Package: insight (via r-universe)

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Type Package

Title Easy Access to Model Information for Various Model Objects

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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 (>= 3.6)

Imports methods, stats, utils

Suggests AER, afex, aod, ape, BayesFactor, bayestestR, bbmle, BSDA, bdsmatrix, betareg, biglm, BH, blavaan (>= 0.5-5), blme, boot, brms, broom, car, carData, censReg, cgam, clubSandwich, cobalt, coxme, cplm, crch, curl, datawizard (>= 1.2.0), dbarts, effectsize, emmeans, epiR, estimatr, feisr, fixest (>= 0.11.2), fungible, fwb, gam, gamlss, gamlss.data, gamlss.dist, gamm4, gbm, gee, geepack, geoR, GLMMadaptive, glmmTMB (>= 1.1.12), glmtoolbox, gmnl, grDevices, gt, httptest2, httr2, interp, ivreg, JM, knitr, lavaan, lavaSearch2, lcmm, lfe, lme4, lmerTest, lmtest, logistf, logitr, marginaleffects (>= 0.29.0), MASS, Matrix, mclogit, mclust, MCMCglmm, merTools, metaBMA, metadat, metafor, metaplus, mgcv, mhurdle, mice (>= 3.17.0), mlogit, mmrm, modelbased (>= 0.9.0), multgee, MuMIn, mvtnorm,

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`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

```
data(mtcars)
data(sleepstudy, package = "lme4")

m1 <- lm(mpg ~ wt + cyl + vs, data = mtcars)
m2 <- lm(mpg ~ wt + cyl, data = mtcars)
m3 <- lme4::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)
```

---

check_if_installed *Checking if needed package is installed*

Description

Checking if needed package is installed

Usage

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

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. Ignored if `quietly = TRUE`.
minimum_version	A character vector, representing the minimum package version that is required for each package. Should be of same length as `package`. If `NULL`, will automatically check the DESCRIPTION file for the correct minimum version. If using `minimum_version` with more than one package, `NA` should be used instead of `NULL` for packages where a specific version is not necessary.

quietly	Logical, if TRUE, invisibly returns a vector of logicals (TRUE for each installed package, FALSE otherwise), and does not stop or throw a warning. If quietly = TRUE, arguments stop and prompt are ignored. Use this argument to internally check for package dependencies without stopping or warnings.
prompt	If TRUE, will prompt the user to install needed package(s). Ignored if quietly = TRUE.
...	Currently ignored

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

```
check_if_installed("insight")
try(check_if_installed("datawizard", stop = FALSE))
try(check_if_installed("rstanarm", stop = FALSE))
try(check_if_installed("nonexistent_package", stop = FALSE))
try(check_if_installed("insight", minimum_version = "99.8.7"))
try(check_if_installed(c("nonexistent", "also_not_here"), stop = FALSE))
try(check_if_installed(c("datawizard", "rstanarm"), stop = FALSE))
try(check_if_installed(c("datawizard", "rstanarm"),
  minimum_version = c(NA, "2.21.1"), stop = FALSE
))
```

---

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

```
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()"
data(cbpp, package = "lme4")
m <- lme4::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` column refers to special model components like *conditional*, *zero_inflated*, or *dispersion*. For models from package **brms**, the various distributional parameters are also included in this column. 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

```
model <- download_model("brms_zi_2")
if (!is.null(model)) {
  clean_parameters(model)
}
```

color_if *Color-formatting for data columns based on condition*

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

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

x, where columns matched by predicate are wrapped into color codes.

Examples

```
# all values in Sepal.Length larger than 5 in green, all remaining in red
x <- color_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)
```

---

compact_character *Remove empty strings from character*

Description

Remove empty strings from character

Usage

```
compact_character(x)
```

Arguments

x
: A single character or a vector of characters.

Value

A character or a character vector with empty strings removed.

Examples

```
compact_character(c("x", "y", NA))
compact_character(c("x", "NULL", "", "y"))
```

`compact_list` *Remove empty elements from lists*

Description

Remove empty elements from lists

Usage

```
compact_list(x, remove_na = FALSE)
```

Arguments

`x`	A list or vector.
`remove_na`	Logical to decide if `NA`s should be removed.

Note

By default, `compact_list()` does not remove "empty" elements from deeper list levels. Only if an element on the first level of a list is "empty", it is removed.

Examples

```
compact_list(list(NULL, 1, c(NA, NA)))
compact_list(c(1, NA, NA))
compact_list(c(1, NA, NA), remove_na = TRUE)

# remove only NULL on top level, don't change deeper lists
compact_list(list(
  a = 1,
  NULL,
  b = list(NULL, list(1, 2, 3), list(list(x = 3, y = 4, NULL))),
  NULL
))
```

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". A special option is "tt", which creates a tinytable::tt() object, where the output format is dependent on the context where the table is used, i.e. it can be markdown format when export_table() is used in markdown files, or LaTex format when creating PDFs etc.

Value

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

Global Options to Customize Output when Printing

- options(easystats_display_format = <value>) will set the default format for the display() methods. Can be one of "markdown", "html", or "tt". See display() for details.

- `options(easystats_table_width = <value>)` sets the default width for tables printed to the console. Tables exceeding this width are wrapped into multiple parts to ensure clean formatting and avoid excessively long lines.
- `options(easystats_ci_separator = <value>)` defines the separator string used between the lower and upper CI limits. Defaults to `", "`, resulting in an output like `[0.3, 0.8]`.
- `options(easystats_ci_brackets = <value>)` determines whether brackets or parentheses are used to enclose formatted CIs. Can be `FALSE` to omit them, `TRUE` to include them (defaults to `[` and `]` for text output), or a character vector of length 2 to define custom opening and closing symbols (e.g., `c("(", ")")`).
- `options(insight_use_symbols = <value>)` accepts `TRUE` or `FALSE`. If `TRUE`, statistical symbols (e.g., eta-squared, omega) are rendered using their corresponding Unicode characters.

Examples

```
display(iris[1:5, ], format = "html")

display(iris[1:5, ], format = "tt")

display(iris[1:5, ], format = "markdown")
```

---

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 = "https://raw.github.com/easystats/circus/master/data/",
  extension = ".rda",
  verbose = TRUE
)
```

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/`.
`extension`	File extension. Default is `.rda`.
`verbose`	Toggle messages and warnings.

Details

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

Value

A model from the *circus*-repository, or NULL if model could not be downloaded (e.g., due to server problems).

References

https://easystats.github.io/circus/

Examples

```
download_model("aov_1")
try(download_model("non_existent_model"))
```

---

easystats_columns *Easystats columns*

Description

Returns all valid column names that are used or defined across easystats packages as character vector.

Usage

```
easystats_columns(select = "all")

broom_columns(select = "all")
```

Arguments

select	String, indicating which columns to return.

Value

A character vector with all (or selected) column names that are in use across the easystats-ecosystem, or broom-alike column names for broom_columns().

Examples

```
easystats_columns("uncertainty")
```

efc_insight *Sample dataset from the EFC Survey*

Description

A sample data set, internally used in tests. Consists of 28 variables from 908 observations. The data set is part of the EUROFAMCARE project, a cross-national survey on informal caregiving in Europe. Useful when testing on "real-life" data sets, including random missing values. This data set also has value and variable label attributes.

ellipsis_info *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

```
ellipsis_info(objects, ...)

## Default S3 method:
ellipsis_info(..., only_models = TRUE, verbose = TRUE)
```

Arguments

objects, ...	Arbitrary number of objects. May also be a list of model objects.
only_models	Only keep supported models (default to TRUE).
verbose	Toggle warnings.

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

```
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

Function to export data frames into tables, which can be printed to the console, or displayed in markdown or HTML format (and thereby, exported to other formats like Word or PDF). The table width is automatically adjusted to fit into the width of the display device (e.g., width of console). Use the `table_width` argument to control this behaviour.

Usage

```
export_table(
  x,
  sep = " | ",
  header = "-",
  cross = NULL,
  empty_line = NULL,
  digits = 2,
  protect_integers = TRUE,
  missing = "",
  width = NULL,
  format = NULL,
  title = NULL,
  caption = title,
  subtitle = NULL,
  footer = NULL,
  column_names = NULL,
  align = NULL,
  by = NULL,
  zap_small = FALSE,
  big_mark = NULL,
  table_width = "auto",
  remove_duplicates = FALSE,
  row_groups = NULL,
  column_groups = 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.
cross	Character that is used where separator and header lines cross.
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. A special option is "tt", which creates a tinytable::tt() object, where the output format is dependent on the context where the table is used, i.e. it can be markdown format when export_table() is used in markdown files, or LaTeX format when creating PDFs etc.
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 you want to force that no title is printed, even if present as attribute, use "", which will never print titles. If x is a list of data frames, caption may be a list of table captions, one for each table. For format = "html" and format = "tt", a list of data frames is shown as one table, and the caption of each data frame is the label of its row group, or the title if all data frames have the same caption. This does not apply if any data frame has a Component, Effects, Group or Response column. For format = "tt", it also does not apply if a data frame has one column, no rows or row groups (indent_rows), if the data frames have different column names, or if by, row_groups or column_groups is given.

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. If NULL, no footer is printed, unless it is stored as attributes (table_footer). If you want to force that no footer is printed, even if present as attribute, use "", which will never print footers. For format = "html" and format = "tt" and a list of data frames, the footer of each data frame is a note of the table, followed by footer if it is a string. The exceptions are the same as for caption. For format = "tt" and a single data frame, the footer is one note. For a list of data frames that is not shown as one table, each element of a list footer is one note.

column_names — Character vector of names that will be used as column names in the table. Must either be of same length as columns in the table, or a named vector, where names (LHS) indicate old column names, and values (RHS) are used as new column names.

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 a string with abbreviated alignment characters, one per column. 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. If format = "html", the characters go to the columns that the table shows, in the order shown (the rowname_col columns first, and the columns of a column_groups spanner where *gt* shows them). "left", "right" and "center" align all shown columns, and "firstleft" left-aligns the first shown column. The group columns Component, Effects, Group and Response, and the by columns given by name, are not shown: with two or more values they become row groups, with one value they are removed. With row_groups, if a group column is removed, the other group columns do not become row groups and are shown. A string with one character per column of x (for a list of data frames, per column of one data frame) skips the characters of the group columns that are not shown. A shorter string is for the shown columns only, and characters beyond the number of shown columns are ignored.

by — Name of column(s) in x that indicates grouping for tables. When format = "html", by is passed down to gt::gt(groupname_col = by). Likewise, for format = "tt", by indicates the name of the variable in the data frame, which is then used to create row headers in the table. For markdown and text format, x is internally split into a list of data frames. See also row_groups to group rows in the printed output.

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.

big_mark — Character used as thousands separator. If NULL (default), no thousands separator is used. Use "," for comma separator or " " for space separator.

table_width — Numeric,"auto", NULL or Inf, indicating the width of the complete table.

- If `table_width = "auto"` (default) 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 multiple parts.
- Else, if `table_width` is numeric and table rows are larger than `table_width`, the table is split into multiple parts. For each new table, the first column is repeated for better orientation.
- Use `NULL` or `Inf` to turn off automatic splitting of the table.
- `options(easystats_table_width = <value>)` can be used to set a default width for tables.

`remove_duplicates`
: Logical, if `TRUE` and table is split into multiple parts, duplicated ("empty") rows will be removed. If `FALSE`, empty rows will be preserved. Only applies when `table_width` is *not* `NULL` (or `Inf`) *and* table is split into multiple parts.

`row_groups`
: Named list, can be used as alternative to by to group rows in the printed output, but in a more flexible way. List elements may either be character vectors that match the names of values in the first column of the data frame that belong to one group, or list elements can be row numbers of those value rows that should belong to one group. The names of the list elements will be used as group names, which will be inserted as "header row". Rows will be re-ordered according to the order used in `row_groups`, while all rows with non-matching values will be added to the end.

`column_groups`
: Named list, can be used to group columns in the printed output. List elements must indicate column indices for columns that should belong to one group. The names of the list elements will be used as group names, which will be inserted as "column header row". Currently only works for `format = "tt"` or `format = "html"`.

`verbose`
: Toggle messages and warnings.

`...`
: Arguments passed to `tinytable::tt()` and `tinytable::style_tt()` when `format = "tt"`. When `format = "html"`, arguments of `gt::gt()`, for example `id` or `rowname_col`, are passed to `gt::gt()`, except `data`, `groupname_col` and `auto_align`. `caption` is not passed, because it is an argument of `export_table()`. With `rowname_col`, the `rowname_col` columns are shown first, so they take the first characters of `align` that go to the shown columns (see `align`), and the remaining columns take the other characters.

Value

If `format = "text"` (or `NULL`), a formatted character string is returned. `format = "markdown"` (or `"md"`) returns a character string of class `knitr_kable`, which renders nicely in markdown files. `format = "html"` returns an `gt` object (created by the **gt** package), which - by default - is displayed in the IDE's viewer pane or default browser. This object can be further modified with the various gt-functions. `format = "tt"` returns a `tinytable::tt()` object, which is a lightweight table format that can be used in markdown, LaTeX, HTML and other formats, depending on the context where the table is used.

