Package ‘broom.mixed’

October 12, 2022

Type Package

Title Tidying Methods for Mixed Models

Version 0.2.9.4

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Description Convert fitted objects from various R mixed-model packages
into tidy data frames along the lines of the 'broom' package.
The package provides three
S3 generics for each model: tidy(), which summarizes a model's statistical findings such as
coefficients of a regression; augment(), which adds columns to the original
data such as predictions, residuals and cluster assignments; and glance(), which
provides a one-row summary of model-level statistics.

Imports broom, coda, dplyr, forcats, methods, nlme, purrr, stringr,
tibble, tidyr, furrr

Suggests brms, dotwhisker, knitr, testthat, gamlss, gamlss.data,
ggplot2, GLMMadaptive, glmmADMB, glmmTMB, lmerTest, lme4,
Matrix, MCMCglmm, mgcv, pander, pbkrtest, rstan, rstanarm,
rstantools, R2jags, TMB, rmarkdown

URL https://github.com/bbolker/broom.mixed

BugReports https://github.com/bbolker/broom.mixed/issues

License GPL-3

Encoding UTF-8

Additional_repositories http://bbolker.github.io/drat

VignetteBuilder knitr

RoxygenNote 7.1.2

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-04-17 17:42:29 UTC

R topics documented:

`augment.ranef.mer` *Augmentation for random effects (for caterpillar plots etc.)*

Description

Augmentation for random effects (for caterpillar plots etc.)

Usage

```
## S3 method for class 'ranef.mer'
augment(x, ci.level = 0.9, reorder = TRUE, order.var = 1, ...)
```

Arguments

x	ranef (conditional mode) information from an lme4 fit, using `ranef(.,condVar=TRUE)`
ci.level	level for confidence intervals
reorder	reorder levels by conditional mode values?
order.var	numeric or character: which variable to use for ordering levels?
...	additional arguments (unused: for generic consistency)

Examples

```
if (require("lme4")) {
   load(system.file("extdata","lme4_example.rda",package="broom.mixed"))
   rr <- ranef(lmm1,condVar=TRUE)
   aa <- broom::augment(rr)
   ## Q-Q plot:
   if (require(ggplot2) && require(dplyr)) {
      g0 <- ggplot(aa,aes(estimate,qq,xmin=lb,xmax=ub))+
          geom_errorbarh(height=0)+
          geom_point()+facet_wrap(~variable,scale="free_x")
      ## regular caterpillar plot:
      g1 <- ggplot(aa,aes(estimate,level,xmin=lb,xmax=ub))+
         geom_errorbarh(height=0)+
         geom_vline(xintercept=0,lty=2)+
         geom_point()+facet_wrap(~variable,scale="free_x")
      ## emphasize extreme values
      aa2 <- group_by(aa,grp,level)
      aa3 <- mutate(aa2, keep=any(estimate/std.error>2))
      ## Update caterpillar plot with extreme levels highlighted
      ##  (highlight all groups with *either* extreme intercept *or*
      ##   extreme slope)
      ggplot(aa3, aes(estimate,level,xmin=lb,xmax=ub,colour=factor(keep)))+
         geom_errorbarh(height=0)+
         geom_vline(xintercept=0,lty=2)+
         geom_point()+facet_wrap(~variable,scale="free_x")+
         scale_colour_manual(values=c("black","red"), guide=FALSE)
   }
}
```

---

brms_tidiers *Tidying methods for a brms model*

Description

These methods tidy the estimates from brmsfit-objects (fitted model objects from the **brms** package) into a summary.

Usage

```
## S3 method for class 'brmsfit'
tidy(
  x,
  parameters = NA,
  effects = c("fixed", "ran_pars"),
  robust = FALSE,
  conf.int = TRUE,
  conf.level = 0.95,
  conf.method = c("quantile", "HPDinterval"),
  fix.intercept = TRUE,
  exponentiate = FALSE,
  ...
)

## S3 method for class 'brmsfit'
glance(x, looic = FALSE, ...)

## S3 method for class 'brmsfit'
augment(x, data = stats::model.frame(x), newdata = NULL, se.fit = TRUE, ...)
```

Arguments

`x`	Fitted model object from the **brms** package. See `brmsfit-class`.
`parameters`	Names of parameters for which a summary should be returned, as given by a character vector or regular expressions. If `NA` (the default) summarized parameters are specified by the `effects` argument.
`effects`	A character vector including one or more of `"fixed"`, `"ran_vals"`, or `"ran_pars"`. See the Value section for details.
`robust`	Whether to use median and median absolute deviation of the posterior distribution, rather than mean and standard deviation, to derive point estimates and uncertainty
`conf.int`	If `TRUE` columns for the lower (`conf.low`) and upper bounds (`conf.high`) of posterior uncertainty intervals are included.
`conf.level`	Defines the range of the posterior uncertainty conf.int, such that `100 * conf.level%` of the parameter's posterior distributio lies within the corresponding interval. Only used if `conf.int = TRUE`.
`conf.method`	method for computing confidence intervals ("quantile" or "HPDinterval")
`fix.intercept`	rename "Intercept" parameter to "(Intercept)", to match behaviour of other model types?
`exponentiate`	whether to exponentiate the fixed-effect coefficient estimates and confidence intervals (common for logistic regression); if `TRUE`, also scales the standard errors by the exponentiated coefficient, transforming them to the new scale
`...`	Extra arguments, not used
`looic`	Should the LOO Information Criterion (and related info) be included? See `loo.stanfit` for details. (This can be slow for models fit to large datasets.)

data	data frame
newdata	new data frame
se.fit	return standard errors of fit?

Value

All tidying methods return a `data.frame` without rownames. The structure depends on the method chosen.

When `parameters` = `NA`, the `effects` argument is used to determine which parameters to summarize.

Generally, `tidy.brmsfit` returns one row for each coefficient, with at least three columns:

term	The name of the model parameter.
estimate	A point estimate of the coefficient (mean or median).
std.error	A standard error for the point estimate (sd or mad).

