Package: tramME (via r-universe)

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Title Transformation Models with Mixed Effects

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Description Likelihood-based estimation of mixed-effects transformation models using the Template Model Builder ('TMB', Kristensen et al., 2016) <doi:10.18637/jss.v070.i05>. The technical details of transformation models are given in Hothorn et al. (2018) <doi:10.1111/sjos.12291>. Likelihood contributions of exact, randomly censored (left, right, interval) and truncated observations are supported. The random effects are assumed to be normally distributed on the scale of the transformation function, the marginal likelihood is evaluated using the Laplace approximation, and the gradients are calculated with automatic differentiation (Tamasi & Hothorn, 2021) <doi:10.32614/RJ-2021-075>. Penalized smooth shift terms can be defined using 'mgcv'.

Depends R (>= 3.6.0), tram (>= 0.3.2), mlt (>= 1.1.0)

Imports alabama, Matrix, methods, mgcv (>= 1.8.34), nlme, TMB (>= 1.7.15), stats, variables (>= 1.0.2), basefun (>= 1.0.6), numDeriv, MASS, coneproj, mvtnorm, reformulas

Suggests lme4 (>= 1.1.19), multcomp, parallel, survival, knitr, coxme, ordinal, ordinalCont, gamm4, gamlss.dist, glmmTMB, xtable

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Contents

`anova.tramME` *Comparison of nested tramME models.*

Description

Calculates information criteria and LR ratio test for nested tramME models. The calculation of the degrees of freedom is problematic, because the parameter space is restricted.

Usage

```
## S3 method for class 'tramME'
anova(object, object2, ...)
```

Arguments

`object`	A `tramME` object.
`object2`	A `tramME` object.
`...`	Optional arguments, for compatibility with the generic. (Ignored)

Details

Currently only supports the comparison of two models. Additional arguments will be ignored.

The nestedness of the models is not checked.

Value

A `data.frame` with the calculated statistics.

Examples

```
data("sleepstudy", package = "lme4")
mod1 <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
mod2 <- LmME(Reaction ~ Days + (Days || Subject), data = sleepstudy)
anova(mod1, mod2)
```

BoxCoxME *Non-normal (Box-Cox-type) Linear Mixed-effects Additive Regression Model*

Description

Estimates a mixed-effects additive transformation model with flexible smooth parameterization for the baseline transformation and the inverse link set to the CDF of the standard Gaussian distribution (see Hothorn et al., 2018).

Usage

```
BoxCoxME(
  formula,
  data,
  subset,
  weights,
  offset,
  na.action = na.omit,
  silent = TRUE,
  resid = FALSE,
  do_update = FALSE,
  estinit = TRUE,
  initpar = NULL,
  fixed = NULL,
  nofit = FALSE,
  control = optim_control(),
  ...
)
```

Arguments

formula	A formula describing the model. Smooth additive terms are defined the way as in mgcv, and random effects consistently with the notation used in lme4.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of case weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
na.action	a function which indicates what should happen when the data contain NAs. The default is set to na.omit.

silent	Logical. Make **TMB** functionality silent.
resid	Logical. If TRUE, the score residuals are also calculated. This comes with some performance cost.
do_update	Logical. If TRUE, the model is set up so that the weights and the offsets are updateable. This comes with some performance cost.
estinit	Logical. Estimate a vector of initial values for the fixed effects parameters from a (fixed effects only) mlt model
initpar	Named list of initial parameter values, if NULL, it is ignored
fixed	a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix
nofit	logical, if TRUE, creates the model object, but does not run the optimization
control	list with controls for optimization
...	Optional arguments to tram

Details

The model extends tram::BoxCox with random effects and (optionally penalized) additive terms. For details on mixed-effect transformation models, see Tamasi and Hothorn (2021).

The elements of the linear predictor are parameterized with negative parameters (i.e. negative = TRUE in tram).

Value

A BoxCoxME model object.

References

Hothorn, Torsten, Lisa Möst, and Peter Bühlmann. "Most Likely Transformations." Scandinavian Journal of Statistics 45, no. 1 (March 2018): 110–34. <doi:10.1111/sjos.12291>

Tamasi, Balint, and Torsten Hothorn. "tramME: Mixed-Effects Transformation Models Using Template Model Builder." The R Journal 13, no. 2 (2021): 398–418. <doi:10.32614/RJ-2021-075>

Examples

```
data("sleepstudy", package = "lme4")
m <- BoxCoxME(Reaction ~ s(Days) + (Days | Subject), data = sleepstudy)
summary(m)
```

coef.LmME — *Extract the coefficients of an* LmME *model*

Description

Extracts the fixed effects coefficents (default behavior), the baseline parameters or all (baseline, fixed and random) coefficients of the model.

Usage

```
## S3 method for class 'LmME'
coef(object, as.lm = FALSE, fixed = TRUE, ...)
```

Arguments

object	An LmME object.
as.lm	If TRUE, return the transformed coefficients as in a lmerMod object.
fixed	If TRUE, also include the fixed parameters.
...	Optional arguments passed to coef.tramME.

Details

See also the documentation of coef.tramME.

Value

A numeric vector of the transformed coefficients.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
coef(fit, as.lm = TRUE)
```

coef.SurvregME — *Extract the coefficients of the fixed effects terms of an SurvregME model.*

Description

Extract the coefficients of the fixed effects terms of an SurvregME model.

Usage

```
## S3 method for class 'SurvregME'
coef(object, as.survreg = FALSE, ...)
```

Arguments

object	An SurvregME object.
as.survreg	If TRUE, return the transformed coefficients as in a survival::survreg object.
...	Optional arguments passed to coef.tramME.

Value

A numeric vector of the transformed coefficients.

Examples

```
library("survival")
fit <- SurvregME(Surv(time, status) ~ rx + (1 | litter), data = rats)
coef(fit, as.survreg = TRUE)
```

---

coef.tramME *Extract the coefficients of a* tramME *model*

Description

Extracts the fixed effects coefficents (default behavior), the baseline parameters or all (baseline, fixed and random) coefficients of the model.

Usage

```
## S3 method for class 'tramME'
coef(object, with_baseline = FALSE, fixed = TRUE, complete = FALSE, ...)
```

Arguments

object	A tramME object.
with_baseline	If TRUE, also include the baseline parameters and the fixed effects parameters from the smooth terms. (Kept for compatibility with tram)
fixed	If TRUE, also include the fixed parameters.
complete	If TRUE, return all parameters that can be seen as coefficients (baseline, fixed, random) in the tramME model. With complete = TRUE, with_baseline = FALSE and fixed = FALSE are ignored. (The behavior of this argument might change in the future).
...	Optional parameters (ignored).

Value

Numeric vector of parameter values.

Examples

```
library("survival")
mod <- SurvregME(Surv(time, status) ~ rx + (1 | litter/rx), data = rats,
                 dist = "exponential", nofit = TRUE)
coef(mod, with_baseline = TRUE)
coef(mod, with_baseline = TRUE, fixed = FALSE)

data("sleepstudy", package = "lme4")
mod2 <- BoxCoxME(Reaction ~ s(Days) + (Days || Subject), data = sleepstudy,
                 nofit = TRUE)
coef(mod2, complete = TRUE)
```

---

coef<-.tramME *Set coefficients of a tramME model.*

Description

Sets the whole vector of fixed-effects coefficients of a tramME model. The parameters of the baseline transformation function should respect the restrictions of the parameter space. This is checked before setting the new parameter values provided that the parameters for the variance components has already been set. If the model contains fixed coefficient parameters, the input should also respect that. When called on a fitted tram object, the function sets it to unfitted and removes all parts that come from the estimation.

Usage

```
## S3 replacement method for class 'tramME'
coef(object) <- value
```

Arguments

object	A tramME object.
value	Numeric vector of new coefficient values.

Value

A tramME object with the new coefficient values.

Examples

```
data("sleepstudy", package = "lme4")
mod <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy, nofit = TRUE)
coef(mod) <- c(-1, 0.5, 1)
```

ColrME *Mixed-effects Additive Continuous Outcome Logistic Regression Model*

Description

Estimates a mixed-effects additive transformation model with flexible smooth parameterization for the baseline transformation and the inverse link set to the CDF of the standard logistic distribution (see Hothorn et al., 2018).

Usage