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

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

# group (split) tables by variables
export_table(head(mtcars, 8), by = "cyl")


# 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)

# rename column names
export_table(x, column_names = letters[1:5])
export_table(x, column_names = c(Species = "a"))


# 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")

# group rows in the table
## Not run:
data(mtcars)

# fit model
mtcars$cyl <- as.factor(mtcars$cyl)
mtcars$gear <- as.factor(mtcars$gear)
model <- lm(mpg ~ hp + gear * vs + cyl + drat, data = mtcars)

# model summary, don't select "Intercept" parameter
mp <- as.data.frame(format(
  parameters::model_parameters(model, drop = "^\\(Intercept")
))

# define groups for the table
groups <- list(
  Engine = c("cyl [6]", "cyl [8]", "vs", "hp"),
  Interactions = c(8, 9),
  Controls = c(2, 3, 7)
)

# export table with groups, using tinytable format
export_table(mp, format = "tt", row_groups = groups)

## End(Not run)
```

`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

```
data(sleepstudy, package = "lme4")
m <- lme4::lmer(Reaction ~ Days + (1 | Subject), data = sleepstudy)
find_algorithm(m)



data(sleepstudy, package = "lme4")
m <- suppressWarnings(rstanarm::stan_lmer(
  Reaction ~ Days + (1 | Subject),
  data = sleepstudy,
  refresh = 0
))
find_algorithm(m)
```

`find_auxiliary` *Find auxiliary (distributional) parameters from models*

Description

Returns the names of all auxiliary / distributional parameters from brms-models, like dispersion, sigma, kappa, phi, or beta... For univariate non-linear models (`nl = TRUE`), the non-linear parameters of `mu` are not auxiliary parameters, and are not returned.

Usage

```
find_auxiliary(x, ...)

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

Arguments

x	A model of class brmsfit.
...	Currently not used.
verbose	Toggle warnings.

Value

The names of all available auxiliary parameters used in the model, or NULL if no auxiliary parameters were found.

---

find_formula *Find model formula*

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, ...)

formula_ok(
  x,
  checks = "all",
  action = "warning",
  prefix_msg = NULL,
  verbose = TRUE,
  ...
)

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

## S3 method for class 'nestedLogit'
find_formula(x, dichotomies = FALSE, verbose = TRUE, ...)
```

Arguments

x	A fitted model.
...	Currently not used.
checks	Indicates what kind of checks are conducted when checking the formula notation. Currently, four different formula specification that can result in unexpected behaviour of downstream-functions are checked. checks can be one or more of: • "dollar": Check if formula contains data name with "$", e.g. mtcars$am. • "T": Check if formula contains poly-term with "raw=T", e.g. poly(x, 2, raw=T). In this case, all.vars() returns T as variable, which is not intended. • "index": Check if formula contains indexed data frames as response variable (e.g., df[, 5] ~ x). • "name": Check if syntactically invalid variable names were used and quoted in backticks. • "all": Checks all of the above mentioned options.
action	Should a message, warning or error be given for an invalid formula? Must be one of "message", "warning" (default) or "error".
prefix_msg	Optional string that will be added to the warning/error message. This can be used to add additional information, e.g. about the specific function that was calling formula_ok() and failed.
verbose	Toggle warnings.
dichotomies	Logical, if model is a nestedLogit objects, returns the formulas for the dichotomies.

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. for models from *brms*, this component is named zi.
- zero_inflated_random, the "random effects" part from the zero-inflation component of the model; for models from *brms*, this component is named zi_random.
- 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

- nonlinear, for nonlinear mixed models like lme4::nlmer() or nlme::nlme(), the nonlinear model as a one-sided formula, like ~ SSlogis(Time, Asym, xmid, scal). For nlme::nlme() models, conditional has the response and the covariates of the fixed-effect parameter formulas, and random has one formula for each grouping level, like ~ Asym | Plot.
- scale, for distributional models such as mgcv::gaulss() family fitted with mgcv::gam(), the formula that describes the scale parameter
- 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".
- bidrange, for models of class oohbchoice (from package **DCchoice**), which indicates the right-hand side of the bar (the bid-range).

For models from package **brms**, distributional parameters are also included.

Note

For models of class lme, nlme, glmmPQL, gls or gnls, the correlation-component is the formula of the fitted correlation structure, e.g. ~ t | Subject for corAR1(form = ~ t | Subject), with the environment of the model formula. For a structure without form, this is the grouping that the model used, like ~1 | Subject. There is no correlation-component when that formula has no variable, e.g. ~1.

Examples

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

m <- lme4::lmer(Sepal.Length ~ Sepal.Width + (1 | Species), data = iris)
f <- find_formula(m)
f
format(f)
```

---

find_interactions *Find interaction terms from models*

Description

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

Usage

```
find_interactions(x, component = "all", 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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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.

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

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- `"smooth_terms"`: returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- `"zero_inflated"` (or `"zi"`): returns the zero-inflation component.

- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

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, as_term = FALSE)
```

Arguments

x	A fitted model.
as_term	Logical, if TRUE, the offset is returned as term, including possible transformations, like log(variable). If FALSE (default), only the variable name is returned.

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), raw_off = off)
dat$y <- rpois(N, exp(yhat)) # Poisson process
dat$y <- ifelse(rbinom(N, 1, 0.3), 0, dat$y) # Zero-inflation process

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

m2 <- pscl::zeroinfl(
  y ~ offset(log(raw_off)) + x | 1,
  data = dat,
  dist = "poisson"
)
find_offset(m2)
find_offset(m2, as_term = TRUE)

m3 <- pscl::zeroinfl(y ~ x | 1, data = dat, offset = logOff, dist = "poisson")
find_offset(m3)
```

`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

```
find_parameters(x, ...)

## Default S3 method:
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.

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.

- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Parameters, Variables, Predictors and Terms

There are four functions that return information about the variables in a model: find_predictors(), find_variables(), find_terms() and find_parameters(). There are some differences between those functions, which are explained using following model. Note that some, but not all of those functions return information about the *dependent* and *independent* variables. In this example, we only show the differences for the independent variables.

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

- `find_terms(model)` returns the model terms, i.e. how the variables were used in the model, e.g. applying transformations like `factor()`, `poly()` etc. `find_terms()` may return a variable name multiple times in case of multiple transformations. The return value would be `"factor(gear)"`.
- `find_parameters(model)` returns the names of the model parameters (coefficients). The return value would be `"(Intercept)"`, `"factor(gear)4"` and `"factor(gear)5"`.
- `find_variables()` returns the original variable names. `find_variables()` returns each variable name only once. The return value would be `"gear"`.
- `find_predictors()` is comparable to `find_variables()` and also returns the original variable names, but excluded the *dependent* (response) variables. The return value would be `"gear"`.

For non-linear models (`nls`, `nlmer` or `nlme`), the parameters of the nonlinear formula are returned by `find_parameters()`, while `find_predictors()` and `find_variables()` only return the variables. Parameters that are elements of a vector, like `b[1]`, are not yet removed.

Examples

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

---

find_parameters.averaging

Find model parameters from models with special components

Description

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

Usage

```
## S3 method for class 'averaging'
find_parameters(x, component = "conditional", 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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes):

- 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, usually requested via the component argument:

- conditional, the "fixed effects" part from the model.
- full, parameters from the full model.
- precision for models of class betareg.
- survival for model of class mjoint.
- extra for models of class glmx.

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".

- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

```
data("GasolineYield", package = "betareg")
m <- betareg::betareg(yield ~ batch + temp, data = GasolineYield)
find_parameters(m)
find_parameters(m, component = "precision")
```

---

find_parameters.betamfx

Find names of model parameters from marginal effects models

Description

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

Usage

```
## S3 method for class 'betamfx'
find_parameters(x, component = "all", 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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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.

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- `"smooth_terms"`: returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- `"zero_inflated"` (or `"zi"`): returns the zero-inflation component.
- `"dispersion"`: returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.

- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

```
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

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

## S3 method for class 'brmsfit'
find_parameters(
  x,
  effects = "all",
  component = "all",
  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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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.
effects	Should variables for fixed effects ("fixed"), random effects ("random") or both ("all") be returned? Only applies to mixed models. May be abbreviated. For models of from packages **brms** or **rstanarm** there are additional options: • "fixed" returns fixed effects. • "random_variance" return random effects parameters (variance and correlation components, e.g. those parameters that start with sd_ or cor_). • "grouplevel" returns random effects group level estimates, i.e. those parameters that start with r_. • "random" returns both "random_variance" and "grouplevel". • "all" returns fixed effects and random effects variances. • "full" returns all parameters.
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. For **brms**, this is named zi.
- zero_inflated_random, the "random effects" part from the zero-inflation component of the model. For **brms**, this is named zi_random.
- smooth_terms, the smooth parameters

Furthermore, some models, especially from **brms**, can also return other auxiliary (distributional) 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)
- and any pre-defined or arbitrary distributional parameter for models from package **brms**, like mu, ndt, kappa, etc.

For univariate non-linear models from **brms** (nl = TRUE), the coefficients of the non-linear parameters of mu are returned in the conditional element, and their group-level terms in the random element.

Models of class **BGGM** additionally can return the elements correlation and intercept.

Models of class **BFBayesFactor** additionally can return the element extra.

Examples

```
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)
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

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

## S3 method for class 'gam'
find_parameters(x, component = "all", 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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • 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

```
data(mtcars)
m <- mgcv::gam(mpg ~ s(hp) + gear, 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

```
## S3 method for class 'glmmTMB'
find_parameters(x, effects = "all", component = "all", flatten = FALSE, ...)
```

Arguments

`x`	A fitted model.
`effects`	Should variables for fixed effects (`"fixed"`), random effects (`"random"`) or both (`"all"`) be returned? Only applies to mixed models. May be abbreviated. For `find_predictors()` and `find_variables()`, it also applies to the correlation part of models from *nlme* (like `gls`).
`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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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, usually returned based on the combination of the `effects` and `component` arguments:

- 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)
- dispersion_random, the "random effects" part from the dispersion parameters (auxiliary parameter)
- nonlinear, the parameters from the nonlinear formula.

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"

- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

```
data(sleepstudy, package = "lme4")
m <- lme4::lmer(
  Reaction ~ Days + (1 + Days | Subject),
  data = sleepstudy
)
find_parameters(m)
```

---

find_parameters.zeroinfl

Find names of model parameters from zero-inflated models

Description

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

Usage

```
## S3 method for class 'zeroinfl'
find_parameters(x, component = "all", 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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes):

- 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.
- zero_inflated, the "fixed effects" part from the zero-inflation component of the model.
- Special models are mhurdle, which also can have the components infrequent_purchase, ip, and auxiliary.

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).

- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

```
data(bioChemists, package = "pscl")
m <- pscl::zeroinfl(
  art ~ fem + mar + kid5 + ment | kid5 + phd,
  data = bioChemists
)
find_parameters(m)
```

---

find_predictors *Find names of model predictors*

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 = "fixed",
  component = "all",
  flatten = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

x	A fitted model.
...	Currently not used.
effects	Should variables for fixed effects ("fixed"), random effects ("random") or both ("all") be returned? Only applies to mixed models. May be abbreviated. For find_predictors() and find_variables(), it also applies to the correlation part of models from *nlme* (like gls).
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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • 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.
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 can have 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. For models from **brms**, this is named zi.
- zero_inflated_random, the "random effects" terms from the zero-inflation component of the model. For models from **brms**, this is named zi_random.
- 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 (without the grouping factor for effects = "fixed")
- nonlinear, for non-linear models (like models of class nlmerMod or nlme), the variables of the nonlinear formula
- smooth_terms returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms)

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Parameters, Variables, Predictors and Terms

There are four functions that return information about the variables in a model: find_predictors(), find_variables(), find_terms() and find_parameters(). There are some differences between those functions, which are explained using following model. Note that some, but not all of those functions return information about the *dependent* and *independent* variables. In this example, we only show the differences for the independent variables.

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

- find_terms(model) returns the model terms, i.e. how the variables were used in the model, e.g. applying transformations like factor(), poly() etc. find_terms() may return a variable name multiple times in case of multiple transformations. The return value would be "factor(gear)".
- find_parameters(model) returns the names of the model parameters (coefficients). The return value would be "(Intercept)", "factor(gear)4" and "factor(gear)5".
- find_variables() returns the original variable names. find_variables() returns each variable name only once. The return value would be "gear".
- find_predictors() is comparable to find_variables() and also returns the original variable names, but excluded the *dependent* (response) variables. The return value would be "gear".

For non-linear models (nls, nlmer or nlme), the parameters of the nonlinear formula are returned by find_parameters(), while find_predictors() and find_variables() only return the variables. Parameters that are elements of a vector, like b[1], are not yet removed.

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.

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. For **brms**, this is named zi_random.
- dispersion_random, the "random effects" terms from the dispersion component of the model

Models of class brmsfit may also contain elements for auxiliary parameters.

Examples

```
data(sleepstudy, package = "lme4")
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 <- lme4::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.

Usage

```
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. For **brms**, this is named `zi_random`.
- `dispersion_random`, the random slopes from the dispersion component of the model

Models of class `brmsfit` may also contain elements for auxiliary parameters.

Examples

```
data(sleepstudy, package = "lme4")
m <- lme4::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, ...)

## S3 method for class 'joint'
find_response(x, combine = TRUE, component = "conditional", ...)
```

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.
component	Character, if x is a joint model, this argument can be used to specify which component to return. Possible values are "conditional", "survival" or "all".

Value

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

Examples

```
data(cbpp, package = "lme4")
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 terms from a model object*

Description

Return the names of smooth terms from a model object.

Usage

```
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

```
data(iris)
model <- mgcv::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

```
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

```
# 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. For the nonlinear formula of nonlinear models, only the variables are returned (see 'Note').

Usage

```
find_terms(x, ...)

