentation reflect that the function…
- #11936: ENH: special: add type stubs for `orthogonal.py`
- #11937: DOC: Add docstring examples to fft2, ifft2, io.savemat
- #11938: MAINT: add helper function for deprecating Cython API functions
- #11942: MAINT: ignore conditional import in _lib/_util
- #11943: MAINT: special: add types for geterr/seterr/errstate
- #11946: MAINT: add py.typed marker
- #11950: TST:MAINT: separated and stabilized heequb tests
- #11952: DOC: update toolchain roadmap for py38, C99, C++11/14
- #11957: MAINT: Use np.errstate context manager instead of np.seterr.
- #11958: MAINT: interpolate: Remove some trailing spaces.
- #11960: MAINT: Cleanup Python2 compatibility code
- #11961: MAINT: Remove numpy/npy_3kcompat.h from _superluobject.c
- #11962: DOC: Fix type of `codes` in docstring of `_vq._vq()`
- #11964: MAINT: Cleanup unused IS_PYPY
- #11969: DOC: add Examples and fix docstring for special.airye
- #11970: BUG: sparse: ‘diagonal’ of sparse matrices fixed to match numpy’s…
- #11974: BUG: Reshape oaconvolve output even when no axes are convolved
- #11976: MAINT: add logo for github actions
- #11977: CI: test bleeding edge Python
- #11979: DOC: add Examples for stats.ranksums() docstring.
- #11982: Fix KMeans++ initialisation slowness
- #11983: DOC: add Examples for stats.mstats.argstoarray() docstring.
- #11986: Avoid bugs in ndimage when the output and input arrays overlap…
- #11988: ENH: Override fit method of Laplace distribution with Maximum…
- #11993: TST, CI: Azure Windows path fixups
- #11995: MAINT, CI: remove custom mingw Azure

- #11996: DOC: add Examples and fix pep warning for fft.set_global_backend…
- #11997: MAINT, CI: Azure OpenBLAS simplify
- #11998: BENCH: Run against current HEAD instead of master
- #12001: ENH: stats: Implement _logpdf for the maxwell distribution.
- #12004: DOC: add examples for integrate.quad_vec() and integrate.quad_explain()
- #12005: MAINT: Use helper functions in ?tbtrs tests
- #12007: MAINT: updated LICENSES_bundled for pybind11 and six
- #12008: DOC: roadmap update
- #12009: ENH: optimize: support 64-bit BLAS in lbfgsb
- #12010: ENH: sparse.linalg: support 64-bit BLAS in isolve
- #12012: DOC: add Examples for interpolate.barycentric_interpolate(),…
- #12013: MAINT: remove last uses of numpy.dual
- #12014: CI: print 10 slowest tests
- #12020: MAINT: Removed handling of circular input in SphericalVoronoi
- #12022: DOC : added default value of absolute_sigma to False in scipy.optimize.curve_fit docs
- #12024: DOC: add Examples for io.hb_read() and io.hb_write()
- #12025: MAINT: Remove numpy/npy_3kcompat.h from nd_image
- #12028: Spelling correction
- #12030: ENH: optimize/_trlib: support ILP64 blas/lapack
- #12036: MAINT: Add some generated C files .gitignore
- #12038: MAINT, CI: Travis rackcdn->conda.org
- #12039: MAINT: signal: Lower the resolution of the plots in the chirp…
- #12040: DOC: add Examples for ndimage.spline_filter1d() and spline_filter()…
- #12044: MAINT: combine apt-get update and apt-get install into one RUN
- #12045: TST: Reduce size of test_diagonal_types to speed up tests
- #12046: MAINT: Remove unused npy_3kcompat.h
- #12047: MAINT: Cython 3.0 compat
- #12050: DOC: add download number badges of PyPI and conda-forge in README.rst
- #12052: DOC: add Examples odr.models.polynomial() and fix odr.odr docstring…
- #12056: ENH: Modifies shapiro to return a named tuple
- #12057: Adding my name into THANKS.txt
- #12060: TST: Reduce number of test_diagonal_types configs
- #12062: TST: Change dec.slow to pytest.mark.slow
- #12068: ENH: Modifies jarque_bera to return a named tuple
- #12070: MAINT, CI: appveyor rack->conda.org
- #12072: TST: filter out factorial(float) deprecation warning

- #12078: TST: Skip test on colab with large memory alloc
- #12079: DOC: Remove Python2 reference from stats tutorial
- #12081: DOC: add Examples docstring for optimize.show_options()
- #12084: BUG: interpolate: fix BarycentricInterpolator with integer input…
- #12089: ENH: spatial/qhull: support ILP64 Lapack
- #12090: ENH: integrate: support ILP64 BLAS in odeint/vode/lsoda
- #12091: ENH: integrate: support ILP64 in quadpack
- #12092: BUG: Fix dropping dt in signal.StateSpace
- #12093: MAINT: Rollback python2.6 workaround
- #12094: MAINT: `openblas_support` hash checks
- #12095: MAINT: ndimage: change `shares_memory` to `may_share_memory`
- #12098: Doc: change 4 model instances of odr to be instances of `Model`…
- #12101: Removed more unused imports and assignments.
- #12107: ENH: Area calculation for 2D inputs in SphericalVoronoi
- #12108: MAINT: ensure attributes have correct data type in `SphericalVoronoi`
- #12109: degree is not order in splines
- #12110: ENH: More helpful/forgiving io.wavfile errors
- #12117: BUG: fix newline
- #12123: [MAINT] Fix error on PyData/Sparse import.
- #12124: TST: Always test matmul now that Python3.5+ is required
- #12126: TST: Cleanup unused matplotlib code.
- #12127: DOC: update docstrings of signal.cspline2d, qspline2d, sepfir2d
- #12130: MAINT: Fixing broken links with linkchecker
- #12135: ENH: linalg: Add the function convolution_matrix.
- #12136: MAINT: Cleanup np.poly1d hack
- #12137: TST, CI: reproduce wheels 32-bit setup
- #12140: TST: stats: add kstwo, ksone to slow tests.
- #12141: Support 64-bit integer size in Fitpack
- #12151: DOC: Correct Rosenbrock function sum
- #12159: BUG: Fix length calculation in upfirdn
- #12160: BUG: Fix M_PI
- #12168: DOC: add an obsolete version checking javascript to doc release…
- #12171: CI, MAINT: Azure OpenBLAS drive flip
- #12172: ENH: Bounds for the Powell minimization method
- #12175: BLD: support more Fortran compilers for ilp64 and macro expansion…
- #12179: BUG: stats: A few distributions didn't accept lists as arguments.

- #12180: MAINT: removed redundant import in SphericalVoronoi tests
- #12181: DOC: for versionwarning don't use $.getScript
- #12182: MAINT: random sampling on the hypersphere in SphericalVoronoi…
- #12194: MAINT: Module and example cleanups for doc build
- #12202: ENH: tool to DL release wheels from Anaconda
- #12210: Remove py.typed marker (at least for the release)
- #12217: BUG: stats: Fix handling of edge cases in median_abs_deviation.
- #12223: BUG: stats: wilcoxon returned p > 1 for certain inputs.
- #12227: BLD: Set macos min version when building rectangular_lsap
- #12229: MAINT: tools/gh_lists.py: fix http header case sensitivity issue
- #12236: DOC: Fix a couple grammatical mistakes in 1.5.0-notes.rst.
- #12276: TST: skip *test_heequb*, it fails intermittently.
- #12285: CI: split travis arm64 run into two
- #12317: BUG: prevent error accumulation in *Rotation* multiplication
- #12318: BUG: sparse: avoid np.prod overflow in check_shape
- #12319: BUG: Make cobyla threadsafe
- #12335: MAINT: Work around Sphinx bug

5.11 SciPy 1.4.1 Release Notes

Contents

- *SciPy 1.4.1 Release Notes*
  - *Authors*
    - *Issues closed for 1.4.1*
    - *Pull requests for 1.4.1*

SciPy 1.4.1 is a bug-fix release with no new features compared to 1.4.0. Importantly, it aims to fix a problem where an older version of pybind11 may cause a segmentation fault when imported alongside incompatible libraries.

5.11.1 Authors

- Ralf Gommers
- Tyler Reddy

Issues closed for 1.4.1

- #11237: Seg fault when importing torch

Pull requests for 1.4.1

- #11238: BLD: update minimum pybind11 version to 2.4.0.

5.12 SciPy 1.4.0 Release Notes

Contents

- *SciPy 1.4.0 Release Notes*
  - *Highlights of this release*
    - *New features*
  - *Infrastructure*
  - `scipy.constants` *improvements*
  - `scipy.fft` *added*
  - `scipy.fftpack` *improvements*
  - `scipy.integrate` *improvements*
  - `scipy.interpolate` *improvements*
  - `scipy.io` *improvements*
  - `scipy.linalg` *improvements*
  - `scipy.ndimage` *improvements*
  - `scipy.optimize` *improvements*
  - `scipy.signal` *improvements*
  - `scipy.sparse` *improvements*
  - `scipy.spatial` *improvements*
  - `scipy.special` *improvements*
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  - `scipy.special` *changes*
  - `scipy.sparse` *changes*
  - `scipy.signal` *changes*
  - `scipy.stats` *changes*

* *Other changes*
* *Authors*

– *Issues closed for 1.4.0*

– *Pull requests for 1.4.0*

SciPy 1.4.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning`s). Our development attention will now shift to bug-fix releases on the 1.4.x branch, and on adding new features on the master branch.

This release requires Python 3.5+ and NumPy >=1.13.3 (for Python 3.5, 3.6), >=1.14.5 (for Python 3.7), >= 1.17.3 (for Python 3.8)

For running on PyPy, PyPy3 6.0+ and NumPy 1.15.0 are required.

5.12.1 Highlights of this release

- a new submodule, *scipy.fft*, now supersedes *scipy.fftpack*; this means support for `long double` transforms, faster multi-dimensional transforms, improved algorithm time complexity, release of the global intepreter lock, and control over threading behavior
- support for `pydata/sparse` arrays in *scipy.sparse.linalg*
- substantial improvement to the documentation and functionality of several *scipy.special* functions, and some new additions
- the generalized inverse Gaussian distribution has been added to *scipy.stats*
- an implementation of the Edmonds-Karp algorithm in *scipy.sparse.csgraph.maximum_flow*
- **scipy.spatial.SphericalVoronoi** ***now supports n-dimensional input,***

  has linear memory complexity, improved performance, and supports single-hemisphere generators

New features

5.12.2 Infrastructure

Documentation can now be built with `runtests.py --doc`

A `Dockerfile` is now available in the `scipy/scipy-dev` repository to facilitate getting started with SciPy development.

5.12.3 scipy.constants improvements

scipy.constants has been updated with the CODATA 2018 constants.

5.12.4 scipy.fft added

scipy.fft is a new submodule that supersedes the *scipy.fftpack* submodule. For the most part, this is a drop-in replacement for `numpy.fft` and *scipy.fftpack* alike. With some important differences, *scipy.fft*: - uses NumPy's conventions for real transforms (`rfft`). This means the return value is a complex array, half the size of the full `fft` output. This is different from the output of `fftpack` which returned a real array representing complex components packed together. - the inverse real to real transforms (`idct` and `idst`) are normalized for `norm=None` in thesame way as `ifft`. This means the identity `idct(dct(x)) == x` is now `True` for all norm modes. - does not include the convolutions or pseudo-differential operators from `fftpack`.

This submodule is based on the `pypocketfft` library, developed by the author of `pocketfft` which was recently adopted by NumPy as well. `pypocketfft` offers a number of advantages over fortran `FFTPACK`: - support for long double (`np.longfloat`) precision transforms. - faster multi-dimensional transforms using vectorisation - Bluestein's algorithm removes the worst-case `O(n^2)` complexity of `FFTPACK` - the global interpreter lock (`GIL`) is released during transforms - optional multithreading of multi-dimensional transforms via the `workers` argument

Note that *scipy.fftpack* has not been deprecated and will continue to be maintained but is now considered legacy. New code is recommended to use *scipy.fft* instead, where possible.

5.12.5 scipy.fftpack improvements

scipy.fftpack now uses pypocketfft to perform its FFTs, offering the same speed and accuracy benefits listed for scipy.fft above but without the improved API.

5.12.6 scipy.integrate improvements

The function *scipy.integrate.solve_ivp* now has an `args` argument. This allows the user-defined functions passed to the function to have additional parameters without having to create wrapper functions or lambda expressions for them.

scipy.integrate.solve_ivp can now return a `y_events` attribute representing the solution of the ODE at event times

New `OdeSolver` is implemented — `DOP853`. This is a high-order explicit Runge-Kutta method originally implemented in Fortran. Now we provide a pure Python implementation usable through `solve_ivp` with all its features.

scipy.integrate.quad provides better user feedback when break points are specified with a weighted integrand.

scipy.integrate.quad_vec is now available for general purpose integration of vector-valued functions

5.12.7 `scipy.interpolate` improvements

scipy.interpolate.pade now handles complex input data gracefully

scipy.interpolate.Rbf can now interpolate multi-dimensional functions

5.12.8 `scipy.io` improvements

scipy.io.wavfile.read can now read data from a *WAV* file that has a malformed header, similar to other modern *WAV* file parsers

scipy.io.FortranFile now has an expanded set of available `Exception` classes for handling poorly-formatted files

5.12.9 `scipy.linalg` improvements

The function `scipy.linalg.subspace_angles(A, B)` now gives correct results for complex-valued matrices. Before this, the function only returned correct values for real-valued matrices.

New boolean keyword argument `check_finite` for *scipy.linalg.norm*; whether to check that the input matrix contains only finite numbers. Disabling may give a performance gain, but may result in problems (crashes, non-termination) if the inputs do contain infinities or NaNs.

scipy.linalg.solve_triangular has improved performance for a C-ordered triangular matrix

`LAPACK` wrappers have been added for `?geequ`, `?geequb`, `?syequb`, and `?heequb`

Some performance improvements may be observed due to an internal optimization in operations involving LAPACK routines via `_compute_lwork`. This is particularly true for operations on small arrays.

Block `QR` wrappers are now available in *scipy.linalg.lapack*

5.12.10 `scipy.ndimage` improvements

5.12.11 `scipy.optimize` improvements

It is now possible to use linear and non-linear constraints with *scipy.optimize.differential_evolution*.

scipy.optimize.linear_sum_assignment has been re-written in C++ to improve performance, and now allows input costs to be infinite.

A `ScalarFunction.fun_and_grad` method was added for convenient simultaneous retrieval of a function and gradient evaluation

scipy.optimize.minimize `BFGS` method has improved performance by avoiding duplicate evaluations in some cases

Better user feedback is provided when an objective function returns an array instead of a scalar.

5.12.12 scipy.signal improvements

Added a new function to calculate convolution using the overlap-add method, named *scipy.signal.oaconvolve*. Like *scipy.signal.fftconvolve*, this function supports specifying dimensions along which to do the convolution.

scipy.signal.cwt now supports complex wavelets.

The implementation of `choose_conv_method` has been updated to reflect the new FFT implementation. In addition, the performance has been significantly improved (with rather drastic improvements in edge cases).

The function `upfirdn` now has a `mode` keyword argument that can be used to select the signal extension mode used at the signal boundaries. These modes are also available for use in `resample_poly` via a newly added `padtype` argument.

scipy.signal.sosfilt now benefits from Cython code for improved performance

scipy.signal.resample should be more efficient by leveraging `rfft` when possible

5.12.13 scipy.sparse improvements

It is now possible to use the LOBPCG method in *scipy.sparse.linalg.svds*.

scipy.sparse.linalg.LinearOperator now supports the operation `rmatmat` for adjoint matrix-matrix multiplication, in addition to `rmatvec`.

Multiple stability updates enable float32 support in the LOBPCG eigenvalue solver for symmetric and Hermitian eigenvalues problems in `scipy.sparse.linalg.lobpcg`.

A solver for the maximum flow problem has been added as *scipy.sparse.csgraph.maximum_flow*.

scipy.sparse.csgraph.maximum_bipartite_matching now allows non-square inputs, no longer requires a perfect matching to exist, and has improved performance.

scipy.sparse.lil_matrix conversions now perform better in some scenarios

Basic support is available for `pydata/sparse` arrays in *scipy.sparse.linalg*

scipy.sparse.linalg.spsolve_triangular now supports the `unit_diagonal` argument to improve call signature similarity with its dense counterpart, *scipy.linalg.solve_triangular*

`assertAlmostEqual` may now be used with sparse matrices, which have added support for `__round__`

5.12.14 scipy.spatial improvements

The bundled Qhull library was upgraded to version 2019.1, fixing several issues. Scipy-specific patches are no longer applied to it.

scipy.spatial.SphericalVoronoi now has linear memory complexity, improved performance, and supports single-hemisphere generators. Support has also been added for handling generators that lie on a great circle arc (geodesic input) and for generators in n-dimensions.

`scipy.spatial.transform.Rotation` now includes functions for calculation of a mean rotation, generation of the 3D rotation groups, and reduction of rotations with rotational symmetries.

`scipy.spatial.transform.Slerp` is now callable with a scalar argument

scipy.spatial.voronoi_plot_2d now supports furthest site Voronoi diagrams

scipy.spatial.Delaunay and *scipy.spatial.Voronoi* now have attributes for tracking whether they are furthest site diagrams

5.12.15 `scipy.special` improvements

The Voigt profile has been added as *scipy.special.voigt_profile*.

A real dispatch has been added for the Wright Omega function (*scipy.special.wrightomega*).

The analytic continuation of the Riemann zeta function has been added. (The Riemann zeta function is the one-argument variant of *scipy.special.zeta*.)

The complete elliptic integral of the first kind (*scipy.special.ellipk*) is now available in `scipy.special.cython_special`.

The accuracy of *scipy.special.hyp1f1* for real arguments has been improved.

The documentation of many functions has been improved.

5.12.16 `scipy.stats` improvements

scipy.stats.multiscale_graphcorr added as an independence test that operates on high dimensional and nonlinear data sets. It has higher statistical power than other *scipy.stats* tests while being the only one that operates on multivariate data.

The generalized inverse Gaussian distribution (*scipy.stats.geninvgauss*) has been added.

It is now possible to efficiently reuse *scipy.stats.binned_statistic_dd* with new values by providing the result of a previous call to the function.

scipy.stats.hmean now handles input with zeros more gracefully.

The beta-binomial distribution is now available in *scipy.stats.betabinom*.

scipy.stats.zscore, *scipy.stats.circmean*, *scipy.stats.circstd*, and *scipy.stats.circvar* now support the `nan_policy` argument for enhanced handling of `NaN` values

scipy.stats.entropy now accepts an `axis` argument

scipy.stats.gaussian_kde.resample now accepts a `seed` argument to empower reproducibility

scipy.stats.kendalltau performance has improved, especially for large inputs, due to improved cache usage

scipy.stats.truncnorm distribution has been rewritten to support much wider tails

Deprecated features

5.12.17 `scipy` deprecations

Support for NumPy functions exposed via the root SciPy namespace is deprecated and will be removed in 2.0.0. For example, if you use `scipy.rand` or `scipy.diag`, you should change your code to directly use `numpy.random.default_rng` or `numpy.diag`, respectively. They remain available in the currently continuing Scipy 1.x release series.

The exception to this rule is using `scipy.fft` as a function – *scipy.fft* is now meant to be used only as a module, so the ability to call `scipy.fft(...)` will be removed in SciPy 1.5.0.

In *scipy.spatial.Rotation* methods `from_dcm`, `as_dcm` were renamed to `from_matrix`, `as_matrix` respectively. The old names will be removed in SciPy 1.6.0.

Method `Rotation.match_vectors` was deprecated in favor of `Rotation.align_vectors`, which provides a more logical and general API to the same functionality. The old method will be removed in SciPy 1.6.0.

Backwards incompatible changes

5.12.18 `scipy.special` changes

The deprecated functions `hyp2f0`, `hyp1f2`, and `hyp3f0` have been removed.

The deprecated function `bessel_diff_formula` has been removed.

The function `i0` is no longer registered with `numpy.dual`, so that `numpy.dual.i0` will unconditionally refer to the NumPy version regardless of whether *scipy.special* is imported.

The function `expn` has been changed to return `nan` outside of its domain of definition (`x, n < 0`) instead of `inf`.

5.12.19 `scipy.sparse` changes

Sparse matrix reshape now raises an error if shape is not two-dimensional, rather than guessing what was meant. The behavior is now the same as before SciPy 1.1.0.

`CSR` and `CSC` sparse matrix classes should now return empty matrices of the same type when indexed out of bounds. Previously, for some versions of SciPy, this would raise an `IndexError`. The change is largely motivated by greater consistency with `ndarray` and `numpy.matrix` semantics.

5.12.20 `scipy.signal` changes

scipy.signal.resample behavior for length-1 signal inputs has been fixed to output a constant (DC) value rather than an impulse, consistent with the assumption of signal periodicity in the FFT method.

scipy.signal.cwt now performs complex conjugation and time-reversal of wavelet data, which is a backwards-incompatible bugfix for time-asymmetric wavelets.

5.12.21 `scipy.stats` changes

scipy.stats.loguniform added with better documentation as (an alias for `scipy.stats.reciprocal`). `loguniform` generates random variables that are equally likely in the log space; e.g., `1`, `10` and `100` are all equally likely if `loguniform(10 ** 0, 10 ** 2).rvs()` is used.

Other changes

The `LSODA` method of *scipy.integrate.solve_ivp* now correctly detects stiff problems.

scipy.spatial.cKDTree now accepts and correctly handles empty input data

scipy.stats.binned_statistic_dd now calculates the standard deviation statistic in a numerically stable way.

scipy.stats.binned_statistic_dd now throws an error if the input data contains either `np.nan` or `np.inf`. Similarly, in *scipy.stats* now all continuous distributions' `.fit()` methods throw an error if the input data contain any instance of either `np.nan` or `np.inf`.

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A total of 142 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

5.12.22 Issues closed for 1.4.0

- #1255: maxiter broken for Scipy.sparse.linalg gmres, in addition to…
- #1301: consolidate multipack.h from interpolate and integrate packages…
- #1739: Single precision FFT insufficiently accurate. (Trac #1212)
- #1795: stats test_distributions.py: replace old fuzz tests (Trac #1269)
- #2233: fftpack segfault with big arrays (Trac #1714)
- #2434: rmatmat and the sophistication of linear operator objects
- #2477: stats.truncnorm.rvs() does not give symmetric results for negative…
- #2629: FFTpack is unacceptably slow on non power of 2
- #2883: UnboundLocalError in scipy.interpolate.splrep
- #2956: Feature Request: axis argument for stats.entropy function
- #3528: Segfault on test_djbfft (possibly MKL-related?)
- #3793: cwt should also return complex array
- #4464: TST: residue/residuez/invres/invresz don't have any tests
- #4561: BUG: tf filter trailing and leading zeros in residuez
- #4669: Rewrite sosfilt to make a single loop over the input?
- #5040: BUG: Empty data handling of (c)KDTrees
- #5112: boxcox transform edge cases could use more care
- #5441: scipy.stats.ncx2 fails for nc=0
- #5502: args keyword not handled in optimize.curve_fit
- #6484: Qhull segmentation fault
- #6900: linear_sum_assignment with infinite weights
- #6966: Hypergeometric Functions documentation is lacking
- #6999: possible false positive corruption check in compressed loadmat()
- #7018: ydata that needs broadcasting renders curve_fit unable to compute…
- #7140: trouble with documentation for windows
- #7327: interpolate.ndgriddata.griddata causes Python to crash rather…
- #7396: MatrixLinearOperator implements _adjoint(), but not _transpose()
- #7400: BUG(?): special: factorial and factorial2 return a 0-dimensional…
- #7434: Testing of scipy.stats continuous distributions misses 25 distributions
- #7491: Several scipy.stats distributions (fisk, burr, burr12, f) return…
- #7759: Overflow in stats.kruskal for large samples
- #7906: Wrong result from scipy.interpolate.UnivariateSpline.integral…

- #8165: ENH: match functionality of R for hmean
- #8417: optimimze.minimize(method='L-BFGS-B', options={'disp': True})…
- #8535: Strictly increasing requirement in UnivariateSpline
- #8815: [BUG] GMRES: number of iteration is only increased if callback…
- #9207: scipy.linalg.solve_triangular speed after scipy.linalg.lu_factor
- #9275: new feature: adding LOBPCG solver in svds in addition to ARPACK
- #9403: range of truncnorm.logpdf could be extended
- #9429: gaussian_kde not working with numpy matrix
- #9515: ndimage implementation relies on undefined behavior
- #9643: arpack returns singular values in ascending order
- #9669: DOC: matthew-brett/build-openblas has been retired
- #9852: scipy.spatial.ConvexHull exit with code 134, free(): invalid…
- #9902: scipy.stats.truncnorm second moment may be wrong
- #9943: Custom sampling methods in shgo do not work
- #9947: DOC: Incorrect documentation for `nan_policy='propagate` in…
- #9994: BUG: sparse: reshape method allows a shape containing an arbitrary…
- #10036: Official Nelder mead tutorial uses xtol instead of xatol, which…
- #10078: possible to get a better error message when objective function…
- #10092: overflow in truncnorm.rvs
- #10121: A little spelling mistake
- #10126: inaccurate std implementation in binned_statistic
- #10161: Error in documentation scipy.special.modstruve
- #10195: Derivative of spline with 'const' extrapolation is also extrapolted…
- #10206: sparse matrices indexing with scipy 1.3
- #10236: Non-descriptive error on type mismatch for functions of scipy.optimize…
- #10258: LOBPCG convergence failure if guess provided
- #10262: distance matrix lacks dtype checks / warnings
- #10271: BUG: optimize failure on wheels
- #10277: scipy.special.zeta(0) = NAN
- #10292: DOC/REL: Some sections of the release notes are not nested correctly.
- #10300: scipy.stats.rv_continuous.fit throws empty RuntimeError when…
- #10319: events in scipy.integrate.solve_ivp: How do I setup an events…
- #10323: Adding more low-level LAPACK wrappers
- #10360: firwin2 inadvertently modifies input and may result in undefined…
- #10388: BLD: TestHerd::test_hetrd core dumps with Python-dbg
- #10395: Remove warning about output shape of zoom

- #10403: DOC: scipy.signal.resample ignores t parameter
- #10421: Yeo-Johnson power transformation fails with integer input data
- #10422: BUG: scipy.fft does not support multiprocessing
- #10427: ENH: convolve numbers should be updated
- #10444: BUG: scipy.spatial.transform.Rotation.match_vectors returns improper…
- #10488: ENH: DCTs/DSTs for scipy.fft
- #10501: BUG: scipy.spatial.HalfspaceIntersection works incorrectly
- #10514: BUG: cKDTree GIL handling is incorrect
- #10535: TST: master branch CI failures
- #10588: scipy.fft and numpy.fft inconsistency when axes=None and shape…
- #10628: Scipy python>3.6 Windows wheels don't ship msvcp*.dll
- #10733: DOC/BUG: min_only result does not match documentation
- #10774: min_only=true djisktra infinite loop with duplicate indices
- #10775: UnboundLocalError in Radau when given a NaN
- #10835: io.wavfile.read unnecessarily raises an error for a bad wav header
- #10838: Error in documentation for scipy.linalg.lu_factor
- #10875: DOC: Graphical guides (using TikZ)
- #10880: setting verbose > 2 in minimize with trust-constr method leads…
- #10887: scipy.signal.signaltools._fftconv_faster has incorrect estimates
- #10948: gammainc(0,x) = nan but should be 1, gammaincc(0,x) = nan but…
- #10952: TestQRdelete_F.test_delete_last_p_col test failure
- #10968: API: Change normalized=False to normalize=True in Rotation
- #10987: Memory leak in shgo triangulation
- #10991: Error running openBlas probably missing a step
- #11033: deadlock on osx for python 3.8
- #11041: Test failure in wheel builds for TestTf2zpk.test_simple
- #11089: Regression in scipy.stats where distribution will not accept loc and scale parameters
- #11100: BUG: multiscale_graphcorr random state seeding and parallel use
- #11121: Calls to `scipy.interpolate.splprep` increase RAM usage.
- #11125: BUG: segfault when slicing a CSR or CSC sparse matrix with slice start index > stop index
- #11198: BUG: sparse eigs (arpack) shift-invert drops the smallest eigenvalue for some k

5.12.23 Pull requests for 1.4.0

- #4591: BUG, TST: Several issues with scipy.signal.residue
- #6629: ENH: sparse: canonicalize on initialization
- #7076: ENH: add complex wavelet support to scipy.signal.cwt.
- #8681: ENH add generalized inverse Gaussian distribution to scipy.stats
- #9064: BUG/ENH: Added default _transpose into LinearOperator. Fixes…
- #9215: ENH: Rbf interpolation of large multi-dimensional data
- #9311: ENH: Added voigt in scipy.special.
- #9642: ENH: integrate: quad() for vector-valued functions
- #9679: DOC: expand docstring of exponweib distribution
- #9684: TST: add ppc64le ci testing
- #9800: WIP : ENH: Refactored _hungarian.py for speed and added a minimize/maximize…
- #9847: DOC: Change integrate tutorial to use solve_ivp instead of odeint
- #9876: ENH: Use rfft when possible in resampling
- #9998: BUG: Do not remove 1s when calling sparse: reshape method #9994
- #10002: ENH: adds constraints for differential evolution
- #10098: ENH: integrate: add args argument to solve_ivp.
- #10099: DOC: Add missing docs for linprog unknown_options
- #10104: BUG: Rewrite of stats.truncnorm distribution.
- #10105: MAINT improve efficiency of rvs_ratio_uniforms in scipy.stats
- #10107: TST: dual_annealing set seed
- #10108: ENH: stats: improve kendall_tau cache usage
- #10110: MAINT: _lib: Fix a build warning.
- #10114: FIX: only print bounds when supported by minimizer (shgo)
- #10115: TST: Add a test with an almost singular design matrix for lsq_linear
- #10118: MAINT: fix rdist methods in scipy.stats
- #10119: MAINT: improve rvs of randint in scipy.stats
- #10127: Fix typo in record array field name (spatial-ckdtree-sparse_distance…
- #10130: MAINT: ndimage: Fix some compiler warnings.
- #10131: DOC: Note the solve_ivp args enhancement in the 1.4.0 release…
- #10133: MAINT: add rvs for semicircular in scipy.stats
- #10138: BUG: special: Invalid arguments to ellip_harm can crash Python.
- #10139: MAINT: spatial: Fix some compiler warnings in the file distance_wrap.c.
- #10140: ENH: add handling of NaN in RuntimeWarning except clause
- #10142: DOC: return value of scipy.special.comb
- #10143: MAINT: Loosen linprog tol

- #10152: BUG: Fix custom sampling input for shgo, add unittest
- #10154: MAINT: add moments and improve doc of mielke in scipy.stats
- #10158: Issue #6999: read zlib checksum before checking bytes read.
- #10166: BUG: Correctly handle broadcasted ydata in curve_fit pcov computation.
- #10167: DOC: special: Add missing factor of `i` to `modstruve` docstring
- #10168: MAINT: stats: Fix an incorrect comment.
- #10169: ENH: optimize: Clarify error when objective function returns…
- #10172: DEV: Run tests in parallel when –parallel flag is passed to…
- #10173: ENH: Implement DOP853 ODE integrator
- #10176: Fixed typo
- #10182: TST: fix test issue for stats.pearsonr
- #10184: MAINT: stats: Simplify zmap and zscore (we can use keepdims now).
- #10191: DOC: fix a formatting issue in the scipy.spatial module docstring.
- #10193: DOC: Updated docstring for optimize.nnls
- #10198: DOC, ENH: special: Make `hyp2f1` references more specific
- #10202: DOC: Format DST and DCT definitions as latex equations
- #10207: BUG: Compressed matrix indexing should return a scalar
- #10210: DOC: Update docs for connection='weak' in connected_components
- #10225: DOC: Clarify new interfaces for legacy functions in 'optimize'
- #10231: DOC, MAINT: gpg2 updates to release docs / pavement
- #10235: LICENSE: split license file in standard BSD 3-clause and bundled.
- #10238: ENH: Add new scipy.fft module using pocketfft
- #10243: BUG: fix ARFF reader regression with quoted values.
- #10248: DOC: update README file
- #10255: CI: bump OpenBLAS to match wheels
- #10264: TST: add tests for stats.tvar with unflattened arrays
- #10280: MAINT: stats: Use a constant value for sqrt(2/PI).
- #10286: Development Documentation Overhaul
- #10290: MAINT: Deprecate NumPy functions in SciPy root
- #10291: FIX: Avoid importing xdist when checking for availability
- #10295: Disable deprecated Numpy API in __odrpack.c
- #10296: ENH: C++ extension for linear assignment problem
- #10298: ENH: Made pade function work with complex inputs
- #10301: DOC: Fix critical value significance levels in stats.anderson_ksamp
- #10307: Minkowski Distance Type Fix (issue #10262)
- #10309: BUG: Pass jac=None directly to lsoda

- #10310: BUG: interpolate: UnivariateSpline.derivative.ext is 'zeros'…
- #10312: FIX: Fixing a typo in a comment
- #10314: scipy.spatial enhancement request
- #10315: DOC: Update integration tutorial to solve_ivp
- #10318: DOC: update the example for PPoly.solve
- #10333: TST: add tests for stats.tvar with unflattened arrays
- #10334: MAINT: special: Remove deprecated `hyp2f0`, `hyp1f2`, and…
- #10336: BUG: linalg/interpolative: fix interp_decomp modifying input
- #10341: BUG: sparse.linalg/gmres: deprecate effect of callback on semantics…
- #10344: DOC: improve wording of mathematical formulation
- #10345: ENH: Tiled QR wrappers for scipy.linalg.lapack
- #10350: MAINT: linalg: Use the new fft subpackage in linalg.dft test…
- #10351: BUG: Fix unstable standard deviation calculation in histogram
- #10353: Bug: interpolate.NearestNDInterpolator (issue #10352)
- #10357: DOC: linalg: Refer to scipy.fft.fft (not fftpack) in the dft…
- #10359: DOC: Update roadmap now scipy.fft has been merged
- #10361: ENH: Prefer scipy.fft to scipy.fftpack in scipy.signal
- #10371: DOC: Tweaks to fft documentation
- #10372: DOC: Fix typos
- #10377: TST, MAINT: adjustments for pytest 5.0
- #10378: ENH: _lib: allow new np.random.Generator in check_random_state
- #10379: BUG: sparse: set writeability to be forward-compatible with numpy>=1.17
- #10381: BUG: Fixes gh-7491, pdf at x=0 of fisk/burr/burr12/f distributions.
- #10387: ENH: optimize/bfgs: don't evaluate twice at initial point for…
- #10392: [DOC] Add an example for _binned_statistic_dd
- #10396: Remove warning about output shape of zoom
- #10397: ENH: Add check_finite to sp.linalg.norm
- #10399: ENH: Add __round__ method to sparse matrix
- #10407: MAINT: drop pybind11 from install_requires, it's only build-time…
- #10408: TST: use pytest.raises, not numpy assert_raises
- #10409: CI: uninstall nose on Travis
- #10410: [ENH] ncx2 dispatch to chi2 when nc=0
- #10411: TST: optimize: test should use assert_allclose for fp comparisons
- #10414: DOC: add pybind11 to the other part of quickstart guides
- #10417: DOC: special: don't mark non-ufuncs with a `[+]`
- #10423: FIX: Use pybind11::isinstace to check array dtypes

- #10424: DOC: add doctest example for binary data for ttest_ind_from_stats
- #10425: ENH: Add missing Hermitian transforms to scipy.fft
- #10426: MAINT: Fix doc build bugs
- #10431: Update numpy version for AIX
- #10433: MAINT: Minor fixes for the stats
- #10434: BUG: special: make `ndtri` return NaN outside domain of definition
- #10435: BUG: Allow integer input data in scipy.stats.yeojohnson
- #10438: [DOC] Add example for kurtosis
- #10440: ENH: special: make `ellipk` a ufunc
- #10443: MAINT: ndimage: malloc fail check
- #10447: BLD: Divert output from test compiles into a temporary directory
- #10451: MAINT: signal: malloc fail check
- #10455: BUG: special: fix values of `hyperu` for negative `x`
- #10456: DOC: Added comment clarifying the call for dcsrch.f in lbfgsb.f
- #10457: BUG: Allow ckdtree to accept empty data input
- #10459: BUG:TST: Compute lwork safely
- #10460: [DOC] Add example to entropy
- #10461: DOC: Quickstart Guide updates
- #10462: TST: special: only show max atol/rtol for test points that failed
- #10465: BUG: Correctly align fft inputs
- #10467: ENH: lower-memory duplicate generator checking in spatial.SphericalVoronoi
- #10470: ENH: Normalise the inverse DCT/DST in scipy.fft
- #10472: BENCH: adjust timeout for slow setup_cache
- #10475: CI: include python debug for Travis-ci
- #10476: TST: special: use `__tracebackhide__` to get better error messages
- #10477: ENH: faster region building in spatial.SphericalVoronoi
- #10479: BUG: stats: Fix a few issues with the distributions' fit method.
- #10480: Add RuntimeError in _distn_infrastructure.py in fit() method
- #10481: BENCH, MAINT: wheel_cache_size has been renamed build_cache_size
- #10494: ENH: faster circumcenter calculation in spatial.SphericalVoronoi
- #10500: Splrep _curfit_cache global variable bugfix
- #10503: BUG: spatial/qhull: get HalfspaceIntersection.dual_points from…
- #10506: DOC: interp2d, note nearest neighbor extrapolation
- #10507: MAINT: Remove fortran fftpack library in favour of pypocketfft
- #10508: TST: fix a bug in the circular import test.
- #10509: MAINT: Set up _build_utils as subpackage

- #10516: BUG: Use nogil contexts in cKDTree
- #10517: ENH: fftconvolve should not FFT broadcastable axes
- #10518: ENH: Speedup fftconvolve
- #10520: DOC: Proper .rst formatting for deprecated features and Backwards…
- #10523: DOC: Improve scipy.signal.resample documentation
- #10524: ENH: Add MGC to scipy.stats
- #10525: [ENH] ncx2.ppf dispatch to chi2 when nc=0
- #10526: DOC: clarify laplacian normalization
- #10528: API: Rename scipy.fft DCT/DST shape argument to s
- #10531: BUG: fixed improper rotations in spatial.transform.rotation.match_vectors
- #10533: [DOC] Add example for winsorize function
- #10539: MAINT: special: don't register `i0` with `numpy.dual`
- #10540: MAINT: Fix Travis and Circle
- #10542: MAINT: interpolate: use cython_lapack
- #10547: Feature request. Add furthest site Voronoi diagrams to scipy.spatial.plotutils.
- #10549: [BUG] Fix bug in trimr when inclusive=False
- #10552: add scipy.signal.upfirdn signal extension modes
- #10555: MAINT: special: move `c_misc` into Cephes
- #10556: [DOC] Add example for trima
- #10562: [DOC] Fix triple string fo trimmed so that __doc__ can show…
- #10563: improve least_squares error msg for mismatched shape
- #10564: ENH: linalg: memoize get_lapack/blas_funcs to speed it up
- #10566: ENH: add implementation of solver for the maximum flow problem
- #10567: BUG: spatial: use c++11 construct for getting start of vector…
- #10568: DOC: special: small tweaks to the `zetac` docstring
- #10571: [ENH] Gaussian_kde can accept matrix dataset
- #10574: ENH: linalg: speed up _compute_lwork by avoiding numpy constructs
- #10582: Fix typos with typos in bundled libraries reverted
- #10583: ENH: special: add the analytic continuation of Riemann zeta
- #10584: MAINT: special: clean up `special.__all__`
- #10586: BUG: multidimensional scipy.fft functions should accept 's' rather…
- #10587: BUG: integrate/lsoda: never abort run, set error istate instead
- #10594: API: Replicate numpy's fftn behaviour when s is given but not…
- #10599: DOC: dev: update documentation vs. github pull request workflow…
- #10603: MAINT: installer scripts removed
- #10604: MAINT: Change c*np.ones(…) to np.full(…, c, …) in many…

- #10608: Univariate splines should require x to be strictly increasing…
- #10613: ENH: Add seed option for gaussian_kde.resample
- #10614: ENH: Add parallel computation to scipy.fft
- #10615: MAINT: interpolate: remove unused header file
- #10616: MAINT: Clean up 32-bit platform xfail markers
- #10618: BENCH: Added 'trust-constr' to minimize benchmarks
- #10621: [MRG] multiple stability updates in lobpcg
- #10622: MAINT: forward port 1.3.1 release notes
- #10624: DOC: stats: Fix spelling of 'support'.
- #10627: DOC: stats: Add references for the alpha distribution.
- #10629: MAINT: special: avoid overflow longer in `zeta` for negative…
- #10630: TST: GH10271, relax test assertion, fixes #10271
- #10631: DOC: nelder-mean uses xatol fixes #10036
- #10633: BUG: interpolate: integral(a, b) should be zero when both limits…
- #10635: DOC: special: complete hypergeometric functions documentation
- #10636: BUG: special: use series for `hyp1f1` when it converges rapidly
- #10641: ENH: allow matching of general bipartite graphs
- #10643: ENH: scipy.sparse.linalg.spsolve triangular unit diagonal
- #10650: ENH: Cythonize sosfilt
- #10654: DOC: Vertical alignment of table entries
- #10655: ENH: Dockerfile for scipy development
- #10660: TST: clean up tests for rvs in scipy.stats
- #10664: Throw error on non-finite input for binned_statistic_dd()
- #10665: DOC: special: improve the docstrings for `gamma` and `gammasgn`
- #10669: TST: Update scipy.fft real transform tests
- #10670: DOC: Clarify docs and error messages for scipy.signal.butter
- #10672: ENH: return solution attribute when using events in solve_ivp
- #10675: MAINT: special: add an explicit NaN check for `iv` arguments
- #10679: DOC: special: Add documentation for `beta` function
- #10681: TST: sparse.linalg: fix arnoldi test seed
- #10682: DOC: special: Add documentation for `betainc` function
- #10684: TST: special: require Mpmath 1.1.0 for `test_hyperu_around_0`
- #10686: FIX: sphinx isattributedescriptor is not available in sphinx…
- #10687: DOC: added Docker quickstart guide by @andyfaff
- #10689: DOC: special: clarify format of parameters/returns sections for…
- #10690: DOC: special: improve docstrings of incomplete gamma functions

- #10692: ENH: higher-dimensional input in `spatial.SphericalVoronoi`
- #10694: ENH: ScalarFunction.fun_and_grad
- #10698: DOC: special: Add documentation for `betaincinv`
- #10699: MAINT: remove time print lbfgsb fixes #8417
- #10701: TST, MAINT: bump OpenBLAS to 0.3.7 stable
- #10702: DOC: clarify iterations consume multiple function calls
- #10703: DOC: iprint doc lbfgsb closes #5482
- #10708: TST: test suggested in gh1758
- #10710: ENH: Added nan_policy to circ functions in `stats`
- #10712: ENH: add axis parameter to stats.entropy
- #10714: DOC: Formatting fix rv_continuous.expect docs
- #10715: DOC: BLD: update doc Makefile for python version; add scipy version…
- #10717: MAINT: modernize doc/Makefile
- #10719: Enable setting minres initial vector
- #10720: DOC: silence random warning in doc build for `stats.binned_statistic_dd`
- #10724: DEV: Add doc option to runtests.py
- #10728: MAINT: get rid of gramA, gramB text files that lobpcg tests leave…
- #10732: DOC: add min_only to docstring for Dijkstra's algorithm
- #10734: DOC: spell out difference between source and target in shortest…
- #10735: Fix for Python 4
- #10739: BUG: optimize/slsqp: deal with singular BFGS update
- #10741: ENH: LAPACK wrappers for ?geequ, ?geequb, ?syequb, ?heequb
- #10742: DOC: special: add to the docstring of `gammaln`
- #10743: ENH: special: add a real dispatch for `wrightomega`
- #10746: MAINT: Fix typos in comments, docs and test name
- #10747: Remove spurious quotes
- #10750: MAINT: make cython code more precise
- #10751: MAINT: Check that scipy.linalg.lapack functions are documented
- #10752: MAINT: special: use `sf_error` in Cephes
- #10755: DOC: cluster: Add 'See Also' and 'Examples' for kmeans2.
- #10763: MAINT: list of minimize methods
- #10768: BUG: Fix corner case for sos2zpk
- #10773: Fix error type for complex input to scipy.fftpack.rfft and irfft
- #10776: ENH: handle geodesic input in `spatial.SphericalVoronoi`
- #10777: MAINT: minimizer–>custom should handle the kinds of bounds/constrain……
- #10781: ENH: solve_triangular C order improvement

- #10787: Fix behavior of `exp1` on branch cut and add docstring
- #10789: DOC: special: add parameters/returns doc sections for erfc/erfcx/erfi
- #10790: Travis CI: sudo is deprecated and Xenial is default distro
- #10792: DOC: special: add full docstring for `expi`
- #10799: DOC: special: add a complete docstring for `expn`
- #10800: Docs edits (GSoD)
- #10802: BUG: fix UnboundLocalError in Radau (scipy#10775)
- #10804: ENH: Speed up next_fast_len with LRU cache
- #10805: DOC: Fix unbalanced quotes in signal.place_poles
- #10809: ENH: Speed up next_fast_len
- #10810: ENH: Raise catchable exceptions for bad Fortran files
- #10811: MAINT: optimize: Remove extra variable from _remove_redundancy_dense
- #10813: MAINT: special: Remove unused variables from _kolmogi and _smirnovi
- #10815: DOC, API: scipy.stats.reciprocal is “log-uniform”
- #10816: MAINT: special: remove deprecated `bessel_diff_formula`
- #10817: DOC: special: complete the docstring for `fresnel`
- #10820: Fixed compiler_helper.py to allow compilation with ICC on Linux
- #10823: DOC: updated reference guide text for consistency in writing…
- #10825: MAINT: special: change some features of the Voigt function
- #10828: MAINT: integrate: Remove unused variable from init_callback
- #10830: Adding LOBPCG solver in svds in addition to ARPACK
- #10837: WIP: ENH: reduction function for `spatial.tranform.Rotation`…
- #10843: ENH: Adding optional parameter to stats.zscores to allow for…
- #10845: Rebase kruskal fix
- #10847: remove redundant __getitem__ from scipy.sparse.lil
- #10848: Better handling of empty (not missing) docstrings
- #10849: ENH: implement rmatmat for LinearOperator
- #10850: MAINT : Refactoring lil List of Lists
- #10851: DOC: add a generative art example to the scipy.spatial tutorial.
- #10852: DOC: linalg: fixed gh-10838 unused imports in example deleted
- #10854: DOC: special: add a full docstring for `pdtr`
- #10861: ENH: option to reuse binnumbers in stats.binned_statistic_dd
- #10863: DOC: partial standardization and validation of scipy.stats reference…
- #10865: BUG: special: fix incomplete gamma functions for infinite `a`
- #10866: ENH: calculation of mean in spatial.transform.Rotation
- #10867: MAINT: Also store latex directory

- #10869: ENH: Implement overlap-add convolution
- #10870: ENH: Do not raise EOF error if wavfile data read
- #10876: ENH: Add beta-binomial distribution to scipy.stats
- #10878: MAINT: Update R project URL
- #10883: MAINT: (ndimage) More robust check for output being a numpy dtype
- #10884: DOC: Added instructions on adding a new distribution to scipy.stats.
- #10885: [BUG] fix lobpcg with maxiter=None results in Exception
- #10899: ENH: Match R functionality for hmean
- #10900: MAINT: stats: Use keepdims to simplify a few lines in power_divergence.
- #10901: ENH: sparse/linalg: support pydata/sparse matrices
- #10907: Check whether `maxiter` is integer
- #10912: ENH: warn user that quad() ignores `points=…` when `weight=…`…
- #10918: CI: fix Travis CI py3.8 build
- #10920: MAINT: Update constants to codata 2018 values (second try)
- #10921: ENH: scipy.sparse.lil: tocsr accelerated
- #10924: BUG: Forbid passing 'args' as kwarg in scipy.optimize.curve_fit
- #10928: DOC: Add examples to io.wavfile docstrings
- #10934: typo fix
- #10935: BUG: Avoid undefined behaviour on float to unsigned conversion
- #10936: DOC: Added missing example to stats.mstats.variation
- #10939: ENH: scipy.sparse.lil: tocsr accelerated depending on density
- #10946: BUG: setting verbose > 2 in minimize with trust-constr method…
- #10947: DOC: special: small improvements to the `poch` docstring
- #10949: BUG: fix return type of erlang_gen._argcheck
- #10951: DOC: fixed Ricker wavelet formula
- #10954: BUG: special: fix `factorial` return type for 0-d inputs
- #10955: MAINT: Relax the assert_unitary atol value
- #10956: WIP: make pdtr(int, double) be pdtr(double, double)
- #10957: BUG: Ensure full binary compatibility of long double test data
- #10964: ENH: Make Slerp callable with a scalar argument
- #10972: BUG: Handle complex gains in zpk2sos
- #10975: TST: skip test_kendalltau ppc64le
- #10978: BUG: boxcox data dimension and constancy check #5112
- #10979: API: Rename dcm to (rotation) matrix in Rotation class
- #10981: MAINT: add support for a==0 and x>0 edge case to igam and igamc
- #10986: MAINT: Remove direct imports from numpy in signaltools.py

- #10988: BUG: signal: fixed issue #10360
- #10989: FIX binned_statistic_dd Mac wheel test fails
- #10990: BUG: Fix memory leak in shgo triangulation
- #10992: TST: Relax tolerance in upfirdn test_modes
- #10993: TST: bump tolerance in optimize tests
- #10997: MAINT: Rework residue and residuez
- #11001: DOC: Updated Windows build tutorial
- #11004: BUG: integrate/quad_vec: fix several bugs in quad_vec
- #11005: TST: add Python 3.8 Win CI
- #11006: DOC: special: add a reference for `kl_div`
- #11012: MAINT: Rework invres and invresz
- #11015: DOC: special: add references for `rel_entr`
- #11017: DOC: numpydoc validation of morestats.py
- #11018: MAINT: Filter unrelated warning
- #11031: MAINT: update choose_conv_method for pocketfft implementation
- #11034: MAINT: TST: Skip tests with multiprocessing that use “spawn”…
- #11036: DOC: update doc/README with some more useful content.
- #11037: DOC: special: add a complete docstring for `rgamma`
- #11038: DOC: special: add a reference for the polygamma function
- #11042: TST: fix tf2zpk test failure due to incorrect complex sorting.
- #11044: MAINT: choose_conv_method can choose fftconvolution for longcomplex
- #11046: TST: Reduce tolerance for ppc64le with reference lapack
- #11048: DOC: special: add reference for orthogonal polynomial functions
- #11049: MAINT: proper random number initialization and readability fix
- #11051: MAINT: pep8 cleanup
- #11054: TST: bump test precision for dual_annealing SLSQP test
- #11055: DOC: special: add a reference for `zeta`
- #11056: API: Deprecated normalized keyword in Rotation
- #11065: DOC: Ubuntu Development Environment Quickstart should not modify…
- #11066: BUG: skip deprecation for numpy top-level types
- #11067: DOC: updated documentation for consistency in writing style
- #11070: DOC: Amendment to Ubuntu Development Environment Quickstart should…
- #11073: DOC: fix 1.4.0 release notes
- #11081: API: Replace Rotation.match_vectors with align_vectors
- #11083: DOC: more 1.4.0 release note fixes
- #11092: BUG: stats: fix freezing of some distributions

- #11096: BUG: scipy.sparse.csgraph: fixed issue #10774
- #11124: fix Cython warnings related to _stats.pyx
- #11126: BUG: interpolate/fitpack: fix memory leak in splprep
- #11127: Avoid potential segfault in CSR and CSC matrix indexing
- #11152: BUG: Fix random state bug multiscale_graphcorr
- #11166: BUG: empty sparse slice shapes
- #11167: BUG: redundant fft in signal.resample
- #11181: TST: Fix tolerance of tests for aarch64
- #11182: TST: Bump up tolerance for test_maxiter_worsening
- #11199: BUG: sparse.linalg: mistake in unsymm. real shift-invert ARPACK eigenvalue selection

5.13 SciPy 1.3.3 Release Notes

Contents

- *SciPy 1.3.3 Release Notes*
  - *Authors*
    - *Issues closed for 1.3.3*
    - *Pull requests for 1.3.3*

SciPy 1.3.3 is a bug-fix release with no new features compared to 1.3.2. In particular, a test suite issue involving multiprocessing was fixed for Windows and Python 3.8 on macOS.

Wheels were also updated to place msvcp140.dll at the appropriate location, which was previously causing issues.

5.13.1 Authors

Ilhan Polat Tyler Reddy Ralf Gommers

Issues closed for 1.3.3

- #11033: deadlock on osx for python 3.8

Pull requests for 1.3.3

- #11034: MAINT: TST: Skip tests with multiprocessing that use “spawn” start method

5.14 SciPy 1.3.2 Release Notes

Contents

- *SciPy 1.3.2 Release Notes*
  - *Authors*
    - *Issues closed for 1.3.2*
    - *Pull requests for 1.3.2*

SciPy 1.3.2 is a bug-fix and maintenance release that adds support for Python 3.8.