When `effects` = `"fixed"`, only population-level effects are returned.

When `effects` = `"ran_vals"`, only group-level effects are returned. In this case, two additional columns are added:

group	The name of the grouping factor.
level	The name of the level of the grouping factor.

Specifying `effects` = `"ran_pars"` selects the standard deviations and correlations of the group-level parameters.

If `conf.int` = `TRUE`, columns for the `lower` and `upper` bounds of the posterior conf.int computed.

Note

The names 'fixed', 'ran_pars', and 'ran_vals' (corresponding to "non-varying", "hierarchical", and "varying" respectively in previous versions of the package), while technically inappropriate in a Bayesian setting where "fixed" and "random" effects are not well-defined, are used for compatibility with other (frequentist) mixed model types.

At present, the components of parameter estimates are separated by parsing the column names of `as_draws` (e.g. `r_patient[1,Intercept]` for the random effect on the intercept for patient 1, or `b_Trt1` for the fixed effect `Trt1`. We try to detect underscores in parameter names and warn, but detection may be imperfect.

See Also

`brms`, `brmsfit-class`

Examples

```
 ## original model
 ## Not run:
    brms_crossedRE <- brm(mpg ~ wt + (1|cyl) + (1+wt|gear), data = mtcars,
           iter = 500, chains = 2)

## End(Not run)
 if (.Platform$OS.type!="windows" && require("brms")) {
   ## too slow on Windows, skip (>5 seconds on r-devel-windows)
   ## load stored object
   load(system.file("extdata", "brms_example.rda", package="broom.mixed"))

   fit <- brms_crossedRE
   tidy(fit)
   tidy(fit, parameters = "^sd_", conf.int = FALSE)
   tidy(fit, effects = "fixed", conf.method="HPDinterval")
   tidy(fit, effects = "ran_vals")
   tidy(fit, effects = "ran_pars", robust = TRUE)
   # glance method
   glance(fit)
   ## this example will give a warning that it should be run with
   ## reloo=TRUE; however, doing this will fail
   ## because the \code{fit} object has been stripped down to save space
   suppressWarnings(glance(fit, looic = TRUE, cores = 1))
   head(augment(fit))
}
```

compact *Remove NULL items in a vector or list*

Description

Remove NULL items in a vector or list

Usage

```
compact(x)
```

Arguments

x	a vector or list

fixef.MCMCglmm — *Extract fixed effects from an* `MCMCglmm` *object*

Description

Function designed to extract the fixed effects from an `MCMCglmm` model object. Can either extract all samples from the fixed effects posteriors or return the posterior means.

Usage

```
## S3 method for class 'MCMCglmm'
fixef(object, use = c("all", "mean"), ...)
```

Arguments

`object`	An `MCMCglmm` model object to extract the effects from
`use`	A character string indicating whether to extract all posterior samples or the mean of the posteriors. Defaults to "all".
`...`	Arguments passed on to the worker function.

Value

A matrix of the fixed effects

See Also

`ranef.MCMCglmm`

Examples

```
## Not run:
  # a simple MCMCglmm model
  data(PlodiaPO)
  m <- MCMCglmm(PO ~ 1, random= ~ FSfamily, data=PlodiaPO, verbose=FALSE)

  # only extract average fixed effects
  fixef(m, use = "mean")

  # histogram of posterior samples of fixed effects
  hist(fixef(m))
  # matches the mean
  rowMeans(fixef(m))

## End(Not run)
```

gamlss_tidiers *Tidying methods for gamlss objects*

Description

Tidying methods for "gamlss" objects from the gamlss package.

Usage

```
## S3 method for class 'gamlss'
tidy(x, quick = FALSE, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

`x`	A "gamlss" object
`quick`	Whether to perform a fast version, and return only the coefficients
`conf.int`	whether to return confidence intervals
`conf.level`	confidence level for CI
`...`	arguments passed to `confint.gamlss`

Value

All tidying methods return a data.frame without rownames, whose structure depends on the method chosen.

A tibble with one row for each coefficient, containing columns:

`parameter`	type of coefficient being estimated: `mu`, `sigma`, `nu`, or `tau`
`term`	term in the model being estimated and tested
`estimate`	estimated coefficient
`std.error`	standard error
`statistic`	t-statistic
`p.value`	two-sided p-value

Examples

```
if (requireNamespace("gamlss", quietly = TRUE) &&
    requireNamespace("gamlss.data", quietly = TRUE)) {
    data(abdom, package="gamlss.data")
    ## Not run:
         mod <- gamlss(y~pb(x), sigma.fo=~pb(x), family=BCT,
                       data=abdom, method=mixed(1,20))

## End(Not run)
    ## load stored object
    mod <- readRDS(system.file("extdata", "gamlss_example.rds",
                   package="broom.mixed"))
    tidy(mod)
}
```

---

get_methods — *Retrieve all method/class combinations currently provided by the broom.mixed package*

Description

Retrieve all method/class combinations currently provided by the broom.mixed package

Usage

```
get_methods()
```

Examples

```
print(get_methods(), n = Inf)
```

---

glmmadmb_tidiers — *Tidying methods for glmmADMB models*

Description

These methods tidy the coefficients of `glmmADMB` models

Usage

```
## S3 method for class 'glmmadmb'
tidy(
  x,
  effects = c("fixed", "ran_pars"),
  component = "cond",
  scales = NULL,
  ran_prefix = NULL,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = "Wald",
  ...
)

