# Package 'mlt'

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**Title** Most Likely Transformations

**Version** 1.8-1

**Description** Likelihood-based estimation of conditional transformation models via the most likely transformation approach described in Hothorn et al. (2018) <DOI:10.1111/sjos.12291> and Hothorn (2020) <DOI:10.18637/jss.v092.i01>. Shift-scale (Siegfried et al, 2023, <DOI:10.1080/00031305.2023.2203177>) and multivariate (Klein et al, 2022, <DOI:10.1111/sjos.12501>) transformation models are part of this package. A package vignette is available from <DOI:10.32614/CRAN.package.mlt.docreg> and more convenient user interfaces to many models from <DOI:10.32614/CRAN.package.tram>.

**Depends** basefun (>= 1.2-1), variables (>= 1.1-0)

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`mlt-package` *General Information on the* **mlt** *Package*

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## Description

The **mlt** package implements maximum likelihood estimation in conditional transformation models as introduced by Hothorn, Möst, and Bühlmann (2018), its multivariate extension by Klein, Hothorn, Barbanti, and Kneib (2022), and location-scale models by Siegfried, Kook, and Hothorn (2023).

An introduction to the package is available in the `mlt` package vignette from package `mlt.docreg` (Hothorn 2020).

Novice users might find the high(er) level interfaces offered by package **tram** more convenient.

## References

Hothorn T (2020). "Most Likely Transformations: The **mlt** Package." *Journal of Statistical Software*, **92**(1), 1–68. doi:10.18637/jss.v092.i01.

Hothorn T, Möst L, Bühlmann P (2018). "Most Likely Transformations." *Scandinavian Journal of Statistics*, **45**(1), 110–134. doi:10.1111/sjos.12291.

Klein N, Hothorn T, Barbanti L, Kneib T (2022). "Multivariate Conditional Transformation Models." *Scandinavian Journal of Statistics*, **49**, 116–142. doi:10.1111/sjos.12501.

Siegfried S, Kook L, Hothorn T (2023). "Distribution-Free Location-Scale Regression." *The American Statistician*, **77**(4), 345–356. doi:10.1080/00031305.2023.2203177.

confband *Confidence Bands*

## Description

Confidence bands for transformation, distribution, survivor or cumulative hazard functions

## Usage

```
confband(object, newdata, level = 0.95, ...)
## S3 method for class 'mlt'
confband(object, newdata, level = 0.95,
       type = c("trafo", "distribution", "survivor", "cumhazard"),
       K = 20, cheat = K, ...)
```

## Arguments

| | |
|---|---|
| object | an object of class mlt |
| newdata | a data frame of observations |
| level | the confidence level |
| type | the function to compute the confidence band for |
| K | number of grid points the function is evaluated at |
| cheat | number of grid points the function is evaluated at when using the quantile obtained for K grid points |
| ... | additional arguments to confint.glht |

## Details

The function is evaluated at K grid points and simultaneous confidence intervals are then interpolated in order to construct the band.

A smoother band can be obtained by setting cheat to something larger than K: The quantile is obtained for K grid points but the number of evaluated grid points cheat can be much larger at no additional cost. Technically, the nominal level is not maintained in this case but the deviation will be small for reasonably large K.

## Value

For each row in newdata the function and corresponding confidence band evaluated at the K (or cheat) grid points is returned.

ctm *Conditional Transformation Models*

## Description

Specification of conditional transformation models

## Usage

```
ctm(response, interacting = NULL, shifting = NULL, scaling = NULL,
    scale_shift = FALSE, data = NULL,
    todistr = c("Normal", "Logistic", "MinExtrVal", "MaxExtrVal",
                "Exponential", "Laplace", "Cauchy"),
    sumconstr = inherits(interacting, c("formula", "formula_basis")), ...)
has_scale(object)
```

## Arguments

| | |
|---|---|
| response | a basis function, ie, an object of class basis |
| interacting | a basis function, ie, an object of class basis |
| shifting | a basis function, ie, an object of class basis |
| scaling | a basis function, ie, an object of class basis |
| scale_shift | a logical choosing between two different model types in the presence of a scaling term |
| data | either a data.frame containing the model variables or a formal description of these variables in an object of class vars |
| todistr | a character vector describing the distribution to be transformed |
| sumconstr | a logical indicating if sum constraints shall be applied |
| object | an object of class ctm |
| ... | arguments to as.basis when shifting is a formula |

## Details

This function only specifies the model which can then be fitted using mlt. The shift term is positive by default. All arguments except response can be missing (in this case an unconditional distribution is estimated). Hothorn, Möst, and Bühlmann (2018) explain the model class.