5.14.1 Authors

- CJ Carey
- Dany Vohl
- Martin Gauch +
- Ralf Gommers
- Matt Haberland
- Eric Larson
- Nikolay Mayorov
- Sam McCormack +
- Andrew Nelson
- Tyler Reddy
- Pauli Virtanen
- Huize Wang +
- Warren Weckesser
- Joseph Weston +

A total of 14 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.3.2

- #4915: Bug in unique_roots in scipy.signal.signaltools.py for roots…
- #5161: Optimizers reporting success when the minimum is NaN
- #5546: ValueError raised if scipy.sparse.linalg.expm recieves array…
- #10124: linprog(method='revised simplex') doctest bug
- #10609: Graph shortest path with Floyd-Warshall removes explicit zeros.
- #10658: BUG: stats: Formula for the variance of the noncentral F distribution…
- #10695: BUG: Assignation issues in csr_matrix with fancy indexing

- #10846: root_scalar fails when passed a function wrapped with functools.lru_cache
- #10902: CI: travis osx build failure
- #10967: macOS build failure in SuperLU on maintenance/1.3.x
- #10976: Typo in sp.stats.wilcoxon docstring

Pull requests for 1.3.2

- #10498: TST: optimize: fixed `linprog` `"disp": True` bug
- #10536: CI: add 3.8-dev to travis
- #10671: BUG: stats: Fix the formula for the variance of the noncentral…
- #10693: BUG: ScalarFunction stores original array
- #10700: BUG: sparse: Loosen checks on sparse fancy assignment
- #10709: BUG: Fix floyd_warshall to support zero-weight edges
- #10756: BUG: optimize: ensure solvers exit with success=False for nan…
- #10833: BUG: Fix subspace_angles for complex values
- #10882: BUG: sparse/arpack: fix incorrect code for complex hermitian…
- #10891: BUG: make C-implemented root finders work with functools.lru_cache
- #10906: BUG: sparse/linalg: fix expm for np.matrix inputs
- #10917: CI: fix travis osx CI
- #10930: MAINT: Updates for 3.8
- #10938: MAINT: Add Python 3.8 to pyproject.toml
- #10943: BLD: update Cython version to 0.29.13
- #10961: BUG: Fix signal.unique_roots
- #10971: MAINT: use 3.8 stable in CI
- #10977: DOC: Fix typo in sp.stats.wilcoxon docsting
- #11025: Update _peak_finding.py

5.15 SciPy 1.3.1 Release Notes

Contents

- *SciPy 1.3.1 Release Notes*
  - *Authors*
    - *Issues closed for 1.3.1*
    - *Pull requests for 1.3.1*

SciPy 1.3.1 is a bug-fix release with no new features compared to 1.3.0.

5.15.1 Authors

- Matt Haberland
- Geordie McBain
- Yu Feng
- Evgeni Burovski
- Sturla Molden
- Tapasweni Pathak
- Eric Larson
- Peter Bell
- Carlos Ramos Carreño +
- Ralf Gommers
- David Hagen
- Antony Lee
- Ayappan P
- Tyler Reddy
- Pauli Virtanen

A total of 15 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.3.1

- #5040: BUG: Empty data handling of (c)KDTrees
- #9901: lsoda fails to detect stiff problem when called from solve_ivp
- #10206: sparse matrices indexing with scipy 1.3
- #10232: Exception in loadarff with quoted nominal attributes in scipy…
- #10292: DOC/REL: Some sections of the release notes are not nested correctly.
- #10303: BUG: optimize: *linprog* failing TestLinprogSimplexBland::test_unbounded_below_no_presolve_corrected
- #10376: TST: Travis CI fails (with pytest 5.0 ?)
- #10384: CircleCI doc build failing on new warnings
- #10398: Scipy 1.3.0 build broken in AIX
- #10501: BUG: scipy.spatial.HalfspaceIntersection works incorrectly
- #10514: BUG: cKDTree GIL handling is incorrect
- #10535: TST: master branch CI failures
- #10572: BUG: ckdtree query_ball_point errors on discontiguous input
- #10597: BUG: No warning on PchipInterpolator changing from bernstein base to local power base

Pull requests for 1.3.1

- #10071: DOC: reconstruct SuperLU permutation matrices avoiding SparseEfficiencyWarning
- #10196: Fewer checks on xdata for curve_fit.
- #10207: BUG: Compressed matrix indexing should return a scalar
- #10233: Fix for ARFF reader regression (#10232)
- #10306: BUG: optimize: Fix for 10303
- #10309: BUG: Pass jac=None directly to lsoda
- #10377: TST, MAINT: adjustments for pytest 5.0
- #10379: BUG: sparse: set writeability to be forward-compatible with numpy>=1.17
- #10426: MAINT: Fix doc build bugs
- #10431: Update numpy version for AIX
- #10457: BUG: Allow ckdtree to accept empty data input
- #10503: BUG: spatial/qhull: get HalfspaceIntersection.dual_points from the correct array
- #10516: BUG: Use nogil contexts in cKDTree
- #10520: DOC: Proper .rst formatting for deprecated features and Backwards incompatible changes
- #10540: MAINT: Fix Travis and Circle
- #10573: BUG: Fix query_ball_point with discontiguous input
- #10600: BUG: interpolate: fix broken conversions between PPoly/BPoly objects

5.16 SciPy 1.3.0 Release Notes

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SciPy 1.3.0 is the culmination of 5 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been some API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning` s). Our development attention will now shift to bug-fix releases on the 1.3.x branch, and on adding new features on the master branch.

This release requires Python 3.5+ and NumPy 1.13.3 or greater.

For running on PyPy, PyPy3 6.0+ and NumPy 1.15.0 are required.

5.16.1 Highlights of this release

- Three new `stats` functions, a rewrite of `pearsonr`, and an exact computation of the Kolmogorov-Smirnov two-sample test.
- A new Cython API for bounded scalar-function root-finders in *`scipy.optimize`*.
- Substantial `CSR` and `CSC` sparse matrix indexing performance improvements.
- Added support for interpolation of rotations with continuous angular rate and acceleration in `RotationSpline`.

5.16.2 New features

`scipy.interpolate` improvements

A new class `CubicHermiteSpline` is introduced. It is a piecewise-cubic interpolator which matches observed values and first derivatives. Existing cubic interpolators `CubicSpline`, `PchipInterpolator` and `Akima1DInterpolator` were made subclasses of `CubicHermiteSpline`.

scipy.io improvements

For the Attribute-Relation File Format (ARFF) *scipy.io.arff.loadarff* now supports relational attributes.

scipy.io.mmread can now parse Matrix Market format files with empty lines.

scipy.linalg improvements

Added wrappers for `?syconv` routines, which convert a symmetric matrix given by a triangular matrix factorization into two matrices and vice versa.

scipy.linalg.clarkson_woodruff_transform now uses an algorithm that leverages sparsity. This may provide a 60-90 percent speedup for dense input matrices. Truly sparse input matrices should also benefit from the improved sketch algorithm, which now correctly runs in `O(nnz(A))` time.

Added new functions to calculate symmetric Fiedler matrices and Fiedler companion matrices, named *scipy.linalg.fiedler* and *scipy.linalg.fiedler_companion*, respectively. These may be used for root finding.

scipy.ndimage improvements

Gaussian filter performances may improve by an order of magnitude in some cases, thanks to the removal of a dependence on `np.polynomial`. This may impact *scipy.ndimage.gaussian_filter* for example.

scipy.optimize improvements

The *scipy.optimize.brute* minimizer obtained a new keyword `workers`, which can be used to parallelize computation.

A Cython API for bounded scalar-function root-finders in *scipy.optimize* is available in a new module *scipy.optimize.cython_optimize* via `cimport`. This API may be used with `nogil` and `prange` to loop over an array of function arguments to solve for an array of roots more quickly than with pure Python.

`'interior-point'` is now the default method for `linprog`, and `'interior-point'` now uses SuiteSparse for sparse problems when the required scikits (scikit-umfpack and scikit-sparse) are available. On benchmark problems (gh-10026), execution time reductions by factors of 2-3 were typical. Also, a new `method='revised simplex'` has been added. It is not as fast or robust as `method='interior-point'`, but it is a faster, more robust, and equally accurate substitute for the legacy `method='simplex'`.

`differential_evolution` can now use a `Bounds` class to specify the bounds for the optimizing argument of a function.

scipy.optimize.dual_annealing performance improvements related to vectorization of some internal code.

scipy.signal improvements

Two additional methods of discretization are now supported by *scipy.signal.cont2discrete*: `impulse` and `foh`.

scipy.signal.firls now uses faster solvers.

scipy.signal.detrend now has a lower physical memory footprint in some cases, which may be leveraged using the new `overwrite_data` keyword argument.

scipy.signal.firwin `pass_zero` argument now accepts new string arguments that allow specification of the desired filter type: `'bandpass'`, `'lowpass'`, `'highpass'`, and `'bandstop'`.

scipy.signal.sosfilt may have improved performance due to lower retention of the global interpreter lock (GIL) in the algorithm.

scipy.sparse improvements

A new keyword was added to `csgraph.dijsktra` that allows users to query the shortest path to ANY of the passed-in indices, as opposed to the shortest path to EVERY passed index.

scipy.sparse.linalg.lsmr performance has been improved by roughly 10 percent on large problems.

Improved performance and reduced physical memory footprint of the algorithm used by *scipy.sparse.linalg.lobpcg*.

`CSR` and `CSC` sparse matrix fancy indexing performance has been improved substantially.

scipy.spatial improvements

scipy.spatial.ConvexHull now has a `good` attribute that can be used alongsize the `QGn` Qhull options to determine which external facets of a convex hull are visible from an external query point.

scipy.spatial.cKDTree.query_ball_point has been modernized to use some newer Cython features, including GIL handling and exception translation. An issue with `return_sorted=True` and scalar queries was fixed, and a new mode named `return_length` was added. `return_length` only computes the length of the returned indices list instead of allocating the array every time.

`scipy.spatial.transform.RotationSpline` has been added to enable interpolation of rotations with continuous angular rates and acceleration.

scipy.stats improvements

Added a new function to compute the Epps-Singleton test statistic, *scipy.stats.epps_singleton_2samp*, which can be applied to continuous and discrete distributions.

New functions *scipy.stats.median_absolute_deviation* and *scipy.stats.gstd* (geometric standard deviation) were added. The *scipy.stats.combine_pvalues* method now supports `pearson`, `tippett` and `mudholkar_george` pvalue combination methods.

The *scipy.stats.ortho_group* and *scipy.stats.special_ortho_group* `rvs(dim)` functions' algorithms were updated from a `O(dim^4)` implementation to a `O(dim^3)` which gives large speed improvements for `dim>100`.

A rewrite of *scipy.stats.pearsonr* to use a more robust algorithm, provide meaningful exceptions and warnings on potentially pathological input, and fix at least five separate reported issues in the original implementation.

Improved the precision of `hypergeom.logcdf` and `hypergeom.logsf`.

Added exact computation for Kolmogorov-Smirnov (KS) two-sample test, replacing the previously approximate computation for the two-sided test *stats.ks_2samp*. Also added a one-sided, two-sample KS test, and a keyword `alternative` to *stats.ks_2samp*.

5.16.3 Backwards-incompatible changes

`scipy.interpolate` changes

Functions from `scipy.interpolate` (`spleval`, `spline`, `splmake`, and `spltopp`) and functions from `scipy.misc` (`bytescale`, `fromimage`, `imfilter`, `imread`, `imresize`, `imrotate`, `imsave`, `imshow`, `toimage`) have been removed. The former set has been deprecated since v0.19.0 and the latter has been deprecated since v1.0.0. Similarly, aliases from `scipy.misc` (`comb`, `factorial`, `factorial2`, `factorialk`, `logsumexp`, `pade`, `info`, `source`, `who`) which have been deprecated since v1.0.0 are removed. SciPy documentation for v1.1.0 can be used to track the new import locations for the relocated functions.

`scipy.linalg` changes

For `pinv`, `pinv2`, and `pinvh`, the default cutoff values are changed for consistency (see the docs for the actual values).

`scipy.optimize` changes

The default method for `linprog` is now `'interior-point'`. The method's robustness and speed come at a cost: solutions may not be accurate to machine precision or correspond with a vertex of the polytope defined by the constraints. To revert to the original simplex method, include the argument `method='simplex'`.

`scipy.stats` changes

Previously, `ks_2samp(data1, data2)` would run a two-sided test and return the approximated p-value. The new signature, `ks_2samp(data1, data2, alternative="two-sided", method="auto")`, still runs the two-sided test by default but returns the exact p-value for small samples and the approximated value for large samples. `method="asymp"` would be equivalent to the old version but `auto` is the better choice.

5.16.4 Other changes

Our tutorial has been expanded with a new section on global optimizers.

There has been a rework of the `stats.distributions` tutorials.

`scipy.optimize` now correctly sets the convergence flag of the result to `CONVERR`, a convergence error, for bounded scalar-function root-finders if the maximum iterations has been exceeded, `disp` is false, and `full_output` is true.

`scipy.optimize.curve_fit` no longer fails if `xdata` and `ydata` dtypes differ; they are both now automatically cast to `float64`.

`scipy.ndimage` functions including `binary_erosion`, `binary_closing`, and `binary_dilation` now require an integer value for the number of iterations, which alleviates a number of reported issues.

Fixed normal approximation in case `zero_method == "pratt"` in *`scipy.stats.wilcoxon`*.

Fixes for incorrect probabilities, broadcasting issues and thread-safety related to stats distributions setting member variables inside `_argcheck()`.

`scipy.optimize.newton` now correctly raises a `RuntimeError` in the following cases: when default arguments are used and if a derivative of value zero is obtained (which is a special case of failing to converge).

A draft toolchain roadmap is now available, laying out a compatibility plan including Python versions, C standards, and NumPy versions.

5.16.5 Authors

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- Gopi Manohar T +
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- Daniel Vargas +
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- VNMabus +
- Stefan van der Walt
- Warren Weckesser
- Josh Wilson
- Nate Yoder +
- Roman Yurchak

A total of 97 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.3.0

- #1320: scipy.stats.distribution: problem with self.a, self.b if they…
- #2002: members set in scipy.stats.distributions.##._argcheck (Trac #1477)
- #2823: distribution methods add tmp
- #3220: Scipy.opimize.fmin_powell direc argument syntax unclear
- #3728: scipy.stats.pearsonr: possible bug with zero variance input
- #6805: error-in-scipy-wilcoxon-signed-rank-test-for-equal-series

- #6873: 'stats.boxcox' return all same values
- #7117: Warn users when using float32 input data to curve_fit and friends
- #7632: it's not possible to tell the `optimize.least_squares` solver…
- #7730: stats.pearsonr: Potential division by zero for dataset of length…
- #7933: stats.truncnorm fails when providing values outside truncation…
- #8033: Add standard filter types to firwin to set pass_zero intuitively…
- #8600: lfilter.c.src zfill has erroneous header
- #8692: Non-negative values of `stats.hypergeom.logcdf`
- #8734: Enable pip build isolation
- #8861: scipy.linalg.pinv gives wrong result while scipy.linalg.pinv2…
- #8915: need to fix macOS build against older numpy versions
- #8980: scipy.stats.pearsonr overflows with high values of x and y
- #9226: BUG: signal: SystemError: <built-in function _linear_filter>…
- #9254: BUG: root finders brentq, etc, flag says "converged" even if…
- #9308: Test failure - test_initial_constraints_as_canonical
- #9353: scipy.stats.pearsonr returns r=1 if r_num/r_den = inf
- #9359: Planck distribution is a geometric distribution
- #9381: linregress should warn user in 2x2 array case
- #9406: BUG: stats: In pearsonr, when r is nan, the p-value must also…
- #9437: Cannot create sparse matrix from size_t indexes
- #9518: Relational attributes in loadarff
- #9551: BUG: scipy.optimize.newton says the root of x^2+1 is zero.
- #9564: rv_sample accepts invalid input in scipy.stats
- #9565: improper handling of multidimensional input in stats.rv_sample
- #9581: Least-squares minimization fails silently when x and y data are…
- #9587: Outdated value for scipy.constants.au
- #9611: Overflow error with new way of p-value calculation in kendall…
- #9645: `scipy.stats.mode` crashes with variable length arrays (`dtype=object`)
- #9734: PendingDeprecationWarning for np.matrix with pytest
- #9786: stats.ks_2samp() misleading for small data sets.
- #9790: Excessive memory usage on detrend
- #9801: dual_annealing does not set the success attribute in OptimizeResult
- #9833: IntegrationWarning from mielke.stats() during build of html doc.
- #9835: scipy.signal.firls seems to be inefficient versus MATLAB firls
- #9864: Curve_fit does not check for empty input data if called with…
- #9869: scipy.ndimage.label: Minor documentation issue

- #9882: format at the wrong paranthesis in scipy.spatial.transform
- #9889: scipy.signal.find_peaks minor documentation issue
- #9890: Minkowski p-norm Issues in cKDTree For Values Other Than 2 Or…
- #9896: scipy.stats._argcheck sets (not just checks) values
- #9905: Memory error in ndimage.binary_erosion
- #9909: binary_dilation/erosion/closing crashes when iterations is float
- #9919: BUG: `coo_matrix` does not validate the `shape` argument.
- #9982: lsq_linear hangs/infinite loop with 'trf' method
- #10003: exponnorm.pdf returns NAN for small K
- #10011: Incorrect check for invalid rotation plane in scipy.ndimage.rotate
- #10024: Fails to build from git
- #10048: DOC: scipy.optimize.root_scalar
- #10068: DOC: scipy.interpolate.splev
- #10074: BUG: `expm` calculates the wrong coefficients in the backward…

Pull requests for 1.3.0

- #7827: ENH: sparse: overhaul of sparse matrix indexing
- #8431: ENH: Cython optimize zeros api
- #8743: DOC: Updated linalg.pinv, .pinv2, .pinvh docstrings
- #8744: DOC: added examples to remez docstring
- #9227: DOC: update description of "direc" parameter of "fmin_powell"
- #9263: ENH: optimize: added "revised simplex" for scipy.optimize.linprog
- #9325: DEP: Remove deprecated functions for 1.3.0
- #9330: Add note on push and pull affine transformations
- #9423: DOC: Clearly state how 2x2 input arrays are handled in stats.linregress
- #9428: ENH: parallelised brute
- #9438: BUG: Initialize coo matrix with size_t indexes
- #9455: MAINT: Speed up get_(lapack,blas)_func
- #9465: MAINT: Clean up optimize.zeros C solvers interfaces/code.
- #9477: DOC: linalg: fix lstsq docstring on residues shape
- #9478: DOC: Add docstring examples for rosen functions
- #9479: DOC: Add docstring example for ai_zeros and bi_zeros
- #9480: MAINT: linalg: lstsq clean up
- #9489: DOC: roadmap update for changes over the last year.
- #9492: MAINT: stats: Improve implementation of chi2 ppf method.
- #9497: DOC: Improve docstrings sparse.linalg.isolve

- #9499: DOC: Replace “Scipy” with “SciPy” in the .rst doc files for consistency.
- #9500: DOC: Document the toolchain and its roadmap.
- #9505: DOC: specify which definition of skewness is used
- #9511: DEP: interpolate: remove deprecated interpolate_wrapper
- #9517: BUG: improve error handling in stats.iqr
- #9522: ENH: Add Fiedler and fiedler companion to special matrices
- #9526: TST: relax precision requirements in signal.correlate tests
- #9529: DOC: fix missing random seed in optimize.newton example
- #9533: MAINT: Use list comprehension when possible
- #9537: DOC: add a “big picture” roadmap
- #9538: DOC: Replace “Numpy” with “NumPy” in .py, .rst and .txt doc files…
- #9539: ENH: add two-sample test (Epps-Singleton) to scipy.stats
- #9559: DOC: add section on global optimizers to tutorial
- #9561: ENH: remove noprefix.h, change code appropriately
- #9562: MAINT: stats: Rewrite pearsonr.
- #9563: BUG: Minor bug fix Callback in linprog(method='simplex')
- #9568: MAINT: raise runtime error for newton with zeroder if disp true,…
- #9570: Correct docstring in show_options in optimize. Fixes #9407
- #9573: BUG fixes range of pk variable pre-check
- #9577: TST: fix minor issue in a signal.stft test.
- #9580: Included blank line before list - Fixes #8658
- #9582: MAINT: drop Python 2.7 and 3.4
- #9588: MAINT: update `constants.astronomical_unit` to new 2012 value.
- #9592: TST: Add 32-bit testing to CI
- #9593: DOC: Replace cumulative density with cumulative distribution
- #9596: TST: remove VC 9.0 from Azure CI
- #9599: Hyperlink DOI to preferred resolver
- #9601: DEV: try to limit GC memory use on PyPy
- #9603: MAINT: improve logcdf and logsf of hypergeometric distribution
- #9605: Reference to pylops in LinearOperator notes and ARPACK example
- #9617: TST: reduce max memory usage for sparse.linalg.lgmres test
- #9619: FIX: Sparse matrix addition/subtraction eliminates explicit zeros
- #9621: bugfix in rv_sample in scipy.stats
- #9622: MAINT: Raise error in directed_hausdorff distance
- #9623: DOC: Build docs with warnings as errors
- #9625: Return the number of calls to 'hessp' (not just 'hess') in trust…

- #9627: BUG: ignore empty lines in mmio
- #9637: Function to calculate the MAD of an array
- #9646: BUG: stats: mode for objects w/ndim > 1
- #9648: Add `stats.contingency` to refguide-check
- #9650: ENH: many lobpcg() algorithm improvements
- #9652: Move misc.doccer to _lib.doccer
- #9660: ENH: add pearson, tippett, and mudholkar-george to combine_pvalues
- #9661: BUG: Fix ksone right-hand endpoint, documentation and tests.
- #9664: ENH: adding multi-target dijsktra performance enhancement
- #9670: MAINT: link planck and geometric distribution in scipy.stats
- #9676: ENH: optimize: change default linprog method to interior-point
- #9685: Added reference to ndimage.filters.median_filter
- #9705: Fix coefficients in expm helper function
- #9711: Release the GIL during sosfilt processing for simple types
- #9721: ENH: Convexhull visiblefacets
- #9723: BLD: Modify rv_generic._construct_doc to print out failing distribution…
- #9726: BUG: Fix small issues with `signal.lfilter'
- #9729: BUG: Typecheck iterations for binary image operations
- #9730: ENH: reduce sizeof(NI_WatershedElement) by 20%
- #9731: ENH: remove suspicious sequence of type castings
- #9739: BUG: qr_updates fails if u is exactly in span Q
- #9749: BUG: MapWrapper.__exit__ should terminate
- #9753: ENH: Added exact computation for Kolmogorov-Smirnov two-sample…
- #9755: DOC: Added example for signal.impulse, copied from impulse2
- #9756: DOC: Added docstring example for iirdesign
- #9757: DOC: Added examples for step functions
- #9759: ENH: Allow pass_zero to act like btype
- #9760: DOC: Added docstring for lp2bs
- #9761: DOC: Added docstring and example for lp2bp
- #9764: BUG: Catch internal warnings for matrix
- #9766: ENH: Speed up _gaussian_kernel1d by removing dependence on np.polynomial
- #9769: BUG: Fix Cubic Spline Read Only issues
- #9773: DOC: Several docstrings
- #9774: TST: bump Azure CI OpenBLAS version to match wheels
- #9775: DOC: Improve clarity of cov_x documentation for scipy.optimize.leastsq
- #9779: ENH: dual_annealing vectorise visit_fn

- #9788: TST, BUG: f2py-related issues with NumPy < 1.14.0
- #9791: BUG: fix amax constraint not enforced in scalar_search_wolfe2
- #9792: ENH: Allow inplace copying in place in "detrend" function
- #9795: DOC: Fix/update docstring for dstn and dst
- #9796: MAINT: Allow None tolerances in least_squares
- #9798: BUG: fixes abort trap 6 error in scipy issue 9785 in unit tests
- #9807: MAINT: improve doc and add alternative keyword to wilcoxon in…
- #9808: Fix PPoly integrate and test for CubicSpline
- #9810: ENH: Add the geometric standard deviation function
- #9811: MAINT: remove invalid derphi default None value in scalar_search_wolfe2
- #9813: Adapt hamming distance in C to support weights
- #9817: DOC: Copy solver description to solver modules
- #9829: ENH: Add FOH and equivalent impulse response discretizations…
- #9831: ENH: Implement RotationSpline
- #9834: DOC: Change mielke distribution default parameters to ensure…
- #9838: ENH: Use faster solvers for firls
- #9854: ENH: loadarff now supports relational attributes.
- #9856: integrate.bvp - improve handling of nonlinear boundary conditions
- #9862: TST: reduce Appveyor CI load
- #9874: DOC: Update requirements in release notes
- #9883: BUG: fixed parenthesis in spatial.rotation
- #9884: ENH: Use Sparsity in Clarkson-Woodruff Sketch
- #9888: MAINT: Replace NumPy aliased functions
- #9892: BUG: Fix 9890 query_ball_point returns wrong result when p is…
- #9893: BUG: curve_fit doesn't check for empty input if called with bounds
- #9894: scipy.signal.find_peaks documentation error
- #9898: BUG: Set success attribute in OptimizeResult. See #9801
- #9900: BUG: Restrict rv_generic._argcheck() and its overrides from setting…
- #9906: fixed a bug in kde logpdf
- #9911: DOC: replace example for "np.select" with the one from numpy…
- #9912: BF(DOC): point to numpy.select instead of plain (python) .select
- #9914: DOC: change ValueError message in _validate_pad of signaltools.
- #9915: cKDTree query_ball_point improvements
- #9918: Update ckdtree.pyx with boxsize argument in docstring
- #9920: BUG: sparse: Validate explicit shape if given with dense argument…
- #9924: BLD: add back pyproject.toml

- #9931: Fix empty constraint
- #9935: DOC: fix references for stats.f_oneway
- #9936: Revert gh-9619: “FIX: Sparse matrix addition/subtraction eliminates…
- #9937: MAINT: fix PEP8 issues and update to pycodestyle 2.5.0
- #9939: DOC: correct `structure` description in `ndimage.label` docstring
- #9940: MAINT: remove extraneous distutils copies
- #9945: ENH: differential_evolution can use Bounds object
- #9949: Added ‘std’ to add doctstrings since it is a `known_stats`…
- #9953: DOC: Documentation cleanup for stats tutorials.
- #9962: __repr__ for Bounds
- #9971: ENH: Improve performance of lsmr
- #9987: CI: pin Sphinx version to 1.8.5
- #9990: ENH: constraint violation
- #9991: BUG: Avoid inplace modification of input array in newton
- #9995: MAINT: sparse.csgraph: Add cdef to stop build warning.
- #9996: BUG: Make minimize_quadratic_1d work with infinite bounds correctly
- #10004: BUG: Fix unbound local error in linprog - simplex.
- #10007: BLD: fix Python 3.7 build with build isolation
- #10009: BUG: Make sure that _binary_erosion only accepts an integer number…
- #10016: Update link to airspeed-velocity
- #10017: DOC: Update `interpolate.LSQSphereBivariateSpline` to include…
- #10018: MAINT: special: Fix a few warnings that occur when compiling…
- #10019: TST: Azure summarizes test failures
- #10021: ENH: Introduce CubicHermiteSpline
- #10022: BENCH: Increase cython version in asv to fix benchmark builds
- #10023: BUG: Avoid exponnorm producing nan for small K values.
- #10025: BUG: optimize: tweaked linprog status 4 error message
- #10026: ENH: optimize: use SuiteSparse in linprog interior-point when…
- #10027: MAINT: cluster: clean up the use of malloc() in the function…
- #10028: Fix rotate invalid plane check
- #10040: MAINT: fix pratt method of wilcox test in scipy.stats
- #10041: MAINT: special: Fix a warning generated when building the AMOS…
- #10044: DOC: fix up spatial.transform.Rotation docstrings
- #10047: MAINT: interpolate: Fix a few build warnings.
- #10051: Add project_urls to setup
- #10052: don’t set flag to “converged” if max iter exceeded

- #10054: MAINT: signal: Fix a few build warnings and modernize some C…
- #10056: BUG: Ensure factorial is not too large in kendaltau
- #10058: Small speedup in samping from ortho and special_ortho groups
- #10059: BUG: optimize: fix #10038 by increasing tol
- #10061: BLD: DOC: make building docs easier by parsing python version.
- #10064: ENH: Significant speedup for ortho and special ortho group
- #10065: DOC: Reword parameter descriptions in `optimize.root_scalar`
- #10066: BUG: signal: Fix error raised by savgol_coeffs when deriv > polyorder.
- #10067: MAINT: Fix the cutoff value inconsistency for pinv2 and pinvh
- #10072: BUG: stats: Fix boxcox_llf to avoid loss of precision.
- #10075: ENH: Add wrappers for ?syconv routines
- #10076: BUG: optimize: fix curve_fit for mixed float32/float64 input
- #10077: DOC: Replace undefined `k` in `interpolate.splev` docstring
- #10079: DOC: Fixed typo, rearranged some doc of stats.morestats.wilcoxon.
- #10080: TST: install scikit-sparse for full TravisCI tests
- #10083: Clean ``_clean_inputs`` in optimize.linprog
- #10088: ENH: optimize: linprog test CHOLMOD/UMFPACK solvers when available
- #10090: MAINT: Fix CubicSplinerInterpolator for pandas
- #10091: MAINT: improve logcdf and logsf of hypergeometric distribution
- #10095: MAINT: Clean ``_clean_inputs`` in linprog
- #10116: MAINT: update scipy-sphinx-theme
- #10135: BUG: fix linprog revised simplex docstring problem failure

5.17 SciPy 1.2.3 Release Notes

Contents

- *SciPy 1.2.3 Release Notes*
  - *Authors*
    - *Issues closed for 1.2.3*
    - *Pull requests for 1.2.3*

SciPy 1.2.3 is a bug-fix release with no new features compared to 1.2.2. It is part of the long-term support (LTS) release series for Python 2.7.

5.17.1 Authors

- Geordie McBain
- Matt Haberland
- David Hagen
- Tyler Reddy
- Pauli Virtanen
- Eric Larson
- Yu Feng
- ananyashreyjain
- Nikolay Mayorov
- Evgeni Burovski
- Warren Weckesser

Issues closed for 1.2.3

- #4915: Bug in unique_roots in scipy.signal.signaltools.py for roots with same magnitude
- #5546: ValueError raised if scipy.sparse.linalg.expm recieves array larger than 200x200
- #7117: Warn users when using float32 input data to curve_fit and friends
- #7906: Wrong result from scipy.interpolate.UnivariateSpline.integral for out-of-bounds
- #9581: Least-squares minimization fails silently when x and y data are different types
- #9901: lsoda fails to detect stiff problem when called from solve_ivp
- #9988: doc build broken with Sphinx 2.0.0
- #10303: BUG: optimize: *linprog* failing TestLinprogSimplexBland::test_unbounded_below_no_presolve_corrected
- #10376: TST: Travis CI fails (with pytest 5.0 ?)
- #10384: CircleCI doc build failing on new warnings
- #10535: TST: master branch CI failures
- #11121: Calls to `scipy.interpolate.splprep` increase RAM usage.
- #11198: BUG: sparse eigs (arpack) shift-invert drops the smallest eigenvalue for some k
- #11266: Sparse matrix constructor data type detection changes on Numpy 1.18.0

Pull requests for 1.2.3

- #9992: MAINT: Undo Sphinx pin
- #10071: DOC: reconstruct SuperLU permutation matrices avoiding SparseEfficiencyWarning
- #10076: BUG: optimize: fix curve_fit for mixed float32/float64 input
- #10138: BUG: special: Invalid arguments to ellip_harm can crash Python.
- #10306: BUG: optimize: Fix for 10303
- #10309: BUG: Pass jac=None directly to lsoda
- #10377: TST, MAINT: adjustments for pytest 5.0
- #10379: BUG: sparse: set writeability to be forward-compatible with numpy>=1.17
- #10426: MAINT: Fix doc build bugs
- #10540: MAINT: Fix Travis and Circle
- #10633: BUG: interpolate: integral(a, b) should be zero when both limits are outside of the interpolation range
- #10833: BUG: Fix subspace_angles for complex values
- #10882: BUG: sparse/arpack: fix incorrect code for complex hermitian M
- #10906: BUG: sparse/linalg: fix expm for np.matrix inputs
- #10961: BUG: Fix signal.unique_roots
- #11126: BUG: interpolate/fitpack: fix memory leak in splprep
- #11199: BUG: sparse.linalg: mistake in unsymm. real shift-invert ARPACK eigenvalue selection
- #11269: Fix: Sparse matrix constructor data type detection changes on Numpy 1.18.0

5.18 SciPy 1.2.2 Release Notes

Contents

- *SciPy 1.2.2 Release Notes*
  - *Authors*
    - *Issues closed for 1.2.2*
    - *Pull requests for 1.2.2*

SciPy 1.2.2 is a bug-fix release with no new features compared to 1.2.1. Importantly, the SciPy 1.2.2 wheels are built with OpenBLAS 0.3.7.dev to alleviate issues with SkylakeX AVX512 kernels.

5.18.1 Authors

- CJ Carey
- Tyler Dawson +
- Ralf Gommers
- Kai Striega
- Andrew Nelson
- Tyler Reddy
- Kevin Sheppard +

A total of 7 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.2.2

- #9611: Overflow error with new way of p-value calculation in kendall tau correlation for perfectly monotonic vectors
- #9964: optimize.newton : overwrites x0 argument when it is a numpy array
- #9784: TST: Minimum NumPy version is not being CI tested
- #10132: Docs: Description of nnz attribute of sparse.csc_matrix misleading

Pull requests for 1.2.2

- #10056: BUG: Ensure factorial is not too large in kendaltau
- #9991: BUG: Avoid inplace modification of input array in newton
- #9788: TST, BUG: f2py-related issues with NumPy < 1.14.0
- #9749: BUG: MapWrapper.__exit__ should terminate
- #10141: Update description for nnz on csc.py

5.19 SciPy 1.2.1 Release Notes

Contents

- *SciPy 1.2.1 Release Notes*
  - *Authors*
    - *Issues closed for 1.2.1*
    - *Pull requests for 1.2.1*

SciPy 1.2.1 is a bug-fix release with no new features compared to 1.2.0. Most importantly, it solves the issue that 1.2.0 cannot be installed from source on Python 2.7 because of non-ascii character issues.

It is also notable that SciPy 1.2.1 wheels were built with OpenBLAS 0.3.5.dev, which may alleviate some linear algebra issues observed in SciPy 1.2.0.

5.19.1 Authors

- Eric Larson
- Mark Mikofski
- Evgeni Burovski
- Ralf Gommers
- Eric Moore
- Tyler Reddy

Issues closed for 1.2.1

- #9606: SyntaxError: Non-ASCII character 'xe2' in file scipy/stats/_continuous_distns.py on line 3346, but no encoding declared
- #9608: Version 1.2.0 introduces *too many indices for array* error in…
- #9709: scipy.stats.gaussian_kde normalizes the weights keyword argument…
- #9733: scipy.linalg.qr_update gives NaN result
- #9724: CI: Is scipy.scipy Windows Python36-32bit-full working?

Pull requests for 1.2.1

- #9612: BUG: don't use array newton unless size is greater than 1
- #9615: ENH: Add test for encoding
- #9720: BUG: stats: weighted KDE does not modify the weights array
- #9739: BUG: qr_updates fails if u is exactly in span Q
- #9725: TST: pin mingw for Azure Win CI
- #9736: TST: adjust to vmImage dispatch in Azure
- #9681: BUG: Fix failing stats tests (partial backport)
- #9662: TST: interpolate: avoid pytest deprecations

5.20 SciPy 1.2.0 Release Notes

Contents

- *SciPy 1.2.0 Release Notes*
  - *Highlights of this release*
  - *New features*

        * scipy.ndimage *improvements*
        * scipy.fftpack *improvements*
        * scipy.interpolate *improvements*
        * scipy.cluster *improvements*
        * scipy.special *improvements*
        * scipy.optimize *improvements*
        * scipy.signal *improvements*
        * scipy.sparse *improvements*
        * scipy.spatial *improvements*
        * scipy.stats *improvements*
        * scipy.linalg *improvements*
    - *Deprecated features*
    - *Backwards-incompatible changes*
    - *Authors*
        * *Issues closed for 1.2.0*
        * *Pull requests for 1.2.0*

SciPy 1.2.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning`s). Our development attention will now shift to bug-fix releases on the 1.2.x branch, and on adding new features on the master branch.

This release requires Python 2.7 or 3.4+ and NumPy 1.8.2 or greater.

Note: This will be the last SciPy release to support Python 2.7. Consequently, the 1.2.x series will be a long term support (LTS) release; we will backport bug-fixes until 1 Jan 2020.

For running on PyPy, PyPy3 6.0+ and NumPy 1.15.0 are required.

5.20.1 Highlights of this release

- 1-D root finding improvements with a new solver, `toms748`, and a new unified interface, `root_scalar`
- new `dual_annealing` optimization method that combines stochastic and local deterministic searching
- a new optimization algorithm, `shgo` (simplicial homology global optimization), for derivative-free optimization problems
- a new category of quaternion-based transformations are available in `scipy.spatial.transform`

5.20.2 New features

`scipy.ndimage` improvements

Proper spline coefficient calculations have been added for the `mirror`, `wrap`, and `reflect` modes of *scipy.ndimage.rotate*.

`scipy.fftpack` improvements

DCT-IV, DST-IV, DCT-I, and DST-I orthonormalization are now supported in *scipy.fftpack*.

`scipy.interpolate` improvements

scipy.interpolate.pade now accepts a new argument for the order of the numerator.

`scipy.cluster` improvements

scipy.cluster.vq.kmeans2 gained a new initialization method, kmeans++.

`scipy.special` improvements

The function `softmax` was added to *scipy.special*.

`scipy.optimize` improvements

The one-dimensional nonlinear solvers have been given a unified interface *scipy.optimize.root_scalar*, similar to the *scipy.optimize.root* interface for multi-dimensional solvers. `scipy.optimize.root_scalar(f, bracket=[a ,b], method="brenth")` is equivalent to `scipy.optimize.brenth(f, a ,b)`. If no `method` is specified, an appropriate one will be selected based upon the bracket and the number of derivatives available.

The so-called Algorithm 748 of Alefeld, Potra and Shi for root-finding within an enclosing interval has been added as *scipy.optimize.toms748*. This provides guaranteed convergence to a root with convergence rate per function evaluation of approximately 1.65 (for sufficiently well-behaved functions).

`differential_evolution` now has the `updating` and `workers` keywords. The first chooses between continuous updating of the best solution vector (the default), or once per generation. Continuous updating can lead to faster convergence. The `workers` keyword accepts an `int` or map-like callable, and parallelises the solver (having the side effect of updating once per generation). Supplying an `int` evaluates the trial solutions in N parallel parts. Supplying a map-like callable allows other parallelisation approaches (such as `mpi4py`, or `joblib`) to be used.

`dual_annealing` (and `shgo` below) is a powerful new general-purpose global optimization (GO) algorithm. `dual_annealing` uses two annealing processes to accelerate the convergence towards the global minimum of an objective mathematical function. The first annealing process controls the stochastic Markov chain searching and the second annealing process controls the deterministic minimization. So, dual annealing is a hybrid method that takes advantage of stochastic and local deterministic searching in an efficient way.

`shgo` (simplicial homology global optimization) is a similar algorithm appropriate for solving black box and derivative-free optimization (DFO) problems. The algorithm generally converges to the global solution in finite time. The convergence holds for non-linear inequality and equality constraints. In addition to returning a global minimum, the algorithm also returns any other global and local minima found after every iteration. This makes it useful for exploring the solutions in a domain.

scipy.optimize.newton can now accept a scalar or an array.

MINPACK usage is now thread-safe, such that MINPACK + callbacks may be used on multiple threads.

scipy.signal improvements

Digital filter design functions now include a parameter to specify the sampling rate. Previously, digital filters could only be specified using normalized frequency, but different functions used different scales (e.g. 0 to 1 for butter vs 0 to π for freqz), leading to errors and confusion. With the fs parameter, ordinary frequencies can now be entered directly into functions, with the normalization handled internally.

find_peaks and related functions no longer raise an exception if the properties of a peak have unexpected values (e.g. a prominence of 0). A PeakPropertyWarning is given instead.

The new keyword argument plateau_size was added to find_peaks. plateau_size may be used to select peaks based on the length of the flat top of a peak.

welch() and csd() methods in *scipy.signal* now support calculation of a median average PSD, using average='mean' keyword.

scipy.sparse improvements

The *scipy.sparse.bsr_matrix.tocsr* method is now implemented directly instead of converting via COO format, and the *scipy.sparse.bsr_matrix.tocsc* method is now also routed via CSR conversion instead of COO. The efficiency of both conversions is now improved.

The issue where SuperLU or UMFPACK solvers crashed on matrices with non-canonical format in *scipy.sparse.linalg* was fixed. The solver wrapper canonicalizes the matrix if necessary before calling the SuperLU or UMFPACK solver.

The largest option of *scipy.sparse.linalg.lobpcg()* was fixed to have a correct (and expected) behavior. The order of the eigenvalues was made consistent with the ARPACK solver (eigs()), i.e. ascending for the smallest eigenvalues, and descending for the largest eigenvalues.

The *scipy.sparse.random* function is now faster and also supports integer and complex values by passing the appropriate value to the dtype argument.

scipy.spatial improvements

The function *scipy.spatial.distance.jaccard* was modified to return 0 instead of np.nan when two all-zero vectors are compared.

Support for the Jensen Shannon distance, the square-root of the divergence, has been added under *scipy.spatial.distance.jensenshannon*.

An optional keyword was added to the function *scipy.spatial.cKDTree.query_ball_point()* to sort or not sort the returned indices. Not sorting the indices can speed up calls.

A new category of quaternion-based transformations are available in scipy.spatial.transform, including spherical linear interpolation of rotations (Slerp), conversions to and from quaternions, Euler angles, and general rotation and inversion capabilities (*spatial.transform.Rotation*), and uniform random sampling of 3D rotations (*spatial.transform.Rotation.random*).

scipy.stats improvements

The Yeo-Johnson power transformation is now supported (`yeojohnson`, `yeojohnson_llf`, `yeojohnson_normmax`, `yeojohnson_normplot`). Unlike the Box-Cox transformation, the Yeo-Johnson transformation can accept negative values.

Added a general method to sample random variates based on the density only, in the new function `rvs_ratio_uniforms`.

The Yule-Simon distribution (`yulesimon`) was added – this is a new discrete probability distribution.

`stats` and `mstats` now have access to a new regression method, `siegelslopes`, a robust linear regression algorithm

`scipy.stats.gaussian_kde` now has the ability to deal with weighted samples, and should have a modest improvement in performance

Levy Stable Parameter Estimation, PDF, and CDF calculations are now supported for *`scipy.stats.levy_stable`*.

The Brunner-Munzel test is now available as `brunnermunzel` in `stats` and `mstats`.

scipy.linalg improvements

`scipy.linalg.lapack` now exposes the LAPACK routines using the Rectangular Full Packed storage (RFP) for upper triangular, lower triangular, symmetric, or Hermitian matrices; the upper trapezoidal fat matrix RZ decomposition routines are now available as well.

5.20.3 Deprecated features

The functions `hyp2f0`, `hyp1f2` and `hyp3f0` in `scipy.special` have been deprecated.

5.20.4 Backwards-incompatible changes

LAPACK version 3.4.0 or later is now required. Building with Apple Accelerate is no longer supported.

The function `scipy.linalg.subspace_angles(A, B)` now gives correct results for all angles. Before this, the function only returned correct values for those angles which were greater than $\pi/4$.

Support for the Bento build system has been removed. Bento had not been maintained for several years, and did not have good Python 3 or wheel support, hence it was time to remove it.

The required signature of *scipy.optimize.lingprog* `method=simplex` callback function has changed. Before iteration begins, the simplex solver first converts the problem into a standard form that does not, in general, have the same variables or constraints as the problem defined by the user. Previously, the simplex solver would pass a user-specified callback function several separate arguments, such as the current solution vector `xk`, corresponding to this standard-form problem. Unfortunately, the relationship between the standard-form problem and the user-defined problem was not documented, limiting the utility of the information passed to the callback function.

In addition to numerous bug-fix changes, the simplex solver now passes a user-specified callback function a single `OptimizeResult` object containing information that corresponds directly to the user-defined problem. In future releases, this `OptimizeResult` object may be expanded to include additional information, such as variables corresponding to the standard-form problem and information concerning the relationship between the standard-form and user-defined problems.

The implementation of *`scipy.sparse.random`* has changed, and this affects the numerical values returned for both `sparse.random` and `sparse.rand` for some matrix shapes and a given seed.

`scipy.optimize.newton` will no longer use Halley's method in cases where it negatively impacts convergence.

5.20.5 Authors

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- Roman Yurchak +
- Roy Zywina +

A total of 137 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.2.0

- #9520: signal.correlate with method='fft' doesn't benefit from long…
- #9547: signature of dual_annealing doesn't match other optimizers
- #9540: SciPy v1.2.0rc1 cannot be imported on Python 2.7.15
- #1240: Allowing multithreaded use of minpack through scipy.optimize…
- #1432: scipy.stats.mode extremely slow (Trac #905)
- #3372: Please add Sphinx search field to online scipy html docs
- #3678: _clough_tocher_2d_single direction between centroids
- #4174: lobpcg "largest" option invalid?
- #5493: anderson_ksamp p-values>1
- #5743: slsqp fails to detect infeasible problem
- #6139: scipy.optimize.linprog failed to find a feasible starting point…
- #6358: stats: docstring for *vonmises_line* points to *vonmises_line*…
- #6498: runtests.py is missing in pypi distfile
- #7426: scipy.stats.ksone(n).pdf(x) returns nan for positive values of…
- #7455: scipy.stats.ksone.pdf(2,x) return incorrect values for x near…
- #7456: scipy.special.smirnov and scipy.special.smirnovi have accuracy…
- #7492: scipy.special.kolmogorov(x)/kolmogi(p) inefficient, inaccurate…
- #7914: TravisCI not failing when it should for -OO run
- #8064: linalg.solve test crashes on Windows
- #8212: LAPACK Rectangular Full Packed routines
- #8256: differential_evolution bug converges to wrong results in complex…
- #8443: Deprecate *hyp2f0*, *hyp1f2*, and *hyp3f0*?
- #8452: DOC: ARPACK tutorial has two conflicting equations
- #8680: scipy fails compilation when building from source
- #8686: Division by zero in _trustregion.py when x0 is exactly equal…
- #8700: _MINPACK_LOCK not held when calling into minpack from least_squares
- #8786: erroneous moment values for t-distribution
- #8791: Checking COLA condition in istft should be optional (or omitted)
- #8843: imresize cannot be deprecated just yet
- #8844: Inverse Wishart Log PDF Incorrect for Non-diagonal Scale Matrix?
- #8878: vonmises and vonmises_line in stats: vonmises wrong and superfluous?
- #8895: v1.1.0 *ndi.rotate* documentation – reused parameters not filled…
- #8900: Missing complex conjugation in scipy.sparse.linalg.LinearOperator
- #8904: BUG: if zero derivative at root, then Newton fails with RuntimeWarning
- #8911: make_interp_spline bc_type incorrect input interpretation

- #8942: MAINT: Refactor *_linprog.py* and *_linprog_ip.py* to remove…
- #8947: np.int64 in scipy.fftpack.next_fast_len
- #9020: BUG: linalg.subspace_angles gives wrong results
- #9033: scipy.stats.normaltest sometimes gives incorrect returns b/c…
- #9036: Bizarre times for `scipy.sparse.rand` function with 'low' density…
- #9044: optimize.minimize(method=`trust-constr`) result dict does not…
- #9071: doc/linalg: add cho_solve_banded to see also of cholesky_banded
- #9082: eigenvalue sorting in scipy.sparse.linalg.eigsh
- #9086: signaltools.py:491: FutureWarning: Using a non-tuple sequence…
- #9091: test_spline_filter failure on 32-bit
- #9122: Typo on scipy minimization tutorial
- #9135: doc error at https://docs.scipy.org/doc/scipy/reference/tutorial/stats/discrete_poisson.html
- #9167: DOC: BUG: typo in ndimage LowLevelCallable tutorial example
- #9169: truncnorm does not work if b < a in scipy.stats
- #9250: scipy.special.tests.test_mpmath::TestSystematic::test_pcfw fails…
- #9259: rv.expect() == rv.mean() is false for rv.mean() == nan (and inf)
- #9286: DOC: Rosenbrock expression in optimize.minimize tutorial
- #9316: SLSQP fails in nested optimization
- #9337: scipy.signal.find_peaks key typo in documentation
- #9345: Example from documentation of scipy.sparse.linalg.eigs raises…
- #9383: Default value for "mode" in "ndimage.shift"
- #9419: dual_annealing off by one in the number of iterations
- #9442: Error in Defintion of Rosenbrock Function
- #9453: TST: test_eigs_consistency() doesn't have consistent results

Pull requests for 1.2.0

- #9526: TST: relax precision requirements in signal.correlate tests
- #9507: CI: MAINT: Skip a ckdtree test on pypy
- #9512: TST: test_random_sampling 32-bit handling
- #9494: TST: test_kolmogorov xfail 32-bit
- #9486: BUG: fix sparse random int handling
- #9550: BUG: scipy/_lib/_numpy_compat: get_randint
- #9549: MAINT: make dual_annealing signature match other optimizers
- #9541: BUG: fix SyntaxError due to non-ascii character on Python 2.7
- #7352: ENH: add Brunner Munzel test to scipy.stats.
- #7373: BUG: Jaccard distance for all-zero arrays would return np.nan

- #7374: ENH: Add PDF, CDF and parameter estimation for Stable Distributions
- #8098: ENH: Add shgo for global optimization of NLPs.
- #8203: ENH: adding simulated dual annealing to optimize
- #8259: Option to follow original Storn and Price algorithm and its parallelisation
- #8293: ENH add ratio-of-uniforms method for rv generation to scipy.stats
- #8294: BUG: Fix slowness in stats.mode
- #8295: ENH: add Jensen Shannon distance to `scipy.spatial.distance`
- #8357: ENH: vectorize scalar zero-search-functions
- #8397: Add *fs*= parameter to filter design functions
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- #8558: ENH: small speedup for stats.gaussian_kde
- #8560: BUG: fix p-value calc of anderson_ksamp in scipy.stats
- #8614: ENH: correct p-values for stats.kendalltau and stats.mstats.kendalltau
- #8670: ENH: Require Lapack 3.4.0
- #8683: Correcting kmeans documentation
- #8725: MAINT: Cleanup scipy.optimize.leastsq
- #8726: BUG: Fix _get_output in scipy.ndimage to support string
- #8733: MAINT: stats: A bit of clean up.
- #8737: BUG: Improve numerical precision/convergence failures of smirnov/kolmogorov
- #8738: MAINT: stats: A bit of clean up in test_distributions.py.
- #8740: BF/ENH: make minpack thread safe
- #8742: BUG: Fix division by zero in trust-region optimization methods
- #8746: MAINT: signal: Fix a docstring of a private function, and fix…
- #8750: DOC clarified description of norminvgauss in scipy.stats
- #8753: DOC: signal: Fix a plot title in the chirp docstring.
- #8755: DOC: MAINT: Fix link to the wheel documentation in developer…
- #8760: BUG: stats: boltzmann wasn't setting the upper bound.
- #8763: [DOC] Improved scipy.cluster.hierarchy documentation
- #8765: DOC: added example for scipy.stat.mstats.tmin
- #8788: DOC: fix definition of optional *disp* parameter
- #8802: MAINT: Suppress dd_real unused function compiler warnings.
- #8803: ENH: Add full_output support to optimize.newton()
- #8804: MAINT: stats cleanup
- #8808: DOC: add note about isinstance for frozen rvs
- #8812: Updated numpydoc submodule
- #8813: MAINT: stats: Fix multinomial docstrings, and do some clean up.