## Default S3 method:
find_terms(x, flatten = FALSE, as_term_labels = 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.
as_term_labels	Logical, if TRUE, extracts model formula and tries to access the "term.labels" attribute. This should better mimic the terms() behaviour even for those models that do not have such a method, but may be insufficient, e.g. for mixed models.
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)

- 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
- nonlinear, for nonlinear models from lme4::nlmer() and nlme::nlme(), the variables of the nonlinear formula (see 'Note')

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

Parameters, Variables, Predictors and Terms

There are four functions that return information about the variables in a model: find_predictors(), find_variables(), find_terms() and find_parameters(). There are some differences between those functions, which are explained using following model. Note that some, but not all of those functions return information about the *dependent* and *independent* variables. In this example, we only show the differences for the independent variables.

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

- find_terms(model) returns the model terms, i.e. how the variables were used in the model, e.g. applying transformations like factor(), poly() etc. find_terms() may return a variable name multiple times in case of multiple transformations. The return value would be "factor(gear)".
- find_parameters(model) returns the names of the model parameters (coefficients). The return value would be "(Intercept)", "factor(gear)4" and "factor(gear)5".
- find_variables() returns the original variable names. find_variables() returns each variable name only once. The return value would be "gear".
- find_predictors() is comparable to find_variables() and also returns the original variable names, but excluded the *dependent* (response) variables. The return value would be "gear".

For non-linear models (nls, nlmer or nlme), the parameters of the nonlinear formula are returned by find_parameters(), while find_predictors() and find_variables() only return the variables. Parameters that are elements of a vector, like b[1], are not yet removed.

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. For non-linear models (nls, nlmer or nlme), the nonlinear formula and the random part return the variables, like find_variables(), because the nonlinear formula also holds the parameters.

Examples

```
data(sleepstudy, package = "lme4")
m <- suppressWarnings(lme4::lmer(
  log(Reaction) ~ Days + I(Days^2) + (1 + Days + exp(Days) | Subject),
  data = sleepstudy
))

find_terms(m)

# sometimes, it is necessary to retrieve terms from "term.labels" attribute
m <- lm(mpg ~ hp * (am + cyl), data = mtcars)
find_terms(m, as_term_labels = TRUE)
```

---

find_transformation *Find possible transformation of model variables*

Description

This functions checks whether any transformation, such as log- or exp-transforming, was applied to the response variable (dependent variable) in a regression formula. Optionally, all model terms can also be checked for any such transformation. Currently, following patterns are detected: `log`, `log1p`, `log2`, `log10`, `exp`, `expm1`, `sqrt`, `log(y+<number>)`, `log-log`, `log(y,base=<number>)`, `power` (e.g. to 2nd power, like `I(y^2)`), `inverse` (like `1/y`), `scale` (e.g., `y/3`), and `box-cox` (e.g., `(y^lambda - 1) / lambda`).

Usage

```
find_transformation(x, ...)

## Default S3 method:
find_transformation(x, include_all = FALSE, ...)
```

Arguments

`x`	A regression model or a character string of the formulation of the (response) variable.
`...`	Currently not used.
`include_all`	Logical, if `TRUE`, does not only check the response variable, but all model terms.

Value

A string, with the name of the function of the applied transformation. Returns `"identity"` for no transformation, and e.g. `"log(y+3)"` when a specific values was added to the response variables before log-transforming. For unknown transformations, returns `NULL`.

Examples

```
# 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 transformation for all model terms
model <- lm(mpg ~ log(wt) + I(gear^2) + exp(am), data = mtcars)
find_transformation(model, include_all = TRUE)

# inverse, response provided as character string
find_transformation("1 / y")
```

---

find_variables *Find names of all variables*

Description

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

Usage

```
find_variables(
  x,
  effects = "all",
  component = "all",
  flatten = FALSE,
  verbose = TRUE
)
```

Arguments

x	A fitted model.
effects	Should variables for fixed effects ("fixed"), random effects ("random") or both ("all") be returned? Only applies to mixed models. May be abbreviated. For find_predictors() and find_variables(), it also applies to the correlation part of models from *nlme* (like gls).
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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes):

- `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.

`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
- `nonlinear`, for nonlinear models from `lme4::nlmer()` and `nlme::nlme()`, the variables of the nonlinear formula
- `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. For **brms**, this is named `zi`.
- `zero_inflated_random`, the names of the random effects (grouping factors). For **brms**, this is named `zi_random`.

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.

- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Parameters, Variables, Predictors and Terms

There are four functions that return information about the variables in a model: find_predictors(), find_variables(), find_terms() and find_parameters(). There are some differences between those functions, which are explained using following model. Note that some, but not all of those functions return information about the *dependent* and *independent* variables. In this example, we only show the differences for the independent variables.

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

- `find_terms(model)` returns the model terms, i.e. how the variables were used in the model, e.g. applying transformations like `factor()`, `poly()` etc. `find_terms()` may return a variable name multiple times in case of multiple transformations. The return value would be `"factor(gear)"`.
- `find_parameters(model)` returns the names of the model parameters (coefficients). The return value would be `"(Intercept)"`, `"factor(gear)4"` and `"factor(gear)5"`.
- `find_variables()` returns the original variable names. `find_variables()` returns each variable name only once. The return value would be `"gear"`.
- `find_predictors()` is comparable to `find_variables()` and also returns the original variable names, but excluded the *dependent* (response) variables. The return value would be `"gear"`.

For non-linear models (`nls`, `nlmer` or `nlme`), the parameters of the nonlinear formula are returned by `find_parameters()`, while `find_predictors()` and `find_variables()` only return the variables. Parameters that are elements of a vector, like `b[1]`, are not yet removed.

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

```
data(cbpp, package = "lme4")
data(sleepstudy, package = "lme4")
# 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 <- lme4::glmer(
  cbind(incidence, size - incidence) ~ period + (1 | herd),
  data = cbpp,
  family = binomial
)
find_variables(m1)

m2 <- lme4::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

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

Arguments

x	A fitted model.
...	Used for objects from package **survey**, to pass the source argument to get_data(). See related documentation of that argument for further details.

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 for count models*

Description

A sample data set, used in tests and some examples. Useful for testing count models.

format_bf *Bayes Factor formatting*

Description

Bayes Factor formatting

Usage

```
format_bf(
  bf,
  stars = FALSE,
  stars_only = FALSE,
  inferiority_star = "°",
  name = "BF",
  protect_ratio = FALSE,
  na_reference = NA,
  exact = FALSE,
  digits = NULL
)
```

Arguments

bf	Bayes Factor.
stars	Add significance stars (e.g., p < .001***). For Bayes factors, the thresholds for "significant" results are values larger than 3, 10, and 30.
stars_only	Return only significance stars.
inferiority_star	String, indicating the symbol that is used to indicate inferiority, i.e. when the Bayes Factor is smaller than one third (the thresholds are smaller than one third, 1/10 and 1/30).
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").
digits	Number of significant digits. Can also be "scientific" (which is identical to exact = TRUE).

Value

A formatted string.

Examples

```
bfs <- c(0.000045, 0.033, NA, 1557, 3.54)
format_bf(bfs)
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)
```

---

format_capitalize *Capitalizes the first letter in a string*

Description

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

Usage

```
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

```
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, ...)

## S3 method for class 'numeric'
format_ci(
  CI_low,
  CI_high,
  ci = 0.95,
  digits = 2,
  brackets = getOption("easystats_ci_brackets", TRUE),
  separator = getOption("easystats_ci_separator", ", "),
  width = NULL,
  width_low = width,
  width_high = width,
  missing = "",
  zap_small = FALSE,
  ci_string = "CI",
  ...
)
```

Arguments

CI_low	Lower CI bound. Usually a numeric value, but can also be a CI output returned bayestestR, in which case the remaining arguments are unnecessary.
...	Arguments passed to or from other methods.
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 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()).
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.
separator	String, used to separate lower and upper CI limit values.

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.

ci_string — String to be used in the output to indicate the type of interval. Default is "CI", but can be changed to "HDI" or anything else, if necessary.

Value

A formatted string.

Examples

```
format_ci(1.20, 3.57, ci = 0.90)
format_ci(1.20, 3.57, ci = NULL)
format_ci(1.20, 3.57, ci = NULL, brackets = FALSE)
format_ci(1.20, 3.57, ci = NULL, brackets = c("(", ")"))
format_ci(1.20, 3.57, ci = NULL, brackets = FALSE, separator = "-")
format_ci(c(1.205645, 23.4), c(3.57, -1.35), ci = 0.90)
format_ci(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 <- format_ci(c(1.205, 23.4, 100.43), c(3.57, -13.35, 9.4))
cat(x, sep = "\n")

x <- format_ci(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 spaces.

format_alert() is a wrapper that combines formatting a string with a call to message(), warning() or stop(). By default, format_alert() creates a message(). format_warning() and format_error() change the default type of exception to warning() and stop(), respectively.

Usage

```
format_message(
  string,
  ...,
  line_length = 0.9 * getOption("width", 80),
  indent = "  "
)

format_alert(
  string,
  ...,
  line_length = 0.9 * getOption("width", 80),
  indent = "  ",
  type = "message",
  call = FALSE,
  immediate = FALSE
)

format_warning(..., immediate = FALSE)

format_error(...)
```

Arguments

string	A string.
...	Further strings that will be concatenated as indented new lines.
line_length	Numeric, the maximum length of a line. The default is 90% of the width of the console window.
indent	Character vector. If further lines are specified in . . . , a user-defined string can be specified to indent subsequent lines. Defaults to " " (two white spaces), hence for each start of the line after the first line, two white space characters are inserted.
type	Type of exception alert to raise. Can be "message" for message(), "warning" for warning(), or "error" for stop().
call	Logical. Indicating if the call should be included in the the error message. This is usually confusing for users when the function producing the warning or error is deep within another function, so the default is FALSE.
immediate	Logical. Indicating if the *warning* should be printed immediately. Only applies to format_warning() or format_alert() with type = "warning". The default is FALSE.

Details

There is an experimental formatting feature implemented in this function. You can use following tags:

- {.b text} for bold formatting

- {.i text} to use italic font style
- {.url www.url.com} formats the string as URL (i.e., enclosing URL in < and >, blue color and italic font style)
- {.pkg packagename} formats the text in blue color.

This features has some limitations: it's hard to detect the exact length for each line when the string has multiple lines (after line breaks) and the string contains formatting tags. Thus, it can happen that lines are wrapped at an earlier length than expected. Furthermore, if you have multiple words in a format tag ({.b one two three}), a line break might occur inside this tag, and the formatting no longer works (messing up the message-string).

Value

For format_message(), a formatted string. For format_alert() and related functions, the requested exception, with the exception formatted using format_message().

Examples

```
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)

msg <- format_message("Much too long string for just one line, I guess!",
  "First new line",
  "Second new line",
  "(not indented)",
  line_length = 30,
  indent = ""
)
message(msg)

# Caution, experimental! See 'Details'
msg <- format_message(
  "This is {.i italic}, visit {.url easystats.github.io/easystats}",
  line_length = 30
)
message(msg)


# message
format_alert("This is a message.")
format_alert("This is a warning.", type = "message")
```

```
# error
try(format_error("This is an error."))


# warning
format_warning("This is a warning.")
```

`format_number` *Convert number to words*

Description

Convert number to words

Usage

```
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

Examples

```
format_number(2)
format_number(45)
format_number(324.68765)
```

format_p *p-values formatting*

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***). For Bayes factors, the thresholds for "significant" results are values larger than 3, 10, and 30.
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.

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***). For Bayes factors, the thresholds for "significant" results are values larger than 3, 10, and 30.
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

```
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

```
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

```
format_string(x, ...)

## S3 method for class 'character'
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

```
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)
```

---

format_table *Parameter table formatting*

Description

This functions takes a data frame (usually 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

```
format_table(
  x,
  pretty_names = TRUE,
  stars = FALSE,
  stars_only = FALSE,
  digits = 2,
  ci_width = "auto",
  ci_brackets = getOption("easystats_ci_brackets", TRUE),
  ci_separator = getOption("easystats_ci_separator", ", "),
  ci_digits = digits,
```

```
  p_digits = 3,
  rope_digits = digits,
  ic_digits = 1,
  zap_small = FALSE,
  preserve_attributes = FALSE,
  exact = TRUE,
  use_symbols = getOption("insight_use_symbols", FALSE),
  select = NULL,
  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	If TRUE, add significance stars (e.g., p < .001***). Can also be a character vector, naming the columns that should include stars for significant values. This is especially useful for Bayesian models, where we might have multiple columns with significant values, e.g. BF for the Bayes factor or pd for the probability of direction. In such cases, use `stars = c("pd", "BF")` to add stars to both columns, or `stars = "BF"` to only add stars to the Bayes factor and exclude the pd column. Currently, following columns are recognized: "BF", "pd" and "p".
stars_only	If TRUE, return significant stars only (and no p-values).
digits, ci_digits, p_digits, rope_digits, ic_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).
ci_separator	String, used to separate lower and upper CI limit values. `options(easystats_ci_separator = "<value>")` can be used to set a default separator string.
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.
exact	Formatting for Bayes factor columns, in case the provided data frame contains such a column (i.e. columns named "BF" or "log_BF"). For `exact = TRUE`, very large or very small values are then either reported with a scientific format (e.g., 4.24e5), else as truncated values (as "> 1000" and "< 1/1000").

use_symbols — Logical, if TRUE, column names that refer to particular effectsizes (like Phi, Omega or Epsilon) include the related unicode-character instead of the written name. This only works on Windows for R >= 4.2, and on OS X or Linux for R >= 4.0. It is possible to define a global option for this setting, see 'Note'.

select — Determines which columns are printed and the table layout. There are two options for this argument:

- **A string expression with layout pattern**
  `select` is a string with "tokens" enclosed in braces. These tokens will be replaced by their associated columns, where the selected columns will be collapsed into one column. Following tokens are replaced by the related coefficients or statistics: `{estimate}`, `{se}`, `{ci}` (or `{ci_low}` and `{ci_high}`), `{p}`, `{pd}` and `{stars}`. The token `{ci}` will be replaced by `{ci_low}, {ci_high}`. Example: `select = "{estimate}{stars} ({ci})"` It is possible to create multiple columns as well. A `|` separates values into new cells/columns. Example: `select = "{estimate} ({ci})|{p}"`.
- **A string indicating a pre-defined layout**
  `select` can be one of the following string values, to create one of the following pre-defined column layouts:
  - `"minimal"`: Estimates, confidence intervals and numeric p-values, in two columns. This is equivalent to `select = "{estimate} ({ci})|{p}"`.
  - `"short"`: Estimate, standard errors and numeric p-values, in two columns. This is equivalent to `select = "{estimate} ({se})|{p}"`.
  - `"ci"`: Estimates and confidence intervals, no asterisks for p-values. This is equivalent to `select = "{estimate} ({ci})"`.
  - `"se"`: Estimates and standard errors, no asterisks for p-values. This is equivalent to `select = "{estimate} ({se})"`.
  - `"ci_p"`: Estimates, confidence intervals and asterisks for p-values. This is equivalent to `select = "{estimate}{stars} ({ci})"`.
  - `"se_p"`: Estimates, standard errors and asterisks for p-values. This is equivalent to `select = "{estimate}{stars} ({se})"`..