Possible choices of the distributions the model transforms to (the inverse link functions $F_Z$) include the standard normal ("Normal"), the standard logistic ("Logistic"), the standard minimum extreme value ("MinExtrVal", also known as Gompertz distribution), and the standard maximum extreme value ("MaxExtrVal", also known as Gumbel distribution) distributions. The exponential distribution ("Exponential") can be used to fit Aalen additive hazard models. Laplace and Cauchy distributions are also available.

Shift-scale models (Siegfried, Kook, and Hothorn 2023) of the form

$$P(Y \leq y \mid X = x) = F_Z(\sqrt{\exp(s(x)^\top \gamma)}[(a(y) \otimes b(x))^\top \vartheta] + d(x)^\top \beta)$$

(`scale_shift = FALSE`) or

$$P(Y \leq y \mid X = x) = F_Z(\sqrt{\exp(s(x)^\top \gamma)}[(a(y) \otimes b(x))^\top \vartheta + d(x)^\top \beta])$$

(`scale_shift = TRUE`) with bases $a(y)$ (`response`), $b(x)$ (`interacting`), $d(x)$ (`shifting`), and $s(x)$ (`scaling`) can be specified as well.

## Value

An object of class `ctm`; and a logical is returned by `has_scale` when a scale term is present in `object`.

## References

Hothorn T, Möst L, Bühlmann P (2018). "Most Likely Transformations." *Scandinavian Journal of Statistics*, **45**(1), 110–134. doi:10.1111/sjos.12291.

Siegfried S, Kook L, Hothorn T (2023). "Distribution-Free Location-Scale Regression." *The American Statistician*, **77**(4), 345–356. doi:10.1080/00031305.2023.2203177.

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`ctm-methods` *Methods for ctm Objects*

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## Description

Methods for objects of class ctm

## Usage

```
## S3 method for class 'ctm'
variable.names(object,
               which = c("all", "response", "interacting",
                         "shifting", "scaling"),
               ...)
## S3 method for class 'ctm'
coef(object, ...)
```

## Arguments

| | |
|---|---|
| `object` | an unfitted conditional transformation model as returned by `ctm` |
| `which` | a character specifying which names shall be returned |
| `...` | additional arguments |

## Details

`coef` can be used to get and set model parameters.

mlt *Most Likely Transformations*

## Description

Likelihood-based model estimation in conditional transformation models

## Usage

```
mlt(model, data, weights = NULL, offset = NULL, fixed = NULL,
    theta = NULL, pstart = NULL, scaleparm = TRUE,
    dofit = TRUE, optim = mltoptim(hessian = has_scale(model)))
```

## Arguments

| | |
|---|---|
| model | a conditional transformation model as specified by ctm |
| data | a data.frame containing all variables specified in model |
| weights | an optional vector of case weights |
| offset | an optional vector of offset values; offsets are not added to an optional scaling term (see link{ctm}) |
| fixed | a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix |
| theta | optional starting values for the model parameters |
| pstart | optional starting values for the distribution function evaluated at the data |
| scaleparm | a logical indicating if (internal) scaling shall be applied to the model parameters; TRUE unless a location-scale model is fitted where the numerically approximated Hessian is only available on the original parameter scale |
| dofit | a logical indicating if the model shall be fitted to the data (TRUE) or not. If theta is given, a model of class mlt (a full "fitted" model) featuring these parameters is returned. Otherwise, an unfitted model of class ctm is returned |
| optim | a list of functions implementing suitable optimisers, requires numerical Hessian for location-scale models |

## Details

This function fits a conditional transformation model by searching for the most likely transformation as described in Hothorn, Möst, and Bühlmann (2018), including location-scale models (Siegfried, Kook, and Hothorn 2023). Implementation details are given in (Hothorn 2020).

## Value

An object of class mlt with corresponding methods.

## References

Hothorn T (2020). "Most Likely Transformations: The **mlt** Package." *Journal of Statistical Software*, **92**(1), 1–68. doi:10.18637/jss.v092.i01.

Hothorn T, Möst L, Bühlmann P (2018). "Most Likely Transformations." *Scandinavian Journal of Statistics*, **45**(1), 110–134. doi:10.1111/sjos.12291.

Siegfried S, Kook L, Hothorn T (2023). "Distribution-Free Location-Scale Regression." *The American Statistician*, **77**(4), 345–356. doi:10.1080/00031305.2023.2203177.

