

Package ‘glmmTMB’

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Title Generalized Linear Mixed Models using Template Model Builder

Version 1.1.6

Description Fit linear and generalized linear mixed models with various extensions, including zero-inflation. The models are fitted using maximum likelihood estimation via 'TMB' (Template Model Builder). Random effects are assumed to be Gaussian on the scale of the linear predictor and are integrated out using the Laplace approximation. Gradients are calculated using automatic differentiation.

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Depends R (>= 3.2.0)

Imports methods, TMB (>= 1.9.0), lme4 (>= 1.1-18.9000), Matrix, nlme, numDeriv

LinkingTo TMB, RcppEigen

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Anova.glmTMB	<i>Downstream methods</i>
--------------	---------------------------

Description

Methods have been written that allow `glmTMB` objects to be used with several downstream packages that enable different forms of inference. For some methods (Anova and `emmeans`, but *not* effects at present), set the component argument to "cond" (conditional, the default), "zi" (zero-inflation) or "disp" (dispersion) in order to produce results for the corresponding part of a `glmTMB` model. Support for **emmeans** also allows additional options `component = "response"` (response means taking both the cond and zi components into account), and `component = "cmean"` (mean of the [possibly truncated] conditional distribution).

In particular,

- `car`: Anova constructs type-II and type-III Anova tables for the fixed effect parameters of any component
- the `emmeans` package computes estimated marginal means (previously known as least-squares means) for the fixed effects of any component, or predictions with `type = "response"` or `type = "component"`. Note: In hurdle models, `component = "cmean"` produces means of the truncated conditional distribution, while `component = "cond"`, `type = "response"` produces means of the *untruncated* conditional distribution.
- the `effects` package computes graphical tabular effect displays (only for the fixed effects of the conditional component)

Usage

```
Anova.glmTMB(
  mod,
  type = c("II", "III", 2, 3),
  test.statistic = c("Chisq", "F"),
  component = "cond",
```

```

vcov. = vcov(mod)[[component]],
singular.ok,
...
)

Effect.glmmTMB(focal.predictors, mod, ...)

```

Arguments

<code>mod</code>	a <code>glmmTMB</code> model
<code>type</code>	type of test, "II", "III", 2, or 3. Roman numerals are equivalent to the corresponding Arabic numerals. See Anova for details.
<code>test.statistic</code>	unused: only valid choice is "Chisq" (i.e., Wald chi-squared test)
<code>component</code>	which component of the model to test/analyze ("cond", "zi", or "disp") or, in emmeans only, "response" or "cmean" as described in Details.
<code>vcov.</code>	variance-covariance matrix (usually extracted automatically)
<code>singular.ok</code>	OK to do ANOVA with singular models (unused) ?
<code>...</code>	Additional parameters that may be supported by the method.
<code>focal.predictors</code>	a character vector of one or more predictors in the model in any order.

Details

While the examples below are disabled for earlier versions of R, they may still work; it may be necessary to refer to private versions of methods, e.g. `glmmTMB:::Anova.glmmTMB(model, ...)`.

Examples

```

warp.lm <- glmmTMB(breaks ~ wool * tension, data = warpbreaks)
salamander1 <- up2date(readRDS(system.file("example_files", "salamander1.rds", package="glmmTMB")))
if (require(emmeans)) withAutoprint({
  emmeans(warp.lm, poly ~ tension | wool)
  emmeans(salamander1, ~ mined, type="response") # conditional means
  emmeans(salamander1, ~ mined, component="cmean") # same as above, but re-gridded
  emmeans(salamander1, ~ mined, component="zi", type="response") # zero probabilities
  emmeans(salamander1, ~ mined, component="response") # response means including both components
})
if (getRversion() >= "3.6.0") {
  if (require(car)) withAutoprint({
    Anova(warp.lm, type="III")
    Anova(salamander1)
    Anova(salamander1, component="zi")
  })
  if (require(effects)) withAutoprint({
    plot(allEffects(warp.lm))
    plot(allEffects(salamander1))
  })
}

```

 checkDepPackageVersion

Check for version mismatch in dependent binary packages

Description

Check for version mismatch in dependent binary packages

Usage

```
checkDepPackageVersion(
  dep_pkg = "TMB",
  this_pkg = "glmmTMB",
  write_file = FALSE,
  warn = TRUE
)
```

Arguments

dep_pkg	upstream package
this_pkg	downstream package
write_file	(logical) write version file and quit?
warn	give warning?

Value

logical: TRUE if the binary versions match

 confint.glmmTMB

Calculate confidence intervals

Description

Calculate confidence intervals

Usage

```
## S3 method for class 'glmmTMB'
confint(
  object,
  parm = NULL,
  level = 0.95,
  method = c("wald", "Wald", "profile", "uniroot"),
  component = c("all", "cond", "zi", "other"),
  estimate = TRUE,
```

```

include_mapped = FALSE,
parallel = c("no", "multicore", "snow"),
ncpus = getOption("profile.ncpus", 1L),
cl = NULL,
full = FALSE,
...
)

```

Arguments

object	glmTMB fitted object.
parm	which parameters to profile, specified <ul style="list-style-type: none"> • by index (position) [<i>after</i> component selection for <code>confint</code>, if any] • by name (matching the row/column names of <code>vcov(object, full=TRUE)</code>) • as "theta_" (random-effects variance-covariance parameters), "beta_" (conditional and zero-inflation parameters), or "disp_" or "sigma" (dispersion parameters) <p>Parameter indexing by number may give unusual results when some parameters have been fixed using the <code>map</code> argument: please report surprises to the package maintainers.</p>
level	Confidence level.
method	'wald', 'profile', or 'uniroot': see <code>Details</code> function)
component	Which of the three components 'cond', 'zi' or 'other' to select. Default is to select 'all'.
estimate	(logical) add a third column with estimate ?
include_mapped	include dummy rows for mapped (i.e. fixed-value) parameters?
parallel	method (if any) for parallel computation
ncpus	number of CPUs/cores to use for parallel computation
cl	cluster to use for parallel computation
full	CI for all parameters (including dispersion) ?
...	arguments may be passed to <code>profile.glmTMB</code> (and possibly from there to <code>tmbprofile</code>) or <code>tmbroot</code>

Details

Available methods are

"wald" These intervals are based on the standard errors calculated for parameters on the scale of their internal parameterization depending on the family. Derived quantities such as standard deviation parameters and dispersion parameters are back-transformed. It follows that confidence intervals for these derived quantities are typically asymmetric.

"profile" This method computes a likelihood profile for the specified parameter(s) using `profile.glmTMB`; fits a spline function to each half of the profile; and inverts the function to find the specified confidence interval.

"uniroot" This method uses the `uniroot` function to find critical values of one-dimensional profile functions for each specified parameter.

At present, "wald" returns confidence intervals for variance parameters on the standard deviation/correlation scale, while "profile" and "uniroot" report them on the underlying ("theta") scale: for each random effect, the first set of parameter values are standard deviations on the log scale, while remaining parameters represent correlations on the scaled Cholesky scale. For a random effects model with two elements (such as a random-slopes model, or a random effect of factor with two levels), there is a single correlation parameter θ ; the correlation is equal to $\rho = \theta/\sqrt{1 + \theta^2}$. For random-effects terms with more than two elements, the mapping is more complicated: see https://github.com/glmmTMB/glmmTMB/blob/master/misc/glmmTMB_corcalcs.ipynb

Examples

```
data(sleepstudy, package="lme4")
model <- glmmTMB(Reaction ~ Days + (1|Subject), sleepstudy)
model2 <- glmmTMB(Reaction ~ Days + (1|Subject), sleepstudy,
  dispformula= ~I(Days>8))
confint(model) ## Wald/delta-method CIs
confint(model,parm="theta_") ## Wald/delta-method CIs
confint(model,parm=1,method="profile")
```

diagnose

diagnose model problems

Description

EXPERIMENTAL. For a given model, this function attempts to isolate potential causes of convergence problems. It checks (1) whether there are any unusually large coefficients; (2) whether there are any unusually scaled predictor variables; (3) if the Hessian (curvature of the negative log-likelihood surface at the MLE) is positive definite (i.e., whether the MLE really represents an optimum). For each case it tries to isolate the particular parameters that are problematic.