  Using `select` to define columns will re-order columns and remove all columns related to uncertainty (standard errors, confidence intervals), test statistics, and p-values (and similar, like `pd` or `BF` for Bayesian models), because these are assumed to be included or intentionally excluded when using `select`. The new column order will be: Parameter columns first, followed by the "glue" columns, followed by all remaining columns. If further columns should also be placed first, add those as `focal_terms` attributes to `x`. I.e., following columns are considers as "parameter columns" and placed first: `c(easystats_columns("parameter"), attributes(x)$focal_terms)`.
  Note: glue-like syntax is still experimental in the case of more complex models (like mixed models) and may not return expected results.

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!

Note

`options(insight_use_symbols = TRUE)` overrides the `use_symbols` argument and always displays symbols, if possible.

See Also

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

Examples

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

m <- lm(Sepal.Length ~ Species * Sepal.Width, data = iris)
x <- parameters::model_parameters(m)
as.data.frame(format_table(x))
as.data.frame(format_table(x, p_digits = "scientific"))
# "glue" columns
as.data.frame(format_table(x, select = "minimal"))
as.data.frame(format_table(x, select = "{estimate}{stars}|{p}"))


model <- rstanarm::stan_glm(
  Sepal.Length ~ Species,
  data = iris,
  refresh = 0,
  seed = 123
)
x <- parameters::model_parameters(model, ci = c(0.69, 0.89, 0.95))
as.data.frame(format_table(x))
```

---

format_value *Numeric Values Formatting*

Description

`format_value()` converts numeric values into formatted string values, where formatting can be something like rounding digits, scientific notation etc. `format_percent()` is a short-cut for `format_value(as_percent = TRUE)`.

Usage

```
format_value(x, ...)

## S3 method for class 'data.frame'
format_value(
  x,
```

```
  digits = 2,
  protect_integers = FALSE,
  missing = "",
  width = NULL,
  as_percent = FALSE,
  zap_small = FALSE,
  lead_zero = TRUE,
  style_positive = "none",
  style_negative = "hyphen",
  decimal_point = getOption("OutDec"),
  big_mark = NULL,
  ...
)

## S3 method for class 'numeric'
format_value(
  x,
  digits = 2,
  protect_integers = FALSE,
  missing = "",
  width = NULL,
  as_percent = FALSE,
  zap_small = FALSE,
  lead_zero = TRUE,
  style_positive = "none",
  style_negative = "hyphen",
  decimal_point = getOption("OutDec"),
  big_mark = NULL,
  ...
)

format_percent(x, ...)
```

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.
lead_zero	Logical, if TRUE (default), includes leading zeros, else leading zeros are dropped.
style_positive	A string that determines the style of positive numbers. May be "none" (default), "plus" to add a plus-sign or "space" to precede the string by a Unicode "figure space", i.e., a space equally as wide as a number or +.
style_negative	A string that determines the style of negative numbers. May be "hyphen" (default), "minus" for a proper Unicode minus symbol or "parens" to wrap the number in parentheses.
decimal_point	Character string containing a single character that is used as decimal point in output conversions.
big_mark	Character used as thousands separator. If NULL (default), no thousands separator is used. Use "," for comma separator or " " for space separator.

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, 0.12, 0.34))
format_value(c(0.0045, 0.12, 0.34), as_percent = TRUE)
format_value(c(0.0045, 0.12, 0.34), digits = "scientific")
format_value(c(0.0045, 0.12, 0.34), digits = "scientific2")
format_value(c(0.045, 0.12, 0.34), lead_zero = FALSE)
format_value(c(0.0045, 0.12, 0.34), decimal_point = ",")
format_value(c(1234567.89, 1234.56), big_mark = ",")
format_value(c(1234567.89, 1234.56), big_mark = " ")

# default
format_value(c(0.0045, 0.123, 0.345))
# significant figures
format_value(c(0.0045, 0.123, 0.345), 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))
```

`get_auxiliary` *Get auxiliary parameters from models*

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,
  ...
)

get_dispersion(x, ...)

## Default S3 method:
get_dispersion(x, ...)
```

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.

Details

Currently, only sigma and the dispersion parameter are returned, and only for a limited set of models.

Value

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

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 σ^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 ϕ 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 σ^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().

Examples

```
# 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
```

---

get_call *Get the model's function call*

Description

Returns the model's function call when available.

Usage

```
get_call(x)
```

Arguments

x	A fitted mixed model.

Value

A function call.

Examples

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

m <- lme4::lmer(Sepal.Length ~ Sepal.Width + (1 | Species), data = iris)
get_call(m)
```

---

get_data *Get the data that was used to fit the model*

Description

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

Usage

```
get_data(x, ...)

## Default S3 method:
get_data(x, source = "environment", verbose = TRUE, ...)

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

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

## S3 method for class 'rma'
get_data(
  x,
  source = "environment",
  verbose = TRUE,
  include_interval = FALSE,
  transf = NULL,
```

```
  transf_args = NULL,
  ci = 0.95,
  ...
)
```

Arguments

x	A fitted model.
...	Currently not used.
source	String, indicating from where data should be recovered. If `source = "environment"` (default), data is recovered from the environment (e.g. if the data is in the workspace). This option is usually the fastest way of getting data and ensures that the original variables used for model fitting are returned. Note that always the *current* data is recovered from the environment. Hence, if the data was modified *after* model fitting (e.g., variables were recoded or rows filtered), the returned data may no longer equal the model data. If a variable used in the model is missing from the data in the environment, but is a column of `model.frame()`, `get_data()` warns and uses the model frame instead. This applies to most, but not all, model classes. Variables used only inside a transformation, like `a` in `log(a)`, are not detected. If `source = "frame"` (or `"mf"`), the data is taken from the model frame. Any transformed variables are back-transformed, if possible. This option returns the data even if it is not available in the environment, however, in certain edge cases back-transforming to the original data may fail. If `source = "environment"` fails to recover the data, it tries to extract the data from the model frame; if `source = "frame"` and data cannot be extracted from the model frame, data will be recovered from the environment. Both ways only returns observations that have no missing data in the variables used for model fitting. For objects from package **survey**, `"mf"` extracts data from the model frame of the survey design object, which is usually equivalent to the original data. `source = "environment"` extracts data from the model-object in the environment, which usually includes processed variables (like the `"(weights)"` variable for weights).
verbose	Toggle messages and warnings.
effects	Should model data for fixed effects (`"fixed"`), random effects (`"random"`) or both (`"all"`) be returned? Only applies to mixed or gee models.
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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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.

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

include_interval — For meta-analysis models, should normal-approximation confidence intervals be added for each response effect size?

transf — For meta-analysis models, if intervals are included, a function applied to each response effect size and its interval.

transf_args — For meta-analysis models, an optional list of arguments passed to the transf function.

ci — For meta-analysis models, the Confidence Interval (CI) level if include_interval = TRUE. Default to 0.95 (95%).

Value

The data that was used to fit the model.

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".

- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, `smooth_terms`, or `instruments` (everything that are fixed or random effects - depending on the `effects` argument - but no auxiliary parameters).
- `"distributional"` (or `"auxiliary"`): components like `sigma`, `dispersion`, `beta` or `precision` (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: `"infrequent_purchase"`, `"ip"`, and `"auxiliary"`
- **BGGM**: `"correlation"` and `"intercept"`
- **BFBayesFactor**, **glmx**: `"extra"`
- **averaging**:`"conditional"` and `"full"`
- **mjoint**: `"survival"`
- **mfx**: `"precision"`, `"marginal"`
- **betareg**, **DirichletRegModel**: `"precision"`
- **mvord**: `"thresholds"` and `"correlation"`
- **clm2**: `"scale"`
- **selection**: `"selection"`, `"outcome"`, and `"auxiliary"`
- **lcmm**: `"membership"`, `"longitudinal"`, `"beta"`, `"splines"`, and `"linear"`

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like `mu`, `ndt`, `kappa`, etc.

Examples

```
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. Usually used to generate predictions using `get_predicted()`. See this vignette for a tutorial on how to create a visualisation matrix using this function.

Alternatively, these can also be used to extract the "grid" columns from objects generated by **emmeans** and **marginaleffects** (see those methods for more info).

Usage

```
get_datagrid(x, ...)

## S3 method for class 'data.frame'
get_datagrid(
  x,
  by = "all",
  factors = "reference",
  numerics = "mean",
  length = 10,
  range = "range",
  weighted = FALSE,
  n_bins = 5,
  preserve_range = FALSE,
  protect_integers = TRUE,
  digits = 3,
  reference = x,
  ...
)

## S3 method for class 'numeric'
get_datagrid(
  x,
  length = 10,
  range = "range",
  protect_integers = TRUE,
  digits = 3,
  ...
)

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

## Default S3 method:
get_datagrid(
  x,
  by = "all",
  factors = "reference",
  numerics = "mean",
  weighted = FALSE,
  n_bins = 5,
  preserve_range = TRUE,
  reference = x,
  include_smooth = TRUE,
  include_random = FALSE,
  include_response = FALSE,
  data = NULL,
  digits = 3,
```