## Examples

```
### set-up conditional transformation model for conditional
### distribution of dist given speed
dist <- numeric_var("dist", support = c(2.0, 100), bounds = c(0, Inf))
speed <- numeric_var("speed", support = c(5.0, 23), bounds = c(0, Inf))
ctmm <- ctm(response = Bernstein_basis(dist, order = 4, ui = "increasing"),
            interacting = Bernstein_basis(speed, order = 3))

### fit model
mltm <- mlt(ctmm, data = cars)

### plot data
plot(cars)
### predict quantiles and overlay data with model via a "quantile sheet"
q <- predict(mltm, newdata = data.frame(speed = 0:24), type = "quantile",
             p = 2:8 / 10, K = 500)
tmp <- apply(q, 1, function(x) lines(0:24, x, type = "l"))
```

---

`mlt-methods` *Methods for mlt Objects*

---

## Description

Methods for objects of class mlt

## Usage

```
## S3 method for class 'mlt'
coef(object, fixed = TRUE, ...)
coef(object) <- value
## S3 method for class 'mlt'
weights(object, ...)
## S3 method for class 'mlt'
logLik(object, parm = coef(object, fixed = FALSE), w = NULL, newdata, ...)
## S3 method for class 'mlt'
vcov(object, parm = coef(object, fixed = FALSE), complete = FALSE, ...)
Hessian(object, ...)
```

```
## S3 method for class 'mlt'
Hessian(object, parm = coef(object, fixed = FALSE), ...)
Gradient(object, ...)
## S3 method for class 'mlt'
Gradient(object, parm = coef(object, fixed = FALSE), ...)
## S3 method for class 'mlt'
estfun(x, parm = coef(x, fixed = FALSE),
       w = NULL, newdata, ...)
## S3 method for class 'mlt'
residuals(object, parm = coef(object, fixed = FALSE),
       w = NULL, newdata, what = c("shifting", "scaling"), ...)
## S3 method for class 'mlt'
mkgrid(object, n, ...)
## S3 method for class 'mlt'
bounds(object)
## S3 method for class 'mlt'
variable.names(object, ...)
## S3 method for class 'mlt_fit'
update(object, weights = stats::weights(object),
      subset = NULL, offset = object$offset, theta = coef(object, fixed = FALSE),
       fixed = NULL, ...)
## S3 method for class 'mlt'
as.mlt(object)
```

## Arguments

| | |
|---|---|
| object, x | a fitted conditional transformation model as returned by mlt |
| fixed | a logical indicating if only estimated coefficients (fixed = FALSE) should be returned OR (for update) a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix |
| value | coefficients to be assigned to the model |
| parm | model parameters |
| w | model weights |
| what | type of residual: shifting means score with respect to a constant intercept for the shift term and scaling means score with respect to a constant intercept in the scaling term. This works whether or not such terms are actually present in the model |
| weights | model weights |
| newdata | an optional data frame of new observations. Allows evaluation of the log-likelihood for a given model object on these new observations. The parameters parm and w are ignored in this situation. |
| n | number of grid points |
| subset | an optional integer vector indicating the subset of observations to be used for fitting. |
| offset | an optional vector of offset values |
| theta | optional starting values for the model parameters |

| | |
|---|---|
| complete | currently ignored |
| ... | additional arguments |

## Details

coef can be used to get and set model parameters, weights and logLik extract weights and evaluate the log-likelihood (also for parameters other than the maximum likelihood estimate). Hessian returns the Hessian (of the *negative* log-likelihood) and vcov the inverse thereof. Gradient gives the negative gradient (minus sum of the score contributions) and estfun the *negative* score contribution by each observation. mkgrid generates a grid of all variables (as returned by variable.names) in the model. update allows refitting the model with alternative weights and potentially different starting values. bounds gets bounds for bounded variables in the model.