## S3 method for class 'glmmadmb'
augment(x, data = stats::model.frame(x), newdata, ...)

## S3 method for class 'glmmadmb'
glance(x, ...)
```

Arguments

`x`	An object of class `glmmadmb` `glmer`, or `nlmer`
`effects`	A character vector including one or more of "fixed" (fixed-effect parameters), "ran_pars" (variances and covariances or standard deviations and correlations of random effect terms) or "ran_vals" (conditional modes/BLUPs/latent variable estimates)
`component`	Which component(s) to report for (e.g., conditional, zero-inflation, dispersion: at present only works for "cond")
`scales`	scales on which to report the variables: for random effects, the choices are ‘"sdcor"’ (standard deviations and correlations: the default if `scales` is `NULL`) or ‘"varcov"’ (variances and covariances). `NA` means no transformation, appropriate e.g. for fixed effects; inverse-link transformations (exponentiation or logistic) are not yet implemented, but may be in the future.
`ran_prefix`	a length-2 character vector specifying the strings to use as prefixes for self- (variance/standard deviation) and cross- (covariance/correlation) random effects terms
`conf.int`	whether to include a confidence interval
`conf.level`	confidence level for CI
`conf.method`	method for computing confidence intervals (see `confint.merMod`)
`...`	extra arguments (not used)
`data`	original data this was fitted on; if not given this will attempt to be reconstructed
`newdata`	new data to be used for prediction; optional

Details

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

All tidying methods return a `tbl_df` without rownames. The structure depends on the method chosen.

`tidy` returns one row for each estimated effect, either with groups depending on the `effects` parameter. It contains the columns

`group`	the group within which the random effect is being estimated: `NA` for fixed effects
`level`	level within group (`NA` except for modes)
`term`	term being estimated
`estimate`	estimated coefficient
`std.error`	standard error

`statistic`	t- or Z-statistic (`NA` for modes)
`p.value`	P-value computed from t-statistic (may be missing/NA)

`augment` returns one row for each original observation, with columns (each prepended by a .) added. Included are the columns

`.fitted`	predicted values
`.resid`	residuals
`.fixed`	predicted values with no random effects

Also added for "merMod" objects, but not for "mer" objects, are values from the response object within the model (of type `lmResp`, `glmResp`, `nlsResp`, etc). These include `".mu",".offset", ".sqrtXwt", ".sqrtrwt", ".eta"`.

`glance` returns one row with the columns

`sigma`	the square root of the estimated residual variance
`logLik`	the data's log-likelihood under the model
`AIC`	the Akaike Information Criterion
`BIC`	the Bayesian Information Criterion
`deviance`	deviance

See Also

na.action

Examples

```
if (require("glmmADMB") && require("lme4")) {
    ## original model
    ## Not run:
        data("sleepstudy", package="lme4")
        lmm1 <- glmmadmb(Reaction ~ Days + (Days | Subject), sleepstudy,
                         family="gaussian")

## End(Not run)
    ## load stored object
    load(system.file("extdata","glmmADMB_example.rda",package="broom.mixed"))
    tidy(lmm1, effects = "fixed")
    tidy(lmm1, effects = "fixed", conf.int=TRUE)
    ## tidy(lmm1, effects = "fixed", conf.int=TRUE, conf.method="profile")
    ## tidy(lmm1, effects = "ran_vals", conf.int=TRUE)
    head(augment(lmm1, sleepstudy))
    glance(lmm1)

    glmm1 <- glmmadmb(cbind(incidence, size - incidence) ~ period + (1 | herd),
                 data = cbpp, family = "binomial")
    tidy(glmm1)
    tidy(glmm1, effects = "fixed")
    head(augment(glmm1, cbpp))
    glance(glmm1)

}
```

glmmTMB_tidiers *Tidying methods for glmmTMB models*

Description

These methods tidy the coefficients of mixed effects models, particularly responses of the `merMod` class

Usage

```
## S3 method for class 'glmmTMB'
tidy(
  x,
  effects = c("ran_pars", "fixed"),
  component = c("cond", "zi"),
  scales = NULL,
  ran_prefix = NULL,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = "Wald",
  exponentiate = FALSE,
  ...
)

## S3 method for class 'glmmTMB'
augment(x, data = stats::model.frame(x), newdata = NULL, ...)

## S3 method for class 'glmmTMB'
glance(x, ...)
```

Arguments

`x`	An object of class `merMod`, such as those from `lmer`, `glmer`, or `nlmer`
`effects`	A character vector including one or more of "fixed" (fixed-effect parameters), "ran_pars" (variances and covariances or standard deviations and correlations of random effect terms) or "ran_vals" (conditional modes/BLUPs/latent variable estimates)
`component`	which component to extract (e.g. `cond` for conditional effects (i.e., traditional fixed effects); `zi` for zero-inflation model; `disp` for dispersion model
`scales`	scales on which to report the variables: for random effects, the choices are ‘"sdcor"’ (standard deviations and correlations: the default if `scales` is `NULL`) or ‘"varcov"’ (variances and covariances). `NA` means no transformation, appropriate e.g. for fixed effects; inverse-link transformations (exponentiation or logistic) are not yet implemented, but may be in the future.

`ran_prefix`	a length-2 character vector specifying the strings to use as prefixes for self- (variance/standard deviation) and cross- (covariance/correlation) random effects terms
`conf.int`	whether to include a confidence interval
`conf.level`	confidence level for CI
`conf.method`	method for computing confidence intervals (see `confint.merMod`)
`exponentiate`	whether to exponentiate the fixed-effect coefficient estimates and confidence intervals (common for logistic regression); if `TRUE`, also scales the standard errors by the exponentiated coefficient, transforming them to the new scale
`...`	extra arguments (not used)
`data`	original data this was fitted on; if not given this will attempt to be reconstructed
`newdata`	new data to be used for prediction; optional

Details

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

All tidying methods return a `tibble`. The structure depends on the method chosen.

`tidy` returns one row for each estimated effect, either with groups depending on the `effects` parameter. It contains the columns

`group`	the group within which the random effect is being estimated: `NA` for fixed effects
`level`	level within group (`NA` except for modes)
`term`	term being estimated
`estimate`	estimated coefficient
`std.error`	standard error
`statistic`	t- or Z-statistic (`NA` for modes)
`p.value`	P-value computed from t-statistic (may be missing/NA)

`augment` returns one row for each original observation, with columns (each prepended by a .) added. Included are the columns

`.fitted`	predicted values
`.resid`	residuals
`.fixed`	predicted values with no random effects

`glance` returns one row with the columns

`sigma`	the square root of the estimated residual variance

`logLik`	the data's log-likelihood under the model
`AIC`	the Akaike Information Criterion
`BIC`	the Bayesian Information Criterion
`deviance`	deviance

Note

zero-inflation parameters (including the intercept) are reported on the logit scale

See Also

na.action

Examples