- #8816: BUG: fixed _stats of t-distribution in scipy.stats
- #8817: BUG: ndimage: Fix validation of the origin argument in correlate…
- #8822: BUG: integrate: Fix crash with repeated t values in odeint.
- #8832: Hyperlink DOIs against preferred resolver
- #8837: BUG: sparse: Ensure correct dtype for sparse comparison operations.
- #8839: DOC: stats: A few tweaks to the linregress docstring.
- #8846: BUG: stats: Fix logpdf method of invwishart.
- #8849: DOC: signal: Fixed mistake in the firwin docstring.
- #8854: DOC: fix type descriptors in ltisys documentation
- #8865: Fix tiny typo in docs for chi2 pdf
- #8870: Fixes related to invertibility of STFT
- #8872: ENH: special: Add the softmax function
- #8874: DOC correct gamma function in docstrings in scipy.stats
- #8876: ENH: Added TOMS Algorithm 748 as 1-d root finder; 17 test function…
- #8882: ENH: Only use Halley's adjustment to Newton if close enough.
- #8883: FIX: optimize: make jac and hess truly optional for 'trust-constr'
- #8885: TST: Do not error on warnings raised about non-tuple indexing.
- #8887: MAINT: filter out np.matrix PendingDeprecationWarning's in numpy…
- #8889: DOC: optimize: separate legacy interfaces from new ones
- #8890: ENH: Add optimize.root_scalar() as a universal dispatcher for…
- #8899: DCT-IV, DST-IV and DCT-I, DST-I orthonormalization support in…
- #8901: MAINT: Reorganize flapack.pyf.src file
- #8907: BUG: ENH: Check if guess for newton is already zero before checking…
- #8908: ENH: Make sorting optional for cKDTree.query_ball_point()
- #8910: DOC: sparse.csgraph simple examples.
- #8914: DOC: interpolate: fix equivalences of string aliases
- #8918: add float_control(precise, on) to _fpumode.c
- #8919: MAINT: interpolate: improve error messages for common *bc_type*…
- #8920: DOC: update Contributing to SciPy to say "prefer no PEP8 only…
- #8924: MAINT: special: deprecate *hyp2f0*, *hyp1f2*, and *hyp3f0*
- #8927: MAINT: special: remove *errprint*
- #8932: Fix broadcasting scale arg of entropy
- #8936: Fix (some) non-tuple index warnings
- #8937: ENH: implement sparse matrix BSR to CSR conversion directly.
- #8938: DOC: add @_ni_docstrings.docfiller in ndimage.rotate
- #8940: Update _discrete_distns.py

- #8943: DOC: Finish dangling sentence in *convolve* docstring
- #8944: MAINT: Address tuple indexing and warnings
- #8945: ENH: spatial.transform.Rotation [GSOC2018]
- #8950: csgraph Dijkstra function description rewording
- #8953: DOC, MAINT: HTTP -> HTTPS, and other linkrot fixes
- #8955: BUG: np.int64 in scipy.fftpack.next_fast_len
- #8958: MAINT: Add more descriptive error message for phase one simplex.
- #8962: BUG: sparse.linalg: add missing conjugate to _ScaledLinearOperator.adjoint
- #8963: BUG: sparse.linalg: downgrade LinearOperator TypeError to warning
- #8965: ENH: Wrapped RFP format and RZ decomposition routines
- #8969: MAINT: doc and code fixes for optimize.newton
- #8970: Added 'average' keyword for welch/csd to enable median averaging
- #8971: Better imresize deprecation warning
- #8972: MAINT: Switch np.where(c) for np.nonzero(c)
- #8975: MAINT: Fix warning-based failures
- #8979: DOC: fix description of count_sort keyword of dendrogram
- #8982: MAINT: optimize: Fixed minor mistakes in test_linprog.py (#8978)
- #8984: BUG: sparse.linalg: ensure expm casts integer inputs to float
- #8986: BUG: optimize/slsqp: do not exit with convergence on steps where…
- #8989: MAINT: use collections.abc in basinhopping
- #8990: ENH extend p-values of anderson_ksamp in scipy.stats
- #8991: ENH: Weighted kde
- #8993: ENH: spatial.transform.Rotation.random [GSOC 2018]
- #8994: ENH: spatial.transform.Slerp [GSOC 2018]
- #8995: TST: time.time in test
- #9007: Fix typo in fftpack.rst
- #9013: Added correct plotting code for two sided output from spectrogram
- #9014: BUG: differential_evolution with inf objective functions
- #9017: BUG: fixed #8446 corner case for asformat(array|dense)
- #9018: MAINT: _lib/ccallback: remove unused code
- #9021: BUG: Issue with subspace_angles
- #9022: DOC: Added "See Also" section to lombscargle docstring
- #9034: BUG: Fix tolerance printing behavior, remove meaningless tol…
- #9035: TST: improve signal.bsplines test coverage
- #9037: ENH: add a new init method for k-means
- #9039: DOC: Add examples to fftpack.irfft docstrings

- #9048: ENH: scipy.sparse.random
- #9050: BUG: scipy.io.hb_write: fails for matrices not in csc format
- #9051: MAINT: Fix slow sparse.rand for k < mn/3 (#9036).
- #9054: MAINT: spatial: Explicitly initialize LAPACK output parameters.
- #9055: DOC: Add examples to scipy.special docstrings
- #9056: ENH: Use one thread in OpenBLAS
- #9059: DOC: Update README with link to Code of Conduct
- #9060: BLD: remove support for the Bento build system.
- #9062: DOC add sections to overview in scipy.stats
- #9066: BUG: Correct “remez” error message
- #9069: DOC: update linalg section of roadmap for LAPACK versions.
- #9079: MAINT: add spatial.transform to refguide check; complete some…
- #9081: MAINT: Add warnings if pivot value is close to tolerance in linprog(method='simplex')
- #9084: BUG fix incorrect p-values of kurtosistest in scipy.stats
- #9095: DOC: add sections to mstats overview in scipy.stats
- #9096: BUG: Add test for Stackoverflow example from issue 8174.
- #9101: ENH: add Siegel slopes (robust regression) to scipy.stats
- #9105: allow resample_poly() to output float32 for float32 inputs.
- #9112: MAINT: optimize: make trust-constr accept constraint dict (#9043)
- #9118: Add doc entry to cholesky_banded
- #9120: eigsh documentation parameters
- #9125: interpolative: correctly reconstruct full rank matrices
- #9126: MAINT: Use warnings for unexpected peak properties
- #9129: BUG: Do not catch and silence KeyboardInterrupt
- #9131: DOC: Correct the typo in scipy.optimize tutorial page
- #9133: FIX: Avoid use of bare except
- #9134: DOC: Update of 'return_eigenvectors' description
- #9137: DOC: typo fixes for discrete Poisson tutorial
- #9139: FIX: Doctest failure in optimize tutorial
- #9143: DOC: missing sigma in Pearson r formula
- #9145: MAINT: Refactor linear programming solvers
- #9149: FIX: Make scipy.odr.ODR ifixx equal to its data.fix if given
- #9156: DOC: special: Mention the sigmoid function in the expit docstring.
- #9160: Fixed a latex delimiter error in levy()
- #9170: DOC: correction / update of docstrings of distributions in scipy.stats
- #9171: better description of the hierarchical clustering parameter

- #9174: domain check for a < b in stats.truncnorm
- #9175: DOC: Minor grammar fix
- #9176: BUG: CloughTocher2DInterpolator: fix miscalculation at neighborless…
- #9177: BUILD: Document the “clean” target in the doc/Makefile.
- #9178: MAINT: make refguide-check more robust for printed numpy arrays
- #9186: MAINT: Remove np.ediff1d occurence
- #9188: DOC: correct typo in extending ndimage with C
- #9190: ENH: Support specifying axes for fftconvolve
- #9192: MAINT: optimize: fixed @pv style suggestions from #9112
- #9200: Fix make_interp_spline(…, k=0 or 1, axis<0)
- #9201: BUG: sparse.linalg/gmres: use machine eps in breakdown check
- #9204: MAINT: fix up stats.spearmanr and match mstats.spearmanr with…
- #9206: MAINT: include benchmarks and dev files in sdist.
- #9208: TST: signal: bump bsplines test tolerance for complex data
- #9210: TST: mark tests as slow, fix missing random seed
- #9211: ENH: add capability to specify orders in pade func
- #9217: MAINT: Include `success` and `nit` in OptimizeResult returned…
- #9222: ENH: interpolate: Use scipy.spatial.distance to speed-up Rbf
- #9229: MNT: Fix Fourier filter double case
- #9233: BUG: spatial/distance: fix pdist/cdist performance regression…
- #9234: FIX: Proper suppression
- #9235: BENCH: rationalize slow benchmarks + miscellaneous fixes
- #9238: BENCH: limit number of parameter combinations in spatial.*KDTree…
- #9239: DOC: stats: Fix LaTeX markup of a couple distribution PDFs.
- #9241: ENH: Evaluate plateau size during peak finding
- #9242: ENH: stats: Implement _ppf and _logpdf for crystalball, and do…
- #9246: DOC: Properly render versionadded directive in HTML documentation
- #9255: DOC: mention RootResults in optimization reference guide
- #9260: TST: relax some tolerances so tests pass with x87 math
- #9264: TST Use assert_raises “match” parameter instead of the “message”…
- #9267: DOC: clarify expect() return val when moment is inf/nan
- #9272: DOC: Add description of default bounds to linprog
- #9277: MAINT: sparse/linalg: make test deterministic
- #9278: MAINT: interpolate: pep8 cleanup in test_polyint
- #9279: Fixed docstring for resample
- #9280: removed first check for float in get_sum_dtype

- #9281: BUG: only accept 1d input for bartlett / levene in scipy.stats
- #9282: MAINT: dense_output and t_eval are mutually exclusive inputs
- #9283: MAINT: add docs and do some cleanups in interpolate.Rbf
- #9288: Run distance_transform_edt tests on all types
- #9294: DOC: fix the formula typo
- #9298: MAINT: optimize/trust-constr: restore .niter attribute for backward-compat
- #9299: DOC: clarification of default rvs method in scipy.stats
- #9301: MAINT: removed unused import sys
- #9302: MAINT: removed unused imports
- #9303: DOC: signal: Refer to fs instead of nyq in the firwin docstring.
- #9305: ENH: Added Yeo-Johnson power transformation
- #9306: ENH - add dual annealing
- #9309: ENH add the yulesimon distribution to scipy.stats
- #9317: Nested SLSQP bug fix.
- #9320: MAINT: stats: avoid underflow in stats.geom.ppf
- #9326: Add example for Rosenbrock function
- #9332: Sort file lists
- #9340: Fix typo in find_peaks documentation
- #9343: MAINT Use np.full when possible
- #9344: DOC: added examples to docstring of dirichlet class
- #9346: DOC: Fix import of scipy.sparse.linalg in example (#9345)
- #9350: Fix interpolate read only
- #9351: MAINT: special.erf: use the x->-x symmetry
- #9356: Fix documentation typo
- #9358: DOC: improve doc for ksone and kstwobign in scipy.stats
- #9362: DOC: Change datatypes of A matrices in linprog
- #9364: MAINT: Adds implicit none to fftpack fortran sources
- #9369: DOC: minor tweak to CoC (updated NumFOCUS contact address).
- #9373: Fix exception if python is called with -OO option
- #9374: FIX: AIX compilation issue with NAN and INFINITY
- #9376: COBLYA -> COBYLA in docs
- #9377: DOC: Add examples integrate: fixed_quad and quadrature
- #9379: MAINT: TST: Make tests NumPy 1.8 compatible
- #9385: CI: On Travis matrix “OPTIMIZE=-OO” flag ignored
- #9387: Fix defaut value for ‘mode’ in ‘ndimage.shift’ in the doc
- #9392: BUG: rank has to be integer in rank_filter: fixed issue 9388

- #9399: DOC: Misc. typos
- #9400: TST: stats: Fix the expected r-value of a linregress test.
- #9405: BUG: np.hstack does not accept generator expressions
- #9408: ENH: linalg: Shorter ill-conditioned warning message
- #9418: DOC: Fix ndimage docstrings and reduce doc build warnings
- #9421: DOC: Add missing docstring examples in scipy.spatial
- #9422: DOC: Add an example to integrate.newton_cotes
- #9427: BUG: Fixed defect with maxiter #9419 in dual annealing
- #9431: BENCH: Add dual annealing to scipy benchmark (see #9415)
- #9435: DOC: Add docstring examples for stats.binom_test
- #9443: DOC: Fix the order of indices in optimize tutorial
- #9444: MAINT: interpolate: use operator.index for checking/coercing…
- #9445: DOC: Added missing example to stats.mstats.kruskal
- #9446: DOC: Add note about version changed for jaccard distance
- #9447: BLD: version-script handling in setup.py
- #9448: TST: skip a problematic linalg test
- #9449: TST: fix missing seed in lobpcg test.
- #9456: TST: test_eigs_consistency() now sorts output

5.21 SciPy 1.1.0 Release Notes

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    - `scipy.ndimage` *improvements*
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    - `scipy.special` *improvements*
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SciPy 1.1.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning`s). Our development attention will now shift to bug-fix releases on the 1.1.x branch, and on adding new features on the master branch.

This release requires Python 2.7 or 3.4+ and NumPy 1.8.2 or greater.

This release has improved but not necessarily 100% compatible with the PyPy Python implementation. For running on PyPy, PyPy 6.0+ and Numpy 1.15.0+ are required.

5.21.1 New features

`scipy.integrate` improvements

The argument `tfirst` has been added to the function *`scipy.integrate.odeint`*. This allows `odeint` to use the same user functions as *`scipy.integrate.solve_ivp`* and *`scipy.integrate.ode`* without the need for wrapping them in a function that swaps the first two arguments.

Error messages from `quad()` are now clearer.

`scipy.linalg` improvements

The function *`scipy.linalg.ldl`* has been added for factorization of indefinite symmetric/hermitian matrices into triangular and block diagonal matrices.

Python wrappers for LAPACK `sygst`, `hegst` added in *`scipy.linalg.lapack`*.

Added *`scipy.linalg.null_space`*, *`scipy.linalg.cdf2rdf`*, *`scipy.linalg.rsf2csf`*.

`scipy.misc` improvements

An electrocardiogram has been added as an example dataset for a one-dimensional signal. It can be accessed through *`scipy.misc.electrocardiogram`*.

`scipy.ndimage` improvements

The routines *`scipy.ndimage.binary_opening`*, and *`scipy.ndimage.binary_closing`* now support masks and different border values.

`scipy.optimize` improvements

The method `trust-constr` has been added to *scipy.optimize.minimize*. The method switches between two implementations depending on the problem definition. For equality-constrained problems it is an implementation of a trust-region sequential quadratic programming solver and, when inequality constraints are imposed, it switches to a trust-region interior point method. Both methods are appropriate for large scale problems. Quasi-Newton options BFGS and SR1 were implemented and can be used to approximate second-order derivatives for this new method. Also, finite-differences can be used to approximate either first-order or second-order derivatives.

Random-to-Best/1/bin and Random-to-Best/1/exp mutation strategies were added to *scipy.optimize.differential_evolution* as `randtobest1bin` and `randtobest1exp`, respectively. Note: These names were already in use but implemented a different mutation strategy. See *Backwards-incompatible changes* below. The `init` keyword for the *scipy.optimize.differential_evolution* function can now accept an array. This array allows the user to specify the entire population.

Added an `adaptive` option to Nelder-Mead to use step parameters adapted to the dimensionality of the problem.

Minor improvements in *scipy.optimize.basinhopping*.

`scipy.signal` improvements

Three new functions for peak finding in one-dimensional arrays were added. *scipy.signal.find_peaks* searches for peaks (local maxima) based on simple value comparison of neighboring samples and returns those peaks whose properties match optionally specified conditions for their height, prominence, width, threshold and distance to each other. *scipy.signal.peak_prominences* and *scipy.signal.peak_widths* can directly calculate the prominences or widths of known peaks.

Added ZPK versions of frequency transformations: *scipy.signal.bilinear_zpk*, *scipy.signal.lp2bp_zpk*, *scipy.signal.lp2bs_zpk*, *scipy.signal.lp2hp_zpk*, *scipy.signal.lp2lp_zpk*.

Added `scipy.signal.windows.dpss`, `scipy.signal.windows.general_cosine` and `scipy.signal.windows.general_hamming`.

`scipy.sparse` improvements

Previously, the `reshape` method only worked on *scipy.sparse.lil_matrix*, and in-place reshaping did not work on any matrices. Both operations are now implemented for all matrices. Handling of shapes has been made consistent with `numpy.matrix` throughout the *scipy.sparse* module (shape can be a tuple or splatted, negative number acts as placeholder, padding and unpadding dimensions of size 1 to ensure length-2 shape).

`scipy.special` improvements

Added Owen's T function as *scipy.special.owens_t*.

Accuracy improvements in `chndtr`, `digamma`, `gammaincinv`, `lambertw`, `zetac`.

`scipy.stats` improvements

The Moyal distribution has been added as *scipy.stats.moyal*.

Added the normal inverse Gaussian distribution as *scipy.stats.norminvgauss*.

5.21.2 Deprecated features

The iterative linear equation solvers in *scipy.sparse.linalg* had a sub-optimal way of how absolute tolerance is considered. The default behavior will be changed in a future Scipy release to a more standard and less surprising one. To silence deprecation warnings, set the `atol=` parameter explicitly.

scipy.signal.windows.slepian is deprecated, replaced by `scipy.signal.windows.dpss`.

The window functions in *scipy.signal* are now available in `scipy.signal.windows`. They will remain also available in the old location in the *scipy.signal* namespace in future Scipy versions. However, importing them from `scipy.signal.windows` is preferred, and new window functions will be added only there.

Indexing sparse matrices with floating-point numbers instead of integers is deprecated.

The function *scipy.stats.itemfreq* is deprecated.

5.21.3 Backwards incompatible changes

Previously, *scipy.linalg.orth* used a singular value cutoff value appropriate for double precision numbers also for single-precision input. The cutoff value is now tunable, and the default has been changed to depend on the input data precision.

In previous versions of Scipy, the `randtobest1bin` and `randtobest1exp` mutation strategies in *scipy.optimize.differential_evolution* were actually implemented using the Current-to-Best/1/bin and Current-to-Best/1/exp strategies, respectively. These strategies were renamed to `currenttobest1bin` and `currenttobest1exp` and the implementations of `randtobest1bin` and `randtobest1exp` strategies were corrected.

Functions in the ndimage module now always return their output array. Before, most functions only returned the output array if it had been allocated by the function, and would return `None` if it had been provided by the user.

Distance metrics in *scipy.spatial.distance* now require non-negative weights.

scipy.special.loggamma now returns real-valued result when the input is real-valued.

5.21.4 Other changes

When building on Linux with GNU compilers, the `.so` Python extension files now hide all symbols except those required by Python, which can avoid problems when embedding the Python interpreter.

5.21.5 Authors

- Saurabh Agarwal +
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- Paul van Mulbregt
- Pauli Virtanen
- Stefan van der Walt
- Warren Weckesser
- Florian Weimer +
- Eric Wieser
- Josh Wilson
- Ted Ying +
- Evgeny Zhurko
- Zé Vinícius
- @Astrofysicus +
- @awakenting +
- @endolith
- @FormerPhysicist +
- @gaulinmp +
- @hugovk
- @ksemb +
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A total of 122 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.1.0

- #979: Allow Hermitian matrices in lobpcg (Trac #452)
- #2694: Solution of iterative solvers can be less accurate than tolerance…
- #3164: RectBivariateSpline usage inconsistent with other interpolation…
- #4161: Missing ITMAX optional argument in scipy.optimize.nnls
- #4354: signal.slepian should use definition of digital window
- #4866: Shouldn't scipy.linalg.sqrtm raise an error if matrix is singular?
- #4953: The dirichlet distribution unnecessarily requires strictly positive…
- #5336: sqrtm on a diagonal matrix can warn "Matrix is singular and may…
- #5922: Suboptimal convergence of Halley's method?
- #6036: Incorrect edge case in scipy.stats.triang.pdf
- #6202: Enhancement: Add LDLt factorization to scipy
- #6589: sparse.random with custom rvs callable does pass on arg to subclass
- #6654: Spearman's rank correlation coefficient slow with nan values…
- #6794: Remove NumarrayType struct with numarray type names from ndimage
- #7136: The dirichlet distribution unnecessarily rejects probabilities…
- #7169: Will it be possible to add LDL' factorization for Hermitian indefinite…
- #7291: fsolve docs should say it doesn't handle over- or under-determined…
- #7453: binary_opening/binary_closing missing arguments
- #7500: linalg.solve test failure on OS X with Accelerate
- #7555: Integratig a function with singularities using the quad routine
- #7624: allow setting both absolute and relative tolerance of sparse…
- #7724: odeint documentation refers to t0 instead of t
- #7746: False CDF values for skew normal distribution
- #7750: mstats.winsorize documentation needs clarification
- #7787: Documentation error in spherical Bessel, Neumann, modified spherical…

- #7836: Scipy mmwrite incorrectly writes the zeros for skew-symmetric,…
- #7839: sqrtm is unable to compute square root of zero matrix
- #7847: solve is very slow since #6775
- #7888: Scipy 1.0.0b1 prints spurious DVODE/ZVODE/lsoda messages
- #7909: bessel kv function in 0 is nan
- #7915: LinearOperator's __init__ runs two times when instantiating the…
- #7958: integrate.quad could use better error messages when given bad…
- #7968: integrate.quad handles decreasing limits (b<a) inconsistently
- #7970: ENH: matching return dtype for loggamma/gammaln
- #7991: *lfilter* segfaults for integer inputs
- #8076: "make dist" for the docs doesn't complete cleanly
- #8080: Use JSON in *special/_generate_pyx.py*?
- #8127: scipy.special.psi(x) very slow for some values of x
- #8145: BUG: ndimage geometric_transform and zoom using deprecated NumPy…
- #8158: BUG: romb print output requires correction
- #8181: loadmat() raises TypeError instead of FileNotFound when reading…
- #8228: bug for log1p on csr_matrix
- #8235: scipy.stats multinomial pmf return nan
- #8271: scipy.io.mmwrite raises type error for uint16
- #8288: Should tests be written for scipy.sparse.linalg.isolve.minres…
- #8298: Broken links on scipy API web page
- #8329: *_gels* fails for fat A matrix
- #8346: Avoidable overflow in scipy.special.binom(n, k)
- #8371: BUG: special: zetac(x) returns 0 for x < -30.8148
- #8382: collections.OrderedDict in test_mio.py
- #8492: Missing documentation for *brute_force* parameter in scipy.ndimage.morphology
- #8532: leastsq needlessly appends extra dimension for scalar problems
- #8544: [feature request] Convert complex diagonal form to real block…
- #8561: [Bug?] Example of Bland's Rule for optimize.linprog (simplex)…
- #8562: CI: Appveyor builds fail because it can't import ConvexHull from…
- #8576: BUG: optimize: *show_options(solver='minimize', method='Newton-CG')*…
- #8603: test_roots_gegenbauer/chebyt/chebyc failures on manylinux
- #8604: Test failures in scipy.sparse test_inplace_dense
- #8616: special: ellpj.c code can be cleaned up a bit
- #8625: scipy 1.0.1 no longer allows overwriting variables in netcdf…
- #8629: gcrotmk.test_atol failure with MKL

- #8632: Sigma clipping on data with the same value
- #8646: scipy.special.sinpi test failures in test_zero_sign on old MSVC
- #8663: linprog with method=interior-point produced incorrect answer…
- #8694: linalg:TestSolve.test_all_type_size_routine_combinations fails…
- #8703: Q: Does runtests.py –refguide-check need env (or other) variables…

Pull requests for 1.1.0

- #6590: BUG: sparse: fix custom rvs callable argument in sparse.random
- #7004: ENH: scipy.linalg.eigsh cannot get all eigenvalues
- #7120: ENH: implemented Owen's T function
- #7483: ENH: Addition/multiplication operators for StateSpace systems
- #7566: Informative exception when passing a sparse matrix
- #7592: Adaptive Nelder-Mead
- #7729: WIP: ENH: optimize: large-scale constrained optimization algorithms…
- #7802: MRG: Add dpss window function
- #7803: DOC: Add examples to spatial.distance
- #7821: Add Returns section to the docstring
- #7833: ENH: Performance improvements in scipy.linalg.special_matrices
- #7864: MAINT: sparse: Simplify sputils.isintlike
- #7865: ENH: Improved speed of copy into L, U matrices
- #7871: ENH: sparse: Add 64-bit integer to sparsetools
- #7879: ENH: re-enabled old sv lapack routine as defaults
- #7889: DOC: Show probability density functions as math
- #7900: API: Soft deprecate signal.* windows
- #7910: ENH: allow *sqrtm* to compute the root of some singular matrices
- #7911: MAINT: Avoid unnecessary array copies in xdist
- #7913: DOC: Clarifies the meaning of *initial* of scipy.integrate.cumtrapz()
- #7916: BUG: sparse.linalg: fix wrong use of __new__ in LinearOperator
- #7921: BENCH: split spatial benchmark imports
- #7927: ENH: added sygst/hegst routines to lapack
- #7934: MAINT: add *io/_test_fortranmodule* to *gitignore*
- #7936: DOC: Fixed typo in scipy.special.roots_jacobi documentation
- #7937: MAINT: special: Mark a test that fails on i686 as a known failure.
- #7941: ENH: LDLt decomposition for indefinite symmetric/hermitian matrices
- #7945: ENH: Implement reshape method on sparse matrices
- #7947: DOC: update docs on releasing and installing/upgrading

- #7954: Basin-hopping changes
- #7964: BUG: test_falker not robust against numerical fuss in eigenvalues
- #7967: QUADPACK Errors - human friendly errors to replace 'Invalid Input'
- #7975: Make sure integrate.quad doesn't double-count singular points
- #7978: TST: ensure negative weights are not allowed in distance metrics
- #7980: MAINT: Truncate the warning msg about ill-conditioning
- #7981: BUG: special: fix hyp2f1 behavior in certain circumstances
- #7983: ENH: special: Add a real dispatch to *loggamma*
- #7989: BUG: special: make *kv* return *inf* at a zero real argument
- #7990: TST: special: test ufuncs in special at *nan* inputs
- #7994: DOC: special: fix typo in spherical Bessel function documentation
- #7995: ENH: linalg: add null_space for computing null spaces via svd
- #7999: BUG: optimize: Protect _minpack calls with a lock.
- #8003: MAINT: consolidate c99 compatibility
- #8004: TST: special: get all *cython_special* tests running again
- #8006: MAINT: Consolidate an additional _c99compat.h
- #8011: Add new example of integrate.quad
- #8015: DOC: special: remove *jn* from the refguide (again)
- #8018: BUG - Issue with uint datatypes for array in get_index_dtype
- #8021: DOC: spatial: Simplify Delaunay plotting
- #8024: Documentation fix
- #8027: BUG: io.matlab: fix saving unicode matrix names on py2
- #8028: BUG: special: some fixes for *lambertw*
- #8030: MAINT: Bump Cython version
- #8034: BUG: sparse.linalg: fix corner-case bug in expm
- #8035: MAINT: special: remove complex division hack
- #8038: ENH: Cythonize pyx files if pxd dependencies change
- #8042: TST: stats: reduce required precision in test_fligner
- #8043: TST: Use diff. values for decimal keyword for single and doubles
- #8044: TST: accuracy of tests made different for singles and doubles
- #8049: Unhelpful error message when calling scipy.sparse.save_npz on…
- #8052: TST: spatial: add a regression test for gh-8051
- #8059: BUG: special: fix ufunc results for *nan* arguments
- #8066: MAINT: special: reimplement inverses of incomplete gamma functions
- #8072: Example for scipy.fftpack.ifft, https://github.com/scipy/scipy/issues/7168
- #8073: Example for ifftn, https://github.com/scipy/scipy/issues/7168

- #8078: Link to CoC in contributing.rst doc
- #8085: BLD: Fix npy_isnan of integer variables in cephes
- #8088: DOC: note version for which new attributes have been added to…
- #8090: BUG: special: add nan check to *_legacy_cast_check* functions
- #8091: Doxy Typos + trivial comment typos (2nd attempt)
- #8096: TST: special: simplify *Arg*
- #8101: MAINT: special: run *_generate_pyx.py* when *add_newdocs.py*…
- #8104: Input checking for scipy.sparse.linalg.inverse()
- #8105: DOC: special: Update the 'euler' docstring.
- #8109: MAINT: fixing code comments and hyp2f1 docstring: see issues…
- #8112: More trivial typos
- #8113: MAINT: special: generate test data npz files in setup.py and…
- #8116: DOC: add build instructions
- #8120: DOC: Clean up README
- #8121: DOC: Add missing colons in docstrings
- #8123: BLD: update Bento build config files for recent C99 changes.
- #8124: Change to avoid use of *fmod* in scipy.signal.chebwin
- #8126: Added examples for mode arg in geometric_transform
- #8128: relax relative tolerance parameter in TestMinumumPhase.test_hilbert
- #8129: ENH: special: use rational approximation for `digamma` on `[1,…
- #8137: DOC Correct matrix width
- #8141: MAINT: optimize: remove unused `__main__` code in L-BSGS-B
- #8147: BLD: update Bento build for removal of .npz scipy.special test…
- #8148: Alias hanning as an explanatory function of hann
- #8149: MAINT: special: small fixes for *digamma*
- #8159: Update version classifiers
- #8164: BUG: riccati solvers don't catch ill-conditioned problems sufficiently…
- #8168: DOC: release note for sparse resize methods
- #8170: BUG: correctly pad netCDF files with null bytes
- #8171: ENH added normal inverse gaussian distribution to scipy.stats
- #8175: DOC: Add example to scipy.ndimage.zoom
- #8177: MAINT: diffev small speedup in ensure constraint
- #8178: FIX: linalg._qz String formatter syntax error
- #8179: TST: Added pdist to asv spatial benchmark suite
- #8180: TST: ensure constraint test improved
- #8183: 0d conj correlate

- #8186: BUG: special: fix derivative of *spherical_jn(1, 0)*
- #8194: Fix warning message
- #8196: BUG: correctly handle inputs with nan's and ties in spearmanr
- #8198: MAINT: stats.triang edge case fixes #6036
- #8200: DOC: Completed "Examples" sections of all linalg funcs
- #8201: MAINT: stats.trapz edge cases
- #8204: ENH: sparse.linalg/lobpcg: change .T to .T.conj() to support…
- #8206: MAINT: missed triang edge case.
- #8214: BUG: Fix memory corruption in linalg._decomp_update C extension
- #8222: DOC: recommend scipy.integrate.solve_ivp
- #8223: ENH: added Moyal distribution to scipy.stats
- #8232: BUG: sparse: Use deduped data for numpy ufuncs
- #8236: Fix #8235
- #8253: BUG: optimize: fix bug related with function call calculation…
- #8264: ENH: Extend peak finding capabilities in scipy.signal
- #8273: BUG fixed printing of convergence message in minimize_scalar…
- #8276: DOC: Add notes to explain constrains on overwrite_<>
- #8279: CI: fixing doctests
- #8282: MAINT: weightedtau, change search for nan
- #8287: Improving documentation of solve_ivp and the underlying solvers
- #8291: DOC: fix non-ascii characters in docstrings which broke the doc…
- #8292: CI: use numpy 1.13 for refguide check build
- #8296: Fixed bug reported in issue #8181
- #8297: DOC: Examples for linalg/decomp eigvals function
- #8300: MAINT: Housekeeping for minimizing the linalg compiler warnings
- #8301: DOC: make public API documentation cross-link to refguide.
- #8302: make sure _onenorm_matrix_power_nnm actually returns a float
- #8313: Change copyright to outdated 2008-2016 to 2008-year
- #8315: TST: Add tests for `scipy.sparse.linalg.isolve.minres`
- #8318: ENH: odeint: Add the argument 'tfirst' to odeint.
- #8328: ENH: optimize: `trust-constr` optimization algorithms [GSoC…
- #8330: ENH: add a maxiter argument to NNLS
- #8331: DOC: tweak the Moyal distribution docstring
- #8333: FIX: Rewrapped ?gels and ?gels_lwork routines
- #8336: MAINT: integrate: handle b < a in quad
- #8337: BUG: special: Ensure zetac(1) returns inf.

- #8347: BUG: Fix overflow in special.binom. Issue #8346
- #8356: DOC: Corrected Documentation Issue #7750 winsorize function
- #8358: ENH: stats: Use explicit MLE formulas in lognorm.fit and expon.fit
- #8374: BUG: gh7854, maxiter for l-bfgs-b closes #7854
- #8379: CI: enable gcov coverage on travis
- #8383: Removed collections.OrderedDict import ignore.
- #8384: TravisCI: tool pep8 is now pycodestyle
- #8387: MAINT: special: remove unused specfun code for Struve functions
- #8393: DOC: Replace old type names in ndimage tutorial.
- #8400: Fix tolerance specification in sparse.linalg iterative solvers
- #8402: MAINT: Some small cleanups in ndimage.
- #8403: FIX: Make scipy.optimize.zeros run under PyPy
- #8407: BUG: sparse.linalg: fix termination bugs for cg, cgs
- #8409: MAINT: special: add a *pxd* file for Cephes functions
- #8412: MAINT: special: remove *cephes/protos.h*
- #8421: Setting “unknown” message in OptimizeResult when calling MINPACK.
- #8423: FIX: Handle unsigned integers in mmio
- #8426: DOC: correct FAQ entry on Apache license compatibility. Closes…
- #8433: MAINT: add *pytest_cache* to the *gitignore*
- #8436: MAINT: scipy.sparse: less copies at transpose method
- #8437: BUG: correct behavior for skew-symmetric matrices in io.mmwrite
- #8440: DOC:Add examples to integrate.quadpack docstrings
- #8441: BUG: sparse.linalg/gmres: deal with exact breakdown in gmres
- #8442: MAINT: special: clean up Cephes header files
- #8448: TST: Generalize doctest stopwords .axis(.plot(
- #8457: MAINT: special: use JSON for function signatures in *_generate_pyx.py*
- #8461: MAINT: Simplify return value of ndimage functions.
- #8464: MAINT: Trivial typos
- #8474: BUG: spatial: make qhull.pyx more pypy-friendly
- #8476: TST: _lib: disable refcounting tests on PyPy
- #8479: BUG: io/matlab: fix issues in matlab i/o on pypy
- #8481: DOC: Example for signal.cmplx_sort
- #8482: TST: integrate: use integers instead of PyCapsules to store pointers
- #8483: ENH: io/netcdf: make mmap=False the default on PyPy
- #8484: BUG: io/matlab: work around issue in to_writeable on PyPy
- #8488: MAINT: special: add const/static specifiers where possible

- #8489: BUG: ENH: use common halley's method instead of parabolic variant
- #8491: DOC: fix typos
- #8496: ENH: special: make Chebyshev nodes symmetric
- #8501: BUG: stats: Split the integral used to compute skewnorm.cdf.
- #8502: WIP: Port CircleCI to v2
- #8507: DOC: Add missing description to *brute_force* parameter.
- #8509: BENCH: forgot to add nelder-mead to list of methods
- #8512: MAINT: Move spline interpolation code to spline.c
- #8513: TST: special: mark a slow test as xslow
- #8514: CircleCI: Share data between jobs
- #8515: ENH: special: improve accuracy of *zetac* for negative arguments
- #8520: TST: Decrease the array sizes for two linalg tests
- #8522: TST: special: restrict range of *test_besselk*/*test_besselk_int*
- #8527: Documentation - example added for voronoi_plot_2d
- #8528: DOC: Better, shared docstrings in ndimage
- #8533: BUG: Fix PEP8 errors introduced in #8528.
- #8534: ENH: Expose additional window functions
- #8538: MAINT: Fix a couple mistakes in .pyf files.
- #8540: ENH: interpolate: allow string aliases in make_interp_spline…
- #8541: ENH: Cythonize peak_prominences
- #8542: Remove numerical arguments from convolve2d / correlate2d
- #8546: ENH: New arguments, documentation, and tests for ndimage.binary_opening
- #8547: Giving both size and input now raises UserWarning (#7334)
- #8549: DOC: stats: invweibull is also known as Frechet or type II extreme…
- #8550: add cdf2rdf function
- #8551: ENH: Port of most of the dd_real part of the qd high-precision…
- #8553: Note in docs to address issue #3164.
- #8554: ENH: stats: Use explicit MLE formulas in uniform.fit()
- #8555: MAINT: adjust benchmark config
- #8557: [DOC]: fix Nakagami density docstring
- #8559: DOC: Fix docstring of diric(x, n)
- #8563: [DOC]: fix gamma density docstring
- #8564: BLD: change default Python version for doc build from 2.7 to…
- #8568: BUG: Fixes Bland's Rule for pivot row/leaving variable, closes…
- #8572: ENH: Add previous/next to interp1d
- #8578: Example for linalg.eig()

- #8580: DOC: update link to asv docs
- #8584: filter_design: switch to explicit arguments, keeping None as…
- #8586: DOC: stats: Add parentheses that were missing in the exponnorm…
- #8587: TST: add benchmark for newton, secant, halley
- #8588: DOC: special: Remove heaviside from "functions not in special"…
- #8591: DOC: cdf2rdf Added version info and "See also"
- #8594: ENH: Cythonize peak_widths
- #8595: MAINT/ENH/BUG/TST: cdf2rdf: Address review comments made after…
- #8597: DOC: add versionadded 1.1.0 for new keywords in ndimage.morphology
- #8605: MAINT: special: improve implementations of *sinpi* and *cospi*
- #8607: MAINT: add 2D benchmarks for convolve
- #8608: FIX: Fix int check
- #8613: fix typo in doc of signal.peak_widths
- #8615: TST: fix failing linalg.qz float32 test by decreasing precision.
- #8617: MAINT: clean up code in ellpj.c
- #8618: add fsolve docs it doesn't handle over- or under-determined problems
- #8620: DOC: add note on dtype attribute of aslinearoperator() argument
- #8627: ENH: Add example 1D signal (ECG) to scipy.misc
- #8630: ENH: Remove unnecessary copying in stats.percentileofscore
- #8631: BLD: fix pdf doc build. closes gh-8076
- #8633: BUG: fix regression in *io.netcdf_file* with append mode.
- #8635: MAINT: remove spurious warning from (z)vode and lsoda. Closes…
- #8636: BUG: sparse.linalg/gcrotmk: avoid rounding error in termination…
- #8637: For pdf build
- #8639: CI: build pdf documentation on circleci
- #8640: TST: fix special test that was importing *np.testing.utils* (deprecated)
- #8641: BUG: optimize: fixed sparse redundancy removal bug
- #8645: BUG: modified sigmaclip to avoid clipping of constant input in…
- #8647: TST: sparse: skip test_inplace_dense for numpy<1.13
- #8657: Latex reduce left margins
- #8659: TST: special: skip sign-of-zero test on 32-bit win32 with old…
- #8661: Fix dblquad and tplquad not accepting float boundaries
- #8666: DOC: fixes #8532
- #8667: BUG: optimize: fixed issue #8663
- #8668: Fix example in docstring of netcdf_file
- #8671: DOC: Replace deprecated matplotlib kwarg

- #8673: BUG: special: Use a stricter tolerance for the chndtr calculation.
- #8674: ENH: In the Dirichlet distribution allow x_i to be 0 if alpha_i…
- #8676: BUG: optimize: partial fix to linprog fails to detect infeasibility…
- #8685: DOC: Add interp1d-next/previous example to tutorial
- #8687: TST: netcdf: explicit mmap=True in test
- #8688: BUG: signal, stats: use Python sum() instead of np.sum for summing…
- #8689: TST: bump tolerances in tests
- #8690: DEP: deprecate stats.itemfreq
- #8691: BLD: special: fix build vs. dd_real.h package
- #8695: DOC: Improve examples in signal.find_peaks with ECG signal
- #8697: BUG: Fix *setup.py build install egg_info*, which did not previously…
- #8704: TST: linalg: drop large size from solve() test
- #8705: DOC: Describe signal.find_peaks and related functions behavior…
- #8706: DOC: Specify encoding of rst file, remove an ambiguity in an…
- #8710: MAINT: fix an import cycle sparse -> special -> integrate ->…
- #8711: ENH: remove an avoidable overflow in scipy.stats.norminvgauss.pdf()
- #8716: BUG: interpolate: allow list inputs for make_interp_spline(…,…
- #8720: np.testing import that is compatible with numpy 1.15
- #8724: CI: don't use pyproject.toml in the CI builds

5.22 SciPy 1.0.1 Release Notes

Contents

- *SciPy 1.0.1 Release Notes*
  - *Authors*
    - *Issues closed for 1.0.1*
    - *Pull requests for 1.0.1*

SciPy 1.0.1 is a bug-fix release with no new features compared to 1.0.0. Probably the most important change is a fix for an incompatibility between SciPy 1.0.0 and `numpy.f2py` in the NumPy master branch.

5.22.1 Authors

- Saurabh Agarwal +
- Alessandro Pietro Bardelli
- Philip DeBoer
- Ralf Gommers
- Matt Haberland
- Eric Larson
- Denis Laxalde
- Mihai Capotă +
- Andrew Nelson
- Oleksandr Pavlyk
- Ilhan Polat
- Anant Prakash +
- Pauli Virtanen
- Warren Weckesser
- @xoviat
- Ted Ying +

A total of 16 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 1.0.1

- #7493: *ndimage.morphology* functions are broken with numpy 1.13.0
- #8118: minimize_cobyla broken if *disp=True* passed
- #8142: scipy-v1.0.0 pdist with metric=`minkowski` raises `ValueError:…
- #8173: `scipy.stats.ortho_group` produces all negative determinants…
- #8207: gaussian_filter seg faults on float16 numpy arrays
- #8234: `scipy.optimize.linprog` *interior-point* presolve bug with trivial…
- #8243: Make csgraph importable again via *from scipy.sparse import**
- #8320: scipy.root segfaults with optimizer 'lm'

Pull requests for 1.0.1

- #8068: BUG: fix numpy deprecation test failures
- #8082: BUG: fix solve_lyapunov import
- #8144: MRG: Fix for cobyla
- #8150: MAINT: resolve UPDATEIFCOPY deprecation errors
- #8156: BUG: missing check on minkowski w kwarg
- #8187: BUG: Sign of elements in random orthogonal 2D matrices in "ortho_group_gen"…
- #8197: CI: uninstall oclint
- #8215: Fixes Numpy datatype compatibility issues
- #8237: BUG: optimize: fix bug when variables fixed by bounds are inconsistent…
- #8248: BUG: declare "gfk" variable before call of terminate() in newton-cg
- #8280: REV: reintroduce csgraph import in scipy.sparse
- #8322: MAINT: prevent scipy.optimize.root segfault closes #8320
- #8334: TST: stats: don't use exact equality check for hdmedian test
- #8477: BUG: signal/signaltools: fix wrong refcounting in PyArray_OrderFilterND
- #8530: BUG: linalg: Fixed typo in flapack.pyf.src.
- #8566: CI: Temporarily pin Cython version to 0.27.3
- #8573: Backports for 1.0.1
- #8581: Fix Cython 0.28 build break of qhull.pyx

5.23 SciPy 1.0.0 Release Notes

Contents

- *SciPy 1.0.0 Release Notes*
  - *Why 1.0 now?*
  - *Some history and perspectives*
  - *Highlights of this release*
  - *Upgrading and compatibility*
    - *New features*
  - `scipy.cluster` *improvements*
  - `scipy.fftpack` *improvements*
  - `scipy.integrate` *improvements*
  - `scipy.linalg` *improvements*
  - `scipy.ndimage` *improvements*

- scipy.optimize *improvements*
- scipy.signal *improvements*
- scipy.sparse *improvements*
- scipy.sparse.linalg *improvements*
- scipy.spatial *improvements*
- scipy.stats *improvements*
  - *Deprecated features*
  - *Backwards incompatible changes*
  - *Other changes*
  - *Authors*
- *Issues closed for 1.0.0*
- *Pull requests for 1.0.0*

We are extremely pleased to announce the release of SciPy 1.0, 16 years after version 0.1 saw the light of day. It has been a long, productive journey to get here, and we anticipate many more exciting new features and releases in the future.

5.23.1 Why 1.0 now?

A version number should reflect the maturity of a project - and SciPy was a mature and stable library that is heavily used in production settings for a long time already. From that perspective, the 1.0 version number is long overdue.

Some key project goals, both technical (e.g. Windows wheels and continuous integration) and organisational (a governance structure, code of conduct and a roadmap), have been achieved recently.

Many of us are a bit perfectionist, and therefore are reluctant to call something "1.0" because it may imply that it's "finished" or "we are 100% happy with it". This is normal for many open source projects, however that doesn't make it right. We acknowledge to ourselves that it's not perfect, and there are some dusty corners left (that will probably always be the case). Despite that, SciPy is extremely useful to its users, on average has high quality code and documentation, and gives the stability and backwards compatibility guarantees that a 1.0 label imply.

5.23.2 Some history and perspectives

- 2001: the first SciPy release
- 2005: transition to NumPy
- 2007: creation of scikits
- 2008: scipy.spatial module and first Cython code added
- 2010: moving to a 6-monthly release cycle
- 2011: SciPy development moves to GitHub
- 2011: Python 3 support
- 2012: adding a sparse graph module and unified optimization interface
- 2012: removal of scipy.maxentropy
- 2013: continuous integration with TravisCI

- 2015: adding Cython interface for BLAS/LAPACK and a benchmark suite
- 2017: adding a unified C API with scipy.LowLevelCallable; removal of scipy.weave
- 2017: SciPy 1.0 release

Pauli Virtanen is SciPy's Benevolent Dictator For Life (BDFL). He says:

Truthfully speaking, we could have released a SciPy 1.0 a long time ago, so I'm happy we do it now at long last. The project has a long history, and during the years it has matured also as a software project. I believe it has well proved its merit to warrant a version number starting with unity.

Since its conception 15+ years ago, SciPy has largely been written by and for scientists, to provide a box of basic tools that they need. Over time, the set of people active in its development has undergone some rotation, and we have evolved towards a somewhat more systematic approach to development. Regardless, this underlying drive has stayed the same, and I think it will also continue propelling the project forward in future. This is all good, since not long after 1.0 comes 1.1.

Travis Oliphant is one of SciPy's creators. He says:

I'm honored to write a note of congratulations to the SciPy developers and the entire SciPy community for the release of SciPy 1.0. This release represents a dream of many that has been patiently pursued by a stalwart group of pioneers for nearly 2 decades. Efforts have been broad and consistent over that time from many hundreds of people. From initial discussions to efforts coding and packaging to documentation efforts to extensive conference and community building, the SciPy effort has been a global phenomenon that it has been a privilege to participate in.

The idea of SciPy was already in multiple people's minds in 1997 when I first joined the Python community as a young graduate student who had just fallen in love with the expressibility and extensibility of Python. The internet was just starting to bringing together like-minded mathematicians and scientists in nascent electronically-connected communities. In 1998, there was a concerted discussion on the matrix-SIG, python mailing list with people like Paul Barrett, Joe Harrington, Perry Greenfield, Paul Dubois, Konrad Hinsen, David Ascher, and others. This discussion encouraged me in 1998 and 1999 to procrastinate my PhD and spend a lot of time writing extension modules to Python that mostly wrapped battle-tested Fortran and C-code making it available to the Python user. This work attracted the help of others like Robert Kern, Pearu Peterson and Eric Jones who joined their efforts with mine in 2000 so that by 2001, the first SciPy release was ready. This was long before Github simplified collaboration and input from others and the "patch" command and email was how you helped a project improve.

Since that time, hundreds of people have spent an enormous amount of time improving the SciPy library and the community surrounding this library has dramatically grown. I stopped being able to participate actively in developing the SciPy library around 2010. Fortunately, at that time, Pauli Virtanen and Ralf Gommers picked up the pace of development supported by dozens of other key contributors such as David Cournapeau, Evgeni Burovski, Josef Perktold, and Warren Weckesser. While I have only been able to admire the development of SciPy from a distance for the past 7 years, I have never lost my love of the project and the concept of community-driven development. I remain driven even now by a desire to help sustain the development of not only the SciPy library but many other affiliated and related open-source projects. I am extremely pleased that SciPy is in the hands of a world-wide community of talented developers who will ensure that SciPy remains an example of how grass-roots, community-driven development can succeed.

Fernando Perez offers a wider community perspective:

The existence of a nascent Scipy library, and the incredible –if tiny by today's standards– community surrounding it is what drew me into the scientific Python world while still a physics graduate student in 2001. Today, I am awed when I see these tools power everything from high school education to the research that led to the 2017 Nobel Prize in physics.

Don't be fooled by the 1.0 number: this project is a mature cornerstone of the modern scientific computing ecosystem. I am grateful for the many who have made it possible, and hope to be able to contribute again to it in the future. My sincere congratulations to the whole team!

5.23.3 Highlights of this release

Some of the highlights of this release are:

- Major build improvements. Windows wheels are available on PyPI for the first time, and continuous integration has been set up on Windows and OS X in addition to Linux.
- A set of new ODE solvers and a unified interface to them (*scipy.integrate.solve_ivp*).
- Two new trust region optimizers and a new linear programming method, with improved performance compared to what *scipy.optimize* offered previously.
- Many new BLAS and LAPACK functions were wrapped. The BLAS wrappers are now complete.

5.23.4 Upgrading and compatibility

There have been a number of deprecations and API changes in this release, which are documented below. Before upgrading, we recommend that users check that their own code does not use deprecated SciPy functionality (to do so, run your code with `python -Wd` and check for `DeprecationWarning` s).

This release requires Python 2.7 or >=3.4 and NumPy 1.8.2 or greater.

This is also the last release to support LAPACK 3.1.x - 3.3.x. Moving the lowest supported LAPACK version to >3.2.x was long blocked by Apple Accelerate providing the LAPACK 3.2.1 API. We have decided that it's time to either drop Accelerate or, if there is enough interest, provide shims for functions added in more recent LAPACK versions so it can still be used.

New features

5.23.5 `scipy.cluster` improvements

scipy.cluster.hierarchy.optimal_leaf_ordering, a function to reorder a linkage matrix to minimize distances between adjacent leaves, was added.

5.23.6 `scipy.fftpack` improvements

N-dimensional versions of the discrete sine and cosine transforms and their inverses were added as `dctn`, `idctn`, `dstn` and `idstn`.

5.23.7 `scipy.integrate` improvements

A set of new ODE solvers have been added to *scipy.integrate*. The convenience function *scipy.integrate.solve_ivp* allows uniform access to all solvers. The individual solvers (`RK23`, `RK45`, `Radau`, `BDF` and `LSODA`) can also be used directly.

5.23.8 `scipy.linalg` improvements

The BLAS wrappers in *scipy.linalg.blas* have been completed. Added functions are `*gbmv`, `*hbmv`, `*hpmv`, `*hpr`, `*hpr2`, `*spmv`, `*spr`, `*tbmv`, `*tbsv`, `*tpmv`, `*tpsv`, `*trsm`, `*trsv`, `*sbmv`, `*spr2`,

Wrappers for the LAPACK functions `*gels`, `*stev`, `*sytrd`, `*hetrd`, `*sytf2`, `*hetrf`, `*sytrf`, `*sycon`, `*hecon`, `*gglse`, `*stebz`, `*stemr`, `*sterf`, and `*stein` have been added.

The function *scipy.linalg.subspace_angles* has been added to compute the subspace angles between two matrices.

The function *scipy.linalg.clarkson_woodruff_transform* has been added. It finds low-rank matrix approximation via the Clarkson-Woodruff Transform.

The functions *scipy.linalg.eigh_tridiagonal* and *scipy.linalg.eigvalsh_tridiagonal*, which find the eigenvalues and eigenvectors of tridiagonal hermitian/symmetric matrices, were added.

5.23.9 `scipy.ndimage` improvements

Support for homogeneous coordinate transforms has been added to *scipy.ndimage.affine_transform*.

The `ndimage` C code underwent a significant refactoring, and is now a lot easier to understand and maintain.

5.23.10 `scipy.optimize` improvements

The methods `trust-region-exact` and `trust-krylov` have been added to the function *scipy.optimize.minimize*. These new trust-region methods solve the subproblem with higher accuracy at the cost of more Hessian factorizations (compared to dogleg) or more matrix vector products (compared to ncg) but usually require less nonlinear iterations and are able to deal with indefinite Hessians. They seem very competitive against the other Newton methods implemented in scipy.

scipy.optimize.linprog gained an interior point method. Its performance is superior (both in accuracy and speed) to the older simplex method.

5.23.11 `scipy.signal` improvements

An argument `fs` (sampling frequency) was added to the following functions: `firwin`, `firwin2`, `firls`, and `remez`. This makes these functions consistent with many other functions in *scipy.signal* in which the sampling frequency can be specified.

scipy.signal.freqz has been sped up significantly for FIR filters.

5.23.12 `scipy.sparse` improvements

Iterating over and slicing of CSC and CSR matrices is now faster by up to ~35%.

The `tocsr` method of COO matrices is now several times faster.

The `diagonal` method of sparse matrices now takes a parameter, indicating which diagonal to return.

5.23.13 `scipy.sparse.linalg` improvements

A new iterative solver for large-scale nonsymmetric sparse linear systems, *scipy.sparse.linalg.gcrotmk*, was added. It implements `GCROT(m,k)`, a flexible variant of `GCROT`.

scipy.sparse.linalg.lsmr now accepts an initial guess, yielding potentially faster convergence.

SuperLU was updated to version 5.2.1.

5.23.14 `scipy.spatial` improvements

Many distance metrics in *scipy.spatial.distance* gained support for weights.

The signatures of *scipy.spatial.distance.pdist* and *scipy.spatial.distance.cdist* were changed to `*args, **kwargs` in order to support a wider range of metrics (e.g. string-based metrics that need extra keywords). Also, an optional `out` parameter was added to `pdist` and `cdist` allowing the user to specify where the resulting distance matrix is to be stored

5.23.15 `scipy.stats` improvements

The methods `cdf` and `logcdf` were added to *scipy.stats.multivariate_normal*, providing the cumulative distribution function of the multivariate normal distribution.

New statistical distance functions were added, namely *scipy.stats.wasserstein_distance* for the first Wasserstein distance and *scipy.stats.energy_distance* for the energy distance.

Deprecated features

The following functions in *scipy.misc* are deprecated: `bytescale`, `fromimage`, `imfilter`, `imread`, `imresize`, `imrotate`, `imsave`, `imshow` and `toimage`. Most of those functions have unexpected behavior (like rescaling and type casting image data without the user asking for that). Other functions simply have better alternatives.

`scipy.interpolate.interpolate_wrapper` and all functions in that submodule are deprecated. This was a never finished set of wrapper functions which is not relevant anymore.

The `fillvalue` of *scipy.signal.convolve2d* will be cast directly to the dtypes of the input arrays in the future and checked that it is a scalar or an array with a single element.