---

# mltoptim *Control Optimisation*

---

## Description

Define optimisers and their control parameters

## Usage

```
mltoptim(
   auglag = list(
        kkt2.check = hessian,         ### turn off/on numerical hessian
             eps = abstol,        ### absolute tolerance for _parameter_ updates
             itmax = 1000L,           ### max number of outer iterations
            method = "BFGS",          ### inner algorithm
             maxit = 500L             ### max number of inner (BFGS) iterations
        ),
    spg = list(
              ftol = abstol,          ### absolute tolerance for _neg. logLik_
             quiet = TRUE,            ### don't talk
         checkGrad = FALSE            ### don't check analytical gradient
    ),
    nloptr = list(
         algorithm = "NLOPT_LD_MMA",  ### inner algorithm
          ftol_rel = reltol,          ### relative change for _neg. logLik_
          ftol_abs = abstol,          ### absolute tolerance for _neg. logLik_
           maxeval = 1000L            ### max number of evaluations
    ),
    constrOptim = list(
            method = "BFGS",          ### inner algorithm
             maxit = 1000L,           ### max number of inner (BFGS) iterations
  outer.iterations = 500L,            ### max number of outer iterations
         outer.eps = reltol          ### relative change for _neg. logLik_
    ),
```

```
  optim = list(
checkconstraints = TRUE,            ### return -Inf if violated
          method = "BFGS",          ### inner algorithm
           maxit = 1000L,           ### max number of inner (BFGS) iterations
          reltol = reltol          ### relative change for _neg. logLik_
  ),
  nlminb = list(
checkconstraints = TRUE,            ### return -Inf if violated
        iter.max = 1000L,           ### max number of iterations
        eval.max = 1500L,           ### max number of function evaluations
         rel.tol = reltol,          ### relative change for _neg. logLik_
         abs.tol = 0.0,             ### absolute tolerance (nll is not >= 0)
          xf.tol = 1e-10
  ),
 abstol = 1e-07,
 reltol = 1e-6,
  trace = FALSE,
hessian = FALSE)
```

## Arguments

| | |
|---|---|
| auglag | A list with control parameters for the auglag optimiser. maxtry is the number of times the algorithm is re-started in case it failed. |
| spg | A list with control parameters for the BBoptim optimiser (calling spg internally). |
| nloptr | A list with control parameters for the nloptr family of optimisers. |
| constrOptim | A list with control parameters for the constrOptim optimiser. |
| optim | A list with control parameters for the optim optimiser producing an unconstrained fit. |
| nlminb | A list with control parameters for the nlminb optimiser producing an unconstrained fit. |
| abstol, reltol | Absolute and relative tolerances used as stopping criterion by various algorithms. |
| trace | A logical switching trace reports by the optimisers off. |
| hessian | A logical indicating if a numerically differentiated Hessian matrix be returned. |

## Details

This function sets-up functions to be called in mlt internally.

## Value

A list of functions with arguments theta (starting values), f (log-likelihood), g (scores), h (Hessian), ui and ci (linear inequality constraints). Adding further such functions is a way to add more optimisers to mlt. The first one in this list converging defines the resulting model.

All procedures except `optim` and `nlminb` perform constained optimisation. The model is only defined for parameters meeting the constraints. For parameter configurations not meeting the constraints, the resulting log-likelihood is `-Inf`. This, however, does not mean that unconstraint optimisation will always produce parameter estimates which lead to valid models, so one should always check the unconstrained (but probably faster obtained) result against the (slower) constrained solution.

## Examples

```
### set-up linear transformation model for conditional
### distribution of dist given speed
dist <- numeric_var("dist", support = c(2.0, 100), bounds = c(0, Inf))
ctmm <- ctm(response = Bernstein_basis(dist, order = 4, ui = "increasing"),
            shifting = ~ speed, data = cars)

### the numerically determined
### hessian is returned as "optim_hessian" slot
op <- mltoptim(hessian = TRUE)
mltm <- mlt(ctmm, data = cars, scale = FALSE, optim = op)

### compare analytical and numerical hessian
all.equal(c(Hessian(mltm)), c(mltm$optim_hessian), tol = 1e-4)
```

---

`mmlt` *Multivariate Conditional Transformation Models*

---

## Description

Conditional transformation models for multivariate continuous, discrete, or a mix of continuous and discrete outcomes

## Usage

```
mmlt(..., formula = ~ 1, data, conditional = FALSE,
     theta = NULL, fixed = NULL, scaleparm = FALSE,
     optim = mltoptim(hessian = TRUE),  ### provides hessian
     args = list(seed = 1, M = 1000),
     dofit = TRUE, domargins = TRUE)
## S3 method for class 'cmmlt'
coef(object, newdata,
     type = c("all", "conditional",
              "Lambda", "Omega", "Lambdainv", "Omegainv",
              "Precision", "PartialCorr", "Sigma", "Corr",
              "Spearman", "Kendall"), fixed = TRUE,
     ...)
## S3 method for class 'mmmlt'
coef(object, newdata,
```

```
     type = c("all", "marginal",
              "Lambda", "Omega", "Lambdainv", "Omegainv",
              "Precision", "PartialCorr", "Sigma", "Corr",
              "Spearman", "Kendall"), fixed = TRUE,
     ...)
## S3 method for class 'mmlt'
predict(object, newdata, margins = 1:J,
        type = c("trafo", "distribution", "survivor", "density", "hazard"),
                 log = FALSE, args = object$args, ...)
## S3 method for class 'mmlt'
simulate(object, nsim = 1L, seed = NULL, newdata, K = 50, ...)
## S3 method for class 'mmlt'
residuals(object, parm = coef(object, fixed = FALSE),
                         w = NULL, newdata = NULL, ...)
```

