

Package ‘glmmTMB’

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Title Generalized Linear Mixed Models using Template Model Builder

Version 1.1.2.2

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 (>= 1.7.14), lme4 (>= 1.1-18.9000), Matrix, nlme, numDeriv

LinkingTo TMB, RcppEigen

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VignetteBuilder knitr

URL <https://github.com/glmmTMB/glmmTMB>

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BugReports <https://github.com/glmmTMB/glmmTMB/issues>

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Anova.glmmTMB	<i>Downstream methods</i>
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Description

Methods have been written that allow `glmmTMB` 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 `glmmTMB` model.

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
- the `effects` package computes graphical tabular effect displays (only for the fixed effects of the conditional component)

Usage

```
Anova.glmmTMB(
  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")
<code>vcov.</code>	variance-covariance matrix (usually extracted automatically)
<code>singular.ok</code>	OK to do ANOVA with singular models (unused) ?

... Additional parameters that may be supported by the method.
 focal.predictors
 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.glmTMB(model, ...)`.

Examples

```
warp.lm <- glmTMB(breaks ~ wool * tension, data = warpbreaks)
salamander1 <- readRDS(system.file("example_files", "salamander1.rds", package="glmmTMB"))
if (require(emmeans)) {
  emmeans(warp.lm, poly ~ tension | wool)
  emmeans(salamander1, ~ mined, type="response")
  emmeans(salamander1, ~ mined, component="zi", type="response")
}
if (getRversion() >= "3.6.0") {
  if (require(car)) {
    Anova(warp.lm, type="III")
    Anova(salamander1)
    Anova(salamander1, component="zi")
  }
  if (require(effects)) {
    plot(allEffects(warp.lm))
    plot(allEffects(salamander1))
  }
}
```

confint.glmTMB

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,
  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 ?
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's for all parameters (including dispersion) ?
...	arguments may be passed to <code>profile.merMod</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 (see the

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,param="theta_") ## Wald/delta-method CIs
confint(model,param=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
)

```

Arguments

fit	a glmmTMB fit
eval_eps	numeric tolerance for 'bad' eigenvalues
evec_eps	numeric tolerance for 'bad' eigenvector elements
big_coef	numeric tolerance for large coefficients
big_sd_log10	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)
big_zstat	numeric tolerance for Z-statistic

check_coefs	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.)
check_zstats	identify parameters with unusually large Z-statistics (ratio of standard error to mean)? Identifies likely failures of Wald confidence intervals/p-values.
check_hessian	identify non-positive-definite Hessian components?
check_scales	identify predictors with unusually small or large scales?

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

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 <- glmTMB(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"])
  for(F in funs[is.na(match(funs, "getME"))]) {
    cat(sprintf("%s:\n----\n", F))
    r <- tryCatch( get(F)(fm), error=identity)
    if (inherits(r, "error")) cat("** Error:", r$message, "\n")
    else tryCatch( print(r) )
    cat(sprintf("---end{%s}-----\n\n", F))
  }
}
options(op)

```

findReTrmClasses

list of specials – taken from enum.R

Description

list of specials – taken from enum.R

Usage

findReTrmClasses()

`fitTMB`*Optimize a TMB model and package results*

Description

This function (called internally by `glmTMB`) runs the actual model optimization, after all of the appropriate structures have been set up. It can be useful to run `glmTMB` 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)
```

Arguments

`TMBStruc` a list contain

Examples

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

`fixef`*Extract fixed-effects estimates*

Description

Extract Fixed Effects

Usage

```
## S3 method for class 'glmTMB'
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 dispersion parameter
unlist(f1)
print.default(f1)
```

formatVC

Format the 'VarCorr' Matrix of Random Effects

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

<code>varcor</code>	a VarCorr (-like) matrix with attributes.
<code>digits</code>	the number of significant digits.
<code>comp</code>	character vector of length one or two indicating which columns out of "Variance" and "Std.Dev." should be shown in the formatted output.
<code>formatter</code>	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 varc.

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 glmTMB 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 glmTMB knows about</i>
-----------------	---

Description

List model options that glmTMB 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!)