```
  verbose = TRUE,
  ...
)
```

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.).
by	Indicates the *focal predictors* (variables) for the reference grid and at which values focal predictors should be represented. If not specified otherwise, representative values for numeric variables or predictors are evenly distributed from the minimum to the maximum, with a total number of `length` values covering that range (see 'Examples'). Possible options for by are:

- **Select variables only:**
  - `"all"`, which will include all variables or predictors. For models from *nlme*, variables that only the correlation structure uses are left out.
  - a character vector of one or more variable or predictor names, like `c("Species", "Sepal.Width")`, which will create a grid of all combinations of unique values.

  Note: If by specifies only variable names, without associated values, the following occurs: factor variables use all their levels, numeric variables use a range of `length` equally spaced values between their minimum and maximum, and character variables use all their unique values.
- **Select variables and values:**
  - by can be a list of named elements, indicating focal predictors and their representative values, e.g. by = `list(mpg = 10:20)`, by = `list(Sepal.Length = c(2, 4), Species = "setosa")`, or by = `list(Sepal.Length = seq(2, 5, 0.5))`.
  - Instead of a list, it is possible to write a string representation, or a character vector of such strings, e.g. by = `"mpg = 10:20"`, by = `c("Sepal.Length = c(2, 4)", "Species = 'setosa'")`, or by = `"Sepal.Length = seq(2, 5, 0.5)"`. Note the usage of single and double quotes to assign strings within strings.
  - In general, any expression after a = will be evaluated as R code, which allows using own functions, e.g.

    ```
    fun <- function(x) x^2
    get_datagrid(iris, by = "Sepal.Width = fun(2:5)")
    ```

  Note: If by specifies variables *with* their associated values, argument `length` is ignored.

There is a special handling of assignments with *brackets*, i.e. values defined inside [and], which create summaries for *numeric* variables. Following "tokens" that creates pre-defined representative values are possible:

- for mean and -/+ 1 SD around the mean: `"x = [sd]"`
- for median and -/+ 1 MAD around the median: `"x = [mad]"`

- for Tukey's five number summary (minimum, lower-hinge, median, upper-hinge, maximum): `"x = [fivenum]"`
- for quartiles: `"x = [quartiles]"` (same as `"x = [fivenum]"`, but *excluding* minimum and maximum)
- for terciles: `"x = [terciles]"`
- for terciles, *including* minimum and maximum: `"x = [terciles2]"`
- for a pretty value range: `"x = [pretty]"`
- for minimum and maximum value: `"x = [minmax]"`
- for 0 and the maximum value: `"x = [zeromax]"`
- for a random sample from all values: `"x = [sample <number>]"`, where `<number>` should be a positive integer, e.g. `"x = [sample 15]"`.

Note: the `length` argument will be ignored when using brackets-tokens.

The remaining variables not specified in `by` will be fixed (see also arguments `factors` and `numerics`).

`factors` Type of summary for factors *not* specified in `by`. 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 *not* specified in `by`. Can be `"all"` (will duplicate the grid for all unique values), any function (`"mean"`, `"median"`, ...) or a value (e.g., `numerics = 0`). Special functions are `"mode"`, which will set the numeric variable to its most common value, and `"integer"`, which returns the rounded mean.

`length` Length of numeric target variables selected in `by` (if no representative values are additionally specified). This arguments controls the number of (equally spread) values that will be taken to represent the continuous (non-integer alike!) variables. A longer length will increase precision, but can also substantially increase the size of the datagrid (especially in case of interactions). If `NA`, will return all the unique values.

In case of multiple continuous target variables, `length` can also be a vector of different values (see 'Examples'). In this case, `length` must be of same length as numeric target variables. If `length` is a named vector, values are matched against the names of the target variables.

When `range = "range"` (the default), `length` is ignored for integer type variables when `length` is larger than the number of unique values *and* `protect_integers` is `TRUE` (default). Set `protect_integers = FALSE` to create a spread of `length` number of values from minimum to maximum for integers, including fractions (i.e., to treat integer variables as regular numeric variables).

`length` is furthermore ignored if "tokens" (in brackets `[` and `]`) are used in `by`, or if representative values are additionally specified in `by`.

`range` Option to control the representative values given in `by`, if no specific values were provided. Use in combination with the `length` argument to control the number of values within the specified range. `range` can be one of the following:

- `"range"` (default), will use the minimum and maximum of the original data vector as end-points (min and max). For integer variables, the `length` argument will be ignored, and `"range"` will only use values that appear in the

data. Set protect_integers = FALSE to override this behaviour for integer variables.

- if an interval type is specified, such as "iqr", "ci", "hdi" or "eti", it will spread the values within that range (the default CI width is 95% but this can be changed by adding for instance ci = 0.90.) See IQR() and bayestestR::ci(). This can be useful to have more robust change and skipping extreme values.
- if "sd" or "mad", it will spread by this dispersion index around the mean or the median, respectively. If the length argument is an even number (e.g., 4), it will have one more step on the positive side (i.e., -1, 0, +1, +2). The result is a named vector. See 'Examples.'
- "grid" will create a reference grid that is useful when plotting predictions, by choosing representative values for numeric variables based on their position in the reference grid. If a numeric variable is the first predictor in by, values from minimum to maximum of the same length as indicated in length are generated. For numeric predictors not specified at first in by, mean and -1/+1 SD around the mean are returned. For factors, all levels are returned.
- "pretty" will create a range "pretty" values, using pretty(), where the value in length is used for the n argument in pretty().

range can also be a vector of different values (see 'Examples'). In this case, range must be of same length as numeric target variables. If range is a named vector, values are matched against the names of the target variables.

weighted — Logical or character. If TRUE, creates a "weighted" data grid, which is a smaller representation of a large data grid. Each unique combination of (categorical) predictors is included only once (i.e., one row per unique combination of predictors specified in by). Numeric predictors are binned (see argument n_bins) and each value is recoded into the mean value for the related bin. A new Weight variable is added that indicates how often each combination appears in the original data. weighted can also be the name of an existing weighting variable in the data. In this case, the new Weight variable represents the sum of the weights for all observations that share the unique combination of predictors.

n_bins — Numeric value indicating the number of bins to use for numeric predictors when creating a weighted data grid (see weighted). Defaults to 5. If a numeric predictor has more unique values than n_bins, it is divided into n_bins equal-sized intervals, and each value is replaced by the mean of its respective bin. If a predictor has fewer unique values than n_bins, it is not binned. If n_bins = NULL or NA, numeric predictors are not used to group the data; instead, they are held constant at their overall mean across the dataset.

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.

protect_integers — Defaults to TRUE. Indicates whether integers (whole numbers) should be treated as integers (i.e., prevent adding any in-between round number values), or - if

FALSE - as regular numeric variables. Only applies to focal predictors (specified in by) and when:

1. range = "range" (the default), or if range = "grid" and the first predictor in by is an integer;
2. length is larger than the number of unique values for the variable.

If length is smaller than the number of unique values, protect_integers is ignored.

digits — Number of digits used for rounding numeric values specified in by. E.g., x = [sd] will round the mean and +-/1 SD in the data grid to digits.

reference — The reference vector from which to compute the mean and SD. Used when standardizing or unstandardizing the grid using effectsize::standardize.

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().

verbose — Toggle warnings.

Details

Data grids are an (artificial or theoretical) representation of the sample. They consists of predictors of interest (so-called focal predictors), and meaningful values, at which the sample characteristics (focal predictors) should be represented. The focal predictors are selected in by. To select meaningful (or representative) values, either use by, or use a combination of the arguments length and range.

Value

Reference grid data frame.

See Also

get_predicted() to extract predictions, for which the data grid is useful, and see the methods for objects generated by **emmeans** and **marginaleffects** to extract the "grid" columns.

Examples

```
# Datagrids of variables and dataframes ====================================
data(iris)
data(mtcars)

# Single variable is of interest; all others are "fixed" ------------------

# Factors, returns all the levels
get_datagrid(iris, by = "Species")
# Specify an expression
get_datagrid(iris, by = "Species = c('setosa', 'versicolor')")

# Numeric variables, default spread length = 10
get_datagrid(iris, by = "Sepal.Length")
# change length
get_datagrid(iris, by = "Sepal.Length", length = 3)

# change non-targets fixing
get_datagrid(iris[2:150, ],
  by = "Sepal.Length",
  factors = "mode", numerics = "median"
)

# change min/max of target
get_datagrid(iris, by = "Sepal.Length", range = "ci", ci = 0.90)

# Manually change min/max
get_datagrid(iris, by = "Sepal.Length = c(0, 1)")

# -1 SD, mean and +1 SD
get_datagrid(iris, by = "Sepal.Length = [sd]")

# rounded to 1 digit
get_datagrid(iris, by = "Sepal.Length = [sd]", digits = 1)

# identical to previous line: -1 SD, mean and +1 SD
get_datagrid(iris, by = "Sepal.Length", range = "sd", length = 3)

# quartiles
get_datagrid(iris, by = "Sepal.Length = [quartiles]")

# Standardization and unstandardization
data <- get_datagrid(iris, by = "Sepal.Length", range = "sd", length = 3)

# It is a named vector (extract names with `names(out$Sepal.Length)`)
data$Sepal.Length
datawizard::standardize(data, select = "Sepal.Length")

# Manually specify values
data <- get_datagrid(iris, by = "Sepal.Length = c(-2, 0, 2)")
data
datawizard::unstandardize(data, select = "Sepal.Length")
```

```
# Multiple variables are of interest, creating a combination --------------

get_datagrid(iris, by = c("Sepal.Length", "Species"), length = 3)
get_datagrid(iris, by = c("Sepal.Length", "Petal.Length"), length = c(3, 2))
get_datagrid(iris, by = c(1, 3), length = 3)
get_datagrid(iris, by = c("Sepal.Length", "Species"), preserve_range = TRUE)
get_datagrid(iris, by = c("Sepal.Length", "Species"), numerics = 0)
get_datagrid(iris, by = c("Sepal.Length = 3", "Species"))
get_datagrid(iris, by = c("Sepal.Length = c(3, 1)", "Species = 'setosa'"))

# specify length individually for each focal predictor
# values are matched by names
get_datagrid(mtcars[1:4], by = c("mpg", "hp"), length = c(hp = 3, mpg = 2))

# Numeric and categorical variables, generating a grid for plots
# default spread when numerics are first: length = 10
get_datagrid(iris, by = c("Sepal.Length", "Species"), range = "grid")

# default spread when numerics are not first: length = 3 (-1 SD, mean and +1 SD)
get_datagrid(iris, by = c("Species", "Sepal.Length"), range = "grid")

# range of values
get_datagrid(iris, by = c("Sepal.Width = 1:5", "Petal.Width = 1:3"))

# With list-style by-argument
get_datagrid(
  iris,
  by = list(Sepal.Length = 1:3, Species = c("setosa", "versicolor"))
)


# Weighted data grid ------------------------------------------------------
data(penguins)
# Adelie appears 152 times in the data, Chinstrap 68 times and Gentoo 124
# times. Instead of a three-row data grid, which assumes that each species
# is present equally often in the data, we now could "weight" each row
# according to their actual frequency in the data
get_datagrid(penguins, "species", weighted = TRUE)

# numeric variables are included and "binned"
get_datagrid(penguins, c("species", "island", "body_mass"), weighted = TRUE)

# numeric variables are included, but set to their mean value
get_datagrid(
  penguins,
  c("species", "island", "body_mass"),
  n_bins = NULL,
  weighted = TRUE
)

# With models ===============================================================
```

```
# Fit a linear regression
model <- lm(Sepal.Length ~ Sepal.Width * Petal.Length, data = iris)

# Get datagrid of predictors
data <- get_datagrid(model, length = c(20, 3), range = c("range", "sd"))
# same as: get_datagrid(model, range = "grid", length = 20)

# Add predictions
data$Sepal.Length <- get_predicted(model, data = data)

# Visualize relationships (each color is at -1 SD, Mean, and + 1 SD of Petal.Length)
plot(data$Sepal.Width, data$Sepal.Length,
  col = data$Petal.Length,
  main = "Relationship at -1 SD, Mean, and + 1 SD of Petal.Length"
)

# weighted data grid
model <- lm(Sepal.Length ~ Species + Sepal.Width, data = iris)
# when `by` is not specified, all predictors are used to create a weighted grid
get_datagrid(model, weighted = TRUE)

# fewer bins for numeric values
get_datagrid(model, n_bins = 3, weighted = TRUE)

# weighted data grid
d <- iris
d$weights <- abs(rnorm(nrow(d), 1, 0.2))

model <- lm(Sepal.Length ~ Species + Sepal.Width, data = d, weights = weights)
get_datagrid(model, "Species", weighted = "weights")
```

`get_datagrid.emmGrid` *Extract a reference grid from objects created by* {emmeans} *and* {marginaleffects}

Description

Extract a reference grid from objects created by {emmeans} and {marginaleffects}

Usage

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

Arguments

x	An object created by a function such as emmeans::emmeans(), marginaleffects::slopes(), etc.
...	Currently not used

Details

Note that for {emmeans} inputs the results is a proper grid (all combinations of values are represented), except when a nesting structure is detected. Additionally, when the input is an emm_list object, the function will rbind() the data-grids of all the elements in the input.

For {marginaleffects} inputs, the output may very well be a non-grid result. See examples.

Value

A data.frame with key columns that identify the rows in x.

Examples

```
data("mtcars")
mtcars$cyl <- factor(mtcars$cyl)

mod <- glm(am ~ cyl + hp + wt,
  family = binomial("logit"),
  data = mtcars
)


em1 <- emmeans::emmeans(mod, ~ cyl + hp, at = list(hp = c(100, 150)))
get_datagrid(em1)

contr1 <- emmeans::contrast(em1, method = "consec", by = "hp")
get_datagrid(contr1)

eml1 <- emmeans::emmeans(mod, pairwise ~ cyl | hp, at = list(hp = c(100, 150)))
get_datagrid(eml1) # not a "true" grid


mfx1 <- marginaleffects::slopes(mod, variables = "hp")
get_datagrid(mfx1) # not a "true" grid

mfx2 <- marginaleffects::slopes(mod, variables = c("hp", "wt"), by = "am")
get_datagrid(mfx2)

contr2 <- marginaleffects::avg_comparisons(mod)
get_datagrid(contr2) # not a "true" grid
```

---

get_deviance *Model Deviance*

Description

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

Usage

```
get_deviance(x, ...)

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

Arguments

x	A model.
...	Not used.
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.

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	Type of approximation for the degrees of freedom. Can be one of the following: • "residual" (aka "analytical") returns the residual degrees of freedom, which usually is what stats::df.residual() returns. If a model object has no method to extract residual degrees of freedom, these are calculated as n-p, i.e. the number of observations minus the number of estimated parameters. If residual degrees of freedom cannot be extracted by either approach, returns Inf. • "wald" returns residual (aka analytical) degrees of freedom for models with t-statistic, 1 for models with Chi-squared statistic, and Inf for all other models. Also returns Inf if residual degrees of freedom cannot be extracted. • "normal" always returns Inf. • "model" returns model-based degrees of freedom, i.e. the number of (estimated) parameters. • For mixed models, can also be "ml1" (or "m-l-1", approximation of degrees of freedom based on a "m-l-1" heuristic as suggested by *Elff et al. 2019*) or "between-within" (or "betwithin"). • For mixed models of class merMod or glmmTMB, type can also be "satterthwaite" or "kenward-roger" (or "kenward"). See 'Details'. Usually, when degrees of freedom are required to calculate p-values or confidence intervals, type = "wald" is likely to be the best choice in most cases.
verbose	Toggle warnings.

Details

Degrees of freedom for mixed models

Inferential statistics (like p-values, confidence intervals and standard errors) may be biased in mixed models when the number of clusters is small (even if the sample size of level-1 units is high). In such cases it is recommended to approximate a more accurate number of degrees of freedom for such inferential statistics (see *Li and Redden 2015*).

m-l-1 degrees of freedom

The *m-l-1* heuristic is an approach that uses a t-distribution with fewer degrees of freedom. In particular for repeated measure designs (longitudinal data analysis), the m-l-1 heuristic is likely to be more accurate than simply using the residual or infinite degrees of freedom, because `get_df(type = "ml1")` returns different degrees of freedom for within-cluster and between-cluster effects. Note that the "m-l-1" heuristic is not applicable (or at least less accurate) for complex multilevel designs, e.g. with cross-classified clusters. In such cases, more accurate approaches like the Kenward-Roger approximation is recommended. However, the "m-l-1" heuristic also applies to generalized mixed models, while approaches like Kenward-Roger or Satterthwaite are limited to linear mixed models only.