```
if (require("glmmTMB") && require("lme4")
    ## &&
    ## make sure package versions are OK
    ## checkDepPackageVersion(dep_pkg = "TMB",
    ##                        this_pkg = "glmmTMB",
    ##                         warn = FALSE) &&
    ## checkDepPackageVersion(dep_pkg = "Matrix",
    ##                        this_pkg = "TMB",
    ##                       warn = FALSE)
)
{
    data("sleepstudy",package="lme4")
    ## original model:
    ## Not run:
        lmm1 <- glmmTMB(Reaction ~ Days + (Days | Subject), sleepstudy)

## End(Not run)
    ## load stored object
    L <- load(system.file("extdata","glmmTMB_example.rda",package="broom.mixed"))
    for (obj in L) {
       assign(obj, glmmTMB::up2date(get(obj)))
    }
    tidy(lmm1)
    tidy(lmm1, effects = "fixed")
    tidy(lmm1, effects = "fixed", conf.int=TRUE)
    tidy(lmm1, effects = "fixed", conf.int=TRUE, conf.method="uniroot")
    ## FIX: tidy(lmm1, effects = "ran_vals", conf.int=TRUE)
    head(augment(lmm1, sleepstudy))
    glance(lmm1)

    ## original model:
    ##  glmm1 <- glmmTMB(incidence/size ~ period + (1 | herd),
    ##                   data = cbpp, family = binomial, weights=size)
    tidy(glmm1)
    tidy(glmm1, effects = "fixed")
    tidy(glmm1, effects = "fixed", exponentiate=TRUE)
    tidy(glmm1, effects = "fixed", conf.int=TRUE, exponentiate=TRUE)
    head(augment(glmm1, cbpp))
    head(augment(glmm1, cbpp, type.residuals="pearson"))
    glance(glmm1)
## Not run:
    ## profile CIs - a little bit slower but more accurate
   tidy(glmm1, effects = "fixed", conf.int=TRUE, exponentiate=TRUE, conf.method="profile")

## End(Not run)
}
```

`insert_NAs` *insert a row of NAs into a data frame wherever another data frame has NAs*

Description

insert a row of NAs into a data frame wherever another data frame has NAs

Usage

```
insert_NAs(x, original)
```

Arguments

`x`	data frame that has one row for each non-NA row in original
`original`	data frame with NAs

`lme4_tidiers` *Tidying methods for mixed effects models*

Description

These methods tidy the coefficients of `lme4::lmer` and `lme4::glmer` models (i.e., `merMod` objects). Methods are also provided for `allFit` objects.

Usage

```
## S3 method for class 'merMod'
tidy(
  x,
  effects = c("ran_pars", "fixed"),
  scales = NULL,
  exponentiate = FALSE,
  ran_prefix = NULL,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = "Wald",
  ddf.method = NULL,
  profile = NULL,
  debug = FALSE,
  ...
)

## S3 method for class 'rlmerMod'
tidy(
  x,
  effects = c("ran_pars", "fixed"),
  scales = NULL,
  exponentiate = FALSE,
  ran_prefix = NULL,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = "Wald",
  ddf.method = NULL,
  profile = NULL,
  debug = FALSE,
  ...
)

## S3 method for class 'merMod'
augment(x, data = stats::model.frame(x), newdata, ...)

## S3 method for class 'merMod'
glance(x, ...)
```

Arguments

`x`	An object of class `merMod`, such as those from `lmer`, `glmer`, or `nlmer`
`effects`	A character vector including one or more of "fixed" (fixed-effect parameters); "ran_pars" (variances and covariances or standard deviations and correlations of random effect terms); "ran_vals" (conditional modes/BLUPs/latent variable estimates); or "ran_coefs" (predicted parameter values for each group, as returned by `coef.merMod`)
`scales`	scales on which to report the variables: for random effects, the choices are ‘"sdcor"’ (standard deviations and correlations: the default if `scales` is `NULL`) or ‘"vcov"’ (variances and covariances). `NA` means no transformation, appropriate e.g. for fixed effects.
`exponentiate`	whether to exponentiate the fixed-effect coefficient estimates and confidence intervals (common for logistic regression); if `TRUE`, also scales the standard errors by the exponentiated coefficient, transforming them to the new scale
`ran_prefix`	a length-2 character vector specifying the strings to use as prefixes for self- (variance/standard deviation) and cross- (covariance/correlation) random effects terms

`conf.int`	whether to include a confidence interval
`conf.level`	confidence level for CI
`conf.method`	method for computing confidence intervals (see `lme4::confint.merMod`)
`ddf.method`	the method for computing the degrees of freedom and t-statistics (only applicable when using the **lmerTest** package: see `summary.lmerModLmerTest`
`profile`	pre-computed profile object, for speed when using `conf.method="profile"`
`debug`	print debugging output?
`...`	Additional arguments (passed to `confint.merMod` for `tidy`; `augment_columns` for `augment`; ignored for `glance`)
`data`	original data this was fitted on; if not given this will attempt to be reconstructed
`newdata`	new data to be used for prediction; optional

Details

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

All tidying methods return a `data.frame` without rownames. The structure depends on the method chosen.

`tidy` returns one row for each estimated effect, either with groups depending on the `effects` parameter. It contains the columns

`group`	the group within which the random effect is being estimated: `"fixed"` for fixed effects
`level`	level within group (`NA` except for modes)
`term`	term being estimated
`estimate`	estimated coefficient
`std.error`	standard error
`statistic`	t- or Z-statistic (`NA` for modes)
`p.value`	P-value computed from t-statistic (may be missing/NA)

`augment` returns one row for each original observation, with columns (each prepended by a .) added. Included are the columns

`.fitted`	predicted values
`.resid`	residuals
`.fixed`	predicted values with no random effects

Also added for "merMod" objects, but not for "mer" objects, are values from the response object within the model (of type `lmResp`, `glmResp`, `nlsResp`, etc). These include `".mu",".offset", ".sqrtXwt", ".sqrtrwt", ".eta"`.

`glance` returns one row with the columns

`nobs`	the number of observations
`sigma`	the square root of the estimated residual variance
`logLik`	the data's log-likelihood under the model
`AIC`	the Akaike Information Criterion
`BIC`	the Bayesian Information Criterion
`deviance`	deviance

See Also

na.action

Examples