`scipy.spatial.distance.matching` is deprecated. It is an alias of *scipy.spatial.distance.hamming*, which should be used instead.

Implementation of *scipy.spatial.distance.wminkowski* was based on a wrong interpretation of the metric definition. In scipy 1.0 it has been just deprecated in the documentation to keep retro-compatibility but is recommended to use the new version of *scipy.spatial.distance.minkowski* that implements the correct behaviour.

Positional arguments of *scipy.spatial.distance.pdist* and *scipy.spatial.distance.cdist* should be replaced with their keyword version.

Backwards incompatible changes

The following deprecated functions have been removed from *scipy.stats*: betai, chisqprob, f_value, histogram, histogram2, pdf_fromgamma, signaltonoise, square_of_sums, ss and threshold.

The following deprecated functions have been removed from *scipy.stats.mstats*: betai, f_value_wilks_lambda, signaltonoise and threshold.

The deprecated a and reta keywords have been removed from *scipy.stats.shapiro*.

The deprecated functions sparse.csgraph.cs_graph_components and sparse.linalg.symeig have been removed from *scipy.sparse*.

The following deprecated keywords have been removed in *scipy.sparse.linalg*: drop_tol from splu, and xtype from bicg, bicgstab, cg, cgs, gmres, qmr and minres.

The deprecated functions expm2 and expm3 have been removed from *scipy.linalg*. The deprecated keyword q was removed from *scipy.linalg.expm*. And the deprecated submodule linalg.calc_lwork was removed.

The deprecated functions C2K, K2C, F2C, C2F, F2K and K2F have been removed from *scipy.constants*.

The deprecated ppform class was removed from *scipy.interpolate*.

The deprecated keyword iprint was removed from *scipy.optimize.fmin_cobyla*.

The default value for the zero_phase keyword of *scipy.signal.decimate* has been changed to True.

The kmeans and kmeans2 functions in *scipy.cluster.vq* changed the method used for random initialization, so using a fixed random seed will not necessarily produce the same results as in previous versions.

scipy.special.gammaln does not accept complex arguments anymore.

The deprecated functions sph_jn, sph_yn, sph_jnyn, sph_in, sph_kn, and sph_inkn have been removed. Users should instead use the functions spherical_jn, spherical_yn, spherical_in, and spherical_kn. Be aware that the new functions have different signatures.

The cross-class properties of *scipy.signal.lti* systems have been removed. The following properties/setters have been removed:

Name - (accessing/setting has been removed) - (setting has been removed)

- StateSpace - (num, den, gain) - (zeros, poles)
- TransferFunction (A, B, C, D, gain) - (zeros, poles)
- ZerosPolesGain (A, B, C, D, num, den) - ()

signal.freqz(b, a) with b or a >1-D raises a ValueError. This was a corner case for which it was unclear that the behavior was well-defined.

The method var of *scipy.stats.dirichlet* now returns a scalar rather than an ndarray when the length of alpha is 1.

Other changes

SciPy now has a formal governance structure. It consists of a BDFL (Pauli Virtanen) and a Steering Committee. See the governance document for details.

It is now possible to build SciPy on Windows with MSVC + gfortran! Continuous integration has been set up for this build configuration on Appveyor, building against OpenBLAS.

Continuous integration for OS X has been set up on TravisCI.

The SciPy test suite has been migrated from `nose` to `pytest`.

`scipy/_distributor_init.py` was added to allow redistributors of SciPy to add custom code that needs to run when importing SciPy (e.g. checks for hardware, DLL search paths, etc.).

Support for PEP 518 (specifying build system requirements) was added - see `pyproject.toml` in the root of the SciPy repository.

In order to have consistent function names, the function `scipy.linalg.solve_lyapunov` is renamed to *`scipy.linalg.solve_continuous_lyapunov`*. The old name is kept for backwards-compatibility.

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A total of 121 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

5.23.16 Issues closed for 1.0.0

- #2300: scipy.misc.toimage (and therefore imresize) converts to uint32…
- #2347: Several `misc.im*` functions incorrectly handle 3 or 4-channeled…
- #2442: scipy.misc.pilutil -> scipy.ndimage?
- #2829: Mingw Gfortran on Windows?
- #3154: scipy.misc.imsave creates wrong bitmap header
- #3505: scipy.linalg.lstsq() residual's help text is a lil strange
- #3808: Is Brent's method for minimizing the value of a function implemented…
- #4121: Add cdf() method to stats.multivariate_normal
- #4458: scipy.misc.imresize changes image range
- #4575: Docs for L-BFGS-B mention non-existent parameter
- #4893: misc.imsave does not work with file type defined
- #5231: Discrepancies in scipy.optimize.minimize(method='L-BFGS-B')
- #5238: Optimal leaf ordering in scipy.cluster.hierarchy.dendrogram
- #5305: Wrong image scaling in scipy/misc/pilutil.py with misc.imsave?
- #5823: test failure in `filter_design`
- #6061: scipy.stats.spearmanr return values outside range -1 to 1
- #6242: Inconsistency / duplication for imread and imshow, imsave
- #6265: BUG: signal.iirfilter of bandpass type is unstable when high…
- #6370: `scipy.optimize.linear_sum_assignment` hangs on undefined matrix
- #6417: scipy.misc.imresize converts images to uint8
- #6618: splrep and splprep inconsistent
- #6854: Support PEP 519 in I/O functions
- #6921: [Feature request] Random unitary matrix
- #6930: `uniform_filter1d` appears to truncate rather than round when output…
- #6949: interp2d function crashes python
- #6959: scipy.interpolate.LSQUnivariateSpline - check for increasing…
- #7005: linear_sum_assignment in scipy.optimize never return if one of…
- #7010: `scipy.statsbinned_statistic_2d`: incorrect binnumbers returned
- #7049: `expm_multiply` is excessively slow when called for intervals
- #7050: Documenting `_argcheck` for `rv_discrete`
- #7077: `coo_matrix.tocsr()` still slow
- #7093: Wheels licensing
- #7122: Sketching-based Matrix Computations
- #7133: Discontinuity of a scipy special function
- #7141: Improve documentation for Elliptic Integrals

- #7181: A change in `numpy.poly1d` is causing the scipy tests to fail.
- #7220: String Formatting Issue in `LinearOperator.__init__`
- #7239: Source tarball distribution
- #7247: genlaguerre poly1d-object doesn't respect 'monic' option at evaluation
- #7248: BUG: regression in Legendre polynomials on master
- #7316: dgels is missing
- #7381: Krogh interpolation fails to produce derivatives for complex…
- #7416: scipy.stats.kappa4(h,k) raise a ValueError for positive integer…
- #7421: scipy.stats.arcsine().pdf and scipy.stats.beta(0.5, 0.5).pdf…
- #7429: `test_matrix_norms()` in scipy/linalg/tests/test_basic.py calls…
- #7444: Doc: stats.dirichlet.var output description is wrong
- #7475: Parameter amax in `scalar_search_wolfe2` is not used
- #7510: Operations between numpy.array and scipy.sparse matrix return…
- #7550: DOC: signal tutorial: Typo in explanation of convolution
- #7551: stdint.h included in SuperLU header files, but does not exist…
- #7553: Build for master broken on OS X
- #7557: Error in scipy.signal.periodogram example
- #7590: OSX test fail - `test_ltisys.TestPlacePoles.test_real`
- #7658: optimize.BenchGlobal broken
- #7669: nan result from multivariate_normal.cdf
- #7733: Inconsistent usage of indices, indptr in `Delaunay.vertex_neighbor_vertices`
- #7747: Numpy changes in np.random.dirichlet cause test failures
- #7772: Fix numpy lstsq rcond= parameter
- #7776: tests require `nose`
- #7798: contributor names for 1.0 release notes
- #7828: 32-bit Linux test errors on TestCephes
- #7893: scipy.spatial.distance.wminkowski behaviour change in 1.0.0b1
- #7898: DOC: Window functions
- #7959: BUG maybe: fmin_bfgs possibly broken in 1.0
- #7969: scipy 1.0.0rc1 windows wheels depend on missing msvcp140.dll

5.23.17 Pull requests for 1.0.0

- #4978: WIP: add pre_center and normalize options to lombscargle
- #5796: TST: Remove all permanent filter changes from tests
- #5910: ENH: sparse.linalg: add GCROT(m,k)
- #6326: ENH: New ODE solvers
- #6480: ENH: Make *signal.decimate* default to `zero_phase=True`
- #6705: ENH: add initial guess to sparse.linalg.lsqr
- #6706: ENH: add initial guess to sparse.linalg.lsmr
- #6769: BUG: optimize: add sufficient descent condition check to CG line…
- #6855: Handle objects supporting PEP 519 in I/O functions
- #6945: MAINT: ckdtree codebase clean up
- #6953: DOC: add a SciPy Project Governance document
- #6998: fix documentation of spearman rank corrcoef
- #7017: ENH: add methods logcdf and cdf to `scipy.stats.multivariate_normal`
- #7027: Add random unitary matrices
- #7030: ENH: Add strictly-increasing checks for x to 1D splines
- #7031: BUG: Fix `linear_sum_assignment` hanging on an undefined matrix
- #7041: DOC: Clairfy that windows are DFT-even by default
- #7048: DOC: modified docs for `find_peak_cwt`. Fixes #6922
- #7056: Fix insufficient precision when calculating spearman/kendall…
- #7057: MAINT: change dtype comparison in `optimize.linear_sum_assignment`.
- #7059: TST: make `Xdist_deprecated_args` cover all metrics
- #7061: Fix msvc 9 and 10 compile errors
- #7070: ENH: sparse: optimizing CSR/CSC slicing fast paths
- #7078: ENH: sparse: defer `sum_duplicates` to csr/csc
- #7079: ENH: sparse: allow subclasses to override specific math operations
- #7081: ENH: sparse: speed up CSR/CSC toarray()
- #7082: MAINT: Add missing `PyType_Ready(&SuperLUGlobalType)` for Py3
- #7083: Corrected typo in the doc of scipy.linalg.lstsq()
- #7086: Fix bug #7049 causing excessive slowness in `expm_multiply`
- #7088: Documented `_argcheck` for `rv_discrete`
- #7094: MAINT: Fix mistake in PR #7082
- #7098: BF: return NULL from failed Py3 module check
- #7105: MAINT: Customize ?TRSYL call in lyapunov solver
- #7111: Fix error message typo in UnivariateSpline
- #7113: FIX: Add add float to return type in documentation

- #7119: ENH: sparse.linalg: remove `_count_nonzero` hack
- #7123: ENH: added "interior-point" method for `scipy.optimize.linprog`
- #7137: DOC: clarify stats.linregress docstring, closes gh-7074
- #7138: DOC: special: Add an example to the airy docstring.
- #7139: DOC: stats: Update stats tutorial
- #7142: BUG: special: prevent segfault in `pbwa`
- #7143: DOC: special: warn about alternate elliptic integral parameterizations
- #7146: fix docstring of NearestNDInterpolator
- #7148: DOC: special: Add Parameters, Returns and Examples to gamma docstring
- #7152: MAINT: spatial: Remove two unused variables in ckdtree/src/distance.h
- #7153: MAINT: special: remove deprecated variant of `gammaln`
- #7154: MAINT: Fix some code that generates C compiler warnings
- #7155: DOC: linalg: Add examples for `solve_banded` and `solve_triangular`
- #7156: DOC: fix docstring of NearestNDInterpolator
- #7159: BUG: special: fix sign of derivative when `x < 0` in `pbwa`
- #7161: MAINT: interpolate: make Rbf.A array a property
- #7163: MAINT: special: return nan for inaccurate regions of `pbwa`
- #7165: ENH: optimize: changes to make BFGS implementation more efficient.
- #7166: BUG: Prevent infinite loop in `optimize._lsq.trf_linear.py`
- #7173: BUG: sparse: return a numpy matrix from `_add_dense`
- #7179: DOC: Fix an error in sparse argmax docstring
- #7180: MAINT: interpolate: A bit of clean up in `interpolate/src/_interpolate.cpp`
- #7182: Allow homogeneous coordinate transforms in `affine_transform`
- #7184: MAINT: Remove hack modifying a readonly attr
- #7185: ENH: Add evaluation of periodic splines #6730
- #7186: MAINT: PPoly: improve error messages for wrong shape/axis
- #7187: DEP: interpolate: deprecate interpolate_wrapper
- #7198: DOC: linalg: Add examples for `solveh_banded` and `solve_toeplitz`.
- #7200: DOC: stats: Added tutorial documentation for the generalized…
- #7208: DOC: Added docstrings to `issparse/isspmatrix(_...)` methods and…
- #7213: DOC: Added examples to circmean, circvar, circstd
- #7215: DOC: Adding examples to scipy.sparse.linalg…. docstrings
- #7223: DOC: special: Add examples for expit and logit.
- #7224: BUG: interpolate: fix integer overflow in fitpack.bispev
- #7225: DOC: update 1.0 release notes for several recent PRs.
- #7226: MAINT: update docs and code for mailing list move to python.org

- #7233: Fix issue #7232: Do not mask exceptions in objective func evaluation
- #7234: MAINT: cluster: cleaning up VQ/k-means code
- #7236: DOC: Fixed typo
- #7238: BUG: fix syntaxerror due to unicode character in `trustregion_exact`.
- #7243: DOC: Update docstring in misc/pilutil.py
- #7246: DEP: misc: deprecate imported names
- #7249: DOC: Add plotted example to scipy.cluster.vq.kmeans
- #7252: Fix 5231: docs of *factr*, *ftol* in sync w/ code
- #7254: ENH: SphericalVoronoi Input Handling
- #7256: fix for issue #7255 - Circular statistics functions give wrong…
- #7263: CI: use python's faulthandler to ease tracing segfaults
- #7288: ENH: linalg: add `subspace_angles` function.
- #7290: BUG: stats: Fix spurious warnings in genextreme.
- #7292: ENH: optimize: added trust region method trust-trlib
- #7296: DOC: stats: Add an example to the `ttest_ind_from_stats` docstring.
- #7297: DOC: signal: Add examples for `chirp()` and `sweep_poly()`.
- #7299: DOC: Made difference between brent and fminbound clearer
- #7305: Simplify if-statements and constructor calls in `integrate._ode`
- #7309: Comply with PEP 518.
- #7313: REL: add `python_requires` to setup.py, fix Python version check.
- #7315: BUG: Fixed bug with Laguerre and Legendre polynomials
- #7320: DOC: clarify meaning of flags in ode.integrate
- #7333: DOC: Add examples to `scipy.ndimage.gaussian_filter1d`
- #7337: ENH: add n-dimensional DCT and IDCT to fftpack
- #7353: Add `_gels` functions
- #7357: DOC: linalg: Add examples to the svdvals docstring.
- #7359: Bump Sphinx version to 1.5.5
- #7361: DOC: linalg: Add some 'See Also' links among special matrices…
- #7362: TST: Fix some Fedora 25 test failures.
- #7363: DOC: linalg: tweak the docstring example of svd
- #7365: MAINT: fix `refguide_check.py` for Sphinx >= 1.5
- #7367: BUG: odrpack: fix invalid stride checks in `d_lpkbls.f`
- #7368: DOC: constants: Add examples to the 'find' docstring.
- #7376: MAINT: bundle Mathjax with built docs
- #7377: MAINT: optimize: Better name for trust-region-exact method.
- #7378: Improve wording in tutorial

- #7383: fix KroghInterpolator.derivatives failure with complex input
- #7389: FIX: Copy mutable window in `resample_poly`
- #7390: DOC: optimize: A few tweaks of the examples in the `curve_fit`
- #7391: DOC: Add examples to scipy.stats
- #7394: "Weight" is actually mass. Add slugs and slinches/blobs to mass
- #7398: DOC: Correct minor typo in optimize.{brenth,brentq}
- #7401: DOC: zeta only accepts real input
- #7413: BUG: fix error messages in `_minimize_trustregion_exact`
- #7414: DOC: fix `ndimage.distance_transform_bf` docstring [ci skip]
- #7415: DOC: fix skew docstring [ci skip]
- #7423: Expand binnumbers with correct dimensions
- #7431: BUG: Extend scipy.stats.arcsine.pdf to endpoints 0 and 1 #7427
- #7432: DOC: Add examples to scipy.cluster.hierarchy
- #7448: ENH: stats: Implement the survival function for pareto.
- #7454: FIX Replaced `np.assert_allclose` with imported `assert_allclose`
- #7460: TST: fix integrate.ivp test that fails on 32-bit Python.
- #7461: Doc: Added tutorial documentation for stats distributions ksone
- #7463: DOC: Fix typos and remove trailing whitespace
- #7465: Fix some ndimage.interpolation endianness bugs
- #7468: del redundance in interpolate.py
- #7470: Initialize "info" in `minpack_lmdif`
- #7478: Added more testing of smirnov/smirnovi functions
- #7479: MAINT: update for new FutureWarning's in numpy 1.13.0
- #7480: DOC: correctly describe output shape of dirichlet.mean() and…
- #7482: signal.lti: Remove deprecated cross-system properties
- #7484: MAINT: Clean-up uses of np.asarray in ndimage
- #7485: ENH: support any order >=0 in `ndimage.gaussian_filter`
- #7486: ENH: Support k!=0 for sparse.diagonal()
- #7498: BUG: sparse: pass assumeSortedIndices option to scikit.umfpack
- #7501: ENH: add optimal leaf ordering for linkage matrices
- #7506: MAINT: remove overflow in Metropolis fixes #7495
- #7507: TST: speed up full test suite by less eval points in mpmath tests.
- #7509: BUG: fix issue when using `python setup.py somecommand --force`.
- #7511: fix some alerts found with lgtm
- #7514: Add explanation what the integer returned mean.
- #7516: BUG: Fix roundoff errors in `ndimage.uniform_filter1d`.

- #7517: TST: fix signal.convolve test that was effectively being skipped.
- #7523: ENH: linalg: allow lstsq to work with 0-shaped arrays
- #7525: TST: Warning cleanup
- #7526: DOC: params in ndimage.interpolation functions not optional
- #7527: MAINT: Encapsulate error message handling in `NI_LineBuffer`.
- #7528: MAINT: Remove ndimage aliases for `NPY_MAXDIMS`.
- #7529: MAINT: Remove `NI_(UN)LIKELY` macros in favor of numpy ones.
- #7537: MAINT: Use accessor function for numpy array internals
- #7541: MAINT: Remove some uses of Numarray types in ndimage.
- #7543: MAINT: Replace all NumarrayTypes uses in `ni_fourier.c`
- #7544: MAINT: Replace all uses of NumarrayTypes in `ni_interpolation.c`
- #7545: MAINT: Replace all uses of NumarrayTypes in `ni_measure.c`
- #7546: MAINT: Replace all uses of NumarrayTypes in `ni_morphology.c`
- #7548: DOC: make a note in benchmarks README on how to run without rebuilding.
- #7549: MAINT: Get rid of NumarrayTypes.
- #7552: TST: Fix new warnings -> error bugs found on OSX
- #7554: Update superlu to 5.2.1 + fix stdint.h issue on MSVC
- #7556: MAINT: Fix some types from #7549 + miscellaneous warnings.
- #7558: MAINT: Use correct #define `NO_IMPORT_ARRAY`, not `NO_ARRAY_IMPORT`…
- #7562: BUG: Copy `import_nose` from numpy.
- #7563: ENH: Add the first Wasserstein and the Cramér-von Mises statistical…
- #7568: Test janitoring
- #7571: Test janitoring pt. 2
- #7572: Pytestifying
- #7574: TST: Remove ignore warnings filters from stats
- #7577: MAINT: Remove unused code in `ndimage/ni_measure.c` and .h
- #7578: TST: Remove ignore warnings filters from sparse, clean up warning…
- #7581: BUG: properly deallocate memory from `PyArray_IntpConverter`.
- #7582: DOC: signal tutorial: Typo in explanation of convolution
- #7583: Remove remaining ignore warnings filters
- #7586: DOC: add note to HACKING.rst on where to find build docs.
- #7587: DOC: Add examples to scipy.optimize
- #7594: TST: Add tests for ndimage converter functions.
- #7596: Added a sanity check to `signal.savgol_filter`
- #7599: _upfirdn_apply stopping condition bugfix
- #7601: MAINT: special: remove `sph_jn` et al.

- #7602: TST: fix test failures in trimmed statistics tests with numpy…
- #7605: Be clear about required dimension order
- #7606: MAINT: Remove unused function `NI_NormalizeType`.
- #7607: TST: add osx to travis matrix
- #7608: DOC: improve HACKING guide - mention reviewing PRs as contribution.
- #7609: MAINT: Remove unnecessary warning filter by avoiding unnecessary…
- #7610: #7557 : fix example code in periodogram
- #7611: #7220 : fix TypeError while raising ValueError for invalid shape
- #7612: Convert yield tests to pytest parametrized tests
- #7613: Add distributor init file
- #7614: fixup header
- #7615: BUG: sparse: Fix assignment w/ non-canonical sparse argument
- #7617: DOC: Clarify digital filter functions
- #7619: ENH: scipy.sparse.spmatrix.astype: casting and copy parameter…
- #7621: Expose VODE/ZVODE/LSODE IDID return code to user
- #7622: MAINT: special: remove out-of-date comment for `ellpk`
- #7625: TST: Add a test for “ignore” warning filters
- #7628: MAINT: refactoring and cleaning distance.py/.c/.h
- #7629: DEP: deprecate args usage in xdist
- #7630: ENH: weighted metrics
- #7634: Follow-up to #6855
- #7635: interpolate.splprep: Test some error cases, give slightly better…
- #7642: Add an example to `interpolate.lagrange`
- #7643: ENH: Added wrappers for LAPACK <s,d>stev
- #7649: Fix #7636, add PEP 519 test coverage to remaining I/O functions
- #7650: DOC: signal: Add ‘Examples’ to the docstring for sosfiltfilt.
- #7651: Fix up ccache usage on Travis + try enabling on OSX
- #7653: DOC: transition of examples from 2 to 3. Closes #7366
- #7659: BENCH: fix optimize.BenchGlobal. Closes gh-7658.
- #7662: CI: speed up continuous integration builds
- #7664: Update odr documentation
- #7665: BUG: wolfe2 line/scalar search now uses amax parameter
- #7671: MAINT: `_lib/ccallback.h`: PyCapsule_GetName returns const `char*`
- #7672: TST: interpolate: test integrating periodic b-splines against…
- #7674: Tests tuning
- #7675: CI: move refguide-check to faster build

- #7676: DOC: bump scipy-sphinx-theme to fix copybutton.js
- #7678: Note the zero-padding of the results of `splrep` and `splprep`
- #7681: MAINT: `_lib`: add user-overridable available memory determination
- #7684: TST: linalg: explicitly close opened npz files
- #7686: MAINT: remove unnecessary shebang lines and executable bits
- #7687: BUG: stats: don't emit invalid warnings if moments are infinite
- #7690: ENH: allow int-like parameters in several routines
- #7691: DOC: Drop non-working source links from docs
- #7694: fix `ma.rray` to `ma.array` in func `median_cihs`
- #7698: BUG: stats: fix nan result from `multivariate_normal.cdf` (#7669)
- #7703: DOC: special: Update the docstrings for noncentral F functions.
- #7709: BLD: integrate: avoid symbol clash between lsoda and vode
- #7711: TST: `_lib`: make `test_parallel_threads` to not fail falsely
- #7712: TST: stats: bump test tolerance in `TestMultivariateNormal.test_broadcasting`
- #7715: MAINT: fix deprecated use of numpy.issubdtype
- #7716: TST: integrate: drop timing tests
- #7717: MAINT: mstats.winsorize inclusion bug fix
- #7719: DOC: stats: Add a note about the special cases of the rdist distribution.
- #7720: DOC: Add example and math to stats.pearsonr
- #7723: DOC: Added Mann-Whitney U statistic reference
- #7727: BUG: special/cdflib: deal with nan and nonfinite inputs
- #7728: BLD: spatial: fix ckdtree depends header list
- #7732: BLD: update Bento build for optimal_leaf_ordering addition
- #7734: DOC: signal: Copy-edit and add examples to the Kaiser-related…
- #7736: BUG: Fixes #7735: Prevent integer overflow in concatenated index…
- #7737: DOC: rename indices/indptr for `spatial.Delaunay vertex_neighbor_vertices`
- #7738: ENH: Speed up freqz computation
- #7739: TST: ignore ncfdtridfn failure in win32 and warn on FPU mode changes
- #7740: Fix overflow in Anderson-Darling k-sample test
- #7742: TST: special: limit expm1 mpmath comparison range
- #7748: TST: stats: don't pass invalid alpha to np.random.dirichlet
- #7749: BUG/DOC: optimize: method is 'interior-point', not 'interior…
- #7751: BUG: optimize: `show_options('linprog', method='interior-point')`…
- #7753: ENH: io: easier syntax for FortranFile read/write of mixed records
- #7754: BLD: add `_lib._fpumode` extension to Bento build.
- #7756: DOC: Show probability density functions as math

- #7757: MAINT: remove outdated OS X build scripts. Fixes pytest failure.
- #7758: MAINT: stats: pep8, wrap lines
- #7760: DOC: special: add instructions on how to add special functions
- #7761: DOC: allow specifying Python version for Sphinx makefile
- #7765: TST: fix test coverage of `mstats_extras.py`
- #7767: DOC: update 1.0 release notes.
- #7768: DOC: update notes on how to release. Also change paver file to…
- #7769: Add the `_sf` and `_logsf` function for planck dist
- #7770: DOC: Replace rotten links in the docstring of minres
- #7771: MAINT: f2py build output cleanup
- #7773: DOC: optimize: Some copy-editing of linprog docs.
- #7774: MAINT: set rcond explicitly for np.linalg.lstsq calls
- #7777: remove leftover `nose` imports
- #7780: ENH: Wrap LAPACK's dsytrd
- #7781: DOC: Link rfft
- #7782: MAINT: run pyx autogeneration in cythonize & remove autogen files
- #7783: FIX: Disallow Wn==1 in digital filters
- #7790: Fix test errors introduced by gh-5910
- #7792: MAINT: fix syntax in pyproject.toml
- #7809: ENH: sketches - Clarkson Woodruff Transform
- #7810: ENH: Add `eig(vals)_tridiagonal`
- #7811: BUG: stats: Fix warnings in `binned_statistics_dd`
- #7814: ENH: signal: Replace 'nyq' and 'Hz' arguments with 'fs'.
- #7820: DOC: update 1.0 release notes and mailmap
- #7823: BUG: memory leak in messagestream / qhull.pyx
- #7830: DOC: linalg: Add an example to the lstsq docstring.
- #7835: ENH: Automatic FIR order for `decimate`
- #7838: MAINT: stats: Deprecate `frechet_l` and `frechet_r`.
- #7841: slsqp PEP8 formatting fixes, typos, etc.
- #7843: ENH: Wrap all BLAS routines
- #7844: DOC: update LICENSE.txt with licenses of bundled libs as needed.
- #7851: ENH: Add wrappers for ?GGLSE, ?(HE/SY)CON, ?SYTF2, ?(HE/SY)TRF
- #7856: ENH: added out argument to Xdist
- #7858: BUG: special/cdflib: fix fatal loss of precision issues in cumfnc
- #7859: FIX: Squash `place_poles` warning corner case
- #7861: dummy statement for undefined `WITH_THREAD`

- #7863: MAINT: add license texts to binary distributions
- #7866: DOC, MAINT: fix links in the doc
- #7867: DOC: fix up descriptions of pdf's in distribution docstrings.
- #7869: DEP: deprecate misc.pilutil functions
- #7870: DEP: remove deprecated functions
- #7872: TST: silence RuntimeWarning for stats.truncnorm test marked as…
- #7874: TST: fix an optimize.linprog test that fails intermittently.
- #7875: TST: filter two integration warnings in stats tests.
- #7876: GEN: Add comments to the tests for clarification
- #7891: ENH: backport #7879 to 1.0.x
- #7902: MAINT: signal: Make freqz handling of multidim. arrays match…
- #7905: REV: restore wminkowski
- #7908: FIX: Avoid bad `__del__` (close) behavior
- #7918: TST: mark two optimize.linprog tests as xfail. See gh-7877.
- #7929: MAINT: changed defaults to lower in sytf2, sytrf and hetrf
- #7939: Fix umfpack solver construction for win-amd64
- #7948: DOC: add note on checking for deprecations before upgrade to…
- #7952: DOC: update SciPy Roadmap for 1.0 release and recent discussions.
- #7960: BUG: optimize: revert changes to bfgs in gh-7165
- #7962: TST: special: mark a failing hyp2f1 test as xfail
- #7973: BUG: fixed keyword in 'info' in `_get_mem_available` utility
- #8001: TST: fix test failures from Matplotlib 2.1 update
- #8010: BUG: signal: fix crash in lfilter
- #8019: MAINT: fix test failures with NumPy master

5.24 SciPy 0.19.1 Release Notes

SciPy 0.19.1 is a bug-fix release with no new features compared to 0.19.0. The most important change is a fix for a severe memory leak in `integrate.quad`.

5.24.1 Authors

- Evgeni Burovski
- Patrick Callier +
- Yu Feng
- Ralf Gommers
- Ilhan Polat

- Eric Quintero
- Scott Sievert
- Pauli Virtanen
- Warren Weckesser

A total of 9 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.19.1

- #7214: Memory use in integrate.quad in scipy-0.19.0
- #7258: `linalg.matrix_balance` gives wrong transformation matrix
- #7262: Segfault in daily testing
- #7273: `scipy.interpolate._bspl.evaluate_spline` gets wrong type
- #7335: scipy.signal.dlti(A,B,C,D).freqresp() fails

Pull requests for 0.19.1

- #7211: BUG: convolve may yield inconsistent dtypes with method changed
- #7216: BUG: integrate: fix refcounting bug in quad()
- #7229: MAINT: special: Rewrite a test of wrightomega
- #7261: FIX: Corrected the transformation matrix permutation
- #7265: BUG: Fix broken axis handling in spectral functions
- #7266: FIX 7262: ckdtree crashes in query_knn.
- #7279: Upcast half- and single-precision floats to doubles in BSpline…
- #7336: BUG: Fix signal.dfreqresp for StateSpace systems
- #7419: Fix several issues in `sparse.load_npz`, `save_npz`
- #7420: BUG: stats: allow integers as kappa4 shape parameters

5.25 SciPy 0.19.0 Release Notes

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    - `scipy.linalg` *improvements*
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        * scipy.optimize *improvements*
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SciPy 0.19.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.19.x branch, and on adding new features on the master branch.

This release requires Python 2.7 or 3.4-3.6 and NumPy 1.8.2 or greater.

Highlights of this release include:

- A unified foreign function interface layer, *scipy.LowLevelCallable*.
- Cython API for scalar, typed versions of the universal functions from the *scipy.special* module, via *cimport scipy.special.cython_special*.

5.25.1 New features

Foreign function interface improvements

scipy.LowLevelCallable provides a new unified interface for wrapping low-level compiled callback functions in the Python space. It supports Cython imported "api" functions, ctypes function pointers, CFFI function pointers, PyCapsules, Numba jitted functions and more. See gh-6509 for details.

`scipy.linalg` improvements

The function *scipy.linalg.solve* obtained two more keywords `assume_a` and `transposed`. The underlying LAPACK routines are replaced with "expert" versions and now can also be used to solve symmetric, hermitian and positive definite coefficient matrices. Moreover, ill-conditioned matrices now cause a warning to be emitted with the estimated condition number information. Old `sym_pos` keyword is kept for backwards compatibility reasons however it is identical to using `assume_a='pos'`. Moreover, the `debug` keyword, which had no function but only printing the `overwrite_<a, b>` values, is deprecated.

The function *scipy.linalg.matrix_balance* was added to perform the so-called matrix balancing using the LAPACK xGEBAL routine family. This can be used to approximately equate the row and column norms through diagonal similarity transformations.

The functions *scipy.linalg.solve_continuous_are* and *scipy.linalg.solve_discrete_are* have numerically more stable algorithms. These functions can also solve generalized algebraic matrix Riccati equations. Moreover, both gained a `balanced` keyword to turn balancing on and off.

`scipy.spatial` improvements

`scipy.spatial.SphericalVoronoi.sort_vertices_of_regions` has been re-written in Cython to improve performance.

scipy.spatial.SphericalVoronoi can handle > 200 k points (at least 10 million) and has improved performance.

The function *scipy.spatial.distance.directed_hausdorff* was added to calculate the directed Hausdorff distance.

`count_neighbors` method of *scipy.spatial.cKDTree* gained an ability to perform weighted pair counting via the new keywords `weights` and `cumulative`. See gh-5647 for details.

scipy.spatial.distance.pdist and *scipy.spatial.distance.cdist* now support non-double custom metrics.

`scipy.ndimage` improvements

The callback function C API supports PyCapsules in Python 2.7

Multidimensional filters now allow having different extrapolation modes for different axes.

`scipy.optimize` improvements

The *scipy.optimize.basinhopping* global minimizer obtained a new keyword, *seed*, which can be used to seed the random number generator and obtain repeatable minimizations.

The keyword *sigma* in *scipy.optimize.curve_fit* was overloaded to also accept the covariance matrix of errors in the data.

`scipy.signal` improvements

The function `scipy.signal.correlate` and `scipy.signal.convolve` have a new optional parameter *method*. The default value of *auto* estimates the fastest of two computation methods, the direct approach and the Fourier transform approach.

A new function has been added to choose the convolution/correlation method, `scipy.signal.choose_conv_method` which may be appropriate if convolutions or correlations are performed on many arrays of the same size.

New functions have been added to calculate complex short time fourier transforms of an input signal, and to invert the transform to recover the original signal: `scipy.signal.stft` and `scipy.signal.istft`. This implementation also fixes the previously incorrect output of `scipy.signal.spectrogram` when complex output data were requested.

The function `scipy.signal.sosfreqz` was added to compute the frequency response from second-order sections.

The function `scipy.signal.unit_impulse` was added to conveniently generate an impulse function.

The function `scipy.signal.iirnotch` was added to design second-order IIR notch filters that can be used to remove a frequency component from a signal. The dual function `scipy.signal.iirpeak` was added to compute the coefficients of a second-order IIR peak (resonant) filter.

The function `scipy.signal.minimum_phase` was added to convert linear-phase FIR filters to minimum phase.

The functions `scipy.signal.upfirdn` and `scipy.signal.resample_poly` are now substantially faster when operating on some n-dimensional arrays when n > 1. The largest reduction in computation time is realized in cases where the size of the array is small (<1k samples or so) along the axis to be filtered.

`scipy.fftpack` improvements

Fast Fourier transform routines now accept *np.float16* inputs and upcast them to *np.float32*. Previously, they would raise an error.

`scipy.cluster` improvements

Methods `"centroid"` and `"median"` of `scipy.cluster.hierarchy.linkage` have been significantly sped up. Long-standing issues with using `linkage` on large input data (over 16 GB) have been resolved.

`scipy.sparse` improvements

The functions `scipy.sparse.save_npz` and `scipy.sparse.load_npz` were added, providing simple serialization for some sparse formats.

The *prune* method of classes *bsr_matrix*, *csc_matrix*, and *csr_matrix* was updated to reallocate backing arrays under certain conditions, reducing memory usage.

The methods *argmin* and *argmax* were added to classes *coo_matrix*, *csc_matrix*, *csr_matrix*, and *bsr_matrix*.

New function `scipy.sparse.csgraph.structural_rank` computes the structural rank of a graph with a given sparsity pattern.

New function `scipy.sparse.linalg.spsolve_triangular` solves a sparse linear system with a triangular left hand side matrix.

`scipy.special` improvements

Scalar, typed versions of universal functions from *scipy.special* are available in the Cython space via `cimport` from the new module `scipy.special.cython_special`. These scalar functions can be expected to be significantly faster then the universal functions for scalar arguments. See the *scipy.special* tutorial for details.

Better control over special-function errors is offered by the functions *scipy.special.geterr* and *scipy.special.seterr* and the context manager *scipy.special.errstate*.

The names of orthogonal polynomial root functions have been changed to be consistent with other functions relating to orthogonal polynomials. For example, `scipy.special.j_roots` has been renamed *scipy.special.roots_jacobi* for consistency with the related functions *scipy.special.jacobi* and *scipy.special.eval_jacobi*. To preserve back-compatibility the old names have been left as aliases.

Wright Omega function is implemented as *scipy.special.wrightomega*.

`scipy.stats` improvements

The function *scipy.stats.weightedtau* was added. It provides a weighted version of Kendall's tau.

New class *scipy.stats.multinomial* implements the multinomial distribution.

New class *scipy.stats.rv_histogram* constructs a continuous univariate distribution with a piecewise linear CDF from a binned data sample.

New class *scipy.stats.argus* implements the Argus distribution.

`scipy.interpolate` improvements

New class *scipy.interpolate.BSpline* represents splines. `BSpline` objects contain knots and coefficients and can evaluate the spline. The format is consistent with FITPACK, so that one can do, for example:

```
>>> t, c, k = splrep(x, y, s=0)
>>> spl = BSpline(t, c, k)
>>> np.allclose(spl(x), y)
```

`spl*` functions, *scipy.interpolate.splev*, *scipy.interpolate.splint*, *scipy.interpolate.splder* and *scipy.interpolate.splantider*, accept both `BSpline` objects and `(t, c, k)` tuples for backwards compatibility.

For multidimensional splines, `c.ndim > 1`, `BSpline` objects are consistent with piecewise polynomials, *scipy.interpolate.PPoly*. This means that `BSpline` objects are not immediately consistent with *scipy.interpolate.splprep*, and one *cannot* do `>>> BSpline(*splprep([x, y])[0])`. Consult the *scipy.interpolate* test suite for examples of the precise equivalence.

In new code, prefer using `scipy.interpolate.BSpline` objects instead of manipulating `(t, c, k)` tuples directly.

New function *scipy.interpolate.make_interp_spline* constructs an interpolating spline given data points and boundary conditions.

New function *scipy.interpolate.make_lsq_spline* constructs a least-squares spline approximation given data points.

`scipy.integrate` improvements

Now *scipy.integrate.fixed_quad* supports vector-valued functions.

5.25.2 Deprecated features

scipy.interpolate.splmake, *scipy.interpolate.spleval* and *scipy.interpolate.spline* are deprecated. The format used by *splmake/spleval* was inconsistent with *splrep/splev* which was confusing to users.

scipy.special.errprint is deprecated. Improved functionality is available in *scipy.special.seterr*.

calling *scipy.spatial.distance.pdist* or *scipy.spatial.distance.cdist* with arguments not needed by the chosen metric is deprecated. Also, metrics *"old_cosine"* and *"old_cos"* are deprecated.

5.25.3 Backwards incompatible changes

The deprecated `scipy.weave` submodule was removed.

scipy.spatial.distance.squareform now returns arrays of the same dtype as the input, instead of always float64.

scipy.special.errprint now returns a boolean.

The function *scipy.signal.find_peaks_cwt* now returns an array instead of a list.

scipy.stats.kendalltau now computes the correct p-value in case the input contains ties. The p-value is also identical to that computed by *scipy.stats.mstats.kendalltau* and by R. If the input does not contain ties there is no change w.r.t. the previous implementation.

The function *scipy.linalg.block_diag* will not ignore zero-sized matrices anymore. Instead it will insert rows or columns of zeros of the appropriate size. See gh-4908 for more details.

5.25.4 Other changes

SciPy wheels will now report their dependency on `numpy` on all platforms. This change was made because Numpy wheels are available, and because the pip upgrade behavior is finally changing for the better (use `--upgrade-strategy=only-if-needed` for `pip >= 8.2`; that behavior will become the default in the next major version of `pip`).

Numerical values returned by *scipy.interpolate.interp1d* with `kind="cubic"` and `"quadratic"` may change relative to previous scipy versions. If your code depended on specific numeric values (i.e., on implementation details of the interpolators), you may want to double-check your results.

5.25.5 Authors

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A total of 121 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.19.0

- #1767: Function definitions in __fitpack.h should be moved. (Trac #1240)
- #1774: _kmeans chokes on large thresholds (Trac #1247)
- #2089: Integer overflows cause segfault in linkage function with large…
- #2190: Are odd-length window functions supposed to be always symmetrical?…
- #2251: solve_discrete_are in scipy.linalg does (sometimes) not solve…
- #2580: scipy.interpolate.UnivariateSpline (or a new superclass of it)…
- #2592: scipy.stats.anderson assumes gumbel_l
- #3054: scipy.linalg.eig does not handle infinite eigenvalues
- #3160: multinomial pmf / logpmf
- #3904: scipy.special.ellipj dn wrong values at quarter period
- #4044: Inconsistent code book initialization in kmeans
- #4234: scipy.signal.flattop documentation doesn't list a source for…
- #4831: Bugs in C code in __quadpack.h
- #4908: bug: unnessesary validity check for block dimension in scipy.sparse.block_diag
- #4917: BUG: indexing error for sparse matrix with ix_
- #4938: Docs on extending ndimage need to be updated.
- #5056: sparse matrix element-wise multiplying dense matrix returns dense…
- #5337: Formula in documentation for correlate is wrong
- #5537: use OrderedDict in io.netcdf
- #5750: [doc] missing data index value in KDTree, cKDTree
- #5755: p-value computation in scipy.stats.kendalltau() in broken in…
- #5757: BUG: Incorrect complex output of signal.spectrogram
- #5964: ENH: expose scalar versions of scipy.special functions to cython
- #6107: scipy.cluster.hierarchy.single segmentation fault with 2**16…
- #6278: optimize.basinhopping should take a RandomState object

- #6296: InterpolatedUnivariateSpline: check_finite fails when w is unspecified
- #6306: Anderson-Darling bad results
- #6314: scipy.stats.kendaltau() p value not in agreement with R, SPSS…
- #6340: Curve_fit bounds and maxfev
- #6377: expm_multiply, complex matrices not working using start,stop,etc…
- #6382: optimize.differential_evolution stopping criterion has unintuitive…
- #6391: Global Benchmarking times out at 600s.
- #6397: mmwrite errors with large (but still 64-bit) integers
- #6413: scipy.stats.dirichlet computes multivariate gaussian differential…
- #6428: scipy.stats.mstats.mode modifies input
- #6440: Figure out ABI break policy for scipy.special Cython API
- #6441: Using Qhull for halfspace intersection : segfault
- #6442: scipy.spatial : In incremental mode volume is not recomputed
- #6451: Documentation for scipy.cluster.hierarchy.to_tree is confusing…
- #6490: interp1d (kind=zero) returns wrong value for rightmost interpolation…
- #6521: scipy.stats.entropy does *not* calculate the KL divergence
- #6530: scipy.stats.spearmanr unexpected NaN handling
- #6541: Test runner does not run scipy._lib/tests?
- #6552: BUG: misc.bytescale returns unexpected results when using cmin/cmax…
- #6556: RectSphereBivariateSpline(u, v, r) fails if min(v) >= pi
- #6559: Differential_evolution maxiter causing memory overflow
- #6565: Coverage of spectral functions could be improved
- #6628: Incorrect parameter name in binomial documentation
- #6634: Expose LAPACK's xGESVX family for linalg.solve ill-conditioned…
- #6657: Confusing documentation for `scipy.special.sph_harm`
- #6676: optimize: Incorrect size of Jacobian returned by `minimize(…,…
- #6681: add a new context manager to wrap `scipy.special.seterr`
- #6700: BUG: scipy.io.wavfile.read stays in infinite loop, warns on wav…
- #6721: scipy.special.chebyt(N) throw a 'TypeError' when N > 64
- #6727: Documentation for scipy.stats.norm.fit is incorrect
- #6764: Documentation for scipy.spatial.Delaunay is partially incorrect
- #6811: scipy.spatial.SphericalVoronoi fails for large number of points
- #6841: spearmanr fails when nan_policy='omit' is set
- #6869: Currently in gaussian_kde, the logpdf function is calculated…
- #6875: SLSQP inconsistent handling of invalid bounds
- #6876: Python stopped working (Segfault?) with minimum/maximum filter…

- #6889: dblquad gives different results under scipy 0.17.1 and 0.18.1
- #6898: BUG: dblquad ignores error tolerances
- #6901: Solving sparse linear systems in CSR format with complex values
- #6903: issue in spatial.distance.pdist docstring
- #6917: Problem in passing drop_rule to scipy.sparse.linalg.spilu
- #6926: signature mismatches for LowLevelCallable
- #6961: Scipy contains shebang pointing to /usr/bin/python and /bin/bash…
- #6972: BUG: special: *generate_ufuncs.py* is broken
- #6984: Assert raises test failure for test_ill_condition_warning
- #6990: BUG: sparse: Bad documentation of the *k* argument in *sparse.linalg.eigs*
- #6991: Division by zero in linregress()
- #7011: possible speed improvment in rv_continuous.fit()
- #7015: Test failure with Python 3.5 and numpy master
- #7055: SciPy 0.19.0rc1 test errors and failures on Windows
- #7096: macOS test failues for test_solve_continuous_are
- #7100: test_distance.test_Xdist_deprecated_args test error in 0.19.0rc2

Pull requests for 0.19.0

- #2908: Scipy 1.0 Roadmap
- #3174: add b-splines
- #4606: ENH: Add a unit impulse waveform function
- #5608: Adds keyword argument to choose faster convolution method
- #5647: ENH: Faster count_neighour in cKDTree / + weighted input data
- #6021: Netcdf append
- #6058: ENH: scipy.signal - Add stft and istft
- #6059: ENH: More accurate signal.freqresp for zpk systems
- #6195: ENH: Cython interface for special
- #6234: DOC: Fixed a typo in ward() help
- #6261: ENH: add docstring and clean up code for signal.normalize
- #6270: MAINT: special: add tests for cdflib
- #6271: Fix for scipy.cluster.hierarchy.is_isomorphic
- #6273: optimize: rewrite while loops as for loops
- #6279: MAINT: Bessel tweaks
- #6291: Fixes gh-6219: remove runtime warning from genextreme distribution
- #6294: STY: Some PEP8 and cleaning up imports in stats/_continuous_distns.py
- #6297: Clarify docs in misc/__init__.py

- #6300: ENH: sparse: Loosen input validation for *diags* with empty inputs
- #6301: BUG: standardizes check_finite behavior re optional weights,…
- #6303: Fixing example in _lazyselect docstring.
- #6307: MAINT: more improvements to gammainc/gammaincc
- #6308: Clarified documentation of hypergeometric distribution.
- #6309: BUG: stats: Improve calculation of the Anderson-Darling statistic.
- #6315: ENH: Descending order of x in PPoly
- #6317: ENH: stats: Add support for nan_policy to stats.median_test
- #6321: TST: fix a typo in test name
- #6328: ENH: sosfreqz
- #6335: Define LinregressResult outside of linregress
- #6337: In anderson test, added support for right skewed gumbel distribution.
- #6341: Accept several spellings for the curve_fit max number of function…
- #6342: DOC: cluster: clarify hierarchy.linkage usage
- #6352: DOC: removed brentq from its own 'see also'
- #6362: ENH: stats: Use explicit formulas for sf, logsf, etc in weibull…
- #6369: MAINT: special: add a comment to hyp0f1_complex
- #6375: Added the multinomial distribution.
- #6387: MAINT: special: improve accuracy of ellipj's *dn* at quarter…
- #6388: BenchmarkGlobal - getting it to work in Python3
- #6394: ENH: scipy.sparse: add save and load functions for sparse matrices
- #6400: MAINT: moves global benchmark run from setup_cache to track_all
- #6403: ENH: seed kwd for basinhopping. Closes #6278
- #6404: ENH: signal: added irrnotch and iirpeak functions.
- #6406: ENH: special: extend *sici*/*shichi* to complex arguments
- #6407: ENH: Window functions should not accept non-integer or negative…
- #6408: MAINT: _differentialevolution now uses _lib._util.check_random_state
- #6427: MAINT: Fix gmpy build & test that mpmath uses gmpy
- #6439: MAINT: ndimage: update callback function c api
- #6443: BUG: Fix volume computation in incremental mode
- #6447: Fixes issue #6413 - Minor documentation fix in the entropy function…
- #6448: ENH: Add halfspace mode to Qhull
- #6449: ENH: rtol and atol for differential_evolution termination fixes…
- #6453: DOC: Add some See Also links between similar functions
- #6454: DOC: linalg: clarify callable signature in *ordqz*
- #6457: ENH: spatial: enable non-double dtypes in squareform

- #6459: BUG: Complex matrices not handled correctly by expm_multiply…
- #6465: TST DOC Window docs, tests, etc.
- #6469: ENH: linalg: better handling of infinite eigenvalues in *eig*/*eigvals*
- #6475: DOC: calling interp1d/interp2d with NaNs is undefined
- #6477: Document magic numbers in optimize.py
- #6481: TST: Supress some warnings from test_windows
- #6485: DOC: spatial: correct typo in procrustes
- #6487: Fix Bray-Curtis formula in pdist docstring
- #6493: ENH: Add covariance functionality to scipy.optimize.curve_fit
- #6494: ENH: stats: Use log1p() to improve some calculations.
- #6495: BUG: Use MST algorithm instead of SLINK for single linkage clustering
- #6497: MRG: Add minimum_phase filter function
- #6505: reset scipy.signal.resample window shape to 1-D
- #6507: BUG: linkage: Raise exception if y contains non-finite elements
- #6509: ENH: _lib: add common machinery for low-level callback functions
- #6520: scipy.sparse.base.__mul__ non-numpy/scipy objects with 'shape'…
- #6522: Replace kl_div by rel_entr in entropy
- #6524: DOC: add next_fast_len to list of functions
- #6527: DOC: Release notes to reflect the new covariance feature in optimize.curve_fit
- #6532: ENH: Simplify _cos_win, document it, add symmetric/periodic arg
- #6535: MAINT: sparse.csgraph: updating old cython loops
- #6540: DOC: add to documentation of orthogonal polynomials
- #6544: TST: Ensure tests for scipy._lib are run by scipy.test()
- #6546: updated docstring of stats.linregress
- #6553: commited changes that I originally submitted for scipy.signal.cspline…
- #6561: BUG: modify signal.find_peaks_cwt() to return array and accept…
- #6562: DOC: Negative binomial distribution clarification
- #6563: MAINT: be more liberal in requiring numpy
- #6567: MAINT: use xrange for iteration in differential_evolution fixes…
- #6572: BUG: "sp.linalg.solve_discrete_are" fails for random data
- #6578: BUG: misc: allow both cmin/cmax and low/high params in bytescale
- #6581: Fix some unfortunate typos
- #6582: MAINT: linalg: make handling of infinite eigenvalues in *ordqz*…
- #6585: DOC: interpolate: correct seealso links to ndimage
- #6588: Update docstring of scipy.spatial.distance_matrix
- #6592: DOC: Replace 'first' by 'smallest' in mode

- #6593: MAINT: remove scipy.weave submodule
- #6594: DOC: distance.squareform: fix html docs, add note about dtype…
- #6598: [DOC] Fix incorrect error message in medfilt2d
- #6599: MAINT: linalg: turn a *solve_discrete_are* test back on
- #6600: DOC: Add SOS goals to roadmap
- #6601: DEP: Raise minimum numpy version to 1.8.2
- #6605: MAINT: 'new' module is deprecated, don't use it
- #6607: DOC: add note on change in wheel dependency on numpy and pip…
- #6609: Fixes #6602 - Typo in docs
- #6616: ENH: generalization of continuous and discrete Riccati solvers…
- #6621: DOC: improve cluster.hierarchy docstrings.
- #6623: CS matrix prune method should copy data from large unpruned arrays
- #6625: DOC: special: complete documentation of *eval_** functions
- #6626: TST: special: silence some deprecation warnings
- #6631: fix parameter name doc for discrete distributions
- #6632: MAINT: stats: change some instances of *special* to *sc*
- #6633: MAINT: refguide: py2k long integers are equal to py3k integers
- #6638: MAINT: change type declaration in cluster.linkage, prevent overflow
- #6640: BUG: fix issue with duplicate values used in cluster.vq.kmeans
- #6641: BUG: fix corner case in cluster.vq.kmeans for large thresholds
- #6643: MAINT: clean up truncation modes of dendrogram
- #6645: MAINT: special: rename **_roots* functions
- #6646: MAINT: clean up mpmath imports
- #6647: DOC: add sqrt to Mahalanobis description for pdist
- #6648: DOC: special: add a section on *cython_special* to the tutorial
- #6649: ENH: Added scipy.spatial.distance.directed_hausdorff
- #6650: DOC: add Sphinx roles for DOI and arXiv links
- #6651: BUG: mstats: make sure mode(…, None) does not modify its input
- #6652: DOC: special: add section to tutorial on functions not in special
- #6653: ENH: special: add the Wright Omega function
- #6656: ENH: don't coerce input to double with custom metric in cdist…
- #6658: Faster/shorter code for computation of discordances
- #6659: DOC: special: make __init__ summaries and html summaries match
- #6661: general.rst: Fix a typo
- #6664: TST: Spectral functions' window correction factor
- #6665: [DOC] Conditions on v in RectSphereBivariateSpline

