

# Package ‘tbn’

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**Title** Transformation Boosting Machines

**Version** 0.3-1

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**Description** Boosting the likelihood of conditional and shift transformation models.

**Depends** mlt ( $\geq 1.0-6$ ), mboost ( $\geq 2.8-2$ )

**Imports** variables, basefun, sandwich, coneproj, methods

**Suggests** TH.data ( $\geq 1.0-9$ ), tram ( $\geq 0.2-3$ ), survival, partykit,  
lattice, latticeExtra, knitr, colorspace, gamlss.data, trtf

**VignetteBuilder** knitr

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

**License** GPL-2

**NeedsCompilation** no

**Author** Torsten Hothorn [aut, cre] (<<https://orcid.org/0000-0001-8301-0471>>)

**Maintainer** Torsten Hothorn <Torsten.Hothorn@R-project.org>

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ctmboost

*Likelihood Boosting for Conditional Transformation Models*


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## 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[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, 2019). 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 (2019). Transformation Boosting Machines. *Statistics and Computing*, in press.

## 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")
}

```

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stmboost

*Likelihood Boosting for Shift Transformation Models*


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## 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[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, 2019). 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 (2019). Transformation Boosting Machines. *Statistics and Computing*, in press.

**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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