## Arguments

| | |
|---|---|
| `...` | marginal transformation models, one for each response, for `mmlt`. Additional arguments for the methods. |
| `formula` | a model formula describing a model for the dependency structure via the lambda parameters. The default is set to `~ 1` for constant lambdas. |
| `data` | a data.frame. |
| `conditional` | logical; parameters are defined conditionally (only possible when all models are probit models). This is the default as described by Klein et al. (2022). If `FALSE`, parameters can be directly interpreted marginally, this is explained in Section 2.6 by Klein et al. (2022). Using `conditional = FALSE` with probit-only models gives the same likelihood but different parameter estimates. |
| `theta` | an optional vector of starting values. |
| `fixed` | an optional named numeric vector of predefined parameter values or a logical (for `coef`) indicating to also return fixed parameters (only when `type = "all"`). |
| `scaleparm` | a logical indicating if (internal) scaling shall be applied to the model parameters. |
| `optim` | a list of optimisers as returned by `mltoptim` |
| `args` | a list of arguments for `lpmvnorm`. |
| `dofit` | logical; parameters are fitted by default, otherwise a list with log-likelihood and score function is returned. |
| `domargins` | logical; all model parameters are fitted by default, including the parameters of marginal models. |
| `object` | an object of class `mmlt`. |
| `newdata` | an optional data.frame coefficients and predictions shall be computed for. |
| `type` | type of coefficient or prediction to be returned. |
| `margins` | indices defining marginal models to be evaluated. Can be single integers giving the marginal distribution of the corresponding variable, or multiple integers (currently only `1:j` implemented). |
| `log` | logical; return log-probabilities or log-densities if `TRUE`. |

| | |
|---|---|
| nsim | number of samples to generate. |
| seed | optional seed for the random number generator. |
| K | number of grid points to generate. |
| parm | parameter vector. |
| w | weights. |

## Details

The function implements core functionality for fitting multivariate conditional transformation models as described by Klein, Hothorn, Barbanti, and Kneib (2022).

## Value

An object of class mmlt with coef and predict methods.

The model is always parameterised in terms of a unit lower-triangular matrix $\Lambda$. If conditional = FALSE (the default), it is standardised to a lower-triangular matrix $\Omega = \Lambda \text{diag}(\Lambda^{-1}\Lambda^{-\top})$ such that $\Sigma = \Omega^{-1}\Omega^{-\top}$ is a correlation matrix. Note that $Omega = \Lambda$ when conditional = TRUE was requested. These concepts are explained in Hothorn (2024), Section 2.

## References

Hothorn T (2024). "On Nonparanormal Likelihoods." arXiv 2408.17346. doi:10.48550/arXiv.2408.17346.

Klein N, Hothorn T, Barbanti L, Kneib T (2022). "Multivariate Conditional Transformation Models." *Scandinavian Journal of Statistics*, **49**, 116–142. doi:10.1111/sjos.12501.

---

# mmlt-methods *Methods for mmlt Objects*

---

## Description

Methods for objects of class mmlt

## Usage

```
## S3 method for class 'mmlt'
weights(object, ...)
## S3 method for class 'mmlt'
logLik(object, parm = coef(object, fixed = FALSE), w = NULL, newdata = NULL, ...)
## S3 method for class 'mmlt'
vcov(object, parm = coef(object, fixed = FALSE), complete = FALSE, ...)
## S3 method for class 'mmlt'
Hessian(object, parm = coef(object, fixed = FALSE), ...)
## S3 method for class 'mmlt'
Gradient(object, parm = coef(object, fixed = FALSE), ...)
## S3 method for class 'mmlt'
estfun(x, parm = coef(x, fixed = FALSE),
```

```
       w = NULL, newdata = NULL, ...)
## S3 method for class 'mmlt'
mkgrid(object, ...)
## S3 method for class 'mmlt'
variable.names(object, response_only = FALSE, ...)
```

## Arguments

| | |
|---|---|
| object, x | a fitted multivariate transformation model as returned by mmlt |
| fixed | a logical indicating if only estimated coefficients (fixed = FALSE) should be returned OR (for update) a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix |
| parm | model parameters |
| w | model weights |
| weights | model weights |
| newdata | an optional data frame of new observations. Allows evaluation of the log-likelihood for a given model object on these new observations. The parameters parm and w are ignored in this situation. |
| response_only | only return the names of the response variables |
| complete | currently ignored |
| ... | additional arguments |

## Details

coef can be used to get and set model parameters, weights and logLik extract weights and evaluate the log-likelihood (also for parameters other than the maximum likelihood estimate). Hessian returns the Hessian (of the *negative* log-likelihood) and vcov the inverse thereof. Gradient gives the negative gradient (minus sum of the score contributions) and estfun the *negative* score contribution by each observation. mkgrid generates a grid of all variables (as returned by variable.names) in the model.