```
if (require("lme4")) {
    ## original model
    ## Not run:
        lmm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)

## End(Not run)
    ## load stored object
    load(system.file("extdata", "lme4_example.rda", package="broom.mixed"))
    (tt <- tidy(lmm1))
    tidy(lmm1, effects = "fixed")
    tidy(lmm1, effects = "fixed", conf.int=TRUE)
    tidy(lmm1, effects = "fixed", conf.int=TRUE, conf.method="profile")
    ## lmm1_prof <- profile(lmm1) # generated by extdata/runexamples
    tidy(lmm1, conf.int=TRUE, conf.method="profile", profile=lmm1_prof)
    ## conditional modes (group-level deviations from population-level estimate)
    tidy(lmm1, effects = "ran_vals", conf.int=TRUE)
    ## coefficients (group-level estimates)
    (rcoef1 <- tidy(lmm1, effects = "ran_coefs"))
    if (require(tidyr) && require(dplyr)) {
       ## reconstitute standard coefficient-by-level table
       spread(rcoef1,key=term,value=estimate)
       ## split ran_pars into type + term; sort fixed/sd/cor
       (tt %>% separate(term,c("type","term"),sep="__",fill="left")
           %>% arrange(!is.na(type),desc(type)))
    }
    head(augment(lmm1, sleepstudy))
    glance(lmm1)

    glmm1 <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
                  data = cbpp, family = binomial)
    tidy(glmm1)
    tidy(glmm1,exponentiate=TRUE)
    tidy(glmm1, effects = "fixed")
    ## suppress warning about influence.merMod
    head(suppressWarnings(augment(glmm1, cbpp)))
    glance(glmm1)

    startvec <- c(Asym = 200, xmid = 725, scal = 350)
    nm1 <- nlmer(circumference ~ SSlogis(age, Asym, xmid, scal) ~ Asym|Tree,
                  Orange, start = startvec)
    ## suppress warnings about var-cov matrix ...
    op <- options(warn=-1)
    tidy(nm1)
    tidy(nm1, effects = "fixed")
    options(op)
    head(augment(nm1, Orange))
    glance(nm1)
    detach("package:lme4")
}
if (require("lmerTest")) {
   lmm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
   tidy(lmm1)
   glance(lmm1)
   detach("package:lmerTest")  # clean up
}
```

nlme_tidiers *Tidying methods for mixed effects models*

Description

These methods tidy the coefficients of mixed effects models of the lme class from functions of the nlme package.

Usage

```
## S3 method for class 'lme'
tidy(
  x,
  effects = c("var_model", "ran_pars", "fixed"),
  scales = NULL,
  conf.int = FALSE,
  conf.level = 0.95,
  ...
)

## S3 method for class 'lme'
augment(x, data = x$data, newdata, ...)

## S3 method for class 'lme'
```

```
glance(x, ...)

## S3 method for class 'gls'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)

## S3 method for class 'gls'
augment(x, data = nlme::getData(x), newdata, ...)
```

Arguments

`x`	An object of class `lme`, such as those from `lme` or `nlme`
`effects`	One or more of "var_model", "ran_pars", "fixed", "ran_vals", and/or "ran_coefs".
`scales`	scales on which to report the variables: for random effects, the choices are ‘"sdcor"’ (standard deviations and correlations: the default if `scales` is `NULL`) or ‘"vcov"’ (variances and covariances). `NA` means no transformation, appropriate e.g. for fixed effects.
`conf.int`	whether to include a confidence interval
`conf.level`	confidence level for CI
`...`	extra arguments (not used)
`data`	original data this was fitted on; if not given this will attempt to be reconstructed
`newdata`	new data to be used for prediction; optional

Details

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

All tidying methods return a `data.frame` without rownames. The structure depends on the method chosen.

`tidy` returns one row for each estimated effect, either random or fixed depending on the `effects` parameter. If `effects = "ran_vals"` (or `"ran_pars"`), it contains the columns

`group`	the group within which the random effect is being estimated
`level`	level within group
`term`	term being estimated
`estimate`	estimated coefficient
`estimated`	This column is only included if some parameters are fixed. TRUE if the residual error is estimated and FALSE if the residual error is fixed.

If `effects="fixed"`, `tidy` returns the columns

`term`	fixed term being estimated
`estimate`	estimate of fixed effect
`std.error`	standard error
`statistic`	t-statistic
`p.value`	P-value computed from t-statistic

If `effects="var_model"` (the `weights` argument to the model), `tidy` returns the columns defined in the help for `tidy.varFunc`.

`augment` returns one row for each original observation, with columns (each prepended by a .) added. Included are the columns

`.fitted`	predicted values
`.resid`	residuals
`.fixed`	predicted values with no random effects

`glance` returns one row with the columns

`sigma`	the square root of the estimated residual variance
`logLik`	the data's log-likelihood under the model
`AIC`	the Akaike Information Criterion
`BIC`	the Bayesian Information Criterion
`deviance`	returned as NA. To quote Brian Ripley on R-help `https://stat.ethz.ch/pipermail/r-help/2006-May/104744.html`, "McCullagh & Nelder (1989) would be the authorative [sic] reference, but the 1982 first edition manages to use 'deviance' in three separate senses on one page."

See Also

na.action

Examples