```
ColrME(
  formula,
  data,
  subset,
  weights,
  offset,
  na.action = na.omit,
  silent = TRUE,
  resid = FALSE,
  do_update = FALSE,
  estinit = TRUE,
  initpar = NULL,
  fixed = NULL,
  nofit = FALSE,
  control = optim_control(),
  ...
)
```

Arguments

formula	A formula describing the model. Smooth additive terms are defined the way as in mgcv, and random effects consistently with the notation used in lme4.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of case weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
na.action	a function which indicates what should happen when the data contain NAs. The default is set to na.omit.

silent	Logical. Make **TMB** functionality silent.
resid	Logical. If TRUE, the score residuals are also calculated. This comes with some performance cost.
do_update	Logical. If TRUE, the model is set up so that the weights and the offsets are updateable. This comes with some performance cost.
estinit	Logical. Estimate a vector of initial values for the fixed effects parameters from a (fixed effects only) mlt model
initpar	Named list of initial parameter values, if NULL, it is ignored
fixed	a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix
nofit	logical, if TRUE, creates the model object, but does not run the optimization
control	list with controls for optimization
...	Optional arguments to tram

Details

The model extends tram::Colr with random effects and (optionally penalized) additive terms. For details on mixed-effect transformation models, see Tamasi and Hothorn (2021).

The elements of the linear predictor are parameterized with positive parameters (i.e. negative = FALSE in tram).

Value

A ColrME model object.

References

Hothorn, Torsten, Lisa Möst, and Peter Bühlmann. "Most Likely Transformations." Scandinavian Journal of Statistics 45, no. 1 (March 2018): 110–34. <doi:10.1111/sjos.12291>

Tamasi, Balint, and Torsten Hothorn. "tramME: Mixed-Effects Transformation Models Using Template Model Builder." The R Journal 13, no. 2 (2021): 398–418. <doi:10.32614/RJ-2021-075>

Examples

```
data("neck_pain", package = "ordinalCont")
m <- ColrME(vas ~ time * laser + (1 | id), data = neck_pain,
            bounds = c(0, 1), support = c(0, 1), order = 6)
summary(m)
```

confband.tramME *Confidence intervals and bands from a* tramME *model*

Description

Pointwise confidence intervals or multiplicity-adjusted confidence bands for transformation, distribution, survivor or cumulative hazard functions.

Usage

```
## S3 method for class 'tramME'
confband(
  object,
  newdata,
  level = 0.95,
  type = c("trafo", "distribution", "survivor", "cumhazard"),
  adjust = FALSE,
  K = 40,
  cheat = K,
  q = NULL,
  baseline_only = FALSE,
  ...
)
```

Arguments

object	The tramME object.
newdata	A data frame of covariate values.
level	Confidence level.
type	The scale on which the condfidence bands are calculated.
adjust	If TRUE, multiplicity-adjusted confidence bands are calculated. (see Details)
K	The number of grid points at which the outcome distribution is evaluated.
cheat	In the case of multiplicity adjustment (adjust = TRUE), an option to decrease the number of grid points (cheat < K), for faster calculations and increased numerical stability. (see Details)
q	The quantiles at which the model is evaluated.
baseline_only	If TRUE, only evaluate the baseline transformation function and ignore the shift terms.
...	Optional arguments passed to confint.glht.

Details

Similarly to confband, this method evaluates the conditional distribution of the outcome on a selected scale given a number of grid-points and claculates the corresponding confidence intervals or bands (adjusting for multiplicity).

The point estimates retured by this function could also be calculated with predict.tramME (when newdata does not contain response values and K is set to the number of grid points). While predict.tramME is designed to calculate a potentially large number of point estimates on a wider range of available scales, confband calculates the asymptotic intervals from the joint covariance matrix of the fixed and random effects. For technical reasons, a smaller set of type options are available, and the calculations are slower than with predict.tramME. The handling of random effects is currently stricter than in predict.tramME: No ranef option is available, and grouping factors for random effects supplied in newdata must have the same levels as the dataset used to fit the model.

The multiplicity adjustment is done using confint.glht. The cheat argument reduces the dimensionality of the multivariate root-finding problem (see qmvt) for speed and (occasionally) numerical stability. The critical value for the confidence bands are obtained for cheat < K grid points, but the confidence bands are calculated for K grid points. As a result, the nominal level of the returned confidence band is not maintained, but the deviation is expected to be small if cheat is reasonably large. It is the user's responsibility to set this value, and by default cheat = K.

Value

A matrix (in the case when newdata has a single row) or a list of matrices for each row of newdata.

Warning

This method implements new functionality. Its user interface may be subject to change.

---

confint.LmME *Confidence intervals for LmME model parameters*

Description

Confidence intervals for model parameters on their original scale, optionally consistent with the linear mixed-model specification. When as.lm = TRUE, only Wald CIs are available.

Usage

```
## S3 method for class 'LmME'
confint(
  object,
  parm = NULL,
  level = 0.95,
  as.lm = FALSE,
  pargroup = c("all", "fixef", "ranef"),
  type = c("Wald", "wald", "profile"),
```

```
  estimate = FALSE,
  ...
)
```

Arguments

object	An LmME object.
parm	Names of the parameters to extract.
level	Confidence level.
as.lm	Logical. If TRUE, return results consistent with the normal linear mixed model parameterization.
pargroup	The name of the parameter group to extract. With as.lm = FALSE, the available options are described in confint.tramME. When as.lm = TRUE, the following options are available: • all: Fixed effects and variance components parameters. • fixef: Fixed effects parameters (including FE parameters of the smooth terms). • ranef: Variance components parameters (including the smoothing parameters of the random effects).
type	Type of the CI: either Wald or profile.
estimate	Logical, add the point estimates in a thrid column.
...	Optional parameters passed to confint.tramME

Value

A matrix with lower and upper bounds.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
confint(fit) ## transformation model parameterization
confint(fit, as.lm = TRUE) ## LMM parameterization
confint(fit, as.lm = TRUE, pargroup = "fixef", estimate = TRUE)
confint(fit, as.lm = TRUE, parm = "(Sigma)") ## error SD
```

---

confint.tramME *Confidence intervals for tramME model parameters*

Description

Confidence intervals for model parameters on their original scale. Either Wald CI or profile CI by root finding. Multicore computations are supported in the case of profile confidence intervals, but snow support is yet to be implemented.

Usage

```
## S3 method for class 'tramME'
confint(
  object,
  parm = NULL,
  level = 0.95,
  pargroup = c("all", "fixef", "shift", "baseline", "ranef", "smooth"),
  type = c("Wald", "wald", "profile"),
  estimate = FALSE,
  pmatch = FALSE,
  parallel = c("no", "multicore", "snow"),
  ncpus = getOption("profile.ncpus", 1L),
  ...
)
```

Arguments

object	A tramME object.
parm	The indices or names of the parameters of interest.
level	Confidence level.
pargroup	The name of the parameter group to return: • all: All parameters. • fixef: Fixed effects parameters. • shift: Shift parameters. • baseline: Parameters of the baseline transformation function. • ranef: Variance components parameters. • smooth: Paramaters that belong to the smooth shift terms (both FE and smoothing parameters).
type	Type of the CI: either Wald or profile.
estimate	Logical, add the point estimates in a thrid column.
pmatch	Logical. If TRUE, partial name matching is allowed.
parallel	Method for parallel computation.
ncpus	Number of cores to use for parallel computation.
...	Optional parameters.

Value

A matrix with lower and upper bounds.

Examples

```
data("sleepstudy", package = "lme4")
fit <- BoxCoxME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
confint(fit)
confint(fit, pargroup = "shift", estimate = TRUE)
exp(confint(fit, 1:2, pargroup = "ranef")) ## CIs for the SDs of the REs
```

CoxphME *Mixed-effects Additive Parametric Cox Regression Model*

Description

Estimates a mixed-effects additive transformation model with flexible smooth parameterization for the baseline transformation (log-cumulative baseline hazard) and the inverse link set to the CDF of the standard minimum extreme value distribution (see Hothorn et al., 2018).

Usage

```
CoxphME(
  formula,
  data,
  subset,
  weights,
  offset,
  na.action = na.omit,
  silent = TRUE,
  resid = FALSE,
  do_update = FALSE,
  estinit = TRUE,
  initpar = NULL,
  fixed = NULL,
  nofit = FALSE,
  control = optim_control(),
  ...
)
```

Arguments

formula	A formula describing the model. Smooth additive terms are defined the way as in mgcv, and random effects consistently with the notation used in lme4.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of case weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
na.action	a function which indicates what should happen when the data contain NAs. The default is set to na.omit.

silent	Logical. Make **TMB** functionality silent.
resid	Logical. If TRUE, the score residuals are also calculated. This comes with some performance cost.
do_update	Logical. If TRUE, the model is set up so that the weights and the offsets are updateable. This comes with some performance cost.
estinit	Logical. Estimate a vector of initial values for the fixed effects parameters from a (fixed effects only) mlt model
initpar	Named list of initial parameter values, if NULL, it is ignored
fixed	a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix
nofit	logical, if TRUE, creates the model object, but does not run the optimization
control	list with controls for optimization
...	Optional arguments to tram

Details

The model extends tram::Coxph with random effects and (optionally penalized) additive terms. For details on mixed-effect transformation models, see Tamasi and Hothorn (2021).

The elements of the linear predictor are parameterized with positive parameters (i.e. negative = FALSE in tram).

Value

A CoxphME model object.

References

Hothorn, Torsten, Lisa Möst, and Peter Bühlmann. "Most Likely Transformations." Scandinavian Journal of Statistics 45, no. 1 (March 2018): 110–34. <doi:10.1111/sjos.12291>

Tamasi, Balint, and Torsten Hothorn. "tramME: Mixed-Effects Transformation Models Using Template Model Builder." The R Journal 13, no. 2 (2021): 398–418. <doi:10.32614/RJ-2021-075>

Examples

```
library("survival")
rats$litter <- factor(rats$litter)
m <- CoxphME(Surv(time, status) ~ rx + (1 | litter), data = rats,
             log_first = TRUE)
summary(m)
```

`edf_smooth.tramME` *EDFs of smooth shift terms*

Description

Returns an estimate of effective degrees of freedom associated with each smooth term.

