Package ‘insight’

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Type Package

Title Easy Access to Model Information for Various Model Objects

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Maintainer Daniel Lüdecke <d.luedecke@uke.de>

Description A tool to provide an easy, intuitive and consistent access to information contained in various R models, like model formulas, model terms, information about random effects, data that was used to fit the model or data from response variables. ‘insight’ mainly revolves around two types of functions: Functions that find (the names of) information, starting with ‘find_’, and functions that get the underlying data, starting with ‘get_’. The package has a consistent syntax and works with many different model objects, where otherwise functions to access these information are missing.

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URL https://easystats.github.io/insight/

BugReports https://github.com/easystats/insight/issues

Depends R (>= 3.4)

Imports methods, stats, utils

Suggests AER, afex, aod, BayesFactor, bayestestR, bbmle, bdsmatrix, betareg, bife, biglm, blavaan, blme, boot, brms, censReg, cgam, clubSandwich, coxme, cplm, crch, datawizard, effectsize, emmeans, epiR, estimatr, feisr, fixest, fungible, gam, gamlss, gamm4, gbm, gee, geepack, GLMMadaptive, glmmTMB, gmln, gt, htr, ivreg, JM, knitr, lavaan, lfe, lme4, lme4test, logistf, MASS, Matrix, mclust, MCMCglmm, merTools, metaBMA, mgcv, mice, mlogit, multgee, nlme, mnet, nonnest2, ordinal, panelr, parameters, parsnip, performance, plm, poorman, pscl, psych, quantreg, rmarkdown, rms, robustbase, robustlmm, rstanarm (>= 2.21.1), rstantools, rstudioapi, sandwich, speedglm, spelling, splines, statmod, survey, survival, testthat, tripack, truncreg, VGAM

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Author Daniel Lüdecke [aut, cre] (<https://orcid.org/0000-0002-8895-3206>, @strengejacke),
Dominique Makowski [aut, ctb] (<https://orcid.org/0000-0001-5375-9967>, @Dom_Makowski),
Indrajeet Patil [aut, ctb] (<https://orcid.org/0000-0003-1995-6531>, @patilindrajeets),
Philip Waggoner [aut, ctb] (<https://orcid.org/0000-0002-7825-7573>),
Mattan S. Ben-Shachar [aut, ctb] (<https://orcid.org/0000-0002-4287-4801>),
Brenton M. Wiernik [aut] (<https://orcid.org/0000-0001-9560-6336>, @bmwiernik),
Vincent Arel-Bundock [ctb] (<https://orcid.org/0000-0003-2042-7063>),
Alex Hayes [rev] (<https://orcid.org/0000-0002-4985-5160>)

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R topics documented:

all_models_equal ................................................. 4
check_if_installed .............................................. 5
clean_names ...................................................... 6
clean_parameters ................................................ 7
color_if ............................................................ 8
display ............................................................ 10
download_model ................................................... 11
ellipsis_info ...................................................... 12
export_table ....................................................... 13
find_algorithm .................................................... 16
find_formula ....................................................... 17
find_interactions ................................................ 18
find_offset ......................................................... 19
find_parameters .................................................. 20
find_parameters.averaging ....................................... 21
find_parameters.betamfx ......................................... 21
find_parameters.BGGM ........................................... 24
find_parameters.emmGrid ......................................... 27
find_parameters.gamlss .......................................... 27
find_parameters.glmmTMB ........................................ 29
find_parameters.zeroinfl ........................................ 30
find_predictors .................................................... 31
find_random ........................................................ 32
R topics documented:

find_random_slopes .................................................. 33
find_response .......................................................... 34
find_smooth .............................................................. 35
find_statistic ............................................................ 36
find_terms ................................................................. 36
findTransformation .................................................... 38
find_variables ............................................................ 38
find_weights ............................................................... 40
fish .......................................................... 41
format_bf ................................................................. 41
format_capitalize ......................................................... 42
format_ci ................................................................. 43
format_message .......................................................... 44
format_number ............................................................ 45
format_p ................................................................. 46
format_pd ................................................................. 47
format_rope ............................................................... 48
format_string ............................................................ 48
format_table ............................................................. 49
format_value .............................................................. 51
get_auxiliary ............................................................ 53
get_call ................................................................. 54
get_data ................................................................. 55
get_datagrid ............................................................. 58
get_deviance .............................................................. 60
get_df ................................................................. 61
get_family ............................................................... 62
get_intercept ............................................................. 62
get_loglikelihood ........................................................ 63
get_modelmatrix .......................................................... 64
get_parameters ........................................................... 65
get_parameters.betamfx .................................................. 66
get_parameters.betareg ................................................... 67
get_parameters.BGGM .................................................... 68
get_parameters.emmGrid .................................................. 72
get_parameters.gamm ...................................................... 73
get_parameters.glmm ..................................................... 74
get_parameters.htest ...................................................... 75
get_parameters.zeroinfl .................................................. 76
get_predicted ............................................................. 77
get_predicted_ci ........................................................... 80
get_predictors ........................................................... 83
get_priors ................................................................. 83
get_random ............................................................... 84
get_residuals .............................................................. 85
get_response ............................................................. 86
get_sigma ................................................................. 87
get_statistic .............................................................. 88
all_models_equal

Checks if all objects are models of same class

Description

Small helper that checks if all objects are supported (regression) model objects and of same class.

Usage

all_models_equal(..., verbose = FALSE)

all_models_same_class(..., verbose = FALSE)

Arguments

... A list of objects.

verbose Toggle off warnings.

Value

A logical, TRUE if x are all supported model objects of same class.
Examples

```r
if (require("lme4")) {
  data(mtcars)
  data(sleepstudy)

  m1 <- lm(mpg ~ wt + cyl + vs, data = mtcars)
  m2 <- lm(mpg ~ wt + cyl, data = mtcars)
  m3 <- lmer(Reaction ~ Days + (1 | Subject), data = sleepstudy)
  m4 <- glm(formula = vs ~ wt, family = binomial(), data = mtcars)

  all_models_same_class(m1, m2)
  all_models_same_class(m1, m2, m3)
  all_models_same_class(m1, m4, m2, m3, verbose = TRUE)
  all_models_same_class(m1, m4, mtcars, m2, m3, verbose = TRUE)
}
```

Description

Checking if needed package is installed

Usage

```r
check_if_installed(
  package,
  reason = "for this function to work",
  stop = TRUE,
  minimum_version = NULL,
  quietly = FALSE,
  ...
)
```

Arguments

- **package**: A character vector naming the package(s), whose installation needs to be checked in any of the libraries.
- **reason**: A phrase describing why the package is needed. The default is a generic description.
- **stop**: Logical that decides whether the function should stop if the needed package is not installed.
- **minimum_version**: String, representing the minimum package version that is required. If `NULL`, no check for minimum version is done. Note that `minimum_version` only works when package is of length 1.
quietly Logical, if TRUE, invisibly returns either TRUE if all packages are installed, FALSE otherwise, and does not stop or throw a warning. If quietly = TRUE, argument stop is ignored. Use this argument to internally check for package dependencies without stopping or warnings.

Value

If stop = TRUE, and package is not yet installed, the function stops and throws an error. Else, a named logical vector is returned, indicating which of the packages are installed, and which not.

Examples

```r
## Not run:
check_if_installed("inexistent_package")
check_if_installed("insight")
check_if_installed("insight", minimum_version = "99.8.7")

x <- check_if_installed(c("inexistent", "also_not_here"), stop = FALSE)
x
```

---

clean_names Get clean names of model terms

Description

This function "cleans" names of model terms (or a character vector with such names) by removing patterns like log() or as.factor() etc.

Usage

```r
clean_names(x, ...)
```

## S3 method for class 'character'
clean_names(x, include_names = FALSE, ...)

Arguments

- `x` A fitted model, or a character vector.
- `...` Currently not used.
- `include_names` Logical, if TRUE, returns a named vector where names are the original values of `x`.

Value

The "cleaned" variable names as character vector, i.e. pattern like `s()` for splines or `log()` are removed from the model terms.
Note

Typically, this method is intended to work on character vectors, in order to remove patterns that obscure the variable names. For convenience reasons it is also possible to call clean_names() also on a model object. If x is a regression model, this function is (almost) equal to calling find_variables(). The main difference is that clean_names() always returns a character vector, while find_variables() returns a list of character vectors, unless flatten = TRUE. See 'Examples'.

Examples

# example from ?stats::glm
counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome <- as.numeric(gl(3, 1, 9))
treatment <- gl(3, 3)
m <- glm(counts ~ log(outcome) + as.factor(treatment), family = poisson())
clean_names(m)

# difference "clean_names()" and "find_variables()"
if (require("lme4")) {
m <- glmer(
  cbind(incidence, size - incidence) ~ period + (1 | herd),
  data = cbpp,
  family = binomial
)

clean_names(m)
find_variables(m)
find_variables(m, flatten = TRUE)
}

---

clean_parameters  Get clean names of model parameters

Description

This function "cleans" names of model parameters by removing patterns like "r_" or "b[]" (mostly applicable to Stan models) and adding columns with information to which group or component parameters belong (i.e. fixed or random, count or zero-inflated...)

The main purpose of this function is to easily filter and select model parameters, in particular of - but not limited to - posterior samples from Stan models, depending on certain characteristics. This might be useful when only selective results should be reported or results from all parameters should be filtered to return only certain results (see print_parameters()).

Usage

clean_parameters(x, ...)

Arguments

x  A fitted model.
... Currently not used.

Details

The Effects column indicate if a parameter is a fixed or random effect. The Component can either be conditional or zero_inflated. For models with random effects, the Group column indicates the grouping factor of the random effects. For multivariate response models from brms or rstanarm, an additional Response column is included, to indicate which parameters belong to which response formula. Furthermore, Cleaned_Parameter column is returned that contains "human readable" parameter names (which are mostly identical to Parameter, except for for models from brms or rstanarm, or for specific terms like smooth- or spline-terms).

Value

A data frame with "cleaned" parameter names and information on effects, component and group where parameters belong to. To be consistent across different models, the returned data frame always has at least four columns Parameter, Effects, Component and Cleaned_Parameter. See 'Details'.

Examples

```r
## Not run:
library(brms)
model <- download_model("brms_zi_2")
clean_parameters(model)
## End(Not run)
```

Description

Convenient function that formats columns in data frames with color codes, where the color is chosen based on certain conditions. Columns are then printed in color in the console.

Usage

```r
color_if(
  x, 
columns, 
predicate = `>`, 
value = 0, 
color_if = "green", 
color_else = "red"),
```
color_if

digits = 2
)
colour_if(
x,
columns,
predicate = `>`,
value = 0,
colour_if = "green",
colour_else = "red",
digits = 2
)

Arguments

x A data frame

columns Character vector with column names of x that should be formatted.
predicate A function that takes columns and value as input and which should return TRUE
or FALSE, based on if the condition (in comparison with value) is met.
value The comparator. May be used in conjunction with predicate to quickly set
up a function which compares elements in columns to value. May be ignored
when predicate is a function that internally computes other comparisons. See
'Examples'.
color_if, colour_if

Character vector, indicating the color code used to format values in x that meet
the condition of predicate and value. May be one of "red", "yellow",
"green", "blue", "violet", "cyan" or "grey". Formatting is also possible
with "bold" or "italic".
color_else, colour_else

See color_if, but only for conditions that are not met.
digits Digits for rounded values.

Details

The predicate-function simply works like this: which(predicate(x[,columns],value))

Value

The .

Examples

# all values in Sepal.Length larger than 5 in green, all remaining in red
x <- colour_if(iris[1:10,], columns = "Sepal.Length", predicate = `>`,
value = 5)
x
cat(x$Sepal.Length)

# all levels "setosa" in Species in green, all remaining in red
x <- color_if(iris, columns = "Species", predicate = `==`, value = "setosa")
cat(x$Species)

# own function, argument "value" not needed here
p <- function(x, y) {
  x >= 4.9 & x <= 5.1
}
# all values in Sepal.Length between 4.9 and 5.1 in green, all remaining in red
x <- color_if(iris[1:10, ], columns = "Sepal.Length", predicate = p)
cat(x$Sepal.Length)

---

display

Generic export of data frames into formatted tables

Description

display() is a generic function to export data frames into various table formats (like plain text, markdown, ...). print_md() usually is a convenient wrapper for display(format = "markdown"). Similar, print_html() is a shortcut for display(format = "html"). See the documentation for the specific objects’ classes.

Usage

display(object, ...)

print_md(x, ...)

print_html(x, ...)

## S3 method for class 'data.frame'
display(object, format = "markdown", ...)

## S3 method for class 'data.frame'
print_md(x, ...)

## S3 method for class 'data.frame'
print_html(x, ...)

Arguments

object, x A data frame.

... Arguments passed to other methods.

format String, indicating the output format. Can be "markdown" or "html".

Value

Depending on format, either an object of class gt_tbl or a character vector of class knitr_kable.
**download_model**

Examples

display(iris[1:5, ])

---

**download_model**  
*Download circus models*

Description

Downloads pre-compiled models from the *circus*-repository. The *circus*-repository contains a variety of fitted models to help the systematic testing of other packages.

Usage

download_model(name, url = NULL)

Arguments

- **name**  
  Model name.

- **url**  
  String with the URL from where to download the model data. Optional, and should only be used in case the repository-URL is changing. By default, models are downloaded from https://raw.github.com/easystats/circus/master/data/.

Details

The code that generated the model is available at the [https://easystats.github.io/circus/reference/index.html](https://easystats.github.io/circus/reference/index.html).

Value

A model from the *circus*-repository.

References

[https://easystats.github.io/circus/](https://easystats.github.io/circus/)
Gather information about objects in ellipsis (dot dot dot)

**Description**

Provides information regarding the models entered in an ellipsis. It detects whether all are models, regressions, nested regressions etc., assigning different classes to the list of objects.

**Usage**

```r
ellipsis_info(objects, ...)
```

## Default S3 method:

```r
elements_info(..., only_models = TRUE)
```

**Arguments**

- `objects, ...` Arbitrary number of objects.
- `only_models` Only keep supported models (default to `TRUE`).

**Value**

The list with objects that were passed to the function, including additional information as attributes (e.g. if models have same response or are nested).

**Examples**

```r
m1 <- lm(Sepal.Length ~ Petal.Width + Species, data = iris)
m2 <- lm(Sepal.Length ~ Species, data = iris)
m3 <- lm(Sepal.Length ~ Petal.Width, data = iris)
m4 <- lm(Sepal.Length ~ 1, data = iris)
m5 <- lm(Petal.Width ~ 1, data = iris)

objects <- ellipsis_info(m1, m2, m3, m4)
class(objects)

objects <- ellipsis_info(m1, m2, m4)
attributes(objects)$is_nested

objects <- ellipsis_info(m1, m2, m5)
attributes(objects)$same_response
```
export_table

Data frame and Tables Pretty Formatting

Description

Data frame and Tables Pretty Formatting

Usage

export_table(
  x,
  sep = " | ",
  header = "=-",
  empty_line = NULL,
  digits = 2,
  protect_integers = TRUE,
  missing = " ",
  width = NULL,
  format = NULL,
  title = NULL,
  caption = title,
  subtitle = NULL,
  footer = NULL,
  align = NULL,
  group_by = NULL,
  zap_small = FALSE,
  table_width = NULL,
  verbose = TRUE
)

Arguments

x A data frame. May also be a list of data frames, to export multiple data frames into multiple tables.
sep Column separator.
header Header separator. Can be NULL.
empty_line Separator used for empty lines. If NULL, line remains empty (i.e. filled with whitespaces).
digits Number of digits for rounding or significant figures. May also be "signif" to return significant figures or "scientific" to return scientific notation. Control the number of digits by adding the value as suffix, e.g. digits = "scientific4" to have scientific notation with 4 decimal places, or digits = "signif5" for 5 significant figures (see also signif()).
protect_integers Should integers be kept as integers (i.e., without decimals)?
missing  Value by which NA values are replaced. By default, an empty string (i.e. ") is returned for NA.

width  Refers to the width of columns (with numeric values). Can be either NULL, a number or a named numeric vector. If NULL, the width for each column is adjusted to the minimum required width. If a number, columns with numeric values will have the minimum width specified in width. If a named numeric vector, value names are matched against column names, and for each match, the specified width is used (see 'Examples'). Only applies to text-format (see format).

format  Name of output-format, as string. If NULL (or "text"), returned output is used for basic printing. Can be one of NULL (the default) resp. "text" for plain text, "markdown" (or "md") for markdown and "html" for HTML output.

title, caption, subtitle  Table title (same as caption) and subtitle, as strings. If NULL, no title or subtitle is printed, unless it is stored as attributes (table_title, or its alias table_caption, and table_subtitle). If x is a list of data frames, caption may be a list of table captions, one for each table.

footer  Table footer, as string. For markdown-formatted tables, table footers, due to the limitation in markdown rendering, are actually just a new text line under the table. If x is a list of data frames, footer may be a list of table captions, one for each table.

align  Column alignment. For markdown-formatted tables, the default align = NULL will right-align numeric columns, while all other columns will be left-aligned. If format = "html", the default is left-align first column and center all remaining. May be a string to indicate alignment rules for the complete table, like "left", "right", "center" or "firstleft" (to left-align first column, center remaining); or maybe a string with abbreviated alignment characters, where the length of the string must equal the number of columns, for instance, align = "lccrl" would left-align the first column, center the second and third, right-align column four and left-align the fifth column. For HTML-tables, may be one of "center", "left" or "right".

group_by  Name of column in x that indicates grouping for tables. Only applies when format = "html". group_by is passed down to gt::gt(groupname_col = group_by).

zap_small  Logical, if TRUE, small values are rounded after digits decimal places. If FALSE, values with more decimal places than digits are printed in scientific notation.

table_width  Numeric, or "auto", indicating the width of the complete table. If table_width = "auto" and the table is wider than the current width (i.e. line length) of the console (or any other source for textual output, like markdown files), the table is split into two parts. Else, if table_width is numeric and table rows are larger than table_width, the table is split into two parts.

verbose  Toggle messages and warnings.