Between-within degrees of freedom

The Between-within denominator degrees of freedom approximation is, similar to the "m-l-1" heuristic, recommended in particular for (generalized) linear mixed models with repeated measurements (longitudinal design). `get_df(type = "betwithin")` implements a heuristic based on the between-within approach, i.e. this type returns different degrees of freedom for within-cluster and between-cluster effects. Note that this implementation does not return exactly the same results as shown in *Li and Redden 2015*, but similar.

Satterthwaite and Kenward-Roger degrees of freedom

Unlike simpler approximation heuristics like the "m-l-1" rule (`type = "ml1"`), the Satterthwaite or Kenward-Roger approximation is also applicable in more complex multilevel designs. However, the "m-l-1" or "between-within" heuristics also apply to generalized mixed models, while approaches like Kenward-Roger or Satterthwaite are limited to linear mixed models only.

References

- Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. Biometrics, 983-997.
- Satterthwaite FE (1946) An approximate distribution of estimates of variance components. Biometrics Bulletin 2 (6):110–4.
- Elff, M.; Heisig, J.P.; Schaeffer, M.; Shikano, S. (2019). Multilevel Analysis with Few Clusters: Improving Likelihood-based Methods to Provide Unbiased Estimates and Accurate Inference, British Journal of Political Science.
- Li, P., Redden, D. T. (2015). Comparing denominator degrees of freedom approximations for the generalized linear mixed model in analyzing binary outcome in small sample cluster-randomized trials. BMC Medical Research Methodology, 15(1), 38

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 alternative to stats::family*

Description

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)

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

```
get_intercept(x, ...)
```

Arguments

x	A model.
...	Not used.

Value

The value of the intercept.

Examples

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


get_intercept(lme4::lmer(Sepal.Length ~ Sepal.Width + (1 | Species), data = iris))


get_intercept(gamm4::gamm4(Sepal.Length ~ s(Petal.Width), data = iris))
```

`get_loglikelihood` *Log-Likelihood and Log-Likelihood correction*

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).

`get_loglikelihood_adjustment()` can be used to correct the log-likelihood for models with transformed response variables. The adjustment value can be added to the log-likelihood to get the corrected value. This is done automatically in `get_loglikelihood()` if `check_response = TRUE`.

Usage

```
get_loglikelihood(x, ...)

loglikelihood(x, ...)

get_loglikelihood_adjustment(x)

## S3 method for class 'lm'
get_loglikelihood(
  x,
  estimator = "ML",
  REML = FALSE,
  check_response = 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. `estimator="REML"` will give same results as `logLik(..., REML=TRUE)`.
`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.

check_response	Logical, if TRUE, checks if the response variable is transformed (like log() or sqrt()), and if so, returns a corrected log-likelihood. To get back to the original scale, the likelihood of the model is multiplied by the Jacobian/derivative of the transformation.
verbose	Toggle warnings and messages.

Value

get_loglikelihood() returns 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.

get_loglikelihood_adjustment() returns the adjustment value to be added to the log-likelihood to correct for transformed response variables, or NULL if the adjustment could not be computed.

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")
```

---

get_mixed_info *Extract various information from mixed models*

Description

Small helper function that returns essential information on coefficients, model matrix, variance and correlation parameters, as well as random effects parameters of mixed effects models as list. Mainly used for internal purposes.

Usage

```
get_mixed_info(model, ...)

## Default S3 method:
get_mixed_info(model, verbose = TRUE, ...)

## S3 method for class 'glmmTMB'
get_mixed_info(model, component = "conditional", verbose = TRUE, ...)
```

Arguments

model	A mixed effects model.
...	Not used.
verbose	Toggle off warnings.
component	For glmmTMB and MixMod models, this argument specifies the component of the model to extract. Possible values are "conditional" (default) and "zero_inflated" (or "zi").

Value

This function returns a list that has the same structure for any mixed models with the following components:

- `beta` (contains fixed effects, as returned by `lme4::fixef(model)`)
- `X` (contains the model matrix, as returned by `lme4::getME(model, "X")`)
- `vc` (contains the variance and correlation parameters, as returned by `lme4::VarCorr(model)`)
- `re` (random effects parameters, as returned by `lme4::ranef(model)`)

`get_model` *Get a model objects that is saved as attribute*

Description

This functions tries to get a model object from the object `x`, where the model object is saved as an (arbitrarily named) attribute. This is useful for example, when a model is fitted and saved as an attribute of a data frame.

Usage

```
get_model(x, name = "model", element = NULL, ...)
```

Arguments

`x`	An object that contains a model object as an attribute. This could be a data frame or any other object that has an attribute containing the model.
`name`	The name of the attribute that contains the model object. Defaults to `"model"`.
`element`	String or character vector. If provided, this argument allows you to specify which element(s) of the model object to return. This can be useful if the model object is a list or has multiple components, and you only want to extract a specific part.
`...`	Not used.

Value

The object that is stored as an attribute of `x` with the name `name`, or the specific element of that object if `element` is provided. If the attribute or element does not exist, an error is raised.

Examples

```
# Example of using get_model
d <- data.frame(x = rnorm(100), y = rnorm(100))
# fit a model and save it as an attribute
model <- lm(y ~ x, data = d)
attr(d, "model") <- model
# get the model back
```

```
get_model(d)
# get the coefficients of the model
get_model(d, element = "coefficients")
```

`get_modelmatrix` *Model Matrix*

Description

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

Usage

```
get_modelmatrix(x, ...)
```

Arguments

`x`	An object.
`...`	Passed down to other methods (mainly `model.matrix()`).

Examples

```
data(mtcars)

model <- lm(am ~ vs, data = mtcars)
get_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`)
- Structural equation models (**lavaan**, **blavaan**)

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

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- `"smooth_terms"`: returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- `"zero_inflated"` (or `"zi"`): returns the zero-inflation component.
- `"dispersion"`: returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- `"instruments"`: for instrumental-variable or some fixed effects regression, returns the instruments.
- `"nonlinear"`: for non-linear models (like models of class `nlmerMod`), returns the nonlinear parameters. Not available for functions that return variables, like `find_predictors()`.

- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

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

---

get_parameters.betamfx

Get model parameters from marginal effects models

Description

Returns the coefficients from a model.

Usage

```
## S3 method for class 'betamfx'
get_parameters(x, component = "all", ...)
```

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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • 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.
...	Currently not used.

Value

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

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().

- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

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

---

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 = "all", ...)
```

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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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.
...	Currently not used.

Value

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

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- `"smooth_terms"`: returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- `"zero_inflated"` (or `"zi"`): returns the zero-inflation component.
- `"dispersion"`: returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- `"instruments"`: for instrumental-variable or some fixed effects regression, returns the instruments.
- `"nonlinear"`: for non-linear models (like models of class `nlmerMod`), returns the nonlinear parameters. Not available for functions that return variables, like `find_predictors()`.

- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

```
data("GasolineYield", package = "betareg")
m <- betareg::betareg(yield ~ batch + temp, data = GasolineYield)
get_parameters(m)
get_parameters(m, component = "precision")
```

---

get_parameters.BGGM *Get model parameters from Bayesian models*

Description

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

Usage

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

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

## S3 method for class 'brmsfit'
get_parameters(
  x,
  effects = "fixed",
  component = "all",
  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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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 only used for models of class brmsfit, where a variable argument can be used, which is directly passed to the as.data.frame() method (i.e., as.data.frame(x, variable = variable)).

effects — Should variables for fixed effects ("fixed"), random effects ("random") or both ("all") be returned? Only applies to mixed models. May be abbreviated.

For models of from packages **brms** or **rstanarm** there are additional options:

- "fixed" returns fixed effects.
- "random_variance" return random effects parameters (variance and correlation components, e.g. those parameters that start with sd_ or cor_).
- "grouplevel" returns random effects group level estimates, i.e. those parameters that start with r_.
- "random" returns both "random_variance" and "grouplevel".
- "all" returns fixed effects and random effects variances.
- "full" returns all parameters.

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). For models of class brmsfit, NULL is returned if no parameter matches the selection of effects, component and parameters.

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()`.

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- `"smooth_terms"`: returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- `"zero_inflated"` (or `"zi"`): returns the zero-inflation component.
- `"dispersion"`: returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- `"instruments"`: for instrumental-variable or some fixed effects regression, returns the instruments.
- `"nonlinear"`: for non-linear models (like models of class `nlmerMod`), returns the nonlinear parameters. Not available for functions that return variables, like `find_predictors()`.
- `"correlation"`: for models with correlation-component, like `gls`, the variables used to describe the correlation structure are returned. The grouping factor (like `Subject` in `~ age | Subject`) is only returned for `effects = "all"`.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, `smooth_terms`, or `instruments` (everything that are fixed or random effects - depending on the `effects` argument - but no auxiliary parameters).
- `"distributional"` (or `"auxiliary"`): components like `sigma`, `dispersion`, `beta` or `precision` (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: `"infrequent_purchase"`, `"ip"`, and `"auxiliary"`
- **BGGM**: `"correlation"` and `"intercept"`
- **BFBayesFactor**, **glmx**: `"extra"`
- **averaging**:`"conditional"` and `"full"`
- **mjoint**: `"survival"`
- **mfx**: `"precision"`, `"marginal"`
- **betareg**, **DirichletRegModel**: `"precision"`

- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

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

---

get_parameters.blavaan

Get model parameters from structural equation models

Description

Returns the coefficients (or posterior samples for **blavaan** models with summary = FALSE) from a structural equation model.

Usage

```
## S3 method for class 'blavaan'
get_parameters(x, summary = FALSE, standardize = FALSE, ...)

## S3 method for class 'lavaan'
get_parameters(x, standardize = FALSE, ...)
```

Arguments

x	A model of class lavaan or blavaan.
summary	Logical. For **blavaan** models, indicates whether the full posterior samples (summary = FALSE) or point estimates (summary = TRUE) should be returned.
standardize	Logical. Only TRUE returns standardized parameters. Other values, such as 1 or NA, return unstandardized parameters.
...	If standardize = TRUE, a type argument can be used, which is passed to lavaan::standardizedSoluti (or to blavaan::standardizedPosterior() for the posterior samples of **blavaan** models). For example, type can be "std.all" (the default), "std.lv" or "std.nox". See lavaan::standardizedSolution() for all values. Other arguments are not passed on.

Value

For **blavaan** models with `summary = FALSE`, the posterior samples as data frame, with one row per draw (chains pooled) and one column per free or defined parameter. If `standardize = TRUE`, fixed parameters are included, too. Else, a data frame with the columns `Parameter`, `Estimate` and `Component`.

Examples

```
m <- lavaan::cfa("visual =~ x1 + x2 + x3", data = lavaan::HolzingerSwineford1939)
get_parameters(m, standardize = TRUE, type = "std.lv")
```

---

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, ...)
```

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 parameters 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)

emm <- emmeans(model, "cyl")
get_parameters(emm)

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

```
## S3 method for class 'gamm'
get_parameters(x, component = "all", ...)
```

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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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.
...	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.

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- `"smooth_terms"`: returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- `"zero_inflated"` (or `"zi"`): returns the zero-inflation component.
- `"dispersion"`: returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- `"instruments"`: for instrumental-variable or some fixed effects regression, returns the instruments.
- `"nonlinear"`: for non-linear models (like models of class `nlmerMod`), returns the nonlinear parameters. Not available for functions that return variables, like `find_predictors()`.
- `"correlation"`: for models with correlation-component, like `gls`, the variables used to describe the correlation structure are returned. The grouping factor (like `Subject` in `~ age | Subject`) is only returned for `effects = "all"`.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, `smooth_terms`, or `instruments` (everything that are fixed or random effects - depending on the `effects` argument - but no auxiliary parameters).
- `"distributional"` (or `"auxiliary"`): components like `sigma`, `dispersion`, `beta` or `precision` (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: `"infrequent_purchase"`, `"ip"`, and `"auxiliary"`
- **BGGM**: `"correlation"` and `"intercept"`
- **BFBayesFactor**, **glmx**: `"extra"`
- **averaging**:`"conditional"` and `"full"`
- **mjoint**: `"survival"`
- **mfx**: `"precision"`, `"marginal"`
- **betareg**, **DirichletRegModel**: `"precision"`
- **mvord**: `"thresholds"` and `"correlation"`
- **clm2**: `"scale"`

- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

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

---

get_parameters.glmmTMB

Get model parameters from mixed models

Description

Returns the coefficients from a model.

Usage

```
## S3 method for class 'glmmTMB'
get_parameters(x, effects = "fixed", component = "all", ...)
```

Arguments

x	A fitted model.
effects	Should variables for fixed effects ("fixed"), random effects ("random") or both ("all") be returned? Only applies to mixed models. May be abbreviated. For find_predictors() and find_variables(), it also applies to the correlation part of models from *nlme* (like gls).
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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • 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.

... Currently not used.

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. See details in the section *Model Components*.

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**).

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: `"infrequent_purchase"`, `"ip"`, and `"auxiliary"`
- **BGGM**: `"correlation"` and `"intercept"`
- **BFBayesFactor**, **glmx**: `"extra"`
- **averaging**:`"conditional"` and `"full"`
- **mjoint**: `"survival"`
- **mfx**: `"precision"`, `"marginal"`
- **betareg**, **DirichletRegModel**: `"precision"`
- **mvord**: `"thresholds"` and `"correlation"`
- **clm2**: `"scale"`
- **selection**: `"selection"`, `"outcome"`, and `"auxiliary"`
- **lcmm**: `"membership"`, `"longitudinal"`, `"beta"`, `"splines"`, and `"linear"`

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like `mu`, `ndt`, `kappa`, etc.