Usage

```
## S3 method for class 'tramME'
edf_smooth(object, ...)
```

Arguments

`object`	A `tramME` object.
`...`	Optional arguments passed to the Hessian calculations.

Details

The EDFs are calculated by summing up the elements of

$$diag(V_\vartheta I)$$

term-by-term. V_ϑ is the joint covariance matrix of fixed and random parameters (the inverse of the joint precision, i.e., Hessian of the negative log-likelihood), and I is the joint precision of the unpenalized negative log-likelihood function. See Wood et al. (2016) or Wood (2017, Chapter 6) for references.

Value

A named vector with the edf values.

References

Wood, Simon N., Natalya Pya, and Benjamin Saefken (2016). "Smoothing Parameter and Model Selection for General Smooth Models." Journal of the American Statistical Association 111, <doi:10.1080/01621459.2016.11

Wood, Simon N. (2017). Generalized Additive Models: An Introduction with R. Second edition. Chapman & Hall/CRC Texts in Statistical Science.

Examples

```
data("mcycle", package = "MASS")
fit <- LmME(accel ~ s(times), data = mcycle)
edf_smooth(fit)
```

LehmannME *Mixed-effects Additive Lehmann-alternative Linear Regression Model*

Description

Estimates a mixed-effects additive transformation model with flexible smooth parameterization for the baseline transformation and the inverse link set to the CDF of the standard maximum extreme value distribution (see Hothorn et al., 2018).

Usage

```
LehmannME(
  formula,
  data,
  subset,
  weights,
  offset,
  na.action = na.omit,
  silent = TRUE,
  resid = FALSE,
  do_update = FALSE,
  estinit = TRUE,
  initpar = NULL,
  fixed = NULL,
  nofit = FALSE,
  control = optim_control(),
  ...
)
```

Arguments

formula	A formula describing the model. Smooth additive terms are defined the way as in mgcv, and random effects consistently with the notation used in lme4.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of case weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
na.action	a function which indicates what should happen when the data contain NAs. The default is set to na.omit.

silent	Logical. Make **TMB** functionality silent.
resid	Logical. If TRUE, the score residuals are also calculated. This comes with some performance cost.
do_update	Logical. If TRUE, the model is set up so that the weights and the offsets are updateable. This comes with some performance cost.
estinit	Logical. Estimate a vector of initial values for the fixed effects parameters from a (fixed effects only) mlt model
initpar	Named list of initial parameter values, if NULL, it is ignored
fixed	a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix
nofit	logical, if TRUE, creates the model object, but does not run the optimization
control	list with controls for optimization
...	Optional arguments to tram

Details

The model extends tram::Lehmann with random effects and (optionally penalized) additive terms. For details on mixed-effect transformation models, see Tamasi and Hothorn (2021).

The elements of the linear predictor are parameterized with negative parameters (i.e. negative = TRUE in tram).

Value

A LehmannME model object.

References

Hothorn, Torsten, Lisa Möst, and Peter Bühlmann. "Most Likely Transformations." Scandinavian Journal of Statistics 45, no. 1 (March 2018): 110–34. <doi:10.1111/sjos.12291>

Tamasi, Balint, and Torsten Hothorn. "tramME: Mixed-Effects Transformation Models Using Template Model Builder." The R Journal 13, no. 2 (2021): 398–418. <doi:10.32614/RJ-2021-075>

Examples

```
data("sleepstudy", package = "lme4")
m <- LehmannME(Reaction ~ s(Days) + (Days | Subject), data = sleepstudy)
summary(m)
```

LmME *Mixed-effects Additive Normal Linear Regression Model*

Description

Estimates the normal linear model parameterized as a linear transformation model.

Usage

```
LmME(
  formula,
  data,
  subset,
  weights,
  offset,
  na.action = na.omit,
  silent = TRUE,
  resid = FALSE,
  do_update = FALSE,
  estinit = TRUE,
  initpar = NULL,
  fixed = NULL,
  nofit = FALSE,
  control = optim_control(),
  ...
)
```

Arguments

formula	A formula describing the model. Smooth additive terms are defined the way as in mgcv, and random effects consistently with the notation used in lme4.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of case weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
na.action	a function which indicates what should happen when the data contain NAs. The default is set to na.omit.
silent	Logical. Make **TMB** functionality silent.

resid	Logical. If TRUE, the score residuals are also calculated. This comes with some performance cost.
do_update	Logical. If TRUE, the model is set up so that the weights and the offsets are updateable. This comes with some performance cost.
estinit	Logical. Estimate a vector of initial values for the fixed effects parameters from a (fixed effects only) mlt model
initpar	Named list of initial parameter values, if NULL, it is ignored
fixed	a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix
nofit	logical, if TRUE, creates the model object, but does not run the optimization
control	list with controls for optimization
...	Optional arguments to tram

Details

The additive mixed-effects normal linear model is a special case of the mixed-effects additive transformation model family, with the transformation function restricted to be linear and the inverse link set to the standard Gaussian CDF (see Hothorn et al., 2018). This function estimates this model with the transformation model parameterization, and offers features that are typically not available in other mixed-effects additive implementations, such as stratum-specific variances, and censored and/or truncated observations.

The model extends tram::Lm with random effects and (optionally penalized) additive terms. For details on mixed-effect transformation models, see Tamasi and Hothorn (2021).

The elements of the linear predictor are parameterized with negative parameters (i.e. negative = TRUE in tram).

The results can be transformed back to the usual linear mixed/additive model parametrization with specific methods provided by tramME. The differences between the two parametrizations are discussed in Tamasi and Hothorn (2021).

Value

A LmME model object.

References

Hothorn, Torsten, Lisa Möst, and Peter Bühlmann. "Most Likely Transformations." Scandinavian Journal of Statistics 45, no. 1 (March 2018): 110–34. <doi:10.1111/sjos.12291>

Tamasi, Balint, and Torsten Hothorn. "tramME: Mixed-Effects Transformation Models Using Template Model Builder." The R Journal 13, no. 2 (2021): 398–418. <doi:10.32614/RJ-2021-075>

Examples

```
library("survival")
data("sleepstudy", package = "lme4")
## Create a version of the response with 200 ms detection limit and 50 ms
## step sizes
```

```
ub <- ceiling(sleepstudy$Reaction / 50) * 50
lb <- floor(sleepstudy$Reaction / 50) * 50
lb[ub == 200] <- 0
sleepstudy$Reaction_ic <- Surv(lb, ub, type = "interval2")
m <- LmME(Reaction_ic ~ Days + (Days | Subject), data = sleepstudy)
summary(m)
coef(m, as.lm = TRUE)
```

`logLik.tramME` *Get the log-likelihood of the tramME model*

Description

Evaluates the log-likelihood function. New parameter values and data can optionally be supplied. In the latter case, the function returns the out-of-sample log-likelihood.

Usage

```
## S3 method for class 'tramME'
logLik(
  object,
  param = NULL,
  newdata = NULL,
  type = c("integrated", "fix_smooth", "penalized"),
  ...
)
```

Arguments

`object`	A `tramME` object.
`param`	An optional named list of parameter values (beta and theta). See details. Optionally, gamma elements can also be added, which leads to 'fixing' those random effects terms at the supplied values.
`newdata`	An optional data.frame to calculate the out-of-sample log-likelihood.
`type`	The type of the likelihood to be calculated: • integrated (default when `newdata = NULL`): The marginal log-likelihood, calculated by integrating out the random effects. • fix_smooth (default when `newdata` is supplied): Treating the penalized parameters of the smooth terms as fixed at their posterior mode predictions and only integrating out the 'true' random effects. (Consistent with the functionality of `ranef.tramME` and `residuals.tramME` when `fix_smooth = TRUE`.) • penalized: Treat all parameters as fixed, return the penalized log-likelihood (conditional log-likelihood + penalty for smooth terms and random effects). This is equivalent to fixing all random effect values. See details.
`...`	Optional argument (for consistency with generic).

Details

By default, `param` is set to the estimated (or previously set) parameters. If the parameter vectors in the model are incomplete (contain `NA` elemets), the returned log-likelihood will also be `NA`, unless the user provides new values.

Setting `type = "fix_smooth"` fixes the random effects terms that correspond to penalized smooths at their estimated values, so that they are not refitted when `newdata` is supplied. This is consistent with treating these parameter regularized fixed terms, i.e. as 'new-style' random effects described by Hodges (2014, Chapter 13).

The `"fix_smooth"` and `"penalized"` options for `type` are just for convenience. The same functionality can be achieved by setting `param$gamma` to the desired values. `"penalized"` respects the values of `param$gamma` if both are supplied, while `"fix_smooth"` overwrites them with the fitted values if there are ambiguities.

Value

A numeric value of the log-likelihood.