Value

A data frame in character format.
Note
The values for caption, subtitle and footer can also be provided as attributes of x, e.g. if
caption = NULL and x has attribute table_caption, the value for this attribute will be used as
table caption. table_subtitle is the attribute for subtitle, and table_footer for footer.

See Also
Vignettes Formatting, printing and exporting tables and Formatting model parameters.

Examples

export_table(head(iris))
export_table(head(iris), sep = " ", header = "*", digits = 1)

# split longer tables
export_table(head(iris), table_width = 30)

## Not run:
# colored footers
data(iris)
x <- as.data.frame(iris[1:5, ])
attr(x, "table_footer") <- c("This is a yellow footer line.", "yellow")
export_table(x)

attr(x, "table_footer") <- list(
  c("\nA yellow line", "yellow"),
  c("\nAnd a red line", "red"),
  c("\nAnd a blue line", "blue")
)
export_table(x)

attr(x, "table_footer") <- list(
  c("Without the ", "yellow"),
  c("new-line character ", "red"),
  c("we can have multiple colors per line.", "blue")
)
export_table(x)

## End(Not run)

# column-width
d <- data.frame(  
x = c(1, 2, 3),
y = c(100, 200, 300),
z = c(10000, 20000, 30000)
)
export_table(d)
export_table(d, width = 8)
export_table(d, width = c(x = 5, z = 10))
export_table(d, width = c(x = 5, y = 5, z = 10), align = "lcr")
find_algorithm

Find sampling algorithm and optimizers

Description

Returns information on the sampling or estimation algorithm as well as optimization functions, or for Bayesian model information on chains, iterations and warmup-samples.

Usage

find_algorithm(x, ...)

Arguments

x
A fitted model.

...  
Currently not used.

Value

A list with elements depending on the model.
For frequentist models:

- algorithm, for instance "OLS" or "ML"
- optimizer, name of optimizing function, only applies to specific models (like gam)

For frequentist mixed models:

- algorithm, for instance "REML" or "ML"
- optimizer, name of optimizing function

For Bayesian models:

- algorithm, the algorithm
- chains, number of chains
- iterations, number of iterations per chain
- warmup, number of warmups per chain

Examples

```r
if (require("lme4")) {
  data(sleepstudy)
  m <- lmer(Reaction ~ Days + (1 | Subject), data = sleepstudy)
  find_algorithm(m)
}
```

```r
## Not run:
library(rstanarm)
m <- stan_lmer(Reaction ~ Days + (1 | Subject), data = sleepstudy)
find_algorithm(m)
```

## End(Not run)
Description
Returns the formula(s) for the different parts of a model (like fixed or random effects, zero-inflated component, ...). formula_ok() checks if a model formula has valid syntax regarding writing TRUE instead of T inside poly() and that no data names are used (i.e. no data$variable, but rather variable).

Usage
find_formula(x, verbose = TRUE, ...)
formula_ok(x, verbose = TRUE, ...)

Arguments
x A fitted model.
verbose Toggle warnings.
... Currently not used.

Value
A list of formulas that describe the model. For simple models, only one list-element, conditional, is returned. For more complex models, the returned list may have following elements:

- conditional, the "fixed effects" part from the model (in the context of fixed-effects or instrumental variable regression, also called regressors). One exception are DirichletRegModel models from DirichletReg, which has two or three components, depending on model.
- random, the "random effects" part from the model (or the id for gee-models and similar)
- zero_inflated, the "fixed effects" part from the zero-inflation component of the model
- zero_inflated_random, the "random effects" part from the zero-inflation component of the model
- dispersion, the dispersion formula
- instruments, for fixed-effects or instrumental variable regressions like ivreg::ivreg(), lfe::felm() or plm::plm(), the instrumental variables
- cluster, for fixed-effects regressions like lfe::felm(), the cluster specification
- correlation, for models with correlation-component like nlme::gls(), the formula that describes the correlation structure
- slopes, for fixed-effects individual-slope models like feisr::feis(), the formula for the slope parameters
- precision, for DirichletRegModel models from DirichletReg, when parametrization (i.e. model) is "alternative".
Note
For models of class \texttt{lme} or \texttt{gls} the correlation-component is only returned, when it is explicitly defined as named argument (\texttt{form}), e.g. \texttt{corAR1(form = ~1 | Mare)}

Examples

data(mtcars)
m <- \texttt{lm(mpg ~ wt + cyl + vs, data = mtcars)}
find_formula(m)

if (require("lme4")){
m <- \texttt{lmer(Sepal.Length ~ Sepal.Width + (1 | Species), data = iris)}
f <- find_formula(m)
f
format(f)
}

\begin{verbatim}
find_interactions       Find interaction terms from models
\end{verbatim}

Description

Returns all lowest to highest order interaction terms from a model.

Usage

\begin{verbatim}
find_interactions(
x,
component = c("all", "conditional", "zi", "zero_inflated", "dispersion",
              "instruments"),
flatten = FALSE
)
\end{verbatim}

Arguments

- \texttt{x} \hspace{1cm} A fitted model.
- \texttt{component} \hspace{1cm} Should all predictor variables, predictor variables for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so called fixed-effects regressions). May be abbreviated. Note that the \textit{conditional} component is also called \textit{count} or \textit{mean} component, depending on the model.
- \texttt{flatten} \hspace{1cm} Logical, if \texttt{TRUE}, the values are returned as character vector, not as list. Duplicated values are removed.
find_offset

Find possible offset terms in a model

Value

A list of character vectors that represent the interaction terms. Depending on component, the returned list has following elements (or NULL, if model has no interaction term):

- conditional, interaction terms that belong to the "fixed effects" terms from the model
- zero_inflated, interaction terms that belong to the "fixed effects" terms from the zero-inflation component of the model
- instruments, for fixed-effects regressions like ivreg, felm or plm, interaction terms that belong to the instrumental variables

Examples

data(mtcars)

m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_interactions(m)

m <- lm(mpg ~ wt * cyl + vs * hp * gear + carb, data = mtcars)
find_interactions(m)

find_offset

Find possible offset terms in a model

Description

Returns a character vector with the name(s) of offset terms.

Usage

find_offset(x)

Arguments

x A fitted model.

Value

A character vector with the name(s) of offset terms.

Examples

# Generate some zero-inflated data
set.seed(123)
N <- 100 # Samples
x <- runif(N, 0, 10) # Predictor
off <- rgamma(N, 3, 2) # Offset variable
yhat <- -1 + x * 0.5 + log(off) # Prediction on log scale
dat <- data.frame(y = NA, x, logOff = log(off))
dat$y <- rpois(N, exp(yhat)) # Poisson process
dat$y <- ifelse(rbinom(N, 1, 0.3), 0, dat$y) # Zero-inflation process

if (require("pscl")) {
  m1 <- zeroinfl(y ~ offset(logOff) + x | 1, data = dat, dist = "poisson")
  find_offset(m1)

  m2 <- zeroinfl(y ~ x | 1, data = dat, offset = logOff, dist = "poisson")
  find_offset(m2)
}

---

find_parameters  

Find names of model parameters

**Description**

Returns the names of model parameters, like they typically appear in the summary() output. For Bayesian models, the parameter names equal the column names of the posterior samples after coercion from as.data.frame(). See the documentation for your object’s class:

- Bayesian models (**rstanarm, brms, MCMCglmm, ...**)
- Generalized additive models (**mgcv, VGAM, ...**)
- Marginal effects models (**mfx**)
- Estimated marginal means (**emmeans**)
- Mixed models (**lme4, glmmTMB, GLMMadaptive, ...**)
- Zero-inflated and hurdle models (**pscl, ...**)
- Models with special components (**betareg, MuMIn, ...**)

**Usage**

```r
find_parameters(x, ...)```

## Default S3 method:
```r
find_parameters(x, flatten = FALSE, verbose = TRUE, ...)
```

**Arguments**

- `x` A fitted model.
- `...` Currently not used.
- `flatten` Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.
- `verbose` Toggle messages and warnings.

**Value**

A list of parameter names. For simple models, only one list-element, `conditional`, is returned.
Examples

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_parameters(m)
```

Description

Returns the names of model parameters, like they typically appear in the `summary()` output.

Usage

```r
## S3 method for class 'averaging'
find_parameters(x, component = c("conditional", "full"), flatten = FALSE, ...)

## S3 method for class 'betareg'
find_parameters(
x,
  component = c("all", "conditional", "precision", "location", "distributional", "auxiliary"),
  flatten = FALSE,
...
)

## S3 method for class 'DirichletRegModel'
find_parameters(
x,
  component = c("all", "conditional", "precision", "location", "distributional", "auxiliary"),
  flatten = FALSE,
...
)

## S3 method for class 'mjoint'
find_parameters(
x,
  component = c("all", "conditional", "survival"),
  flatten = FALSE,
...
)

## S3 method for class 'glmx'
find_parameters(
x,
```
Arguments

x A fitted model.

component Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, the instrumental variables or marginal effects be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variables (so called fixed-effects regressions), or models with marginal effects from mfx. May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model. There are three convenient shortcuts: component = "all" returns all possible parameters. If component = "location", location parameters such as conditional, zero_inflated, smooth_terms, or instruments are returned (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters). For component = "distributional" (or "auxiliary"), components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

flatten Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.

... Currently not used.

Value

A list of parameter names. The returned list may have following elements:

• conditional, the "fixed effects" part from the model.
• full, parameters from the full model.

Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_parameters(m)

Description

Returns the names of model parameters, like they typically appear in the summary() output.
find_parameters.betamfx

Usage

## S3 method for class 'betamfx'
find_parameters(
  x,
  component = c("all", "conditional", "precision", "marginal", "location",
                 "distributional", "auxiliary"),
  flatten = FALSE,
  ...
)

## S3 method for class 'logitmfx'
find_parameters(
  x,
  component = c("all", "conditional", "marginal", "location"),
  flatten = FALSE,
  ...
)

Arguments

x
A fitted model.

component
Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, the instrumental variables or marginal effects be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variables (so called fixed-effects regressions), or models with marginal effects from mfx. May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model. There are three convenient shortcuts: component = "all" returns all possible parameters. If component = "location", location parameters such as conditional, zero_inflated, smooth_terms, or instruments are returned (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters). For component = "distributional" (or "auxiliary"), components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

flatten
Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.

...
Currently not used.

Value

A list of parameter names. The returned list may have following elements:

- conditional, the "fixed effects" part from the model.
- marginal, the marginal effects.
- precision, the precision parameter.
Examples

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_parameters(m)
```

---

### find_parameters.BGGM

*Find names of model parameters from Bayesian models*

**Description**

Returns the names of model parameters, like they typically appear in the `summary()` output. For Bayesian models, the parameter names equal the column names of the posterior samples after coercion from `as.data.frame()`.

**Usage**

```r
## S3 method for class 'BGGM'
find_parameters(
  x,
  component = c("correlation", "conditional", "intercept", "all"),
  flatten = FALSE,
  ...
)

## S3 method for class 'BFBayesFactor'
find_parameters(
  x,
  effects = c("all", "fixed", "random"),
  component = c("all", "extra"),
  flatten = FALSE,
  ...
)

## S3 method for class 'MCMCglmm'
find_parameters(x, effects = c("all", "fixed", "random"), flatten = FALSE, ...)

## S3 method for class 'bamlss'
find_parameters(
  x,
  flatten = FALSE,
  component = c("all", "conditional", "location", "distributional", "auxiliary"),
  parameters = NULL,
  ...
)

## S3 method for class 'brmsfit'
find_parameters(
```
find_parameters.BGGM

x,  
effects = "all",  
component = "all",  
flatten = FALSE,  
parameters = NULL,  
...  
)

## S3 method for class 'bayesx'
find_parameters(
  x,  
  component = c("all", "conditional", "smooth_terms"),  
  flatten = FALSE,  
  parameters = NULL,  
...  
)

## S3 method for class 'stanreg'
find_parameters(
  x,  
  effects = c("all", "fixed", "random"),  
  component = c("location", "all", "conditional", "smooth_terms", "sigma",  
  "distributional", "auxiliary"),  
  flatten = FALSE,  
  parameters = NULL,  
...  
)

## S3 method for class 'sim.merMod'
find_parameters(
  x,  
  effects = c("all", "fixed", "random"),  
  flatten = FALSE,  
  parameters = NULL,  
...  
)

Arguments

x A fitted model.

component Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, the instrumental variables or marginal effects be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variables (so called fixed-effects regressions), or models with marginal effects from mfx. May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model. There are three convenient shortcuts: component = "all" returns all possible parameters. If component = "location", ...
location parameters such as conditional, zero_inflated, smooth_terms, or instruments are returned (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters). For component = "distributional" (or "auxiliary"), components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

flatten Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.

effects Should parameters for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.

parameters Regular expression pattern that describes the parameters that should be returned.

Value

A list of parameter names. For simple models, only one list-element, conditional, is returned. For more complex models, the returned list may have following elements:

- conditional, the "fixed effects" part from the model
- random, the "random effects" part from the model
- zero_inflated, the "fixed effects" part from the zero-inflation component of the model
- zero_inflated_random, the "random effects" part from the zero-inflation component of the model
- smooth_terms, the smooth parameters

Furthermore, some models, especially from brms, can also return auxiliary parameters. These may be one of the following:

- sigma, the residual standard deviation (auxiliary parameter)
- dispersion, the dispersion parameters (auxiliary parameter)
- beta, the beta parameter (auxiliary parameter)
- simplex, simplex parameters of monotonic effects (brms only)
- mix, mixture parameters (brms only)
- shiftprop, shifted proportion parameters (brms only)

Examples

```R
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_parameters(m)
```
find_parameters.emmGrid

Find model parameters from estimated marginal means objects

Description

Returns the parameter names from a model.

Usage

## S3 method for class 'emmGrid'
find_parameters(x, flatten = FALSE, merge_parameters = FALSE, ...)

Arguments

x

A fitted model.

flatten

Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.

merge_parameters

Logical, if TRUE and x has multiple columns for parameter names (like emmGrid objects may have), these are merged into a single parameter column, with parameters names and values as values.

...

Currently not used.

Value

A list of parameter names. For simple models, only one list-element, conditional, is returned.

Examples

data(mtcars)
model <- lm(mpg ~ wt * factor(cyl), data = mtcars)
if (require("emmeans", quietly = TRUE)) {
  emm <- emmeans(model, c("wt", "cyl"))
  find_parameters(emm)
}

find_parameters.gamlss

Find names of model parameters from generalized additive models

Description

Returns the names of model parameters, like they typically appear in the summary() output.
Usage

```r
## S3 method for class 'gamlss'
find_parameters(x, flatten = FALSE, ...)

## S3 method for class 'gam'
find_parameters(
  x,
  component = c("all", "conditional", "smooth_terms", "location"),
  flatten = FALSE,
  ...
)
```

Arguments

- **x**: A fitted model.
- **flatten**: Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.
- **...**: Currently not used.
- **component**: Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, the instrumental variables or marginal effects be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variables (so called fixed-effects regressions), or models with marginal effects from mfx. May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model. There are three convenient shortcuts: component = "all" returns all possible parameters. If component = "location", location parameters such as conditional, zero_inflated, smooth_terms, or instruments are returned (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters). For component = "distributional" (or "auxiliary"), components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Value

A list of parameter names. The returned list may have following elements:

- conditional, the "fixed effects" part from the model.
- smooth_terms, the smooth parameters.

Examples

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_parameters(m)
```
find_parameters.glmmTMB

Find names of model parameters from mixed models

Description

Returns the names of model parameters, like they typically appear in the summary() output.

Usage

```r
## S3 method for class 'glmmTMB'
find_parameters(
x, 
effects = c("all", "fixed", "random"),
component = c("all", "conditional", "zi", "zero_inflated", "dispersion"),
flatten = FALSE,
...)
```

```r
## S3 method for class 'merMod'
find_parameters(x, effects = c("all", "fixed", "random"), flatten = FALSE, ...)
```

Arguments

- `x` A fitted model.
- `effects` Should parameters for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
- `component` Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model or the dispersion term? Applies to models with zero-inflated and/or dispersion formula. Note that the conditional component is also called count or mean component, depending on the model. There are three convenient shortcuts: component = "all" returns all possible parameters. If component = "location", location parameters such as conditional or zero_inflated are returned (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters). For component = "distributional" (or "auxiliary"), components like sigma or dispersion (and other auxiliary parameters) are returned.
- `flatten` Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.
- `...` Currently not used.