Usage

```
diagnose(
  fit,
  eval_eps = 1e-05,
  evec_eps = 0.01,
  big_coef = 10,
  big_sd_log10 = 3,
  big_zstat = 5,
  check_coefs = TRUE,
  check_zstats = TRUE,
  check_hessian = TRUE,
  check_scales = TRUE,
  explain = TRUE
)
```

Arguments

<code>fit</code>	a <code>glmmTMB</code> fit
<code>eval_eps</code>	numeric tolerance for 'bad' eigenvalues
<code>evect_eps</code>	numeric tolerance for 'bad' eigenvector elements
<code>big_coef</code>	numeric tolerance for large coefficients
<code>big_sd_log10</code>	numeric tolerance for badly scaled parameters (log10 scale), i.e. for default value of 3, predictor variables with sd less than 1e-3 or greater than 1e3 will be flagged)
<code>big_zstat</code>	numeric tolerance for Z-statistic
<code>check_coefs</code>	identify large-magnitude coefficients? (Only checks conditional-model parameters if a (log, logit, cloglog, probit) link is used. Always checks zero-inflation, dispersion, and random-effects parameters. May produce false positives if predictor variables have extremely large scales.)
<code>check_zstats</code>	identify parameters with unusually large Z-statistics (ratio of standard error to mean)? Identifies likely failures of Wald confidence intervals/p-values.
<code>check_hessian</code>	identify non-positive-definite Hessian components?
<code>check_scales</code>	identify predictors with unusually small or large scales?
<code>explain</code>	provide detailed explanation of each test?

Details

Problems in one category (e.g. complete separation) will generally also appear in "downstream" categories (e.g. non-positive-definite Hessians). Therefore, it is generally advisable to try to deal with problems in order, e.g. address problems with complete separation first, then re-run the diagnostics to see whether Hessian problems persist.

Value

a logical value based on whether anything questionable was found

`dtruncated_nbinom2` *truncated distributions*

Description

Probability functions for k-truncated Poisson and negative binomial distributions.

Usage

```
dtruncated_nbinom2(x, size, mu, k = 0, log = FALSE)
```

```
dtruncated_poisson(x, lambda, k = 0, log = FALSE)
```

```
dtruncated_nbinom1(x, phi, mu, k = 0, log = FALSE)
```


Arguments

x	value
size	number of trials/overdispersion parameter
mu	mean parameter
k	truncation parameter
log	(logical) return log-probability?
lambda	mean parameter
phi	overdispersion parameter

 epil2

Seizure Counts for Epileptics - Extended

Description

Extended version of the epil dataset of the **MASS** package. The three transformed variables `Visit`, `Base`, and `Age` used by Booth et al. (2003) have been added to epil.

Usage

```
epil2
```

Format

A data frame with 236 observations on the following 12 variables:

`y` an integer vector.

`trt` a factor with levels "placebo" and "progabide".

`base` an integer vector.

`age` an integer vector.

`V4` an integer vector.

`subject` an integer vector.

`period` an integer vector.

`lbase` a numeric vector.

`lage` a numeric vector.

Visit $(\text{rep}(1:4, 59) - 2.5) / 5$.

Base $\log(\text{base}/4)$.

Age $\log(\text{age})$.

References

Booth, J.G., G. Casella, H. Friedl, and J.P. Hobert. (2003) Negative binomial loglinear mixed models. *Statistical Modelling* **3**, 179–191.

Examples

```

epil2$subject <- factor(epil2$subject)
op <- options(digits=3)
(fm <- glmmTMB(y ~ Base*trt + Age + Visit + (Visit|subject),
              data=epil2, family=nbinom2))
meths <- methods(class = class(fm))
if((Rv <- getRversion()) > "3.1.3") {
  funs <- attr(meths, "info")[, "generic"]
  funs <- setdiff(funs, "profile") ## too slow! pkgdown is trying to run this??
  for(fun in funs[is.na(match(funs, "getME"))]) {
    cat(sprintf("%s:\n----\n", fun))
    r <- tryCatch( get(fun)(fm), error=identity)
    if (inherits(r, "error")) cat("** Error:", r$message, "\n")
    else tryCatch( print(r) )
    cat(sprintf("---end{%s}-----\n\n", fun))
  }
}
options(op)

```

expandGrpVar

apply

Description

apply

Usage

expandGrpVar(f)

Arguments

f a language object (an atom of a formula) `expandGrpVar(quote(x*y))` `expandGrpVar(quote(x/y))`

family_params

Retrieve family-specific parameters

Description

Most conditional distributions have only parameters governing their location (retrieved via `predict`) and scale (`sigma`). A few (e.g. Tweedie, Student t, ordered beta) are characterized by one or more additional parameters.

Usage

```
family_params(object)
```

Arguments

```
object          glmmTMB object
```

Value

a named numeric vector

findReTrmClasses	<i>list of specials – taken from enum.R</i>
------------------	---

Description

list of specials – taken from enum.R

Usage

```
findReTrmClasses()
```

fitTMB	<i>Optimize a TMB model and package results</i>
--------	---

Description

This function (called internally by `glmmTMB`) runs the actual model optimization, after all of the appropriate structures have been set up. It can be useful to run `glmmTMB` with `doFit=TRUE`, adjust the components as required, and then finish the fitting process with `fitTMB` (however, it is the user's responsibility to make sure that any modifications create an internally consistent final fitted object).

Usage

```
fitTMB(TMBStruc, doOptim = TRUE)
```

Arguments

```
TMBStruc      a list containing lots of stuff ...
doOptim      logical; do optimization? If FALSE, return TMB object
```

Examples

```
m0 <- glmmTMB(count ~ mined + (1|site),
              family=poisson, data=Salamanders, doFit=FALSE)
names(m0)
fitTMB(m0)
```

fixef	<i>Extract fixed-effects estimates</i>
-------	--

Description

Extract Fixed Effects

Usage

```
## S3 method for class 'glmmTMB'  
fixef(object, ...)
```

Arguments

object	any fitted model object from which fixed effects estimates can be extracted.
...	optional additional arguments. Currently none are used in any methods.

Details

Extract fixed effects from a fitted `glmmTMB` model.

The print method for `fixef.glmmTMB` object *only displays non-trivial components*: in particular, the dispersion parameter estimate is not printed for models with a single (intercept) dispersion parameter (see examples)

Value

an object of class `fixef.glmmTMB` comprising a list of components (`cond`, `zi`, `disp`), each containing a (possibly zero-length) numeric vector of coefficients

Examples

```
data(sleepstudy, package = "lme4")  
fm1 <- glmmTMB(Reaction ~ Days, sleepstudy)  
(f1 <- fixef(fm1))  
f1$cond  
## show full coefficients, including empty z-i model and  
## constant dispersion parameter  
print(f1, print_trivials = TRUE)
```

formatVC	<i>Format the 'VarCorr' Matrix of Random Effects</i>
----------	--

Description

"format()" the 'VarCorr' matrix of the random effects – for print()ing and show()ing

Usage

```
formatVC(
  varcor,
  digits = max(3, getOption("digits") - 2),
  comp = "Std.Dev.",
  formatter = format,
  useScale = attr(varcor, "useSc"),
  ...
)
```

Arguments

varcor	a VarCorr (-like) matrix with attributes.
digits	the number of significant digits.
comp	character vector of length one or two indicating which columns out of "Variance" and "Std.Dev." should be shown in the formatted output.
formatter	the function to be used for formatting the standard deviations and or variances (but <i>not</i> the correlations which (currently) are always formatted as "0.nnn")
useScale	whether to report a scale parameter (e.g. residual standard deviation)
...	optional arguments for formatter(*) in addition to the first (numeric vector) and digits.