Type of the log-likelihood

By default, `logLik` calculates the _integrated_ (or marginal) log-likelihood by integrating over the random effects. By fixing the random effects, the value of the log-likelihood changes, because TMB won't integrate over these random effects. This will result in the _penalized_ log-likelihood (conditional log-likelihood + penalty for smooth terms and random effects, see example).

By setting `type = "penalized"`, the function will 'fix' all random effects and penalized parameters of the smooth terms at their predicted levels, and calcualte the penalized log-likelihood. In this sense, setting `type = "fix_smooth"` will result in a hybrid log-likelihood value, where the 'true' random effects (c.f. Hodges 2014, Ch. 13) are integrated out, while it includes the penalty values for the penalized parameters of the smooths terms.

In general, it is not clear which type of log-likelihood we should calculate when we want to evaluate models based on their out-of-sample log-likelihood values. The context and the model setup are key in these cases. Please make sure you know what you want to calculate to avoid misunderstandings.

References

Hodges, James S. (2014). Richly Parameterized Linear Models: Additive, Time Series, and Spatial Models Using Random Effects. Chapman & Hall/CRC Texts in Statistical Science Series.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
logLik(fit)

data("mcycle", package = "MASS")
fit <- LmME(accel ~ s(times), data = mcycle)
logLik(fit) < logLik(fit, type = "penalized")
```

`model.frame.tramME` *Extract model frame from a tramME model*

Description

Extract model frame from a tramME model

Usage

```
## S3 method for class 'tramME'
model.frame(
  formula,
  data = NULL,
  group_as_factor = FALSE,
  ignore_response = FALSE,
  ...
)
```

Arguments

`formula`	A `tramME` object.
`data`	a data frame, list or environment (or object coercible by `as.data.frame` to a data frame), containing the variables in `formula`. Neither a matrix nor an array will be accepted.
`group_as_factor`	Logical; If `TRUE`, automatically convert the grouping variables of the random effects to factors. (not used, might not be needed) ## FIXME
`ignore_response`	Logical; If `TRUE`, the response is not added to the result. In this case the function won't look for it in `data`.
`...`	Optional arguments, passed to `model.frame`.

Details

In `mlt`, the basis functions expect the response variables in the data to be evaluated, i.e. instead of `x` and `y` columns we should have a `` `Surv(x, y)` `` column when the response is a `Surv` object. `model.frame.tramME` builds the model frame accordingly, assigning to the resulting object the class `tramME_data` to indicate this structure to other functions that use its results. If the input `data` is a `tramME_data` is also expects this structure.

Value

A `tramME_data` object, which is also a `data.frame`.

Examples

```
data("sleepstudy", package = "lme4")
mod <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy, nofit = TRUE)
model.frame(mod)
```

`model.matrix.tramME` *Model matrices for* `tramME` *models*

Description

Model matrix for fixed effects, random effects, and baseline transformations (with interacting terms if present).

Usage

```
## S3 method for class 'tramME'
model.matrix(
  object,
  data = model.frame(object),
  type = c("Y", "X", "Zt"),
  drop_unused_groups = FALSE,
  keep_sign = TRUE,
  simplify = FALSE,
  ...
)
```

Arguments

`object`	A `tramME` object.
`data`	A `data.frame` containing the variable values.
`type`	"X": Fixed effects model matrix. "Zt": Random effects model matrix (transposed). "Y": Model matrices for the baseline transfromations.
`drop_unused_groups`	Logical; remove unused levels of the random effects. (see `drop.unused.levels` argument of `mkReTrms`)
`keep_sign`	Logical; the terms will have the same sign as in the `tramME` model if `TRUE`.
`simplify`	Logical; Remove empty `Y` matrices.
`...`	Optional arguments.

Details

Creates model matrices for fixed effects (`type = "X"`) and random effects (`type = "Zt"`) and baseline transfromation (`type = "Y"`), by evaluating the respective basis functions given a new dataset.

The response values may be exact, censored (left, right, interval) and truncated (left, right, interval), and the function returns several, potentially empty, model matrices:

- Ye: Exact observations.
- Yeprime: The model matrix corresponding to the first derivative of the baseline transformation, evaluated at exact observations.
- Yl: Left-censored observations.
- Yr: Rigt-censored observations.
- Yil and Yir: Interval-censored observations evaluated at the left and right bounds of the interval.
- Ytl: Left-truncated observations.
- Ytr: Rigt-truncated observations.
- Ytil and Ytir: Interval-truncated observations evaluated at the left and right bounds of the interval.

for the baseline transfromations (unless `simplify = TRUE`).

Value

List of requested model matrices.

Note

The model matrix of the random effects is a sparse matrix and it is transposed to be directly used with `Matrix::crossprod` which is faster than transposing and multiplying ("Zt" instead of "Z").

Examples

```
library("survival")
rats$litter <- factor(rats$litter)
m <- CoxphME(Surv(time, status) ~ rx + (1 | litter), data = rats,
             log_first = TRUE, nofit = TRUE)
mm <- model.matrix(m)
nd <- model.frame(m)[rep(1, 100), ]
nd[[1]] <- seq(1, 120, length.out = 100)
mm2 <- model.matrix(m, data = nd, simplify = TRUE)
mm3 <- model.matrix(m, data = nd, simplify = TRUE, drop_unused_groups = TRUE)
## compare mm2$Zt & mm3$Zt
```

---

optim_control *Set up and control optimization parameters*

Description

Set up and control optimization parameters

Usage

```
optim_control(
  method = c("nlminb", "BFGS", "CG", "L-BFGS-B"),
  scale = TRUE,
  trace = FALSE,
  ntry = 5,
  ok_warnings = "NA/NaN function evaluation",
  ...
)
```

Arguments

method	Optimization procedure.
scale	Logical; if TRUE rescale the fixed effects design matrix to improve convergence.
trace	Logical; print trace of the optimization.
ntry	Number of restarts with new random initialization if optimization fails to converge.
ok_warnings	Control for what warnings will be reported during optimization. If TRUE, no warnings will be reported, if FALSE all warnings are displayed. In case of a character vector, the matching warnings are treated as unimportant, and not reported. See also Notes.
...	Optional arguments passed to auglag, nlminb or optim as a list of control parameters.

Note

Irrespective of the value of the ok_warnings argument, all warnings are collected in the opt$warnings element of the tramME object.

---

plot.smooth.tramME *Plot smooth terms of a tramME model.*

Description

Plot smooth terms of a tramME model.

Usage

```
## S3 method for class 'smooth.tramME'
plot(
  x,
  which = seq_along(x),
  col = 1,
  fill = grey(0.5, 0.25),
  trafo = I,
```

```
  add = FALSE,
  ...
)
```

Arguments

x	A smooth.tramME object.
which	Select terms to be printed by their indices
col	Line color for the point estimates.
fill	Fill color for the confidence intervals.
trafo	Monotonic transformation to be applied on the smooth terms
add	Add the plot to an existing figure.
...	Optional parameters passed to the plotting functions.

Examples

```
data("mcycle", package = "MASS")
fit <- LmME(accel ~ s(times), data = mcycle)
plot(smooth_terms(fit, as.lm = TRUE))
```

---

plot.tramME *Plotting method for tramME objects*

Description

Plot the conditional distribution evaluated at a grid of possible response values and a set of covariate and random effects values on a specified scale.

Usage

```
## S3 method for class 'tramME'
plot(
  x,
  newdata = model.frame(x),
  ranef = NULL,
  fix_smooth = TRUE,
  type = c("trafo", "distribution", "logdistribution", "survivor", "logsurvivor",
   "density", "logdensity", "hazard", "loghazard", "cumhazard", "logcumhazard", "odds",
    "logodds", "quantile"),
  ...
)
```

Arguments

x	A tramME object.
newdata	an optional data frame of observations
ranef	Random effects (either in named list format or a numeric vector) or the word "zero". See Details.
fix_smooth	If FALSE, the random effects coefficients of the smooth terms are refitted to newdata. It's probably not what you want to do.
type	The scale on which the predictions are evaluated: • trafo: The prediction evaluated on the scale of the transformation function. • (log)distribution: The prediction evaluated on the scale of the conditional (log-)CDF. • (log)survivor: The prediction evaluated on the scale of the (conditional) (log-)survivor function. • (log)density: The prediction evaluated on the scale of the conditional (log-)PDF. • (log)hazard: The prediction evaluated on the (log-)hazard scale. • (log)cumhazard: The prediction evaluated on the (log-)cumulative hazard scale. • (log)odds: The prediction evaluated on the (log-)odds scale. • quantile: Return the quantiles of the conditional outcome distribution corresponding to newdata. For more information, see Details.
...	Additional arguments, passed to plot.mlt.

Details

When ranef is equal to "zero", a vector of zeros with the right size is substituted. For more details, see predict.tramME.

For more information on how to control the grid on which the functions are evaluated, see the documentation of predict.mlt.

Value

A numeric matrix of the predicted values invisibly.

Examples

```
data("sleepstudy", package = "lme4")
fit <- BoxCoxME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
plot(fit, K = 100, type = "density")
```

plot_ci *Plot confidence bands from* tramME *models*

Description

Plotting method for confband.tramME objects.

Usage