---

# plot-predict-simulate *Plots, Predictions and Samples from mlt Objects*

---

## Description

Plot, predict and sample from objects of class mlt

## Usage

```
## S3 method for class 'ctm'
plot(x, newdata, type = c(
         "distribution", "logdistribution",
         "survivor", "logsurvivor",
         "density", "logdensity",
```

```
          "hazard", "loghazard",
          "cumhazard", "logcumhazard",
          "odds", "logodds",
          "quantile", "trafo"),
     q = NULL, prob = 1:(K - 1) / K, K = 50, col = rgb(.1, .1, .1, .1), lty = 1,
     add = FALSE, ...)
## S3 method for class 'mlt'
plot(x, ...)
## S3 method for class 'ctm'
predict(object, newdata, type = c("trafo",
          "distribution", "logdistribution",
          "survivor", "logsurvivor",
          "density", "logdensity",
          "hazard", "loghazard",
          "cumhazard", "logcumhazard",
          "odds", "logodds",
          "quantile"),
          terms = c("bresponse", "binteracting", "bshifting"),
          q = NULL, prob = NULL, K = 50, interpolate = FALSE, ...)
## S3 method for class 'mlt'
predict(object, newdata = object$data, ...)
## S3 method for class 'ctm'
simulate(object, nsim = 1, seed = NULL, newdata, K = 50, q = NULL,
          interpolate = FALSE, bysim = TRUE, ...)
## S3 method for class 'mlt'
simulate(object, nsim = 1, seed = NULL, newdata = object$data, bysim = TRUE, ...)
```

## Arguments

| | |
|---|---|
| object | a fitted conditional transformation model as returned by mlt or an unfitted conditional transformation model as returned by ctm |
| x | a fitted conditional transformation model as returned by mlt |
| newdata | an optional data frame of observations |
| type | type of prediction or plot to generate |
| q | quantiles at which to evaluate the model |
| prob | probabilities for the evaluation of the quantile function (type = "quantile") |
| terms | terms to evaluate for the predictions, corresponds to the argument response, interacting and shifting in ctm |
| K | number of grid points to generate (in the absence of q) |
| col | color for the lines to plot |
| lty | line type for the lines to plot |
| add | logical indicating if a new plot shall be generated (the default) |
| interpolate | logical indicating if quantiles shall be interpolated linearily. This unnecessary option is no longer implemented (starting with 1.2-1). |
| nsim | number of samples to generate |

| | |
|---|---|
| seed | optional seed for the random number generator |
| bysim | logical, if TRUE a list with nsim elements is returned, each element is of length nrow(newdata) and contains one sample from the conditional distribution for each row of newdata. If FALSE, a list of length nrow(newdata) is returned, its ith element of length nsim contains nsim samples from the conditional distribution given newdata[i,]. |
| ... | additional arguments |

## Details

plot evaluates the transformation function over a grid of q values for all observations in newdata and plots these functions (according to type). predict evaluates the transformation function over a grid of q values for all observations in newdata and returns the result as a matrix (where _columns_ correspond to _rows_ in newdata, see examples). Lack of type = "mean" is a feature and not a bug.

Argument type defines the scale of the plots or predictions: type = "distribution" means the cumulative distribution function, type = "survivor" is the survivor function (one minus distribution function), type = "density" the absolute continuous or discrete density (depending on the response), type = "hazard", type = "cumhazard", and type = "odds" refers to the hazard (absolute continuous or discrete), cumulative hazard (defined as minus log-survivor function in both the absolute continuous and discrete cases), and odds (distribution divided by survivor) functions. The quantile function can be evaluated for probabilities prob by type = "quantile".

Note that the predict method for ctm objects requires all model coefficients to be specified in this unfitted model. simulate draws samples from object by numerical inversion of the quantile function.

Note that offsets are ALWAYS IGNORED when computing predictions. If you want the methods to pay attention to offsets, specify them as a variable in the model with fixed regression coefficient using the fixed argument in mlt.