Value

a character matrix of formatted VarCorr entries from var.c.

formula.glmTMB	<i>Extract the formula of a glmTMB object</i>
----------------	---

Description

Extract the formula of a glmTMB object

Usage

```
## S3 method for class 'glmTMB'
formula(x, fixed.only = FALSE, component = c("cond", "zi", "disp"), ...)
```

Arguments

x	a glmmTMB object
fixed.only	(logical) drop random effects, returning only the fixed-effect component of the formula?
component	formula for which component of the model to return (conditional, zero-inflation, or dispersion)
...	unused, for generic consistency

getCapabilities	<i>List model options that glmmTMB knows about</i>
-----------------	--

Description

List model options that glmmTMB knows about

Usage

```
getCapabilities(what = "all", check = FALSE)
```

Arguments

what	(character) which type of model structure to report on ("all", "family", "link", "covstruct")
check	(logical) do brute-force checking to test whether families are really implemented (only available for what="family")

Value

if check==FALSE, returns a vector of the names (or a list of name vectors) of allowable entries; if check==TRUE, returns a logical vector of working families

Note

these are all the options that are *defined* internally; they have not necessarily all been *implemented* (FIXME!)

getME.glmTMB	<i>Extract or Get Generalize Components from a Fitted Mixed Effects Model</i>
--------------	---

Description

Extract or Get Generalize Components from a Fitted Mixed Effects Model

Usage

```
## S3 method for class 'glmTMB'
getME(object, name = c("X", "Xzi", "Z", "Zzi", "Xd", "theta", "beta"), ...)
```

Arguments

object	a fitted glmTMB object
name	of the component to be retrieved
...	ignored, for method compatibility

See Also

[getME](#) Get generic and re-export:

getReStruc	<i>Calculate random effect structure Calculates number of random effects, number of parameters, block size and number of blocks. Mostly for internal use.</i>
------------	---

Description

Calculate random effect structure Calculates number of random effects, number of parameters, block size and number of blocks. Mostly for internal use.

Usage

```
getReStruc(reTrms, ss = NULL, aa = NULL, reXterms = NULL, fr = NULL)
```

Arguments

reTrms	random-effects terms list
ss	a character string indicating a valid covariance structure. Must be one of names(glmTMB:::valid_covs) default is to use an unstructured variance-covariance matrix ("us") for all blocks).
aa	additional arguments (i.e. rank)
reXterms	terms objects corresponding to each RE term
fr	model frame

Value

a list

blockNumTheta number of variance covariance parameters per term

blockSize size (dimension) of one block

blockReps number of times the blocks are repeated (levels)

covCode structure code

Examples

```
data(sleepstudy, package="lme4")
rt <- lme4::lFormula(Reaction~Days+(1|Subject)+(0+Days|Subject),
  sleepstudy)$reTrms
rt2 <- lme4::lFormula(Reaction~Days+(Days|Subject),
  sleepstudy)$reTrms
getReStruc(rt)
```

getXReTrms

Create X and random effect terms from formula

Description

Create X and random effect terms from formula

Usage

```
getXReTrms(formula, mf, fr, ranOK = TRUE, type = "", contrasts, sparse = FALSE)
```

Arguments

formula current formula, containing both fixed & random effects

mf matched call

fr full model frame

ranOK random effects allowed here?

type label for model type

contrasts a list of contrasts (see ?glmmTMB)

sparse (logical) return sparse model matrix?

Value

a list composed of

X	design matrix for fixed effects
Z	design matrix for random effects
reTrms	output from <code>mkReTrms</code> from lme4
ss	splitform of the formula
aa	additional arguments, used to obtain rank
terms	terms for the fixed effects
offset	offset vector, or vector of zeros if offset not specified
reXterms	terms for the model matrix in each RE term

get_cor	<i>translate vector of correlation parameters to correlation values</i>
---------	---

Description

translate vector of correlation parameters to correlation values

Usage

```
get_cor(theta)
```

```
put_cor(C)
```

Arguments

theta	vector of internal correlation parameters (elements of scaled Cholesky factor, in <i>row-major</i> order)
C	a correlation matrix

Details

These functions follow the definition at http://kaskr.github.io/adcomp/classdensity_1_1UNSTRUCTURED__CORR__t.html: if L is the lower-triangular matrix with 1 on the diagonal and the correlation parameters in the lower triangle, then the correlation matrix is defined as $\Sigma = D^{-1/2}LL^T D^{-1/2}$, where $D = \text{diag}(LL^T)$. For a single correlation parameter θ_0 , this works out to $\rho = \theta_0/\sqrt{1 + \theta_0^2}$. The `get_cor` function returns the elements of the lower triangle of the correlation matrix, in column-major order.

Value

a vector of correlation values (`get_cor`) or glmmTMB scaled-correlation parameters (`put_cor`)

Examples

```

th0 <- 0.5
stopifnot(all.equal(get_cor(th0), th0/sqrt(1+th0^2)))
get_cor(c(0.5,0.2,0.5))
C <- matrix(c(1, 0.2, 0.1,
              0.2, 1, -0.2,
              0.1,-0.2, 1),
            3, 3)
## test: round-trip (almostl results in lower triangle only)
stopifnot(all.equal(get_cor(put_cor(C)),
                    C[lower.tri(C)]))

```

glmmTMB

*Fit Models with TMB***Description**

Fit a generalized linear mixed model (GLMM) using Template Model Builder (TMB).

Usage

```

glmmTMB(
  formula,
  data = NULL,
  family = gaussian(),
  ziformula = ~0,
  dispformula = ~1,
  weights = NULL,
  offset = NULL,
  contrasts = NULL,
  na.action,
  se = TRUE,
  verbose = FALSE,
  doFit = TRUE,
  control = glmmTMBControl(),
  REML = FALSE,
  start = NULL,
  map = NULL,
  sparseX = NULL
)

```

Arguments

formula	combined fixed and random effects formula, following lme4 syntax.
data	data frame (tibbles are OK) containing model variables. Not required, but strongly recommended; if data is not specified, downstream methods such as prediction

with new data (`predict(fitted_model, newdata = ...)`) will fail. If it is necessary to call `glmmTMB` with model variables taken from the environment rather than from a data frame, specifying `data=NULL` will suppress the warning message.

<code>family</code>	a family function, a character string naming a family function, or the result of a call to a family function (variance/link function) information. See family for a generic discussion of families or family_glmmTMB for details of <code>glmmTMB</code> -specific families.
<code>ziformula</code>	a <i>one-sided</i> (i.e., no response variable) formula for zero-inflation combining fixed and random effects: the default <code>~0</code> specifies no zero-inflation. Specifying <code>~.</code> sets the zero-inflation formula identical to the right-hand side of <code>formula</code> (i.e., the conditional effects formula); terms can also be added or subtracted. When using <code>~.</code> as the zero-inflation formula in models where the conditional effects formula contains an offset term, the offset term will automatically be dropped. The zero-inflation model uses a logit link.
<code>dispformula</code>	a <i>one-sided</i> formula for dispersion containing only fixed effects: the default <code>~1</code> specifies the standard dispersion given any family. The argument is ignored for families that do not have a dispersion parameter. For an explanation of the dispersion parameter for each family, see sigma . The dispersion model uses a log link. In Gaussian mixed models, <code>dispformula=~0</code> fixes the residual variance to be 0 (actually a small non-zero value), forcing variance into the random effects. The precise value can be controlled via <code>control=glmmTMBControl(zero_dispval=...)</code> ; the default value is <code>sqrt(.Machine\$double.eps)</code> .
<code>weights</code>	weights, as in <code>glm</code> . Not automatically scaled to have sum 1.
<code>offset</code>	offset for conditional model (only).
<code>contrasts</code>	an optional list, e.g., <code>list(fac1="contr.sum")</code> . See the <code>contrasts.arg</code> of model.matrix.default .
<code>na.action</code>	a function that specifies how to handle observations containing NAs. The default action (<code>na.omit</code> , inherited from the 'factory fresh' value of <code>getOption("na.action")</code>) strips any observations with any missing values in any variables. Using <code>na.action = na.exclude</code> will similarly drop observations with missing values while fitting the model, but will fill in NA values for the predicted and residual values for cases that were excluded during the fitting process because of missingness.
<code>se</code>	whether to return standard errors.
<code>verbose</code>	whether progress indication should be printed to the console.
<code>doFit</code>	whether to fit the full model, or (if <code>FALSE</code>) return the preprocessed data and parameter objects, without fitting the model.
<code>control</code>	control parameters, see glmmTMBControl .
<code>REML</code>	whether to use REML estimation rather than maximum likelihood.
<code>start</code>	starting values, expressed as a list with possible components <code>beta</code> , <code>betazi</code> , <code>betad</code> (fixed-effect parameters for conditional, zero-inflation, dispersion models); <code>b</code> , <code>bzi</code> (conditional modes for conditional and zero-inflation models); <code>theta</code> , <code>thetazi</code> (random-effect parameters, on the standard deviation/Cholesky scale, for conditional and z-i models); <code>psi</code> (extra family parameters, e.g., shape for Tweedie models).