```
if (require("nlme") && require("lme4")) {
    data("sleepstudy", package="lme4")
    ## original model
    ## Not run: 
         lmm1 <- lme(Reaction ~ Days, random=~ Days|Subject, sleepstudy)

## End(Not run)
    ## load stored object
    load(system.file("extdata","nlme_example.rda", package="broom.mixed"))
    tidy(lmm1)
    tidy(lmm1, effects = "fixed")
    tidy(lmm1, conf.int = TRUE)
    tidy(lmm1, effects = "ran_pars")
    tidy(lmm1, effects = "ran_vals")
    tidy(lmm1, effects = "ran_coefs")
    head(augment(lmm1, sleepstudy))
    glance(lmm1)

    startvec <- c(Asym = 200, xmid = 725, scal = 350)
    nm1 <- nlme(circumference ~ SSlogis(age, Asym, xmid, scal),
                  data = Orange,
                  fixed = Asym + xmid + scal ~1,
                  random = Asym ~1,
                  start = startvec)
    tidy(nm1)
    tidy(nm1, effects = "fixed")
    head(augment(nm1, Orange))
    glance(nm1)

    gls1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
                         correlation = corAR1(form = ~ 1 | Mare))
    tidy(gls1)
    glance(gls1)
    head(augment(gls1))
}
```

---

ranef.MCMCglmm *Extract random effects from an* MCMCglmm *object*

Description

Function designed to extract the random effects from an MCMCglmm model object. Can either extract all samples from the random effects posteriors or return the posterior means.

Usage

```
## S3 method for class 'MCMCglmm'
ranef(object, use = c("all", "mean"), ...)
```

Arguments

object	An MCMCglmm model object to extract the effects from
use	A character string indicating whether to extract all posterior samples or the mean of the posteriors. Defaults to "all".
...	Arguments passed on to the worker function.

Value

A matrix of the fixed effects

See Also

fixef.MCMCglmm

Examples

```
## Not run:
  # a simple MCMCglmm model
  data(PlodiaPO)
  m <- MCMCglmm(PO ~ 1, random= ~ FSfamily, data=PlodiaPO, pr=TRUE, verbose=FALSE)

  # only extract average fixed effects
  head(ranef(m, use = "mean"))

  # histogram of posterior samples of fixed effects
  hist(ranef(m)[1, ])
  # matches the mean
  rowMeans(ranef(m)[1:6, ])

## End(Not run)
```

`ranefLevels` *Extract the levels of factors used for random effects in* `MCMCglmm` *objects*

Description

Extract the levels of factors used for random effects in `MCMCglmm` objects

Usage

```
ranefLevels(object, data, ...)
```

Arguments

`object`	An `MCMCglmm` model object
`data`	The dataset used for the model
`...`	Not currently used

See Also

`paramNamesMCMCglmm`, `ranef.MCMCglmm`

Examples

```
## Not run:
  # a simple MCMCglmm model
  data(PlodiaPO)
  m <- MCMCglmm(PO ~ 1, random = ~ FSfamily, data = PlodiaPO, verbose=FALSE)

  # extract the random effects levels
  ranefLevels(m, PlodiaPO)

## End(Not run)
```

rstanarm_tidiers *Tidying methods for an rstanarm model*

Description

These methods tidy the estimates from `rstanarm` fits (`stan_glm`, `stan_glmer`, etc.) into a summary.

Usage

```
## S3 method for class 'stanreg'
tidy(
  x,
  effects = "fixed",
  conf.int = FALSE,
  conf.level = 0.9,
  conf.method = c("quantile", "HPDinterval"),
  ...
)

## S3 method for class 'stanreg'
glance(x, looic = FALSE, ...)
```

Arguments

`x`	Fitted model object from the **rstanarm** package. See `stanreg-objects`.
`effects`	A character vector including one or more of `"fixed"`, `"ran_vals"`, or `"ran_pars"`. See the Value section for details.
`conf.int`	If `TRUE` columns for the lower (`conf.low`) and upper (`conf.high`) bounds of the `100*prob%` posterior uncertainty intervals are included. See `posterior_interval` for details.
`conf.level`	See `posterior_interval`.
`conf.method`	method for computing confidence intervals ("quantile" or "HPDinterval")
`...`	For `glance`, if `looic=TRUE`, optional arguments to `loo.stanfit`.
`looic`	Should the LOO Information Criterion (and related info) be included? See `loo.stanfit` for details. (This can be slow for models fit to large datasets.)

Value

All tidying methods return a `data.frame` without rownames. The structure depends on the method chosen.

When `effects="fixed"` (the default), `tidy.stanreg` returns one row for each coefficient, with three columns:

`term`	The name of the corresponding term in the model.

`estimate`	A point estimate of the coefficient (posterior median).
`std.error`	A standard error for the point estimate based on `mad`. See the *Uncertainty estimates* section in `print.stanreg` for more details.

For models with group-specific parameters (e.g., models fit with `stan_glmer`), setting `effects="ran_vals"` selects the group-level parameters instead of the non-varying regression coefficients. Addtional columns are added indicating the `level` and `group`. Specifying `effects="ran_pars"` selects the standard deviations and (for certain models) correlations of the group-level parameters.

Setting `effects="auxiliary"` will select parameters other than those included by the other options. The particular parameters depend on which **rstanarm** modeling function was used to fit the model. For example, for models fit using `stan_glm` the overdispersion parameter is included if `effects="aux"`, for `stan_lm` the auxiliary parameters include the residual SD, R^2, and log(fit_ratio), etc.

`glance` returns one row with the columns

`algorithm`	The algorithm used to fit the model.
`pss`	The posterior sample size (except for models fit using optimization).
`nobs`	The number of observations used to fit the model.
`sigma`	The square root of the estimated residual variance, if applicable. If not applicable (e.g., for binomial GLMs), `sigma` will be given the value `1` in the returned object.

If `looic=TRUE`, then the following additional columns are also included:

`looic`	The LOO Information Criterion.
`elpd_loo`	The expected log predictive density (`elpd_loo` = `-2` * `looic`).
`p_loo`	The effective number of parameters.

See Also

`summary,stanfit-method`

Examples

