

Package ‘tbm’

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Title Transformation Boosting Machines

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Description Boosting the likelihood of conditional and shift transformation models as introduced in <[DOI:10.1007/s11222-019-09870-4](https://doi.org/10.1007/s11222-019-09870-4)>.

Depends mlt (>= 1.0-6), mboost (>= 2.8-2)

Imports variables, basefun, sandwich, coneproj, methods

Suggests TH.data (>= 1.0-9), tram (>= 0.2-3), survival, partykit, lattice, latticeExtra, knitr, colorspace, gamlss.data, trtf

VignetteBuilder knitr

URL <http://ctm.R-forge.R-project.org>

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NeedsCompilation no

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ctmboost

*Likelihood Boosting for Conditional Transformation Models***Description**

Employs maximisation of the likelihood for estimation of conditional transformation models

Usage

```
ctmboost(model, formula, data = list(), weights = NULL,
         method = quote(mboost::mboost), ...)
```

Arguments

model	an object of class <code>mlt</code> as returned by <code>mlt</code> .
formula	a model formula describing how the parameters of <code>model</code> depend on explanatory variables, see <code>mboost</code> .
data	an optional data frame of observations.
weights	an optional vector of weights.
method	a call to <code>mboost</code> , <code>gamboost</code> , or <code>blackboost</code> .
...	additional arguments to <code>method</code> .

Details

The parameters of `model` depend on explanatory variables in a possibly structured additive way (see Hothorn, 2020). The number of boosting iterations is a hyperparameter which needs careful tuning.

Value

An object of class `ctmboost` with `predict` and `logLik` methods.

References

Torsten Hothorn (2020). Transformation Boosting Machines. *Statistics and Computing*, **30**, 141–152.

Examples

```
if (require("TH.data") && require("tram")) {
  data("bodyfat", package = "TH.data")

  ### estimate unconditional model
  m_mlt <- BoxCox(DEXfat ~ 1, data = bodyfat, prob = c(.1, .99))
  ### get corresponding in-sample log-likelihood
  logLik(m_mlt)

  ### estimate conditional transformation model
```

```

bm <- ctmbboost(m_mlt, formula = DEXfat ~ ., data = bodyfat,
               method = quote(mboost::mboost))
### in-sample log-likelihood (NEEDS TUNING OF mstop!)
logLik(bm)

### evaluate conditional densities for two observations
predict(bm, newdata = bodyfat[1:2,], type = "density")
}

```

stmboost

*Likelihood Boosting for Shift Transformation Models***Description**

Employs maximisation of the likelihood for estimation of shift transformation models

Usage

```

stmboost(model, formula, data = list(), weights = NULL,
         method = quote(mboost::mboost), mltargs = list(), ...)

```

Arguments

<code>model</code>	an object of class <code>mlt</code> as returned by mlt .
<code>formula</code>	a model formula describing how the parameters of <code>model</code> depend on explanatory variables, see mboost .
<code>data</code>	an optional data frame of observations.
<code>weights</code>	an optional vector of weights.
<code>method</code>	a call to mboost , gamboost , or blackboost .
<code>mltargs</code>	a list with arguments to be passed to mlt .
<code>...</code>	additional arguments to <code>method</code> .

Details

The parameters of `model` depend on explanatory variables in a possibly structured additive way (see Hothorn, 2020). The number of boosting iterations is a hyperparameter which needs careful tuning.

Value

An object of class `stmboost` with `predict` and `logLik` methods.

References

Torsten Hothorn (2020). Transformation Boosting Machines. *Statistics and Computing*, **30**, 141–152.

Examples

```
if (require("TH.data") && require("tram")) {  
  data("bodyfat", package = "TH.data")  
  
  ### estimate unconditional model  
  m_mlt <- BoxCox(DEXfat ~ 1, data = bodyfat, prob = c(.1, .99))  
  ### get corresponding in-sample log-likelihood  
  logLik(m_mlt)  
  
  ### estimate conditional transformation model  
  bm <- stmboost(m_mlt, formula = DEXfat ~ ., data = bodyfat,  
                 method = quote(mboost::mboost))  
  ### in-sample log-likelihood (NEEDS TUNING OF mstop!)  
  logLik(bm)  
  
  ### evaluate conditional densities for two observations  
  predict(bm, newdata = bodyfat[1:2,], type = "density")  
}
```

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