Value

A list of parameter names. The returned list may have following elements:

- conditional, the "fixed effects" part from the model.
• random, the "random effects" part from the model.
• zero_inflated, the "fixed effects" part from the zero-inflation component of the model.
• zero_inflated_random, the "random effects" part from the zero-inflation component of the model.
• dispersion, the dispersion parameters (auxiliary parameter)

Examples

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_parameters(m)
```

Description

Returns the names of model parameters, like they typically appear in the `summary()` output.

Usage

```r
## S3 method for class 'zeroinfl'
find_parameters(
x,
component = c("all", "conditional", "zi", "zero_inflated"),
flatten = FALSE,
...
)
```

```r
## S3 method for class 'mhurdle'
find_parameters(
x,
component = c("all", "conditional", "zi", "zero_inflated", "infrequent_purchase", "ip", "auxiliary"),
flatten = FALSE,
...
)
```

Arguments

- `x`: A fitted model.
- `component`: Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, the instrumental variables or marginal effects be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variables (so called...
find_predictors

fixed-effects regressions), or models with marginal effects from mfx. May be
abbreviated. Note that the conditional component is also called count or mean
component, depending on the model. There are three convenient shortcuts:
component = "all" returns all possible parameters. If component = "location",
location parameters such as conditional, zero_inflated, smooth_terms, or
instruments are returned (everything that are fixed or random effects - depend-
ing on the effects argument - but no auxiliary parameters). For component =
distributional" (or "auxiliary"), components like sigma, dispersion,
beta or precision (and other auxiliary parameters) are returned.

find_predictors

find_predictors
Find names of model predictors

value

A list of parameter names. The returned list may have following elements:
• conditional, the "fixed effects" part from the model.
• zero_inflated, the "fixed effects" part from the zero-inflation component of the model.

Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_parameters(m)

find_predictors(x, ...)

# Default S3 method:
find_predictors(
x,
effects = c("fixed", "random", "all"),
component = c("all", "conditional", "zi", "zero_inflated", "dispersion",
"instruments", "correlation", "smooth_terms"),
flatten = FALSE,
verbose = TRUE,
...)

Description

Returns the names of the predictor variables for the different parts of a model (like fixed or random
effects, zero-inflated component, ...). Unlike find_parameters(), the names from find_predictors()
match the original variable names from the data that was used to fit the model.

Usage

find_predictors(x, ...)

# Default S3 method:
find_predictors(
x,
effects = c("fixed", "random", "all"),
component = c("all", "conditional", "zi", "zero_inflated", "dispersion",
"instruments", "correlation", "smooth_terms"),
flatten = FALSE,
verbose = TRUE,
...)


find_random

Arguments

x A fitted model.

... Currently not used.
effects Should variables for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.

component Should all predictor variables, predictor variables for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so called fixed-effects regressions). May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model.

flatten Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.

verbose Toggle warnings.

Value

A list of character vectors that represent the name(s) of the predictor variables. Depending on the combination of the arguments effects and component, the returned list has following elements:

- conditional, the "fixed effects" terms from the model
- random, the "random effects" terms from the model
- zero_inflated, the "fixed effects" terms from the zero-inflation component of the model
- zero_inflated_random, the "random effects" terms from the zero-inflation component of the model
- dispersion, the dispersion terms
- instruments, for fixed-effects regressions like ivreg, felm or plm, the instrumental variables
- correlation, for models with correlation-component like gls, the variables used to describe the correlation structure

Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_predictors(m)

find_random Find names of random effects

Description

Return the name of the grouping factors from mixed effects models.
find_random_slopes

Usage

find_random(x, split_nested = FALSE, flatten = FALSE)

Arguments

x A fitted mixed model.

split_nested Logical, if TRUE, terms from nested random effects will be returned as separated elements, not as single string with colon. See 'Examples'.

flatten Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.

Value

A list of character vectors that represent the name(s) of the random effects (grouping factors). Depending on the model, the returned list has following elements:

- random, the "random effects" terms from the conditional part of model
- zero_inflated_random, the "random effects" terms from the zero-inflation component of the model

Examples

if (require("lme4")) {
  data(sleepstudy)
  sleepstudy$mygrp <- sample(1:5, size = 180, replace = TRUE)
  sleepstudy$mysubgrp <- NA
  for (i in 1:5) {
    filter_group <- sleepstudy$mygrp == i
    sleepstudy$mysubgrp[filter_group] <- 
      sample(1:30, size = sum(filter_group), replace = TRUE)
  }

  m <- lmer(
    Reaction ~ Days + (1 | mygrp / mysubgrp) + (1 | Subject),
    data = sleepstudy
  )

  find_random(m)
  find_random(m, split_nested = TRUE)
}

find_random_slopes Find names of random slopes

Description

Return the name of the random slopes from mixed effects models.
find_random_slopes(x)

Arguments

x

A fitted mixed model.

Value

A list of character vectors with the name(s) of the random slopes, or NULL if model has no random slopes. Depending on the model, the returned list has following elements:

• random, the random slopes from the conditional part of model
• zero_inflated_random, the random slopes from the zero-inflation component of the model

Examples

if (require("lme4")) {
  data(sleepstudy)
  m <- lmer(Reaction ~ Days + (1 + Days | Subject), data = sleepstudy)
  find_random_slopes(m)
}

find_response

Find name of the response variable

Description

Returns the name(s) of the response variable(s) from a model object.

Usage

find_response(x, combine = TRUE, ...)

Arguments

x

A fitted model.

combine

Logical, if TRUE and the response is a matrix-column, the name of the response matches the notation in formula, and would for instance also contain patterns like "cbind(...)". Else, the original variable names from the matrix-column are returned. See 'Examples'.

...

Currently not used.

Value

The name(s) of the response variable(s) from x as character vector, or NULL if response variable could not be found.
Examples

```r
if (require("lme4")) {
  data(cbpp)
  cbpp$trials <- cbpp$size - cbpp$incidence
  m <- glm(cbind(incidence, trials) ~ period, data = cbpp, family = binomial)

  find_response(m, combine = TRUE)
  find_response(m, combine = FALSE)
}
```

find_smooth

---

**find_smooth**  
*Find smooth terms from a model object*

Description

Return the names of smooth terms from a model object.

Usage

```r
find_smooth(x, flatten = FALSE)
```

Arguments

- `x`  
  A (gam) model.
- `flatten`  
  Logical, if `TRUE`, the values are returned as character vector, not as list. Duplicated values are removed.

Value

A character vector with the name(s) of the smooth terms.

Examples

```r
if (require("mgcv")) {
  data(iris)
  model <- gam(Petal.Length ~ Petal.Width + s(Sepal.Length), data = iris)
  find_smooth(model)
}
```
find_statistic  

Find statistic for model

**Description**

Returns the statistic for a regression model (t-statistic, z-statistic, etc.).

Small helper that checks if a model is a regression model object and return the statistic used.

**Usage**

```r
find_statistic(x, ...)
```

**Arguments**

- `x`  
  An object.
- `...`  
  Currently not used.

**Value**

A character describing the type of statistic. If there is no statistic available with a distribution, NULL will be returned.

**Examples**

```r
# regression model object
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
find_statistic(m)
```

find_terms  

Find all model terms

**Description**

Returns a list with the names of all terms, including response value and random effects, "as is". This means, on-the-fly tranformations or arithmetic expressions like log(), I(), as.factor() etc. are preserved.

**Usage**

```r
find_terms(x, flatten = FALSE, verbose = TRUE, ...)
```
Arguments

- **x**: A fitted model.
- **flatten**: Logical; if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.
- **verbose**: Toggle warnings.
- **...**: Currently not used.

Value

A list with (depending on the model) following elements (character vectors):

- **response**, the name of the response variable
- **conditional**, the names of the predictor variables from the *conditional* model (as opposed to the zero-inflated part of a model)
- **random**, the names of the random effects (grouping factors)
- **zero_inflated**, the names of the predictor variables from the *zero-inflated* part of the model
- **zero_inflated_random**, the names of the random effects (grouping factors)
- **dispersion**, the name of the dispersion terms
- **instruments**, the names of instrumental variables

Returns **NULL** if no terms could be found (for instance, due to problems in accessing the formula).

Note

The difference to *find_variables()* is that *find_terms()* may return a variable multiple times in case of multiple transformations (see examples below), while *find_variables()* returns each variable name only once.

Examples

```r
if (require("lme4")) {
  data(sleepstudy)
  m <- lmer(
    log(Reaction) ~ Days + I(Days^2) + (1 + Days + exp(Days) | Subject),
    data = sleepstudy
  )

  find_terms(m)
}
```
find_transformation  
*Find possible transformation of response variables*

**Description**

This function checks whether any transformation, such as log- or exp-transforming, was applied to the response variable (dependent variable) in a regression formula. Currently, following patterns are detected: log, log1p, exp, expm1, sqrt, log(x+<number>) and log-log.

**Usage**

```r
find_transformation(x)
```

**Arguments**

- `x`  
  A regression model.

**Value**

A string, with the name of the function of the applied transformation. Returns "identity" for no transformation, and e.g. "log(x+3)" when a specific value was added to the response variables before log-transforming.

**Examples**

```r
# identity, no transformation
model <- lm(Sepal.Length ~ Species, data = iris)
find_transformation(model)

# log-transformation
model <- lm(log(Sepal.Length) ~ Species, data = iris)
find_transformation(model)

# log+2
model <- lm(log(Sepal.Length + 2) ~ Species, data = iris)
find_transformation(model)
```

---

find_variables  
*Find names of all variables*

**Description**

Returns a list with the names of all variables, including response value and random effects.
Usage

```r
find_variables(
  x,
  effects = c("all", "fixed", "random"),
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion",
                 "instruments", "smooth_terms"),
  flatten = FALSE,
  verbose = TRUE
)
```

Arguments

- `x` A fitted model.
- `effects` Should variables for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
- `component` Should all predictor variables, predictor variables for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so called fixed-effects regressions). May be abbreviated. Note that the `conditional` component is also called `count` or `mean` component, depending on the model.
- `flatten` Logical, if `TRUE`, the values are returned as character vector, not as list. Duplicated values are removed.
- `verbose` Toggle warnings.

Value

A list with (depending on the model) following elements (character vectors):

- `response`, the name of the response variable
- `conditional`, the names of the predictor variables from the `conditional` model (as opposed to the zero-inflated part of a model)
- `cluster`, the names of cluster or grouping variables
- `dispersion`, the name of the dispersion terms
- `instruments`, the names of instrumental variables
- `random`, the names of the random effects (grouping factors)
- `zero_inflated`, the names of the predictor variables from the `zero-inflated` part of the model
- `zero_inflated_random`, the names of the random effects (grouping factors)

Note

The difference to `find_terms()` is that `find_variables()` returns each variable name only once, while `find_terms()` may return a variable multiple times in case of transformations or when arithmetic expressions were used in the formula.
**Examples**

```r
if (require("lme4")) {
    data(cbpp)
data(sleepstudy)
    # some data preparation...
cbpp$trials <- cbpp$size - cbpp$incidence
sleepstudy$mygrp <- sample(1:5, size = 180, replace = TRUE)
sleepstudy$mysubgrp <- NA
for (i in 1:5) {
    filter_group <- sleepstudy$mygrp == i
    sleepstudy$mysubgrp[filter_group] <- sample(1:30, size = sum(filter_group), replace = TRUE)
}
m1 <- glmer(
    cbind(incidence, size - incidence) ~ period + (1 | herd),
    data = cbpp,
    family = binomial
)find_variables(m1)

m2 <- lmer(
    Reaction ~ Days + (1 | mygrp / mysubgrp) + (1 | Subject),
    data = sleepstudy
)find_variables(m2)
find_variables(m2, flatten = TRUE)
}
```

---

**find_weights**

*Find names of model weights*

**Description**

Returns the name of the variable that describes the weights of a model.

**Usage**

```r
find_weights(x, ...)
```

**Arguments**

- `x` A fitted model.
- `...` Currently not used.

**Value**

The name of the weighting variable as character vector, or NULL if no weights were specified.
Examples

data(mtcars)
mtcars$weight <- rnorm(nrow(mtcars), 1, .3)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars, weights = weight)
find_weights(m)

---

### fish

**Sample data set**

**Description**

A sample data set, used in tests and some examples.

---

### format_bf

**Bayes Factor formatting**

**Description**

Bayes Factor formatting

**Usage**

```r
format_bf(
  bf,
  stars = FALSE,
  stars_only = FALSE,
  name = "BF",
  protect_ratio = FALSE,
  na_reference = NA,
  exact = FALSE
)
```

**Arguments**

- **bf**: Bayes Factor.
- **stars**: Add significance stars (e.g., p < .001***).
- **stars_only**: Return only significance stars.
- **name**: Name prefixing the text. Can be NULL.
- **protect_ratio**: Should values smaller than 1 be represented as ratios?
- **na_reference**: How to format missing values (NA).
- **exact**: Should very large or very small values be reported with a scientific format (e.g., 4.24e5), or as truncated values (as "> 1000" and "< 1/1000").
Value

A formatted string.

Examples

```r
format_bf(bfs <- c(0.000045, 0.033, NA, 1557, 3.54))
format_bf(bfs, exact = TRUE, name = NULL)
format_bf(bfs, stars = TRUE)
format_bf(bfs, protect_ratio = TRUE)
format_bf(bfs, protect_ratio = TRUE, exact = TRUE)
format_bf(bfs, na_reference = 1)
```

---

```r
format_capitalize x, with first letter capitalized.
```

Description

This function converts the first letter in a string into upper case.

Usage

```r
format_capitalize(x, verbose = TRUE)
```

Arguments

- `x` A character vector or a factor. The latter is coerced to character. All other objects are returned unchanged.
- `verbose` Toggle warnings.

Value

`x`, with first letter capitalized.

Examples

```r
format_capitalize("hello")
format_capitalize(c("hello", "world"))
unique(format_capitalize(iris$Species))
```
format_ci

Confidence/Credible Interval (CI) Formatting

Description

Confidence/Credible Interval (CI) Formatting

Usage

format_ci(
  CI_low,
  CI_high,
  ci = 0.95,
  digits = 2,
  brackets = TRUE,
  width = NULL,
  width_low = width,
  width_high = width,
  missing = "",
  zap_small = FALSE
)

Arguments

CI_low
  Lower CI bound.

CI_high
  Upper CI bound.

ci
  CI level in percentage.

digits
  Number of digits for rounding or significant figures. May also be "signif" to return significant figures or "scientific" to return scientific notation. Control the number of digits by addingthe value as suffix, e.g. digits = "scientific4" to have scientific notation with 4 decimal places, or digits = "signif5" for 5 significant figures (see also signif()).

brackets
  Either a logical, and if TRUE (default), values are encompassed in square brackets. If FALSE or NULL, no brackets are used. Else, a character vector of length two, indicating the opening and closing brackets.

width
  Minimum width of the returned string. If not NULL and width is larger than the string’s length, leading whitespaces are added to the string. If width="auto", width will be set to the length of the longest string.

width_low, width_high
  Like width, but only applies to the lower or higher confidence interval value. This can be used when the values for the lower and upper CI are of very different length.

missing
  Value by which NA values are replaced. By default, an empty string (i.e. "") is returned for NA.
zap_small Logical, if TRUE, small values are rounded after digits decimal places. If FALSE, values with more decimal places than digits are printed in scientific notation.

Value
A formatted string.

Examples

```r
format_ci(1.20, 3.57, ci = 0.90)
fraction(1.20, 3.57, ci = NULL)
fraction(1.20, 3.57, ci = NULL, brackets = FALSE)
fraction(1.20, 3.57, ci = NULL, brackets = c("([", "]"))
fraction(c(1.205645, 23.4), c(3.57, -1.35), ci = 0.90)
fraction(c(1.20, NA, NA), c(3.57, -1.35, NA), ci = 0.90)

# automatic alignment of width, useful for printing multiple CIs in columns
x <- fraction(c(1.205, 23.4, 100.43), c(3.57, -13.35, 9.4))
cat(x, sep = "\n")

x <- fraction(c(1.205, 23.4, 100.43), c(3.57, -13.35, 9.4), width = "auto")
cat(x, sep = "\n")
```

format_message Format messages and warnings

Description
Inserts line breaks into a longer message or warning string. Line length is adjusted to maximum length of the console, if the width can be accessed. By default, new lines are indented by two whitespace.

Usage
```
format_message(string, ..., line_length = options()$width)
```

Arguments

- `string` A string.
- `...` Further strings that will be concatenated as indented new lines.
- `line_length` Numeric, the maximum length of a line.

Value
A formatted string.
**Examples**

```r
msg <- format_message("Much too long string for just one line, I guess!",
  line_length = 15
)
message(msg)

msg <- format_message("Much too long string for just one line, I guess!",
  "First new line",
  "Second new line",
  "{both indented}"
  line_length = 30
)
message(msg)
```

---

**format_number**

*Convert number to words*

---

**Description**

Convert number to words

**Usage**

```r
format_number(x, textual = TRUE, ...)
```

**Arguments**

- `x`: Number.
- `textual`: Return words. If FALSE, will run `format_value()`.
- `...`: Arguments to be passed to `format_value()` if `textual` is FALSE.

**Value**

A formatted string.

**Note**

The code has been adapted from here [https://github.com/ateucher/useful_code/blob/master/R/numbers2words.r](https://github.com/ateucher/useful_code/blob/master/R/numbers2words.r)

**Examples**

```r
format_number(2)
format_number(45)
format_number(324.68765)
```
Description

Format p-values.

Usage

format_p(
  p,
  stars = FALSE,
  stars_only = FALSE,
  whitespace = TRUE,
  name = "p",
  missing = "",
  decimal_separator = NULL,
  digits = 3,
  ...
)

Arguments

- **p**: value or vector of p-values.
- **stars**: Add significance stars (e.g., p < .001***).
- **stars_only**: Return only significance stars.
- **whitespace**: Logical, if TRUE (default), preserves whitespaces. Else, all whitespace characters are removed from the returned string.
- **name**: Name prefixing the text. Can be NULL.
- **missing**: Value by which NA values are replaced. By default, an empty string (i.e. "") is returned for NA.
- **decimal_separator**: Character, if not NULL, will be used as decimal separator.
- **digits**: Number of significant digits. May also be "scientific" to return exact p-values in scientific notation, or "apa" to use an APA 7th edition-style for p-values (equivalent to digits = 3). If "scientific", control the number of digits by adding the value as a suffix, e.g.m digits = "scientific4" to have scientific notation with 4 decimal places.
  ...
- **...**: Arguments from other methods.

Value

A formatted string.
format_pd

Examples

format_p(c(.02, .065, 0, .23))
format_p(c(.02, .065, 0, .23), name = NULL)
format_p(c(.02, .065, 0, .23), stars_only = TRUE)

model <- lm(mpg ~ wt + cyl, data = mtcars)
p <- coef(summary(model))[, 4]
format_p(p, digits = "apa")
format_p(p, digits = "scientific")
format_p(p, digits = "scientific2")

format_pd

Probability of direction (pd) formatting

Description

Probability of direction (pd) formatting

Usage

format_pd(pd, stars = FALSE, stars_only = FALSE, name = "pd")

Arguments

pd        Probability of direction (pd).
stars     Add significance stars (e.g., p < .001***).
stars_only Return only significance stars.
name      Name prefixing the text. Can be NULL.

Value

A formatted string.

Examples

format_pd(0.12)
format_pd(c(0.12, 1, 0.9999, 0.98, 0.995, 0.96), name = NULL)
format_pd(c(0.12, 1, 0.9999, 0.98, 0.995, 0.96), stars = TRUE)
### format_rope  

**Percentage in ROPE formatting**

**Description**

Percentage in ROPE formatting

**Usage**