- #6668: DOC: Mention negative masses for center of mass
- #6675: MAINT: special: remove outdated README
- #6677: BUG: Fixes computation of p-values.
- #6679: BUG: optimize: return correct Jacobian for method 'SLSQP' in…
- #6680: ENH: Add structural rank to sparse.csgraph
- #6686: TST: Added Airspeed Velocity benchmarks for SphericalVoronoi
- #6687: DOC: add section "deciding on new features" to developer guide.
- #6691: ENH: Clearer error when fmin_slsqp obj doesn't return scalar
- #6702: TST: Added airspeed velocity benchmarks for scipy.spatial.distance.cdist
- #6707: TST: interpolate: test fitpack wrappers, not _impl
- #6709: TST: fix a number of test failures on 32-bit systems
- #6711: MAINT: move function definitions from __fitpack.h to _fitpackmodule.c
- #6712: MAINT: clean up wishlist in stats.morestats, and copyright statement.
- #6715: DOC: update the release notes with BSpline et al.
- #6716: MAINT: scipy.io.wavfile: No infinite loop when trying to read…
- #6717: some style cleanup
- #6723: BUG: special: cast to float before in-place multiplication in…
- #6726: address performance regressions in interp1d
- #6728: DOC: made code examples in *integrate* tutorial copy-pasteable
- #6731: DOC: scipy.optimize: Added an example for wrapping complex-valued…
- #6732: MAINT: cython_special: remove *errprint*
- #6733: MAINT: special: fix some pyflakes warnings
- #6734: DOC: sparse.linalg: fixed matrix description in *bicgstab* doc
- #6737: BLD: update *cythonize.py* to detect changes in pxi files
- #6740: DOC: special: some small fixes to docstrings
- #6741: MAINT: remove dead code in interpolate.py
- #6742: BUG: fix `linalg.block_diag` to support zero-sized matrices.
- #6744: ENH: interpolate: make PPoly.from_spline accept BSpline objects
- #6746: DOC: special: clarify use of Condon-Shortley phase in *sph_harm*/*lpmv*
- #6750: ENH: sparse: avoid densification on broadcasted elem-wise mult
- #6751: sinm doc explained cosm
- #6753: ENH: special: allow for more fine-tuned error handling
- #6759: Move logsumexp and pade from scipy.misc to scipy.special and…
- #6761: ENH: argmax and argmin methods for sparse matrices
- #6762: DOC: Improve docstrings of sparse matrices
- #6763: ENH: Weighted tau

- #6768: ENH: cythonized spherical Voronoi region polygon vertex sorting
- #6770: Correction of Delaunay class' documentation
- #6775: ENH: Integrating LAPACK "expert" routines with conditioning warnings…
- #6776: MAINT: Removing the trivial f2py warnings
- #6777: DOC: Update rv_continuous.fit doc.
- #6778: MAINT: cluster.hierarchy: Improved wording of error msgs
- #6786: BLD: increase minimum Cython version to 0.23.4
- #6787: DOC: expand on `linalg.block_diag` changes in 0.19.0 release…
- #6789: ENH: Add further documentation for norm.fit
- #6790: MAINT: Fix a potential problem in nn_chain linkage algorithm
- #6791: DOC: Add examples to scipy.ndimage.fourier
- #6792: DOC: fix some numpydoc / Sphinx issues.
- #6793: MAINT: fix circular import after moving functions out of misc
- #6796: TST: test importing each submodule. Regression test for gh-6793.
- #6799: ENH: stats: Argus distribution
- #6801: ENH: stats: Histogram distribution
- #6803: TST: make sure tests for `_build_utils` are run.
- #6804: MAINT: more fixes in *loggamma*
- #6806: ENH: Faster linkage for 'centroid' and 'median' methods
- #6810: ENH: speed up upfirdn and resample_poly for n-dimensional arrays
- #6812: TST: Added ConvexHull asv benchmark code
- #6814: ENH: Different extrapolation modes for different dimensions in…
- #6826: Signal spectral window default fix
- #6828: BUG: SphericalVoronoi Space Complexity (Fixes #6811)
- #6830: RealData docstring correction
- #6834: DOC: Added reference for skewtest function. See #6829
- #6836: DOC: Added mode='mirror' in the docstring for the functions accepting…
- #6838: MAINT: sparse: start removing old BSR methods
- #6844: handle incompatible dimensions when input is not an ndarray in…
- #6847: Added maxiter to golden search.
- #6850: BUG: added check for optional param scipy.stats.spearmanr
- #6858: MAINT: Removing redundant tests
- #6861: DEP: Fix escape sequences deprecated in Python 3.6.
- #6862: DOC: dx should be float, not int
- #6863: updated documentation curve_fit
- #6866: DOC : added some documentation to j1 referring to spherical_jn

- #6867: DOC: cdist move long examples list into Notes section
- #6868: BUG: Make stats.mode return a ModeResult namedtuple on empty…
- #6871: Corrected documentation.
- #6874: ENH: gaussian_kde.logpdf based on logsumexp
- #6877: BUG: ndimage: guard against footprints of all zeros
- #6881: python 3.6
- #6885: Vectorized integrate.fixed_quad
- #6886: fixed typo
- #6891: TST: fix failures for linalg.dare/care due to tightened test…
- #6892: DOC: fix a bunch of Sphinx errors.
- #6894: TST: Added asv benchmarks for scipy.spatial.Voronoi
- #6908: BUG: Fix return dtype for complex input in spsolve
- #6909: ENH: fftpack: use float32 routines for float16 inputs.
- #6911: added min/max support to binned_statistic
- #6913: Fix 6875: SLSQP raise ValueError for all invalid bounds.
- #6914: DOCS: GH6903 updating docs of Spatial.distance.pdist
- #6916: MAINT: fix some issues for 32-bit Python
- #6924: BLD: update Bento build for scipy.LowLevelCallable
- #6932: ENH: Use OrderedDict in io.netcdf. Closes gh-5537
- #6933: BUG: fix LowLevelCallable issue on 32-bit Python.
- #6936: BUG: sparse: handle size-1 2D indexes correctly
- #6938: TST: fix test failures in special on 32-bit Python.
- #6939: Added attributes list to cKDTree docstring
- #6940: improve efficiency of dok_matrix.tocoo
- #6942: DOC: add link to liac-arff package in the io.arff docstring.
- #6943: MAINT: Docstring fixes and an additional test for linalg.solve
- #6944: DOC: Add example of odeint with a banded Jacobian to the integrate…
- #6946: ENH: hypergeom.logpmf in terms of betaln
- #6947: TST: speedup distance tests
- #6948: DEP: Deprecate the keyword “debug” from linalg.solve
- #6950: BUG: Correctly treat large integers in MMIO (fixes #6397)
- #6952: ENH: Minor user-friendliness cleanup in LowLevelCallable
- #6956: DOC: improve description of ‘output’ keyword for convolve
- #6957: ENH more informative error in sparse.bmat
- #6962: Shebang fixes
- #6964: DOC: note argmin/argmax addition

- #6965: BUG: Fix issues passing error tolerances in dblquad and tplquad.
- #6971: fix the docstring of signaltools.correlate
- #6973: Silence expected numpy warnings in scipy.ndimage.interpolation.zoom()
- #6975: BUG: special: fix regex in *generate_ufuncs.py*
- #6976: Update docstring for griddata
- #6978: Avoid division by zero in zoom factor calculation
- #6979: BUG: ARE solvers did not check the generalized case carefully
- #6985: ENH: sparse: add scipy.sparse.linalg.spsolve_triangular
- #6994: MAINT: spatial: updates to plotting utils
- #6995: DOC: Bad documentation of k in sparse.linalg.eigs See #6990
- #6997: TST: Changed the test with a less singular example
- #7000: DOC: clarify interp1d 'zero' argument
- #7007: BUG: Fix division by zero in linregress() for 2 data points
- #7009: BUG: Fix problem in passing drop_rule to scipy.sparse.linalg.spilu
- #7012: speed improvment in _distn_infrastructure.py
- #7014: Fix Typo: add a single quotation mark to fix a slight typo
- #7021: MAINT: stats: use machine constants from np.finfo, not machar
- #7026: MAINT: update .mailmap
- #7032: Fix layout of rv_histogram docs
- #7035: DOC: update 0.19.0 release notes
- #7036: ENH: Add more boundary options to signal.stft
- #7040: TST: stats: skip too slow tests
- #7042: MAINT: sparse: speed up setdiag tests
- #7043: MAINT: refactory and code cleaning Xdist
- #7053: Fix msvc 9 and 10 compile errors
- #7060: DOC: updated release notes with #7043 and #6656
- #7062: MAINT: Change defaut STFT boundary kwarg to "zeros"
- #7064: Fix ValueError: path is on mount 'X:', start on mount 'D:' on…
- #7067: TST: Fix PermissionError: [Errno 13] Permission denied on Windows
- #7068: TST: Fix UnboundLocalError: local variable 'data' referenced…
- #7069: Fix OverflowError: Python int too large to convert to C long…
- #7071: TST: silence RuntimeWarning for nan test of stats.spearmanr
- #7072: Fix OverflowError: Python int too large to convert to C long…
- #7084: TST: linalg: bump tolerance in test_falker
- #7095: TST: linalg: bump more tolerances in test_falker
- #7101: TST: Relax solve_continuous_are test case 2 and 12

- #7106: BUG: stop cdist "correlation" modifying input
- #7116: Backports to 0.19.0rc2

5.26 SciPy 0.18.1 Release Notes

SciPy 0.18.1 is a bug-fix release with no new features compared to 0.18.0.

5.26.1 Authors

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A total of 9 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.18.1

- #6357: scipy 0.17.1 piecewise cubic hermite interpolation does not return…
- #6420: circmean() changed behaviour from 0.17 to 0.18
- #6421: scipy.linalg.solve_banded overwrites input 'b' when the inversion…
- #6425: cKDTree INF bug
- #6435: scipy.stats.ks_2samp returns different values on different computers
- #6458: Error in scipy.integrate.dblquad when using variable integration…

Pull requests for 0.18.1

- #6405: BUG: sparse: fix elementwise divide for CSR/CSC
- #6431: BUG: result for insufficient neighbours from cKDTree is wrong.
- #6432: BUG Issue #6421: scipy.linalg.solve_banded overwrites input 'b'…
- #6455: DOC: add links to release notes
- #6462: BUG: interpolate: fix .roots method of PchipInterpolator
- #6492: BUG: Fix regression in dblquad: #6458
- #6543: fix the regression in circmean

- #6545: Revert gh-5938, restore ks_2samp
- #6557: Backports for 0.18.1

5.27 SciPy 0.18.0 Release Notes

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    - *Pull requests for 0.18.0*

SciPy 0.18.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and

optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.19.x branch, and on adding new features on the master branch.

This release requires Python 2.7 or 3.4-3.5 and NumPy 1.7.1 or greater.

Highlights of this release include:

- A new ODE solver for two-point boundary value problems, *scipy.optimize.solve_bvp*.
- A new class, *CubicSpline*, for cubic spline interpolation of data.
- N-dimensional tensor product polynomials, *scipy.interpolate.NdPPoly*.
- Spherical Voronoi diagrams, *scipy.spatial.SphericalVoronoi*.
- Support for discrete-time linear systems, *scipy.signal.dlti*.

5.27.1 New features

scipy.integrate improvements

A solver of two-point boundary value problems for ODE systems has been implemented in *scipy.integrate.solve_bvp*. The solver allows for non-separated boundary conditions, unknown parameters and certain singular terms. It finds a C1 continious solution using a fourth-order collocation algorithm.

scipy.interpolate improvements

Cubic spline interpolation is now available via *scipy.interpolate.CubicSpline*. This class represents a piecewise cubic polynomial passing through given points and C2 continuous. It is represented in the standard polynomial basis on each segment.

A representation of n-dimensional tensor product piecewise polynomials is available as the *scipy.interpolate.NdPPoly* class.

Univariate piecewise polynomial classes, *PPoly* and *Bpoly*, can now be evaluated on periodic domains. Use `extrapolate="periodic"` keyword argument for this.

scipy.fftpack improvements

scipy.fftpack.next_fast_len function computes the next "regular" number for FFTPACK. Padding the input to this length can give significant performance increase for *scipy.fftpack.fft*.

scipy.signal improvements

Resampling using polyphase filtering has been implemented in the function *scipy.signal.resample_poly*. This method upsamples a signal, applies a zero-phase low-pass FIR filter, and downsamples using *scipy.signal.upfirdn* (which is also new in 0.18.0). This method can be faster than FFT-based filtering provided by *scipy.signal.resample* for some signals.

scipy.signal.firls, which constructs FIR filters using least-squares error minimization, was added.

scipy.signal.sosfiltfilt, which does forward-backward filtering like *scipy.signal.filtfilt* but for second-order sections, was added.

Discrete-time linear systems

scipy.signal.dlti provides an implementation of discrete-time linear systems. Accordingly, the *StateSpace*, *TransferFunction* and *ZerosPolesGain* classes have learned a the new keyword, *dt*, which can be used to create discrete-time instances of the corresponding system representation.

`scipy.sparse` improvements

The functions *sum*, *max*, *mean*, *min*, *transpose*, and *reshape* in *scipy.sparse* have had their signatures augmented with additional arguments and functionality so as to improve compatibility with analogously defined functions in `numpy`.

Sparse matrices now have a *count_nonzero* method, which counts the number of nonzero elements in the matrix. Unlike *getnnz()* and `nnz` property, which return the number of stored entries (the length of the data attribute), this method counts the actual number of non-zero entries in data.

`scipy.optimize` improvements

The implementation of Nelder-Mead minimization, *scipy.minimize(..., method="Nelder-Mead")*, obtained a new keyword, *initial_simplex*, which can be used to specify the initial simplex for the optimization process.

Initial step size selection in CG and BFGS minimizers has been improved. We expect that this change will improve numeric stability of optimization in some cases. See pull request gh-5536 for details.

Handling of infinite bounds in SLSQP optimization has been improved. We expect that this change will improve numeric stability of optimization in the some cases. See pull request gh-6024 for details.

A large suite of global optimization benchmarks has been added to `scipy/benchmarks/go_benchmark_functions`. See pull request gh-4191 for details.

Nelder-Mead and Powell minimization will now only set defaults for maximum iterations or function evaluations if neither limit is set by the caller. In some cases with a slow converging function and only 1 limit set, the minimization may continue for longer than with previous versions and so is more likely to reach convergence. See issue gh-5966.

`scipy.stats` improvements

Trapezoidal distribution has been implemented as `scipy.stats.trapz`. Skew normal distribution has been implemented as *scipy.stats.skewnorm*. Burr type XII distribution has been implemented as *scipy.stats.burr12*. Three- and four-parameter kappa distributions have been implemented as *scipy.stats.kappa3* and *scipy.stats.kappa4*, respectively.

New *scipy.stats.iqr* function computes the interquartile region of a distribution.

Random matrices

scipy.stats.special_ortho_group and *scipy.stats.ortho_group* provide generators of random matrices in the SO(N) and O(N) groups, respectively. They generate matrices in the Haar distribution, the only uniform distribution on these group manifolds.

scipy.stats.random_correlation provides a generator for random correlation matrices, given specified eigenvalues.

scipy.linalg improvements

scipy.linalg.svd gained a new keyword argument, `lapack_driver`. Available drivers are `gesdd` (default) and `gesvd`.

scipy.linalg.lapack.ilaver returns the version of the LAPACK library SciPy links to.

scipy.spatial improvements

Boolean distances, *scipy.spatial.pdist*, have been sped up. Improvements vary by the function and the input size. In many cases, one can expect a speed-up of x2–x10.

New class *scipy.spatial.SphericalVoronoi* constructs Voronoi diagrams on the surface of a sphere. See pull request gh-5232 for details.

scipy.cluster improvements

A new clustering algorithm, the nearest neighbor chain algorithm, has been implemented for *scipy.cluster.hierarchy.linkage*. As a result, one can expect a significant algorithmic improvement ($O(N^2)$ instead of $O(N^3)$) for several linkage methods.

scipy.special improvements

The new function *scipy.special.loggamma* computes the principal branch of the logarithm of the Gamma function. For real input, `loggamma` is compatible with *scipy.special.gammaln*. For complex input, it has more consistent behavior in the complex plane and should be preferred over `gammaln`.

Vectorized forms of spherical Bessel functions have been implemented as *scipy.special.spherical_jn*, *scipy.special.spherical_kn*, *scipy.special.spherical_in* and *scipy.special.spherical_yn*. They are recommended for use over `sph_*` functions, which are now deprecated.

Several special functions have been extended to the complex domain and/or have seen domain/stability improvements. This includes *spence*, *digamma*, *log1p* and several others.

5.27.2 Deprecated features

The cross-class properties of *lti* systems have been deprecated. The following properties/setters will raise a *DeprecationWarning*:

Name - (accessing/setting raises warning) - (setting raises warning) * StateSpace - (*num*, *den*, *gain*) - (*zeros*, *poles*) * TransferFunction (*A*, *B*, *C*, *D*, *gain*) - (*zeros*, *poles*) * ZerosPolesGain (*A*, *B*, *C*, *D*, *num*, *den*) - ()

Spherical Bessel functions, `sph_in`, `sph_jn`, `sph_kn`, `sph_yn`, `sph_jnyn` and `sph_inkn` have been deprecated in favor of *scipy.special.spherical_jn* and `spherical_kn`, `spherical_yn`, `spherical_in`.

The following functions in *scipy.constants* are deprecated: `C2K`, `K2C`, `C2F`, `F2C`, `F2K` and `K2F`. They are superceded by a new function *scipy.constants.convert_temperature* that can perform all those conversions plus to/from the Rankine temperature scale.

5.27.3 Backwards incompatible changes

scipy.optimize

The convergence criterion for `optimize.bisect`, `optimize.brentq`, `optimize.brenth`, and `optimize.ridder` now works the same as `numpy.allclose`.

scipy.ndimage

The offset in `ndimage.iterpolation.affine_transform` is now consistently added after the matrix is applied, independent of if the matrix is specified using a one-dimensional or a two-dimensional array.

scipy.stats

`stats.ks_2samp` used to return nonsensical values if the input was not real or contained nans. It now raises an exception for such inputs.

Several deprecated methods of *scipy.stats* distributions have been removed: `est_loc_scale`, `vecfunc`, `veccdf` and `vec_generic_moment`.

Deprecated functions `nanmean`, `nanstd` and `nanmedian` have been removed from *scipy.stats*. These functions were deprecated in scipy 0.15.0 in favor of their `numpy` equivalents.

A bug in the `rvs()` method of the distributions in *scipy.stats* has been fixed. When arguments to `rvs()` were given that were shaped for broadcasting, in many cases the returned random samples were not random. A simple example of the problem is `stats.norm.rvs(loc=np.zeros(10))`. Because of the bug, that call would return 10 identical values. The bug only affected code that relied on the broadcasting of the shape, location and scale parameters.

The `rvs()` method also accepted some arguments that it should not have. There is a potential for backwards incompatibility in cases where `rvs()` accepted arguments that are not, in fact, compatible with broadcasting. An example is

```
stats.gamma.rvs([2, 5, 10, 15], size=(2,2))
```

The shape of the first argument is not compatible with the requested size, but the function still returned an array with shape (2, 2). In scipy 0.18, that call generates a `ValueError`.

scipy.io

`scipy.io.netcdf` masking now gives precedence to the `_FillValue` attribute over the `missing_value` attribute, if both are given. Also, data are only treated as missing if they match one of these attributes exactly: values that differ by roundoff from `_FillValue` or `missing_value` are no longer treated as missing values.

scipy.interpolate

scipy.interpolate.PiecewisePolynomial class has been removed. It has been deprecated in scipy 0.14.0, and *scipy.interpolate.BPoly.from_derivatives* serves as a drop-in replacement.

5.27.4 Other changes

Scipy now uses `setuptools` for its builds instead of plain distutils. This fixes usage of `install_requires='scipy'` in the `setup.py` files of projects that depend on Scipy (see Numpy issue gh-6551 for details). It potentially affects the way that build/install methods for Scipy itself behave though. Please report any unexpected behavior on the Scipy issue tracker.

PR #6240 changes the interpretation of the *maxfun* option in *L-BFGS-B* based routines in the `scipy.optimize` module. An *L-BFGS-B* search consists of multiple iterations, with each iteration consisting of one or more function evaluations. Whereas the old search strategy terminated immediately upon reaching *maxfun* function evaluations, the new strategy allows the current iteration to finish despite reaching *maxfun*.

The bundled copy of Qhull in the `scipy.spatial` subpackage has been upgraded to version 2015.2.

The bundled copy of ARPACK in the `scipy.sparse.linalg` subpackage has been upgraded to arpack-ng 3.3.0.

The bundled copy of SuperLU in the `scipy.sparse` subpackage has been upgraded to version 5.1.1.

5.27.5 Authors

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A total of 99 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.18.0

- #1484: SVD using `*GESVD` lapack drivers (Trac #957)
- #1547: Inconsistent use of offset in ndimage.interpolation.affine_transform()…
- #1609: special.hyp0f1 returns nan (Trac #1082)
- #1656: fmin_slsqp enhancement (Trac #1129)
- #2069: stats broadcasting in rvs (Trac #1544)
- #2165: sph_jn returns false results for some orders/values (Trac #1640)
- #2255: Incorrect order of translation and rotation in affine_transform…
- #2332: hyp0f1 args and return values are unnumpyic (Trac #1813)
- #2534: The sparse .sum() method with uint8 dtype does not act like the…
- #3113: Implement ufuncs for CSPHJY, SPHJ, SPHY, CSPHIK, SPHI, SPHIK…
- #3568: SciPy 0.13.3 - CentOS5 - Errors in test_arpack
- #3581: optimize: stepsize in fmin_bfgs is "bad"
- #4476: scipy.sparse non-native endian bug
- #4484: ftol in optimize.fmin fails to work
- #4510: sparsetools.cxx call_thunk can segfault due to out of bounds…
- #5051: ftol and xtol for _minimize_neldermead are absolute instead of…
- #5097: proposal: spherical Voronoi diagrams
- #5123: Call to *`scipy.sparse.coo_matrix`* fails when passed Cython typed…
- #5220: scipy.cluster.hierarchy.{ward,median,centroid} does not work…
- #5379: Add a build step at the end of .travis.yml that uploads working…
- #5440: scipy.optimize.basinhopping: accept_test returning `numpy.bool_`…
- #5452: Error in scipy.integrate.nquad when using variable integration…
- #5520: Cannot inherit csr_matrix properly
- #5533: Kendall tau implementation uses Python mergesort
- #5553: stats.tiecorrect overflows
- #5589: Add the Type XII Burr distribution to stats.
- #5612: sparse.linalg factorizations slow for small k due to default…
- #5626: io.netcdf masking should use masked_equal rather than masked_value
- #5637: Simple cubic spline interpolation?

- #5683: BUG: Akima1DInterpolator may return nans given multidimensional…
- #5686: scipy.stats.ttest_ind_from_stats does not accept arrays
- #5702: scipy.ndimage.interpolation.affine_transform lacks documentation…
- #5718: Wrong computation of weighted minkowski distance in cdist
- #5745: move to setuptools for next release
- #5752: DOC: solve_discrete_lyapunov equation puts transpose in wrong…
- #5760: signal.ss2tf doesn't handle zero-order state-space models
- #5764: Hypergeometric function hyp0f1 behaves incorrectly for complex…
- #5814: stats NaN Policy Error message inconsistent with code
- #5833: docstring of stats.binom_test() needs an update
- #5853: Error in scipy.linalg.expm for complex matrix with shape (1,1)
- #5856: Specify Nelder-Mead initial simplex
- #5865: scipy.linalg.expm fails for certain numpy matrices
- #5915: optimize.basinhopping - variable referenced before assignment.
- #5916: LSQUnivariateSpline fitting failed with knots generated from…
- #5927: unicode vs. string comparison in scipy.stats.binned_statistic_dd
- #5936: faster implementation of ks_2samp
- #5948: csc matrix .mean returns single element matrix rather than scalar
- #5959: BUG: optimize test error for root when using lgmres
- #5972: Test failures for sparse sum tests on 32-bit Python
- #5976: Unexpected exception in scipy.sparse.bmat while using 0 x 0 matrix
- #6008: scipy.special.kl_div not available in 0.14.1
- #6011: The von-Mises entropy is broken
- #6016: python crashes for linalg.interpolative.svd with certain large…
- #6017: Wilcoxon signed-rank test with zero_method="pratt" or "zsplit"…
- #6028: stats.distributions does not have trapezoidal distribution
- #6035: Wrong link in f_oneway
- #6056: BUG: signal.decimate should only accept discrete LTI objects
- #6093: Precision error on Linux 32 bit with openblas
- #6101: Barycentric transforms test error on Python3, 32-bit Linux
- #6105: scipy.misc.face docstring is incorrect
- #6113: scipy.linalg.logm fails for a trivial matrix
- #6128: Error in dot method of sparse COO array, when used with numpy…
- #6132: Failures with latest MKL
- #6136: Failures on *master* with MKL
- #6162: fmin_l_bfgs_b returns inconsistent results (fmin $\neq$ f(xmin)) and…

- #6165: optimize.minimize infinite loop with Newton-CG
- #6167: incorrect distribution fitting for data containing boundary values.
- #6194: lstsq() and others detect numpy.complex256 as real
- #6216: ENH: improve accuracy of ppf cdf roundtrip for bradford
- #6217: BUG: weibull_min.logpdf return nan for c=1 and x=0
- #6218: Is there a method to cap shortest path search distances?
- #6222: PchipInterpolator no longer handles a 2-element array
- #6226: ENH: improve accuracy for logistic.ppf and logistic.isf
- #6227: ENH: improve accuracy for rayleigh.logpdf and rayleigh.logsf…
- #6228: ENH: improve accuracy of ppf cdf roundtrip for gumbel_l
- #6235: BUG: alpha.pdf and alpha.logpdf returns nan for x=0
- #6245: ENH: improve accuracy for ppf-cdf and sf-isf roundtrips for invgamma
- #6263: BUG: stats: Inconsistency in the multivariate_normal docstring
- #6292: Python 3 unorderable type errors in test_sparsetools.TestInt32Overflow
- #6316: TestCloughTocher2DInterpolator.test_dense crashes python3.5.2rc1_64bit…
- #6318: Scipy interp1d 'nearest' not working for high values on x-axis

Pull requests for 0.18.0

- #3226: DOC: Change *nb* and *na* to conventional m and n
- #3867: allow cKDTree.query taking a list input in k.
- #4191: ENH: Benchmarking global optimizers
- #4356: ENH: add PPoly.solve(y) for solving `p(x) == y`
- #4370: DOC separate boolean distance functions for clarity
- #4678: BUG: sparse: ensure index dtype is large enough to pass all parameters…
- #4881: scipy.signal: Add the class dlti for linear discrete-time systems….
- #4901: MAINT: add benchmark and improve docstring for signal.lfilter
- #5043: ENH: sparse: add count_nonzero method
- #5136: Attribute kurtosistest() to Anscombe & Glynn (1983)
- #5186: ENH: Port upfirdn
- #5232: ENH: adding spherical Voronoi diagram algorithm to scipy.spatial
- #5279: ENH: Bessel filters with different normalizations, high order
- #5384: BUG: Closes #5027 distance function always casts bool to double
- #5392: ENH: Add zero_phase kwarg to signal.decimate
- #5394: MAINT: sparse: non-canonical test cleanup and fixes
- #5424: DOC: add Scipy developers guide
- #5442: STY: PEP8 amendments

- #5472: Online QR in LGMRES
- #5526: BUG: stats: Fix broadcasting in the rvs() method of the distributions.
- #5530: MAINT: sparse: set *format* attr explicitly
- #5536: optimize: fix up cg/bfgs initial step sizes
- #5548: PERF: improves performance in stats.kendalltau
- #5549: ENH: Nearest-neighbor chain algorithm for hierarchical clustering
- #5554: MAINT/BUG: closes overflow bug in stats.tiecorrect
- #5557: BUG: modify optimize.bisect to achieve desired tolerance
- #5581: DOC: Tutorial for least_squares
- #5606: ENH: differential_evolution - moving core loop of solve method…
- #5609: [MRG] test against numpy dev
- #5611: use setuptools for bdist_egg distributions
- #5615: MAINT: linalg: tighten _decomp_update + special: remove unused…
- #5622: Add SO(N) rotation matrix generator
- #5623: ENH: special: Add vectorized spherical Bessel functions.
- #5627: Response to issue #5160, implements the skew normal distribution…
- #5628: DOC: Align the description and operation
- #5632: DOC: special: Expanded docs for Airy, elliptic, Bessel functions.
- #5633: MAINT: linalg: unchecked malloc in _decomp_update
- #5634: MAINT: optimize: tighten _group_columns
- #5640: Fixes for io.netcdf masking
- #5645: MAINT: size 0 vector handling in cKDTree range queries
- #5649: MAINT: update license text
- #5650: DOC: Clarify Exponent Order in ltisys.py
- #5651: DOC: Clarify Documentation for scipy.special.gammaln
- #5652: DOC: Fixed scipy.special.betaln Doc
- #5653: [MRG] ENH: CubicSpline interpolator
- #5654: ENH: Burr12 distribution to stats module
- #5659: DOC: Define BEFORE/AFTER in runtests.py -h for bench-compare
- #5660: MAINT: remove functions deprecated before 0.16.0
- #5662: ENH: Circular statistic optimization
- #5663: MAINT: remove uses of np.testing.rand
- #5665: MAINT: spatial: remove matching distance implementation
- #5667: Change some HTTP links to HTTPS
- #5669: DOC: zpk2sos can't do analog, array_like, etc.
- #5670: Update conf.py

- #5672: MAINT: move a sample distribution to a subclass of rv_discrete
- #5678: MAINT: stats: remove est_loc_scale method
- #5679: MAINT: DRY up generic computations for discrete distributions
- #5680: MAINT: stop shadowing builtins in stats.distributions
- #5681: forward port ENH: Re-enable broadcasting of fill_value
- #5684: BUG: Fix Akima1DInterpolator returning nans
- #5690: BUG: fix stats.ttest_ind_from_stats to handle arrays.
- #5691: BUG: fix generator in io._loadarff to comply with PEP 0479
- #5693: ENH: use math.factorial for exact factorials
- #5695: DOC: dx might be a float, not only an integer
- #5699: MAINT: io: micro-optimize Matlab reading code for size
- #5701: Implement OptimizeResult.__dir__
- #5703: ENH: stats: make R^2 printing optional in probplot
- #5704: MAINT: typo ouf->out
- #5705: BUG: fix typo in query_pairs
- #5707: DOC:Add some explanation for ftol xtol in scipy.optimize.fmin
- #5708: DOC: optimize: PEP8 minimize docstring
- #5709: MAINT: optimize Cython code for speed and size
- #5713: [DOC] Fix broken link to reference
- #5717: DOC: curve_fit raises RuntimeError on failure.
- #5724: forward port gh-5720
- #5728: STY: remove a blank line
- #5729: ENH: spatial: speed up boolean distances
- #5732: MAINT: differential_evolution changes to default keywords break…
- #5733: TST: differential_evolution - population initiation tests
- #5736: Complex number support in log1p, expm1, and xlog1py
- #5741: MAINT: sparse: clean up extraction functions
- #5742: DOC: signal: Explain fftbins in get_window
- #5748: ENH: Add O(N) random matrix generator
- #5749: ENH: Add polyphase resampling
- #5756: RFC: Bump the minimum numpy version, drop older python versions
- #5761: DOC: Some improvements to least squares docstrings
- #5762: MAINT: spatial: distance refactoring
- #5768: DOC: Fix io.loadmat docstring for mdict param
- #5770: BUG: Accept anything np.dtype can handle for a dtype in sparse.random
- #5772: Update sparse.csgraph.laplacian docstring

- #5777: BUG: fix special.hyp0f1 to work correctly for complex inputs.
- #5780: DOC: Update PIL error install URL
- #5781: DOC: Fix documentation on solve_discrete_lyapunov
- #5782: DOC: cKDTree and KDTree now reference each other
- #5783: DOC: Clarify finish behaviour in scipy.optimize.brute
- #5784: MAINT: Change default tolerances of least_squares to 1e-8
- #5787: BUG: Allow Processing of Zero Order State Space Models in signal.ss2tf
- #5788: DOC, BUG: Clarify and Enforce Input Types to 'Data' Objects
- #5789: ENH: sparse: speedup LIL matrix slicing (was #3338)
- #5791: DOC: README: remove coveralls.io
- #5792: MAINT: remove uses of deprecated np.random.random_integers
- #5794: fix affine_transform (fixes #1547 and #5702)
- #5795: DOC: Removed uniform method from kmeans2 doc
- #5797: DOC: Clarify the computation of weighted minkowski
- #5798: BUG: Ensure scipy's _asfarray returns ndarray
- #5799: TST: Mpmath testing patch
- #5801: allow reading of certain IDL 8.0 .sav files
- #5803: DOC: fix module name in error message
- #5804: DOC: special: Expanded docs for special functions.
- #5805: DOC: Fix order of returns in _spectral_helper
- #5806: ENH: sparse: vectorized coo_matrix.diagonal
- #5808: ENH: Added iqr function to compute IQR metric in scipy/stats/stats.py
- #5810: MAINT/BENCH: sparse: Benchmark cleanup and additions
- #5811: DOC: sparse.linalg: shape, not size
- #5813: Update sparse ARPACK functions min *ncv* value
- #5815: BUG: Error message contained wrong values
- #5816: remove dead code from stats tests
- #5820: "in"->"a" in order_filter docstring
- #5821: DOC: README: INSTALL.txt was renamed in 2014
- #5825: DOC: typo in the docstring of least_squares
- #5826: MAINT: sparse: increase test coverage
- #5827: NdPPoly rebase
- #5828: Improve numerical stability of hyp0f1 for large orders
- #5829: ENH: sparse: Add copy parameter to all .toXXX() methods in sparse…
- #5830: DOC: rework INSTALL.rst.txt
- #5831: Adds plotting options to voronoi_plot_2d

- #5834: Update stats.binom_test() docstring
- #5836: ENH, TST: Allow SIMO tf's for tf2ss
- #5837: DOC: Image examples
- #5838: ENH: sparse: add eliminate_zeros() to coo_matrix
- #5839: BUG: Fixed name of NumpyVersion.__repr__
- #5845: MAINT: Fixed typos in documentation
- #5847: Fix bugs in sparsetools
- #5848: BUG: sparse.linalg: add locks to ensure ARPACK threadsafety
- #5849: ENH: sparse.linalg: upgrade to superlu 5.1.1
- #5851: ENH: expose lapack's ilaver to python to allow lapack verion…
- #5852: MAINT: runtests.py: ensure Ctrl-C interrupts the build
- #5854: DOC: Minor update to documentation
- #5855: Pr 5640
- #5859: ENH: Add random correlation matrix generator
- #5862: BUG: Allow expm for complex matrix with shape (1, 1)
- #5863: FIX: Fix test
- #5864: DOC: add a little note about the Normal survival function (Q-function)
- #5867: Fix for #5865
- #5869: extend normal distribution cdf to complex domain
- #5872: DOC: Note that morlet and cwt don't work together
- #5875: DOC: interp2d class description
- #5876: MAINT: spatial: remove a stray print statement
- #5878: MAINT: Fixed noisy UserWarnings in ndimage tests. Fixes #5877
- #5879: MAINT: sparse.linalg/superlu: add explicit casts to resolve compiler…
- #5880: MAINT: signal: import gcd from math and not fractions when on…
- #5887: Neldermead initial simplex
- #5894: BUG: _CustomLinearOperator unpickalable in python3.5
- #5895: DOC: special: slightly improve the multigammaln docstring
- #5900: Remove duplicate assignment.
- #5901: Update bundled ARPACK
- #5904: ENH: Make convolve and correlate order-agnostic
- #5905: ENH: sparse.linalg: further LGMRES cleanups
- #5906: Enhancements and cleanup in scipy.integrate (attempt #2)
- #5907: ENH: Change sparse *sum* and *mean* dtype casting to match…
- #5909: changes for convolution symmetry
- #5913: MAINT: basinhopping remove instance test closes #5440

- #5919: MAINT: uninitialised var if basinhopping niter=0. closes #5915
- #5920: BLD: Fix missing lsame.c error for MKL
- #5921: DOC: interpolate: add example showing how to work around issue…
- #5926: MAINT: spatial: upgrade to Qhull 2015.2
- #5928: MAINT: sparse: optimize DIA sum/diagonal, csgraph.laplacian
- #5929: Update info/URL for octave-maintainers discussion
- #5930: TST: special: silence DeprecationWarnings from sph_yn
- #5931: ENH: implement the principle branch of the logarithm of Gamma.
- #5934: Typo: “mush” => “must”
- #5935: BUG:string comparison stats._binned_statistic closes #5927
- #5938: Cythonize stats.ks_2samp for a ~33% gain in speed.
- #5939: DOC: fix optimize.fmin convergence docstring
- #5941: Fix minor typo in squareform docstring
- #5942: Update linregress stderr description.
- #5943: ENH: Improve numerical accuracy of lognorm
- #5944: Merge vonmises into stats pyx
- #5945: MAINT: interpolate: Tweak declaration to avoid cython warning…
- #5946: MAINT: sparse: clean up format conversion methods
- #5949: BUG: fix sparse .mean to return a scalar instead of a matrix
- #5955: MAINT: Replace calls to *hanning* with *hann*
- #5956: DOC: Missing periods interfering with parsing
- #5958: MAINT: add a test for lognorm.sf underflow
- #5961: MAINT _centered(): rename size to shape
- #5962: ENH: constants: Add multi-scale temperature conversion function
- #5965: ENH: special: faster way for calculating comb() for exact=True
- #5975: ENH: Improve FIR path of signal.decimate
- #5977: MAINT/BUG: sparse: remove overzealous bmat checks
- #5978: minimize_neldermead() stop at user requested maxiter or maxfev
- #5983: ENH: make sparse *sum* cast dtypes like NumPy *sum* for 32-bit…
- #5985: BUG, API: Add *jac* parameter to curve_fit
- #5989: ENH: Add firls least-squares fitting
- #5990: BUG: read tries to handle 20-bit WAV files but shouldn’t
- #5991: DOC: Cleanup wav read/write docs and add tables for common types
- #5994: ENH: Add gesvd method for svd
- #5996: MAINT: Wave cleanup
- #5997: TST: Break up upfirdn tests & compare to lfilter

- #6001: Filter design docs
- #6002: COMPAT: Expand compatibility fromnumeric.py
- #6007: ENH: Skip conversion of TF to TF in freqresp
- #6009: DOC: fix incorrect versionadded for entr, rel_entr, kl_div
- #6013: Fixed the entropy calculation of the von Mises distribution.
- #6014: MAINT: make gamma, rgamma use loggamma for complex arguments
- #6020: WIP: ENH: add exact=True factorial for vectors
- #6022: Added 'lanczos' to the image interpolation function list.
- #6024: BUG: optimize: do not use dummy constraints in SLSQP when no…
- #6025: ENH: Boundary value problem solver for ODE systems
- #6029: MAINT: Future imports for optimize._lsq
- #6030: ENH: stats.trap - adding trapezoidal distribution closes #6028
- #6031: MAINT: Some improvements to optimize._numdiff
- #6032: MAINT: Add special/_comb.c to .gitignore
- #6033: BUG: check the requested approximation rank in interpolative.svd
- #6034: DOC: Doc for mannwhitneyu in stats.py corrected
- #6040: FIX: Edit the wrong link in f_oneway
- #6044: BUG: (ordqz) always increase parameter lwork by 1.
- #6047: ENH: extend special.spence to complex arguments.
- #6049: DOC: Add documentation of PR #5640 to the 0.18.0 release notes
- #6050: MAINT: small cleanups related to loggamma
- #6070: Add asarray to explicitly cast list to numpy array in wilcoxon…
- #6071: DOC: antialiasing filter and link decimate resample, etc.
- #6075: MAINT: reimplement special.digamma for complex arguments
- #6080: avoid multiple computation in kstest
- #6081: Clarified pearson correlation return value
- #6085: ENH: allow long indices of sparse matrix with umfpack in spsolve()
- #6086: fix description for associated Laguerre polynomials
- #6087: Corrected docstring of splrep.
- #6094: ENH: special: change zeta signature to zeta(x, q=1)
- #6095: BUG: fix integer overflow in special.spence
- #6106: Fixed Issue #6105
- #6116: BUG: matrix logarithm edge case
- #6119: TST: DeprecationWarnings in stats on python 3.5 closes #5885
- #6120: MAINT: sparse: clean up sputils.isintlike
- #6122: DOC: optimize: linprog docs should say minimize instead of maximize

- #6123: DOC: optimize: document the *fun* field in `scipy.optimize.OptimizeResult`
- #6124: Move FFT zero-padding calculation from signaltools to fftpack
- #6125: MAINT: improve special.gammainc in the `a ~ x` regime.
- #6130: BUG: sparse: Fix COO dot with zero columns
- #6138: ENH: stats: Improve behavior of genextreme.sf and genextreme.isf
- #6146: MAINT: simplify the expit implementation
- #6151: MAINT: special: make generate_ufuncs.py output deterministic
- #6152: TST: special: better test for gammainc at large arguments
- #6153: ENH: Make next_fast_len public and faster
- #6154: fix typo “mush”–>”must”
- #6155: DOC: Fix some incorrect RST definition lists
- #6160: make logsumexp error out on a masked array
- #6161: added missing bracket to rosen documentation
- #6163: ENH: Added “kappa4” and “kappa3” distributions.
- #6164: DOC: Minor clean-up in integrate._bvp
- #6169: Fix mpf_assert_allclose to handle iterable results, such as maps
- #6170: Fix pchip_interpolate convenience function
- #6172: Corrected misplaced bracket in doc string
- #6175: ENH: sparse.csgraph: Pass indices to shortest_path
- #6178: TST: increase test coverage of sf and isf of a generalized extreme…
- #6179: TST: avoid a deprecation warning from numpy
- #6181: ENH: Boundary conditions for CubicSpline
- #6182: DOC: Add examples/graphs to max_len_seq
- #6183: BLD: update Bento build config files for recent changes.
- #6184: BUG: fix issue in io/wavfile for float96 input.
- #6186: ENH: Periodic extrapolation for PPoly and BPoly
- #6192: MRG: Add circle-CI
- #6193: ENH: sparse: avoid setitem densification
- #6196: Fixed missing sqrt in docstring of Mahalanobis distance in cdist,…
- #6206: MAINT: Minor changes in solve_bvp
- #6207: BUG: linalg: for BLAS, downcast complex256 to complex128, not…
- #6209: BUG: io.matlab: avoid buffer overflows in read_element_into
- #6210: BLD: use setuptools when building.
- #6214: BUG: sparse.linalg: fix bug in LGMRES breakdown handling
- #6215: MAINT: special: make loggamma use zdiv
- #6220: DOC: Add parameter

- #6221: ENH: Improve Newton solver for solve_bvp
- #6223: pchip should work for length-2 arrays
- #6224: signal.lti: deprecate cross-class properties/setters
- #6229: BUG: optimize: avoid an infinite loop in Newton-CG
- #6230: Add example for application of gaussian filter
- #6236: MAINT: gumbel_l accuracy
- #6237: MAINT: rayleigh accuracy
- #6238: MAINT: logistic accuracy
- #6239: MAINT: bradford distribution accuracy
- #6240: MAINT: avoid bad fmin in l-bfgs-b due to maxfun interruption
- #6241: MAINT: weibull_min accuracy
- #6246: ENH: Add _support_mask to distributions
- #6247: fixed a print error for an example of ode
- #6249: MAINT: change x-axis label for stats.probplot to "theoretical…
- #6250: DOC: fix typos
- #6251: MAINT: constants: filter out test noise from deprecated conversions
- #6252: MAINT: io/arff: remove unused variable
- #6253: Add examples to scipy.ndimage.filters
- #6254: MAINT: special: fix some build warnings
- #6258: MAINT: inverse gamma distribution accuracy
- #6260: MAINT: signal.decimate - Use discrete-time objects
- #6262: BUG: odr: fix string formatting
- #6267: TST: fix some test issues in interpolate and stats.
- #6269: TST: fix some warnings in the test suite
- #6274: ENH: Add sosfiltfilt
- #6276: DOC: update release notes for 0.18.0
- #6277: MAINT: update the author name mapping
- #6282: DOC: Correcting references for scipy.stats.normaltest
- #6283: DOC: some more additions to 0.18.0 release notes.
- #6284: Add *versionadded::* directive to *loggamma*.
- #6285: BUG: stats: Inconsistency in the multivariate_normal docstring…
- #6290: Add author list, gh-lists to 0.18.0 release notes
- #6293: TST: special: relax a test's precision
- #6295: BUG: sparse: stop comparing None and int in bsr_matrix constructor
- #6313: MAINT: Fix for python 3.5 travis-ci build problem.
- #6327: TST: signal: use assert_allclose for testing near-equality in…

- #6330: BUG: spatial/qhull: allocate qhT via malloc to ensure CRT likes…
- #6332: TST: fix stats.iqr test to not emit warnings, and fix line lengths.
- #6334: MAINT: special: fix a test for hyp0f1
- #6347: TST: spatial.qhull: skip a test on 32-bit platforms
- #6350: BUG: optimize/slsqp: don't overwrite an array out of bounds
- #6351: BUG: #6318 Interp1d 'nearest' integer x-axis overflow issue fixed
- #6355: Backports for 0.18.0

5.28 SciPy 0.17.1 Release Notes

SciPy 0.17.1 is a bug-fix release with no new features compared to 0.17.0.

5.28.1 Issues closed for 0.17.1

- #5817: BUG: skew, kurtosis return np.nan instead of "propagate"
- #5850: Test failed with sgelsy
- #5898: interpolate.interp1d crashes using float128
- #5953: Massive performance regression in cKDTree.query with L_inf distance…
- #6062: mannwhitneyu breaks backward compatibility in 0.17.0
- #6134: T test does not handle nans

5.28.2 Pull requests for 0.17.1

- #5902: BUG: interpolate: make interp1d handle np.float128 again
- #5957: BUG: slow down with p=np.inf in 0.17 cKDTree.query
- #5970: Actually propagate nans through stats functions with nan_policy="propagate"
- #5971: BUG: linalg: fix lwork check in `*gelsy`
- #6074: BUG: special: fixed violation of strict aliasing rules.
- #6083: BUG: Fix dtype for sum of linear operators
- #6100: BUG: Fix mannwhitneyu to be backward compatible
- #6135: Don't pass null pointers to LAPACK, even during workspace queries.
- #6148: stats: fix handling of nan values in T tests and kendalltau

5.29 SciPy 0.17.0 Release Notes

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    - `scipy.signal` *improvements*
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    - `scipy.sparse` *improvements*
    - `scipy.spatial` *improvements*
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SciPy 0.17.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.17.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.5 and NumPy 1.6.2 or greater.

Release highlights:

- New functions for linear and nonlinear least squares optimization with constraints: *scipy.optimize.lsq_linear* and *scipy.optimize.least_squares*
- Support for fitting with bounds in *scipy.optimize.curve_fit*.
- Significant improvements to *scipy.stats*, providing many functions with better handing of inputs which have NaNs or are empty, improved documentation, and consistent behavior between *scipy.stats* and *scipy.stats.mstats*.
- Significant performance improvements and new functionality in *scipy.spatial.cKDTree*.

5.29.1 New features

`scipy.cluster` improvements

A new function *scipy.cluster.hierarchy.cut_tree*, which determines a cut tree from a linkage matrix, was added.

`scipy.io` improvements

scipy.io.mmwrite gained support for symmetric sparse matrices.

`scipy.io.netcdf` gained support for masking and scaling data based on data attributes.

`scipy.optimize` improvements

Linear assignment problem solver

scipy.optimize.linear_sum_assignment is a new function for solving the linear sum assignment problem. It uses the Hungarian algorithm (Kuhn-Munkres).

Least squares optimization

A new function for *nonlinear* least squares optimization with constraints was added: *scipy.optimize.least_squares*. It provides several methods: Levenberg-Marquardt for unconstrained problems, and two trust-region methods for constrained ones. Furthermore it provides different loss functions. New trust-region methods also handle sparse Jacobians.

A new function for *linear* least squares optimization with constraints was added: *scipy.optimize.lsq_linear*. It provides a trust-region method as well as an implementation of the Bounded-Variable Least-Squares (BVLS) algorithm.

scipy.optimize.curve_fit now supports fitting with bounds.

`scipy.signal` improvements

A `mode` keyword was added to *scipy.signal.spectrogram*, to let it return other spectrograms than power spectral density.

`scipy.stats` improvements

Many functions in *scipy.stats* have gained a `nan_policy` keyword, which allows specifying how to treat input with NaNs in them: propagate the NaNs, raise an error, or omit the NaNs.

Many functions in *scipy.stats* have been improved to correctly handle input arrays that are empty or contain infs/nans.

A number of functions with the same name in *scipy.stats* and *scipy.stats.mstats* were changed to have matching signature and behavior. See gh-5474 for details.

scipy.stats.binom_test and *scipy.stats.mannwhitneyu* gained a keyword `alternative`, which allows specifying the hypothesis to test for. Eventually all hypothesis testing functions will get this keyword.

For methods of many continuous distributions, complex input is now accepted.

Matrix normal distribution has been implemented as *scipy.stats.matrix_normal*.

`scipy.sparse` improvements

The *axis* keyword was added to sparse norms, *scipy.sparse.linalg.norm*.

`scipy.spatial` improvements

scipy.spatial.cKDTree was partly rewritten for improved performance and several new features were added to it:

- the `query_ball_point` method became significantly faster
- `query` and `query_ball_point` gained an `n_jobs` keyword for parallel execution
- build and query methods now release the GIL
- full pickling support
- support for periodic spaces
- the `sparse_distance_matrix` method can now return and sparse matrix type

`scipy.interpolate` improvements

Out-of-bounds behavior of *scipy.interpolate.interp1d* has been improved. Use a two-element tuple for the `fill_value` argument to specify separate fill values for input below and above the interpolation range. Linear and nearest interpolation kinds of *scipy.interpolate.interp1d* support extrapolation via the `fill_value="extrapolate"` keyword.

`fill_value` can also be set to an array-like (or a two-element tuple of array-likes for separate below and above values) so long as it broadcasts properly to the non-interpolated dimensions of an array. This was implicitly supported by previous versions of scipy, but support has now been formalized and gets compatibility-checked before use. For example, a set of `y` values to interpolate with shape `(2, 3, 5)` interpolated along the last axis (2) could accept a `fill_value` array with shape `()` (singleton), `(1,)`, `(2, 1)`, `(1, 3)`, `(3,)`, or `(2, 3)`; or it can be a 2-element tuple to specify separate below and above bounds, where each of the two tuple elements obeys proper broadcasting rules.

`scipy.linalg` improvements

The default algorithm for *scipy.linalg.leastsq* has been changed to use LAPACK's function `*gelsd`. Users wanting to get the previous behavior can use a new keyword `lapack_driver="gelss"` (allowed values are "gelss", "gelsd" and "gelsy").

`scipy.sparse` matrices and linear operators now support the matmul (`@`) operator when available (Python 3.5+). See [PEP 465](https://legacy.python.org/dev/peps/pep-0465/)

A new function *scipy.linalg.ordqz*, for QZ decomposition with reordering, has been added.

5.29.2 Deprecated features

`scipy.stats.histogram` is deprecated in favor of `np.histogram`, which is faster and provides the same functionality.

`scipy.stats.threshold` and `scipy.mstats.threshold` are deprecated in favor of `np.clip`. See issue #617 for details.

`scipy.stats.ss` is deprecated. This is a support function, not meant to be exposed to the user. Also, the name is unclear. See issue #663 for details.

`scipy.stats.square_of_sums` is deprecated. This too is a support function not meant to be exposed to the user. See issues #665 and #663 for details.

`scipy.stats.f_value`, `scipy.stats.f_value_multivariate`, `scipy.stats.f_value_wilks_lambda`, and `scipy.mstats.f_value_wilks_lambda` are deprecated. These are related to ANOVA, for which `scipy.stats` provides quite limited functionality and these functions are not very useful standalone. See issues #660 and #650 for details.

`scipy.stats.chisqprob` is deprecated. This is an alias. `stats.chi2.sf` should be used instead.

`scipy.stats.betai` is deprecated. This is an alias for `special.betainc` which should be used instead.

5.29.3 Backwards incompatible changes

The functions `stats.trim1` and `stats.trimboth` now make sure the elements trimmed are the lowest and/or highest, depending on the case. Slicing without at least partial sorting was previously done, but didn't make sense for unsorted input.

When `variable_names` is set to an empty list, `scipy.io.loadmat` now correctly returns no values instead of all the contents of the MAT file.

Element-wise multiplication of sparse matrices now returns a sparse result in all cases. Previously, multiplying a sparse matrix with a dense matrix or array would return a dense matrix.

The function `misc.lena` has been removed due to license incompatibility.

The constructor for `sparse.coo_matrix` no longer accepts `(None, (m,n))` to construct an all-zero matrix of shape `(m,n)`. This functionality was deprecated since at least 2007 and was already broken in the previous SciPy release. Use `coo_matrix((m,n))` instead.

The Cython wrappers in `linalg.cython_lapack` for the LAPACK routines `*gegs`, `*gegv`, `*gelsx`, `*geqpf`, `*ggsvd`, `*ggsvp`, `*lahrd`, `*latzm`, `*tzrqf` have been removed since these routines are not present in the new LAPACK 3.6.0 release. With the exception of the routines `*ggsvd` and `*ggsvp`, these were all deprecated in favor of routines that are currently present in our Cython LAPACK wrappers.