map	a list specifying which parameter values should be fixed to a constant value rather than estimated. map should be a named list containing factors corresponding to a subset of the internal parameter names (see <code>start</code> parameter). Distinct factor values are fitted as separate parameter values, NA values are held fixed: e.g., <code>map=list(beta=factor(c(1,2,3,NA)))</code> would fit the first three fixed-effect parameters of the conditional model and fix the fourth parameter to its starting value. In general, users will probably want to use <code>start</code> to specify non-default starting values for fixed parameters. See MakeADFun for more details.
sparseX	a named logical vector containing (possibly) elements named "cond", "zi", "disp" to indicate whether fixed-effect model matrices for particular model components should be generated as sparse matrices, e.g. <code>c(cond=TRUE)</code> . Default is all FALSE

Details

- Binomial models with more than one trial (i.e., not binary/Bernoulli) can either be specified in the form `prob ~ . . . , weights = N`, or in the more typical two-column matrix `cbind(successes, failures) ~ . . .` form.
- Behavior of `REML=TRUE` for Gaussian responses matches `lme4::lmer`. It may also be useful in some cases with non-Gaussian responses (Millar 2011). Simulations should be done first to verify.
- Because the `df.residual` method for `glmmTMB` currently counts the dispersion parameter, users should multiply this value by `sqrt(nobs(fit) / (1+df.residual(fit)))` when comparing with `lm`.
- Although models can be fitted without specifying a data argument, its use is strongly recommended; drawing model components from the global environment, or using `df$var` notation within model formulae, can lead to confusing (and sometimes hard-to-detect) errors.
- By default, vector-valued random effects are fitted with unstructured (general symmetric positive definite) variance-covariance matrices. Structured variance-covariance matrices can be specified in the form `struc(terms|group)`, where `struc` is one of
 - `diag` (diagonal, heterogeneous variance)
 - `ar1` (autoregressive order-1, homogeneous variance)
 - `cs` (compound symmetric, heterogeneous variance)
 - `ou` (* Ornstein-Uhlenbeck, homogeneous variance)
 - `exp` (* exponential autocorrelation)
 - `gau` (* Gaussian autocorrelation)
 - `mat` (* Matérn process correlation)
 - `toep` (* Toeplitz)
 - `rr` (reduced rank/factor-analytic model)
 - `homdiag` (diagonal, homogeneous variance)

Structures marked with * are experimental/untested. See `vignette("covstruct", package = "glmmTMB")` for more information.

- For backward compatibility, the `family` argument can also be specified as a list comprising the name of the distribution and the link function (e.g. `list(family="binomial", link="logit")`). However, **this alternative is now deprecated**; it produces a warning and will be removed at some point in the future. Furthermore, certain capabilities such as Pearson residuals or predictions on the data scale will only be possible if components such as variance and `linkfun` are present, see [family](#).

Note

For more information about the **glmmTMB** package, see Brooks et al. (2017) and the vignette(package="glmmTMB") collection. For the underlying **TMB** package that performs the model estimation, see Kristensen et al. (2016).

References

Brooks, M. E., Kristensen, K., van Benthem, K. J., Magnusson, A., Berg, C. W., Nielsen, A., Skaug, H. J., Mächler, M. and Bolker, B. M. (2017). glmmTMB balances speed and flexibility among packages for zero-inflated generalized linear mixed modeling. *The R Journal*, **9**(2), 378–400.

Kristensen, K., Nielsen, A., Berg, C. W., Skaug, H. and Bell, B. (2016). TMB: Automatic differentiation and Laplace approximation. *Journal of Statistical Software*, **70**, 1–21.

Millar, R. B. (2011). *Maximum Likelihood Estimation and Inference: With Examples in R, SAS and ADMB*. Wiley, New York.

Examples

```
(m1 <- glmmTMB(count ~ mined + (1|site),
  zi=~mined,
  family=poisson, data=Salamanders))
summary(m1)
##' ## Zero-inflated negative binomial model
(m2 <- glmmTMB(count ~ spp + mined + (1|site),
  zi=~spp + mined,
  family=nbinom2, data=Salamanders))

## Hurdle Poisson model
(m3 <- glmmTMB(count ~ spp + mined + (1|site),
  zi=~spp + mined,
  family=truncated_poisson, data=Salamanders))

## Binomial model
data(cbpp, package="lme4")
(bovine <- glmmTMB(cbind(incidence, size-incidence) ~ period + (1|herd),
  family=binomial, data=cbpp))

## Dispersion model
sim1 <- function(nfac=40, nt=100, facsd=0.1, tsd=0.15, mu=0, residsd=1)
{
  dat <- expand.grid(fac=factor(letters[1:nfac]), t=1:nt)
  n <- nrow(dat)
  dat$REfac <- rnorm(nfac, sd=facsd)[dat$fac]
  dat$REt <- rnorm(nt, sd=tsd)[dat$t]
  dat$x <- rnorm(n, mean=mu, sd=residsd) + dat$REfac + dat$REt
  dat
}
set.seed(101)
d1 <- sim1(mu=100, residsd=10)
d2 <- sim1(mu=200, residsd=5)
d1$sd <- "ten"
```

```

d2$sd <- "five"
dat <- rbind(d1, d2)
m0 <- glmmTMB(x ~ sd + (1|t), dispformula=~sd, data=dat)
fixef(m0)$disp
c(log(5^2), log(10^2)-log(5^2)) # expected dispersion model coefficients

## Using 'map' to fix random-effects SD to 10
m1_map <- update(m1, map=list(theta=factor(NA)),
                 start=list(theta=log(10)))
VarCorr(m1_map)

```

glmmTMBControl

Control parameters for glmmTMB optimization

Description

Control parameters for glmmTMB optimization

Usage

```

glmmTMBControl(
  optCtrl = NULL,
  optArgs = list(),
  optimizer = nlminb,
  profile = FALSE,
  collect = FALSE,
  parallel = getOption("glmmTMB.cores", 1L),
  eigval_check = TRUE,
  zerodisp_val = log(sqrt(.Machine$double.eps)),
  start_method = list(method = NULL, jitter.sd = 0),
  rank_check = c("warning", "adjust", "stop", "skip"),
  conv_check = c("warning", "skip")
)

```

Arguments

optCtrl	Passed as argument control to optimizer. Default value (if default nlminb optimizer is used): <code>list(iter.max=300, eval.max=400)</code>
optArgs	additional arguments to be passed to optimizer function (e.g.: <code>list(method="BFGS")</code>) when optimizer=optim)
optimizer	Function to use in model fitting. See Details for required properties of this function.
profile	(logical) Experimental option to improve speed and robustness when a model has many fixed effects

collect	(logical) Experimental option to improve speed by recognizing duplicated observations.
parallel	(integer) Set number of OpenMP threads to evaluate the negative log-likelihood in parallel. The default is to evaluate models serially (i.e. single-threaded); users can set a default value for an R session via <code>options(glmmTMB.cores=<value>)</code> . At present reduced-rank models (i.e., a covariance structure using <code>rr(...)</code>) cannot be fitted in parallel; the number of threads will be automatically set to 1, with a warning if this overrides the user-specified value.
eigval_check	Check eigenvalues of variance-covariance matrix? (This test may be very slow for models with large numbers of fixed-effect parameters.)
zerodisp_val	value of the dispersion parameter when <code>dispformula=~0</code> is specified
start_method	(list) Options to initialize the starting values when fitting models with reduced-rank (rr) covariance structures; <code>jitter.sd</code> adds variation to the starting values of latent variables when <code>method = "res"</code> .
rank_check	Check whether all parameters in fixed-effects models are identifiable? This test may be slow for models with large numbers of fixed-effect parameters, therefore default value is 'warning'. Alternatives include 'skip' (no check), 'stop' (throw an error), and 'adjust' (drop redundant columns from the fixed-effect model matrix).
conv_check	Do basic checks of convergence (check for non-positive definite Hessian and non-zero convergence code from optimizer). Default is 'warning'; 'skip' ignores these tests (not recommended for general use!)