More examples can be found in (Hothorn 2020).

## References

Hothorn T (2020). "Most Likely Transformations: The **mlt** Package." *Journal of Statistical Software*, **92**(1), 1–68. doi:10.18637/jss.v092.i01.

## Examples

```
library("survival")
op <- options(digits = 2)

### GBSG2 dataset
data("GBSG2", package = "TH.data")

### right-censored response
GBSG2$y <- with(GBSG2, Surv(time, cens))

### define Bernstein(log(time)) parameterisation
### of transformation function. The response
### is bounded (log(0) doesn't work, so we use log(1))
```

```
### support defines the support of the Bernstein polynomial
### and add can be used to make the grid wider (see below)
rvar <- numeric_var("y", bounds = c(0, Inf),
                    support = c(100, 2000))
rb <- Bernstein_basis(rvar, order = 6, ui = "increasing")
### dummy coding of menopausal status
hb <- as.basis(~ 0 + menostat, data = GBSG2)
### treatment contrast of hormonal treatment
xb <- as.basis(~ horTh, data = GBSG2, remove_intercept = TRUE)

### set-up and fit Cox model, stratified by menopausal status
m <- ctm(rb, interacting = hb, shifting = xb, todistr = "MinExtrVal")
fm <- mlt(m, data = GBSG2)

### generate grid for all three variables
### note that the response grid ranges between 1 (bounds[1])
### and 2000 (support[2])
(d <- mkgrid(m, n = 10))
### data.frame of menopausal status and treatment
nd <- do.call("expand.grid", d[-1])

### plot model on different scales, for all four combinations
### of menopausal status and hormonal treatment
typ <- c("distribution", "survivor", "density", "hazard",
         "cumhazard", "odds")
layout(matrix(1:6, nrow = 2))
nl <- sapply(typ, function(tp)
    ### K = 500 makes densities and hazards smooth
    plot(fm, newdata = nd, type = tp, col = 1:nrow(nd), K = 500))
legend("topleft", lty = 1, col = 1:nrow(nd),
       legend = do.call("paste", nd), bty = "n")

### plot calls predict, which generates a grid with K = 50
### response values
### note that a K x nrow(newdata) matrix is returned
### (for reasons explained in the next example)
predict(fm, newdata = nd, type = "survivor")

### newdata can take a list, and evaluates the survivor
### function on the grid defined by newdata
### using a linear array model formulation and is
### extremely efficient (wrt computing time and memory)
### d[1] (the response grid) varies fastest
### => the first dimension of predict() is always the response,
### not the dimension of the predictor variables (like one
### might expect)
predict(fm, newdata = d, type = "survivor")

### owing to this structure, the result can be quickly stored in
### a data frame as follows
cd <- do.call("expand.grid", d)
cd$surv <- c(S <- predict(fm, newdata = d, type = "survivor"))
```

```
### works for distribution functions
all.equal(1 - S, predict(fm, newdata = d, type = "distribution"))
### cumulative hazard functions
all.equal(-log(S), predict(fm, newdata = d, type = "cumhazard"))
### log-cumulative hazard functions (= trafo, for Cox models)
all.equal(log(-log(S)), predict(fm, newdata = d, type = "logcumhazard"))
all.equal(log(-log(S)), predict(fm, newdata = d, type = "trafo"))
### densities, hazards, or odds functions
predict(fm, newdata = d, type = "density")
predict(fm, newdata = d, type = "hazard")
predict(fm, newdata = d, type = "odds")
### and quantiles (10 and 20%)
predict(fm, newdata = d[-1], type = "quantile", prob = 1:2 / 10)

### note that some quantiles are only defined as intervals
### (> 2000, in this case). Intervals are returned as an "response"
### object, see ?R. Unfortunately, these can't be stored as array, so
### a data.frame is returned where the quantile varies first
p <- c(list(prob = 1:9/10), d[-1])
np <- do.call("expand.grid", p)
(Q <- predict(fm, newdata = d[-1], type = "quantile", prob = 1:9 / 10))
np$Q <- Q
np

### simulating from the model works by inverting the distribution
### function; some obs are right-censored at 2000
(s <- simulate(fm, newdata = nd, nsim = 3))
### convert to Surv
sapply(s, as.Surv)

### generate 3 parametric bootstrap samples from the model
tmp <- GBSG2[, c("menostat", "horTh")]
s <- simulate(fm, newdata = tmp, nsim = 3)
### refit the model using the simulated response
lapply(s, function(y) {
  tmp$y <- y
  coef(mlt(m, data = tmp))
})

options(op)
```