```r
format_rope(rope_percentage, name = "in ROPE", digits = 2)
```

**Arguments**

- `rope_percentage`  
  Value or vector of percentages in ROPE.
- `name`  
  Name prefixing the text. Can be NULL.
- `digits`  
  Number of significant digits. May also be "scientific" to return exact p-values in scientific notation, or "apa" to use an APA 7th edition-style for p-values (equivalent to digits = 3). If "scientific", control the number of digits by adding the value as a suffix, e.g.m digits = "scientific4" to have scientific notation with 4 decimal places.

**Value**

A formatted string.

**Examples**

```r
format_rope(c(0.02, 0.12, 0.357, 0))
format_rope(c(0.02, 0.12, 0.357, 0), name = NULL)
```

### format_string  

**String Values Formatting**

**Description**

String Values Formatting

**Usage**

```r
format_string(x, ...)
```

**### S3 method for class 'character'**

```r
format_string(x, length = NULL, abbreviate = "...", ...)
```
Arguments

- **x**: String value.
- **...**: Arguments passed to or from other methods.
- **length**: Numeric, maximum length of the returned string. If not NULL, will shorten the string to a maximum length, however, it will not truncate inside words. I.e., if the string length happens to be inside a word, this word is removed from the returned string, so the returned string has a maximum length of length, but might be shorter.
- **abbreviate**: String that will be used as suffix, if x was shortened.

Value

A formatted string.

Examples

```r
s <- "This can be considered as very long string!"
# string is shorter than max.length, so returned as is
format_string(s, 60)

# string is shortened to as many words that result in
# a string of maximum 20 chars
format_string(s, 20)
```

Description

This function takes a data frame with model parameters as input and formats certain columns into a more readable layout (like collapsing separate columns for lower and upper confidence interval values). Furthermore, column names are formatted as well. Note that `format_table()` converts all columns into character vectors!

Usage

```r
format_table(
  x,
  pretty_names = TRUE,
  stars = FALSE,
  digits = 2,
  ci_width = "auto",
  ci_brackets = TRUE,
  ci_digits = 2,
  p_digits = 3,
  rope_digits = 2,
)```
parameters_table(
  x,
  pretty_names = TRUE,
  stars = FALSE,
  digits = 2,
  ci_width = "auto",
  ci_brackets = TRUE,
  ci_digits = 2,
  p_digits = 3,
  rope_digits = 2,
  zap_small = FALSE,
  preserve_attributes = FALSE,
  verbose = TRUE,
  ...
)

Arguments

x
A data frame of model’s parameters, as returned by various functions of the easystats-packages. May also be a result from broom::tidy().

pretty_names
Return "pretty" (i.e. more human readable) parameter names.

stars
Add significance stars (e.g., p < .001***).

digits, ci_digits, p_digits, rope_digits
Number of digits for rounding or significant figures. May also be "signif" to return significant figures or "scientific" to return scientific notation. Control the number of digits by adding the value as suffix, e.g. digits = "scientific4" to have scientific notation with 4 decimal places, or digits = "signif5" for 5 significant figures (see also signif()).

ci_width
Minimum width of the returned string for confidence intervals. If not NULL and width is larger than the string’s length, leading whitespaces are added to the string. If width="auto", width will be set to the length of the longest string.

ci_brackets
Logical, if TRUE (default), CI-values are encompassed in square brackets (else in parentheses).

zap_small
Logical, if TRUE, small values are rounded after digits decimal places. If FALSE, values with more decimal places than digits are printed in scientific notation.

preserve_attributes
Logical, if TRUE, preserves all attributes from the input data frame.

verbose
Toggle messages and warnings.

... Arguments passed to or from other methods.
Value

A data frame. Note that `format_table()` converts all columns into character vectors!

See Also

Vignettes `Formatting, printing and exporting tables` and `Formatting model parameters`.

Examples

```r
format_table(head(iris), digits = 1)

if (require("parameters")) {
  x <- model_parameters(lm(Sepal.Length ~ Species * Sepal.Width, data = iris))
  as.data.frame(format_table(x))
  as.data.frame(format_table(x, p_digits = "scientific"))
}
if (require("rstanarm", warn.conflicts = FALSE) && require("parameters", warn.conflicts = FALSE)) {
  model <- stan_glm(Sepal.Length ~ Species, data = iris, refresh = 0, seed = 123)
  x <- model_parameters(model, ci = c(0.69, 0.89, 0.95))
  as.data.frame(format_table(x))
}
```

format_value

**Numeric Values Formatting**

Description

Numeric Values Formatting

Usage

```r
format_value(x, ...)
```

## S3 method for class 'data.frame'

```r
format_value(
  x,
  digits = 2,
  protect_integers = FALSE,
  missing = "",
  width = NULL,
  as_percent = FALSE,
  zap_small = FALSE,
  ...
)
```
## S3 method for class 'numeric'
format_value(
  x,
  digits = 2,
  protect_integers = FALSE,
  missing = "",
  width = NULL,
  as_percent = FALSE,
  zap_small = FALSE,
  ...
)

Arguments

 x Numeric value.
 ... Arguments passed to or from other methods.
 digits Number of digits for rounding or significant figures. May also be "signif" to return significant figures or "scientific" to return scientific notation. Control the number of digits by adding the value as suffix, e.g. digits = "scientific4" to have scientific notation with 4 decimal places, or digits = "signif5" for 5 significant figures (see also signif()).
 protect_integers Should integers be kept as integers (i.e., without decimals)?
 missing Value by which NA values are replaced. By default, an empty string (i.e. "") is returned for NA.
 width Minimum width of the returned string. If not NULL and width is larger than the string's length, leading whitespaces are added to the string.
 as_percent Logical, if TRUE, value is formatted as percentage value.
 zap_small Logical, if TRUE, small values are rounded after digits decimal places. If FALSE, values with more decimal places than digits are printed in scientific notation.

Value

 A formatted string.

Examples

 format_value(1.20)
 format_value(1.2)
 format_value(1.2012313)
 format_value(c(0.0045, 234, -23))
 format_value(c(0.0045, .12, .34))
 format_value(c(0.0045, .12, .34), as_percent = TRUE)
 format_value(c(0.0045, .12, .34), digits = "scientific")
 format_value(c(0.0045, .12, .34), digits = "scientific2")

# default
get_auxiliary

get_auxiliary(x, type = "sigma", summary = TRUE, centrality = "mean", verbose = TRUE, ...)

Arguments

x A model.
type The name of the auxiliary parameter that should be retrieved. "sigma" is available for most models, "dispersion" for models of class glm, glmerMod or glmmTMB as well as brmsfit. "beta" and other parameters are currently only returned for brmsfit models. See 'Details'.
summary Logical, indicates whether the full posterior samples (summary = FALSE) or the summarized centrality indices of the posterior samples (summary = TRUE) should be returned as estimates.
centrality Only for models with posterior samples, and when summary = TRUE. In this case, centrality = "mean" would calculate means of posterior samples for each parameter, while centrality = "median" would use the more robust median value as measure of central tendency.
verbose Toggle warnings.
... Currently not used.

Description

Returns the requested auxiliary parameters from models, like dispersion, sigma, or beta...

Usage

get_auxiliary(x, type = "sigma", summary = TRUE, centrality = "mean", verbose = TRUE, ...)

Examples

format_value(c(0.0045, .123, .345))
# significant figures
format_value(c(0.0045, .123, .345), digits = "signif")

format_value(as.factor(c("A", "B", "A")))
format_value(iris$Species)

format_value(3)
format_value(3, protect_integers = TRUE)

format_value(head(iris))
Currently, only sigma and the dispersion parameter are returned, and only for a limited set of models.

**Sigma Parameter:** See `get_sigma()`.

**Dispersion Parameter:** There are many different definitions of "dispersion", depending on the context. `get_auxiliary()` returns the dispersion parameters that usually can be considered as variance-to-mean ratio for generalized (linear) mixed models. Exceptions are models of class `glmmTMB`, where the dispersion equals $\sigma^2$. In detail, the computation of the dispersion parameter for generalized linear models is the ratio of the sum of the squared working-residuals and the residual degrees of freedom. For mixed models of class `glmer`, the dispersion parameter is also called $\phi$ and is the ratio of the sum of the squared Pearson-residuals and the residual degrees of freedom. For models of class `glmmTMB`, dispersion is $\sigma^2$.

**brms models:** For models of class `brmsfit`, there are different options for the `type` argument. See a list of supported auxiliary parameters here: `find_parameters.BGGM()`.

The requested auxiliary parameter, or `NULL` if this information could not be accessed.

```r
# from ?glm
clotting <- data.frame(
  u = c(5, 10, 15, 20, 30, 40, 60, 80, 100),
  lot1 = c(118, 58, 42, 35, 27, 25, 21, 19, 18),
  lot2 = c(69, 35, 26, 21, 18, 16, 13, 12, 12)
)
model <- glm(lot1 ~ log(u), data = clotting, family = Gamma())
get_auxiliary(model, type = "dispersion")  # same as summary(model)$dispersion
```

---

**Description**

Returns the model's function call when available.

**Usage**

```r
get_call(x)
```

**Arguments**

- `x` A fitted mixed model.
**get_data**

**Value**

A function call.

**Examples**

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_call(m)

if (require("lme4")) {
  m <- lmer(Sepal.Length ~ Sepal.Width + (1 | Species), data = iris)
  get_call(m)
}
```

**Description**

This function tries to get the data that was used to fit the model and returns it as a data frame.

**Usage**

```r
get_data(x, ...)
```

## S3 method for class 'gee'
```r
get_data(x, effects = c("all", "fixed", "random"), verbose = TRUE, ...)
```

## S3 method for class 'rqss'
```r
get_data(
  x,
  component = c("all", "conditional", "smooth_terms"),
  verbose = TRUE,
  ...
)
```

## S3 method for class 'hurdle'
```r
get_data(
  x,
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion"),
  verbose = TRUE,
  ...
)
```

## S3 method for class 'zcpglm'
```r
get_data(
  x,
```
get_data

component = c("all", "conditional", "zi", "zero_inflated"),
verbose = TRUE,
...

## S3 method for class 'glmmTMB'
get_data(
  x,
  effects = c("all", "fixed", "random"),
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion"),
  verbose = TRUE,
  ...
)

## S3 method for class 'merMod'
get_data(x, effects = c("all", "fixed", "random"), verbose = TRUE, ...)

## S3 method for class 'glmmadmb'
get_data(x, effects = c("all", "fixed", "random"), verbose = TRUE, ...)

## S3 method for class 'rlmerMod'
get_data(x, effects = c("all", "fixed", "random"), ...)

## S3 method for class 'clmm'
get_data(x, effects = c("all", "fixed", "random"), ...)

## S3 method for class 'mixed'
get_data(x, effects = c("all", "fixed", "random"), ...)

## S3 method for class 'afex_aov'
get_data(x, shape = c("long", "wide"), ...)

## S3 method for class 'lme'
get_data(x, effects = c("all", "fixed", "random"), ...)

## S3 method for class 'MixMod'
get_data(
  x,
  effects = c("all", "fixed", "random"),
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion"),
  verbose = TRUE,
  ...
)

## S3 method for class 'brmsfit'
get_data(x, effects = "all", component = "all", verbose = TRUE, ...)

## S3 method for class 'stanreg'
get_data

get_data(x, effects = c("all", "fixed", "random"), verbose = TRUE, ...)

## S3 method for class 'MCMCglmm'
get_data(x, effects = c("all", "fixed", "random"), verbose = TRUE, ...)

Arguments

x A fitted model.

... Currently not used.

effects Should model data for fixed effects, random effects or both be returned? Only applies to mixed models.

verbose Toggle messages and warnings.

component Should all predictor variables, predictor variables for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so called fixed-effects regressions). May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model.

shape Return long or wide data? Only applicable in repeated measures designs.

Value

The data that was used to fit the model.

Note

Unlike model.frame(), which may contain transformed variables (e.g. if poly() or scale() was used inside the formula to specify the model), get_data() aims at returning the "original", untransformed data (if possible). Consequently, column names are changed accordingly, i.e. "log(x)" will become "x" etc. for all data columns with transformed values.

Examples

if (require("lme4")) {
  data(cbpp, package = "lme4")
  cbpp$trials <- cbpp$size - cbpp$incidence
  m <- glm(cbind(incidence, trials) ~ period, data = cbpp, family = binomial)
  head(get_data(m))
}
get_datagrid

Create a reference grid

Description

Create a reference matrix, useful for visualisation, with evenly spread and combined values.

Usage

get_datagrid(x, ...)

## S3 method for class 'data.frame'
get_datagrid(
  x,
  at = "all",
  factors = "reference",
  numerics = "mean",
  preserve_range = FALSE,
  reference = x,
  ...
)

## S3 method for class 'numeric'
get_datagrid(x, length = 10, range = "range", ...)

## S3 method for class 'factor'
get_datagrid(x, ...)

## Default S3 method:
get_datagrid(
  x,
  at = "all",
  factors = "reference",
  numerics = "mean",
  preserve_range = TRUE,
  reference = x,
  include_smooth = TRUE,
  include_random = FALSE,
  include_response = FALSE,
  data = NULL,
  ...
)

Arguments

x An object from which to construct the reference grid.
Arguments passed to or from other methods (for instance, length or range to control the spread of numeric variables.).

at
Can be "all" or list of characters indicating columns of interest. Can also contain assignments (as named list, e.g. `at = list(c(Sepal.Length = c(2,4),Species = "setosa"), or as string, e.g. `at = "Sepal.Length = 2" or `at = c("Sepal.Length = 2","Species = 'setosa'") - note the usage of single and double quotes to assign strings within strings). The remaining variables will be fixed.

factors
Type of summary for factors. Can be "reference" (set at the reference level), "mode" (set at the most common level) or "all" to keep all levels.

numerics
Type of summary for numeric values. Can be "all" (will duplicate the grid for all unique values), any function ("mean", "median", ...) or a value (e.g., numerics = 0).

preserve_range
In the case of combinations between numeric variables and factors, setting `preserve_range = TRUE` will drop the observations where the value of the numeric variable is originally not present in the range of its factor level. This leads to an unbalanced grid. Also, if you want the minimum and the maximum to closely match the actual ranges, you should increase the `length` argument.

reference
The reference vector from which to compute the mean and SD.

length
Length of numeric "at" variables.

range
Can be one of "range", "iqr", "ci", "hdi" or "eti". If "range" (default), will use the minimum and maximum of the original vector as end-points. If any other interval, will spread within the range (the default CI width is 95% but this can be changed by setting something else, e.g., `ci = 0.90`). See `IQR()` and `bayestestR::ci()`.

include_smooth
If `x` is a model object, decide whether smooth terms should be included in the data grid or not.

include_random
If `x` is a mixed model object, decide whether random effect terms should be included in the data grid or not. If `include_random` is FALSE, but `x` is a mixed model with random effects, these will still be included in the returned grid, but set to their "population level" value (e.g., NA for `glmmTMB` or 0 for `merMod`). This ensures that common `predict()` methods work properly, as these usually need data with all variables in the model included.

include_response
If `x` is a model object, decide whether the response variable should be included in the data grid or not.

data
Optional, the data frame that was used to fit the model. Usually, the data is retrieved via `get_data()`.

Value
Reference grid data frame.

Examples

```r
# Add one row to change the "mode" of Species
data <- rbind(iris, iris[149, ], make.row.names = FALSE)
```
get_deviance

Description

Returns model deviance (see stats::deviance()).

Usage

get_deviance(x, ...)

## Default S3 method:
get_deviance(x, verbose = TRUE, ...)

Arguments

x A model.
...
verbose Toggle warnings and messages.

Details

For GLMMs of class glmerMod, glmmTMB or MixMod, the absolute unconditional deviance is returned (see 'Details' in ?lme4::merMod-class"), i.e. minus twice the log-likelihood. To get the relative conditional deviance (relative to a saturated model, conditioned on the conditional modes of random effects), use deviance(). The value returned ‘get_deviance()’ usually equals the deviance-value from the ‘summary()’. 

Value

The model deviance.
get_df

Examples

data(mtcars)
  x <- lm(mpg ~ cyl, data = mtcars)
  get_deviance(x)

get_df

Extract degrees of freedom

Description

Estimate or extract residual or model-based degrees of freedom from regression models.

Usage

get_df(x, ...)

## Default S3 method:
get_df(x, type = "residual", verbose = TRUE, ...)

Arguments

x  A statistical model.
...
 Currently not used.

 type  Can be "residual", "model" or "analytical". "residual" tries to extract residual degrees of freedoms. If residual degrees of freedom could not be extracted, returns analytical degrees of freedom, i.e. n-k (number of observations minus number of parameters). "model" returns model-based degrees of freedom, i.e. the number of (estimated) parameters.

verbose  Toggle warnings.

Examples

model <- lm(Sepal.Length ~ Petal.Length * Species, data = iris)
get_df(model) # same as df.residual(model)
get_df(model, type = "model") # same as attr(logLik(model), "df")
get_family

A robust and resilient alternative to stats::family. To avoid issues with models like gamm4.

Usage

get_family(x, ...)

Arguments

x
A statistical model.
...
Further arguments passed to methods.

Examples

data(mtcars)
x <- glm(vs ~ wt, data = mtcars, family = "binomial")
get_family(x)

if (require("mgcv")) {
  x <- mgcv::gamm(
    vs ~ am + s(wt),
    random = list(cyl = ~1),
    data = mtcars,
    family = "binomial"
  )
  get_family(x)
}

get_intercept

Get the value at the intercept

Description

Returns the value at the intercept (i.e., the intercept parameter), and NA if there isn’t one.

Usage

gcet_intercept(x, ...)

Arguments

x
A model.
...
Not used.
get_loglikelihood

Value

The value of the intercept.

Examples