Details

By default, `glmmTMB` uses the nonlinear optimizer `nlm` for parameter estimation. Users may sometimes need to adjust optimizer settings in order to get models to converge. For instance, the warning 'iteration limit reached without convergence' may be fixed by increasing the number of iterations using (e.g.)

```
glmmTMBControl(optCtrl=list(iter.max=1e3,eval.max=1e3)).
```

Setting `profile=TRUE` allows `glmmTMB` to use some special properties of the optimization problem in order to speed up estimation in cases with many fixed effects.

Control parameters may depend on the model specification. The value of the controls is evaluated inside an R object that is derived from the output of the `mkTMBStruc` function. For example, to specify that `profile` should be enabled if the model has more than 5 fixed-effect parameters, specify `profile=quote(length(parameters$beta)>=5)`

The optimizer argument can be any optimization (minimizing) function, provided that:

- the first three arguments, in order, are the starting values, objective function, and gradient function;
- the function also takes a control argument;
- the function returns a list with elements (at least) `par`, `objective`, `convergence` (0 if convergence is successful) and `message` (`glmmTMB` automatically handles output from `optim()`, by renaming the value component to `objective`)

Examples

```
## fit with default (nlminb) and alternative (optim/BFGS) optimizer
m1 <- glmTMB(count~ mined, family=poisson, data=Salamanders)
m1B <- update(m1, control=glmTMBControl(optimizer=optim,
    optArgs=list(method="BFGS")))
## estimates are *nearly* identical:
all.equal(fixef(m1), fixef(m1B))
```

isLMM.glmTMB

support methods for parametric bootstrapping

Description

see [refit](#) and [isLMM](#) for details

Usage

```
## S3 method for class 'glmTMB'
isLMM(x, ...)

## S3 method for class 'glmTMB'
refit(object, newresp, ...)
```

Arguments

x	a fitted glmTMB object
...	additional arguments (for generic consistency; ignored)
object	a fitted glmTMB object
newresp	a new response vector

Details

These methods are still somewhat experimental (check your results carefully!), but they should allow parametric bootstrapping. They work by copying and replacing the original response column in the data frame passed to glmTMB, so they will only work properly if (1) the data frame is still available in the environment and (2) the response variable is specified as a single symbol (e.g. proportion or a two-column matrix constructed on the fly with cbind()). Untested with binomial models where the response is specified as a factor.

Examples

```
if (requireNamespace("lme4")) {
## Not run:
  fm1 <- glmTMB(count~mined+(1|spp),
    ziformula=~mined,
    data=Salamanders,
    family=nbinom1)
```



```

## single parametric bootstrap step: refit with data simulated from original model
fm1R <- refit(fm1, simulate(fm1)[[1]])
## the bootMer function from lme4 provides a wrapper for doing multiple refits
## with a specified summary function
b1 <- lme4::bootMer(fm1, FUN=function(x) fixef(x)$zi, nsim=20, .progress="txt")
if (requireNamespace("boot")) {
  boot.ci(b1,type="perc")
}
## can run in parallel: may need to set up cluster explicitly,
## use clusterEvalQ() to load packages on workers
if (requireNamespace("parallel")) {
  cl <- parallel::makeCluster(2)
  parallel::clusterEvalQ(cl, library("lme4"))
  parallel::clusterEvalQ(cl, library("glmmTMB"))
  b2 <- lme4::bootMer(fm1, FUN = function(x) fixef(x)$cond,
    nsim = 10, ncpus = 2, cl = cl, parallel = "snow")
}

## End(Not run)
}

```

nbinom2

Family functions for glmmTMB

Description

Family functions for glmmTMB

Usage

```

nbinom2(link = "log")

nbinom1(link = "log")

compois(link = "log")

truncated_compois(link = "log")

genpois(link = "log")

truncated_genpois(link = "log")

truncated_poisson(link = "log")

truncated_nbinom2(link = "log")

truncated_nbinom1(link = "log")

beta_family(link = "logit")

```

```
betabinomial(link = "logit")
tweedie(link = "log")
ziGamma(link = "inverse")
t_family(link = "identity")
ordbeta(link = "logit")
```

Arguments

link (character) link function for the conditional mean ("log", "logit", "probit", "inverse", "cloglog", "identity", or "sqrt")

Details

If specified, the dispersion model uses a log link. Denoting the variance as V , the dispersion parameter as $\phi = \exp(\eta)$ (where η is the linear predictor from the dispersion model), and the predicted mean as μ :

gaussian (from base R): constant $V = \phi$

Gamma (from base R) ϕ is the shape parameter. $V = \mu\phi$

ziGamma a modified version of Gamma that skips checks for zero values, allowing it to be used to fit hurdle-Gamma models

nbinom2 Negative binomial distribution: quadratic parameterization (Hardin & Hilbe 2007). $V = \mu(1 + \mu/\phi) = \mu + \mu^2/\phi$.

nbinom1 Negative binomial distribution: linear parameterization (Hardin & Hilbe 2007). $V = \mu(1 + \phi)$

truncated_nbinom2 Zero-truncated version of nbinom2: variance expression from Shonkwiler 2016. Simulation code (for this and the other truncated count distributions) is taken from C. Geyer's functions in the `aster` package; the algorithms are described in [this vignette](#).

compois Conway-Maxwell Poisson distribution: parameterized with the exact mean (Huang 2017), which differs from the parameterization used in the **COMPOISSONReg** package (Sellers & Shmueli 2010, Sellers & Lotze 2015). $V = \mu\phi$.

genpois Generalized Poisson distribution (Consul & Famoye 1992). $V = \mu \exp(\eta)$. (Note that Consul & Famoye (1992) define ϕ differently.) Our implementation is taken from the `HMMpa` package, based on Joe and Zhu (2005) and implemented by Vitali Witowski.

beta Beta distribution: parameterization of Ferrari and Cribari-Neto (2004) and the **betareg** package (Cribari-Neto and Zeileis 2010); $V = \mu(1 - \mu)/(\phi + 1)$

betabinomial Beta-binomial distribution: parameterized according to Morris (1997). $V = \mu(1 - \mu)(n(\phi + n)/(\phi + 1))$

tweedie Tweedie distribution: $V = \phi\mu^{power}$. The power parameter is restricted to the interval $1 < power < 2$. Code taken from the `tweedie` package, written by Peter Dunn.

t_family Student-t distribution with adjustable scale and location parameters (also called a **Pearson type VII distribution**). The shape (degrees of freedom parameter) is fitted with a log link; it may be often be useful to fix the shape parameter using `start = list(psi = log(fixed_df))`, `map = list(psi = factor(NA))`.

ordbeta Ordered beta regression from Kubinec (2022); fits continuous (e.g. proportion) data in the *closed* interval [0,1].

Value

returns a list with (at least) components

family	length-1 character vector giving the family name
link	length-1 character vector specifying the link function
variance	a function of either 1 (mean) or 2 (mean and dispersion parameter) arguments giving a value proportional to the predicted variance (scaled by <code>sigma(.)</code>)

References

- Consul PC & Famoye F (1992). "Generalized Poisson regression model." *Communications in Statistics: Theory and Methods* 21:89–109.
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- Joe H, Zhu R (2005). "Generalized Poisson Distribution: The Property of Mixture of Poisson and Comparison with Negative Binomial Distribution." *Biometrical Journal* 47(2): 219–29. doi: [10.1002/bimj.200410102](https://doi.org/10.1002/bimj.200410102).
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- Sellers K & Shmueli G (2010) "A Flexible Regression Model for Count Data." *Annals of Applied Statistics* 4(2), 943–61. doi: [10.1214/09AOAS306](https://doi.org/10.1214/09AOAS306).
- Shonkwiler, J. S. (2016). "Variance of the truncated negative binomial distribution." *Journal of Econometrics* 195(2), 209–210. doi: [10.1016/j.jeconom.2016.09.002](https://doi.org/10.1016/j.jeconom.2016.09.002).

numFactor	<i>Factor with numeric interpretable levels.</i>
-----------	--

Description

Create a factor with numeric interpretable factor levels.

Usage

```
numFactor(x, ...)
```

```
parseNumLevels(levels)
```

Arguments

x	Vector, matrix or data.frame that constitute the coordinates.
...	Additional vectors, matrices or data.frames that constitute the coordinates.
levels	Character vector to parse into numeric values.