---

R *Response Variables*

---

## Description

Represent a possibly censored or truncated response variable

## Usage

```
R(object, ...)
## S3 method for class 'numeric'
R(object = NA, cleft = NA, cright = NA,
   tleft = NA, tright = NA, tol = sqrt(.Machine$double.eps),
   as.R.ordered = FALSE, as.R.interval = FALSE, ...)
## S3 method for class 'ordered'
R(object, cleft = NA, cright = NA, ...)
## S3 method for class 'integer'
R(object, cleft = NA, cright = NA,
   bounds = c(min(object, na.rm = TRUE), Inf), ...)
## S3 method for class 'factor'
R(object, ...)
## S3 method for class 'Surv'
R(object, as.R.ordered = FALSE, as.R.interval = FALSE, ...)
as.Surv(object)
## S3 method for class 'response'
as.Surv(object)
## S3 method for class 'response'
as.double(x, ...)
```

## Arguments

| | |
|---|---|
| object | A vector of (conceptually) exact measurements or an object of class response (for as.Surv) or a list. |
| x | same as object. |
| cleft | A vector of left borders of censored measurements |
| cright | A vector of right borders of censored measurements |
| tleft | A vector of left truncations |
| tright | A vector of right truncations |
| tol | Tolerance for checking if cleft < cright |
| bounds | Range of possible values for integers |
| as.R.ordered | logical, should numeric responses or right-censored (and possible left-truncated survival) times be coded as ordered factor? This leads to a parameterisation allowing to maximise the nonparametric maximum likelihood |
| as.R.interval | logical, should numeric responses be coded for the nonparametric maximum likelihood |
| ... | other arguments, ignored except for tleft and tright to R.ordered and R.integer |

## Details

R is basically an extention of Surv for the representation of arbitrarily censored or truncated measurements at any scale. The storage.mode of object determines if models are fitted by the discrete likelihood (integers or factors) or the continuous likelihood (log-density for numeric objects). Interval-censoring is given by intervals (cleft, cright], also for integers and factors (see example

below). Left- and right-truncation can be defined by the `tleft` and `tright` arguments. Existing `Surv` objects can be converted using `R(Surv(...))$` and, in some cases, an `as.Surv()` method exists for representing `response` objects as `Surv` objects.

`R` applied to a list calls `R` for each of the list elements and returns a joint object.

More examples can be found in (Hothorn 2020) and in `vignette("tram", package = "tram")`.

## References

Hothorn T (2020). "Most Likely Transformations: The **mlt** Package." *Journal of Statistical Software*, **92**(1), 1–68. doi:10.18637/jss.v092.i01.

## Examples

```
library("survival")

### randomly right-censored continuous observations
time <- as.double(1:9)
event <- rep(c(FALSE, TRUE), length = length(time))

Surv(time, event)
R(Surv(time, event))

### right-censoring, left-truncation
ltm <- 1:9 / 10
Surv(ltm, time, event)
R(Surv(ltm, time, event))

### interval-censoring
Surv(ltm, time, type = "interval2")
R(Surv(ltm, time, type = "interval2"))

### interval-censoring, left/right-truncation
lc <- as.double(1:4)
lt <- c(NA, NA, 7, 8)
rt <- c(NA, 9, NA, 10)
x <- c(3, NA, NA, NA)
rc <- as.double(11:14)
R(x, cleft = lt, cright = rt)
as.Surv(R(x, cleft = lt, cright = rt))
R(x, tleft = 1, cleft = lt, cright = rt)
R(x, tleft = 1, cleft = lt, cright = rt, tright = 15)
R(x, tleft = lc, cleft = lt, cright = rt, tright = rc)

### discrete observations: counts
x <- 0:9
R(x)
### partially interval-censored counts
rx <- c(rep(NA, 6), rep(15L, 4))
R(x, cright = rx)

### ordered factor
x <- gl(5, 2, labels = LETTERS[1:5], ordered = TRUE)
```

```
R(x)
### interval-censoring (ie, observations can have multiple levels)
lx <- ordered(c("A", "A", "B", "C", "D", "E"),
              levels = LETTERS[1:5], labels = LETTERS[1:5])
rx <- ordered(c("B", "D", "E", "D", "D", "E"),
              levels = LETTERS[1:5], labels = LETTERS[1:5])
R(rx, cleft = lx, cright = rx)

### facilitate nonparametric maximum likelihood
(y <- round(runif(10), 1))
R(y, as.R.ordered = TRUE)

R(Surv(time, event), as.R.ordered = TRUE)
R(Surv(ltm, time, event), as.R.ordered = TRUE)
```

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