```
## S3 method for class 'confband.tramME'
plot(
  x,
  col,
  lty,
  fill,
  add = FALSE,
  single_plot = FALSE,
  trafo_x = identity,
  trafo_y = identity,
  align_xlim = FALSE,
  align_ylim = FALSE,
  ...
)
```

Arguments

x	The object containing the confidence intervals.
col	Color of the point estimates.
lty	Line type of the point estimates.
fill	Fill color for the intervals.
add	If TRUE, no new plot is created, the interval is added to the current plot.
single_plot	If TRUE, a single new plot is created, and all intervals are plotted on it.
trafo_x	Transform x-axis before plotting.
trafo_y	Transform y-axis before plotting.
align_xlim	If TRUE, align the x-axis limits across all subplots.
align_ylim	If TRUE, align the y-axis limits across all subplots.
...	Optional arguments passed to plot.default and plot.xy.

PolrME *Mixed-effects Additive Transformation Models for Ordered Categorical Responses*

Description

Estimates mixed-effects additive transformation models for ordered categorical responses with various link functions.

Usage

```
PolrME(
  formula,
  data,
  subset,
  weights,
  offset,
  na.action = na.omit,
  method = c("logistic", "probit", "loglog", "cloglog"),
  silent = TRUE,
  resid = FALSE,
  do_update = FALSE,
  estinit = TRUE,
  initpar = NULL,
  fixed = NULL,
  nofit = FALSE,
  control = optim_control(),
  ...
)
```

Arguments

formula	A formula describing the model. Smooth additive terms are defined the way as in mgcv, and random effects consistently with the notation used in lme4.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of case weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
na.action	a function which indicates what should happen when the data contain NAs. The default is set to na.omit.

method	a character describing the link function.
silent	Logical. Make **TMB** functionality silent.
resid	Logical. If TRUE, the score residuals are also calculated. This comes with some performance cost.
do_update	Logical. If TRUE, the model is set up so that the weights and the offsets are updateable. This comes with some performance cost.
estinit	Logical. Estimate a vector of initial values for the fixed effects parameters from a (fixed effects only) mlt model
initpar	Named list of initial parameter values, if NULL, it is ignored
fixed	a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix
nofit	logical, if TRUE, creates the model object, but does not run the optimization
control	list with controls for optimization
...	Optional arguments to tram

Details

The transformation function is parameterized as a step function on a scale defined by the link function (see Hothorn et al., 2018).

The model extends tram::Polr with random effects and (optionally penalized) additive terms. For details on mixed-effect transformation models, see Tamasi and Hothorn (2021).

The elements of the linear predictor are parameterized with negative parameters (i.e. negative = TRUE in tram).

Value

A PolrME model object.

References

Hothorn, Torsten, Lisa Möst, and Peter Bühlmann. "Most Likely Transformations." Scandinavian Journal of Statistics 45, no. 1 (March 2018): 110–34. <doi:10.1111/sjos.12291>

Tamasi, Balint, and Torsten Hothorn. "tramME: Mixed-Effects Transformation Models Using Template Model Builder." The R Journal 13, no. 2 (2021): 398–418. <doi:10.32614/RJ-2021-075>

Examples

```
data("soup", package = "ordinal")
m <- PolrME(SURENESS | SOUPFREQ ~ PROD + (1 | RESP/PROD),
            data = soup, method = "probit")
summary(m)
```

predict.tramME *Predict method for tramME objects*

Description

Evaluates the _conditional_ distribution implied by a tramME model, given by a set of covariates and random effects on a selected scale.

Usage

```
## S3 method for class 'tramME'
predict(
  object,
  newdata = model.frame(object),
  ranef = NULL,
  fix_smooth = TRUE,
 type = c("lp", "trafo", "distribution", "logdistribution", "survivor", "logsurvivor",
  "density", "logdensity", "hazard", "loghazard", "cumhazard", "logcumhazard", "odds",
   "logodds", "quantile"),
  ...
)
```

Arguments

object	A tramME object.
newdata	an optional data frame of observations
ranef	Random effects it can be a ranef.tramME object, a named list, an unnamed list, NULL or the word "zero". See Details.
fix_smooth	If FALSE, the random effects coefficients of the smooth terms are refitted to newdata. It's probably not what you want to do.
type	The scale on which the predictions are evaluated: • lp: Linear predictor (Xb + Zg). For more information, see Details. • trafo: The prediction evaluated on the scale of the transformation function. • (log)distribution: The prediction evaluated on the scale of the conditional (log-)CDF. • (log)survivor: The prediction evaluated on the scale of the (conditional) (log-)survivor function. • (log)density: The prediction evaluated on the scale of the conditional (log-)PDF. • (log)hazard: The prediction evaluated on the (log-)hazard scale. • (log)cumhazard: The prediction evaluated on the (log-)cumulative hazard scale. • (log)odds: The prediction evaluated on the (log-)odds scale. • quantile: Return the quantiles of the conditional outcome distribution corresponding to newdata. For more information, see Details.
...	Additional arguments, passed to predict.mlt.

Details

When newdata contains values of the response variable, prediction is only done for those values. In this case, if random effects vector (ranef) is not supplied by the user, the function predicts the random effects from the model using newdata.

When no response values are supplied in newdata, the prediction is done on a grid of values for each line of the dataset (see predict.mlt for information on how to control the setup of this grid). In this case, the user has to specify the vector of random effects to avoid ambiguities.

The linear predictor (type = "lp") equals to the shift terms plus the random effects terms _without the baseline transfromation function_.

The linear predictor (type = "lp") and the conditional quantile function (type = "quantile") are special in that they do not return results evaluated on a grid, even when the response variable in newdata is missing. The probabilities for the evaluation of the quantile function can be supplied with the prob argument of predict.mlt.

In the case of type = "quantile", when the some of the requested conditonal quantiles fall outside of the support of the response distribution (specified when the model was set up), the inversion of the CDF cannot be done exactly and tramME returns censored values.

ranef can be different objects based on what we want to calculate and what the other inputs are. If ranef is a ranef.tramME, we assume that it contains the full set of random effects, but not the penalized coefficients of the smooth terms. In this case fix_smooth must be TRUE. If ranef is a named vector, we are fixing the supplied random effects (and penalized coefficients) and predict the rest from newdata (fix_smooth may also be used in this case). In this case, the random effects are identified with the same naming convention as in object$param$gamma.

If ranef is an unnamed vector, the function expects the full set of necessary random effects (with or without penalized coefficients, depending on fix_smooth). If ranef = NULL (the default), all random effects and optionally penalized parameters (although this is not recommended) are predicted from newdata. Finally, if ranef is equal to "zero", a vector of zeros with the right size is used.

Value

A numeric vector/matrix of the predicted values (depending on the inputs) or a response object, when the some of the requested conditonal quantiles fall outside of the support of the response distribution specified when the model was set up (only can occur with type = "quantile").

Examples

```
data("sleepstudy", package = "lme4")
fit <- BoxCoxME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
predict(fit, type = "trafo") ## evaluate on the transformation function scale
nd <- sleepstudy
nd$Reaction <- NULL
pr <- predict(fit, newdata = nd, ranef = ranef(fit), type = "distribution",
              K = 100)
```

predict.tramTMB *Post-estimation calculations in a tramTMB model*

Description

Post-estimation calculations in a tramTMB model

Usage

```
## S3 method for class 'tramTMB'
predict(
  object,
  newdata,
  parameters = .get_par(object, full = TRUE),
  scale = c("lp", "trafo"),
  cov = FALSE,
  as.lm = FALSE,
  ...
)
```

Arguments

object	A tramTMB object
newdata	A named list with elements Y, X and Z (not all necessary)
parameters	A named list of parameter values
scale	The scale on which the post-estimation calculations are done
cov	Logical; If TRUE, calculate the full covariance matrix of the calculated values
as.lm	Logical; reparameterize as a LMM
...	Optional arguments (ignored).

print.anova.tramME *Printing* anova.tramME *table*

Description

Printing anova.tramME table

Usage

```
## S3 method for class 'anova.tramME'
print(
  x,
  digits = max(getOption("digits") - 2L, 3L),
  signif.stars = getOption("show.signif.stars"),
  ...
)
```

Arguments

x	A anova.tramME object.
digits	minimum number of significant digits to be used for most numbers.
signif.stars	logical; if TRUE, P-values are additionally encoded visually as 'significance stars' in order to help scanning of long coefficient tables. It defaults to the show.signif.stars slot of options.
...	Optional arguments passed to printCoefmat

Value

Invisibly retrurns the anova.tramME object.

---

print.summary.tramME *Print method for tramME model summary*

Description

Print method for tramME model summary

Usage

```
## S3 method for class 'summary.tramME'
print(
  x,
  fancy = !isTRUE(getOption("knitr.in.progress")) && interactive(),
  digits = max(getOption("digits") - 2L, 3L),
  signif.stars = getOption("show.signif.stars"),
  ...
)
```

Arguments

x	A summary.tramME object.
fancy	Logical, if TRUE, use color in outputs.
digits	minimum number of significant digits to be used for most numbers.
signif.stars	logical; if TRUE, P-values are additionally encoded visually as 'significance stars' in order to help scanning of long coefficient tables. It defaults to the show.signif.stars slot of options.
...	Optional arguments passed to printCoefmat

Value

The input summary.tramME object, invisibly.

print.tramME *Print tramME model*

Description

Print tramME model

Usage