```
if (require("rstanarm")) {
## Not run:
#'     ## original model
    fit <- stan_glmer(mpg ~ wt + (1|cyl) + (1+wt|gear), data = mtcars,
                      iter = 300, chains = 2)

## End(Not run)
## load example data
fit <- readRDS(system.file("extdata", "rstanarm_example.rds", package="broom.mixed"))

  # non-varying ("population") parameters
  tidy(fit, conf.int = TRUE, prob = 0.5)
  tidy(fit, conf.int = TRUE, conf.method = "HPDinterval", prob = 0.5)
  # hierarchical sd & correlation parameters
  tidy(fit, effects = "ran_pars")

  # group-specific deviations from "population" parameters
  tidy(fit, effects = "ran_vals")

  # glance method
   glance(fit)
  ## Not run:
     glance(fit, looic = TRUE, cores = 1)

## End(Not run)
} ## if require("rstanarm")
```

`stdranef` *Extract standard deviation of "random" effects from an* `MCMCglmm` *object*

Description

Function designed to extract the standard deviation of the random effects from an `MCMCglmm` model object. Note that this is not the same as the posterior distribution of (co)variance matrices. It is based on the posterior distribution of the random effects. This also means it requires `pr=TRUE` to be set in the model for the information to be saved. Can optionally return standard deviation of random effects after back transforming to the response metric. Currently probabilities, but only for ordinal family models (`family="ordinal"`).

Usage

```
stdranef(object, which, type = c("lp", "response"), ...)
```

Arguments

`object`	An `MCMCglmm` model object to extract the effects from
`which`	A list of random effects to extract or their numeric positions If there are two numbers in a list, effects are simulataneous.
`type`	A character string indicating whether to calculate the standard deviation on the linear predictor metric, 'lp' or response, 'response'.
`...`	Not currently used.

Value

A list of class postMCMCglmmRE with means (`M`) and individual estimates (`Data`)

Examples

```
## Not run:
  # a simple MCMCglmm model
  data(PlodiaPO)
  PlodiaPO <- within(PlodiaPO, {
    PO2 <- cut(PO, quantile(PO, c(0, .33, .66, 1)))
    plate <- factor(plate)
  })

  m <- MCMCglmm(PO2 ~ 1, random = ~ FSfamily + plate,
    family = "ordinal", data = PlodiaPO,
    prior = list(
      R = list(V = 1, fix = 1),
      G = list(
        G1 = list(V = 1, nu = .002),
        G2 = list(V = 1, nu = .002)
      )
    ), verbose=FALSE, thin=1, pr=TRUE)

  # summary of the model
  summary(m)

  # examples of extracting standard deviations of
  # different random effects on the linear predictor metric
  # or after transformation to probabilities (only for ordinal)
  stdranef(m, which = list(1), type = "lp")
  stdranef(m, which = list(2), type = "lp")
  stdranef(m, which = list(1, 2, c(1, 2)), type = "lp")
  stdranef(m, type = "lp")

  ## error because no 3rd random effect
  #stdranef(m, which = list(1, 2, 3), type = "lp")

  stdranef(m, which = list("FSfamily", "plate"), type = "lp")

  # mean standard deviations on the probability metric
  # also the full distributions, if desired in the Data slot.
  res <- stdranef(m, type = "response")
  res$M # means
  hist(res$Data$FSfamily[, 1]) # histogram

## End(Not run)
```

`tidy.MCMCglmm` *Tidying methods for MCMC (Stan, JAGS, etc.) fits*

Description

Tidying methods for MCMC (Stan, JAGS, etc.) fits

Usage

```
## S3 method for class 'MCMCglmm'
tidy(x, effects = c("fixed", "ran_pars"), scales = NULL, ...)

tidyMCMC(
  x,
  pars,
  robust = FALSE,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = c("quantile", "HPDinterval"),
  drop.pars = c("lp__", "deviance"),
  rhat = FALSE,
  ess = FALSE,
  index = FALSE,
  ...
)

## S3 method for class 'rjags'
tidy(
  x,
  robust = FALSE,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = "quantile",
  ...
)

## S3 method for class 'stanfit'
tidy(
  x,
  pars,
  robust = FALSE,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = c("quantile", "HPDinterval"),
  drop.pars = c("lp__", "deviance"),
  rhat = FALSE,
  ess = FALSE,
  index = FALSE,
  ...
)

## S3 method for class 'mcmc'
tidy(
  x,
  pars,
  robust = FALSE,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = c("quantile", "HPDinterval"),
  drop.pars = c("lp__", "deviance"),
  rhat = FALSE,
  ess = FALSE,
  index = FALSE,
  ...
)

## S3 method for class 'mcmc.list'
tidy(
  x,
  pars,
  robust = FALSE,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = c("quantile", "HPDinterval"),
  drop.pars = c("lp__", "deviance"),
  rhat = FALSE,
  ess = FALSE,
  index = FALSE,
  ...
)
```

Arguments

`x`	a model fit to be converted to a data frame
`effects`	which effects (fixed, random, etc.) to return
`scales`	scales on which to report results
`...`	mostly unused; for `tidy.MCMCglmm`, these represent options passed through to `tidy.mcmc` (e.g. `robust`, `conf.int`, `conf.method`, ...)
`pars`	(character) specification of which parameters to include
`robust`	use mean and standard deviation (if FALSE) or median and mean absolute deviation (if TRUE) to compute point estimates and uncertainty?
`conf.int`	(logical) include confidence interval?
`conf.level`	probability level for CI
`conf.method`	method for computing confidence intervals ("quantile" or "HPDinterval")
`drop.pars`	Parameters not to include in the output (such as log-probability information)
`rhat, ess`	(logical) include Rhat and/or effective sample size estimates?
`index`	Add index column, remove index from term. For example, `term a[13]` becomes `term a` and `index 13`.

Examples