Details

Some glmmTMB covariance structures require extra information, such as temporal or spatial coordinates. numFactor allows to associate such extra information as part of a factor via the factor levels. The original numeric coordinates are recoverable without loss of precision using the function parseNumLevels. Factor levels are sorted coordinate wise from left to right: first coordinate is fastest running.

Value

Factor with specialized coding of levels.

Examples

```
## 1D example
numFactor(sample(1:5,20,TRUE))
## 2D example
coords <- cbind( sample(1:5,20,TRUE), sample(1:5,20,TRUE) )
(f <- numFactor(coords))
parseNumLevels(levels(f)) ## Sorted
## Used as part of a model.matrix
model.matrix( ~f )
## parseNumLevels( colnames(model.matrix( ~f )) )
## Error: 'Failed to parse numeric levels: (Intercept)'
parseNumLevels( colnames(model.matrix( ~ f-1 )) )
```

omp_check	<i>Check OpenMP status</i>
-----------	----------------------------

Description

Checks whether OpenMP has been successfully enabled for this installation of the package. (Use the `parallel` argument to `glmmTMBControl`, or set `options(glmmTMB.cores=[value])`, to specify that computations should be done in parallel.)

Usage

```
omp_check()
```

Value

TRUE or FALSE depending on availability of OpenMP

See Also

[benchmark](#), [glmmTMBControl](#)

Owls	<i>Begging by Owl Nestlings</i>
------	---------------------------------

Description

Begging by owl nestlings

Usage

```
data(Owls)
```

Format

The Owls data set is a data frame with 599 observations on the following variables:

`Nest` a factor describing individual nest locations

`FoodTreatment` (factor) food treatment: Deprived or Satiated

`SexParent` (factor) sex of provisioning parent: Female or Male

`ArrivalTime` a numeric vector

`SiblingNegotiation` a numeric vector

`BroodSize` brood size

`NegPerChick` number of negotiations per chick

Note

Access to data kindly provided by Alain Zuur

Source

Roulin, A. and L. Bersier (2007) Nestling barn owls beg more intensely in the presence of their mother than in the presence of their father. *Animal Behaviour* **74** 1099–1106. doi: [10.1016/j.anbehav.2007.01.027](https://doi.org/10.1016/j.anbehav.2007.01.027); <http://www.highstat.com/Books/Book2/ZuurDataMixedModelling.zip>

References

Zuur, A. F., E. N. Ieno, N. J. Walker, A. A. Saveliev, and G. M. Smith (2009) *Mixed Effects Models and Extensions in Ecology with R*; Springer.

Examples

```
data(Owls, package = "glmmTMB")
require("lattice")
bwplot(reorder(Nest,NegPerChick) ~ NegPerChick | FoodTreatment:SexParent,
       data=Owls)
dotplot(reorder(Nest,NegPerChick) ~ NegPerChick| FoodTreatment:SexParent,
        data=Owls)
## Not run:
## Fit negative binomial model with "constant" Zero Inflation :
owls_nb1 <- glmmTMB(SiblingNegotiation ~ FoodTreatment*SexParent +
                  (1|Nest)+offset(log(BroodSize)),
                  family = nbinom1(), zi = ~1, data=Owls)
owls_nb1_bs <- update(owls_nb1,
                    . ~ . - offset(log(BroodSize)) + log(BroodSize))
fixef(owls_nb1_bs)

## End(Not run)
```

predict.glmTMB

prediction

Description

prediction

Usage

```
## S3 method for class 'glmmTMB'
predict(
  object,
  newdata = NULL,
  newparams = NULL,
  se.fit = FALSE,
```

```

cov.fit = FALSE,
re.form = NULL,
allow.new.levels = FALSE,
type = c("link", "response", "conditional", "zprob", "zlink", "disp"),
zitype = NULL,
na.action = na.pass,
fast = NULL,
debug = FALSE,
...
)

```

Arguments

object	a glmTMB object
newdata	new data for prediction
newparams	new parameters for prediction
se.fit	return the standard errors of the predicted values?
cov.fit	return the covariance matrix of the predicted values?
re.form	NULL to specify individual-level predictions; ~ 0 or NA to specify population-level predictions (i.e., setting all random effects to zero)
allow.new.levels	allow previously unobserved levels in random-effects variables? see details.
type	Denoting μ as the mean of the conditional distribution and p as the zero-inflation probability, the possible choices are: "link" conditional mean on the scale of the link function, or equivalently the linear predictor of the conditional model "response" expected value; this is $\mu * (1 - p)$ for zero-inflated models and μ otherwise "conditional" mean of the conditional response; μ for all models (i.e., synonymous with "response" in the absence of zero-inflation) "zprob" the probability of a structural zero (returns 0 for non-zero-inflated models) "zlink" predicted zero-inflation probability on the scale of the logit link function (returns $-\text{Inf}$ for non-zero-inflated models) "disp" dispersion parameter however it is defined for that particular family as described in sigma.glmTMB
zitype	deprecated: formerly used to specify type of zero-inflation probability. Now synonymous with type
na.action	how to handle missing values in newdata (see na.action); the default (<code>na.pass</code>) is to predict NA
fast	predict without expanding memory (default is TRUE if newdata and newparams are NULL and population-level prediction is not being done)
debug	(logical) return the TMBstruc object that will be used internally for debugging?
...	unused - for method compatibility

Details

- To compute population-level predictions for a given grouping variable (i.e., setting all random effects for that grouping variable to zero), set the grouping variable values to NA. Finer-scale control of conditioning (e.g. allowing variation among groups in intercepts but not slopes when predicting from a random-slopes model) is not currently possible.
- Prediction of new random effect levels is possible as long as the model specification (fixed effects and parameters) is kept constant. However, to ensure intentional usage, a warning is triggered if `allow.new.levels=FALSE` (the default).
- Prediction using "data-dependent bases" (variables whose scaling or transformation depends on the original data, e.g. `poly`, `ns`, or `poly`) should work properly; however, users are advised to check results extra-carefully when using such variables. Models with different versions of the same data-dependent basis type in different components (e.g. `formula= y ~ poly(x, 3)`, `dispformula= ~poly(x, 2)`) will probably *not* produce correct predictions.

Examples

```
data(sleepstudy, package="lme4")
g0 <- glmmTMB(Reaction~Days+(Days|Subject), sleepstudy)
predict(g0, sleepstudy)
## Predict new Subject
nd <- sleepstudy[1,]
nd$Subject <- "new"
predict(g0, newdata=nd, allow.new.levels=TRUE)
## population-level prediction
nd_pop <- data.frame(Days=unique(sleepstudy$Days),
                    Subject=NA)
predict(g0, newdata=nd_pop)
```

`print.VarCorr.glmTMB` *Printing The Variance and Correlation Parameters of a glmmTMB*

Description

Printing The Variance and Correlation Parameters of a glmmTMB

Usage

```
## S3 method for class 'VarCorr.glmTMB'
print(
  x,
  digits = max(3, getOption("digits") - 2),
  comp = "Std.Dev.",
  formatter = format,
  ...
)
```


Arguments

x	a result of <code>VarCorr(<glmTMB>)</code> .
digits	number of significant digits to use.
comp	a string specifying the component to format and print.
formatter	a function .
...	optional further arguments, passed the next <code>print</code> method.

profile.glmTMB	<i>Compute likelihood profiles for a fitted model</i>
----------------	---

Description

Compute likelihood profiles for a fitted model

Usage

```
## S3 method for class 'glmTMB'
profile(
  fitted,
  parm = NULL,
  level_max = 0.99,
  npts = 8,
  stepfac = 1/4,
  stderr = NULL,
  trace = FALSE,
  parallel = c("no", "multicore", "snow"),
  ncpus = getOption("profile.ncpus", 1L),
  cl = NULL,
  ...
)

## S3 method for class 'profile.glmTMB'
confint(object, parm = NULL, level = 0.95, ...)
```

Arguments

fitted	a fitted glmTMB object
parm	which parameters to profile, specified <ul style="list-style-type: none"> • by index (position) • by name (matching the row/column names of <code>vcov(object, full=TRUE)</code>) • as "theta_" (random-effects variance-covariance parameters) or "beta_" (conditional and zero-inflation parameters)
level_max	maximum confidence interval target for profile
npts	target number of points in (each half of) the profile (<i>approximate</i>)

stepfac	initial step factor (fraction of estimated standard deviation)
stderr	standard errors to use as a scaling factor when picking step sizes to compute the profile; by default (if stderr is NULL, or NA for a particular element), uses the estimated (Wald) standard errors of the parameters
trace	print tracing information? If trace=FALSE or 0, no tracing; if trace=1, print names of parameters currently being profiled; if trace>1, turn on tracing for the underlying <code>tmbprofile</code> function
parallel	method (if any) for parallel computation
ncpus	number of CPUs/cores to use for parallel computation
cl	cluster to use for parallel computation
...	additional arguments passed to <code>tmbprofile</code>
object	a fitted profile (<code>profile.glmmTMB</code>) object
level	confidence level

Details

Fits natural splines separately to the points from each half of the profile for each specified parameter (i.e., values above and below the MLE), then finds the inverse functions to estimate the endpoints of the confidence interval

Value

An object of class `profile.glmmTMB`, which is also a data frame, with columns `.par` (parameter being profiled), `.focal` (value of focal parameter), `value` (negative log-likelihood).