```
## S3 method for class 'tramME'
print(x, digits = max(getOption("digits") - 2L, 3L), ...)
```

Arguments

x	A tramME object.
digits	Number of significant digits
...	Optional arguments (for consistency with the generic)

Value

The original tramME object invisibly

print.VarCorr.tramME *Print method for the variance-correlation parameters of a tramME object*

Description

Print method for the variance-correlation parameters of a tramME object

Usage

```
## S3 method for class 'VarCorr.tramME'
print(x, sd = TRUE, digits = max(getOption("digits") - 2L, 3L), ...)
```

Arguments

x	A VarCorr.tramME object.
sd	Logical. Print standard deviations instead of variances.
digits	Number of digits
...	optional arguments

Value

Invisibly returns the input VarCorr.tramME object.

ranef.LmME *Extract the conditional modes of random effects of an LmME model*

Description

The condVar option is not implemented for ranef.LmME. Setting raw=TURE will return the raw random effects estimates from the transformation model parameterization.

Usage

```
## S3 method for class 'LmME'
ranef(object, as.lm = FALSE, ...)
```

Arguments

object	A fitted LmME object.
as.lm	If TRUE, return the transformed conditional modes as in a normal linear mixed effects model.
...	Optional parameters passed to ranef.tramME.

Value

A numeric vector or a ranef.tramME object depending on the inputs.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
ranef(fit, raw = TRUE) ## transformation model parameterization!
ranef(fit, as.lm = TRUE)
```

ranef.tramME *Point estimates and conditional variances of random effects.*

Description

Extract the conditional modes and conditional variances of random effects in a formatted or unformatted way.

Usage

```
## S3 method for class 'tramME'
ranef(
  object,
  param = NULL,
  newdata = NULL,
  fix_smooth = !is.null(newdata),
  condVar = FALSE,
  raw = FALSE,
  ...
)
```

Arguments

object	A tramME object.
param	An optional named list of parameter values (beta and theta). See details. Optionally, gamma elements can also be added, which leads to 'fixing' those random effects terms at the supplied values.
newdata	An optional data.frame of new observations for which the new random effects values are predicted.
fix_smooth	Logical; it is set to TRUE by default, if newdata is supplied. The random effects parameters corresponding the smooth terms are fixed and not fitted (posterior mode) to newdata instead they are treated just like fixed effects parameters. See details.
condVar	If TRUE, include the conditional variances as attributes. Only works with raw = FALSE.
raw	Return the unformatted RE estimates as fitted by the model.
...	Optional arguments (for consistency with generic)

Details

raw = TRUE returns the whole vector of random effects (i.e. with parameters of smooth shift terms), while raw = FALSE only returns the formatted list of actual random effects (i.e. for grouped observations) values. For the conceptual differences between the two types of random effects, see Hodges (2014, Chapter 13).

The conditional variances of the fixed random effects are set to NA.

Value

Depending on the value of raw, either a numeric vector or a ranef.tramME object which contains the conditional mode and variance estimates by grouping factors.

Warning

The function has several optional arguments that allow great flexibilty beyond its most basic usage. The user should be careful with setting these, because some combinations might not return sensical results. Only limited sanity checks are performed.

References

Hodges, James S. (2014). Richly Parameterized Linear Models: Additive, Time Series, and Spatial Models Using Random Effects. Chapman & Hall/CRC Texts in Statistical Science Series.

Examples

```
data("sleepstudy", package = "lme4")
fit <- BoxCoxME(Reaction ~ Days + (Days | Subject), data = sleepstudy, order = 5)
ranef(fit, raw = TRUE)
ranef(fit)
```

`residuals.LmME` *Residuals of a LmME model*

Description

Calculates the score residuals of an intercept term fixed at 0. In the case of an LmME model, this is equal to the residual of an LMM.

Usage

```
## S3 method for class 'LmME'
residuals(object, as.lm = FALSE, ...)
```

Arguments

`object`	An `LmME` object.
`as.lm`	If `TRUE`, return the residuals as in a normal linear mixed effects model.
`...`	Optional arguments (for consistency with generic)

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
resid(fit)
```

`residuals.tramME` *Residuals of a tramME model*

Description

Calculates the score residuals of an intercept term fixed at 0.

Usage

```
## S3 method for class 'tramME'
residuals(
  object,
  param = NULL,
  newdata = NULL,
  fix_smooth = !is.null(newdata),
  ...
)
```

Arguments

`object`	A `tramME` object.
`param`	An optional named list of parameter values (beta and theta). See details. Optionally, gamma elements can also be added, which leads to 'fixing' those random effects terms at the supplied values.
`newdata`	An optional `data.frame` of observations for which we want to calculate the residuals.
`fix_smooth`	Logical; it is set to `TRUE` by default, if `newdata` is supplied. The random effects parameters corresponding the smooth terms are fixed and not fitted (posterior mode) to `newdata` instead they are treated just like fixed effects parameters. See details.
`...`	Optional arguments (for consistency with generic)

Examples

```
library("survival")
fit <- SurvregME(Surv(time, status) ~ rx + (1 | litter), data = rats)
resid(fit)
```

Resp *Response objects*

Description

Response objects to represent censored and truncated observations

Usage

```
Resp(
  cleft,
  cright,
  tleft,
  tright,
  bounds = c(-Inf, Inf),
  open_lwr_bnd = TRUE,
  tol = sqrt(.Machine$double.eps)
)

## S3 method for class 'Resp'
R(object, ...)

## S3 method for class 'Resp'
print(x, ...)

## S3 method for class 'Resp'
x[i, j, drop = FALSE]

## S3 method for class 'Resp'
is.na(x)

## S3 method for class 'Resp'
length(x)

## S3 method for class 'Resp'
format(x, ...)
```

Arguments

cleft	A vector of left borders of censoring intervals
cright	A vector of right borders of censoring intervals
tleft	A vector of left truncation values
tright	A vector of right truncation values
bounds	An optional numeric vector of two elements (c(a, b)) that denotes the lower and upper boundaries of the outcome.

open_lwr_bnd	Logical; if TRUE, the lower boundary of the outcome is open, and we want to enforce this.
tol	Tolerance level.
object	A Resp object
...	Optional arguments
x	A Resp object
i	Row index (typically the only index)
j	Column index (typically missing)
drop	If TRUE the result is coerced to the lowest possible dimension

Details

Resp extends the functionality of Surv class by allowing cases that cannot be defined with it. An example is an interval-censored outcome with left truncatation (see Examples).

Censored and exactly observed data can be defined similarly to type = "interval2" objects in Surv. NA values for left or right censoring borders mean left- or right-censored observations, respectively. If both borders are NA, the observation is considered NA by is.na(). Truncation times (tleft and tright arguments) can be omitted or take NA values, which means no truncation. If only the censoring intervals are provided, i.e., no trunction is present, the function returns a Surv object.

Resp also provides a limited interface between tramME and the response class (technically, inherits from it) of mlt (see R), which uses an internal representation that is not compatible with tramME.

The optional argument open_lwr_bnd can be used to enforce lower boundaries of the outcome. Left boundaries in the Resp object (cleft and tleft) that are equal to the first element of bounds will be increased with one tol value to avoid downstream numerical problems in mlt. This adjustment is recorded and reversed when we print the object.

Value

A Resp object or a Surv object

Methods (by generic)

- R(Resp): Converting Resp objects to response (from mlt) objects (see R)
- print(Resp): Print method for the Resp class
- [: Subsetting Resp objects
- is.na(Resp): Missing values
- length(Resp): Length of a Resp object
- format(Resp): format method for a Resp object

Warning

This function is experimental and currently limited to continuous outcome types. It may be subject to change.

Examples

```
dat <- data.frame(x1 = 1:10, x2 = c(2:10, NA), x3 = c(NA, 0:8))
dat$r <- with(dat, Resp(x1, x2, x3))

dat$r
dat[1:3, ]$r
dat$r[1:3]

is.na(dat$r)

model.frame(r ~ 1, data = dat, na.action = na.omit)
```

---

sigma.LmME *Extract the SD of the error term of an LmME model.*

Description

Extract the SD of the error term of an LmME model.

Usage

```
## S3 method for class 'LmME'
sigma(object, ...)
```

Arguments

object	An LmME object.
...	Optional argument (for consistency with generic).

Value

A numeric value of the transformed sigma parameter.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
sigma(fit)
```

simulate.tramME *Simulate from a* tramME *model*

Description

Simulate from a tramME model

Usage

```
## S3 method for class 'tramME'
simulate(
  object,
  nsim = 1,
  seed = NULL,
  newdata = model.frame(object),
  type = c("ranef", "response", "joint"),
  ...
)
```

Arguments

object	A tramME object.
nsim	number of samples to generate
seed	optional seed for the random number generator
newdata	an optional data frame of observations
type	Defaults to "ranef". Currently the only avalable option.
...	Additional arguments, passed to simulate.mlt.