Because the LAPACK `*gegv` routines were removed in LAPACK 3.6.0. The corresponding Python wrappers in `scipy.linalg.lapack` are now deprecated and will be removed in a future release. The source files for these routines have been temporarily included as a part of `scipy.linalg` so that SciPy can be built against LAPACK versions that do not provide these deprecated routines.

5.29.4 Other changes

Html and pdf documentation of development versions of Scipy is now automatically rebuilt after every merged pull request.

scipy.constants is updated to the CODATA 2014 recommended values.

Usage of *scipy.fftpack* functions within Scipy has been changed in such a way that PyFFTW can easily replace *scipy.fftpack* functions (with improved performance). See gh-5295 for details.

The `imread` functions in *scipy.misc* and *scipy.ndimage* were unified, for which a `mode` argument was added to *scipy.misc.imread*. Also, bugs for 1-bit and indexed RGB image formats were fixed.

`runtests.py`, the development script to build and test Scipy, now allows building in parallel with `--parallel`.

5.29.5 Authors

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- Peter Yin +

A total of 101 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.17.0

- #1923: problem with numpy 0's in stats.poisson.rvs (Trac #1398)
- #2138: scipy.misc.imread segfaults on 1 bit png (Trac #1613)
- #2237: distributions do not accept complex arguments (Trac #1718)
- #2282: scipy.special.hyp1f1(0.5, 1.5, -1000) fails (Trac #1763)
- #2618: poisson.pmf returns NaN if mu is 0
- #2957: hyp1f1 precision issue
- #2997: FAIL: test_qhull.TestUtilities.test_more_barycentric_transforms
- #3129: No way to set ranges for fitting parameters in Optimize functions
- #3191: interp1d should contain a fill_value_below and a fill_value_above…
- #3453: PchipInterpolator sets slopes at edges differently than Matlab's…
- #4106: ndimage._ni_support._normalize_sequence() fails with numpy.int64
- #4118: `scipy.integrate.ode.set_solout` called after `scipy.integrate.ode.set_initial_value` fails silently
- #4233: 1D scipy.interpolate.griddata using method=nearest produces nans…
- #4375: All tests fail due to bad file permissions
- #4580: scipy.ndimage.filters.convolve documenation is incorrect
- #4627: logsumexp with sign indicator - enable calculation with negative…
- #4702: logsumexp with zero scaling factor
- #4834: gammainc should return 1.0 instead of NaN for infinite x
- #4838: enh: exprel special function
- #4862: the scipy.special.boxcox function is inaccurate for denormal…
- #4887: Spherical harmonic incongruences
- #4895: some scipy ufuncs have inconsistent output dtypes?
- #4923: logm does not aggressively convert complex outputs to float
- #4932: BUG: stats: The *fit* method of the distributions silently ignores…
- #4956: Documentation error in `scipy.special.bi_zeros`
- #4957: Docstring for *pbvv_seq* is wrong
- #4967: block_diag should look at dtypes of all arguments, not only the…
- #5037: scipy.optimize.minimize error messages are printed to stdout…

- #5039: Cubic interpolation: On entry to DGESDD parameter number 12 had…
- #5163: Base case example of Hierarchical Clustering (offer)
- #5181: BUG: stats.genextreme.entropy should use the explicit formula
- #5184: Some? wheels don't express a numpy dependency
- #5197: mstats: test_kurtosis fails (ULP max is 2)
- #5260: Typo causing an error in splrep
- #5263: Default epsilon in rbf.py fails for colinear points
- #5276: Reading empty (no data) arff file fails
- #5280: 1d scipy.signal.convolve much slower than numpy.convolve
- #5326: Implementation error in scipy.interpolate.PchipInterpolator
- #5370: Test issue with test_quadpack and libm.so as a linker script
- #5426: ERROR: test_stats.test_chisquare_masked_arrays
- #5427: Automate installing correct numpy versions in numpy-vendor image
- #5430: Python3 : Numpy scalar types "not iterable"; specific instance…
- #5450: BUG: spatial.ConvexHull triggers a seg. fault when given nans.
- #5478: clarify the relation between matrix normal distribution and *multivariate_normal*
- #5539: lstsq related test failures on windows binaries from numpy-vendor
- #5560: doc: scipy.stats.burr pdf issue
- #5571: lstsq test failure after lapack_driver change
- #5577: ordqz segfault on Python 3.4 in Wine
- #5578: scipy.linalg test failures on python 3 in Wine
- #5607: Overloaded 'isnan(double&)' is ambiguous when compiling with…
- #5629: Test for lstsq randomly failed
- #5630: memory leak with scipy 0.16 spatial cKDEtree
- #5689: isnan errors compiling scipy/special/Faddeeva.cc with clang++
- #5694: fftpack test failure in test_import
- #5719: curve_fit(method!="lm") ignores initial guess

Pull requests for 0.17.0

- #3022: hyp1f1: better handling of large negative arguments
- #3107: ENH: Add ordered QZ decomposition
- #4390: ENH: Allow axis and keepdims arguments to be passed to scipy.linalg.norm.
- #4671: ENH: add axis to sparse norms
- #4796: ENH: Add cut tree function to scipy.cluster.hierarchy
- #4809: MAINT: cauchy moments are undefined
- #4821: ENH: stats: make distribution instances picklable

- #4839: ENH: Add scipy.special.exprel relative error exponential ufunc
- #4859: Logsumexp fixes - allows sign flags and b==0
- #4865: BUG: scipy.io.mmio.write: error with big indices and low precision
- #4869: add as_inexact option to _lib._util._asarray_validated
- #4884: ENH: Finite difference approximation of Jacobian matrix
- #4890: ENH: Port cKDTree query methods to C++, allow pickling on Python…
- #4892: how much doctesting is too much?
- #4896: MAINT: work around a possible numpy ufunc loop selection bug
- #4898: MAINT: A bit of pyflakes-driven cleanup.
- #4899: ENH: add 'alternative' keyword to hypothesis tests in stats
- #4903: BENCH: Benchmarks for interpolate module
- #4905: MAINT: prepend underscore to mask_to_limits; delete masked_var.
- #4906: MAINT: Benchmarks for optimize.leastsq
- #4910: WIP: Trimmed statistics functions have inconsistent API.
- #4912: MAINT: fix typo in stats tutorial. Closes gh-4911.
- #4914: DEP: deprecate *scipy.stats.ss* and *scipy.stats.square_of_sums*.
- #4924: MAINT: if the imaginary part of logm of a real matrix is small,…
- #4930: BENCH: Benchmarks for signal module
- #4941: ENH: update *find_repeats*.
- #4942: MAINT: use np.float64_t instead of np.float_t in cKDTree
- #4944: BUG: integer overflow in correlate_nd
- #4951: do not ignore invalid kwargs in distributions fit method
- #4958: Add some detail to docstrings for special functions
- #4961: ENH: stats.describe: add bias kw and empty array handling
- #4963: ENH: scipy.sparse.coo.coo_matrix.__init__: less memory needed
- #4968: DEP: deprecate `stats.f_value*` and `mstats.f_value*` functions.
- #4969: ENH: review *stats.relfreq* and *stats.cumfreq*; fixes to *stats.histogram*
- #4971: Extend github source links to line ranges
- #4972: MAINT: impove the error message in validate_runtests_log
- #4976: DEP: deprecate *scipy.stats.threshold*
- #4977: MAINT: more careful dtype treatment in block diagonal matrix…
- #4979: ENH: distributions, complex arguments
- #4984: clarify dirichlet distribution error handling
- #4992: ENH: *stats.fligner* and *stats.bartlett* empty input handling.
- #4996: DOC: fix stats.spearmanr docs
- #4997: Fix up boxcox for underflow / loss of precision

- #4998: DOC: improved documentation for *stats.ppcc_max*
- #5000: ENH: added empty input handling *scipy.moment*; doc enhancements
- #5003: ENH: improves rankdata algorithm
- #5005: scipy.stats: numerical stability improvement
- #5007: ENH: nan handling in functions that use *stats._chk_asarray*
- #5009: remove coveralls.io
- #5010: Hypergeometric distribution log survival function
- #5014: Patch to compute the volume and area of convex hulls
- #5015: DOC: Fix mistaken variable name in sawtooth
- #5016: DOC: resample example
- #5017: DEP: deprecate *stats.betai* and *stats.chisqprob*
- #5018: ENH: Add test on random inpu to volume computations
- #5026: BUG: Fix return dtype of lil_matrix.getnnz(axis=0)
- #5030: DOC: resample slow for prime output too
- #5033: MAINT: integrate, special: remove unused R1MACH and Makefile
- #5034: MAINT: signal: lift max_len_seq validation out of Cython
- #5035: DOC/MAINT: refguide / doctest drudgery
- #5041: BUG: fixing some small memory leaks detected by cppcheck
- #5044: [GSoC] ENH: New least-squares algorithms
- #5050: MAINT: C fixes, trimmed a lot of dead code from Cephes
- #5057: ENH: sparse: avoid densifying on sparse/dense elementwise mult
- #5058: TST: stats: add a sample distribution to the test loop
- #5061: ENH: spatial: faster 2D Voronoi and Convex Hull plotting
- #5065: TST: improve test coverage for *stats.mvsdist* and *stats.bayes_mvs*
- #5066: MAINT: fitpack: remove a noop
- #5067: ENH: empty and nan input handling for *stats.kstat* and *stats.kstatvar*
- #5071: DOC: optimize: Correct paper reference, add doi
- #5072: MAINT: scipy.sparse cleanup
- #5073: DOC: special: Add an example showing the relation of diric to…
- #5075: DOC: clarified parameterization of stats.lognorm
- #5076: use int, float, bool instead of np.int, np.float, np.bool
- #5078: DOC: Rename fftpack docs to README
- #5081: BUG: Correct handling of scalar ‘b’ in lsmr and lsqr
- #5082: loadmat variable_names: don’t confuse [] and None.
- #5083: Fix integrate.fixed_quad docstring to indicate None return value
- #5086: Use solve() instead of inv() for gaussian_kde

- #5090: MAINT: stats: add explicit _sf, _isf to gengamma distribution
- #5094: ENH: scipy.interpolate.NearestNDInterpolator: cKDTree configurable
- #5098: DOC: special: fix typesetting in `*_roots quadrature` functions
- #5099: DOC: make the docstring of stats.moment raw
- #5104: DOC/ENH fixes and micro-optimizations for scipy.linalg
- #5105: enh: made l-bfgs-b parameter for the maximum number of line search…
- #5106: TST: add NIST test cases to *stats.f_oneway*
- #5110: [GSoC]: Bounded linear least squares
- #5111: MAINT: special: Cephes cleanup
- #5118: BUG: FIR path failed if len(x) < len(b) in lfilter.
- #5124: ENH: move the filliben approximation to a publicly visible function
- #5126: StatisticsCleanup: *stats.kruskal* review
- #5130: DOC: update PyPi trove classifiers. Beta -> Stable. Add license.
- #5131: DOC: differential_evolution, improve docstring for mutation and…
- #5132: MAINT: differential_evolution improve init_population_lhs comments…
- #5133: MRG: rebased mmio refactoring
- #5135: MAINT: *stats.mstats* consistency with *stats.stats*
- #5139: TST: linalg: add a smoke test for gh-5039
- #5140: EHN: Update constants.codata to CODATA 2014
- #5145: added ValueError to docstring as possible error raised
- #5146: MAINT: Improve implementation details and doc in *stats.shapiro*
- #5147: [GSoC] ENH: Upgrades to curve_fit
- #5150: Fix misleading wavelets/cwt example
- #5152: BUG: cluster.hierarchy.dendrogram: missing font size doesn't…
- #5153: add keywords to control the summation in discrete distributions…
- #5156: DOC: added comments on algorithms used in Legendre function
- #5158: ENH: optimize: add the Hungarian algorithm
- #5162: FIX: Remove lena
- #5164: MAINT: fix cluster.hierarchy.dendrogram issues and docs
- #5166: MAINT: changed *stats.pointbiserialr* to delegate to *stats.pearsonr*
- #5167: ENH: add nan_policy to *stats.kendalltau*.
- #5168: TST: added nist test case (Norris) to *stats.linregress*.
- #5169: update lpmv docstring
- #5171: Clarify metric parameter in linkage docstring
- #5172: ENH: add mode keyword to signal.spectrogram
- #5177: DOC: graphical example for KDTree.query_ball_point

- #5179: MAINT: stats: tweak the formula for ncx2.pdf
- #5188: MAINT: linalg: A bit of clean up.
- #5189: BUG: stats: Use the explicit formula in stats.genextreme.entropy
- #5193: BUG: fix uninitialized use in lartg
- #5194: BUG: properly return error to fortran from ode_jacobian_function
- #5198: TST: Fix TestCtypesQuad failure on Python 3.5 for Windows
- #5201: allow extrapolation in interp1d
- #5209: MAINT: Change complex parameter to boolean in Y_()
- #5213: BUG: sparse: fix logical comparison dtype conflicts
- #5216: BUG: sparse: fixing unbound local error
- #5218: DOC and BUG: Bessel function docstring improvements, fix array_like,…
- #5222: MAINT: sparse: fix COO ctor
- #5224: DOC: optimize: type of OptimizeResult.hess_inv varies
- #5228: ENH: Add maskandscale support to netcdf; based on pupynere and…
- #5229: DOC: sparse.linalg.svds doc typo fixed
- #5234: MAINT: sparse: simplify COO ctor
- #5235: MAINT: sparse: warn on todia() with many diagonals
- #5236: MAINT: ndimage: simplify thread handling/recursion + constness
- #5239: BUG: integrate: Fixed issue 4118
- #5241: qr_insert fixes, closes #5149
- #5246: Doctest tutorial files
- #5247: DOC: optimize: typo/import fix in linear_sum_assignment
- #5248: remove inspect.getargspec and test python 3.5 on Travis CI
- #5250: BUG: Fix sparse multiply by single-element zero
- #5261: Fix bug causing a TypeError in splrep when a runtime warning…
- #5262: Follow up to 4489 (Addition LAPACK routines in linalg.lstsq)
- #5264: ignore zero-length edges for default epsilon
- #5269: DOC: Typos and spell-checking
- #5272: MAINT: signal: Convert array syntax to memoryviews
- #5273: DOC: raw strings for docstrings with math
- #5274: MAINT: sparse: update cython code for MST
- #5278: BUG: io: Stop guessing the data delimiter in ARFF files.
- #5289: BUG: misc: Fix the Pillow work-around for 1-bit images.
- #5291: ENH: call np.correlate for 1d in scipy.signal.correlate
- #5294: DOC: special: Remove a potentially misleading example from the…
- #5295: Simplify replacement of fftpack by pyfftw

- #5296: ENH: Add matrix normal distribution to stats
- #5297: Fixed leaf_rotation and leaf_font_size in Python 3
- #5303: MAINT: stats: rewrite find_repeats
- #5307: MAINT: stats: remove unused Fortran routine
- #5313: BUG: sparse: fix diags for nonsquare matrices
- #5315: MAINT: special: Cephes cleanup
- #5316: fix input check for sparse.linalg.svds
- #5319: MAINT: Cython code maintenance
- #5328: BUG: Fix place_poles return values
- #5329: avoid a spurious divide-by-zero in Student t stats
- #5334: MAINT: integrate: miscellaneous cleanup
- #5340: MAINT: Printing Error Msg to STDERR and Removing iterate.dat
- #5347: ENH: add Py3.5-style matmul operator (e.g. A @ B) to sparse linear…
- #5350: FIX error, when reading 32-bit float wav files
- #5351: refactor the PCHIP interpolant's algorithm
- #5354: MAINT: construct csr and csc matrices from integer lists
- #5359: add a fast path to interp1d
- #5364: Add two fill_values to interp1d.
- #5365: ABCD docstrings
- #5366: Fixed typo in the documentation for scipy.signal.cwt() per #5290.
- #5367: DOC updated scipy.spatial.Delaunay example
- #5368: ENH: Do not create a throwaway class at every function call
- #5372: DOC: spectral: fix reference formatting
- #5375: PEP8 amendments to ffpack_basic.py
- #5377: BUG: integrate: builtin name no longer shadowed
- #5381: PEP8ified fftpack_pseudo_diffs.py
- #5385: BLD: fix Bento build for changes to optimize and spatial
- #5386: STY: PEP8 amendments to interpolate.py
- #5387: DEP: deprecate stats.histogram
- #5388: REL: add "make upload" command to doc/Makefile.
- #5389: DOC: updated origin param of scipy.ndimage.filters.convolve
- #5395: BUG: special: fix a number of edge cases related to $x = np.inf$.
- #5398: MAINT: stats: avoid spurious warnings in lognorm.pdf(0, s)
- #5407: ENH: stats: Handle mu=0 in stats.poisson
- #5409: Fix the behavior of discrete distributions at the right-hand…
- #5412: TST: stats: skip a test to avoid a spurious log(0) warning

- #5413: BUG: linalg: work around LAPACK single-precision lwork computation…
- #5414: MAINT: stats: move creation of namedtuples outside of function…
- #5415: DOC: fix up sections in ToC in the pdf reference guide
- #5416: TST: fix issue with a ctypes test for integrate on Fedora.
- #5418: DOC: fix bugs in signal.TransferFunction docstring. Closes gh-5287.
- #5419: MAINT: sparse: fix usage of NotImplementedError
- #5420: Raise proper error if maxiter < 1
- #5422: DOC: changed documentation of brent to be consistent with bracket
- #5444: BUG: gaussian_filter, BPoly.from_derivatives fail on numpy int…
- #5445: MAINT: stats: fix incorrect deprecation warnings and test noise
- #5446: DOC: add note about PyFFTW in fftpack tutorial.
- #5459: DOC: integrate: Some improvements to the differential equation…
- #5465: BUG: Relax mstats kurtosis test tolerance by a few ulp
- #5471: ConvexHull should raise ValueError for NaNs.
- #5473: MAINT: update decorators.py module to version 4.0.5
- #5476: BUG: imsave searches for wrong channel axis if image has 3 or…
- #5477: BLD: add numpy to setup/install_requires for OS X wheels
- #5479: ENH: return Jacobian/Hessian from BasinHopping
- #5484: BUG: fix ttest zero division handling
- #5486: Fix crash on kmeans2
- #5491: MAINT: Expose parallel build option to runtests.py
- #5494: Sort OptimizeResult.__repr__ by key
- #5496: DOC: update the author name mapping
- #5497: Enhancement to binned_statistic: option to unraveled returned…
- #5498: BUG: sparse: fix a bug in sparsetools input dtype resolution
- #5500: DOC: detect unprintable characters in docstrings
- #5505: BUG: misc: Ensure fromimage converts mode 'P' to 'RGB' or 'RGBA'.
- #5514: DOC: further update the release notes
- #5515: ENH: optionally disable fixed-point acceleration
- #5517: DOC: Improvements and additions to the matrix_normal doc
- #5518: Remove wrappers for LAPACK deprecated routines
- #5521: TST: skip a linalg.orth memory test on 32-bit platforms.
- #5523: DOC: change a few floats to integers in docstring examples
- #5524: DOC: more updates to 0.17.0 release notes.
- #5525: Fix to minor typo in documentation for scipy.integrate.ode
- #5527: TST: bump arccosh tolerance to allow for inaccurate numpy or…

- #5535: DOC: signal: minor clarification to docstring of TransferFunction.
- #5538: DOC: signal: fix find_peaks_cwt documentation
- #5545: MAINT: Fix typo in linalg/basic.py
- #5547: TST: mark TestEig.test_singular as knownfail in master.
- #5550: MAINT: work around lstsq driver selection issue
- #5556: BUG: Fixed broken dogbox trust-region radius update
- #5561: BUG: eliminate warnings, exception (on Win) in test_maskandscale;…
- #5567: TST: a few cleanups in the test suite; run_module_suite and clearer…
- #5568: MAINT: simplify poisson's _argcheck
- #5569: TST: bump GMean test tolerance to make it pass on Wine
- #5572: TST: lstsq: bump test tolerance for TravisCI
- #5573: TST: remove use of np.fromfile from cluster.vq tests
- #5576: Lapack deprecations
- #5579: TST: skip tests of linalg.norm axis keyword on numpy <= 1.7.x
- #5582: Clarify language of survival function documentation
- #5583: MAINT: stats/tests: A bit of clean up.
- #5588: DOC: stats: Add a note that stats.burr is the Type III Burr distribution.
- #5595: TST: fix test_lamch failures on Python 3
- #5600: MAINT: Ignore spatial/ckdtree.cxx and .h
- #5602: Explicitly numbered replacement fields for maintainability
- #5605: MAINT: collection of small fixes to test suite
- #5614: Minor doc change.
- #5624: FIX: Fix interpolate
- #5625: BUG: msvc9 binaries crash when indexing std::vector of size 0
- #5635: BUG: misspelled __dealloc__ in cKDTree.
- #5642: STY: minor fixup of formatting of 0.17.0 release notes.
- #5643: BLD: fix a build issue in special/Faddeeva.cc with isnan.
- #5661: TST: linalg tests used stdlib random instead of numpy.random.
- #5682: backports for 0.17.0
- #5696: Minor improvements to least_squares' docstring.
- #5697: BLD: fix for isnan/isinf issues in special/Faddeeva.cc
- #5720: TST: fix for file opening error in fftpack test_import.py
- #5722: BUG: Make curve_fit respect an initial guess with bounds
- #5726: Backports for v0.17.0rc2
- #5727: API: Changes to least_squares API

5.30 SciPy 0.16.1 Release Notes

SciPy 0.16.1 is a bug-fix release with no new features compared to 0.16.0.

5.30.1 Issues closed for 0.16.1

- #5077: cKDTree not indexing properly for arrays with too many elements
- #5127: Regression in 0.16.0: solve_banded errors out in patsy test suite
- #5149: linalg tests apparently cause python to crash with numpy 1.10.0b1
- #5154: 0.16.0 fails to build on OS X; can't find Python.h
- #5173: failing stats.histogram test with numpy 1.10
- #5191: Scipy 0.16.x - TypeError: _asarray_validated() got an unexpected…
- #5195: tarballs missing documentation source
- #5363: FAIL: test_orthogonal.test_j_roots, test_orthogonal.test_js_roots

5.30.2 Pull requests for 0.16.1

- #5088: BUG: fix logic error in cKDTree.sparse_distance_matrix
- #5089: BUG: Don't overwrite b in lfilter's FIR path
- #5128: BUG: solve_banded failed when solving 1x1 systems
- #5155: BLD: fix missing Python include for Homebrew builds.
- #5192: BUG: backport as_inexact kwarg to _asarray_validated
- #5203: BUG: fix uninitialized use in lartg 0.16 backport
- #5204: BUG: properly return error to fortran from ode_jacobian_function…
- #5207: TST: Fix TestCtypesQuad failure on Python 3.5 for Windows
- #5352: TST: sparse: silence warnings about boolean indexing
- #5355: MAINT: backports for 0.16.1 release
- #5356: REL: update Paver file to ensure sdist contents are OK for releases.
- #5382: 0.16.x backport: MAINT: work around a possible numpy ufunc loop…
- #5393: TST:special: bump tolerance levels for test_j_roots and test_js_roots
- #5417: MAINT: stats: move namedtuple creating outside function calls.

5.31 SciPy 0.16.0 Release Notes

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- *SciPy 0.16.0 Release Notes*
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    - `scipy.sparse` *improvements*
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SciPy 0.16.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.16.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.6.2 or greater.

Highlights of this release include:

- A Cython API for BLAS/LAPACK in `scipy.linalg`
- A new benchmark suite. It's now straightforward to add new benchmarks, and they're routinely included with performance enhancement PRs.
- Support for the second order sections (SOS) format in `scipy.signal`.

5.31.1 New features

Benchmark suite

The benchmark suite has switched to using Airspeed Velocity for benchmarking. You can run the suite locally via `python runtests.py --bench`. For more details, see `benchmarks/README.rst`.

`scipy.linalg` improvements

A full set of Cython wrappers for BLAS and LAPACK has been added in the modules *scipy.linalg.cython_blas* and *scipy.linalg.cython_lapack*. In Cython, these wrappers can now be cimported from their corresponding modules and used without linking directly against BLAS or LAPACK.

The functions *scipy.linalg.qr_delete*, *scipy.linalg.qr_insert* and *scipy.linalg.qr_update* for updating QR decompositions were added.

The function *scipy.linalg.solve_circulant* solves a linear system with a circulant coefficient matrix.

The function *scipy.linalg.invpascal* computes the inverse of a Pascal matrix.

The function *scipy.linalg.solve_toeplitz*, a Levinson-Durbin Toeplitz solver, was added.

Added wrapper for potentially useful LAPACK function `*lasd4`. It computes the square root of the i-th updated eigenvalue of a positive symmetric rank-one modification to a positive diagonal matrix. See its LAPACK documentation and unit tests for it to get more info.

Added two extra wrappers for LAPACK least-square solvers. Namely, they are `*gelsd` and `*gelsy`.

Wrappers for the LAPACK `*lange` functions, which calculate various matrix norms, were added.

Wrappers for `*gtsv` and `*ptsv`, which solve `A*X = B` for tri-diagonal matrix `A`, were added.

`scipy.signal` improvements

Support for second order sections (SOS) as a format for IIR filters was added. The new functions are:

- *scipy.signal.sosfilt*
- *scipy.signal.sosfilt_zi*,
- *scipy.signal.sos2tf*
- *scipy.signal.sos2zpk*
- *scipy.signal.tf2sos*
- *scipy.signal.zpk2sos*.

Additionally, the filter design functions *iirdesign*, *iirfilter*, *butter*, *cheby1*, *cheby2*, *ellip*, and *bessel* can return the filter in the SOS format.

The function *scipy.signal.place_poles*, which provides two methods to place poles for linear systems, was added.

The option to use Gustafsson's method for choosing the initial conditions of the forward and backward passes was added to *scipy.signal.filtfilt*.

New classes `TransferFunction`, `StateSpace` and `ZerosPolesGain` were added. These classes are now returned when instantiating *scipy.signal.lti*. Conversion between those classes can be done explicitly now.

An exponential (Poisson) window was added as `scipy.signal.exponential`, and a Tukey window was added as `scipy.signal.tukey`.

The function for computing digital filter group delay was added as *scipy.signal.group_delay*.

The functionality for spectral analysis and spectral density estimation has been significantly improved: *scipy.signal.welch* became ~8x faster and the functions *scipy.signal.spectrogram*, *scipy.signal.coherence* and *scipy.signal.csd* (cross-spectral density) were added.

scipy.signal.lsim was rewritten - all known issues are fixed, so this function can now be used instead of `lsim2`; `lsim` is orders of magnitude faster than `lsim2` in most cases.

`scipy.sparse` improvements

The function *scipy.sparse.norm*, which computes sparse matrix norms, was added.

The function *scipy.sparse.random*, which allows to draw random variates from an arbitrary distribution, was added.

`scipy.spatial` improvements

scipy.spatial.cKDTree has seen a major rewrite, which improved the performance of the `query` method significantly, added support for parallel queries, pickling, and options that affect the tree layout. See pull request 4374 for more details.

The function *scipy.spatial.procrustes* for Procrustes analysis (statistical shape analysis) was added.

`scipy.stats` improvements

The Wishart distribution and its inverse have been added, as *scipy.stats.wishart* and *scipy.stats.invwishart*.

The Exponentially Modified Normal distribution has been added as *scipy.stats.exponnorm*.

The Generalized Normal distribution has been added as *scipy.stats.gennorm*.

All distributions now contain a `random_state` property and allow specifying a specific `numpy.random.RandomState` random number generator when generating random variates.

Many statistical tests and other *scipy.stats* functions that have multiple return values now return `namedtuples`. See pull request 4709 for details.

`scipy.optimize` improvements

A new derivative-free method DF-SANE has been added to the nonlinear equation system solving function *scipy.optimize.root*.

5.31.2 Deprecated features

`scipy.stats.pdf_fromgamma` is deprecated. This function was undocumented, untested and rarely used. Statsmodels provides equivalent functionality with `statsmodels.distributions.ExpandedNormal`.

`scipy.stats.fastsort` is deprecated. This function is unnecessary, `numpy.argsort` can be used instead.

`scipy.stats.signaltonoise` and `scipy.stats.mstats.signaltonoise` are deprecated. These functions did not belong in `scipy.stats` and are rarely used. See issue #609 for details.

`scipy.stats.histogram2` is deprecated. This function is unnecessary, `numpy.histogram2d` can be used instead.

5.31.3 Backwards incompatible changes

The deprecated global optimizer `scipy.optimize.anneal` was removed.

The following deprecated modules have been removed: `scipy.lib.blas`, `scipy.lib.lapack`, `scipy.linalg.cblas`, `scipy.linalg.fblas`, `scipy.linalg.clapack`, `scipy.linalg.flapack`. They had been deprecated since Scipy 0.12.0, the functionality should be accessed as *scipy.linalg.blas* and *scipy.linalg.lapack*.

The deprecated function `scipy.special.all_mat` has been removed.

The deprecated functions `fprob`, `ksprob`, `zprob`, `randwcdf` and `randwppf` have been removed from *scipy.stats*.

5.31.4 Other changes

The version numbering for development builds has been updated to comply with PEP 440.

Building with `python setup.py develop` is now supported.

5.31.5 Authors

- @axiru +
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- Helmut Toplitzer +
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- Anastasiia Tsyplia +
- Jacob Vanderplas
- Pauli Virtanen
- Matteo Visconti +
- Warren Weckesser
- Florian Wilhelm +
- Nathan Woods
- Haochen Wu +
- Daan Wynen +

A total of 93 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed for 0.16.0

- #1063: Implement a whishart distribution (Trac #536)
- #1885: Rbf: floating point warnings - possible bug (Trac #1360)
- #2020: Rbf default epsilon too large (Trac #1495)
- #2325: extending distributions, hypergeom, to degenerate cases (Trac…
- #3502: [ENH] linalg.hessenberg should use ORGHR for calc_q=True
- #3603: Passing array as window into signal.resample() fails
- #3675: Intermittent failures for signal.slepian on Windows
- #3742: Pchipinterpolator inconvenient as ppoly
- #3786: add procrustes?
- #3798: scipy.io.savemat fails for empty dicts
- #3975: Use RandomState in scipy.stats
- #4022: savemat incorrectly saves logical arrays
- #4028: scipy.stats.geom.logpmf(1,1) returns nan. The correct value is…
- #4030: simplify scipy.stats.betaprime.cdf
- #4031: improve accuracy of scipy.stats.gompertz distribution for small…
- #4033: improve accuracy of scipy.stats.lomax distribution for small…
- #4034: improve accuracy of scipy.stats.rayleigh distribution for large…
- #4035: improve accuracy of scipy.stats.truncexpon distribution for small…
- #4081: Error when reading matlab file: buffer is too small for requested…
- #4100: Why does qr(a, lwork=0) not fail?
- #4134: scipy.stats: rv_frozen has no expect() method
- #4204: Please add docstring to scipy.optimize.RootResults
- #4206: Wrap LAPACK tridiagonal solve routine *gtsv*
- #4208: Empty sparse matrices written to MAT file cannot be read by MATLAB
- #4217: use a TravisCI configuration with numpy built with NPY_RELAXED_STRIDES_CHECKING=1
- #4282: integrate.odeint raises an exception when full_output=1 and the…
- #4301: scipy and numpy version names do not follow pep 440
- #4355: PPoly.antiderivative() produces incorrect output
- #4391: spsolve becomes extremely slow with large b matrix
- #4393: Documentation glitsch in sparse.linalg.spilu
- #4408: Vector-valued constraints in minimize() et al
- #4412: Documentation of scipy.signal.cwt error

- #4428: dok.__setitem__ problem with negative indices
- #4434: Incomplete documentation for sparse.linalg.spsolve
- #4438: linprog() documentation example wrong
- #4445: Typo in scipy.special.expit doc
- #4467: Documentation Error in scipy.optimize options for TNC
- #4492: solve_toeplitz benchmark is bitrotting already
- #4506: lobpcg/sparse performance regression Jun 2014?
- #4520: g77_abi_wrappers needed on Linux for MKL as well
- #4521: Broken check in uses_mkl for newer versions of the library
- #4523: rbf with gaussian kernel seems to produce more noise than original…
- #4526: error in site documentation for poisson.pmf() method
- #4527: KDTree example doesn't work in Python 3
- #4550: `scipy.stats.mode` - UnboundLocalError on empty sequence
- #4554: filter out convergence warnings in optimization tests
- #4565: odeint messages
- #4569: remez: "ValueError: Failure to converge after 25 iterations….
- #4582: DOC: optimize: _minimize_scalar_brent does not have a disp option
- #4585: DOC: Erroneous latex-related characters in tutorial.
- #4590: sparse.linalg.svds should throw an exception if which not in…
- #4594: scipy.optimize.linprog IndexError when a callback is providen
- #4596: scipy.linalg.block_diag misbehavior with empty array inputs (v0.13.3)
- #4599: scipy.integrate.nquad should call _OptFunc when called with only…
- #4612: Crash in signal.lfilter on nd input with wrong shaped zi
- #4613: scipy.io.readsav error on reading sav file
- #4673: scipy.interpolate.RectBivariateSpline construction locks PyQt…
- #4681: Broadcasting in signal.lfilter still not quite right.
- #4705: kmeans k_or_guess parameter error if guess is not square array
- #4719: Build failure on 14.04.2
- #4724: GenGamma _munp function fails due to overflow
- #4726: FAIL: test_cobyla.test_vector_constraints
- #4734: Failing tests in stats with numpy master.
- #4736: qr_update bug or incompatibility with numpy 1.10?
- #4746: linprog returns solution violating equality constraint
- #4757: optimize.leastsq docstring mismatch
- #4774: Update contributor list for v0.16
- #4779: circmean and others do not appear in the documentation

- #4788: problems with scipy sparse linalg isolve iterative.py when complex
- #4791: BUG: scipy.spatial: incremental Voronoi doesn't increase size…

Pull requests for 0.16.0

- #3116: sparse: enhancements for DIA format
- #3157: ENH: linalg: add the function 'solve_circulant' for solving a…
- #3442: ENH: signal: Add Gustafsson's method as an option for the filtfilt…
- #3679: WIP: fix sporadic slepian failures
- #3680: Some cleanups in stats
- #3717: ENH: Add second-order sections filtering
- #3741: Dltisys changes
- #3956: add note to scipy.signal.resample about prime sample numbers
- #3980: Add check_finite flag to UnivariateSpline
- #3996: MAINT: stricter linalg argument checking
- #4001: BUG: numerical precision in dirichlet
- #4012: ENH: linalg: Add a function to compute the inverse of a Pascal…
- #4021: ENH: Cython api for lapack and blas
- #4089: Fixes for various PEP8 issues.
- #4116: MAINT: fitpack: trim down compiler warnings (unused labels, variables)
- #4129: ENH: stats: add a random_state property to distributions
- #4135: ENH: Add Wishart and inverse Wishart distributions
- #4195: improve the interpolate docs
- #4200: ENH: Add t-test from descriptive stats function.
- #4202: Dendrogram threshold color
- #4205: BLD: fix a number of Bento build warnings.
- #4211: add an ufunc for the inverse Box-Cox transfrom
- #4212: MRG:fix for gh-4208
- #4213: ENH: specific warning if matlab file is empty
- #4215: Issue #4209: splprep documentation updated to reflect dimensional…
- #4219: DOC: silence several Sphinx warnings when building the docs
- #4223: MAINT: remove two redundant lines of code
- #4226: try forcing the numpy rebuild with relaxed strides
- #4228: BLD: some updates to Bento config files and docs. Closes gh-3978.
- #4232: wrong references in the docs
- #4242: DOC: change example sample spacing
- #4245: Arff fixes

- #4246: MAINT: C fixes
- #4247: MAINT: remove some unused code
- #4249: Add routines for updating QR decompositions
- #4250: MAINT: Some pyflakes-driven cleanup in linalg and sparse
- #4252: MAINT trim away >10 kLOC of generated C code
- #4253: TST: stop shadowing ellip* tests vs boost data
- #4254: MAINT: special: use NPY_PI, not M_PI
- #4255: DOC: INSTALL: use Py3-compatible print syntax, and don't mention…
- #4256: ENH: spatial: reimplement cdist_cosine using np.dot
- #4258: BUG: io.arff #4429 #2088
- #4261: MAINT: signal: PEP8 and related style clean up.
- #4262: BUG: newton_krylov() was ignoring norm_tol argument, closes #4259
- #4263: MAINT: clean up test noise and optimize tests for docstrings…
- #4266: MAINT: io: Give an informative error when attempting to read…
- #4268: MAINT: fftpack benchmark integer division vs true division
- #4269: MAINT: avoid shadowing the eigvals function
- #4272: BUG: sparse: Fix bench_sparse.py
- #4276: DOC: remove confusing parts of the documentation related to writing…
- #4281: Sparse matrix multiplication: only convert array if needed (with…
- #4284: BUG: integrate: odeint crashed when the integration time was…
- #4286: MRG: fix matlab output type of logical array
- #4287: DEP: deprecate stats.pdf_fromgamma. Closes gh-699.
- #4291: DOC: linalg: fix layout in cholesky_banded docstring
- #4292: BUG: allow empty dict as proxy for empty struct
- #4293: MAINT: != -> not_equal in hamming distance implementation
- #4295: Pole placement
- #4296: MAINT: some cleanups in tests of several modules
- #4302: ENH: Solve toeplitz linear systems
- #4306: Add benchmark for conjugate gradient solver.
- #4307: BLD: PEP 440
- #4310: BUG: make stats.geom.logpmf(1,1) return 0.0 instead of nan
- #4311: TST: restore a test that uses slogdet now that we have dropped…
- #4313: Some minor fixes for stats.wishart addition.
- #4315: MAINT: drop numpy 1.5 compatibility code in sparse matrix tests
- #4318: ENH: Add random_state to multivariate distributions
- #4319: MAINT: fix hamming distance regression for exotic arrays, with…

- #4320: TST: a few changes like self.assertTrue(x == y, message) -> assert_equal(x,…
- #4321: TST: more changes like self.assertTrue(x == y, message) -> assert_equal(x,…
- #4322: TST: in test_signaltools, changes like self.assertTrue(x == y,…
- #4323: MAINT: clean up benchmarks so they can all be run as single files.
- #4324: Add more detailed committer guidelines, update MAINTAINERS.txt
- #4326: TST: use numpy.testing in test_hierarchy.py
- #4329: MAINT: stats: rename check_random_state test function
- #4330: Update distance tests
- #4333: MAINT: import comb, factorial from scipy.special, not scipy.misc
- #4338: TST: more conversions from nose to numpy.testing
- #4339: MAINT: remove the deprecated all_mat function from special_matrices.py
- #4340: add several features to frozen distributions
- #4344: BUG: Fix/test invalid lwork param in qr
- #4345: Fix test noise visible with Python 3.x
- #4347: Remove deprecated blas/lapack imports, rename lib to _lib
- #4349: DOC: add a nontrivial example to stats.binned_statistic.
- #4350: MAINT: remove optimize.anneal for 0.16.0 (was deprecated in 0.14.0).
- #4351: MAINT: fix usage of deprecated Numpy C API in optimize…
- #4352: MAINT: fix a number of special test failures
- #4353: implement cdf for betaprime distribution
- #4357: BUG: piecewise polynomial antiderivative
- #4358: BUG: integrate: fix handling of banded Jacobians in odeint, plus…
- #4359: MAINT: remove a code path taken for Python version < 2.5
- #4360: MAINT: stats.mstats: Remove some unused variables (thanks, pyflakes).
- #4362: Removed erroneous reference to smoothing parameter #4072
- #4363: MAINT: interpolate: clean up in fitpack.py
- #4364: MAINT: lib: don't export "partial" from decorator
- #4365: svdvals now returns a length-0 sequence of singular values given…
- #4367: DOC: slightly improve TeX rendering of wishart/invwishart docstring
- #4373: ENH: wrap gtsv and ptsv for solve_banded and solveh_banded.
- #4374: ENH: Enhancements to spatial.cKDTree
- #4376: BF: fix reading off-spec matlab logical sparse
- #4377: MAINT: integrate: Clean up some Fortran test code.
- #4378: MAINT: fix usage of deprecated Numpy C API in signal
- #4380: MAINT: scipy.optimize, removing further anneal references
- #4381: ENH: Make DCT and DST accept int and complex types like fft

- #4392: ENH: optimize: add DF-SANE nonlinear derivative-free solver
- #4394: Make reordering algorithms 64-bit clean
- #4396: BUG: bundle cblas.h in Accelerate ABI wrappers to enable compilation…
- #4398: FIX pdist bug where wminkowski's w.dtype != double
- #4402: BUG: fix stat.hypergeom argcheck
- #4404: MAINT: Fill in the full symmetric squareform in the C loop
- #4405: BUG: avoid X += X.T (refs #4401)
- #4407: improved accuracy of gompertz distribution for small x
- #4414: DOC:fix error in scipy.signal.cwt documentation.
- #4415: ENH: Improve accuracy of lomax for small x.
- #4416: DOC: correct a parameter name in docstring of SuperLU.solve….
- #4419: Restore scipy.linalg.calc_lwork also in master
- #4420: fix a performance issue with a sparse solver
- #4423: ENH: improve rayleigh accuracy for large x.
- #4424: BUG: optimize.minimize: fix overflow issue with integer x0 input.
- #4425: ENH: Improve accuracy of truncexpon for small x
- #4426: ENH: improve rayleigh accuracy for large x.
- #4427: MAINT: optimize: cleanup of TNC code
- #4429: BLD: fix build failure with numpy 1.7.x and 1.8.x.
- #4430: BUG: fix a sparse.dok_matrix set/get copy-paste bug
- #4433: Update _minimize.py
- #4435: ENH: release GIL around batch distance computations
- #4436: Fixed incomplete documentation for spsolve
- #4439: MAINT: integrate: Some clean up in the tests.
- #4440: Fast permutation t-test
- #4442: DOC: optimize: fix wrong result in docstring
- #4447: DOC: signal: Some additional documentation to go along with the…
- #4448: DOC: tweak the docstring of lapack.linalg module
- #4449: fix a typo in the expit docstring
- #4451: ENH: vectorize distance loops with gcc
- #4456: MAINT: don't fail large data tests on MemoryError
- #4461: CI: use travis_retry to deal with network timeouts
- #4462: DOC: rationalize minimize() et al. documentation
- #4470: MAINT: sparse: inherit dok_matrix.toarray from spmatrix
- #4473: BUG: signal: Fix validation of the zi shape in sosfilt.
- #4475: BLD: setup.py: update min numpy version and support "setup.py…

- #4481: ENH: add a new linalg special matrix: the Helmert matrix
- #4485: MRG: some changes to allow reading bad mat files
- #4490: [ENH] linalg.hessenberg: use orghr - rebase
- #4491: ENH: linalg: Adding wrapper for potentially useful LAPACK function…
- #4493: BENCH: the solve_toeplitz benchmark used outdated syntax and…
- #4494: MAINT: stats: remove duplicated code
- #4496: References added for watershed_ift algorithm
- #4499: DOC: reshuffle stats distributions documentation
- #4501: Replace benchmark suite with airspeed velocity
- #4502: SLSQP should strictly satisfy bound constraints
- #4503: DOC: forward port 0.15.x release notes and update author name…
- #4504: ENH: option to avoid computing possibly unused svd matrix
- #4505: Rebase of PR 3303 (sparse matrix norms)
- #4507: MAINT: fix lobpcg performance regression
- #4509: DOC: sparse: replace dead link
- #4511: Fixed differential evolution bug
- #4512: Change to fully PEP440 compliant dev version numbers (always…
- #4525: made tiny style corrections (pep8)
- #4533: Add exponentially modified gaussian distribution (scipy.stats.expongauss)
- #4534: MAINT: benchmarks: make benchmark suite importable on all scipy…
- #4535: BUG: Changed zip() to list(zip()) so that it could work in Python…
- #4536: Follow up to pr 4348 (exponential window)
- #4540: ENH: spatial: Add procrustes analysis
- #4541: Bench fixes
- #4542: TST: NumpyVersion dev -> dev0
- #4543: BUG: Overflow in savgol_coeffs
- #4544: pep8 fixes for stats
- #4546: MAINT: use reduction axis arguments in one-norm estimation
- #4549: ENH : Added group_delay to scipy.signal
- #4553: ENH: Significantly faster moment function
- #4556: DOC: document the changes of the sparse.linalg.svds (optional…
- #4559: DOC: stats: describe loc and scale parameters in the docstring…
- #4563: ENH: rewrite of stats.ppcc_plot
- #4564: Be more (or less) forgiving when user passes +-inf instead of…
- #4566: DEP: remove a bunch of deprecated function from scipy.stats,…
- #4570: MNT: Suppress LineSearchWarning's in scipy.optimize tests

- #4572: ENH: Extract inverse hessian information from L-BFGS-B
- #4576: ENH: Split signal.lti into subclasses, part of #2912
- #4578: MNT: Reconcile docstrings and function signatures
- #4581: Fix build with Intel MKL on Linux
- #4583: DOC: optimize: remove references to unused disp kwarg
- #4584: ENH: scipy.signal - Tukey window
- #4587: Hermite asymptotic
- #4593: DOC - add example to RegularGridInterpolator
- #4595: DOC: Fix erroneous latex characters in tutorial/optimize.
- #4600: Add return codes to optimize.tnc docs
- #4603: ENH: Wrap LAPACK `*lange` functions for matrix norms
- #4604: scipy.stats: generalized normal distribution
- #4609: MAINT: interpolate: fix a few inconsistencies between docstrings…
- #4610: MAINT: make runtest.py –bench-compare use asv continuous and…
- #4611: DOC: stats: explain rice scaling; add a note to the tutorial…
- #4614: BUG: lfilter, the size of zi was not checked correctly for nd…
- #4617: MAINT: integrate: Clean the C code behind odeint.
- #4618: FIX: Raise error when window length != data length
- #4619: Issue #4550: *scipy.stats.mode* - UnboundLocalError on empty…
- #4620: Fixed a problem (#4590) with svds accepting wrong eigenvalue…
- #4621: Speed up special.ai_zeros/bi_zeros by 10x
- #4623: MAINT: some tweaks to spatial.procrustes (private file, html…
- #4628: Speed up signal.lfilter and add a convolution path for FIR filters
- #4629: Bug: integrate.nquad; resolve issue #4599
- #4631: MAINT: integrate: Remove unused variables in a Fortran test function.
- #4633: MAINT: Fix convergence message for remez
- #4635: PEP8: indentation (so that pep8 bot does not complain)
- #4637: MAINT: generalize a sign function to do the right thing for complex…
- #4639: Amended typo in apple_sgemv_fix.c
- #4642: MAINT: use lapack for scipy.linalg.norm
- #4643: RBF default epsilon too large 2020
- #4646: Added atleast_1d around poly in invres and invresz
- #4647: fix doc pdf build
- #4648: BUG: Fixes #4408: Vector-valued constraints in minimize() et…
- #4649: Vonmisesfix
- #4650: Signal example clean up in Tukey and place_poles

- #4652: DOC: Fix the error in convolve for same mode
- #4653: improve erf performance
- #4655: DEP: deprecate scipy.stats.histogram2 in favour of np.histogram2d
- #4656: DEP: deprecate scipy.stats.signaltonoise
- #4660: Avoid extra copy for sparse compressed [:, seq] and [seq, :]…
- #4661: Clean, rebase of #4478, adding ?gelsy and ?gelsd wrappers
- #4662: MAINT: Correct odeint messages
- #4664: Update _monotone.py
- #4672: fix behavior of scipy.linalg.block_diag for empty input
- #4675: Fix lsim
- #4676: Added missing colon to :math: directive in docstring.
- #4679: ENH: sparse randn
- #4682: ENH: scipy.signal - Addition of CSD, coherence; Enhancement of…
- #4684: BUG: various errors in weight calculations in orthogonal.py
- #4685: BUG: Fixes #4594: optimize.linprog IndexError when a callback…
- #4686: MAINT: cluster: Clean up duplicated exception raising code.
- #4688: Improve is_distance_dm exception message
- #4692: MAINT: stats: Simplify the calculation in tukeylambda._ppf
- #4693: ENH: added functionality to handle scalars in *stats._chk_asarray*
- #4694: Vectorization of Anderson-Darling computations.
- #4696: Fix singleton expansion in lfilter.
- #4698: MAINT: quiet warnings from cephes.
- #4701: add Bpoly.antiderivatives / integrals
- #4703: Add citation of published paper
- #4706: MAINT: special: avoid out-of-bounds access in specfun
- #4707: MAINT: fix issues with np.matrix as input to functions related…
- #4709: ENH: `scipy.stats` now returns namedtuples.
- #4710: scipy.io.idl: make reader more robust to missing variables in…
- #4711: Fix crash for unknown chunks at the end of file
- #4712: Reduce onenormest memory usage
- #4713: MAINT: interpolate: no need to pass dtype around if it can be…
- #4714: BENCH: Add benchmarks for stats module
- #4715: MAINT: polish signal.place_poles and signal/test_ltisys.py
- #4716: DEP: deprecate mstats.signaltonoise …
- #4717: MAINT: basinhopping: fix error in tests, silence /0 warning,…
- #4718: ENH: stats: can specify f-shapes to fix in fitting by name

- #4721: Document that imresize converts the input to a PIL image
- #4722: MAINT: PyArray_BASE is not an lvalue unless the deprecated API…
- #4725: Fix gengamma _nump failure
- #4728: DOC: add poch to the list of scipy special function descriptions
- #4735: MAINT: stats: avoid (a spurious) division-by-zero in skew
- #4738: TST: silence runtime warnings for some corner cases in *stats*…
- #4739: BLD: try to build numpy instead of using the one on TravisCI
- #4740: DOC: Update some docstrings with 'versionadded'.
- #4742: BLD: make sure that relaxed strides checking is in effect on…
- #4750: DOC: special: TeX typesetting of rel_entr, kl_div and pseudo_huber
- #4751: BENCH: add sparse null slice benchmark
- #4753: BUG: Fixed compilation with recent Cython versions.
- #4756: BUG: Fixes #4733: optimize.brute finish option is not compatible…
- #4758: DOC: optimize.leastsq default maxfev clarification
- #4759: improved stats mle fit
- #4760: MAINT: count bfgs updates more carefully
- #4762: BUGS: Fixes #4746 and #4594: linprog returns solution violating…
- #4763: fix small linprog bugs
- #4766: BENCH: add signal.lsim benchmark
- #4768: fix python syntax errors in docstring examples
- #4769: Fixes #4726: test_cobyla.test_vector_constraints
- #4770: Mark FITPACK functions as thread safe.
- #4771: edited scipy/stats/stats.py to fix doctest for fisher_exact
- #4773: DOC: update 0.16.0 release notes.
- #4775: DOC: linalg: add funm_psd as a docstring example
- #4778: Use a dictionary for function name synonyms
- #4780: Include apparently-forgotten functions in docs
- #4783: Added many missing special functions to docs
- #4784: add an axis attribute to PPoly and friends
- #4785: Brief note about origin of Lena image
- #4786: DOC: reformat the Methods section of the KDE docstring
- #4787: Add rice cdf and ppf.
- #4792: CI: add a kludge for detecting test failures which try to disguise…
- #4795: Make refguide_check smarter about false positives
- #4797: BUG/TST: numpoints not updated for incremental Voronoi
- #4799: BUG: spatial: Fix a couple edge cases for the Mahalanobis metric…

- #4801: BUG: Fix TypeError in scipy.optimize._trust-region.py when disp=True.
- #4803: Issues with relaxed strides in QR updating routines
- #4806: MAINT: use an informed initial guess for cauchy fit
- #4810: PEP8ify codata.py
- #4812: BUG: Relaxed strides cleanup in decomp_update.pyx.in
- #4820: BLD: update Bento build for sgemv fix and install cython blas/lapack…
- #4823: ENH: scipy.signal - Addition of spectrogram function
- #4827: DOC: add csd and coherence to __init__.py
- #4833: BLD: fix issue in linalg `*lange` wrappers for g77 builds.
- #4841: TST: fix test failures in scipy.special with mingw32 due to test…
- #4842: DOC: update site.cfg.example. Mostly taken over from Numpy
- #4845: BUG: signal: Make spectrogram's return values order match the…
- #4849: DOC:Fix error in ode docstring example
- #4856: BUG: fix typo causing memleak

5.32 SciPy 0.15.1 Release Notes

SciPy 0.15.1 is a bug-fix release with no new features compared to 0.15.0.

5.32.1 Issues fixed

- #4413: BUG: Tests too strict, f2py doesn't have to overwrite this array
- #4417: BLD: avoid using NPY_API_VERSION to check not using deprecated…
- #4418: Restore and deprecate scipy.linalg.calc_work

5.33 SciPy 0.15.0 Release Notes

Contents

- *SciPy 0.15.0 Release Notes*
  - *New features*
    - *Linear Programming Interface*
    - *Differential evolution, a global optimizer*
    - *`scipy.signal` improvements*
    - *`scipy.integrate` improvements*
    - *`scipy.linalg` improvements*
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        * scipy.special improvements
        * scipy.sparse.csgraph improvements
        * scipy.stats improvements
    - Deprecated features
    - Backwards incompatible changes
        * scipy.ndimage
        * scipy.integrate
    - Authors
        * Issues closed
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SciPy 0.15.0 is the culmination of 6 months of hard work. It contains several new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.16.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.5.1 or greater.