Examples

```
data(Salamanders, package = "glmmTMB")
m <- glmmTMB::glmmTMB(
  count ~ mined + (1 | site),
  ziformula = ~mined,
  family = poisson(),
  data = Salamanders
)
get_parameters(m)
```

---

get_parameters.htest *Get model parameters from htest-objects*

Description

Returns the parameters from a hypothesis test.

Usage

```
## S3 method for class 'htest'
get_parameters(x, ...)
```

Arguments

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

Value

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

Examples

```
get_parameters(t.test(1:10, y = c(7:20)))
```

---

get_parameters.zeroinfl

Get model parameters from zero-inflated and hurdle models

Description

Returns the coefficients from a model.

Usage

```
## S3 method for class 'zeroinfl'
get_parameters(x, component = "all", ...)
```

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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • `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.
...	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.

Model components

Possible values for the `component` argument depend on the model class. Following are valid options:

- `"all"`: returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- `"conditional"`: only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- `"smooth_terms"`: returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- `"zero_inflated"` (or `"zi"`): returns the zero-inflation component.
- `"dispersion"`: returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- `"instruments"`: for instrumental-variable or some fixed effects regression, returns the instruments.
- `"nonlinear"`: for non-linear models (like models of class `nlmerMod`), returns the nonlinear parameters. Not available for functions that return variables, like `find_predictors()`.
- `"correlation"`: for models with correlation-component, like `gls`, the variables used to describe the correlation structure are returned. The grouping factor (like `Subject` in `~ age | Subject`) is only returned for `effects = "all"`.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, `smooth_terms`, or `instruments` (everything that are fixed or random effects - depending on the `effects` argument - but no auxiliary parameters).
- `"distributional"` (or `"auxiliary"`): components like `sigma`, `dispersion`, `beta` or `precision` (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: `"infrequent_purchase"`, `"ip"`, and `"auxiliary"`
- **BGGM**: `"correlation"` and `"intercept"`
- **BFBayesFactor**, **glmx**: `"extra"`
- **averaging**:`"conditional"` and `"full"`
- **mjoint**: `"survival"`
- **mfx**: `"precision"`, `"marginal"`
- **betareg**, **DirichletRegModel**: `"precision"`
- **mvord**: `"thresholds"` and `"correlation"`
- **clm2**: `"scale"`

- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

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

---

get_predicted *Model predictions (robust) and their confidence intervals*

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.

get_predicted_ci() returns the confidence (or prediction) interval (CI) associated with predictions made by a model. This function can be called separately on a vector of predicted values. get_predicted() usually returns confidence intervals (included as attribute, and accessible via the as.data.frame() method) by default. It is preferred to rely on the get_predicted() function for standard errors and confidence intervals - use get_predicted_ci() only if standard errors and confidence intervals are not available otherwise.

Usage

```
get_predicted(x, ...)

## Default S3 method:
get_predicted(
  x,
  data = NULL,
  predict = "expectation",
  ci = NULL,
  ci_type = "confidence",
  ci_method = NULL,
  dispersion_method = "sd",
  vcov = NULL,
  vcov_args = NULL,
```

```
  verbose = TRUE,
  ...
)

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

## S3 method for class 'nestedLogit'
get_predicted(
  x,
  data = NULL,
  predict = "expectation",
  submodel = "nested",
  ci = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'stanreg'
get_predicted(
  x,
  data = NULL,
  predict = "expectation",
  iterations = NULL,
  ci = NULL,
  ci_method = NULL,
  include_random = "default",
  include_smooth = TRUE,
  verbose = TRUE,
  ...
)

## S3 method for class 'gam'
get_predicted(
  x,
  data = NULL,
  predict = "expectation",
  ci = NULL,
  include_random = TRUE,
  include_smooth = TRUE,
```

```
  iterations = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'lmerMod'
get_predicted(
  x,
  data = NULL,
  predict = "expectation",
  ci = NULL,
  ci_method = NULL,
  include_random = "default",
  iterations = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'principal'
get_predicted(x, data = NULL, ...)
```

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 the model's `predict()` method, or `get_predicted_ci()`.
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. Visualization matrices can be generated using `get_datagrid()`.
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). This option should also be used for finite mixture models (currently only family `brms::mixture()` from package *brms*), when predicted values of the response for each class is required. • `"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"` is relevant only for binomial, ordinal or mixture models. – For binomial models, `predict = "classification"` will additionally transform the predictions into the original response's type (for instance, to a factor).

  - For ordinal models (e.g., classes `clm` or `multinom`), gives the predicted response class membership, defined as highest probability prediction.
  - For finite mixture models (currently only family `brms::mixture()` from package *brms*) also returns the predicted response class membership (similar as for ordinal models).
- Other strings are passed directly to the `type` argument of the `predict()` method supplied by the modelling package.
- Specifically for models of class `brmsfit` (package *brms*), the `predict` argument can be any valid option for the `dpar` argument, to predict distributional parameters (such as `"sigma"`, `"beta"`, `"kappa"`, `"phi"` and so on, see `?brms::brmsfamily`).
- 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 four 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.

`ci` The interval level. Default is `NULL`, to be fast even for larger models. Set the interval level to an explicit value, e.g. `0.95`, for `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]`).

`ci_method` The method for computing p values and confidence intervals. Possible values depend on model type.

- `NULL` uses the default method, which varies based on the model type.
- Most frequentist models: `"wald"` (default), `"residual"` or `"normal"`.
- Bayesian models: `"quantile"` (default), `"hdi"`, `"eti"`, and `"spi"`.
- Mixed effects **lme4** models: `"wald"` (default), `"residual"`, `"normal"`, `"satterthwaite"`, and `"kenward-roger"`.

See `get_df()` for details.

`dispersion_method`
Bootstrap dispersion and Bayesian posterior summary: `"sd"` or `"mad"`.

vcov

Variance-covariance matrix used to compute uncertainty estimates (e.g., for robust standard errors). This argument accepts a covariance matrix, a function which returns a covariance matrix, or a string which identifies the function to be used to compute the covariance matrix.

- A covariance matrix
- A function which returns a covariance matrix (e.g., `stats::vcov()`)
- A string which indicates the kind of uncertainty estimates to return.
  - Heteroskedasticity-consistent: `"HC"`, `"HC0"`, `"HC1"`, `"HC2"`, `"HC3"`, `"HC4"`, `"HC4m"`, `"HC5"`. See `?sandwich::vcovHC`
  - Cluster-robust: `"CR"`, `"CR0"`, `"CR1"`, `"CR1p"`, `"CR1S"`, `"CR2"`, `"CR3"`. See `?clubSandwich::vcovCR`
  - Bootstrap: `"BS"`, `"xy"`, `"residual"`, `"wild"`, `"mammen"`, `"fractional"`, `"jackknife"`, `"norm"`, `"webb"`. See `?sandwich::vcovBS`
  - Other `sandwich` package functions: `"HAC"`, `"PC"`, `"CL"`, `"OPG"`, `"PL"`.
  - Kenward-Roger approximation: `"kenward-roger"`. See `?pbkrtest::vcovAdj`.
  - Finite Population Correction: `"fpc"` applies the finite population correction. Requires the `population_size` to be specified in `vcov_args`. For mixed models, FPC is based on *Lai et al. 2018*. When `vcov = "fpc"`, at least one of `population_size` (size of the finite population, must be larger than the number of observations in the model) or `cluster_size` (the finite size of cluster groups in the population, must be larger than the number of groups of the random effects) in the `vcov_args` argument. You can additionally apply the Kenward-Roger approximation with the `kr` argument, e.g. `vcov_args = list(cluster_size = 15, kr = TRUE)`.

Exceptions are following models:

- Model of class `glmgee`, which have pre-defined options for the variance-covariance matrix calculation. These are `"robust"`, `"df-adjusted"`, `"model"`, `"bias-corrected"`, and `"jackknife"`. See `?glmtoolbox::vcov.glmgee` for details.
- Model of class `glmmTMB` currently only support the `"HC0"` option.
- Models of class `fixest` use the `vcov()` method of the **fixest** package, so `vcov` accepts the types listed in `?fixest::vcov.fixest`. Of the heteroskedasticity-consistent types, `"HC0"` to `"HC3"` are supported. `"HC0"` uses `vcov = "hetero"` without the small-sample adjustment (`ssc = fixest::ssc(K.adj = FALSE)`).

vcov_args

List of arguments to be passed to the function identified by the `vcov` argument. This function is typically supplied by the **sandwich** or **clubSandwich** packages. Please refer to their documentation (e.g., `?sandwich::vcovHAC`) to see the list of available arguments. If no estimation type (argument `type`) is given, the default type for `"HC"` equals the default from the **sandwich** package; for type `"CR"`, the default is set to `"CR3"`. For `vcov = "fpc"`, `vcov_args` must specify either `population_size` or `cluster_size`, depending on the model.

verbose

Toggle warnings.

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(..., keep_iterations = TRUE)` on the output.

`submodel` Only applies to models of class `nestedLogit`. Can be `"nested"` or `"dichotomies"`. If `"nested"` (default), the fitted probabilities under the nested logit model are returned. For `"dichotomies"`, `predict()` is invoked for each binary logit model.

`include_random` If `"default"`, include all random effects in the prediction, unless random effect variables are not in the data. If `TRUE`, include all random effects in the prediction (in this case, it will be checked if actually all random effect variables are in `data`). 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 `data` is provided, make sure to include the random effect variables in `data` 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**.

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()`.

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. For ordinal or mixture models, it returns the predicted class membership, based on the highest probability of classification.

Heteroscedasticity consistent standard errors

The arguments `vcov` 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.

Finite mixture models

For finite mixture models (currently, only the `mixture()` family from package *brms* is supported), use `predict = "classification"` to predict the class membership. To predict outcome values by class, use `predict = "link"`. Other `predict` options will return predicted values of the outcome for the full data, not stratified by class membership.

Bayesian and Bootstrapped models and iterations

For predictions based on multiple iterations, for instance in the case of Bayesian models and bootstrapped predictions, the function used to compute the centrality (point-estimate predictions) can be modified via the `centrality_function` argument. For instance, `get_predicted(model, centrality_function = stats::median)`. The default is `mean`. Individual draws can be accessed by running `iter <- as.data.frame(get_predicted(model))`, and their iterations can be reshaped into a long format by `bayestestR::reshape_iterations(iter)`.

Hypothesis tests

There is limited support for hypothesis tests, i.e. objects of class `htest`:

- `chisq.test()`: returns the expected values of the contingency table.

See Also

`get_datagrid()`

Examples

```
data(mtcars)
x <- lm(mpg ~ cyl + hp, data = mtcars)

predictions <- get_predicted(x, ci = 0.95)
predictions

# Options and methods ---------------------
get_predicted(x, predict = "prediction")

# Get CI
```

```
as.data.frame(predictions)

# Bootstrapped
as.data.frame(get_predicted(x, iterations = 4))
# Same as as.data.frame(..., keep_iterations = FALSE)
summary(get_predicted(x, iterations = 4))

# Different prediction types ------------------------
data(iris)
data <- droplevels(iris[1:100, ])

# Fit a logistic model
x <- glm(Species ~ Sepal.Length, data = data, family = "binomial")

# Expectation (default): response scale + CI
pred <- get_predicted(x, predict = "expectation", ci = 0.95)
head(as.data.frame(pred))

# Prediction: response scale + PI
pred <- get_predicted(x, predict = "prediction", ci = 0.95)
head(as.data.frame(pred))

# Link: link scale + CI
pred <- get_predicted(x, predict = "link", ci = 0.95)
head(as.data.frame(pred))

# Classification: classification "type" + PI
pred <- get_predicted(x, predict = "classification", ci = 0.95)
head(as.data.frame(pred))
```