Examples

```
## Not run:
m1 <- glmmTMB(count~ mined + (1|site),
              zi=~mined, family=poisson, data=Salamanders)
salamander_prof1 <- profile(m1, parallel="multicore",
                           ncpus=2, trace=1)

## testing
salamander_prof1 <- profile(m1, trace=1,parm=1)
salamander_prof1M <- profile(m1, trace=1,parm=1, npts = 4)
salamander_prof2 <- profile(m1, parm="theta_")

## End(Not run)
salamander_prof1 <- readRDS(system.file("example_files", "salamander_prof1.rds", package="glmmTMB"))
if (require("ggplot2")) {
  ggplot(salamander_prof1, aes(.focal, sqrt(value))) +
    geom_point() + geom_line()+
    facet_wrap(~.par, scale="free_x")+
    geom_hline(yintercept=1.96, linetype=2)
}
salamander_prof1 <- readRDS(system.file("example_files", "salamander_prof1.rds", package="glmmTMB"))
confint(salamander_prof1)
confint(salamander_prof1, level=0.99)
```

ranef.glmTMB	<i>Extract Random Effects</i>
--------------	-------------------------------

Description

Extract random effects from a fitted glmTMB model, both for the conditional model and zero inflation.

Usage

```
## S3 method for class 'glmTMB'
ranef(object, condVar = TRUE, ...)

## S3 method for class 'ranef.glmTMB'
as.data.frame(x, ...)

## S3 method for class 'glmTMB'
coef(object, condVar = FALSE, ...)
```

Arguments

object	a glmTMB model.
condVar	whether to include conditional variances in result.
...	some methods for this generic function require additional arguments (they are unused here and will trigger an error)
x	a ranef.glmTMB object (i.e., the result of running ranef on a fitted glmTMB model)

Value

- For ranef, an object of class ranef.glmTMB with two components:
 - cond** a list of data frames, containing random effects for the conditional model.
 - zi** a list of data frames, containing random effects for the zero inflation.

If condVar=TRUE, the individual list elements within the cond and zi components (corresponding to individual random effects terms) will have associated condVar attributes giving the conditional variances of the random effects values. These are in the form of three-dimensional arrays: see [ranef.merMod](#) for details. The only difference between the packages is that the attributes are called 'postVar' in **lme4**, vs. 'condVar' in **glmTMB**.
- For coef.glmTMB: a similar list, but containing the overall coefficient value for each level, i.e., the sum of the fixed effect estimate and the random effect value for that level. *Conditional variances are not yet available as an option for coef.glmTMB.*
- For as.data.frame: a data frame with components
 - component** part of the model to which the random effects apply (conditional or zero-inflation)
 - grpvar** grouping variable

term random-effects term (e.g., intercept or slope)

grp group, or level of the grouping variable

condval value of the conditional mode

condsd conditional standard deviation

Note

When a model has no zero inflation, the `ranef` and `coef` print methods simplify the structure shown, by default. To show the full list structure, use `print(ranef(model), simplify=FALSE)` or the analogous code for `coef`. In all cases, the full list structure is used to access the data frames, see example.

See Also

[fixef.glmmTMB](#).

Examples

```
if (requireNamespace("lme4")) {
  data(sleepstudy, package="lme4")
  model <- glmmTMB(Reaction ~ Days + (1|Subject), sleepstudy)
  rr <- ranef(model)
  print(rr, simplify=FALSE)
  ## extract Subject conditional modes for conditional model
  rr$cond$Subject
  as.data.frame(rr)
}
```

reinstalling

Reinstalling binary dependencies

Description

The `glmmTMB` package depends on several upstream packages, which it uses in a way that depends heavily on their internal (binary) structure. Sometimes, therefore, installing an update to one of these packages will require that you re-install a *binary-compatible* version of `glmmTMB`, i.e. a version that has been compiled with the updated version of the upstream package.

- If you have development tools (compilers etc.) installed, you should be able to re-install a binary-compatible version of the package by running `install.packages("glmmTMB", type="source")`. If you want to install the development version of `glmmTMB` instead, you can use `remotes::install_github("glmmTMB/development")`. (On Windows, you can install development tools following the instructions at <https://cran.r-project.org/bin/windows/Rtools/>; on MacOS, see <https://mac.r-project.org/tools/>.)
- If you do *not* have development tools and can't/don't want to install them (and so can't install packages with compiled code from source), you have two choices:
 - revert the upstream package(s) to their previous binary version. For example, using the checkpoint package:

```
## load (installing if necessary) the checkpoint package
while (!require("checkpoint")) install.packages("checkpoint")
## retrieve build date of installed version of glmmTMB
bd <- as.character(asDateBuilt(
  packageDescription("glmmTMB", fields="Built")))
oldrepo <- getOption("repos")
use_mran_snapshot(bd) ## was setSnapshot() pre-checkpoint v1.0.0
install.packages("TMB")
options(repos=oldrepo) ## restore original repo
```

A similar recipe (substituting Matrix for TMB and TMB for glmmTMB) can be used if you get warnings about an incompatibility between TMB and Matrix.

- hope that the glmmTMB maintainers have posted a binary version of the package that works with your system; try installing it via `install.packages("glmmTMB", repos="https://glmmTMB.github.io")`. If this doesn't work, please file an issue (with full details about your operating system and R version) asking the maintainers to build and post an appropriate binary version of the package.

residuals.glmmTMB *Compute residuals for a glmmTMB object*

Description

Compute residuals for a glmmTMB object

Usage

```
## S3 method for class 'glmmTMB'
residuals(object, type = c("response", "pearson", "working"), ...)
```

Arguments

object	a “glmmTMB” object
type	(character) residual type
...	ignored, for method compatibility

RHSForm *extract right-hand side of a formula*

Description

extract right-hand side of a formula

Usage

```
RHSForm(form, as.form = FALSE)
```

Arguments

`form` a formula object
`as.form` (logical) return a formula (TRUE) or as a call/symbolic object (FALSE) ?

Salamanders *Repeated counts of salamanders in streams*

Description

A data set containing counts of salamanders with site covariates and sampling covariates. Each of 23 sites was sampled 4 times. When using this data set, please cite Price et al. (2016) as well as the Dryad data package (Price et al. 2015).

Usage

```
data(Salamanders)
```

Format

A data frame with 644 observations on the following 10 variables:

site name of a location where repeated samples were taken
mined factor indicating whether the site was affected by mountain top removal coal mining
cover amount of cover objects in the stream (scaled)
sample repeated sample
DOP Days since precipitation (scaled)
Wtemp water temperature (scaled)
DOY day of year (scaled)
spp abbreviated species name, possibly also life stage
count number of salamanders observed

References

Price SJ, Muncy BL, Bonner SJ, Drayer AN, Barton CD (2016) Effects of mountaintop removal mining and valley filling on the occupancy and abundance of stream salamanders. *Journal of Applied Ecology* **53** 459–468. doi: [10.1111/13652664.12585](https://doi.org/10.1111/13652664.12585)

Price SJ, Muncy BL, Bonner SJ, Drayer AN, Barton CD (2015) Data from: Effects of mountaintop removal mining and valley filling on the occupancy and abundance of stream salamanders. *Dryad Digital Repository*. doi: [10.5061/dryad.5m8f6](https://doi.org/10.5061/dryad.5m8f6)

Examples

```
require("glmmTMB")
data(Salamanders)

zipm3 = glmmTMB(count~spp * mined + (1|site), zi=~spp * mined, Salamanders, family="poisson")
```

sigma.glmmTMB	<i>Extract residual standard deviation or dispersion parameter</i>
---------------	--

Description

For Gaussian models, sigma returns the value of the residual standard deviation; for other families, it returns the dispersion parameter, *however it is defined for that particular family*. See details for each family below.