```
if (require("MCMCglmm")) {
  ## original model
  ## Not run:
      mm0 <- MCMCglmm(Reaction ~ Days,
                 random = ~Subject, data = sleepstudy,
                 nitt=4000,
                 pr = TRUE
             )

## End(Not run)
   ## load stored object
   load(system.file("extdata","MCMCglmm_example.rda",
                                   package="broom.mixed"))
   tidy(mm0)
   tidy(mm1)
   tidy(mm2)
   tail(tidy(mm0,effects="ran_vals"))
}

# Using example from "RStan Getting Started"
# https://github.com/stan-dev/rstan/wiki/RStan-Getting-Started

model_file <- system.file("extdata", "8schools.stan", package = "broom.mixed")
schools_dat <- list(J = 8,
                    y = c(28,  8, -3,  7, -1,  1, 18, 12),
                    sigma = c(15, 10, 16, 11,  9, 11, 10, 18))
## original model
## Not run:
    set.seed(2015)
    rstan_example <- rstan::stan(file = model_file, data = schools_dat,
                         iter = 1000, chains = 2, save_dso = FALSE)

## End(Not run)
if (require(rstan)) {
   ## load stored object
  rstan_example <- readRDS(system.file("extdata", "rstan_example.rds", package = "broom.mixed"))
   tidy(rstan_example)
   tidy(rstan_example, conf.int = TRUE, pars = "theta")
   td_mean <- tidy(rstan_example, conf.int = TRUE)
   td_median <- tidy(rstan_example, conf.int = TRUE, robust = TRUE)

   if (require(dplyr) && require(ggplot2)) {
       tds <- (dplyr::bind_rows(list(mean=td_mean, median=td_median), .id="method")
          %>% mutate(type=ifelse(grepl("^theta",term),"theta",
            ifelse(grepl("^eta",term),"eta",
                  "other")))
      )

     ggplot(tds, aes(estimate, term)) +
      geom_errorbarh(aes(xmin = conf.low, xmax = conf.high),height=0) +
      geom_point(aes(color = method))+
      facet_wrap(~type,scale="free",ncol=1)
 } ## require(dplyr,ggplot2)
} ## require(rstan)
if (require(R2jags)) {
   ## see help("jags",package="R2jags")
   ## and  example("jags",package="R2jags")
   ## for details
   ## load stored object
  R2jags_example <- readRDS(system.file("extdata", "R2jags_example.rds", package = "broom.mixed"))
   tidy(R2jags_example)
   tidy(R2jags_example, conf.int=TRUE, conf.method="quantile")
}
```

tidy.TMB *Tidying methods for TMB models*

Description

Tidying methods for TMB models

Usage

```
## S3 method for class 'TMB'
tidy(
  x,
  effects = c("fixed", "random"),
  conf.int = FALSE,
  conf.level = 0.95,
  conf.method = c("wald", "uniroot", "profile"),
  ...
)
```

Arguments

`x`	An object of class `TMB` (you may need to use `class(obj) <- "TMB"` on your results from TMB)
`effects`	which effects should be returned?
`conf.int`	whether to include a confidence interval
`conf.level`	confidence level for CI
`conf.method`	method for computing confidence intervals
`...`	additional arguments passed to confint function (tmbroot, tmbprofile)

Examples

```
if (require("TMB")) {

    ## Not run:
       runExample("simple",thisR=TRUE)
       class(obj) <- "TMB"
       tidy(obj,conf.int=TRUE,conf.method="wald")

## End(Not run)
    ## Not run: tidy(obj,conf.int=TRUE,conf.method="uniroot")
    ## Not run: tidy(obj,conf.int=TRUE,conf.method="profile")
}
```

`tidy.varFunc` *Tidy variance structure for the* `nlme` *package.*

Description

Returns a tibble with the following columns:

- grouptype of varFunc, along with the right hand side of the formula in parentheses e.g. `"varExp(age | Sex)"`.
- termterms included in the formula of the variance model, specifically the names of the coefficients. If the value is fixed, it will be appended with `" ; fixed"`.
- estimateestimated coefficient
- estimatedThis column is only included if some parameters are fixed. TRUE if the parameter is estimated and FALSE if the parameter is fixed.

Usage

```
## S3 method for class 'varFunc'
tidy(x, ...)

## S3 method for class 'varComb'
tidy(x, ...)
```

Arguments

`x`	An object of class `varFunc`, such as those used as the `weights` argument from the `nlme` package
`...`	Ignored

Value

If the `varFunc` is uninitialized or has no parameters, the function will return an empty tibble. Otherwise, it will return a tibble with names described in the details section.

Examples

```
## Not run:
if (require("nlme")) {
ChickWeight_arbitrary_group <- datasets::ChickWeight
ChickWeight_arbitrary_group$group_arb_n <-
  1 + (
    as.integer(ChickWeight_arbitrary_group$Chick) >
    median(as.integer(ChickWeight_arbitrary_group$Chick))
  )
ChickWeight_arbitrary_group$group_arb <- c("low", "high")[ChickWeight_arbitrary_group$group_arb_n]

fit_with_fixed <-
  lme(
    weight ~ Diet * Time,
    random = ~Time | Chick,
    data =ChickWeight_arbitrary_group,
    weights=varIdent(fixed=c("low"=5), form=~1|group_arb)
  )
# Show all parameters
tidy(fit_with_fixed)
# Exclude fixed parameters
tidy(fit_with_fixed) %>%
  filter(across(any_of("estimated"), ~.x))
}

## End(Not run)
```

---

unrowname *strip rownames from an object*

Description

strip rownames from an object

Usage

```
unrowname(x)
```

Arguments

x	a data frame

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