5.33.1 New features

Linear Programming Interface

The new function `scipy.optimize.linprog` provides a generic linear programming similar to the way `scipy.optimize.minimize` provides a generic interface to nonlinear programming optimizers. Currently the only method supported is *simplex* which provides a two-phase, dense-matrix-based simplex algorithm. Callbacks functions are supported, allowing the user to monitor the progress of the algorithm.

Differential evolution, a global optimizer

A new `scipy.optimize.differential_evolution` function has been added to the `optimize` module. Differential Evolution is an algorithm used for finding the global minimum of multivariate functions. It is stochastic in nature (does not use gradient methods), and can search large areas of candidate space, but often requires larger numbers of function evaluations than conventional gradient based techniques.

`scipy.signal` improvements

The function `scipy.signal.max_len_seq` was added, which computes a Maximum Length Sequence (MLS) signal.

`scipy.integrate` improvements

It is now possible to use *scipy.integrate* routines to integrate multivariate ctypes functions, thus avoiding callbacks to Python and providing better performance.

`scipy.linalg` improvements

The function *scipy.linalg.orthogonal_procrustes* for solving the procrustes linear algebra problem was added.

BLAS level 2 functions `her`, `syr`, `her2` and `syr2` are now wrapped in `scipy.linalg`.

`scipy.sparse` improvements

scipy.sparse.linalg.svds can now take a `LinearOperator` as its main input.

`scipy.special` improvements

Values of ellipsoidal harmonic (i.e. Lame) functions and associated normalization constants can be now computed using `ellip_harm`, `ellip_harm_2`, and `ellip_normal`.

New convenience functions `entr`, `rel_entr` `kl_div`, `huber`, and `pseudo_huber` were added.

`scipy.sparse.csgraph` improvements

Routines `reverse_cuthill_mckee` and `maximum_bipartite_matching` for computing reorderings of sparse graphs were added.

`scipy.stats` improvements

Added a Dirichlet multivariate distribution, *scipy.stats.dirichlet*.

The new function *scipy.stats.median_test* computes Mood's median test.

The new function *scipy.stats.combine_pvalues* implements Fisher's and Stouffer's methods for combining p-values.

scipy.stats.describe returns a namedtuple rather than a tuple, allowing users to access results by index or by name.

5.33.2 Deprecated features

The *scipy.weave* module is deprecated. It was the only module never ported to Python 3.x, and is not recommended to be used for new code - use Cython instead. In order to support existing code, `scipy.weave` has been packaged separately: https://github.com/scipy/weave. It is a pure Python package, and can easily be installed with `pip install weave`.

`scipy.special.bessel_diff_formula` is deprecated. It is a private function, and therefore will be removed from the public API in a following release.

`scipy.stats.nanmean`, `nanmedian` and `nanstd` functions are deprecated in favor of their numpy equivalents.

5.33.3 Backwards incompatible changes

scipy.ndimage

The functions *scipy.ndimage.minimum_positions*, *scipy.ndimage.maximum_positions*` and `scipy.ndimage.extrema` return positions as ints instead of floats.

scipy.integrate

The format of banded Jacobians in `scipy.integrate.ode` solvers is changed. Note that the previous documentation of this feature was erroneous.

5.33.4 Authors

- Abject +
- Ankit Agrawal +
- Sylvain Bellemare +
- Matthew Brett
- Christian Brodbeck
- Christian Brueffer
- Lars Buitinck
- Evgeni Burovski
- Pierre de Buyl +
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- Thomas A Caswell
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- Kevin Davies +
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- Jesse Engel +
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- André Gaul
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- Axl West +
- Nathan Woods
- Benda Xu +

- Víctor Zabalza +
- Tiziano Zito +

A total of 99 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed

- #1431: ellipk(x) extending its domain for x<0 (Trac #904)
- #1727: consistency of std interface (Trac #1200)
- #1851: Shape parameter negated in genextreme (relative to R, MATLAB,…
- #1889: interp2d is weird (Trac #1364)
- #2188: splev gives wrong values or crashes outside of support when der…
- #2343: scipy.insterpolate's splrep function fails with certain combinations…
- #2669: .signal.ltisys.ss2tf should only apply to MISO systems in current…
- #2911: interpolate.splder() failure on Fedora
- #3171: future of weave in scipy
- #3176: Suggestion to improve error message in scipy.integrate.odeint
- #3198: pdf() and logpdf() methods for scipy.stats.gaussian_kde
- #3318: Travis CI is breaking on test("full")
- #3329: scipy.stats.scoreatpercentile backward-incompatible change not…
- #3362: Reference cycle in scipy.sparse.linalg.eigs with shift-invert…
- #3364: BUG: linalg.hessenberg broken (wrong results)
- #3376: stats f_oneway needs floats
- #3379: Installation of scipy 0.13.3 via zc.buildout fails
- #3403: hierarchy.linkage raises an ugly exception for a compressed 2x2…
- #3422: optimize.curve_fit() handles NaN by returning all parameters…
- #3457: linalg.fractional_matrix_power has no docstring
- #3469: DOC: *ndimage.find_object* ignores zero-values
- #3491: optimize.leastsq() documentation should mention it does not work…
- #3499: cluster.vq.whiten return nan for all zeros column in observations
- #3503: minimize attempts to do vector addition when numpy arrays are…
- #3508: exponweib.logpdf fails for valid parameters
- #3509: libatlas3-base-dev does not exist
- #3550: BUG: anomalous values computed by special.ellipkinc
- #3555: `scipy.ndimage` positions are float instead of int
- #3557: UnivariateSpline.__call__ should pass all relevant args through…
- #3569: No license statement for test data imported from boost?

- #3576: mstats test failure (too sensitive?)
- #3579: Errors on scipy 0.14.x branch using MKL, Ubuntu 14.04 x86_64
- #3580: Operator overloading with sparse matrices
- #3587: Wrong alphabetical order in continuous statistical distribution…
- #3596: scipy.signal.fftconvolve no longer threadsafe
- #3623: BUG: signal.convolve takes longer than it needs to
- #3655: Integer returned from integer data in scipy.signal.periodogram…
- #3662: Travis failure on Numpy 1.5.1 (not reproducible?)
- #3668: dendogram(orientation='foo')
- #3669: KroghInterpolator doesn't pass through points
- #3672: Inserting a knot in a spline
- #3682: misleading documentation of scipy.optimize.curve_fit
- #3699: BUG?: minor problem with scipy.signal.lfilter w/initial conditions
- #3700: Inconsistent exceptions raised by scipy.io.loadmat
- #3703: TypeError for RegularGridInterpolator with big-endian data
- #3714: Misleading error message in eigsh: k must be between 1 and rank(A)-1
- #3720: coo_matrix.setdiag() fails
- #3740: Scipy.Spatial.KdTree (Query) Return Type?
- #3761: Invalid result from scipy.special.btdtri
- #3784: DOC - Special Functions - Drum example fix for higher modes
- #3785: minimize() should have friendlier args=
- #3787: BUG: signal: Division by zero in lombscargle
- #3800: BUG: scipy.sparse.csgraph.shortest_path overwrites input matrix
- #3817: Warning in calculating moments from Binomial distribution for…
- #3821: review scipy usage of *np.ma.is_masked*
- #3829: Linear algebra function documentation doesn't mention default…
- #3830: A bug in Docstring of scipy.linalg.eig
- #3844: Issue with shape parameter returned by genextreme
- #3858: "ImportError: No module named Cython.Compiler.Main" on install
- #3876: savgol_filter not in release notes and has no versionadded
- #3884: scipy.stats.kendalltau empty array error
- #3895: ValueError: illegal value in 12-th argument of internal gesdd…
- #3898: skimage test broken by minmax filter change
- #3901: scipy sparse errors with numpy master
- #3905: DOC: optimize: linprog docstring has two "Returns" sections
- #3915: DOC: sphinx warnings because of ***kwds* in the stats distributions…

- #3935: Split stats.distributions files in tutorial
- #3969: gh-3607 breaks backward compatibility in ode solver banded jacobians
- #4025: DOC: signal: The return value of find_peaks_cwt is not documented.
- #4029: scipy.stats.nbinom.logpmf(0,1,1) returns nan. Correct value is…
- #4032: ERROR: test_imresize (test_pilutil.TestPILUtil)
- #4038: errors do not propagate through scipy.integrate.odeint properly
- #4171: orthogonal_procrustes always returns scale.
- #4176: Solving the Discrete Lyapunov Equation does not work with matrix…

Pull requests

- #3109: ENH Added Fisher's method and Stouffer's Z-score method
- #3225: Add the limiting distributions to generalized Pareto distribution…
- #3262: Implement back end of faster multivariate integration
- #3266: ENH: signal: add type=False as parameter for periodogram and…
- #3273: Add PEP8 check to Travis-CI
- #3342: ENH: linprog function for linear programming
- #3348: BUG: add proper error handling when using interp2d on regular…
- #3351: ENH: Add MLS method
- #3382: ENH: scipy.special information theory functions
- #3396: ENH: improve stats.nanmedian more by assuming nans are rare
- #3398: Added two wrappers to the gaussian_kde class.
- #3405: BUG: cluster.linkage array conversion to double dtype
- #3407: MAINT: use assert_warns instead of a more complicated mechanism
- #3409: ENH: change to use array view in signal/_peak_finding.py
- #3416: Issue 3376 : stats f_oneway needs floats
- #3419: BUG: tools: Fix list of FMA instructions in detect_cpu_extensions_wine.py
- #3420: DOC: stats: Add 'entropy' to the stats package-level documentation.
- #3429: BUG: close intermediate file descriptor right after it is used…
- #3430: MAINT: Fix some cython variable declarations to avoid warnings…
- #3433: Correcting the normalization of chebwin window function
- #3435: Add more precise link to R's quantile documentation
- #3446: ENH: scipy.optimize - adding differential_evolution
- #3450: MAINT: remove unused function scipy.stats.mstats_basic._kolmog1
- #3458: Reworked version of PR-3084 (mstats-stats comparison)
- #3462: MAINT : Returning a warning for low attenuation values of chebwin…
- #3463: DOC: linalg: Add examples to functions in matfuncs.py

- #3477: ENH: sparse: release GIL in sparsetools routines
- #3480: DOC: Add more details to deconvolve docstring
- #3484: BLD: fix Qhull build issue with MinGW-w64. Closes gh-3237.
- #3498: MAINT: io: remove old warnings from idl.py
- #3504: BUG: cluster.vq.whiten returns nan or inf when std==0
- #3510: MAINT: stats: Reimplement the pdf and logpdf methods of exponweib.
- #3512: Fix PEP8 errors showing up on TravisCI after pep8 1.5 release
- #3514: DOC: libatlas3-base-dev seems to have never been a thing
- #3516: DOC improve scipy.sparse docstrings
- #3517: ENH: speed-up ndimage.filters.min(max)imum_filter1d
- #3518: Issues in scipy.misc.logsumexp
- #3526: DOC: graphical example for cwt, and use a more interesting signal
- #3527: ENH: Implement min(max)imum_filter1d using the MINLIST algorithm
- #3537: STY: reduce number of C compiler warnings
- #3540: DOC: linalg: add docstring to fractional_matrix_power
- #3542: kde.py Doc Typo
- #3545: BUG: stats: stats.levy.cdf with small arguments loses precision.
- #3547: BUG: special: erfcinv with small arguments loses precision.
- #3553: DOC: Convolve examples
- #3561: FIX: in ndimage.measurements return positions as int instead…
- #3564: Fix test failures with numpy master. Closes gh-3554
- #3565: ENH: make interp2d accept unsorted arrays for interpolation.
- #3566: BLD: add numpy requirement to metadata if it can't be imported.
- #3567: DOC: move matfuncs docstrings to user-visible functions
- #3574: Fixes multiple bugs in mstats.theilslopes
- #3577: TST: decrease sensitivity of an mstats test
- #3585: Cleanup of code in scipy.constants
- #3589: BUG: sparse: allow operator overloading
- #3594: BUG: lobpcg returned wrong values for small matrices (n < 10)
- #3598: MAINT: fix coverage and coveralls
- #3599: MAINT: symeig – now that's a name I've not heard in a long time
- #3602: MAINT: clean up the new optimize.linprog and add a few more tests
- #3607: BUG: integrate: Fix some bugs and documentation errors in the…
- #3609: MAINT integrate/odepack: kill dead Fortran code
- #3616: FIX: Invalid values
- #3617: Sort netcdf variables in a Python-3 compatible way

- #3622: DOC: Added 0.15.0 release notes entry for linprog function.
- #3625: Fix documentation for cKDTree.sparse_distance_matrix
- #3626: MAINT: linalg.orth memory efficiency
- #3627: MAINT: stats: A bit of clean up
- #3628: MAINT: signal: remove a useless function from wavelets.py
- #3632: ENH: stats: Add Mood's median test.
- #3636: MAINT: cluster: some clean up
- #3638: DOC: docstring of optimize.basinhopping confuses singular and…
- #3639: BUG: change ddof default to 1 in mstats.sem, consistent with…
- #3640: Weave: deprecate the module and disable slow tests on TravisCI
- #3641: ENH: Added support for date attributes to io.arff.arffread
- #3644: MAINT: stats: remove superfluous alias in mstats_basic.py
- #3646: ENH: adding *sum_duplicates* method to COO sparse matrix
- #3647: Fix for #3596: Make fftconvolve threadsafe
- #3650: BUG: sparse: smarter random index selection
- #3652: fix wrong option name in power_divergence dosctring example
- #3654: Changing EPD to Canopy
- #3657: BUG: signal.welch: ensure floating point dtype regardless of…
- #3660: TST: mark a test as known fail
- #3661: BLD: ignore pep8 E302 (expected 2 blank lines, found 1)
- #3663: BUG: fix leaking errstate, and ignore invalid= errors in a test
- #3664: BUG: correlate was extremely slow when in2.size > in1.size
- #3667: ENH: Adds default params to pdfs of multivariate_norm
- #3670: ENH: Small speedup of FFT size check
- #3671: DOC: adding differential_evolution function to 0.15 release notes
- #3673: BUG: interpolate/fitpack: arguments to fortran routines may not…
- #3674: Add support for appending to existing netcdf files
- #3681: Speed up test('full'), solve Travis CI timeout issues
- #3683: ENH: cluster: rewrite and optimize *vq* in Cython
- #3684: Update special docs
- #3688: Spacing in special docstrings
- #3692: ENH: scipy.special: Improving sph_harm function
- #3693: Update refguide entries for signal and fftpack
- #3695: Update continuous.rst
- #3696: ENH: check for valid 'orientation' kwarg in dendrogram()
- #3701: make 'a' and 'b' coefficients atleast_1d array in filtfilt

- #3702: BUG: cluster: _vq unable to handle large features
- #3704: BUG: special: ellip(k,e)inc nan and double expected value
- #3707: BUG: handle fill_value dtype checks correctly in RegularGridInterpolator
- #3708: Reraise exception on failure to read mat file.
- #3709: BUG: cast 'x' to correct dtype in KroghInterpolator._evaluate
- #3712: ENH: cluster: reimplement the update-step of K-means in Cython
- #3713: FIX: Check type of lfiltic
- #3718: Changed INSTALL file extension to rst
- #3719: address svds returning nans for zero input matrix
- #3722: MAINT: spatial: static, unused code, sqrt(sqeuclidean)
- #3725: ENH: use numpys nanmedian if available
- #3727: TST: add a new fixed_point test and change some test function…
- #3731: BUG: fix romb in scipy.integrate.quadrature
- #3734: DOC: simplify examples with semilogx
- #3735: DOC: Add minimal docstrings to lti.impulse/step
- #3736: BUG: cast pchip arguments to floats
- #3744: stub out inherited methods of Akima1DInterpolator
- #3746: DOC: Fix formatting for Raises section
- #3748: ENH: Added discrete Lyapunov transformation solve
- #3750: Enable automated testing with Python 3.4
- #3751: Reverse Cuthill-McKee and Maximum Bipartite Matching reorderings…
- #3759: MAINT: avoid indexing with a float array
- #3762: TST: filter out RuntimeWarning in vq tests
- #3766: TST: cluster: some cleanups in test_hierarchy.py
- #3767: ENH/BUG: support negative m in elliptic integrals
- #3769: ENH: avoid repeated matrix inverse
- #3770: BUG: signal: In lfilter_zi, b was not rescaled correctly when…
- #3772: STY avoid unnecessary transposes in csr_matrix.getcol/row
- #3773: ENH: Add ext parameter to UnivariateSpline call
- #3774: BUG: in integrate/quadpack.h, put all declarations before statements.
- #3779: Incbet fix
- #3788: BUG: Fix lombscargle ZeroDivisionError
- #3791: Some maintenance for doc builds
- #3795: scipy.special.legendre docstring
- #3796: TYPO: sheroidal -> spheroidal
- #3801: BUG: shortest_path overwrite

- #3803: TST: lombscargle regression test related to atan vs atan2
- #3809: ENH: orthogonal procrustes solver
- #3811: ENH: scipy.special, Implemented Ellipsoidal harmonic function:…
- #3819: BUG: make a fully connected csgraph from an ndarray with no zeros
- #3820: MAINT: avoid spurious warnings in binom(n, p=0).mean() etc
- #3825: Don't claim scipy.cluster does distance matrix calculations.
- #3827: get and set diagonal of coo_matrix, and related csgraph laplacian…
- #3832: DOC: Minor additions to integrate/nquad docstring.
- #3845: Bug fix for #3842: Bug in scipy.optimize.line_search
- #3848: BUG: edge case where the covariance matrix is exactly zero
- #3850: DOC: typo
- #3851: DOC: document default argument values for some arpack functions
- #3860: DOC: sparse: add the function 'find' to the module-level docstring
- #3861: BUG: Removed unnecessary storage of args as instance variables…
- #3862: BUG: signal: fix handling of multi-output systems in ss2tf.
- #3865: Feature request: ability to read heterogeneous types in FortranFile
- #3866: MAINT: update pip wheelhouse for installs
- #3871: MAINT: linalg: get rid of calc_lwork.f
- #3872: MAINT: use scipy.linalg instead of np.dual
- #3873: BLD: show a more informative message if Cython wasn't installed.
- #3874: TST: cluster: cleanup the hierarchy test data
- #3877: DOC: Savitzky-Golay filter version added
- #3878: DOC: move versionadded to notes
- #3879: small tweaks to the docs
- #3881: FIX incorrect sorting during fancy assignment
- #3885: kendalltau function now returns a nan tuple if empty arrays used…
- #3886: BUG: fixing linprog's kwarg order to match docs
- #3888: BUG: optimize: In _linprog_simplex, handle the case where the…
- #3891: BUG: stats: Fix ValueError message in chi2_contingency.
- #3892: DOC: sparse.linalg: Fix lobpcg docstring.
- #3894: DOC: stats: Assorted docstring edits.
- #3896: Fix 2 mistakes in MatrixMarket format parsing
- #3897: BUG: associated Legendre function of second kind for 1<x<1.0001
- #3899: BUG: fix undefined behavior in alngam
- #3906: MAINT/DOC: Whitespace tweaks in several docstrings.
- #3907: TST: relax bounds of interpolate test to accomodate rounding…

- #3909: MAINT: Create a common version of *count_nonzero* for compatibility…
- #3910: Fix a couple of test errors in master
- #3911: Use MathJax for the html docs
- #3914: Rework the _roots functions and document them.
- #3916: Remove all linpack_lite code and replace with LAPACK routines
- #3917: splines, constant extrapolation
- #3918: DOC: tweak the rv_discrete docstring example
- #3919: Quadrature speed-up: scipy.special.orthogonal.p_roots with cache
- #3920: DOC: Clarify docstring for *sigma* parameter for *curve_fit*
- #3922: Fixed Docstring issues in linprog (Fixes #3905).
- #3924: Coerce args into tuple if necessary.
- #3926: DOC: Surround stats class methods in docstrings with backticks.
- #3927: Changed doc for romb's dx parameter to int.
- #3928: check FITPACK conditions in LSQUnivariateSpline
- #3929: Added a warning about leastsq using with NaNs.
- #3930: ENH: optimize: curve_fit now warns if pcov is undetermined
- #3932: Clarified the k > n case.
- #3933: DOC: remove *import scipy as sp* abbreviation here and there
- #3936: Add license and copyright holders to test data imported from…
- #3938: DOC: Corrected documentation for return types.
- #3939: DOC: fitpack: add a note about Sch-W conditions to splrep docstring
- #3940: TST: integrate: Remove an invalid test of odeint.
- #3942: FIX: Corrected error message of eigsh.
- #3943: ENH: release GIL for filter and interpolation of ndimage
- #3944: FIX: Raise value error if window data-type is unsupported
- #3946: Fixed signal.get_window with unicode window name
- #3947: MAINT: some docstring fixes and style cleanups in stats.mstats
- #3949: DOC: fix a couple of issues in stats docstrings.
- #3950: TST: sparse: remove known failure that doesn't fail
- #3951: TST: switch from Rackspace wheelhouse to numpy/cython source…
- #3952: DOC: stats: Small formatting correction to the 'chi' distribution…
- #3953: DOC: stats: Several corrections and small additions to docstrings.
- #3955: signal.__init__.py: remove duplicated *get_window* entry
- #3959: TST: sparse: more "known failures" for DOK that don't fail
- #3960: BUG: io.netcdf: do not close mmap if there are references left…
- #3965: DOC: Fix a few more sphinx warnings that occur when building…

- #3966: DOC: add guidelines for using test generators in HACKING
- #3968: BUG: sparse.linalg: make Inv objects in arpack garbage-collectable…
- #3971: Remove all linpack_lite code and replace with LAPACK routines
- #3972: fix typo in error message
- #3973: MAINT: better error message for multivariate normal.
- #3981: turn the cryptically named scipy.special information theory functions…
- #3984: Wrap her, syr, her2, syr2 blas routines
- #3990: improve UnivariateSpline docs
- #3991: ENH: stats: return namedtuple for describe output
- #3993: DOC: stats: percentileofscore references np.percentile
- #3997: BUG: linalg: pascal(35) was incorrect: last element overflowed…
- #3998: MAINT: use isMaskedArray instead of is_masked to check type
- #3999: TST: test against all of boost data files.
- #4000: BUG: stats: Fix edge-case handling in a few distributions.
- #4003: ENH: using python's warnings instead of prints in fitpack.
- #4004: MAINT: optimize: remove a couple unused variables in zeros.c
- #4006: BUG: Fix C90 compiler warnings in *NI_MinOrMaxFilter1D*
- #4007: MAINT/DOC: Fix spelling of 'decomposition' in several files.
- #4008: DOC: stats: Split the descriptions of the distributions in the…
- #4015: TST: logsumexp regression test
- #4016: MAINT: remove some inf-related warnings from logsumexp
- #4020: DOC: stats: fix whitespace in docstrings of several distributions
- #4023: Exactly one space required before assignments
- #4024: In dendrogram(): Correct an argument name and a grammar issue…
- #4041: BUG: misc: Ensure that the 'size' argument of PIL's 'resize'…
- #4049: BUG: Return of _logpmf
- #4051: BUG: expm of integer matrices
- #4052: ENH: integrate: odeint: Handle exceptions in the callback functions.
- #4053: BUG: stats: Refactor argument validation to avoid a unicode issue.
- #4057: Added newline to scipy.sparse.linalg.svds documentation for correct…
- #4058: MAINT: stats: Add note about change to scoreatpercentile in release…
- #4059: ENH: interpolate: Allow splev to accept an n-dimensional array.
- #4064: Documented the return value for scipy.signal.find_peaks_cwt
- #4074: ENH: Support LinearOperator as input to svds
- #4084: BUG: Match exception declarations in scipy/io/matlab/streams.pyx…
- #4091: DOC: special: more clear instructions on how to evaluate polynomials

- #4105: BUG: Workaround for SGEMV segfault in Accelerate
- #4107: DOC: get rid of 'import *' in examples
- #4113: DOC: fix typos in distance.yule
- #4114: MAINT C fixes
- #4117: deprecate nanmean, nanmedian and nanstd in favor of their numpy…
- #4126: scipy.io.idl: support description records and fix bug with null…
- #4131: ENH: release GIL in more ndimage functions
- #4132: MAINT: stats: fix a typo [skip ci]
- #4145: DOC: Fix documentation error for nc chi-squared dist
- #4150: Fix _nd_image.geometric_transform endianness bug
- #4153: MAINT: remove use of deprecated numpy API in lib/lapack/ f2py…
- #4156: MAINT: optimize: remove dead code
- #4159: MAINT: optimize: clean up Zeros code
- #4165: DOC: add missing special functions to __doc__
- #4172: DOC: remove misleading procrustes docstring line
- #4175: DOC: sparse: clarify CSC and CSR constructor usage
- #4177: MAINT: enable np.matrix inputs to solve_discrete_lyapunov
- #4179: TST: fix an intermittently failing test case for special.legendre
- #4181: MAINT: remove unnecessary null checks before free
- #4182: Ellipsoidal harmonics
- #4183: Skip Cython build in Travis-CI
- #4184: Pr 4074
- #4187: Pr/3923
- #4190: BUG: special: fix up ellip_harm build
- #4193: BLD: fix msvc compiler errors
- #4194: BUG: fix buffer dtype mismatch on win-amd64
- #4199: ENH: Changed scipy.stats.describe output from datalen to nobs
- #4201: DOC: add blas2 and nan* deprecations to the release notes
- #4243: TST: bump test tolerances

5.34 SciPy 0.14.1 Release Notes

SciPy 0.14.1 is a bug-fix release with no new features compared to 0.14.0.

5.34.1 Issues closed

- #3630: NetCDF reading results in a segfault
- #3631: SuperLU object not working as expected for complex matrices
- #3733: segfault from map_coordinates
- #3780: Segfault when using CSR/CSC matrix and uint32/uint64
- #3781: BUG: sparse: fix omitted types in sparsetools typemaps
- #3802: 0.14.0 API breakage: _gen generators are missing from scipy.stats.distributions API
- #3805: ndimage test failures with numpy 1.10
- #3812: == sometimes wrong on csr_matrix
- #3853: Many scipy.sparse test errors/failures with numpy 1.9.0b2
- #4084: fix exception declarations for Cython 0.21.1 compatibility
- #4093: BUG: fitpack: avoid a memory error in splev(x, tck, der=k)
- #4104: BUG: Workaround SGEMV segfault in Accelerate (maintenance 0.14.x)
- #4143: BUG: fix ndimage functions for large data
- #4149: Bug in expm for integer arrays
- #4154: Backport gh-4041 for 0.14.1 (Ensure that the 'size' argument of PIL's 'resize' method is a tuple)
- #4163: Backport #4142 (ZeroDivisionError in scipy.sparse.linalg.lsqr)
- #4164: Backport gh-4153 (remove use of deprecated numpy API in lib/lapack/ f2py wrapper)
- #4180: backport pil resize support tuple fix
- #4168: Lots of arpack test failures on windows 32 bits with numpy 1.9.1
- #4203: Matrix multiplication in 0.14.x is more than 10x slower compared…
- #4218: attempt to make ndimage interpolation compatible with numpy relaxed…
- #4225: BUG: off-by-one error in PPoly shape checks
- #4248: BUG: optimize: fix issue with incorrect use of closure for slsqp.

5.35 SciPy 0.14.0 Release Notes

Contents

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    * scipy.signal improvements
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    * anneal
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SciPy 0.14.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.14.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.2-3.4 and NumPy 1.5.1 or greater.

5.35.1 New features

`scipy.interpolate` improvements

A new wrapper function `scipy.interpolate.interpn` for interpolation on regular grids has been added. *interpn* supports linear and nearest-neighbor interpolation in arbitrary dimensions and spline interpolation in two dimensions.

Faster implementations of piecewise polynomials in power and Bernstein polynomial bases have been added as `scipy.interpolate.PPoly` and `scipy.interpolate.BPoly`. New users should use these in favor of *scipy.interpolate.PiecewisePolynomial*.

`scipy.interpolate.interp1d` now accepts non-monotonic inputs and sorts them. If performance is critical, sorting can be turned off by using the new `assume_sorted` keyword.

Functionality for evaluation of bivariate spline derivatives in `scipy.interpolate` has been added.

The new class `scipy.interpolate.Akima1DInterpolator` implements the piecewise cubic polynomial interpolation scheme devised by H. Akima.

Functionality for fast interpolation on regular, unevenly spaced grids in arbitrary dimensions has been added as *scipy.interpolate.RegularGridInterpolator*.

scipy.linalg improvements

The new function *scipy.linalg.dft* computes the matrix of the discrete Fourier transform.

A condition number estimation function for matrix exponential, *scipy.linalg.expm_cond*, has been added.

scipy.optimize improvements

A set of benchmarks for optimize, which can be run with `optimize.bench()`, has been added.

scipy.optimize.curve_fit now has more controllable error estimation via the `absolute_sigma` keyword.

Support for passing custom minimization methods to `optimize.minimize()` and `optimize.minimize_scalar()` has been added, currently useful especially for combining `optimize.basinhopping()` with custom local optimizer routines.

scipy.stats improvements

A new class *scipy.stats.multivariate_normal* with functionality for multivariate normal random variables has been added.

A lot of work on the `scipy.stats` distribution framework has been done. Moment calculations (skew and kurtosis mainly) are fixed and verified, all examples are now runnable, and many small accuracy and performance improvements for individual distributions were merged.

The new function *scipy.stats.anderson_ksamp* computes the k-sample Anderson-Darling test for the null hypothesis that k samples come from the same parent population.

scipy.signal improvements

`scipy.signal.iirfilter` and related functions to design Butterworth, Chebyshev, elliptical and Bessel IIR filters now all use pole-zero ("zpk") format internally instead of using transformations to numerator/denominator format. The accuracy of the produced filters, especially high-order ones, is improved significantly as a result.

The Savitzky-Golay filter was added with the new functions *scipy.signal.savgol_filter* and *scipy.signal.savgol_coeffs*.

The new function *scipy.signal.vectorstrength* computes the vector strength, a measure of phase synchrony, of a set of events.

scipy.special improvements

The functions *scipy.special.boxcox* and *scipy.special.boxcox1p*, which compute the Box-Cox transformation, have been added.

`scipy.sparse` improvements

- Significant performance improvement in CSR, CSC, and DOK indexing speed.
- When using Numpy >= 1.9 (to be released in MM 2014), sparse matrices function correctly when given to arguments of `np.dot`, `np.multiply` and other ufuncs. With earlier Numpy and Scipy versions, the results of such operations are undefined and usually unexpected.
- Sparse matrices are no longer limited to `2^31` nonzero elements. They automatically switch to using 64-bit index data type for matrices containing more elements. User code written assuming the sparse matrices use int32 as the index data type will continue to work, except for such large matrices. Code dealing with larger matrices needs to accept either int32 or int64 indices.

5.35.2 Deprecated features

`anneal`

The global minimization function *scipy.optimize.anneal* is deprecated. All users should use the *`scipy.optimize.basinhopping`* function instead.

`scipy.stats`

`randwcdf` and `randwppf` functions are deprecated. All users should use distribution-specific `rvs` methods instead.

Probability calculation aliases `zprob`, `fprob` and `ksprob` are deprecated. Use instead the `sf` methods of the corresponding distributions or the `special` functions directly.

`scipy.interpolate`

`PiecewisePolynomial` class is deprecated.

5.35.3 Backwards incompatible changes

scipy.special.lpmn

`lpmn` no longer accepts complex-valued arguments. A new function `clpmn` with uniform complex analytic behavior has been added, and it should be used instead.

scipy.sparse.linalg

Eigenvectors in the case of generalized eigenvalue problem are normalized to unit vectors in 2-norm, rather than following the LAPACK normalization convention.

The deprecated UMFPACK wrapper in `scipy.sparse.linalg` has been removed due to license and install issues. If available, `scikits.umfpack` is still used transparently in the `spsolve` and `factorized` functions. Otherwise, SuperLU is used instead in these functions.

scipy.stats

The deprecated functions `glm`, `oneway` and `cmedian` have been removed from `scipy.stats`.

`stats.scoreatpercentile` now returns an array instead of a list of percentiles.

scipy.interpolate

The API for computing derivatives of a monotone piecewise interpolation has changed: if *p* is a `PchipInterpolator` object, *p.derivative(der)* returns a callable object representing the derivative of *p*. For in-place derivatives use the second argument of the *__call__* method: *p(0.1, der=2)* evaluates the second derivative of *p* at *x=0.1*.

The method *p.derivatives* has been removed.

5.35.4 Other changes

5.35.5 Authors

- Marc Abramowitz +
- Anders Bech Borchersen +
- Vincent Arel-Bundock +
- Petr Baudis +
- Max Bolingbroke
- François Boulogne
- Matthew Brett
- Lars Buitinck
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- Daniel B. Smith
- Patrick Snape +
- Thomas Spura +
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- Julian Taylor
- Tomas Tomecek
- Richard Tsai
- Jacob Vanderplas
- Joris Vankerschaver +
- Pauli Virtanen
- Warren Weckesser

A total of 80 people contributed to this release. People with a "+" by their names contributed a patch for the first time. This list of names is automatically generated, and may not be fully complete.

Issues closed

- #1325: add custom axis keyword to dendrogram function in scipy.cluster.hierarchy…
- #1437: Wrong pochhammer symbol for negative integers (Trac #910)
- #1555: scipy.io.netcdf leaks file descriptors (Trac #1028)
- #1569: sparse matrix failed with element-wise multiplication using numpy.multiply()…
- #1833: Sparse matrices are limited to 2^32 non-zero elements (Trac #1307)
- #1834: scipy.linalg.eig does not normalize eigenvector if B is given…
- #1866: stats for invgamma (Trac #1340)
- #1886: stats.zipf floating point warnings (Trac #1361)
- #1887: Stats continuous distributions - floating point warnings (Trac…
- #1897: scoreatpercentile() does not handle empty list inputs (Trac #1372)
- #1918: splint returns incorrect results (Trac #1393)

- #1949: kurtosistest fails in mstats with type error (Trac #1424)
- #2092: scipy.test leaves darwin27compiled_catalog, cpp and so files…
- #2106: stats ENH: shape parameters in distribution docstrings (Trac…
- #2123: Bad behavior of sparse matrices in a binary ufunc (Trac #1598)
- #2152: Fix mmio/fromfile on gzip on Python 3 (Trac #1627)
- #2164: stats.rice.pdf(x, 0) returns nan (Trac #1639)
- #2169: scipy.optimize.fmin_bfgs not handling functions with boundaries…
- #2177: scipy.cluster.hierarchy.ClusterNode.pre_order returns IndexError…
- #2179: coo.todense() segfaults (Trac #1654)
- #2185: Precision of scipy.ndimage.gaussian_filter*() limited (Trac #1660)
- #2186: scipy.stats.mstats.kurtosistest crashes on 1d input (Trac #1661)
- #2238: Negative p-value on hypergeom.cdf (Trac #1719)
- #2283: ascending order in interpolation routines (Trac #1764)
- #2288: mstats.kurtosistest is incorrectly converting to float, and fails…
- #2396: lpmn wrong results for `|z| > 1` (Trac #1877)
- #2398: ss2tf returns num as 2D array instead of 1D (Trac #1879)
- #2406: linkage does not take Unicode strings as method names (Trac #1887)
- #2443: IIR filter design should not transform to tf representation internally
- #2572: class method solve of splu return object corrupted or falsely…
- #2667: stats endless loop ?
- #2671: .stats.hypergeom documentation error in the note about pmf
- #2691: BUG scipy.linalg.lapack: potrf/ptroi interpret their ‘lower’…
- #2721: Allow use of ellipsis in scipy.sparse slicing
- #2741: stats: deprecate and remove alias for special functions
- #2742: stats add rvs to rice distribution
- #2765: bugs stats entropy
- #2832: argrelextrema returns tuple of 2 empty arrays when no peaks found…
- #2861: scipy.stats.scoreatpercentile broken for vector *per*
- #2891: COBYLA successful termination when constraints violated
- #2919: test failure with the current master
- #2922: ndimage.percentile_filter ignores origin argument for multidimensional…
- #2938: Sparse/dense matrix inplace operations fail due to __numpy_ufunc__
- #2944: MacPorts builds yield 40Mb worth of build warnings
- #2945: FAIL: test_random_complex (test_basic.TestDet)
- #2947: FAIL: Test some trivial edge cases for savgol_filter()
- #2953: Scipy Delaunay triangulation is not oriented

- #2971: scipy.stats.mstats.winsorize documentation error
- #2980: Problems running what seems a perfectly valid example
- #2996: entropy for rv_discrete is incorrect?!
- #2998: Fix numpy version comparisons
- #3002: python setup.py install fails
- #3014: Bug in stats.fisher_exact
- #3030: relative entropy using scipy.stats.distribution.entropy when…
- #3037: scipy.optimize.curve_fit leads to unexpected behavior when input…
- #3047: mstats.ttest_rel axis=None, requires masked array
- #3059: BUG: Slices of sparse matrices return incorrect dtype
- #3063: range keyword in binned_statistics incorrect
- #3067: cumtrapz not working as expected
- #3069: sinc
- #3086: standard error calculation inconsistent between 'stats' and 'mstats'
- #3094: Add a *perm* function into `scipy.misc` and an enhancement of…
- #3111: scipy.sparse.[hv]stack don't respect anymore the dtype parameter
- #3172: optimize.curve_fit uses different nomenclature from optimize.leastsq
- #3196: scipy.stats.mstats.gmean does not actually take dtype
- #3212: Dot product of csr_matrix causes segmentation fault
- #3227: ZeroDivisionError in broyden1 when initial guess is the right…
- #3238: lbfgsb output not suppressed by disp=0
- #3249: Sparse matrix min/max/etc don't support axis=-1
- #3251: cdist performance issue with 'sqeuclidean' metric
- #3279: logm fails for singular matrix
- #3285: signal.chirp(method='hyp') disallows hyperbolic upsweep
- #3299: MEMORY LEAK: fmin_tnc
- #3330: test failures with the current master
- #3345: scipy and/or numpy change is causing tests to fail in another…
- #3363: splu does not work for non-vector inputs
- #3385: expit does not handle large arguments well
- #3395: specfun.f doesn't compile with MinGW
- #3399: Error message bug in scipy.cluster.hierarchy.linkage
- #3404: interpolate._ppoly doesn't build with MinGW
- #3412: Test failures in signal
- #3466: `` `scipy.sparse.csgraph.shortest_path` `` does not work on `` `scipy.sparse.csr_matrix` `` or `` `lil_matrix` ``

Pull requests

- #442: ENH: sparse: enable 64-bit index arrays & nnz > 2**31
- #2766: DOC: remove doc/seps/technology-preview.rst
- #2772: TST: stats: Added a regression test for stats.wilcoxon. Closes…
- #2778: Clean up stats._support, close statistics review issues
- #2792: BUG io: fix file descriptor closing for netcdf variables
- #2847: Rice distribution: extend to b=0, add an explicit rvs method.
- #2878: [stats] fix formulas for higher moments of dweibull distribution
- #2904: ENH: moments for the zipf distribution
- #2907: ENH: add coverage info with coveralls.io for Travis runs.
- #2932: BUG+TST: setdiag implementation for dia_matrix (Close #2931)…
- #2942: Misc fixes pointed out by Eclipse PyDev static code analysis
- #2946: ENH: allow non-monotonic input in interp1d
- #2986: BUG: runtests: chdir away from root when running tests
- #2987: DOC: linalg: don't recommend np.linalg.norm
- #2992: ENH: Add "limit" parameter to dijkstra calculation
- #2995: ENH: Use int shape
- #3006: DOC: stats: add a log base note to the docstring
- #3007: DEP: stats: Deprecate randwppf and randwcdf
- #3008: Fix mstats.kurtosistest, and test coverage for skewtest/normaltest
- #3009: Minor reST typo
- #3010: Add *scipy.optimize.Result* to API docs
- #3012: Corrects documentation error
- #3052: PEP-8 conformance improvements
- #3064: Binned statistic
- #3068: Fix Issue #3067 fix cumptrapz that was raising an exception when…
- #3073: Arff reader with nominal value of 1 character
- #3074: Some maintenance work
- #3080: Review and clean up all Box-Cox functions
- #3083: Bug: should return 0 if no regions found
- #3085: BUG: Use zpk in IIR filter design to improve accuracy
- #3101: refactor stats tests a bit
- #3112: ENH: implement Akima interpolation in 1D
- #3123: MAINT: an easier way to make ranges from slices
- #3124: File object support for imread and imsave
- #3126: pep8ify stats/distributions.py

- #3134: MAINT: split distributions.py into three files
- #3138: clean up tests for discrete distributions
- #3155: special: handle the edge case lambda=0 in pdtr, pdtrc and pdtrik
- #3156: Rename optimize.Result to OptimizeResult
- #3166: BUG: make curve_fit() work with array_like input. Closes gh-3037.
- #3170: Fix numpy version checks
- #3175: use numpy sinc
- #3177: Update numpy version warning, remove oldnumeric import
- #3178: DEP: remove deprecated umfpack wrapper. Closes gh-3002.
- #3179: DOC: add BPoly to the docs
- #3180: Suppress warnings when running stats.test()
- #3181: altered sem func in mstats to match stats
- #3182: Make weave tests behave
- #3183: ENH: Add k-sample Anderson-Darling test to stats module
- #3186: Fix stats.scoreatpercentile
- #3187: DOC: make curve_fit nomenclature same as leastsq
- #3201: Added axis keyword to dendrogram function
- #3207: Make docstring examples in stats.distributions docstrings runnable
- #3218: BUG: integrate: Fix banded jacobian handling in the “vode” and…
- #3222: BUG: limit input ranges in special.nctdtr
- #3223: Fix test errors with numpy master
- #3224: Fix int32 overflows in sparsetools
- #3228: DOC: tf2ss zpk2ss note controller canonical form
- #3234: Add See Also links and Example graphs to filter design `*ord` functions
- #3235: Updated the buttord function to be consistent with the other…
- #3239: correct doc for pchip interpolation
- #3240: DOC: fix ReST errors in the BPoly docstring
- #3241: RF: check write attr of fileobject without writing
- #3243: a bit of maintanence work in stats
- #3245: BUG/ENH: stats: make frozen distributions hold separate instances
- #3247: ENH function to return nnz per row/column in some sparse matrices
- #3248: ENH much more efficient sparse min/max with axis
- #3252: Fast sqeuclidean
- #3253: FIX support axis=-1 and -2 for sparse reduce methods
- #3254: TST tests for non-canonical input to sparse matrix operations
- #3272: BUG: sparse: fix bugs in dia_matrix.setdiag

- #3278: Also generate a tar.xz when running paver sdist
- #3286: DOC: update 0.14.0 release notes.
- #3289: TST: remove insecure mktemp use in tests
- #3292: MAINT: fix a backwards incompatible change to stats.distributions.__all__
- #3293: ENH: signal: Allow upsweeps of frequency in the 'hyperbolic'…
- #3302: ENH: add dtype arg to stats.mstats.gmean and stats.mstats.hmean
- #3307: DOC: add note about different ba forms in tf2zpk
- #3309: doc enhancements to scipy.stats.mstats.winsorize
- #3310: DOC: clarify matrix vs array in mmio docstrings
- #3314: BUG: fix scipy.io.mmread() of gzipped files under Python3
- #3323: ENH: Efficient interpolation on regular grids in arbitrary dimensions
- #3332: DOC: clean up scipy.special docs
- #3335: ENH: improve nanmedian performance
- #3347: BUG: fix use of np.max in stats.fisher_exact
- #3356: ENH: sparse: speed up LIL indexing + assignment via Cython
- #3357: Fix "imresize does not work with size = int"
- #3358: MAINT: rename AkimaInterpolator to Akima1DInterpolator
- #3366: WHT: sparse: reindent `dsolve/*.c *.h`
- #3367: BUG: sparse/dsolve: fix dense matrix fortran order bugs in superlu…
- #3369: ENH minimize, minimize_scalar: Add support for user-provided…
- #3371: scipy.stats.sigmaclip doesn't appear in the html docs.
- #3373: BUG: sparse/dsolve: detect invalid LAPACK parameters in superlu…
- #3375: ENH: sparse/dsolve: make the L and U factors of splu and spilu…
- #3377: MAINT: make travis build one target against Numpy 1.5
- #3378: MAINT: fftpack: Remove the use of `'import *'` in a couple test…
- #3381: MAINT: replace np.isinf(x) & (x>0) -> np.isposinf(x) to avoid…
- #3383: MAINT: skip float96 tests on platforms without float96
- #3384: MAINT: add pyflakes to Travis-CI
- #3386: BUG: stable evaluation of expit
- #3388: BUG: SuperLU: fix missing declaration of dlamch
- #3389: BUG: sparse: downcast 64-bit indices safely to intp when required
- #3390: BUG: nonlinear solvers are not confused by lucky guess
- #3391: TST: fix sparse test errors due to axis=-1,-2 usage in np.matrix.sum().
- #3392: BUG: sparse/lil: fix up Cython bugs in fused type lookup
- #3393: BUG: sparse/compressed: work around bug in np.unique in earlier…
- #3394: BUG: allow ClusterNode.pre_order() for non-root nodes

- #3400: BUG: cluster.linkage ValueError typo bug
- #3402: BUG: special: In specfun.f, replace the use of CMPLX with DCMPLX,…
- #3408: MAINT: sparse: Numpy 1.5 compatibility fixes
- #3410: MAINT: interpolate: fix blas defs in _ppoly
- #3411: MAINT: Numpy 1.5 fixes in interpolate
- #3413: Fix more test issues with older numpy versions
- #3414: TST: signal: loosen some error tolerances in the filter tests….
- #3415: MAINT: tools: automated close issue + pr listings for release…
- #3440: MAINT: wrap sparsetools manually instead via SWIG
- #3460: TST: open image file in binary mode
- #3467: BUG: fix validation in csgraph.shortest_path

5.36 SciPy 0.13.2 Release Notes

SciPy 0.13.2 is a bug-fix release with no new features compared to 0.13.1.

5.36.1 Issues fixed

- 3096: require Cython 0.19, earlier versions have memory leaks in fused types
- 3079: `ndimage.label` fix swapped 64-bitness test
- 3108: `optimize.fmin_slsqp` constraint violation

5.37 SciPy 0.13.1 Release Notes

SciPy 0.13.1 is a bug-fix release with no new features compared to 0.13.0. The only changes are several fixes in `ndimage`, one of which was a serious regression in `ndimage.label` (Github issue 3025), which gave incorrect results in 0.13.0.

5.37.1 Issues fixed

- 3025: `ndimage.label` returns incorrect results in scipy 0.13.0
- 1992: `ndimage.label` return type changed from int32 to uint32
- 1992: `ndimage.find_objects` doesn't work with int32 input in some cases

5.38 SciPy 0.13.0 Release Notes

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    - *Deprecated `radon` function removed*
    - *Removed deprecated keywords `xa` and `xb` from `stats.distributions`*

        * *Changes to MATLAB file readers / writers*
    - *Other changes*
    - *Authors*

SciPy 0.13.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.13.x branch, and on adding new features on the master branch.

This release requires Python 2.6, 2.7 or 3.1-3.3 and NumPy 1.5.1 or greater. Highlights of this release are:

- support for fancy indexing and boolean comparisons with sparse matrices
- interpolative decompositions and matrix functions in the linalg module
- two new trust-region solvers for unconstrained minimization

5.38.1 New features

`scipy.integrate` improvements

N-dimensional numerical integration

A new function *`scipy.integrate.nquad`*, which provides N-dimensional integration functionality with a more flexible interface than `dblquad` and `tplquad`, has been added.

`dopri*` improvements

The intermediate results from the `dopri` family of ODE solvers can now be accessed by a *solout* callback function.

`scipy.linalg` improvements

Interpolative decompositions

Scipy now includes a new module *`scipy.linalg.interpolative`* containing routines for computing interpolative matrix decompositions (ID). This feature is based on the ID software package by P.G. Martinsson, V. Rokhlin, Y. Shkolnisky, and M. Tygert, previously adapted for Python in the PymatrixId package by K.L. Ho.

Polar decomposition

A new function *`scipy.linalg.polar`*, to compute the polar decomposition of a matrix, was added.

BLAS level 3 functions

The BLAS functions `symm`, `syrk`, `syr2k`, `hemm`, `herk` and `her2k` are now wrapped in *`scipy.linalg`*.

Matrix functions

Several matrix function algorithms have been implemented or updated following detailed descriptions in recent papers of Nick Higham and his co-authors. These include the matrix square root (`sqrtm`), the matrix logarithm (`logm`), the matrix exponential (`expm`) and its Frechet derivative (`expm_frechet`), and fractional matrix powers (`fractional_matrix_power`).

`scipy.optimize` improvements

Trust-region unconstrained minimization algorithms

The `minimize` function gained two trust-region solvers for unconstrained minimization: `dogleg` and `trust-ncg`.

`scipy.sparse` improvements

Boolean comparisons and sparse matrices

All sparse matrix types now support boolean data, and boolean operations. Two sparse matrices A and B can be compared in all the expected ways $A < B$, $A >= B$, $A != B$, producing similar results as dense Numpy arrays. Comparisons with dense matrices and scalars are also supported.

CSR and CSC fancy indexing

Compressed sparse row and column sparse matrix types now support fancy indexing with boolean matrices, slices, and lists. So where A is a (CSC or CSR) sparse matrix, you can do things like:

```
>>> A[A > 0.5] = 1  # since Boolean sparse matrices work
>>> A[:2, :3] = 2
>>> A[[1,2], 2] = 3
```

`scipy.sparse.linalg` improvements

The new function `onenormest` provides a lower bound of the 1-norm of a linear operator and has been implemented according to Higham and Tisseur (2000). This function is not only useful for sparse matrices, but can also be used to estimate the norm of products or powers of dense matrices without explicitly building the intermediate matrix.

The multiplicative action of the matrix exponential of a linear operator (`expm_multiply`) has been implemented following the description in Al-Mohy and Higham (2011).

Abstract linear operators (*`scipy.sparse.linalg.LinearOperator`*) can now be multiplied, added to each other, and exponentiated, producing new linear operators. This enables easier construction of composite linear operations.

`scipy.spatial` improvements

The vertices of a *ConvexHull* can now be accessed via the *vertices* attribute, which gives proper orientation in 2-D.

`scipy.signal` improvements

The cosine window function `scipy.signal.cosine` was added.

`scipy.special` improvements

New functions *scipy.special.xlogy* and *scipy.special.xlog1py* were added. These functions can simplify and speed up code that has to calculate `x * log(y)` and give 0 when `x == 0`.

`scipy.io` improvements

Unformatted Fortran file reader

The new class *scipy.io.FortranFile* facilitates reading unformatted sequential files written by Fortran code.

`scipy.io.wavfile` enhancements

scipy.io.wavfile.write now accepts a file buffer. Previously it only accepted a filename.

scipy.io.wavfile.read and *scipy.io.wavfile.write* can now handle floating point WAV files.

`scipy.interpolate` improvements

B-spline derivatives and antiderivatives

scipy.interpolate.splder and *scipy.interpolate.splantider* functions for computing B-splines that represent derivatives and antiderivatives of B-splines were added. These functions are also available in the class-based FITPACK interface as `UnivariateSpline.derivative` and `UnivariateSpline.antiderivative`.

`scipy.stats` improvements

Distributions now allow using keyword parameters in addition to positional parameters in all methods.

The function *scipy.stats.power_divergence* has been added for the Cressie-Read power divergence statistic and goodness of fit test. Included in this family of statistics is the "G-test" (https://en.wikipedia.org/wiki/G-test).

scipy.stats.mood now accepts multidimensional input.

An option was added to *scipy.stats.wilcoxon* for continuity correction.

scipy.stats.chisquare now has an *axis* argument.

scipy.stats.mstats.chisquare now has *axis* and *ddof* arguments.

5.38.2 Deprecated features

`expm2` and `expm3`

The matrix exponential functions *scipy.linalg.expm2* and *scipy.linalg.expm3* are deprecated. All users should use the numerically more robust *scipy.linalg.expm* function instead.

`scipy.stats` functions

scipy.stats.oneway is deprecated; *scipy.stats.f_oneway* should be used instead.

scipy.stats.glm is deprecated. *scipy.stats.ttest_ind* is an equivalent function; more full-featured general (and generalized) linear model implementations can be found in statsmodels.

scipy.stats.cmedian is deprecated; `numpy.median` should be used instead.

5.38.3 Backwards incompatible changes

LIL matrix assignment

Assigning values to LIL matrices with two index arrays now works similarly as assigning into ndarrays:

```
>>> x = lil_matrix((3, 3))
>>> x[[0,1,2],[0,1,2]]=[0,1,2]
>>> x.todense()
matrix([[ 0.,  0.,  0.],
        [ 0.,  1.,  0.],
        [ 0.,  0.,  2.]])
```

rather than giving the result:

```
>>> x.todense()
matrix([[ 0.,  1.,  2.],
        [ 0.,  1.,  2.],
        [ 0.,  1.,  2.]])
```

Users relying on the previous behavior will need to revisit their code. The previous behavior is obtained by `x[numpy.ix_([0,1,2],[0,1,2])] = ...`.

Deprecated `radon` function removed

The `misc.radon` function, which was deprecated in scipy 0.11.0, has been removed. Users can find a more full-featured `radon` function in scikit-image.

Removed deprecated keywords `xa` and `xb` from `stats.distributions`

The keywords `xa` and `xb`, which were deprecated since 0.11.0, have been removed from the distributions in `scipy.stats`.