<code>getME.glmTMB</code>	<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

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

See Also

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

<code>getReStruc</code>	<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(<code>glmmTMB:::valid_covs</code>) 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 <code>?glmmTMB</code>)
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)
```

Arguments

theta vector of internal correlation parameters

Details

This function follows the definition at http://kaskr.github.io/adcomp/classUNSTRUCTURED_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 function returns the elements of the lower triangle of the correlation matrix, in column-major order.

Value

a vector of correlation values

Examples

```
th0 <- 0.5
stopifnot(all.equal(get_cor(th0), th0/sqrt(1+th0^2)))
get_cor(c(0.5, 0.2, 0.5))
```

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 = na.fail,
  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 containing model variables. Not required, but strongly recommended: see
family	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 glmmTMB-specific families.
ziformula	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 formula (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>	how to handle missing values, see na.action and model.frame . From <code>lm</code> : "The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The 'factory-fresh' default is <code>na.omit</code> ."
<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>thetaf</code> (extra family parameters, e.g., shape for Tweedie models).
<code>map</code>	a list specifying which parameter values should be fixed to a constant value rather than estimated. <code>map</code> 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.
<code>sparseX</code>	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 <code>FALSE</code>

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)

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)

```

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)
)
```

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> .

Details

By default, `glmmTMB` uses the nonlinear optimizer `nlminb` 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.)

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

Setting `profile=TRUE` allows `glmTMB` 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` (`glmTMB` automatically handles output from `optim()`, by renaming the value component to `objective`)

Examples

```
## fit with default (nlnmb) 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(object)

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

Arguments

<code>object</code>	a fitted <code>glmTMB</code> object
<code>newresp</code>	a new response vector
<code>...</code>	additional arguments (for generic consistency; ignored)

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 `glmmTMB`, 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 <- glmmTMB(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")
  }

  ## 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")
```

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

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.
- 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.
- 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.
- Morris W (1997). "Disentangling Effects of Induced Plant Defenses and Food Quantity on Herbivores by Fitting Nonlinear Models." *American Naturalist* 150:299-327.
- 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>
- Sellers K & Shmueli G (2010) "A Flexible Regression Model for Count Data." *Annals of Applied Statistics* 4(2), 943–61. <https://doi.org/10.1214/09-AOAS306>.
- 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

numFactor

Factor with numeric interpretable levels.

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

Check OpenMP status

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

Begging by Owl Nestlings

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	<i>prediction</i>
----------------	-------------------

Description

prediction

Usage

```

## S3 method for class 'glmmTMB'
predict(
  object,
  newdata = NULL,
  newparams = NULL,
  se.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 glmmTMB object
newdata	new data for prediction

<code>newparams</code>	new parameters for prediction
<code>se.fit</code>	return the standard errors of the predicted values?
<code>re.form</code>	NULL to specify individual-level predictions; ~ 0 or NA to specify population-level predictions (i.e., setting all random effects to zero)
<code>allow.new.levels</code>	allow previously unobserved levels in random-effects variables? see details.
<code>type</code>	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 (gives an error for non-zero-inflated models) "zlink" predicted zero-inflation probability on the scale of the logit link function "disp" dispersion parameter however it is defined for that particular family as described in sigma.glmTMB
<code>zitype</code>	deprecated: formerly used to specify type of zero-inflation probability. Now synonymous with <code>type</code>
<code>na.action</code>	how to handle missing values in <code>newdata</code> (see na.action); the default (<code>na.pass</code>) is to predict NA
<code>fast</code>	predict without expanding memory (default is TRUE if <code>newdata</code> and <code>newparams</code> are NULL and population-level prediction is not being done)
<code>debug</code>	(logical) return the <code>TMBStruc</code> object that will be used internally for debugging?
<code>...</code>	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 <- glmTMB(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 glmTMB*

Description

Printing The Variance and Correlation Parameters of a glmTMB

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 print method.

profile.glmmTMB *Compute likelihood profiles for a fitted model*

Description

Compute likelihood profiles for a fitted model

Usage

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

Arguments

fitted	a fitted glmmTMB 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)
}
```

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"), ...)
```

Arguments

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

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

*Extract residual standard deviation or dispersion parameter***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(deviance/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 the internal function `glmmTMB:::tweedie_power`.

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.

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

Description

Methods for extracting developer-level information from glmmTMB models

Usage

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

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

Arguments

x	a fitted glmmTMB 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 <code>model.frame</code>)
object	a fitted glmmTMB object

vcov.glmmTMB	<i>Calculate Variance-Covariance Matrix for a Fitted glmmTMB model</i>
--------------	--

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	<i>Extract weights from a glmTMB object</i>
----------------	---

Description

Extract weights from a glmTMB object

Usage

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

Arguments

object	a fitted glmTMB object
type	weights type
...	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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