Value

A length nsim list of draws.

Warning

This method is under active development and may be subject to change. It is currently limited to simulating random effects.

Examples

```
data("sleepstudy", package = "lme4")
fit <- BoxCoxME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
sim <- simulate(fit, nsim = 10, seed = 123)
```

smooth_terms.LmME *Evaluate smooth terms of a* LmME *model.*

Description

Evaluate smooth terms of a LmME model.

Usage

```
## S3 method for class 'LmME'
smooth_terms(object, as.lm = FALSE, k = 100, newdata = NULL, ...)
```

Arguments

object	A tramME object.
as.lm	Logical; if TRUE return the rescaled values according to a LMM parametrization.
k	Integer, the number of points to be used to evaluate the smooth terms. Ignored when newdata is supplied.
newdata	A data.frame with new values for the smooth terms. If NULL, the new data is set up based on the model.frame and k. Smooths for which the supplied information in this input is incomplete will be ignored.
...	Optional arguments. as.lm is passed through this when it is necessary.

Value

A list of results from evaluating the smooth terms of the model.

Examples

```
data("mcycle", package = "MASS")
fit <- LmME(accel ~ s(times), data = mcycle)
plot(smooth_terms(fit, as.lm = TRUE))
```

smooth_terms.tramME *Extract and evaluate the smooth terms of a tramME model*

Description

Extract and evaluate the smooth terms of a tramME model

Usage

```
## S3 method for class 'tramME'
smooth_terms(object, k = 100, newdata = NULL, ...)
```

Arguments

object	A tramME object.
k	Integer, the number of points to be used to evaluate the smooth terms. Ignored when newdata is supplied.
newdata	A data.frame with new values for the smooth terms. If NULL, the new data is set up based on the model.frame and k. Smooths for which the supplied information in this input is incomplete will be ignored.
...	Optional arguments. as.lm is passed through this when it is necessary.

Value

A list of results from evaluating the smooth terms of the model.

Examples

```
data("mcycle", package = "MASS")
fit <- LmME(accel ~ s(times), data = mcycle)
plot(smooth_terms(fit))
```

---

summary.tramME *Summary method for tramME model*

Description

Summary method for tramME model

Usage

```
## S3 method for class 'tramME'
summary(object, ...)
```

Arguments

object	A tramME object
...	Optional arguments (for consistency with the generic)

Value

A summary.tramME object.

SurvregME *Mixed-effects Additive Parametric Survival Models*

Description

Estimates various mixed-effects additive parametric models (not exclusively) for survival analysis.

Usage

```
SurvregME(
  formula,
  data,
  subset,
  weights,
  offset,
  na.action = na.omit,
 dist = c("weibull", "logistic", "gaussian", "exponential", "rayleigh", "loggaussian",
    "lognormal", "loglogistic"),
  scale = 0,
  silent = TRUE,
  resid = FALSE,
  do_update = FALSE,
  estinit = TRUE,
  initpar = NULL,
  fixed = NULL,
  nofit = FALSE,
  control = optim_control(),
  ...
)
```

Arguments

formula	A formula describing the model. Smooth additive terms are defined the way as in mgcv, and random effects consistently with the notation used in lme4.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of case weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.
na.action	a function which indicates what should happen when the data contain NAs. The default is set to na.omit.

dist	character defining the conditional distribution of the (not necessarily positive) response, current choices include Weibull, logistic, normal, exponential, Rayleigh, log-normal (same as log-gaussian), or log-logistic.
scale	a fixed value for the scale parameter(s).
silent	Logical. Make **TMB** functionality silent.
resid	Logical. If TRUE, the score residuals are also calculated. This comes with some performance cost.
do_update	Logical. If TRUE, the model is set up so that the weights and the offsets are updateable. This comes with some performance cost.
estinit	Logical. Estimate a vector of initial values for the fixed effects parameters from a (fixed effects only) mlt model
initpar	Named list of initial parameter values, if NULL, it is ignored
fixed	a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix
nofit	logical, if TRUE, creates the model object, but does not run the optimization
control	list with controls for optimization
...	Optional arguments to tram

Details

The parameterization is slightly different from survival::survreg, see Hothorn et al. (2018). The results can be transformed back to the survreg parameterization with specific methods provided by tramME.

The model extends tram::Survreg with random effects and (optionally penalized) additive terms. For details on mixed-effect transformation models, see Tamasi and Hothorn (2021).

The elements of the linear predictor are parameterized with negative parameters (i.e. negative = TRUE in tram).

Value

A SurvregME model object.

References

Hothorn, Torsten, Lisa Möst, and Peter Bühlmann. "Most Likely Transformations." Scandinavian Journal of Statistics 45, no. 1 (March 2018): 110–34. <doi:10.1111/sjos.12291>

Tamasi, Balint, and Torsten Hothorn. "tramME: Mixed-Effects Transformation Models Using Template Model Builder." The R Journal 13, no. 2 (2021): 398–418. <doi:10.32614/RJ-2021-075>

Examples

```
library("survival")
rats$litter <- factor(rats$litter)
m <- SurvregME(Surv(time, status) ~ rx + (1 | litter), data = rats,
               dist = "weibull")
summary(m)
coef(m, as.survreg = TRUE)
```

tramME *Mixed-effects Additive transformation models*

Description

A general function to define and fit tramME models.

Usage

```
tramME(
  formula,
  data,
  subset,
  weights,
  offset,
  na.action,
  tram = NULL,
  call = NULL,
  ctm = NULL,
  smooth = NULL,
  negative = NULL,
  silent = TRUE,
  resid = FALSE,
  do_update = FALSE,
  estinit = TRUE,
  initpar = NULL,
  fixed = NULL,
  nofit = FALSE,
  control = optim_control(),
  ...
)
```

Arguments

formula	A formula describing the model. Smooth additive terms are defined the way as in mgcv, and random effects consistently with the notation used in lme4.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of case weights to be used in the fitting process. Should be NULL or a numeric vector. If present, the weighted log-likelihood is maximised.
offset	this can be used to specify an _a priori_ known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases.

na.action	a function which indicates what should happen when the data contain NAs. The default is set to na.omit.
tram	Parameter vector for the tram model type.
call	The original function call (to be passed from the wrapper).
ctm	A model object of the ctm class that descibes the fixed-effects part of the tramME model.
smooth	A tramME_smooth object that describes the smooth additive elements of the tramME model.
negative	Logical; if TRUE, the model is parameterized with negative coefficinets for the elements of the linear predictor.
silent	Logical. Make **TMB** functionality silent.
resid	Logical. If TRUE, the score residuals are also calculated. This comes with some performance cost.
do_update	Logical. If TRUE, the model is set up so that the weights and the offsets are updateable. This comes with some performance cost.
estinit	Logical. Estimate a vector of initial values for the fixed effects parameters from a (fixed effects only) mlt model
initpar	Named list of initial parameter values, if NULL, it is ignored
fixed	a named vector of fixed regression coefficients; the names need to correspond to column names of the design matrix
nofit	logical, if TRUE, creates the model object, but does not run the optimization
control	list with controls for optimization
...	Optional arguments to tram

Details

The specific model functions (LmME, BoxCoxME, ColrME, etc.) are wrappers around this function.

For a general description of the transformation model family, see Hothorn et al. (2018), for details on the mixed-effects extension, see Tamasi and Hothorn (2021).

Warning

Typically, the tramME function shouldn't be called directly; it is only exported to allow the advanced users to define their tramME models in a more flexible way from their basic building blocks.

References

Hothorn, Torsten, Lisa Möst, and Peter Bühlmann. "Most Likely Transformations." Scandinavian Journal of Statistics 45, no. 1 (March 2018): 110–34. <doi:10.1111/sjos.12291>

Tamasi, Balint, and Torsten Hothorn. "tramME: Mixed-Effects Transformation Models Using Template Model Builder." The R Journal 13, no. 2 (2021): 398–418. <doi:10.32614/RJ-2021-075>

`tramTMB` *Create a tramTMB object*

Description

Create a tramTMB object

Usage

```
tramTMB(
  data,
  parameters,
  constraint,
  negative,
  map = list(),
  resid = FALSE,
  do_update = FALSE,
  check_const = TRUE,
  no_int = FALSE,
  ...
)
```

Arguments

`data`	List of data objects (vectors, matrices, arrays, factors, sparse matrices) required by the user template (order does not matter and un-used components are allowed).
`parameters`	List of all parameter objects required by the user template (both random and fixed effects).
`constraint`	list describing the constarints on the parameters
`negative`	logical, whether the model is parameterized with negative values
`map`	same as map argument of `TMB::MakeADFun`
`resid`	logical, indicating whether the score residuals are calculated from the resulting object
`do_update`	logical, indicating whether the model should be set up with updateable offsets and weights
`check_const`	Logical; if `TRUE` check the parameter constraints before evaluating the returned functions.
`no_int`	Logical; if `FALSE` skip the numerical integration step.
`...`	optional parameters passed to `TMB::MakeADFun`

Value

A tramTMB object.