Changes to MATLAB file readers / writers

The major change is that 1D arrays in numpy now become row vectors (shape 1, N) when saved to a MATLAB 5 format file. Previously 1D arrays saved as column vectors (N, 1). This is to harmonize the behavior of writing MATLAB 4 and 5 formats, and adapt to the defaults of numpy and MATLAB - for example `np.atleast_2d` returns 1D arrays as row vectors.

Trying to save arrays of greater than 2 dimensions in MATLAB 4 format now raises an error instead of silently reshaping the array as 2D.

`scipy.io.loadmat('afile')` used to look for *afile* on the Python system path (`sys.path`); now `loadmat` only looks in the current directory for a relative path filename.

5.38.4 Other changes

Security fix: `scipy.weave` previously used temporary directories in an insecure manner under certain circumstances.

Cython is now required to build *unreleased* versions of scipy. The C files generated from Cython sources are not included in the git repo anymore. They are however still shipped in source releases.

The code base received a fairly large PEP8 cleanup. A `tox pep8` command has been added; new code should pass this test command.

Scipy cannot be compiled with gfortran 4.1 anymore (at least on RH5), likely due to that compiler version not supporting entry constructs well.

5.38.5 Authors

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

- Jorge Cañardo Alastuey +
- Tom Aldcroft +
- Max Bolingbroke +
- Joseph Jon Booker +
- François Boulogne
- Matthew Brett
- Christian Brodbeck +
- Per Brodtkorb +
- Christian Brueffer +
- Lars Buitinck
- Evgeni Burovski +
- Tim Cera
- Lawrence Chan +
- David Cournapeau
- Dražen Lučanin +
- Alexander J. Dunlap +
- endolith
- André Gaul +
- Christoph Gohlke
- Ralf Gommers
- Alex Griffing +
- Blake Griffith +

- Charles Harris
- Bob Helmbold +
- Andreas Hilboll
- Kat Huang +
- Oleksandr (Sasha) Huziy +
- Gert-Ludwig Ingold +
- Thouis (Ray) Jones
- Juan Luis Cano Rodríguez +
- Robert Kern
- Andreas Kloeckner +
- Sytse Knypstra +
- Gustav Larsson +
- Denis Laxalde
- Christopher Lee
- Tim Leslie
- Wendy Liu +
- Clemens Novak +
- Takuya Oshima +
- Josef Perktold
- Illia Polosukhin +
- Przemek Porebski +
- Steve Richardson +
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- Skipper Seabold
- Fazlul Shahriar
- Leo Singer +
- Rohit Sivaprasad +
- Daniel B. Smith +
- Julian Taylor
- Louis Thibault +
- Tomas Tomecek +
- John Travers
- Richard Tsai +
- Jacob Vanderplas
- Patrick Varilly
- Pauli Virtanen

- Stefan van der Walt
- Warren Weckesser
- Pedro Werneck +
- Nils Werner +
- Michael Wimmer +
- Nathan Woods +
- Tony S. Yu +

A total of 65 people contributed to this release. People with a "+" by their names contributed a patch for the first time.

5.39 SciPy 0.12.1 Release Notes

SciPy 0.12.1 is a bug-fix release with no new features compared to 0.12.0. The single issue fixed by this release is a security issue in `scipy.weave`, which was previously using temporary directories in an insecure manner under certain circumstances.

5.40 SciPy 0.12.0 Release Notes

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        * scipy.lib.lapack
        * fblas *and* cblas
    - *Backwards incompatible changes*
        * *Removal of* `scipy.io.save_as_module`
        * axis *argument added to* `scipy.stats.scoreatpercentile`
    - *Authors*

SciPy 0.12.0 is the culmination of 7 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.12.x branch, and on adding new features on the master branch.

Some of the highlights of this release are:

- Completed QHull wrappers in scipy.spatial.
- cKDTree now a drop-in replacement for KDTree.
- A new global optimizer, basinhopping.
- Support for Python 2 and Python 3 from the same code base (no more 2to3).

This release requires Python 2.6, 2.7 or 3.1-3.3 and NumPy 1.5.1 or greater. Support for Python 2.4 and 2.5 has been dropped as of this release.

5.40.1 New features

`scipy.spatial` improvements

cKDTree feature-complete

Cython version of KDTree, cKDTree, is now feature-complete. Most operations (construction, query, query_ball_point, query_pairs, count_neighbors and sparse_distance_matrix) are between 200 and 1000 times faster in cKDTree than in KDTree. With very minor caveats, cKDTree has exactly the same interface as KDTree, and can be used as a drop-in replacement.

Voronoi diagrams and convex hulls

`scipy.spatial` now contains functionality for computing Voronoi diagrams and convex hulls using the Qhull library. (Delaunay triangulation was available since Scipy 0.9.0.)

Delaunay improvements

It's now possible to pass in custom Qhull options in Delaunay triangulation. Coplanar points are now also recorded, if present. Incremental construction of Delaunay triangulations is now also possible.

Spectral estimators (`scipy.signal`)

The functions `scipy.signal.periodogram` and `scipy.signal.welch` were added, providing DFT-based spectral estimators.

`scipy.optimize` improvements

Callback functions in L-BFGS-B and TNC

A callback mechanism was added to L-BFGS-B and TNC minimization solvers.

Basin hopping global optimization (`scipy.optimize.basinhopping`)

A new global optimization algorithm. Basinhopping is designed to efficiently find the global minimum of a smooth function.

`scipy.special` improvements

Revised complex error functions

The computation of special functions related to the error function now uses a new Faddeeva library from MIT which increases their numerical precision. The scaled and imaginary error functions `erfcx` and `erfi` were also added, and the Dawson integral `dawsn` can now be evaluated for a complex argument.

Faster orthogonal polynomials

Evaluation of orthogonal polynomials (the `eval_*` routines) in now faster in `scipy.special`, and their `out=` argument functions properly.

`scipy.sparse.linalg` features

- In `scipy.sparse.linalg.spsolve`, the `b` argument can now be either a vector or a matrix.
- `scipy.sparse.linalg.inv` was added. This uses `spsolve` to compute a sparse matrix inverse.
- `scipy.sparse.linalg.expm` was added. This computes the exponential of a sparse matrix using a similar algorithm to the existing dense array implementation in `scipy.linalg.expm`.

Listing Matlab(R) file contents in `scipy.io`

A new function `whosmat` is available in `scipy.io` for inspecting contents of MAT files without reading them to memory.

Documented BLAS and LAPACK low-level interfaces (`scipy.linalg`)

The modules *`scipy.linalg.blas`* and *`scipy.linalg.lapack`* can be used to access low-level BLAS and LAPACK functions.

Polynomial interpolation improvements (`scipy.interpolate`)

The barycentric, Krogh, piecewise and pchip polynomial interpolators in `scipy.interpolate` accept now an `axis` argument.

5.40.2 Deprecated features

scipy.lib.lapack

The module *scipy.lib.lapack* is deprecated. You can use *scipy.linalg.lapack* instead. The module *scipy.lib.blas* was deprecated earlier in Scipy 0.10.0.

fblas and *cblas*

Accessing the modules *scipy.linalg.fblas*, *cblas*, *flapack*, *clapack* is deprecated. Instead, use the modules *scipy.linalg.lapack* and *scipy.linalg.blas*.

5.40.3 Backwards incompatible changes

Removal of `scipy.io.save_as_module`

The function `scipy.io.save_as_module` was deprecated in Scipy 0.11.0, and is now removed.

Its private support modules `scipy.io.dumbdbm_patched` and `scipy.io.dumb_shelve` are also removed.

axis argument added to `scipy.stats.scoreatpercentile`

The function *scipy.stats.scoreatpercentile* has been given an *axis* argument. The default argument is *axis=None*, which means the calculation is done on the flattened array. Before this change, *scoreatpercentile* would act as if *axis=0* had been given. Code using *scoreatpercentile* with a multidimensional array will need to add *axis=0* to the function call to preserve the old behavior. (This API change was not noticed until long after the release of 0.12.0.)

5.40.4 Authors

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- Anne Archibald
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A total of 75 people contributed to this release. People with a "+" by their names contributed a patch for the first time.

5.41 SciPy 0.11.0 Release Notes

Contents

- *SciPy 0.11.0 Release Notes*
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  - *Authors*

SciPy 0.11.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. Highlights of this release are:

- A new module has been added which provides a number of common sparse graph algorithms.
- New unified interfaces to the existing optimization and root finding functions have been added.

All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Our development attention will now shift to bug-fix releases on the 0.11.x branch, and on adding new features on the master branch.

This release requires Python 2.4-2.7 or 3.1-3.2 and NumPy 1.5.1 or greater.

5.41.1 New features

Sparse Graph Submodule

The new submodule *scipy.sparse.csgraph* implements a number of efficient graph algorithms for graphs stored as sparse adjacency matrices. Available routines are:

- *connected_components* - determine connected components of a graph
- *laplacian* - compute the laplacian of a graph
- *shortest_path* - compute the shortest path between points on a positive graph
- *dijkstra* - use Dijkstra's algorithm for shortest path
- *floyd_warshall* - use the Floyd-Warshall algorithm for shortest path
- *breadth_first_order* - compute a breadth-first order of nodes
- *depth_first_order* - compute a depth-first order of nodes
- *breadth_first_tree* - construct the breadth-first tree from a given node
- *depth_first_tree* - construct a depth-first tree from a given node
- *minimum_spanning_tree* - construct the minimum spanning tree of a graph

`scipy.optimize` improvements

The optimize module has received a lot of attention this release. In addition to added tests, documentation improvements, bug fixes and code clean-up, the following improvements were made:

- A unified interface to minimizers of univariate and multivariate functions has been added.
- A unified interface to root finding algorithms for multivariate functions has been added.
- The L-BFGS-B algorithm has been updated to version 3.0.

Unified interfaces to minimizers

Two new functions `scipy.optimize.minimize` and `scipy.optimize.minimize_scalar` were added to provide a common interface to minimizers of multivariate and univariate functions respectively. For multivariate functions, `scipy.optimize.minimize` provides an interface to methods for unconstrained optimization (*fmin*, *fmin_powell*, *fmin_cg*, *fmin_ncg*, *fmin_bfgs* and *anneal*) or constrained optimization (*fmin_l_bfgs_b*, *fmin_tnc*, *fmin_cobyla* and *fmin_slsqp*). For univariate functions, `scipy.optimize.minimize_scalar` provides an interface to methods for unconstrained and bounded optimization (*brent*, *golden*, *fminbound*). This allows for easier comparing and switching between solvers.

Unified interface to root finding algorithms

The new function `scipy.optimize.root` provides a common interface to root finding algorithms for multivariate functions, embedding *fsolve*, *leastsq* and *nonlin* solvers.

`scipy.linalg` improvements

New matrix equation solvers

Solvers for the Sylvester equation (`scipy.linalg.solve_sylvester`, discrete and continuous Lyapunov equations (`scipy.linalg.solve_lyapunov`, `scipy.linalg.solve_discrete_lyapunov`) and discrete and continuous algebraic Riccati equations (`scipy.linalg.solve_continuous_are`, `scipy.linalg.solve_discrete_are`) have been added to `scipy.linalg`. These solvers are often used in the field of linear control theory.

QZ and QR Decomposition

It is now possible to calculate the QZ, or Generalized Schur, decomposition using `scipy.linalg.qz`. This function wraps the LAPACK routines sgges, dgges, cgges, and zgges.

The function `scipy.linalg.qr_multiply`, which allows efficient computation of the matrix product of Q (from a QR decomposition) and a vector, has been added.

Pascal matrices

A function for creating Pascal matrices, `scipy.linalg.pascal`, was added.

Sparse matrix construction and operations

Two new functions, `scipy.sparse.diags` and `scipy.sparse.block_diag`, were added to easily construct diagonal and block-diagonal sparse matrices respectively.

`scipy.sparse.csc_matrix` and `csr_matrix` now support the operations `sin`, `tan`, `arcsin`, `arctan`, `sinh`, `tanh`, `arcsinh`, `arctanh`, `rint`, `sign`, `expm1`, `log1p`, `deg2rad`, `rad2deg`, `floor`, `ceil` and `trunc`. Previously, these operations had to be performed by operating on the matrices' `data` attribute.

LSMR iterative solver

LSMR, an iterative method for solving (sparse) linear and linear least-squares systems, was added as `scipy.sparse.linalg.lsmr`.

Discrete Sine Transform

Bindings for the discrete sine transform functions have been added to `scipy.fftpack`.

`scipy.interpolate` improvements

For interpolation in spherical coordinates, the three classes `scipy.interpolate.SmoothSphereBivariateSpline`, `scipy.interpolate.LSQSphereBivariateSpline`, and `scipy.interpolate.RectSphereBivariateSpline` have been added.

Binned statistics (`scipy.stats`)

The stats module has gained functions to do binned statistics, which are a generalization of histograms, in 1-D, 2-D and multiple dimensions: `scipy.stats.binned_statistic`, `scipy.stats.binned_statistic_2d` and `scipy.stats.binned_statistic_dd`.

5.41.2 Deprecated features

`scipy.sparse.cs_graph_components` has been made a part of the sparse graph submodule, and renamed to `scipy.sparse.csgraph.connected_components`. Calling the former routine will result in a deprecation warning.

`scipy.misc.radon` has been deprecated. A more full-featured radon transform can be found in scikits-image.

`scipy.io.save_as_module` has been deprecated. A better way to save multiple Numpy arrays is the `numpy.savez` function.

The *xa* and *xb* parameters for all distributions in `scipy.stats.distributions` already weren't used; they have now been deprecated.

5.41.3 Backwards incompatible changes

Removal of `scipy.maxentropy`

The `scipy.maxentropy` module, which was deprecated in the 0.10.0 release, has been removed. Logistic regression in scikits.learn is a good and modern alternative for this functionality.

Minor change in behavior of `splev`

The spline evaluation function now behaves similarly to `interp1d` for size-1 arrays. Previous behavior:

```
>>> from scipy.interpolate import splev, splrep, interp1d
>>> x = [1,2,3,4,5]
>>> y = [4,5,6,7,8]
>>> tck = splrep(x, y)
>>> splev([1], tck)
4.
>>> splev(1, tck)
4.
```

Corrected behavior:

```
>>> splev([1], tck)
array([ 4.])
>>> splev(1, tck)
array(4.)
```

This affects also the `UnivariateSpline` classes.

Behavior of `scipy.integrate.complex_ode`

The behavior of the `y` attribute of `complex_ode` is changed. Previously, it expressed the complex-valued solution in the form:

```
z = ode.y[::2] + 1j * ode.y[1::2]
```

Now, it is directly the complex-valued solution:

```
z = ode.y
```

Minor change in behavior of T-tests

The T-tests `scipy.stats.ttest_ind`, `scipy.stats.ttest_rel` and `scipy.stats.ttest_1samp` have been changed so that 0 / 0 now returns NaN instead of 1.

5.41.4 Other changes

The SuperLU sources in `scipy.sparse.linalg` have been updated to version 4.3 from upstream.

The function `scipy.signal.bode`, which calculates magnitude and phase data for a continuous-time system, has been added.

The two-sample T-test `scipy.stats.ttest_ind` gained an option to compare samples with unequal variances, i.e. Welch's T-test.

`scipy.misc.logsumexp` now takes an optional `axis` keyword argument.

5.41.5 Authors

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

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- Thouis (Ray) Jones
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- Scott Sinclair
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A total of 55 people contributed to this release. People with a "+" by their names contributed a patch for the first time.

5.42 SciPy 0.10.1 Release Notes

Contents

- *SciPy 0.10.1 Release Notes*
  - *Main changes*
  - *Other issues fixed*

SciPy 0.10.1 is a bug-fix release with no new features compared to 0.10.0.

5.42.1 Main changes

The most important changes are:

1. The single precision routines of `eigs` and `eigsh` in `scipy.sparse.linalg` have been disabled (they internally use double precision now).
2. A compatibility issue related to changes in NumPy macros has been fixed, in order to make scipy 0.10.1 compile with the upcoming numpy 1.7.0 release.

5.42.2 Other issues fixed

- #835: stats: nan propagation in stats.distributions
- #1202: io: netcdf segfault
- #1531: optimize: make curve_fit work with method as callable.
- #1560: linalg: fixed mistake in eig_banded documentation.
- #1565: ndimage: bug in ndimage.variance
- #1457: ndimage: standard_deviation does not work with sequence of indexes
- #1562: cluster: segfault in linkage function
- #1568: stats: One-sided fisher_exact() returns $p < 1$ for 0 successful attempts
- #1575: stats: zscore and zmap handle the axis keyword incorrectly

5.43 SciPy 0.10.0 Release Notes

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    - *Enhancements to `scipy.signal`*
    - *Additional decomposition options (`scipy.linalg`)*
    - *Additional special matrices (`scipy.linalg`)*
    - *Enhancements to `scipy.stats`*
    - *Enhancements to `scipy.special`*
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    - `scipy.lib.blas`
    - *Numscons build system*
  - *Backwards-incompatible changes*
  - *Other changes*
  - *Authors*

SciPy 0.10.0 is the culmination of 8 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a limited number of deprecations and backwards-incompatible changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.10.x branch, and on adding new features on the development master branch.

Release highlights:

- Support for Bento as optional build system.
- Support for generalized eigenvalue problems, and all shift-invert modes available in ARPACK.

This release requires Python 2.4-2.7 or 3.1- and NumPy 1.5 or greater.

5.43.1 New features

Bento: new optional build system

Scipy can now be built with Bento. Bento has some nice features like parallel builds and partial rebuilds, that are not possible with the default build system (distutils). For usage instructions see BENTO_BUILD.txt in the scipy top-level directory.

Currently Scipy has three build systems, distutils, numscons and bento. Numscons is deprecated and is planned and will likely be removed in the next release.

Generalized and shift-invert eigenvalue problems in `scipy.sparse.linalg`

The sparse eigenvalue problem solver functions `scipy.sparse.eigs/eigh` now support generalized eigenvalue problems, and all shift-invert modes available in ARPACK.

Discrete-Time Linear Systems (`scipy.signal`)

Support for simulating discrete-time linear systems, including `scipy.signal.dlsim`, `scipy.signal.dimpulse`, and `scipy.signal.dstep`, has been added to SciPy. Conversion of linear systems from continuous-time to discrete-time representations is also present via the `scipy.signal.cont2discrete` function.

Enhancements to `scipy.signal`

A Lomb-Scargle periodogram can now be computed with the new function `scipy.signal.lombscargle`.

The forward-backward filter function `scipy.signal.filtfilt` can now filter the data in a given axis of an n-dimensional numpy array. (Previously it only handled a 1-dimensional array.) Options have been added to allow more control over how the data is extended before filtering.

FIR filter design with `scipy.signal.firwin2` now has options to create filters of type III (zero at zero and Nyquist frequencies) and IV (zero at zero frequency).

Additional decomposition options (`scipy.linalg`)

A sort keyword has been added to the Schur decomposition routine (`scipy.linalg.schur`) to allow the sorting of eigenvalues in the resultant Schur form.

Additional special matrices (`scipy.linalg`)

The functions `hilbert` and `invhilbert` were added to `scipy.linalg`.

Enhancements to `scipy.stats`

- The *one-sided form* of Fisher's exact test is now also implemented in `stats.fisher_exact`.
- The function `stats.chi2_contingency` for computing the chi-square test of independence of factors in a contingency table has been added, along with the related utility functions `stats.contingency.margins` and `stats.contingency.expected_freq`.

Enhancements to `scipy.special`

The functions `logit(p) = log(p/(1-p))` and `expit(x) = 1/(1+exp(-x))` have been implemented as `scipy.special.logit` and `scipy.special.expit` respectively.

Basic support for Harwell-Boeing file format for sparse matrices

Both read and write are support through a simple function-based API, as well as a more complete API to control number format. The functions may be found in scipy.sparse.io.

The following features are supported:

- Read and write sparse matrices in the CSC format
- Only real, symmetric, assembled matrix are supported (RUA format)

5.43.2 Deprecated features

`scipy.maxentropy`

The maxentropy module is unmaintained, rarely used and has not been functioning well for several releases. Therefore it has been deprecated for this release, and will be removed for scipy 0.11. Logistic regression in scikits.learn is a good alternative for this functionality. The `scipy.maxentropy.logsumexp` function has been moved to `scipy.misc`.

`scipy.lib.blas`

There are similar BLAS wrappers in `scipy.linalg` and `scipy.lib`. These have now been consolidated as `scipy.linalg.blas`, and `scipy.lib.blas` is deprecated.

Numscons build system

The numscons build system is being replaced by Bento, and will be removed in one of the next scipy releases.

5.43.3 Backwards-incompatible changes

The deprecated name *invnorm* was removed from `scipy.stats.distributions`, this distribution is available as *invgauss*.

The following deprecated nonlinear solvers from `scipy.optimize` have been removed:

```
- ``broyden_modified`` (bad performance)
- ``broyden1_modified`` (bad performance)
- ``broyden_generalized`` (equivalent to ``anderson``)
- ``anderson2`` (equivalent to ``anderson``)
- ``broyden3`` (obsoleted by new limited-memory broyden methods)
- ``vackar`` (renamed to ``diagbroyden``)
```

5.43.4 Other changes

`scipy.constants` has been updated with the CODATA 2010 constants.

`__all__` dicts have been added to all modules, which has cleaned up the namespaces (particularly useful for interactive work).

An API section has been added to the documentation, giving recommended import guidelines and specifying which submodules are public and which aren't.

5.43.5 Authors

This release contains work by the following people (contributed at least one patch to this release, names in alphabetical order):

- Jeff Armstrong +
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- FI$H 2000 +
- Michael McNeil Forbes +
- Matty G +
- Christoph Gohlke
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- Yaroslav Halchenko
- Charles Harris
- Thouis (Ray) Jones +
- Chris Jordan-Squire +
- Robert Kern
- Chris Lasher +
- Wes McKinney +
- Travis Oliphant
- Fabian Pedregosa
- Josef Perktold
- Thomas Robitaille +

- Pim Schellart +
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- Skipper Seabold +
- Fazlul Shahriar +
- David Simcha +
- Scott Sinclair +
- Andrey Smirnov +
- Collin RM Stocks +
- Martin Teichmann +
- Jake Vanderplas +
- Gaël Varoquaux +
- Pauli Virtanen
- Stefan van der Walt
- Warren Weckesser
- Mark Wiebe +

A total of 35 people contributed to this release. People with a "+" by their names contributed a patch for the first time.

5.44 SciPy 0.9.0 Release Notes

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    - *Nonlinear equation solvers (`scipy.optimize`)*
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    - *Improved statistical tests (`scipy.stats`)*
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    - *Obsolete nonlinear solvers (in `scipy.optimize`)*
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        * *scipy.sparse*
        * *scipy.sparse.linalg.arpack.speigs*
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SciPy 0.9.0 is the culmination of 6 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.9.x branch, and on adding new features on the development trunk.

This release requires Python 2.4 - 2.7 or 3.1 - and NumPy 1.5 or greater.

Please note that SciPy is still considered to have "Beta" status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have "Beta" status, we are committed to making them as bug-free as possible.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function's call signatures.

5.44.1 Python 3

Scipy 0.9.0 is the first SciPy release to support Python 3. The only module that is not yet ported is `scipy.weave`.

5.44.2 Scipy source code location to be changed

Soon after this release, Scipy will stop using SVN as the version control system, and move to Git. The development source code for Scipy can from then on be found at

https://github.com/scipy/scipy

5.44.3 New features

Delaunay tessellations (`scipy.spatial`)

Scipy now includes routines for computing Delaunay tessellations in N dimensions, powered by the Qhull computational geometry library. Such calculations can now make use of the new `scipy.spatial.Delaunay` interface.

N-dimensional interpolation (scipy.interpolate)

Support for scattered data interpolation is now significantly improved. This version includes a `scipy.interpolate.griddata` function that can perform linear and nearest-neighbour interpolation for N-dimensional scattered data, in addition to cubic spline (C1-smooth) interpolation in 2D and 1D. An object-oriented interface to each interpolator type is also available.

Nonlinear equation solvers (scipy.optimize)

Scipy includes new routines for large-scale nonlinear equation solving in `scipy.optimize`. The following methods are implemented:

- Newton-Krylov (`scipy.optimize.newton_krylov`)
- (Generalized) secant methods:
  - Limited-memory Broyden methods (`scipy.optimize.broyden1`, `scipy.optimize.broyden2`)
  - Anderson method (`scipy.optimize.anderson`)
- Simple iterations (`scipy.optimize.diagbroyden`, `scipy.optimize.excitingmixing`, `scipy.optimize.linearmixing`)

The `scipy.optimize.nonlin` module was completely rewritten, and some of the functions were deprecated (see above).

New linear algebra routines (scipy.linalg)

Scipy now contains routines for effectively solving triangular equation systems (`scipy.linalg.solve_triangular`).

Improved FIR filter design functions (scipy.signal)

The function `scipy.signal.firwin` was enhanced to allow the design of highpass, bandpass, bandstop and multi-band FIR filters.

The function `scipy.signal.firwin2` was added. This function uses the window method to create a linear phase FIR filter with an arbitrary frequency response.

The functions `scipy.signal.kaiser_atten` and `scipy.signal.kaiser_beta` were added.

Improved statistical tests (scipy.stats)

A new function `scipy.stats.fisher_exact` was added, that provides Fisher's exact test for 2x2 contingency tables.

The function `scipy.stats.kendalltau` was rewritten to make it much faster (O(n log(n)) vs O(n^2)).

5.44.4 Deprecated features

Obsolete nonlinear solvers (in `scipy.optimize`)

The following nonlinear solvers from `scipy.optimize` are deprecated:

- `broyden_modified` (bad performance)
- `broyden1_modified` (bad performance)
- `broyden_generalized` (equivalent to `anderson`)
- `anderson2` (equivalent to `anderson`)
- `broyden3` (obsoleted by new limited-memory broyden methods)
- `vackar` (renamed to `diagbroyden`)

5.44.5 Removed features

The deprecated modules `helpmod`, `pexec` and `ppimport` were removed from `scipy.misc`.

The `output_type` keyword in many `scipy.ndimage` interpolation functions has been removed.

The `econ` keyword in `scipy.linalg.qr` has been removed. The same functionality is still available by specifying `mode='economic'`.

Old correlate/convolve behavior (in `scipy.signal`)

The old behavior for `scipy.signal.convolve`, `scipy.signal.convolve2d`, `scipy.signal.correlate` and `scipy.signal.correlate2d` was deprecated in 0.8.0 and has now been removed. Convolve and correlate used to swap their arguments if the second argument has dimensions larger than the first one, and the mode was relative to the input with the largest dimension. The current behavior is to never swap the inputs, which is what most people expect, and is how correlation is usually defined.

`scipy.stats`

Many functions in `scipy.stats` that are either available from numpy or have been superseded, and have been deprecated since version 0.7, have been removed: *std*, *var*, *mean*, *median*, *cov*, *corrcoef*, *z*, *zs*, *stderr*, *samplestd*, *samplevar*, *pdfapprox*, *pdf_moments* and *erfc*. These changes are mirrored in `scipy.stats.mstats`.

`scipy.sparse`

Several methods of the sparse matrix classes in `scipy.sparse` which had been deprecated since version 0.7 were removed: *save*, *rowcol*, *getdata*, *listprint*, *ensure_sorted_indices*, *matvec*, *matmat* and *rmatvec*.

The functions `spkron`, `speye`, `spidentity`, `lil_eye` and `lil_diags` were removed from `scipy.sparse`. The first three functions are still available as `scipy.sparse.kron`, `scipy.sparse.eye` and `scipy.sparse.identity`.

The *dims* and *nzmax* keywords were removed from the sparse matrix constructor. The *colind* and *rowind* attributes were removed from CSR and CSC matrices respectively.

scipy.sparse.linalg.arpack.speigs

A duplicated interface to the ARPACK library was removed.

5.44.6 Other changes

ARPACK interface changes

The interface to the ARPACK eigenvalue routines in `scipy.sparse.linalg` was changed for more robustness.

The eigenvalue and SVD routines now raise `ArpackNoConvergence` if the eigenvalue iteration fails to converge. If partially converged results are desired, they can be accessed as follows:

```
import numpy as np
from scipy.sparse.linalg import eigs, ArpackNoConvergence

m = np.random.randn(30, 30)
try:
    w, v = eigs(m, 6)
except ArpackNoConvergence, err:
    partially_converged_w = err.eigenvalues
    partially_converged_v = err.eigenvectors
```

Several bugs were also fixed.

The routines were moreover renamed as follows:

- eigen –> eigs
- eigen_symmetric –> eigsh
- svd –> svds

5.45 SciPy 0.8.0 Release Notes

Contents

- *SciPy 0.8.0 Release Notes*
  - *Python 3*
  - *Major documentation improvements*
  - *Deprecated features*
    - *Swapping inputs for correlation functions (scipy.signal)*
    - *Obsolete code deprecated (scipy.misc)*
    - *Additional deprecations*
  - *New features*
    - *DCT support (scipy.fftpack)*
    - *Single precision support for fft functions (scipy.fftpack)*

        * *Correlation functions now implement the usual definition (scipy.signal)*
        * *Additions and modification to LTI functions (scipy.signal)*
        * *Improved waveform generators (scipy.signal)*
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        * *Lambert W function*
        * *Improved hypergeometric 2F1 function*
        * *More flexible interface for Radial basis function interpolation*
    - *Removed features*
        * *scipy.io*

SciPy 0.8.0 is the culmination of 17 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.8.x branch, and on adding new features on the development trunk. This release requires Python 2.4 - 2.6 and NumPy 1.4.1 or greater.

Please note that SciPy is still considered to have "Beta" status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have "Beta" status, we are committed to making them as bug-free as possible.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function's call signatures.

5.45.1 Python 3

Python 3 compatibility is planned and is currently technically feasible, since Numpy has been ported. However, since the Python 3 compatible Numpy 1.5 has not been released yet, support for Python 3 in Scipy is not yet included in Scipy 0.8. SciPy 0.9, planned for fall 2010, will very likely include experimental support for Python 3.

5.45.2 Major documentation improvements

SciPy documentation is greatly improved.

5.45.3 Deprecated features

Swapping inputs for correlation functions (scipy.signal)

Concern correlate, correlate2d, convolve and convolve2d. If the second input is larger than the first input, the inputs are swapped before calling the underlying computation routine. This behavior is deprecated, and will be removed in scipy 0.9.0.

Obsolete code deprecated (scipy.misc)

The modules *helpmod*, *ppimport* and *pexec* from `scipy.misc` are deprecated. They will be removed from SciPy in version 0.9.

Additional deprecations

- linalg: The function *solveh_banded* currently returns a tuple containing the Cholesky factorization and the solution to the linear system. In SciPy 0.9, the return value will be just the solution.
- The function *constants.codata.find* will generate a DeprecationWarning. In Scipy version 0.8.0, the keyword argument 'disp' was added to the function, with the default value 'True'. In 0.9.0, the default will be 'False'.
- The *qshape* keyword argument of *signal.chirp* is deprecated. Use the argument *vertex_zero* instead.
- Passing the coefficients of a polynomial as the argument *f0* to *signal.chirp* is deprecated. Use the function *signal.sweep_poly* instead.
- The *io.recaster* module has been deprecated and will be removed in 0.9.0.

5.45.4 New features

DCT support (scipy.fftpack)

New realtransforms have been added, namely dct and idct for Discrete Cosine Transform; type I, II and III are available.

Single precision support for fft functions (scipy.fftpack)

fft functions can now handle single precision inputs as well: fft(x) will return a single precision array if x is single precision.

At the moment, for FFT sizes that are not composites of 2, 3, and 5, the transform is computed internally in double precision to avoid rounding error in FFTPACK.

Correlation functions now implement the usual definition (scipy.signal)

The outputs should now correspond to their matlab and R counterparts, and do what most people expect if the old_behavior=False argument is passed:

- correlate, convolve and their 2d counterparts do not swap their inputs depending on their relative shape anymore;
- correlation functions now conjugate their second argument while computing the slided sum-products, which correspond to the usual definition of correlation.

Additions and modification to LTI functions (scipy.signal)

- The functions *impulse2* and *step2* were added to `scipy.signal`. They use the function `scipy.signal.lsim2` to compute the impulse and step response of a system, respectively.
- The function `scipy.signal.lsim2` was changed to pass any additional keyword arguments to the ODE solver.

Improved waveform generators (scipy.signal)

Several improvements to the *chirp* function in `scipy.signal` were made:

- The waveform generated when *method="logarithmic"* was corrected; it now generates a waveform that is also known as an "exponential" or "geometric" chirp. (See https://en.wikipedia.org/wiki/Chirp.)
- A new *chirp* method, "hyperbolic", was added.
- Instead of the keyword *qshape*, *chirp* now uses the keyword *vertex_zero*, a boolean.
- *chirp* no longer handles an arbitrary polynomial. This functionality has been moved to a new function, *sweep_poly*.

A new function, *sweep_poly*, was added.

New functions and other changes in scipy.linalg

The functions *cho_solve_banded*, *circulant*, *companion*, *hadamard* and *leslie* were added to `scipy.linalg`.

The function *block_diag* was enhanced to accept scalar and 1D arguments, along with the usual 2D arguments.

New function and changes in scipy.optimize

The *curve_fit* function has been added; it takes a function and uses non-linear least squares to fit that to the provided data.

The *leastsq* and *fsolve* functions now return an array of size one instead of a scalar when solving for a single parameter.

New sparse least squares solver

The *lsqr* function was added to *scipy.sparse*. This routine finds a least-squares solution to a large, sparse, linear system of equations.

ARPACK-based sparse SVD

A naive implementation of SVD for sparse matrices is available in scipy.sparse.linalg.eigen.arpack. It is based on using an symmetric solver on <A, A>, and as such may not be very precise.

Alternative behavior available for `scipy.constants.find`

The keyword argument *disp* was added to the function *scipy.constants.find*, with the default value *True*. When *disp* is *True*, the behavior is the same as in Scipy version 0.7. When *False*, the function returns the list of keys instead of printing them. (In SciPy version 0.9, the default will be reversed.)

Incomplete sparse LU decompositions

Scipy now wraps SuperLU version 4.0, which supports incomplete sparse LU decompositions. These can be accessed via *scipy.sparse.linalg.spilu*. Upgrade to SuperLU 4.0 also fixes some known bugs.

Faster matlab file reader and default behavior change

We've rewritten the matlab file reader in Cython and it should now read matlab files at around the same speed that Matlab does.

The reader reads matlab named and anonymous functions, but it can't write them.

Until scipy 0.8.0 we have returned arrays of matlab structs as numpy object arrays, where the objects have attributes named for the struct fields. As of 0.8.0, we return matlab structs as numpy structured arrays. You can get the older behavior by using the optional `struct_as_record=False` keyword argument to *scipy.io.loadmat* and friends.

There is an inconsistency in the matlab file writer, in that it writes numpy 1D arrays as column vectors in matlab 5 files, and row vectors in matlab 4 files. We will change this in the next version, so both write row vectors. There is a *FutureWarning* when calling the writer to warn of this change; for now we suggest using the `oned_as='row'` keyword argument to *scipy.io.savemat* and friends.

Faster evaluation of orthogonal polynomials

Values of orthogonal polynomials can be evaluated with new vectorized functions in *scipy.special*: *eval_legendre*, *eval_chebyt*, *eval_chebyu*, *eval_chebyc*, *eval_chebys*, *eval_jacobi*, *eval_laguerre*, *eval_genlaguerre*, *eval_hermite*, *eval_hermitenorm*, *eval_gegenbauer*, *eval_sh_legendre*, *eval_sh_chebyt*, *eval_sh_chebyu*, *eval_sh_jacobi*. This is faster than constructing the full coefficient representation of the polynomials, which was previously the only available way.

Note that the previous orthogonal polynomial routines will now also invoke this feature, when possible.

Lambert W function

`scipy.special.lambertw` can now be used for evaluating the Lambert W function.

Improved hypergeometric 2F1 function

Implementation of `scipy.special.hyp2f1` for real parameters was revised. The new version should produce accurate values for all real parameters.

More flexible interface for Radial basis function interpolation

The `scipy.interpolate.Rbf` class now accepts a callable as input for the "function" argument, in addition to the built-in radial basis functions which can be selected with a string argument.

5.45.5 Removed features

scipy.stsci: the package was removed

The module *scipy.misc.limits* was removed.

scipy.io

The IO code in both NumPy and SciPy is being extensively reworked. NumPy will be where basic code for reading and writing NumPy arrays is located, while SciPy will house file readers and writers for various data formats (data, audio, video, images, matlab, etc.).

Several functions in `scipy.io` are removed in the 0.8.0 release including: *npfile*, *save*, *load*, *create_module*, *create_shelf*, *objload*, *objsave*, *fopen*, *read_array*, *write_array*, *fread*, *fwrite*, *bswap*, *packbits*, *unpackbits*, and *convert_objectarray*. Some of these functions have been replaced by NumPy's raw reading and writing capabilities, memory-mapping capabilities, or array methods. Others have been moved from SciPy to NumPy, since basic array reading and writing capability is now handled by NumPy.

5.46 SciPy 0.7.2 Release Notes

Contents

- *SciPy 0.7.2 Release Notes*

SciPy 0.7.2 is a bug-fix release with no new features compared to 0.7.1. The only change is that all C sources from Cython code have been regenerated with Cython 0.12.1. This fixes the incompatibility between binaries of SciPy 0.7.1 and NumPy 1.4.

5.47 SciPy 0.7.1 Release Notes

Contents

- *SciPy 0.7.1 Release Notes*
  - *scipy.io*
  - *scipy.odr*
  - *scipy.signal*
  - *scipy.sparse*
  - *scipy.special*
  - *scipy.stats*
  - *Windows binaries for python 2.6*
  - *Universal build for scipy*

SciPy 0.7.1 is a bug-fix release with no new features compared to 0.7.0.

5.47.1 scipy.io

Bugs fixed:

- Several fixes in Matlab file IO

5.47.2 scipy.odr

Bugs fixed:

- Work around a failure with Python 2.6

5.47.3 scipy.signal

Memory leak in lfilter have been fixed, as well as support for array object

Bugs fixed:

- #880, #925: lfilter fixes
- #871: bicgstab fails on Win32

5.47.4 scipy.sparse

Bugs fixed:

- #883: scipy.io.mmread with scipy.sparse.lil_matrix broken
- lil_matrix and csc_matrix reject now unexpected sequences, cf. http://thread.gmane.org/gmane.comp.python.scientific.user/19996 (dead link)

5.47.5 scipy.special

Several bugs of varying severity were fixed in the special functions:

- #503, #640: iv: problems at large arguments fixed by new implementation
- #623: jv: fix errors at large arguments
- #679: struve: fix wrong output for v < 0
- #803: pbdv produces invalid output
- #804: lqmn: fix crashes on some input
- #823: betainc: fix documentation
- #834: exp1 strange behavior near negative integer values
- #852: jn_zeros: more accurate results for large s, also in jnp/yn/ynp_zeros
- #853: jv, yv, iv: invalid results for non-integer v < 0, complex x
- #854: jv, yv, iv, kv: return nan more consistently when out-of-domain
- #927: ellipj: fix segfault on Windows
- #946: ellpj: fix segfault on Mac OS X/python 2.6 combination.
- ive, jve, yve, kv, kve: with real-valued input, return nan for out-of-domain instead of returning only the real part of the result.

Also, when `scipy.special.errprint(1)` has been enabled, warning messages are now issued as Python warnings instead of printing them to stderr.

5.47.6 scipy.stats

- linregress, mannwhitneyu, describe: errors fixed
- kstwobign, norm, expon, exponweib, exponpow, frechet, genexpon, rdist, truncexpon, planck: improvements to numerical accuracy in distributions

5.47.7 Windows binaries for python 2.6

python 2.6 binaries for windows are now included. The binary for python 2.5 requires numpy 1.2.0 or above, and the one for python 2.6 requires numpy 1.3.0 or above.

5.47.8 Universal build for scipy

Mac OS X binary installer is now a proper universal build, and does not depend on gfortran anymore (libgfortran is statically linked). The python 2.5 version of scipy requires numpy 1.2.0 or above, the python 2.6 version requires numpy 1.3.0 or above.

5.48 SciPy 0.7.0 Release Notes

Contents

- *SciPy 0.7.0 Release Notes*
  - *Python 2.6 and 3.0*
  - *Major documentation improvements*
  - *Running Tests*
  - *Building SciPy*
  - *Sandbox Removed*
  - *Sparse Matrices*
  - *Statistics package*
  - *Reworking of IO package*
  - *New Hierarchical Clustering module*
  - *New Spatial package*
  - *Reworked fftpack package*
  - *New Constants package*
  - *New Radial Basis Function module*
  - *New complex ODE integrator*
  - *New generalized symmetric and hermitian eigenvalue problem solver*
  - *Bug fixes in the interpolation package*
  - *Weave clean up*
  - *Known problems*

SciPy 0.7.0 is the culmination of 16 months of hard work. It contains many new features, numerous bug-fixes, improved test coverage and better documentation. There have been a number of deprecations and API changes in this release, which are documented below. All users are encouraged to upgrade to this release, as there are a large number of bug-fixes and optimizations. Moreover, our development attention will now shift to bug-fix releases on the 0.7.x branch, and on adding new features on the development trunk. This release requires Python 2.4 or 2.5 and NumPy 1.2 or greater.

Please note that SciPy is still considered to have "Beta" status, as we work toward a SciPy 1.0.0 release. The 1.0.0 release will mark a major milestone in the development of SciPy, after which changing the package structure or API will be much more difficult. Whilst these pre-1.0 releases are considered to have "Beta" status, we are committed to making them as bug-free as possible. For example, in addition to fixing numerous bugs in this release, we have also doubled the number of unit tests since the last release.

However, until the 1.0 release, we are aggressively reviewing and refining the functionality, organization, and interface. This is being done in an effort to make the package as coherent, intuitive, and useful as possible. To achieve this, we need help from the community of users. Specifically, we need feedback regarding all aspects of the project - everything - from which algorithms we implement, to details about our function's call signatures.

Over the last year, we have seen a rapid increase in community involvement, and numerous infrastructure improvements to lower the barrier to contributions (e.g., more explicit coding standards, improved testing infrastructure, better documentation tools). Over the next year, we hope to see this trend continue and invite everyone to become more involved.

5.48.1 Python 2.6 and 3.0

A significant amount of work has gone into making SciPy compatible with Python 2.6; however, there are still some issues in this regard. The main issue with 2.6 support is NumPy. On UNIX (including Mac OS X), NumPy 1.2.1 mostly works, with a few caveats. On Windows, there are problems related to the compilation process. The upcoming NumPy 1.3 release will fix these problems. Any remaining issues with 2.6 support for SciPy 0.7 will be addressed in a bug-fix release.

Python 3.0 is not supported at all; it requires NumPy to be ported to Python 3.0. This requires immense effort, since a lot of C code has to be ported. The transition to 3.0 is still under consideration; currently, we don't have any timeline or roadmap for this transition.

5.48.2 Major documentation improvements

SciPy documentation is greatly improved; you can view a HTML reference manual online or download it as a PDF file. The new reference guide was built using the popular Sphinx tool.

This release also includes an updated tutorial, which hadn't been available since SciPy was ported to NumPy in 2005. Though not comprehensive, the tutorial shows how to use several essential parts of Scipy. It also includes the `ndimage` documentation from the `numarray` manual.

Nevertheless, more effort is needed on the documentation front. Luckily, contributing to Scipy documentation is now easier than before: if you find that a part of it requires improvements, and want to help us out, please register a user name in our web-based documentation editor at https://docs.scipy.org/ and correct the issues.

5.48.3 Running Tests

NumPy 1.2 introduced a new testing framework based on nose. Starting with this release, SciPy now uses the new NumPy test framework as well. Taking advantage of the new testing framework requires `nose` version 0.10, or later. One major advantage of the new framework is that it greatly simplifies writing unit tests - which has all ready paid off, given the rapid increase in tests. To run the full test suite:

```
>>> import scipy
>>> scipy.test('full')
```

For more information, please see The NumPy/SciPy Testing Guide.

We have also greatly improved our test coverage. There were just over 2,000 unit tests in the 0.6.0 release; this release nearly doubles that number, with just over 4,000 unit tests.

5.48.4 Building SciPy

Support for NumScons has been added. NumScons is a tentative new build system for NumPy/SciPy, using SCons at its core.

SCons is a next-generation build system, intended to replace the venerable `Make` with the integrated functionality of `autoconf`/`automake` and `ccache`. Scons is written in Python and its configuration files are Python scripts. NumScons is meant to replace NumPy's custom version of `distutils` providing more advanced functionality, such as `autoconf`, improved fortran support, more tools, and support for `numpy.distutils`/`scons` cooperation.

5.48.5 Sandbox Removed

While porting SciPy to NumPy in 2005, several packages and modules were moved into `scipy.sandbox`. The sandbox was a staging ground for packages that were undergoing rapid development and whose APIs were in flux. It was also a place where broken code could live. The sandbox has served its purpose well, but was starting to create confusion. Thus `scipy.sandbox` was removed. Most of the code was moved into `scipy`, some code was made into a `scikit`, and the remaining code was just deleted, as the functionality had been replaced by other code.

5.48.6 Sparse Matrices

Sparse matrices have seen extensive improvements. There is now support for integer dtypes such `int8`, `uint32`, etc. Two new sparse formats were added:

- new class `dia_matrix` : the sparse DIAgonal format
- new class `bsr_matrix` : the Block CSR format

Several new sparse matrix construction functions were added:

- `sparse.kron` : sparse Kronecker product
- `sparse.bmat` : sparse version of `numpy.bmat`
- `sparse.vstack` : sparse version of `numpy.vstack`
- `sparse.hstack` : sparse version of `numpy.hstack`

Extraction of submatrices and nonzero values have been added:

- `sparse.tril` : extract lower triangle
- `sparse.triu` : extract upper triangle
- `sparse.find` : nonzero values and their indices

`csr_matrix` and `csc_matrix` now support slicing and fancy indexing (e.g., `A[1:3, 4:7]` and `A[[3,2,6,8], :]`). Conversions among all sparse formats are now possible:

- using member functions such as `.tocsr()` and `.tolil()`
- using the `.asformat()` member function, e.g. `A.asformat('csr')`
- using constructors `A = lil_matrix([[1,2]]); B = csr_matrix(A)`

All sparse constructors now accept dense matrices and lists of lists. For example:

- `A = csr_matrix( rand(3,3) )` and `B = lil_matrix( [[1,2],[3,4]] )`

The handling of diagonals in the `spdiags` function has been changed. It now agrees with the MATLAB(TM) function of the same name.

Numerous efficiency improvements to format conversions and sparse matrix arithmetic have been made. Finally, this release contains numerous bugfixes.

5.48.7 Statistics package

Statistical functions for masked arrays have been added, and are accessible through `scipy.stats.mstats`. The functions are similar to their counterparts in `scipy.stats` but they have not yet been verified for identical interfaces and algorithms.

Several bugs were fixed for statistical functions, of those, `kstest` and `percentileofscore` gained new keyword arguments.

Added deprecation warning for `mean`, `median`, `var`, `std`, `cov`, and `corrcoef`. These functions should be replaced by their numpy counterparts. Note, however, that some of the default options differ between the `scipy.stats` and numpy versions of these functions.

Numerous bug fixes to `stats.distributions`: all generic methods now work correctly, several methods in individual distributions were corrected. However, a few issues remain with higher moments (`skew`, `kurtosis`) and entropy. The maximum likelihood estimator, `fit`, does not work out-of-the-box for some distributions - in some cases, starting values have to be carefully chosen, in other cases, the generic implementation of the maximum likelihood method might not be the numerically appropriate estimation method.

We expect more bugfixes, increases in numerical precision and enhancements in the next release of scipy.

5.48.8 Reworking of IO package

The IO code in both NumPy and SciPy is being extensively reworked. NumPy will be where basic code for reading and writing NumPy arrays is located, while SciPy will house file readers and writers for various data formats (data, audio, video, images, matlab, etc.).

Several functions in `scipy.io` have been deprecated and will be removed in the 0.8.0 release including `npfile`, `save`, `load`, `create_module`, `create_shelf`, `objload`, `objsave`, `fopen`, `read_array`, `write_array`, `fread`, `fwrite`, `bswap`, `packbits`, `unpackbits`, and `convert_objectarray`. Some of these functions have been replaced by NumPy's raw reading and writing capabilities, memory-mapping capabilities, or array methods. Others have been moved from SciPy to NumPy, since basic array reading and writing capability is now handled by NumPy.

The Matlab (TM) file readers/writers have a number of improvements:

- default version 5
- v5 writers for structures, cell arrays, and objects
- v5 readers/writers for function handles and 64-bit integers
- new struct_as_record keyword argument to `loadmat`, which loads struct arrays in matlab as record arrays in numpy
- string arrays have `dtype='U...'` instead of `dtype=object`
- `loadmat` no longer squeezes singleton dimensions, i.e. `squeeze_me=False` by default

5.48.9 New Hierarchical Clustering module

This module adds new hierarchical clustering functionality to the `scipy.cluster` package. The function interfaces are similar to the functions provided MATLAB(TM)'s Statistics Toolbox to help facilitate easier migration to the NumPy/SciPy framework. Linkage methods implemented include single, complete, average, weighted, centroid, median, and ward.

In addition, several functions are provided for computing inconsistency statistics, cophenetic distance, and maximum distance between descendants. The `fcluster` and `fclusterdata` functions transform a hierarchical clustering into a set of flat clusters. Since these flat clusters are generated by cutting the tree into a forest of trees, the `leaders` function takes a linkage and a flat clustering, and finds the root of each tree in the forest. The `ClusterNode` class represents a hierarchical clusterings as a field-navigable tree object. `to_tree` converts a matrix-encoded hierarchical clustering to a `ClusterNode` object. Routines for converting between MATLAB and SciPy linkage encodings are provided. Finally, a `dendrogram` function plots hierarchical clusterings as a dendrogram, using matplotlib.

5.48.10 New Spatial package

The new spatial package contains a collection of spatial algorithms and data structures, useful for spatial statistics and clustering applications. It includes rapidly compiled code for computing exact and approximate nearest neighbors, as well as a pure-python kd-tree with the same interface, but that supports annotation and a variety of other algorithms. The API for both modules may change somewhat, as user requirements become clearer.

It also includes a `distance` module, containing a collection of distance and dissimilarity functions for computing distances between vectors, which is useful for spatial statistics, clustering, and kd-trees. Distance and dissimilarity functions provided include Bray-Curtis, Canberra, Chebyshev, City Block, Cosine, Dice, Euclidean, Hamming, Jaccard, Kulsinski, Mahalanobis, Matching, Minkowski, Rogers-Tanimoto, Russell-Rao, Squared Euclidean, Standardized Euclidean, Sokal-Michener, Sokal-Sneath, and Yule.

The `pdist` function computes pairwise distance between all unordered pairs of vectors in a set of vectors. The `cdist` computes the distance on all pairs of vectors in the Cartesian product of two sets of vectors. Pairwise distance matrices are stored in condensed form; only the upper triangular is stored. `squareform` converts distance matrices between square and condensed forms.

5.48.11 Reworked fftpack package

FFTW2, FFTW3, MKL and DJBFFT wrappers have been removed. Only (NETLIB) fftpack remains. By focusing on one backend, we hope to add new features - like float32 support - more easily.

5.48.12 New Constants package

`scipy.constants` provides a collection of physical constants and conversion factors. These constants are taken from CODATA Recommended Values of the Fundamental Physical Constants: 2002. They may be found at physics.nist.gov/constants. The values are stored in the dictionary physical_constants as a tuple containing the value, the units, and the relative precision - in that order. All constants are in SI units, unless otherwise stated. Several helper functions are provided.

5.48.13 New Radial Basis Function module

`scipy.interpolate` now contains a Radial Basis Function module. Radial basis functions can be used for smoothing/interpolating scattered data in n-dimensions, but should be used with caution for extrapolation outside of the observed data range.

5.48.14 New complex ODE integrator

`scipy.integrate.ode` now contains a wrapper for the ZVODE complex-valued ordinary differential equation solver (by Peter N. Brown, Alan C. Hindmarsh, and George D. Byrne).

5.48.15 New generalized symmetric and hermitian eigenvalue problem solver

`scipy.linalg.eigh` now contains wrappers for more LAPACK symmetric and hermitian eigenvalue problem solvers. Users can now solve generalized problems, select a range of eigenvalues only, and choose to use a faster algorithm at the expense of increased memory usage. The signature of the `scipy.linalg.eigh` changed accordingly.

5.48.16 Bug fixes in the interpolation package

The shape of return values from `scipy.interpolate.interp1d` used to be incorrect, if interpolated data had more than 2 dimensions and the axis keyword was set to a non-default value. This has been fixed. Moreover, `interp1d` returns now a scalar (0D-array) if the input is a scalar. Users of `scipy.interpolate.interp1d` may need to revise their code if it relies on the previous behavior.

5.48.17 Weave clean up

There were numerous improvements to `scipy.weave`. `blitz++` was relicensed by the author to be compatible with the SciPy license. `wx_spec.py` was removed.

5.48.18 Known problems

Here are known problems with scipy 0.7.0:

- weave test failures on windows: those are known, and are being revised.
- weave test failure with gcc 4.3 (std::labs): this is a gcc 4.3 bug. A workaround is to add #include <cstdlib> in scipy/weave/blitz/blitz/funcs.h (line 27). You can make the change in the installed scipy (in site-packages).

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