```r
get_intercept(lm(Sepal.Length ~ Petal.Width, data = iris))
get_intercept(lm(Sepal.Length ~ 0 + Petal.Width, data = iris))

if (require("lme4")) {
  get_intercept(lme4::lmer(Sepal.Length ~ Sepal.Width + (1 | Species), data = iris))
}
if (require("gamm4")) {
  get_intercept(gamm4::gamm4(Sepal.Length ~ s(Petal.Width), data = iris))
}
```

get_loglikelihood  Log-Likelihood

Description

A robust function to compute the log-likelihood of a model, as well as individual log-likelihoods (for each observation) whenever possible. Can be used as a replacement for `stats::logLik()` out of the box, as the returned object is of the same class (and it gives the same results by default).

Usage

```r
get_loglikelihood(x, ...)
loglikelihood(x, ...)
```

```r
## S3 method for class 'lm'
get_loglikelihood(x, estimator = "ML", REML = FALSE, verbose = TRUE, ...)
```

Arguments

- `x`: A model.
- `...`: Passed down to `logLik()`, if possible.
- `estimator`: Corresponds to the different estimators for the standard deviation of the errors. If `estimator="ML"` (default), the scaling is done by `n` (the biased ML estimator), which is then equivalent to using `stats::logLik()`. If `estimator="OLS"`, it returns the unbiased OLS estimator.
- `REML`: Only for linear models. This argument is present for compatibility with `stats::logLik()`. Setting it to `TRUE` will overwrite the `estimator` argument and is thus equivalent to setting `estimator="REML"`. It will give the same results as `stats::logLik(..., REML=TRUE)`. Note that individual log-likelihoods are not available under REML.
- `verbose`: Toggle warnings and messages.
get_modelmatrix

Value

An object of class "logLik", also containing the log-likelihoods for each observation as a per_observation attribute (attributes(get_loglikelihood(x))$per_observation) when possible. The code was partly inspired from the nonnest2 package.

Examples

x <- lm(Sepal.Length ~ Petal.Width + Species, data = iris)

get_loglikelihood(x, estimator = "ML") # Equivalent to stats::logLik(x)
get_loglikelihood(x, estimator = "REML") # Equivalent to stats::logLik(x, REML=TRUE)
get_loglikelihood(x, estimator = "OLS")

generate_modelmatrix

Model Matrix

Description

Creates a design matrix from the description. Any character variables are coerced to factors.

Usage

generate_modelmatrix(x, ...)

Arguments

x          An object.
...

Passed down to other methods (mainly model.matrix()).

Examples

data(mtcars)

model <- lm(am ~ vs, data = mtcars)

generate_modelmatrix(model)
get_parameters

Get model parameters

Description

Returns the coefficients (or posterior samples for Bayesian models) from a model. See the documentation for your object’s class:

- Bayesian models (rstanarm, brms, MCMCglmm, ...)
- Estimated marginal means (emmeans)
- Generalized additive models (mgcv, VGAM, ...)
- Marginal effects models (mfx)
- Mixed models (lme4, glmmTMB, GLMMadaptive, ...)
- Zero-inflated and hurdle models (pscl, ...)
- Models with special components (betareg, MuMIn, ...)
- Hypothesis tests (htest)

Usage

get_parameters(x, ...)

## Default S3 method:
get_parameters(x, verbose = TRUE, ...)

Arguments

x
A fitted model.

... Currently not used.

verbose Toggle messages and warnings.

Details

In most cases when models either return different "effects" (fixed, random) or "components" (conditional, zero-inflated, ...), the arguments effects and component can be used.

get_parameters() is comparable to coef(), however, the coefficients are returned as data frame (with columns for names and point estimates of coefficients). For Bayesian models, the posterior samples of parameters are returned.

Value

- for non-Bayesian models, a data frame with two columns: the parameter names and the related point estimates.
- for Anova (aov()) with error term, a list of parameters for the conditional and the random effects parameters
Examples

```r
data(mtcars)
model <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_parameters(model)
```

---

get_parameters.betamfx

*Get model parameters from marginal effects models*

Description

Returns the coefficients from a model.

Usage

```r
## S3 method for class 'betamfx'
get_parameters(
x, 
component = c("all", "conditional", "precision", "marginal"),
...
)
```

```r
## S3 method for class 'logitmfx'
get_parameters(x, component = c("all", "conditional", "marginal"), ...)
```

Arguments

- **x**: A fitted model.
- **component**: Should all predictor variables, predictor variables for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so called fixed-effects regressions). May be abbreviated. Note that the `conditional` component is also called `count` or `mean` component, depending on the model.
- **...**: Currently not used.

Value

A data frame with three columns: the parameter names, the related point estimates and the component.

Examples

```r
data(mtcars)
model <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_parameters(model)
```
get_parameters.betareg

Get model parameters from models with special components

Description

Returns the coefficients from a model.

Usage

## S3 method for class 'betareg'
get_parameters(
x,  
component = c("all", "conditional", "precision", "location", "distributional",  
"auxiliary"),  
...  
)

## S3 method for class 'DirichletRegModel'
get_parameters(
x,  
component = c("all", "conditional", "precision", "location", "distributional",  
"auxiliary"),  
...  
)

## S3 method for class 'averaging'
get_parameters(x, component = c("conditional", "full"), ...)

## S3 method for class 'glmx'
get_parameters(
x,  
component = c("all", "conditional", "extra", "location", "distributional",  
"auxiliary"),  
...  
)

## S3 method for class 'clm2'
get_parameters(x, component = c("all", "conditional", "scale"), ...)

## S3 method for class 'mvord'
get_parameters(
x,  
component = c("all", "conditional", "thresholds", "correlation"),  
...  
)
## S3 method for class 'mjoint'
get_parameters(x, component = c("all", "conditional", "survival"), ...)

**Arguments**

- **x**
  A fitted model.

- **component**
  Should all predictor variables, predictor variables for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so called fixed-effects regressions). May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model.

- **...**
  Currently not used.

**Value**

A data frame with three columns: the parameter names, the related point estimates and the component.

**Examples**

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_parameters(m)
```

---

### get_parameters.BGGM

*Get model parameters from Bayesian models*

#### Description

Returns the coefficients (or posterior samples for Bayesian models) from a model.

#### Usage

```r
## S3 method for class 'BGGM'
get_parameters(
x,
  component = c("correlation", "conditional", "intercept", "all"),
  summary = FALSE,
  centrality = "mean",
  ...
)
```

```r
## S3 method for class 'MCMCglmm'
get_parameters(
x,
  effects = c("fixed", "random", "all"),
```
get_parameters.BGGM

summary = FALSE,
centrality = "mean",
...
)

## S3 method for class 'BFBayesFactor'
get_parameters(
  x,
  effects = c("all", "fixed", "random"),
  component = c("all", "extra"),
  iterations = 4000,
  progress = FALSE,
  verbose = TRUE,
  summary = FALSE,
  centrality = "mean",
  ...
)

## S3 method for class 'stanmvreg'
get_parameters(
  x,
  effects = c("fixed", "random", "all"),
  parameters = NULL,
  summary = FALSE,
  centrality = "mean",
  ...
)

## S3 method for class 'brmsfit'
get_parameters(
  x,
  effects = "fixed",
  component = "all",
  parameters = NULL,
  summary = FALSE,
  centrality = "mean",
  ...
)

## S3 method for class 'stanreg'
get_parameters(
  x,
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
               "distributional", "auxiliary"),
  parameters = NULL,
  summary = FALSE,
  centrality = "mean",
  ...
... }  

## S3 method for class 'bayesx'
get_parameters(  
  x,  
  component = c("conditional", "smooth_terms", "all"),  
  summary = FALSE,  
  centrality = "mean",  
  ... 
)  

## S3 method for class 'bamlss'
get_parameters(  
  x,  
  component = c("all", "conditional", "smooth_terms", "location", "distributional",  
  "auxiliary"),  
  parameters = NULL,  
  summary = FALSE,  
  centrality = "mean",  
  ... 
)  

## S3 method for class 'sim.merMod'
get_parameters(  
  x,  
  effects = c("fixed", "random", "all"),  
  parameters = NULL,  
  summary = FALSE,  
  centrality = "mean",  
  ... 
)  

## S3 method for class 'sim'
get_parameters(x, parameters = NULL, summary = FALSE, centrality = "mean", ...)  

Arguments

x  
A fitted model.

component  
Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, the instrumental variables or marginal effects be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variables (so called fixed-effects regressions), or models with marginal effects from mfx. May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model. There are three convenient shortcuts: component = "all" returns all possible parameters. If component = "location", location parameters such as conditional, zero_inflated, smooth_terms, or
instruments are returned (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters). For component = "distributional" (or "auxiliary"), components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

**summary** Logical, indicates whether the full posterior samples (summary = FALSE) or the summarized centrality indices of the posterior samples (summary = TRUE) should be returned as estimates.

**centrality** Only for models with posterior samples, and when summary = TRUE. In this case, centrality = "mean" would calculate means of posterior samples for each parameter, while centrality = "median" would use the more robust median value as measure of central tendency.

... Currently not used.

**effects** Should parameters for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.

**iterations** Number of posterior draws.

**progress** Display progress.

**verbose** Toggle messages and warnings.

**parameters** Regular expression pattern that describes the parameters that should be returned.

### Details

In most cases when models either return different "effects" (fixed, random) or "components" (conditional, zero-inflated, ...), the arguments effects and component can be used.

### Value

The posterior samples from the requested parameters as data frame. If summary = TRUE, returns a data frame with two columns: the parameter names and the related point estimates (based on centrality).

### BFBayesFactor Models

Note that for BFBayesFactor models (from the `BayesFactor` package), posteriors are only extracted from the first numerator model (i.e., model[1]). If you want to apply some function `foo()` to another model stored in the BFBayesFactor object, index it directly, e.g. `foo(model[2])`, `foo(1/model[5])`, etc. See also `bayestestR::weighted_posteriors()`.

### Examples

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_parameters(m)
```
get_parameters.emmGrid

Get model parameters from estimated marginal means objects

Description

Returns the coefficients from a model.

Usage

## S3 method for class 'emmGrid'
get_parameters(x, summary = FALSE, merge_parameters = FALSE, ...)

## S3 method for class 'emm_list'
get_parameters(x, summary = FALSE, ...)

Arguments

x
A fitted model.

summary
Logical, indicates whether the full posterior samples (summary = FALSE) or
the summarized centrality indices of the posterior samples (summary = TRUE))
should be returned as estimates.

merge_parameters
Logical, if TRUE and x has multiple columns for parameter names (like emmGrid
objects may have), these are merged into a single parameter column, with pa-
rameters names and values as values.

...
Currently not used.

Value

A data frame with two columns: the parameter names and the related point estimates.

Note

Note that emmGrid or emm_list objects returned by functions from emmeans have a different
structure compared to usual regression models. Hence, the Parameter column does not always
contain names of variables, but may rather contain values, e.g. for contrasts. See an example for
pairwise comparisons below.

Examples

data(mtcars)
model <- lm(mpg ~ wt * factor(cyl), data = mtcars)
if (require("emmeans", quietly = TRUE)) {
  emm <- emmeans(model, "cyl")
  get_parameters(emm)
```r
emm <- emmeans(model, pairwise ~ cyl)
get_parameters(emm)
```

---

**get_parameters.gamm**  
*Get model parameters from generalized additive models*

**Description**

Returns the coefficients from a model.

**Usage**

```r
## S3 method for class 'gamm'
get_parameters(
  x,
  component = c("all", "conditional", "smooth_terms", "location"),
  ...)
## S3 method for class 'gam'
get_parameters(
  x,
  component = c("all", "conditional", "smooth_terms", "location"),
  ...)
## S3 method for class 'rqss'
get_parameters(x, component = c("all", "conditional", "smooth_terms"), ...)
```

**Arguments**

- **x**  
  A fitted model.

- **component**  
  Should all predictor variables, predictor variables for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so-called fixed-effects regressions). May be abbreviated. Note that the *conditional* component is also called *count* or *mean* component, depending on the model.

- **...**  
  Currently not used.

**Value**

For models with smooth terms or zero-inflation component, a data frame with three columns: the parameter names, the related point estimates and the component.
Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_parameters(m)

get_parameters.glmm  Get model parameters from mixed models

description

Returns the coefficients from a model.

Usage

## S3 method for class 'glmm'
get_parameters(x, effects = c("all", "fixed", "random"), ...)

## S3 method for class 'coxme'
get_parameters(x, effects = c("fixed", "random"), ...)

## S3 method for class 'merMod'
get_parameters(x, effects = c("fixed", "random"), ...)

## S3 method for class 'glmmTMB'
get_parameters(
  x,
  effects = c("fixed", "random"),
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion"),
  ...
)

## S3 method for class 'glimML'
get_parameters(x, effects = c("fixed", "random", "all"), ...)

Arguments

x  A fitted model.
effects  Should parameters for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
...  Currently not used.
component  Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model or the dispersion term? Applies to models with zero-inflated and/or dispersion formula. Note that the conditional component is also called count or mean component, depending on the model. There are three convenient shortcuts: component = "all" returns all possible parameters. If component = "location", location parameters such as
get_parameters.htest

conditional or zero_inflated are returned (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters). For component = "distributional" (or "auxiliary"), components like sigma or dispersion (and other auxiliary parameters) are returned.

Details

In most cases when models either return different "effects" (fixed, random) or "components" (conditional, zero-inflated, ...), the arguments effects and component can be used.

Value

If effects = "fixed", a data frame with two columns: the parameter names and the related point estimates. If effects = "random", a list of data frames with the random effects (as returned by ranef()), unless the random effects have the same simplified structure as fixed effects (e.g. for models from MCMCglmm).

Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_parameters(m)

data(iris)
t <- t.test(iris$Sepal.Length, iris$Species)
get_parameters(t, ...)
Get model parameters from zero-inflated and hurdle models

**Description**

Returns the coefficients from a model.

**Usage**

```r
## S3 method for class 'zeroinfl'
get_parameters(
  x,
  component = c("all", "conditional", "zi", "zero_inflated"),
  ...
)

## S3 method for class 'zcpglm'
get_parameters(
  x,
  component = c("all", "conditional", "zi", "zero_inflated"),
  ...
)

## S3 method for class 'mhurdle'
get_parameters(
  x,
  component = c("all", "conditional", "zi", "zero_inflated", "infrequent_purchase", "ip", "auxiliary"),
  ...
)
```

**Arguments**

- `x` A fitted model.
- `component` Should all predictor variables, predictor variables for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so called fixed-effects regressions). May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model.
- `...` Currently not used.

**Value**

For models with smooth terms or zero-inflation component, a data frame with three columns: the parameter names, the related point estimates and the component.
Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_parameters(m)

get_predicted

Model Predictions (robust)

Description

The get_predicted() function is a robust, flexible and user-friendly alternative to base R predict() function. Additional features and advantages include availability of uncertainty intervals (CI), bootstrapping, a more intuitive API and the support of more models than base R’s predict function. However, although the interface are simplified, it is still very important to read the documentation of the arguments. This is because making "predictions" (a lose term for a variety of things) is a non-trivial process, with lots of caveats and complications. Read the Details section for more information.

Usage

general(x, ...)

## S3 method for class 'lm'
general(
x,
data = NULL,
predict = "expectation",
iterations = NULL,
verbose = TRUE,
...
)

## S3 method for class 'stanreg'
general(
x,
data = NULL,
predict = "expectation",
iterations = NULL,
include.random = TRUE,
include.smooth = TRUE,
verbose = TRUE,
...
)
Arguments

- **x**: A statistical model (can also be a data.frame, in which case the second argument has to be a model).
- **...**: Other argument to be passed, for instance to `get_predicted_ci()`. This can be used to request confidence intervals based on robust standard errors, e.g. by specifying the `vcov_*` arguments from `get_predicted_ci()` directly in the call to `get_predicted()`.
- **data**: An optional data frame in which to look for variables with which to predict. If omitted, the data used to fit the model is used.
- **predict**: string or `NULL`
  - "link" returns predictions on the model’s link-scale (for logistic models, that means the log-odds scale) with a confidence interval (CI).
  - "expectation" (default) also returns confidence intervals, but this time the output is on the response scale (for logistic models, that means probabilities).
  - "prediction" also gives an output on the response scale, but this time associated with a prediction interval (PI), which is larger than a confidence interval (though it mostly make sense for linear models).
  - "classification" only differs from "prediction" for binomial models where it additionally transforms the predictions into the original response’s type (for instance, to a factor).
  - Other strings are passed directly to the `type` argument of the `predict()` method supplied by the modelling package.
  - When `predict = NULL`, alternative arguments such as `type` will be captured by the ... ellipsis and passed directly to the `predict()` method supplied by the modelling package. Note that this might result in conflicts with multiple matching `type` arguments - thus, the recommendation is to use the predict argument for those values.
  - Notes: You can see the 4 options for predictions as on a gradient from "close to the model" to "close to the response data": "link", "expectation", "prediction", "classification". The predict argument modulates two things: the scale of the output and the type of certainty interval. Read more about in the Details section below.
- **iterations**: For Bayesian models, this corresponds to the number of posterior draws. If `NULL`, will return all the draws (one for each iteration of the model). For frequentist models, if not `NULL`, will generate bootstrapped draws, from which bootstrapped CIs will be computed. Iterations can be accessed by running `as.data.frame()` on the output.
- **verbose**: Toggle warnings.
- **include_random**: If TRUE (default), include all random effects in the prediction. If FALSE, don’t take them into account. Can also be a formula to specify which random effects to condition on when predicting (passed to the `re.form` argument). If `include_random = TRUE` and `newdata` is provided, make sure to include the random effect variables in `newdata` as well.
include_smooth  For General Additive Models (GAMs). If FALSE, will fix the value of the smooth to its average, so that the predictions are not depending on it. (default), mean(), or bayestestR::map_estimate().

Details

In insight::get_predicted(), the predict argument jointly modulates two separate concepts, the scale and the uncertainty interval.

Confidence Interval (CI) vs. Prediction Interval (PI):

• **Linear models** - lm(): For linear models, Prediction intervals (predict="prediction") show the range that likely contains the value of a new observation (in what range it is likely to fall), whereas confidence intervals (predict="expectation" or predict="link") reflect the uncertainty around the estimated parameters (and gives the range of uncertainty of the regression line). In general, Prediction Intervals (PIs) account for both the uncertainty in the model's parameters, plus the random variation of the individual values. Thus, prediction intervals are always wider than confidence intervals. Moreover, prediction intervals will not necessarily become narrower as the sample size increases (as they do not reflect only the quality of the fit, but also the variability within the data).

• **Generalized Linear models** - glm(): For binomial models, prediction intervals are somewhat useless (for instance, for a binomial (Bernoulli) model for which the dependent variable is a vector of 1s and 0s, the prediction interval is... [0, 1]).

Link scale vs. Response scale: When users set the predict argument to "expectation", the predictions are returned on the response scale, which is arguably the most convenient way to understand and visualize relationships of interest. When users set the predict argument to "link", predictions are returned on the link scale, and no transformation is applied. For instance, for a logistic regression model, the response scale corresponds to the predicted probabilities, whereas the link-scale makes predictions of log-odds (probabilities on the logit scale). Note that when users select predict="classification" in binomial models, the get_predicted() function will first calculate predictions as if the user had selected predict="expectation". Then, it will round the responses in order to return the most likely outcome.

Heteroscedasticity consistent standard errors: The arguments vcov_estimation, vcov_type and vcov_args can be used to calculate robust standard errors for confidence intervals of predictions. These arguments, when provided in get_predicted(), are passed down to get_predicted_ci(), thus, see the related documentation there for more details.

Value

The fitted values (i.e. predictions for the response). For Bayesian or bootstrapped models (when iterations != NULL), iterations (as columns and observations are rows) can be accessed via as.data.frame.

See Also

get_predicted_ci()
get_predicted_ci

Confidence and Prediction Interval for Model Predictions

Description

Returns the Confidence (or Prediction) Interval (CI) associated with predictions made by a model.
Usage