Usage

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

Arguments

object	a “glmmTMB” fitted object
...	(ignored; for method compatibility)

Details

The value returned varies by family:

gaussian returns the *maximum likelihood* estimate of the standard deviation (i.e., smaller than the results of `sigma(lm(...))` by a factor of $(n-1)/n$)

nbinom1 returns a dispersion parameter (usually denoted α as in Hardin and Hilbe (2007)): such that the variance equals $\mu(1 + \alpha)$.

nbinom2 returns a dispersion parameter (usually denoted θ or k); in contrast to most other families, larger θ corresponds to a *lower* variance which is $\mu(1 + \mu/\theta)$.

Gamma Internally, glmmTMB fits Gamma responses by fitting a mean and a shape parameter; sigma is estimated as $(1/\sqrt{\text{shape}})$, which will typically be close (but not identical to) that estimated by `stats::sigma.default`, which uses $\sqrt{\text{deviance}/\text{df.residual}}$

beta returns the value of ϕ , where the conditional variance is $\mu(1 - \mu)/(1 + \phi)$ (i.e., increasing ϕ decreases the variance.) This parameterization follows Ferrari and Cribari-Neto (2004) (and the `betareg` package):

betabinomial This family uses the same parameterization (governing the Beta distribution that underlies the binomial probabilities) as beta.

genpois returns the index of dispersion ϕ^2 , where the variance is $\mu\phi^2$ (Consul & Famoye 1992)

compois returns the value of $1/\nu$. When $\nu = 1$, `compois` is equivalent to the Poisson distribution. There is no closed form equation for the variance, but it is approximately undersidpersed when $1/\nu < 1$ and approximately oversidpersed when $1/\nu > 1$. In this implementation, μ is exactly the mean (Huang 2017), which differs from the `COMPoissonReg` package (Sellers & Lotze 2015).

tweedie returns the value of ϕ , where the variance is $\phi\mu^p$. The value of p can be extracted using `family_params`

The most commonly used GLM families (binomial, poisson) have fixed dispersion parameters which are internally ignored.

References

- Consul PC, and Famoye F (1992). "Generalized Poisson regression model. Communications in Statistics: Theory and Methods" 21:89–109.
- Ferrari SLP, Cribari-Neto F (2004). "Beta Regression for Modelling Rates and Proportions." *J. Appl. Stat.* 31(7), 799-815.
- Hardin JW & Hilbe JM (2007). "Generalized linear models and extensions." Stata press.
- Huang A (2017). "Mean-parametrized Conway–Maxwell–Poisson regression models for dispersed counts. " *Statistical Modelling* 17(6), 1-22.
- Sellers K & Lotze T (2015). "COMpoissonReg: Conway-Maxwell Poisson (COM-Poisson) Regression". R package version 0.3.5. <https://CRAN.R-project.org/package=COMpoissonReg>

simulate.glmTMB

Simulate from a glmTMB fitted model

Description

Simulate from a glmTMB fitted model

Usage

```
## S3 method for class 'glmTMB'
simulate(object, nsim = 1, seed = NULL, ...)
```

Arguments

object	glmTMB fitted model
nsim	number of response lists to simulate. Defaults to 1.
seed	random number seed
...	extra arguments

Details

Random effects are also simulated from their estimated distribution. Currently, it is not possible to condition on estimated random effects.

Value

returns a list of vectors. The list has length nsim. Each simulated vector of observations is the same size as the vector of response variables in the original data set. In the binomial family case each simulation is a two-column matrix with success/failure.

simulate_new	<i>Simulate from covariate/metadata in the absence of a real data set (EXPERIMENTAL)</i>
--------------	--

Description

See vignette("sim", package = "glmmTMB") for more details and examples, and vignette("covstruct", package = "glmmTMB") for more information on the parameterization of different covariance structures.

Usage

```
simulate_new(
  object,
  nsim = 1,
  seed = NULL,
  newdata,
  newparams,
  ...,
  show_pars = FALSE
)
```

Arguments

object	a <i>one-sided</i> model formula (e.g. $\sim a + b + c$ (peculiar naming is for consistency with the generic function, which typically takes a fitted model object))
nsim	number of simulations
seed	random-number seed
newdata	a data frame containing all variables listed in the formula, <i>including</i> the response variable (which needs to fall within the domain of the conditional distribution, and should probably not be all zeros, but whose value is otherwise irrelevant)
newparams	a list of parameters containing sub-vectors (beta, betazi, betad, theta, etc.) to be used in the model
...	other arguments to glmmTMB (e.g. family)
show_pars	(logical) print structure of parameter vector and stop without simulating?

Examples

```
## use Salamanders data for structure/covariates
simulate_new(~ mined + (1|site),
             zi = ~ mined,
             newdata = Salamanders, show_pars = TRUE)
sim_count <- simulate_new(~ mined + (1|site),
                          newdata = Salamanders,
                          zi = ~ mined,
                          family = nbinom2,
```

```

newparams = list(beta = c(2, 1),
                 betazi = c(-0.5, 0.5), ## logit-linear model for zi
                 betad = log(2), ## log(NB dispersion)
                 theta = log(1)) ## log(among-site SD)
)
head(sim_count[[1]])

```

terms.glmTMB	<i>Methods for extracting developer-level information from glmTMB models</i>
--------------	--

Description

Methods for extracting developer-level information from glmTMB models

Usage

```

## S3 method for class 'glmTMB'
terms(x, component = "cond", part = "fixed", ...)

## S3 method for class 'glmTMB'
model.matrix(object, component = "cond", part = "fixed", ...)

```

Arguments

x	a fitted glmTMB object
component	model component ("cond", "zi", or "disp"; not all models contain all components)
part	whether to return results for the fixed or random effect part of the model (at present only part="fixed" is implemented for most methods)
...	additional arguments (ignored or passed to model.frame)
object	a fitted glmTMB object

up2date	<i>conditionally update glmTMB object fitted with an old TMB version</i>
---------	--

Description

conditionally update glmTMB object fitted with an old TMB version
 Load data from system file, updating glmTMB objects

Usage

```

up2date(oldfit)

gt_load(fn, verbose = FALSE, mustWork = FALSE)

```

Arguments

oldfit	a fitted glmmTMB object
fn	partial path to system file (e.g. test_data/foo.rda)
verbose	print names of updated objects?
mustWork	fail if file not found?

vcov.glmmTMB

*Calculate Variance-Covariance Matrix for a Fitted glmmTMB model***Description**

Calculate Variance-Covariance Matrix for a Fitted glmmTMB model

Usage

```
## S3 method for class 'glmmTMB'
vcov(object, full = FALSE, include_mapped = FALSE, ...)
```

Arguments

object	a “glmmTMB” fit
full	return a full variance-covariance matrix?
include_mapped	include mapped variables? (these will be given variances and covariances of NA)
...	ignored, for method compatibility

Value

By default (`full==FALSE`), a list of separate variance-covariance matrices for each model component (conditional, zero-inflation, dispersion). If `full==TRUE`, a single square variance-covariance matrix for *all* top-level model parameters (conditional, dispersion, and variance-covariance parameters)

`weights.glmTMB`*Extract weights from a glmTMB object*

Description

Extract weights from a glmTMB object

Usage

```
## S3 method for class 'glmTMB'  
weights(object, type = "prior", ...)
```

Arguments

<code>object</code>	a fitted glmTMB object
<code>type</code>	weights type
<code>...</code>	additional arguments (not used; for methods compatibility)

Details

At present only explicitly specified *prior weights* (i.e., weights specified in the `weights` argument) can be extracted from a fitted model.

- Unlike other GLM-type models such as `glm` or `glmer`, `weights()` does not currently return the total number of trials when binomial responses are specified as a two-column matrix.
- Since glmTMB does not fit models via iteratively weighted least squares, working weights (see `weights.glm`) are unavailable.

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