Note

The post-estimation parameters are supplied as a part of `data`

`VarCorr.LmME` *Variances and correlation matrices of random effects of an LmME object*

Description

The returned parameters are the transformed versions of the original parameters that correspond to the normal linear mixed model parameterization.

Usage

```
## S3 method for class 'LmME'
VarCorr(x, sigma = 1, as.lm = FALSE, ...)
```

Arguments

`x`	An `LmME` object.
`sigma`	Standard deviation of the error term in the LMM parameterization (should not be set manually, only for consistency with the generic method)
`as.lm`	If `TRUE`, return the variances and correlations that correspond to a normal linear mixed model (i.e. `lmerMod`).
`...`	Optional arguments (for consistency with generic)

Details

The function only returns the correlation matrices that belong to actual random effects (defined for groups in the data) and ignores the random effects parameters of the smooth shift terms. To extract these, the user should use `varcov` with `full = TRUE`.

Value

A list of vectors with variances and correlation matrices corresponding to the various grouping variables.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
VarCorr(fit) ## tranformation model parameterization
VarCorr(fit, as.lm = TRUE) ## LMM parameterization
```

VarCorr.tramME *Variances and correlation matrices of random effects*

Description

This function calculates the variances and correlations from `varcov.tramME`.

Usage

```
## S3 method for class 'tramME'
VarCorr(x, ...)
```

Arguments

`x`	A `tramME` object
`...`	optional arguments (for consistency with the generic method)

Details

The function only returns the correlation matrices that belong to actual random effects (defined for groups in the data) and ignores the random effects parameters of the smooth shift terms. To extract these, the user should use `varcov` with `full = TRUE`.

Note that, by default, `print.VarCorr.tramME` prints the standard deviations of the random effects, similarly to `lme4`.

Value

A list of vectors with variances and correlation matrices corresponding to the various grouping variables.

Examples

```
data("sleepstudy", package = "lme4")
fit <- BoxCoxME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
VarCorr(fit)
```

varcov *Generic method for* `varcov`

Description

Generic method for `varcov`

Usage

```
varcov(object, ...)
```

Arguments

object	A model object.
...	Optional inputs.

Value

A variance-covariance matrix.

`varcov.LmME` *Extract the variance-covariance matrix of the random effects of an LmME model*

Description

Extract the variance-covariance matrix of the random effects of an LmME model

Usage

```
## S3 method for class 'LmME'
varcov(object, as.lm = FALSE, as.theta = FALSE, full = FALSE, ...)
```

Arguments

object	A LmME object.
as.lm	If TRUE, the returned values correspond to the LMM parameterization.
as.theta	Logical value, if TRUE, the values are returned in their reparameterized form.
full	Logical value; if TRUE, return all random effects elements, if FALSE, do not return the random effects parameters of the smooth terms.
...	Optional arguments (unused).

Value

A list of the covariance matrices or a vector of theta values.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
varcov(fit, as.lm = TRUE)
varcov(fit, as.theta = TRUE, as.lm = TRUE)
```

varcov.tramME *Extract the variance-covariance matrix of the random effects*

Description

Returns the covariance matrix of the random effects as saved in the tramME object. The returned values correspond to the transformation model parametrization.

Usage

```
## S3 method for class 'tramME'
varcov(object, as.theta = FALSE, full = FALSE, ...)
```

Arguments

object	A tramME object.
as.theta	Logical value, if TRUE, the values are returned in their reparameterized form.
full	Logical value; if TRUE, return all random effects elements, if FALSE, do not return the random effects parameters of the smooth terms.
...	Optional arguments (unused).

Value

A list of the covariance matrices or a vector of theta values.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
varcov(fit)
varcov(fit, as.theta = TRUE)
```

varcov<- *Generic method for "varcov<-"*

Description

Generic method for "varcov<-"

Usage

```
varcov(object, ...) <- value
```

Arguments

object	A model object.
...	Optional inputs.
value	The new value of the covariance matrix.

Value

An object with the same class as object, with updated variance-covariance matrix of random effects.

---

varcov<-.tramME *Set the values of the random effects covariance matrices of a tramME model.*

Description

Sets the list containing the covariance matrices of a tramME model. The matrices have to be positive definite. Just as in "coef<-", when the function is called on a fitted object, the function will remove the infromation about the optimization.

Usage

```
## S3 replacement method for class 'tramME'
varcov(object, as.theta = FALSE, ...) <- value
```

Arguments

object	A tramME object.
as.theta	Logical value, if TRUE, indicating that the new values are supplied in their reparameterized form.
...	Optional arguments (ignored).
value	A list of positive definite covariance matrices.

Details

The supplied list has to be named with the same names as implied by the model. Hence, it might be a good idea to call varcov first, and modify this list to make sure that the input has the right structure.

The new values can also be supplied in a form that corresponds to the reparametrization used by the tramTMB model (see the option as.theta = TRUE).

All random effects variance parameters must be supplied. When there are penalized smooth terms in the model variance parameters corresponding to these should also be part of the input list.

Value

A new tramME object with the new coefficient values.

Examples

```
data("sleepstudy", package = "lme4")
mod <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy, nofit = TRUE)
vc <- varcov(mod)
vc[[1]] <- matrix(c(1, 0, 0, 2), ncol = 2)
varcov(mod) <- vc
```

`variable.names.tramME` *Return variable names.*

Description

Returns the variable names corresponding to different variable groups in a tramME model.

Usage

```
## S3 method for class 'tramME'
variable.names(
  object,
 which = c("all", "response", "grouping", "shifting", "interacting", "smooth", "ranef"),
  ...
)
```

Arguments

`object`	a tramME object (fitted or unfitted)
`which`	1. all: all variables, 2. response: response variable, 3. grouping: grouping factors for random effects, 4. shifting: shifting variables, 5. interacting: interacting variables, 6. smooth: variables in smooth terms, 7. ranef: all random effects variables (covariates with random slopes and grouping factors).
`...`	optional parameters

Details

The returned names are the names as they are used by tramME. For example, when the response is a `Surv` object, `variable.names` returns the name of that object, and not the names of the variables used to create it.

Value

A vector of variable names.

Examples

```
data("sleepstudy", package = "lme4")
mod <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy, nofit = TRUE)
variable.names(mod)
variable.names(mod, "response")
```

`vcov.LmME` *Get the variance-covariance matrix of the parameters of an LmME model*

Description

Get the variance-covariance matrix of the parameters of an LmME model

Usage

```
## S3 method for class 'LmME'
vcov(
  object,
  as.lm = FALSE,
  parm = NULL,
  pargroup = c("all", "fixef", "ranef"),
  ...
)
```

Arguments

`object`	A fitted `LmME` object.
`as.lm`	If `TRUE`, return the covariance matrix of the same parameterization as used by `lmer`.
`parm`	Names of the parameters to extract.
`pargroup`	The name of the parameter group to extract. With `as.lm = FALSE`, the available options are described in `confint.tramME`. When `as.lm = TRUE`, the following options are available: • all: Fixed effects and variance components parameters. • fixef: Fixed effects parameters (including FE parameters of the smooth terms). • ranef: Variance components parameters (including the smoothing parameters of the random effects).
`...`	Optional parameters passed to `confint.tramME`

Value

A numeric covariance matrix.

Examples

```
data("sleepstudy", package = "lme4")
fit <- LmME(Reaction ~ Days + (Days | Subject), data = sleepstudy)
vcov(fit) ## transformation model parameterization
vcov(fit, as.lm = TRUE) ## LMM parameterization
vcov(fit, as.lm = TRUE, pargroup = "fixef") ## cov of fixed effects
```

`vcov.tramME` *Calculate the variance-covariance matrix of the parameters*

Description

Extracts the covariance matrix of the selected parameters. The returned values are on the same scale as the estimated parameter values, i.e. the standard deviations of the random effect terms are on log scale.

Usage

```
## S3 method for class 'tramME'
vcov(
  object,
  parm = NULL,
  pargroup = c("all", "fixef", "shift", "baseline", "ranef", "smooth"),
  pmatch = FALSE,
  ...
)
```

Arguments

`object`	A fitted tramME object.
`parm`	The names of the parameters of interest. See in details.
`pargroup`	The name of the parameter group to return: • all: All parameters. • fixef: Fixed effects parameters. • shift: Shift parameters. • baseline: Parameters of the baseline transformation function. • ranef: Variance components parameters. • smooth: Paramaters that belong to the smooth shift terms (both FE and smoothing parameters).
`pmatch`	Logical. If `TRUE`, partial name matching is allowed.
`...`	Optional arguments passed to `vcov.tramTMB`

Details

Access to variances and covariances of penalized parameters is currently provided by the `parm` argument. Parameter names must be consistent with names in `object$param`.

Value

A numeric covariance matrix.

Examples

```
data("sleepstudy", package = "lme4")
fit <- BoxCoxME(Reaction ~ Days + (Days | Subject), data = sleepstudy, order = 10)
vcov(fit)
vcov(fit, pargroup = "ranef")
vcov(fit, pargroup = "baseline")
vcov(fit, parm = "Reaction") ## same as previous
```

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