

Package: **tbm** (via r-universe)

June 10, 2026

Title Transformation Boosting Machines

Version 0.3-11

Date 2026-06-10

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 (>= 1.7-0), mboost (>= 2.8-2)

Imports variables, basefun, sandwich, coneproj, methods

Suggests TH.data (>= 1.0-9), tram (>= 1.3-0), survival, partykit, lattice, latticeExtra, knitr, colorspace, gamlss.data, trtf

VignetteBuilder knitr

URL <https://codeberg.org/thothorn/tram>

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NeedsCompilation no

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Repository <https://cran.r-universe.dev>

Date/Publication 2026-06-10 17:10:02 UTC

RemoteUrl <https://github.com/cran/tbm>

RemoteRef HEAD

RemoteSha 6389d652cb104f4bf37e3b3692a2438df2c76890

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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 <- ctboost(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

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> .
mltargs	a list with arguments to be passed to <code>mlt</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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