```r
get_predicted_ci(x, predictions = NULL, ...)
```

## Default S3 method:
```r
get_predicted_ci(  
  x,  
  predictions = NULL,  
  data = NULL,  
  se = NULL,  
  ci = 0.95,  
  ci_type = "confidence",  
  ci_method = "quantile",  
  dispersion_method = "sd",  
  vcov_estimation = NULL,  
  vcov_type = NULL,  
  vcov_args = NULL,  
  ...
)
```

Arguments

- **x**: A statistical model (can also be a data.frame, in which case the second argument has to be a model).
- **predictions**: A vector of predicted values (as obtained by `stats::fitted()`, `stats::predict()` or `get_predicted()`).
- **...**: Not used for now.
- **data**: An optional data frame in which to look for variables with which to predict. If omitted, the data used to fit the model is used.
- **se**: Numeric vector of standard error of predicted values. If `NULL`, standard errors are calculated based on the variance-covariance matrix.
- **ci**: The interval level (default 0.95, i.e., 95% CI).
- **ci_type**: Can be "prediction" or "confidence". Prediction intervals show the range that likely contains the value of a new observation (in what range it would fall), whereas confidence intervals reflect the uncertainty around the estimated parameters (and gives the range of the link; for instance of the regression line in a linear regressions). Prediction intervals account for both the uncertainty in the model’s parameters, plus the random variation of the individual values. Thus, prediction intervals are always wider than confidence intervals. Moreover, prediction intervals will not necessarily become narrower as the sample size increases (as they do not reflect only the quality of the fit). This applies mostly for "simple" linear models (like `lm`), as for other models (e.g., `glm`), prediction intervals are somewhat useless (for instance, for a binomial model for which the dependent variable is a vector of 1s and 0s, the prediction interval is... [0, 1]).
- **dispersion_method**, **ci_method**: These arguments are only used in the context of bootstrapped and Bayesian models. Possible values are `dispersion_method = c("sd","mad")` and `ci_method`
get_predicted_ci

= c("quantile","hdi","eti"). For the latter, the bayestestR package is required.

cov_estimation

Either a matrix, or a string, indicating the suffix of the vcov()-function from the sandwich or clubSandwich package, e.g. vcov_estimation = "CL" (which calls sandwich::vcovCL() to compute clustered covariance matrix estimators), or vcov_estimation = "HC" (which calls sandwich::vcovHC() to compute heteroskedasticity-consistent covariance matrix estimators).

cov_type

Character vector, specifying the estimation type for the robust covariance matrix estimation (see sandwich::vcovHC() or clubSandwich::vcovCR() for details). Only applies if vcov_estimation is a string, and not a matrix.

cov_args

List of named vectors, used as additional arguments that are passed down to the sandwich-function specified in vcov_estimation. Only applies if vcov_estimation is a string, and not a matrix.

Value

The Confidence (or Prediction) Interval (CI).

Examples

data(mtcars)

# Linear model
# ------------
x <- lm(mpg ~ cyl + hp, data = mtcars)
predictions <- predict(x)

###
ci_vals <- get_predicted_ci(x, predictions, ci_type = "prediction")

###
head(ci_vals)

###
ci_vals <- get_predicted_ci(x, predictions, ci_type = "confidence")

###
head(ci_vals)

###
ci_vals <- get_predicted_ci(x, predictions, ci = c(0.8, 0.9, 0.95))

###
head(ci_vals)

# Bootstrapped
# -------------
predictions <- get_predicted(x, iterations = 500)

get_predicted_ci(x, predictions)

if (require("datawizard")) {

  ###
ci_vals <- get_predicted_ci(x, predictions, ci = c(0.80, 0.95))

  ###
head(ci_vals)

datawizard::reshape_ci(ci_vals)

  ###
ci_vals <- getpredicted_ci(x,

dispersio

  ###

  ###

  ###
}

head(ci_vals)
# Logistic model
# --------------
x <- glm(vs ~ wt, data = mtcars, family = "binomial")
predictions <- predict(x, type = "link")
ci_vals <- get_predicted_ci(x, predictions, ci_type = "prediction")
head(ci_vals)
ci_vals <- get_predicted_ci(x, predictions, ci_type = "confidence")
head(ci_vals)

get_predictors  Get the data from model predictors

Description

Returns the data from all predictor variables (fixed effects).

Usage

generatePredictors(x, verbose = TRUE)

Arguments

x    A fitted model.
verbose    Toggle messages and warnings.

Value

The data from all predictor variables, as data frame.

Examples

m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
head(get_predictors(m))

get_priors  Get summary of priors used for a model

Description

Provides a summary of the prior distributions used for the parameters in a given model.
Usage

get_priors(x, ...)

## S3 method for class 'brmsfit'
get_priors(x, verbose = TRUE, ...)

Arguments

x A Bayesian model.
...
verbose Toggle warnings and messages.

Value

A data frame with a summary of the prior distributions used for the parameters in a given model.

Examples

## Not run:
library(rstanarm)
model <- stan_glm(Sepal.Width ~ Species * Petal.Length, data = iris)
get_priors(model)
## End(Not run)

Description

Returns the data from all random effects terms.

Usage

get_random(x)

Arguments

x A fitted mixed model.

Value

The data from all random effects terms, as data frame. Or NULL if model has no random effects.
get_residuals

Examples

```r
if (require("lme4")) {
  data(sleepstudy)
  # prepare some data...
  sleepstudy$mygrp <- sample(1:5, size = 180, replace = TRUE)
  sleepstudy$mysubgrp <- NA
  for (i in 1:5) {
    filter_group <- sleepstudy$mygrp == i
    sleepstudy$mysubgrp[filter_group] <-
      sample(1:30, size = sum(filter_group), replace = TRUE)
  }

  m <- lmer(
    Reaction ~ Days + (1 | mygrp / mysubgrp) + (1 | Subject),
    data = sleepstudy
  )

  head(get_random(m))
}
```

get_residuals

Extract model residuals

Description

Returns the residuals from regression models.

Usage

```r
get_residuals(x, ...)
```

## Default S3 method:
```r
get_residuals(x, weighted = FALSE, verbose = TRUE, ...)
```

Arguments

- `x`: A model.
- `...`: Passed down to residuals(), if possible.
- `weighted`: Logical, if TRUE, returns weighted residuals.
- `verbose`: Toggle warnings and messages.

Value

The residuals, or NULL if this information could not be accessed.
Note

This function returns the default type of residuals, i.e. for the response from linear models, the deviance residuals for models of class glm etc. To access different types, pass down the type argument (see 'Examples').

This function is a robust alternative to residuals(), as it works for some special model objects that otherwise do not respond properly to calling residuals().

Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_residuals(m)

m <- glm(vs ~ wt + cyl + mpg, data = mtcars, family = binomial())
get_residuals(m) # type = "deviance" by default
get_residuals(m, type = "response")

get_response

Get the values from the response variable

Description

Returns the values the response variable(s) from a model object. If the model is a multivariate response model, a data frame with values from all response variables is returned.

Usage

get_response(x, select = NULL, verbose = TRUE)

Arguments

x
A fitted model.

select
Optional name(s) of response variables for which to extract values. Can be used in case of regression models with multiple response variables.

verbose
Toggle warnings.

Value

The values of the response variable, as vector, or a data frame if x has more than one defined response variable.
Examples

```r
if (require("lme4")) {
  data(cbpp)
  cbpp$trials &lt;= cbpp$size - cbpp$incidence

  m &lt;- glm(cbind(incidence, trials) ~ period, data = cbpp, family = binomial)
  head(get_response(m))
  get_response(m, select = "incidence")
}

data(mtcars)
  m &lt;- lm(mpg ~ wt + cyl + vs, data = mtcars)
  get_response(m)
```

---

**get_sigma**

*Get residual standard deviation from models*

**Description**

Returns sigma, which corresponds the estimated standard deviation of the residuals. This function extends the `sigma()` base R generic for models that don’t have implemented it. It also computes the confidence interval (CI), which is stored as an attribute.

Sigma is a key-component of regression models, and part of the so-called auxiliary parameters that are estimated. Indeed, linear models for instance assume that the residuals comes from a normal distribution with mean 0 and standard deviation sigma. See the details section below for more information about its interpretation and calculation.

**Usage**

```r
get_sigma(x, ci = NULL, verbose = TRUE)
```

**Arguments**

- `x`: A model.
- `ci`: Scalar, the CI level. The default (NULL) returns no CI.
- `verbose`: Toggle messages and warnings.

**Details**

**Interpretation of Sigma:** The residual standard deviation, σ, indicates that the predicted outcome will be within +/- σ units of the linear predictor for approximately 68% of the data points (Gelman, Hill & Vehtari 2020, p.84). In other words, the residual standard deviation indicates the accuracy for a model to predict scores, thus it can be thought of as “a measure of the average distance each observation falls from its prediction from the model” (Gelman, Hill & Vehtari 2020, p.168). σ can be considered as a measure of the unexplained variation in the data, or of the precision of inferences about regression coefficients.
**Calculation of Sigma:** By default, `get_sigma()` tries to extract sigma by calling `stats::sigma()`. If the model-object has no `sigma()` method, the next step is calculating sigma as square-root of the model-deviance divided by the residual degrees of freedom. Finally, if even this approach fails, and `x` is a mixed model, the residual standard deviation is accessed using the square-root from `get_variance_residual()`.

**Value**

The residual standard deviation (sigma), or `NULL` if this information could not be accessed.

**References**


**Examples**

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_sigma(m)
```

---

**get_statistic**

*Get statistic associated with estimates*

**Description**

Returns the statistic (t, z, ...) for model estimates. In most cases, this is the related column from `coef(summary())`.

**Usage**

```r
get_statistic(x, ...)
```

## Default S3 method:

```r
get_statistic(x, column_index = 3, verbose = TRUE, ...)
```

## S3 method for class `lm`

```r
get_statistic(x, component = c("all", "conditional", "zi", "zero_inflated", "dispersion"), ...)
```

## S3 method for class `glmmTMB`

```r
get_statistic(x, component = c("all", "conditional", "scale"), ...)
```

## S3 method for class `betamfx`

```r
get_statistic(x, ...)
```
Arguments

x  A model.

...  Currently not used.

column_index  For model objects that have no defined get_statistic() method yet, the
default method is called. This method tries to extract the statistic column from
coef(summary()), where the index of the column that is being pulled is column_index.
Defaults to 3, which is the default statistic column for most models' summary-
output.

verbose  Toggle messages and warnings.

component  Should all parameters, parameters for the conditional model, or for the zero-
inflated part of the model be returned? Applies to models with zero-inflated
component. component may be one of "conditional", "zi", "zero-inflated"
or "all" (default). For models with smooth terms, component = "smooth_terms"
is also possible. May be abbreviated. Note that the conditional component is
also called count or mean component, depending on the model.

ci  Confidence Interval (CI) level. Default to 0.95 (95%). Currently only applies
to objects of class emmGrid.

adjust  Character value naming the method used to adjust p-values or confidence inter-
vals. See ?emmeans::summary.emmGrid for details.

merge_parameters  Logical, if TRUE and x has multiple columns for parameter names (like emmGrid
objects may have), these are merged into a single parameter column, with pa-
rameters names and values as values.

robust  Logical, if TRUE, test statistic based on robust standard errors is returned.
get_transformation

Value

A data frame with the model’s parameter names and the related test statistic.

Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
get_statistic(m)

Description

This function checks whether any transformation, such as log- or exp-transforming, was applied to
the response variable (dependent variable) in a regression formula, and returns the related function
that was used for transformation.

Usage

get_transformation(x)

Arguments

  x       A regression model.

Value

A list of two functions: $transformation, the function that was used to transform the response vari-
able; $inverse, the inverse-function of $transformation (can be used for “back-transformation”). If
no transformation was applied, both list-elements $transformation and $inverse just return function(x)
x.

Examples

# identity, no transformation
model <- lm(Sepal.Length ~ Species, data = iris)
get_transformation(model)

# log-transformation
model <- lm(log(Sepal.Length) ~ Species, data = iris)
get_transformation(model)

# log-function
get_transformation(model)$transformation(.3)
log(.3)

# inverse function is exp()
get_transformation(model)$inverse(.3)
exp(.3)
get_varcov

Get variance-covariance matrix from models

Description

Returns the variance-covariance, as retrieved by stats::vcov(), but works for more model objects that probably don't provide a vcov()-method.

Usage

get_varcov(x, ...)

## Default S3 method:
get_varcov(x, verbose = TRUE, ...)

## S3 method for class 'betareg'
get_varcov(
x,
  component = c("conditional", "precision", "all"),
  verbose = TRUE,
  ...
)

## S3 method for class 'DirichletRegModel'
get_varcov(
x,
  component = c("conditional", "precision", "all"),
  verbose = TRUE,
  ...
)

## S3 method for class 'clm2'
get_varcov(x, component = c("all", "conditional", "scale"), ...)

## S3 method for class 'truncreg'
get_varcov(x, component = c("conditional", "all"), ...)

## S3 method for class 'gamlss'
get_varcov(x, component = c("conditional", "all"), ...)

## S3 method for class 'hurdle'
get_varcov(x, component = c("conditional", "zero_inflated", "zi", "all"), ...)

## S3 method for class 'zcpglm'
get_varcov(x, component = c("conditional", "zero_inflated", "zi", "all"), ...)

## S3 method for class 'glmmTMB'
get_varcov(
  x,
  component = c("conditional", "zero_inflated", "zi", "dispersion", "all"),
  ...
)

## S3 method for class 'MixMod'
get_varcov(
  x,
  effects = c("fixed", "random"),
  component = c("conditional", "zero_inflated", "zi", "dispersion", "auxiliary", "all"),
  robust = FALSE,
  verbose = TRUE,
  ...
)

## S3 method for class 'brmsfit'
get_varcov(x, component = "conditional", ...)

## S3 method for class 'betamfx'
get_varcov(x, component = c("conditional", "precision", "all"), ...)

## S3 method for class 'aov'
get_varcov(x, complete = FALSE, ...)

## S3 method for class 'mixor'
get_varcov(x, effects = c("all", "fixed", "random"), ...)

Arguments

x A model.

... Currently not used.

verbose Toggle warnings.

cOMPONENT Should the complete variance-covariance matrix of the model be returned, or only for specific model components only (like count or zero-inflated model parts)? Applies to models with zero-inflated component, or models with precision (e.g. betareg) component. component may be one of "conditional", "zi", "zero-inflated", "dispersion", "precision", or "all". May be abbreviated. Note that the conditional component is also called count or mean component, depending on the model.

effects Should the complete variance-covariance matrix of the model be returned, or only for specific model parameters only? Currently only applies to models of class mixor.

robust Logical, if TRUE, returns a robust variance-covariance matrix using sandwich estimation.

complete Logical, if TRUE, for aov, returns the full variance-covariance matrix.
Value

The variance-covariance matrix, as matrix-object.

Note

gtext_varcov() tries to return the nearest positive definite matrix in case of a negative variance-covariance matrix.

Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
gtext_varcov(m)

get_variance

Get variance components from random effects models

Description

This function extracts the different variance components of a mixed model and returns the result as list. Functions like get_variance_residual(x) or get_variance_fixed(x) are shortcuts for get_variance(x, component = "residual") etc.

Usage

gtext_variance(x, 
component = c("all", "fixed", "random", "residual", "distribution", "dispersion", 
"intercept", "slope", "rho01", "rho00"), 
verbose = TRUE, 
...)

gtext_variance_residual(x, verbose = TRUE, ...)

gtext_variance_fixed(x, verbose = TRUE, ...)

gtext_variance_random(x, verbose = TRUE, tolerance = 1e-05, ...)

gtext_variance_distribution(x, verbose = TRUE, ...)

gtext_variance_dispersion(x, verbose = TRUE, ...)

gtext_variance_intercept(x, verbose = TRUE, ...)

gtext_variance_slope(x, verbose = TRUE, ...)
get_correlation_slopes(x, verbose = TRUE, ...)

Arguments

x: A mixed effects model.

component: Character value, indicating the variance component that should be returned. By default, all variance components are returned. The distribution-specific ("distribution") and residual ("residual") variance are the most computational intensive components, and hence may take a few seconds to calculate.

verbose: Toggle off warnings.

... Currently not used.

tolerance: Tolerance for singularity check of random effects, to decide whether to compute random effect variances or not. Indicates up to which value the convergence result is accepted. The larger tolerance is, the stricter the test will be. See performance::check_singularity().

Details

This function returns different variance components from mixed models, which are needed, for instance, to calculate r-squared measures or the intraclass-correlation coefficient (ICC).

**Fixed effects variance:** The fixed effects variance, $\sigma^2_f$, is the variance of the matrix-multiplication $\beta \times X$ (parameter vector by model matrix).

**Random effects variance:** The random effect variance, $\sigma^2_r$, represents the mean random effect variance of the model. Since this variance reflect the "average" random effects variance for mixed models, it is also appropriate for models with more complex random effects structures, like random slopes or nested random effects. Details can be found in Johnson 2014, in particular equation 10. For simple random-intercept models, the random effects variance equals the random-intercept variance.

**Distribution-specific variance:** The distribution-specific variance, $\sigma^2_d$, depends on the model family. For Gaussian models, it is $\sigma^2$ (i.e. sigma(model)^2). For models with binary outcome, it is $\pi^2/3$ for logit-link, 1 for probit-link, and $\pi^2/6$ for cloglog-links. Models from Gamma-families use $\mu^2$ (as obtained from family$\$variance()). For all other models, the distribution-specific variance is based on lognormal approximation, $\log(1 + var(x)/\mu^2)$ (see Nakagawa et al. 2017). The expected variance of a zero-inflated model is computed according to Zuur et al. 2012, p277.

**Variance for the additive overdispersion term:** The variance for the additive overdispersion term, $\sigma^2_e$, represents "the excess variation relative to what is expected from a certain distribution" (Nakagawa et al. 2017). In (most? many?) cases, this will be 0.

**Residual variance:** The residual variance, $\sigma^2_\epsilon$, is simply $\sigma^2_d + \sigma^2_e$.

**Random intercept variance:** The random intercept variance, or between-subject variance ($\tau_{00}$), is obtained from VarCorr(). It indicates how much groups or subjects differ from each other, while the residual variance $\sigma^2_\epsilon$ indicates the within-subject variance.
Random slope variance: The random slope variance ($\tau_{11}$) is obtained from `VarCorr()`. This measure is only available for mixed models with random slopes.

Random slope-intercept correlation: The random slope-intercept correlation ($\rho_{01}$) is obtained from `VarCorr()`. This measure is only available for mixed models with random intercepts and slopes.

Value

A list with following elements:

- `var.fixed`, variance attributable to the fixed effects
- `var.random`, (mean) variance of random effects
- `var.residual`, residual variance (sum of dispersion and distribution)
- `var.distribution`, distribution-specific variance
- `var.dispersion`, variance due to additive dispersion
- `var.intercept`, the random-intercept-variance, or between-subject-variance ($\tau_{00}$)
- `var.slope`, the random-slope-variance ($\tau_{11}$)
- `cor.slope_intercept`, the random-slope-intercept-correlation ($\rho_{01}$)
- `cor.slopes`, the correlation between random slopes ($\rho_{00}$)

Note

This function supports models of class `merMod` (including models from `blme`, `clmm`, `cpglmm`, `glmmadmb`, `glmmTMB`, `MixMod`, `lme`, `mixed`, `rlmerMod`, `stanreg`, `brmsfit` or `wbm`). Support for objects of class `MixMod` (`GLMMadaptive`), `lme` (`nlme`) or `brmsfit` (`brms`) is experimental and may not work for all models.

References


Examples

```r
## Not run:
library(lme4)
data(sleepstudy)
m <- lmer(Reaction ~ Days + (1 + Days | Subject), data = sleepstudy)
get_variance(m)
```
get_weights

Get the values from model weights

Description

Returns weighting variable of a model.

Usage

going_weights(x, ...)

## Default S3 method:
going_weights(x, na_rm = FALSE, null_as_ones = FALSE, ...)

Arguments

x

A fitted model.

...

Currently not used.

na_rm

Logical, if TRUE, removes possible missing values.

null_as_ones

Logical, if TRUE, will return a vector of 1 if no weights were specified in the model (as if the weights were all set to 1).

Value

The weighting variable, or NULL if no weights were specified or if weights were 1. If the weighting variable should also be returned (instead of NULL), when all weights are set to 1 (i.e. no weighting), set null_as_ones = TRUE.

Examples

data(mtcars)
set.seed(123)
mtcars$weight <- rnorm(nrow(mtcars), 1, .3)

# LMs
m <- lm(mpg ~ wt + cyl + vs, data = mtcars, weights = weight)
get_weights(m)

gerget_weights(lm(mpg ~ wt, data = mtcars), null_as_ones = TRUE)

# GLMs
m <- glm(vs ~ disp + mpg, data = mtcars, weights = weight, family = quasibinomial)
ger_weights(m)
m <- glm(cbind(cyl, gear) ~ mpg, data = mtcars, weights = weight, family = binomial)
ger_weights(m)
**has_intercept**

*Checks if model has an intercept*

**Description**

Checks if model has an intercept.

**Usage**

```r
has_intercept(x, verbose = TRUE)
```

**Arguments**

- `x`: A model object.
- `verbose`: Toggle warnings.

**Value**

TRUE if `x` has an intercept, FALSE otherwise.

**Examples**

```r
model <- lm(mpg ~ 0 + gear, data = mtcars)
have_intercept(model)
```

```r
model <- lm(mpg ~ gear, data = mtcars)
have_intercept(model)
```

```r
if (require("lme4")) {
  model <- lmer(Reaction ~ 0 + Days + (Days | Subject), data = sleepstudy)
have_intercept(model)

  model <- lmer(Reaction ~ Days + (Days | Subject), data = sleepstudy)
have_intercept(model)
}
```

---

**is_gam_model**

*Checks if a model is a generalized additive model*

**Description**

Small helper that checks if a model is a generalized additive model.

**Usage**

```r
is_gam_model(x)
```
is_mixed_model

Arguments

x A model object.

Value

A logical, TRUE if x is a mixed model.

Note

This function only returns TRUE when the model inherits from a typical GAM model class and when smooth terms are present in the model formula. If model has no smooth terms or is not from a typical gam class, FALSE is returned.

Examples

if (require("mgcv")) {
  data(iris)
  model1 <- lm(Petal.Length ~ Petal.Width + Sepal.Length, data = iris)
  model2 <- gam(Petal.Length ~ Petal.Width + s(Sepal.Length), data = iris)
  is_gam_model(model1)
  is_gam_model(model2)
}

is_mixed_model Checks if a model is a mixed effects model

Description

Small helper that checks if a model is a mixed effects model, i.e. if it the model has random effects.

Usage

is_mixed_model(x)

Arguments

x A model object.

Value

A logical, TRUE if x is a mixed model.
is_model

Checks if an object is a regression model or statistical test object

Description
Small helper that checks if a model is a regression model or a statistical object. is_regression_model() is stricter and only returns TRUE for regression models, but not for, e.g., htest objects.

Usage
is_model(x)

is_regression_model(x)

Arguments
x An object.

Details
This function returns TRUE if x is a model object.

Value
A logical, TRUE if x is a (supported) model object.

Examples
data(mtcars)
model <- lm(mpg ~ wt + cyl + vs, data = mtcars)
is_model(model)

if (require("lme4")) {
data(sleepstudy)
model <- lmer(Reaction ~ Days + (1 | Subject), data = sleepstudy)
is_mixed_model(model)
}

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
is_model(m)
is_model(mtcars)
test <- t.test(1:10, y = c(7:20))
is_model(test)
is_regression_model(test)
is_model_supported

Checks if an object is a regression model object supported in insight package.

Description
Small helper that checks if a model is a supported (regression) model object. supported_models() prints a list of currently supported model classes.

Usage

is_model_supported(x)

supported_models()

Arguments

x
An object.

Details
This function returns TRUE if x is a model object that works with the package’s functions. A list of supported models can also be found here: https://github.com/easystats/insight.

Value
A logical, TRUE if x is a (supported) model object.

Examples

data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)

is_model_supported(m)
is_model_supported(mtcars)

is_multivariate

Checks if an object stems from a multivariate response model

Description
Small helper that checks if a model is a multivariate response model, i.e. a model with multiple outcomes.

Usage

is_multivariate(x)
is_nested_models

Arguments

x  A model object, or an object returned by a function from this package.

Value

A logical, TRUE if either x is a model object and is a multivariate response model, or TRUE if a return value from a function of insight is from a multivariate response model.

Examples

## Not run:
library(rstanarm)
data("pbcLong")
model <- stan_mvmer(
  formula = list(
    logBili ~ year + (1 | id),
    albumin ~ sex + year + (year | id)
  ),
  data = pbcLong,
  chains = 1, cores = 1, seed = 12345, iter = 1000
)

f <- find_formula(model)
is_multivariate(model)
is_multivariate(f)

## End(Not run)

is_nested_models  Checks whether a list of models are nested models

Description

Checks whether a list of models are nested models, strictly following the order they were passed to the function.

Usage

is_nested_models(...)

Arguments

...  Multiple regression model objects.

Value

TRUE if models are nested, FALSE otherwise. If models are nested, also returns two attributes that indicate whether nesting of models is in decreasing or increasing order.
Examples

m1 <- lm(Sepal.Length ~ Petal.Width + Species, data = iris)
m2 <- lm(Sepal.Length ~ Species, data = iris)
m3 <- lm(Sepal.Length ~ Petal.Width, data = iris)
m4 <- lm(Sepal.Length ~ 1, data = iris)

is_nested_models(m1, m2, m4)
is_nested_models(m4, m2, m1)
is_nested_models(m1, m2, m3)

is_nullmodel

Checks if model is a null-model (intercept-only)

Description

Checks if model is a null-model (intercept-only), i.e. if the conditional part of the model has no predictors.

Usage

is_nullmodel(x)

Arguments

x A model object.

Value

TRUE if x is a null-model, FALSE otherwise.

Examples

model <- lm(mpg ~ 1, data = mtcars)
is_nullmodel(model)

model <- lm(mpg ~ gear, data = mtcars)
is_nullmodel(model)

if (require("lme4")) {
  model <- lmer(Reaction ~ 1 + (Days | Subject), data = sleepstudy)
is_nullmodel(model)

  model <- lmer(Reaction ~ Days + (Days | Subject), data = sleepstudy)
is_nullmodel(model)
}
link_function

Get link-function from model object

Description

Returns the link-function from a model object.

Usage

link_function(x, ...)

## S3 method for class 'betamix'
link_function(x, what = c("mean", "precision"), ...)

## S3 method for class 'gamlss'
link_function(x, what = c("mu", "sigma", "nu", "tau"), ...)

## S3 method for class 'betareg'
link_function(x, what = c("mean", "precision"), ...)

## S3 method for class 'DirichletRegModel'
link_function(x, what = c("mean", "precision"), ...)

Arguments

x             A fitted model.
...            Currently not used.
what           For gamlss models, indicates for which distribution parameter the link (inverse) function should be returned; for betareg or DirichletRegModel, can be "mean" or "precision".

Value

A function, describing the link-function from a model-object. For multivariate-response models, a list of functions is returned.

Examples

# example from ?stats::glm
 counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
 outcome <- gl(3, 1, 9)
 treatment <- gl(3, 3)
 m <- glm(counts ~ outcome + treatment, family = poisson())

link_function(m)(.3)
# same as
log(.3)
Get link-inverse function from model object

Description

Returns the link-inverse function from a model object.

Usage

link_inverse(x, ...)

## S3 method for class 'betareg'
link_inverse(x, what = c("mean", "precision"), ...)

## S3 method for class 'DirichletRegModel'
link_inverse(x, what = c("mean", "precision"), ...)

## S3 method for class 'betamfx'
link_inverse(x, what = c("mean", "precision"), ...)

## S3 method for class 'gamlss'
link_inverse(x, what = c("mu", "sigma", "nu", "tau"), ...)

Arguments

x       A fitted model.
...     Currently not used.
what    For gamlss models, indicates for which distribution parameter the link (inverse) function should be returned; for betareg or DirichletRegModel, can be "mean" or "precision".

Value

A function, describing the inverse-link function from a model-object. For multivariate-response models, a list of functions is returned.

Examples

# example from ?stats::glm
counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome <- gl(3, 1, 9)
treatment <- gl(3, 3)
m <- glm(counts ~ outcome + treatment, family = poisson())

link_inverse(m)(.3)
# same as
exp(.3)
Description

Retrieve information from model objects.

Usage

model_info(x, ...)

## Default S3 method:
model_info(x, verbose = TRUE, ...)

Arguments

x       A fitted model.
...
   Currently not used.
verbose   Toggle off warnings.

Details

model_info() returns a list with information about the model for many different model objects. Following information is returned, where all values starting with is_ are logicals.

• is_binomial: family is binomial (but not negative binomial)
• is_bernoulli: special case of binomial models: family is Bernoulli
• is_poisson: family is poisson
• is_negbin: family is negative binomial
• is_count: model is a count model (i.e. family is either poisson or negative binomial)
• is_beta: family is beta
• is_betabinomial: family is beta-binomial
• is_dirichlet: family is dirichlet
• is_exponential: family is exponential (e.g. Gamma or Weibull)
• is_logit: model has logit link
• is_probit: model has probit link
• is_linear: family is gaussian
• is_tweedie: family is tweedie
• isOrdinal: family is ordinal or cumulative link
• is_cumulative: family is ordinal or cumulative link
• is_multinomial: family is multinomial or categorical link
• is_categorical: family is categorical link
• `is_censored`: model is a censored model (has a censored response, including survival models)

• `is_truncated`: model is a truncated model (has a truncated response)

• `is_survival`: model is a survival model

• `is_zero_influenced`: model has zero-inflation component

• `is_hurdle`: model has zero-inflation component and is a hurdle-model (truncated family distribution)

• `is_dispersion`: model has dispersion component

• `is_mixed`: model is a mixed effects model (with random effects)

• `is_multivariate`: model is a multivariate response model (currently only works for `brmsfit` objects)

• `is_trial`: model response contains additional information about the trials

• `is_bayesian`: model is a Bayesian model

• `is_gam`: model is a generalized additive model

• `is_anova`: model is an Anova object

• `is_ttest`: model is an an object of class `htest`, returned by `t.test()`

• `is_correlation`: model is an an object of class `htest`, returned by `cor.test()`

• `is_ranktest`: model is an an object of class `htest`, returned by `cor.test()` (if Spearman’s rank correlation), `wilcox.test()` or `kruskal.test()`.

• `is_levenetest`: model is an an object of class `anova`, returned by `car::leveneTest()`.

• `is_onewaytest`: model is an an object of class `htest`, returned by `oneway.test()`

• `is_proptest`: model is an an object of class `htest`, returned by `prop.test()`

• `is_binomtest`: model is an an object of class `htest`, returned by `binom.test()`

• `is_chi2test`: model is an an object of class `htest`, returned by `chisq.test()`

• `is_xtab`: model is an an object of class `htest` or `BFBayesFactor`, and test-statistic stems from a contingency table (i.e. `chisq.test()` or `BayesFactor::contingencyTableBF()`).

• `link_function`: the link-function

• `family`: the family-object

• `n_obs`: number of observations

• `model_terms`: a list with all model terms, including terms such as random effects or from zero-inflated model parts.

**Value**

A list with information about the model, like family, link-function etc. (see ’Details’).
Examples

```r
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20 - numdead)
dat <- data.frame(ldose, sex, SF, stringsAsFactors = FALSE)
m <- glm(SF ~ sex * ldose, family = binomial)
```

```r
model_info(m)
## Not run:
library(glmmTMB)
data("Salamanders")
m <- glmmTMB(
  count ~ spp + cover + mined + (1 | site),
  ziformula = ~ spp + mined,
  dispformula = ~DOY,
  data = Salamanders,
  family = nbinom2
)
## End(Not run)
model_info(m)
```

Description

Returns the "name" (class attribute) of a model, possibly including further information.

Usage

```r
model_name(x, ...)
```

## Default S3 method:
```r
model_name(x, include_formula = FALSE, include_call = FALSE, ...)
```

Arguments

- `x` A model.
- `...` Currently not used.
- `include_formula` Should the name include the model’s formula.
- `include_call` If TRUE, will return the function call as a name.

Value

A character string of a name (which usually equals the model’s class attribute).
null_model

Compute intercept-only model for regression models

Description

This function computes the null-model (i.e. \( y \sim 1 \)) of a model. For mixed models, the null-model takes random effects into account.

Usage

null_model(model, verbose = TRUE, ...)

Arguments

- **model**: A (mixed effects) model.
- **verbose**: Toggle off warnings.
- **...**: Arguments passed to or from other methods.

Value

The null-model of x

Examples

```r
if (require("lme4")) {
  data(sleepstudy)
  m <- lmer(Reaction ~ Days + (1 + Days | Subject), data = sleepstudy)
  summary(m)
  summary(null_model(m))
}
```
**n_obs**

*Get number of observations from a model*

---

**Description**

This method returns the number of observation that were used to fit the model, as numeric value.

**Usage**

```r
n_obs(x, ...)  
## S3 method for class 'glm'
n_obs(x, disaggregate = FALSE, ...)

## S3 method for class 'svyolr'
n_obs(x, weighted = FALSE, ...)

## S3 method for class 'afex_aov'
n_obs(x, shape = c("long", "wide"), ...)

## S3 method for class 'stanmvreg'
n_obs(x, select = NULL, ...)
```

**Arguments**

- `x`: A fitted model.
- `...`: Currently not used.
- `disaggregate`: For binomial models with aggregated data, `n_obs()` returns the number of data rows by default. If `disaggregate = TRUE`, the total number of trials is returned instead (determined by summing the results of `weights()` for aggregated data, which will be either the weights input for proportion success response or the row sums of the response matrix if matrix response, see 'Examples').
- `weighted`: For survey designs, returns the weighted sample size.
- `shape`: Return long or wide data? Only applicable in repeated measures designs.
- `select`: Optional name(s) of response variables for which to extract values. Can be used in case of regression models with multiple response variables.

**Value**

The number of observations used to fit the model, or NULL if this information is not available.

**Examples**

```r
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
n_obs(m)
```
if (require("lme4")) {
  data(cbpp, package = "lme4")
  m <- glm(
    cbind(incidence, size - incidence) ~ period,
    data = cbpp,
    family = binomial(link = "logit")
  )
  n_obs(m)
  n_obs(m, disaggregate = TRUE)
}

n_parameters  Count number of parameters in a model

Description

Returns the number of parameters (coefficients) of a model.

Usage

n_parameters(x, ...)

## Default S3 method:
n_parameters(x, remove_nonestimable = FALSE, ...)

## S3 method for class 'merMod'
n_parameters(
  x,
  effects = c("fixed", "random"),
  remove_nonestimable = FALSE,
  ...
)

## S3 method for class 'glmmTMB'
n_parameters(
  x,
  effects = c("fixed", "random"),
  component = c("all", "conditional", "zi", "zero_inflated"),
  remove_nonestimable = FALSE,
  ...
)

## S3 method for class 'zeroinfl'
n_parameters(
  x,
  component = c("all", "conditional", "zi", "zero_inflated"),
  remove_nonestimable = FALSE,
n_parameters

...)

## S3 method for class 'gam'
n_parameters(
x,
  component = c("all", "conditional", "smooth_terms"),
  remove_nonestimable = FALSE,
  ...
)

## S3 method for class 'brmsfit'
n_parameters(x, effects = "all", component = "all", ...)

Arguments

x A statistical model.

... Arguments passed to or from other methods.

remove_nonestimable Logical, if TRUE, removes (i.e. does not count) non-estimable parameters (which may occur for models with rank-deficient model matrix).

effects Should number of parameters for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.

component Should total number of parameters, number parameters for the conditional model, the zero-inflated part of the model, the dispersion term or the instrumental variables be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variable (so called fixed-effects regressions). May be abbreviated.

Value

The number of parameters in the model.

Note

This function returns the number of parameters for the fixed effects by default, as returned by find_parameters(x, effects = "fixed"). It does not include all estimated model parameters, i.e. auxiliary parameters like sigma or dispersion are not counted. To get the number of all estimated parameters, use get_df(x, type = "model").

Examples

data(iris)
model <- lm(Sepal.Length ~ Sepal.Width * Species, data = iris)
n_parameters(model)
print_color  
Coloured console output

Description
Convenient function that allows coloured output in the console. Mainly implemented to reduce package dependencies.

Usage

print_color(text, color)
print_colour(text, colour)
color_text(text, color)
colour_text(text, colour)
color_theme()

Arguments

- text: The text to print.
- color, colour: Character vector, indicating the colour for printing. May be one of "red", "yellow", "green", "blue", "violet", "cyan" or "grey". Formatting is also possible with "bold" or "italic".

Details
This function prints text directly to the console using cat(), so no string is returned. color_text(), however, returns only the formatted string, without using cat(). color_theme() either returns "dark" when RStudio is used with dark color scheme, "light" when it’s used with light theme, and NULL if the theme could not be detected.

Value
Nothing.

Examples

print_color("I'm blue dabedi dabedei", "blue")
**Description**

This function takes a data frame, typically a data frame with information on summaries of model parameters like `bayestestR::describe_posterior()`, `bayestestR::hdi()` or `parameters::model_parameters()`, as input and splits this information into several parts, depending on the model. See details below.

**Usage**

```r
print_parameters(
  x,
  ..., 
  split_by = c("Effects", "Component", "Group", "Response"), 
  format = "text", 
  parameter_column = "Parameter", 
  keep_parameter_column = TRUE, 
  remove_empty_column = FALSE, 
  titles = NULL, 
  subtitles = NULL 
)
```

**Arguments**

- `x`: A fitted model, or a data frame returned by `clean_parameters()`.
- `...`: One or more objects (data frames), which contain information about the model parameters and related statistics (like confidence intervals, HDI, ROPE, ...).
- `split_by`: split_by should be a character vector with one or more of the following elements: "Effects", "Component", "Response" and "Group". These are the column names returned by `clean_parameters()`, which is used to extract the information from which the group or component model parameters belong. If `NULL`, the merged data frame is returned. Else, the data frame is split into a list, split by the values from those columns defined in `split_by`.
- `format`: Name of output-format, as string. If `NULL` (or "text"), assumed use for output is basic printing. If "markdown", markdown-format is assumed. This only affects the style of title- and table-caption attributes, which are used in `export_table()`.
- `parameter_column`: String, name of the column that contains the parameter names. Usually, for data frames returned by functions the easystats-packages, this will be "Parameter".
- `keep_parameter_column`: Logical, if `TRUE`, the data frames in the returned list have both a "Cleaned_Parameter" and "Parameter" column. If `FALSE`, the (unformatted) "Parameter" is removed, and the column with cleaned parameter names ("Cleaned_Parameter") is renamed into "Parameter".
remove_empty_column
Logical, if TRUE, columns with completely empty character values will be removed.

titles, subtitles
By default, the names of the model components (like fixed or random effects, count or zero-inflated model part) are added as attributes "table_title" and "table_subtitle" to each list element returned by print_parameters(). These attributes are then extracted and used as table (sub) titles in export_table(). Use titles and subtitles to override the default attribute values for "table_title" and "table_subtitle". titles and subtitles may be any length from 1 to same length as returned list elements. If titles and subtitles are shorter than existing elements, only the first default attributes are overwritten.

Details
This function prepares data frames that contain information about model parameters for clear printing.

First, x is required, which should either be a model object or a prepared data frame as returned by clean_parameters(). If x is a model, clean_parameters() is called on that model object to get information with which model components the parameters are associated.

Then, ... take one or more data frames that also contain information about parameters from the same model, but also have additional information provided by other methods. For instance, a data frame in ... might be the result of, for instance, bayestestR::describe_posterior(), or parameters::model_parameters(), where we have a) a Parameter column and b) columns with other parameter values (like CI, HDI, test statistic, etc.).

Now we have a data frame with model parameters and information about the association to the different model components, a data frame with model parameters, and some summary statistics. print_parameters() then merges these data frames, so the parameters or statistics of interest are also associated with the different model components. The data frame is split into a list, so for a clear printing. Users can loop over this list and print each component for a better overview. Further, parameter names are "cleaned", if necessary, also for a cleaner print. See also 'Examples'.

Value
A data frame or a list of data frames (if split_by is not NULL). If a list is returned, the element names reflect the model components where the extracted information in the data frames belong to, e.g. random.zero_inflated.Intercept: persons. This is the data frame that contains the parameters for the random effects from group-level "persons" from the zero-inflated model component.

Examples
## Not run:
library(bayestestR)
model <- download_model("brms_zi_2")
x <- hdi(model, effects = "all", component = "all")

# hdi() returns a data frame; here we use only the
standardize_column_order

Standardize column order

Description

Standardizes order of columns for dataframes and other objects from easystats and broom ecosystem packages.

Usage

standardize_column_order(data, ...)

## S3 method for class 'parameters_model'
standardize_column_order(data, style = c("easystats", "broom"), ...)

Arguments

data A data frame. In particular, objects from easystats package functions like parameters::model_parameters or effectsize::effectsize() are accepted, but also data frames returned by broom::tidy() are valid objects.

... Currently not used.

style Standardization can either be based on the naming conventions from the easystats-project, or on broom’s naming scheme.

Value

A data frame, with standardized column order.
Examples

```r
# easystats conventions
df1 <- cbind.data.frame(
  CI_low = -2.873,
  t = 5.494,
  CI_high = -1.088,
  p = 0.00001,
  Parameter = -1.980,
  CI = 0.95,
  df = 29.234,
  Method = "Student's t-test"
)

standardize_column_order(df1, style = "easystats")

# broom conventions
df2 <- cbind.data.frame(
  conf.low = -2.873,
  statistic = 5.494,
  conf.high = -1.088,
  p.value = 0.00001,
  estimate = -1.980,
  conf.level = 0.95,
  df = 29.234,
  method = "Student's t-test"
)

standardize_column_order(df2, style = "broom")
```

---

**standardize_names**  
*Standardize column names*

**Description**

Standardize column names from data frames, in particular objects returned from `parameters::model_parameters()`, so column names are consistent and the same for any model object.

**Usage**

```r
standardize_names(data, ...)

## S3 method for class 'parameters_model'
standardize_names(
  data,
  style = c("easystats", "broom"),
  ignore_estimate = FALSE,
  ...)
```
Arguments

- **data**: A data frame. In particular, objects from `easystats` package functions like `parameters::model_parameters()` or `effectsize::effectsize()` are accepted, but also data frames returned by `broom::tidy()` are valid objects.
- **...**: Currently not used.
- **style**: Standardization can either be based on the naming conventions from the `easystats-project`, or on `broom`'s naming scheme.
- **ignore_estimate**: Logical, if TRUE, column names like "mean" or "median" will not be converted to "Coefficient" resp. "estimate".

Details

This method is in particular useful for package developers or users who use, e.g., `parameters::model_parameters()` in their own code or functions to retrieve model parameters for further processing. As `model_parameters()` returns a data frame with varying column names (depending on the input), accessing the required information is probably not quite straightforward. In such cases, `standardize_names()` can be used to get consistent, i.e. always the same column names, no matter what kind of model was used in `model_parameters()`.

For `style = "broom"`, column names are renamed to match `broom`'s naming scheme, i.e. Parameter is renamed to term, Coefficient becomes estimate and so on.

For `style = "easystats"`, when `data` is an object from `broom::tidy()`, column names are converted from "broom"-style into "easystats"-style.

Value

A data frame, with standardized column names.

Examples

```r
if (require("parameters")) {
  model <- lm(mpg ~ wt + cyl, data = mtcars)
  mp <- model_parameters(model)

  as.data.frame(mp)
  standardize_names(mp)
  standardize_names(mp, style = "broom")
}
```

---

text_remove_backticks  Remove backticks from a string

Description

This function removes backticks from a string.
Usage

text_remove_backticks(x, ...)

## S3 method for class 'data.frame'
text_remove_backticks(x, column = "Parameter", verbose = FALSE, ...)

Arguments

x  A character vector, a data frame or a matrix. If a matrix, backticks are removed from the column and row names, not from values of a character vector.

...  Currently not used.

column  If x is a data frame, specify the column of character vectors, where backticks should be removed. If NULL, all character vectors are processed.

verbose  Toggle warnings.

Value

x, where all backticks are removed.

Note

If x is a character vector or data frame, backticks are removed from the elements of that character vector (or character vectors from the data frame.) If x is a matrix, the behaviour slightly differs: in this case, backticks are removed from the column and row names. The reason for this behaviour is that this function mainly serves formatting coefficient names. For vcov() (a matrix), row and column names equal the coefficient names and therefore are manipulated then.

Examples

# example model
data(iris)
iris$'a m' <- iris$Species
iris"Sepal Width" <- iris$Sepal.Width
model <- lm("Sepal Width" ~ Petal.Length + 'a m', data = iris)

# remove backticks from string
names(coef(model))
text_remove_backticks(names(coef(model)))

# remove backticks from character variable in a data frame
# column defaults to "Parameter".
d <- data.frame(Parameter = names(coef(model)),
    Estimate = unname(coef(model)))
d
text_remove_backticks(d)
Index

* data
  fish, 41
  all_models_equal, 4
  all_models_same_class
    (all_models_equal), 4

Bayesian models, 20, 65
bayestestR::ci(), 59
bayestestR::describe_posterior(), 113, 114
bayestestR::hdi(), 113
bayestestR::weighted_posteriors(), 71

check_if_installed, 5
clean_names, 6
clean_parameters(), 113, 114
color_if, 8
color_text (print_color), 112
colour_theme (print_color), 112
colour_if (color_if), 8
colour_text (print_color), 112

display, 10
download_model, 11
effectsize::effectsize(), 115, 117
ellipsis_info, 12
Estimated marginal means, 20, 65
export_table, 13
export_table(), 113, 114

find_algorithm, 16
find_formula, 17
find_interactions, 18
find_offset, 19
find_parameters(), 20
find_parameters(), 31
find_parameters.averaging, 21

find_parameters.bamlss
  (find_parameters.BGGM), 24
find_parameters.bayesx
  (find_parameters.BGGM), 24
find_parameters.betamfx, 22
find_parameters.betareg
  (find_parameters.averaging), 21
find_parameters.BFBayesFactor
  (find_parameters.BGGM), 24
find_parameters.BGGM, 24
find_parameters.BGGM(), 54
find_parameters.brmsfit
  (find_parameters.BGGM), 24
find_parameters.DirichletRegModel
  (find_parameters.averaging), 21
find_parameters.emmGrid, 27
find_parameters.gam
  (find_parameters.gamlss), 27
find_parameters.gamlss, 27
find_parameters.glmmTMB, 29
find_parameters.glmx
  (find_parameters.averaging), 21
find_parameters.logitmfx
  (find_parameters.betamfx), 22
find_parameters.MCMCglmm
  (find_parameters.BGGM), 24
find_parameters.merMod
  (find_parameters.glmmTMB), 29
find_parameters.mhurdle
  (find_parameters.zeroinfl), 30
find_parameters.mjoint
  (find_parameters.averaging), 21
find_parameters.sim.merMod
  (find_parameters.BGGM), 24
find_parameters.stanreg
  (find_parameters.BGGM), 24
find_parameters.zeroinfl, 30
find_predictors, 31
find_random, 32
INDEX

find_random_slopes, 33
find_response, 34
find_smooth, 35
find_statistic, 36
find_terms, 36
find_terms(), 39
find_transformation, 38
find_variables, 38
find_variables(), 37
find_weights, 40
fish, 41
format_bf, 41
format_capitalize, 42
format_ci, 43
format_message, 44
format_number, 45
format_p, 46
format_pd, 47
format_rope, 48
format_string, 48
format_table, 49
format_value, 51
format_value(), 45
formula_ok(find_formula), 17

generalized additive models, 20, 65
get_auxiliary, 53
get_call, 54
get_correlation_slope_intercept
  (get_variance), 93
get_correlation_slopes(get_variance), 93
get_data, 55
get_datagrid, 58
get_deviance, 60
get_df, 61
get_family, 62
get_intercept, 62
get_loglikelihood, 63
get_modelmatrix, 64
get_parameters, 65
get_parameters.averaging
  (get_parameters.betareg), 67
get_parameters.bamlss
  (get_parameters.BGGM), 68
get_parameters.bayesx
  (get_parameters.BGGM), 68
get_parameters.betamfx, 66
get_parameters.betareg, 67
get_parameters.BFBayesFactor
  (get_parameters.BFBayesFactor), 68
get_parameters.BGGM, 68
get_parameters.brmsfit
  (get_parameters.BGGM), 68
get_parameters.clm2
  (get_parameters.betareg), 67
get_parameters.coxme
  (get_parameters.glmm), 74
get_parameters.DirichletRegModel
  (get_parameters.betareg), 67
get_parameters.emm_list
  (get_parameters.emmGrid), 72
get_parameters.emmGrid, 72
get_parameters.gam
  (get_parameters.gam), 73
get_parameters.gamm, 73
get_parameters.glimML
  (get_parameters.glimML), 74
get_parameters.glmm, 74
get_parameters.glmmTMB
  (get_parameters.glmmTMB), 74
get_parameters.glmx
  (get_parameters.betareg), 67
get_parameters.htest, 75
get_parameters.logitmfx
  (get_parameters.betamfx), 66
get_parameters.MCMCglmm
  (get_parameters.BGGM), 68
get_parameters.merMod
  (get_parameters.glmm), 74
get_parameters.mhurdle
  (get_parameters.zeroinfl), 76
get_parameters.mjoint
  (get_parameters.betareg), 67
get_parameters.mvord
  (get_parameters.betareg), 67
get_parameters.rqss
  (get_parameters.gamm), 73
get_parameters.sim
  (get_parameters.BGGM), 68
get_parameters.stanmvreg
  (get_parameters.BGGM), 68
get_parameters.stanreg
  (get_parameters.BGGM), 68
get_parameters.zcpglm
  (get_parameters.zeroinfl), 76
get_parameters.zeroinfl, 76
INDEX

get_predicted, 77
get_predicted(), 81
get_predicted_ci, 80
get_predicted_ci(), 78, 79
get_predictors, 83
get_priors, 83
get_random, 84
get_residuals, 85
get_response, 86
get_sigma, 87
get_sigma(), 54
get_statistic, 88
get_transformation, 90
get_variance, 93
get_variance_dispersion (get_variance), 93
get_variance_distribution
  (get_variance), 93
get_variance_fixed (get_variance), 93
get_variance_intercept (get_variance), 93
get_variance_random (get_variance), 93
get_variance_residual (get_variance), 93
get_variance_slope (get_variance), 93
get_weights, 96

has_intercept, 97
Hypothesis tests, 65

IQR(), 59
is_gam_model, 97
is_mixed_model, 98
is_model, 99
is_model_supported, 100
is_multivariate, 100
is_nested_models, 101
is_nullmodel, 102
is_regression_model (is_model), 99

link_function, 103
link_inverse, 104
loglikelihood (get_loglikelihood), 63

Marginal effects models, 20, 65
Mixed models, 20, 65
model_info, 105
model_name, 107
Models with special components, 20, 65

n_obs, 109
n_parameters, 110
null_model, 108

parameters::model_parameters(), 113–117
parameters_table (format_table), 49
performance::check_singularity(), 94
predict(), 77
print_color, 112
print_colour (print_color), 112
print_html (display), 10
print_md (display), 10
print_parameters, 113
print_parameters(), 7

sandwich::vcovCL(), 82
sandwich::vcovHC(), 82
signif(), 13, 43, 50, 52
standardize_column_order, 115
standardize_names, 116
supported_models (is_model_supported), 100

text_remove_backticks, 117

Zero-inflated and hurdle models, 20, 65