`get_predicted_ci` *Confidence intervals around predicted values*

Description

Confidence intervals around predicted values

Usage

```
get_predicted_ci(x, ...)

## Default S3 method:
get_predicted_ci(
  x,
  predictions = NULL,
  data = NULL,
  se = NULL,
  ci = 0.95,
```

```
  ci_type = "confidence",
  ci_method = NULL,
  dispersion_method = "sd",
  vcov = NULL,
  vcov_args = NULL,
  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 the model's `predict()` method, or `get_predicted_ci()`.
predictions	A vector of predicted values (as obtained by `stats::fitted()`, `stats::predict()` or `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. Visualization matrices can be generated using `get_datagrid()`.
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 is `NULL`, to be fast even for larger models. Set the interval level to an explicit value, e.g. `0.95`, for `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]`).
ci_method	The method for computing p values and confidence intervals. Possible values depend on model type. • `NULL` uses the default method, which varies based on the model type. • Most frequentist models: `"wald"` (default), `"residual"` or `"normal"`. • Bayesian models: `"quantile"` (default), `"hdi"`, `"eti"`, and `"spi"`. • Mixed effects **lme4** models: `"wald"` (default), `"residual"`, `"normal"`, `"satterthwaite"`, and `"kenward-roger"`. See `get_df()` for details.
dispersion_method	Bootstrap dispersion and Bayesian posterior summary: `"sd"` or `"mad"`.

vcov

Variance-covariance matrix used to compute uncertainty estimates (e.g., for robust standard errors). This argument accepts a covariance matrix, a function which returns a covariance matrix, or a string which identifies the function to be used to compute the covariance matrix.

- A covariance matrix
- A function which returns a covariance matrix (e.g., `stats::vcov()`)
- A string which indicates the kind of uncertainty estimates to return.
  - Heteroskedasticity-consistent: `"HC"`, `"HC0"`, `"HC1"`, `"HC2"`, `"HC3"`, `"HC4"`, `"HC4m"`, `"HC5"`. See `?sandwich::vcovHC`
  - Cluster-robust: `"CR"`, `"CR0"`, `"CR1"`, `"CR1p"`, `"CR1S"`, `"CR2"`, `"CR3"`. See `?clubSandwich::vcovCR`
  - Bootstrap: `"BS"`, `"xy"`, `"residual"`, `"wild"`, `"mammen"`, `"fractional"`, `"jackknife"`, `"norm"`, `"webb"`. See `?sandwich::vcovBS`
  - Other `sandwich` package functions: `"HAC"`, `"PC"`, `"CL"`, `"OPG"`, `"PL"`.
  - Kenward-Roger approximation: `"kenward-roger"`. See `?pbkrtest::vcovAdj`.
  - Finite Population Correction: `"fpc"` applies the finite population correction. Requires the `population_size` to be specified in `vcov_args`. For mixed models, FPC is based on *Lai et al. 2018*. When `vcov = "fpc"`, at least one of `population_size` (size of the finite population, must be larger than the number of observations in the model) or `cluster_size` (the finite size of cluster groups in the population, must be larger than the number of groups of the random effects) in the `vcov_args` argument. You can additionally apply the Kenward-Roger approximation with the `kr` argument, e.g. `vcov_args = list(cluster_size = 15, kr = TRUE)`.

Exceptions are following models:

- Model of class `glmgee`, which have pre-defined options for the variance-covariance matrix calculation. These are `"robust"`, `"df-adjusted"`, `"model"`, `"bias-corrected"`, and `"jackknife"`. See `?glmtoolbox::vcov.glmgee` for details.
- Model of class `glmmTMB` currently only support the `"HC0"` option.
- Models of class `fixest` use the `vcov()` method of the **fixest** package, so `vcov` accepts the types listed in `?fixest::vcov.fixest`. Of the heteroskedasticity-consistent types, `"HC0"` to `"HC3"` are supported. `"HC0"` uses `vcov = "hetero"` without the small-sample adjustment (`ssc = fixest::ssc(K.adj = FALSE)`).

vcov_args

List of arguments to be passed to the function identified by the `vcov` argument. This function is typically supplied by the **sandwich** or **clubSandwich** packages. Please refer to their documentation (e.g., `?sandwich::vcovHAC`) to see the list of available arguments. If no estimation type (argument `type`) is given, the default type for `"HC"` equals the default from the **sandwich** package; for type `"CR"`, the default is set to `"CR3"`. For `vcov = "fpc"`, `vcov_args` must specify either `population_size` or `cluster_size`, depending on the model.

verbose

Toggle warnings.

Details

Typically, `get_predicted()` returns confidence intervals based on the standard errors as returned by the `predict()`-function, assuming normal distribution (`+/- 1.96 * SE`) resp. a Student's t-distribution (if degrees of freedom are available). If `predict()` for a certain class does *not* return standard errors (for example, *merMod*-objects), these are calculated manually, based on following steps: matrix-multiply `X` by the parameter vector `B` to get the predictions, then extract the variance-covariance matrix `V` of the parameters and compute `XVX'` to get the variance-covariance matrix of the predictions. The square-root of the diagonal of this matrix represent the standard errors of the predictions, which are then multiplied by the critical test-statistic value (e.g., ~1.96 for normal distribution) for the confidence intervals.

If `ci_type = "prediction"`, prediction intervals are calculated. These are wider than confidence intervals, because they also take into account the uncertainty of the model itself. Before taking the square-root of the diagonal of the variance-covariance matrix, `get_predicted_ci()` adds the residual variance to these values. For mixed models, `get_variance_residual()` is used, while `get_sigma()^2` is used for non-mixed models.

Nonlinear mixed models of class `nlme` (from `nlme::nlme()`) have no model matrix `X`. For these models, the standard errors are calculated with the delta method: `X` is replaced by the Jacobian of the predictions with respect to the fixed effects, computed by central differences of `predict()`, with the random effects held at their predicted values. So the standard errors do not include the uncertainty of the random effects. `get_predicted()` uses the level of its predictions. A direct call to `get_predicted_ci()` uses the `level` argument, or the default level of `predict()` if `level` is missing. Only Wald confidence intervals are available. Prediction intervals, the `vcov` and `vcov_args` arguments, other values of `ci_method` and a `level` with more than one value are not yet supported for these models.

It is preferred to rely on standard errors returned by `get_predicted()` (i.e. returned by the `predict()`-function), because these are more accurate than manually calculated standard errors. Use `get_predicted_ci()` only if standard errors are not available otherwise. An exception are Bayesian models or bootstrapped predictions, where `get_predicted_ci()` returns quantiles of the posterior distribution or bootstrapped samples of the predictions. These are actually accurate standard errors resp. confidence (or uncertainty) intervals.

Examples

```
# Confidence Intervals for Model Predictions
# ------------------------------------------

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)

ci_vals <- get_predicted_ci(x, predictions, ci = c(0.80, 0.95))
head(ci_vals)
datawizard::reshape_ci(ci_vals)

ci_vals <- get_predicted_ci(x,
  predictions,
  dispersion_method = "MAD",
  ci_method = "HDI"
)
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

```
get_predictors(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.
...	Currently not used.
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

```
library(rstanarm)
model <- stan_glm(Sepal.Width ~ Species * Petal.Length, data = iris)
get_priors(model)
```

get_random *Get the data from random effects*

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.

Examples

```
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

```
get_residuals(x, ...)

## Default S3 method:
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, ...)

## Default S3 method:
get_response(
  x,
  select = NULL,
  as_proportion = TRUE,
  source = "environment",
  verbose = TRUE,
  ...
)

## S3 method for class 'nestedLogit'
get_response(x, dichotomies = FALSE, source = "environment", ...)
```

Arguments

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

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

`as_proportion` Logical, if `TRUE` and the response value is a proportion (e.g. `y1 / y2`), then the returned response value will be a vector with the result of this proportion. Else, always a data frame is returned.

`source` String, indicating from where data should be recovered. If `source = "environment"` (default), data is recovered from the environment (e.g. if the data is in the workspace). This option is usually the fastest way of getting data and ensures that the original variables used for model fitting are returned. Note that always the *current* data is recovered from the environment. Hence, if the data was modified *after* model fitting (e.g., variables were recoded or rows filtered), the returned data may no longer equal the model data. If a variable used in the model is missing from the data in the environment, but is a column of `model.frame()`, `get_data()` warns and uses the model frame instead. This applies to most, but not all, model classes. Variables used only inside a transformation, like `a` in `log(a)`, are not detected. If `source = "frame"` (or `"mf"`), the data is taken from the model frame. Any transformed variables are back-transformed, if possible. This option returns the data even if it is not available in the environment, however, in certain edge cases back-transforming to the original data may fail. If `source = "environment"` fails to recover the data, it tries to extract the data from the model frame; if `source = "frame"` and data cannot be extracted from the model frame, data will be recovered from the environment. Both ways only returns observations that have no missing data in the variables used for model fitting.

For objects from package **survey**, `"mf"` extracts data from the model frame of the survey design object, which is usually equivalent to the original data. `source = "environment"` extracts data from the model-object in the environment, which usually includes processed variables (like the `"(weights)"` variable for weights).

`verbose` Toggle warnings.

`dichotomies` Logical, if model is a `nestedLogit` objects, returns the response values for the dichotomies.

Value

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

Examples

```
data(cbpp)
cbpp$trials <- cbpp$size - cbpp$incidence
dat <<- cbpp

m <- glm(cbind(incidence, trials) ~ period, data = dat, family = binomial)
head(get_response(m))
get_response(m, select = "incidence")
```

```
data(mtcars)
m <- 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

```
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.
`...`	For internal use.

Value

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

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()`.

References

Gelman, A., Hill, J., & Vehtari, A. (2020). Regression and Other Stories. Cambridge University Press.

Examples

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

---

get_simulated *Simulate values from fitted models*

Description

Simulate responses from fitted statistical models.

Usage

```
get_simulated(x, ...)

## S3 method for class 'lm'
get_simulated(
  x,
  data = NULL,
  iterations = 1,
  include_data = FALSE,
  seed = NULL,
  ...
)

## S3 method for class 'glmmTMB'
get_simulated(
  x,
  data = NULL,
  iterations = 1,
  include_data = FALSE,
  seed = NULL,
  centrality = NULL,
  re.form = NULL,
  ...
)

## S3 method for class 'merMod'
get_simulated(
  x,
  data = NULL,
```

```
  iterations = 1,
  include_data = FALSE,
  seed = NULL,
  use.u = FALSE,
  re.form = NA,
  newparams = NULL,
  family = NULL,
  cluster.rand = stats::rnorm,
  allow.new.levels = FALSE,
  na.action = stats::na.pass,
  ...
)

## Default S3 method:
get_simulated(x, ...)

## S3 method for class 'data.frame'
get_simulated(x, data = NULL, include_data = FALSE, ...)
```

Arguments

x	A model.
...	Additional arguments passed to the underlying prediction or simulation methods.
data	An optional data frame in which to evaluate predictions before simulation. This can be a data grid created with get_datagrid().
iterations	Number of response vectors to simulate.
include_data	Logical, if TRUE, data is returned alongside with the simulated draws. If data = NULL, the data used to fit the model is included.
seed	An optional integer random seed.
centrality	Function, indicating how to summarize aggregated simulated values when data is a data grid. Only applies to models from package glmmTMB, because a special handling for the data argument is required here. simulate.glmmTMB() always returns simulated draws for the full data that was used to fit the model. If a data grid is passed via data, get_simulated.glmmTMB() internally, first, filters the results using datawizard::data_match() with the model data and data. This may return more than one row of simulated draws per group defined in data, thus, in a second step, the filtered data are aggregated by the groups defined in data. Resulting estimates of simulated values are summarized using centrylity, which, by default is the mode for categorical, ordinal or count response variables, or the mean otherwise.
re.form	For glmmTMB and merMod models, random effects formula passed to simulation (NULL, NA or ~0).
use.u	For merMod models, logical indicating whether to condition on the current conditional modes of the random effects when simulating.

newparams	For merMod models, optional list or vector of alternative parameter values (e.g., fixed- and random-effect parameters) to be used for simulation instead of those from the fitted model.
family	For merMod models, optional family object or function to override the model's family when simulating responses.
cluster.rand	For merMod models, function used to generate random draws for the random effects (e.g., rnorm).
allow.new.levels	For merMod models, logical indicating whether new levels of grouping variables are allowed in data when simulating.
na.action	For merMod models, function specifying how to handle missing values in data before simulation (e.g., "na.pass").

Value

A data frame with one column per simulation (iter_1, iter_2, ...). The attribute seed contains information about the RNG state used.

Examples

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

# Simulations on the original data
get_simulated(m, iterations = 2, seed = 123)

# Simulations on a data grid
dg <- get_datagrid(m, wt = c(2, 3), cyl = c(4, 6))
get_simulated(dg, m, iterations = 2, seed = 123)
```

---

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

```
get_statistic(x, ...)

## Default S3 method:
get_statistic(x, column_index = 3, verbose = TRUE, ...)

## S3 method for class 'glmmTMB'
```

```
get_statistic(x, component = "all", ...)

## S3 method for class 'gam'
get_statistic(x, re_test = TRUE, ...)

## S3 method for class 'emmGrid'
get_statistic(x, ci = 0.95, adjust = "none", merge_parameters = FALSE, ...)

## S3 method for class 'gee'
get_statistic(x, robust = FALSE, ...)
```

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 warnings.
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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • 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.
re_test	Logical, if TRUE (default), tests for random effects terms are performed. Only applies to mgcv::gam() model. For large models these tests can be computationally expensive, in which case it is recommended to set this argument to FALSE.
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 intervals. 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 parameters names and values as values.

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

Value

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

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().
- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"

- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Examples

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

---

get_transformation *Return function of transformed response variables*

Description

This functions 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. See find_transformation() for an overview of supported transformations that are detected.

Usage

```
get_transformation(x, include_all = FALSE, verbose = TRUE)
```

Arguments

x	A regression model or a character string of the formulation of the (response) variable.
include_all	Logical, if TRUE, does not only check the response variable, but all model terms.
verbose	Logical, if TRUE, prints a warning if the transformation could not be determined.

Value

A list of two functions: $transformation, the function that was used to transform the response variable; $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. If transformation is unknown, NULL is returned.

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(0.3)
log(0.3)

# inverse function is exp()
get_transformation(model)$inverse(0.3)
exp(0.3)

# get transformations for all model terms
model <- lm(mpg ~ log(wt) + I(gear^2) + exp(am), data = mtcars)
get_transformation(model, include_all = TRUE)
```

---

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, vcov = NULL, vcov_args = NULL, ...)

## S3 method for class 'glmgee'
get_varcov(x, verbose = TRUE, vcov = "robust", ...)

## S3 method for class 'hurdle'
get_varcov(
  x,
  component = "conditional",
  vcov = NULL,
  vcov_args = NULL,
  verbose = TRUE,
  ...
)
```

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

## S3 method for class 'mixor'
get_varcov(x, effects = "all", verbose = TRUE, ...)
```

Arguments

x	A model.
...	Currently not used.
verbose	Toggle warnings.
vcov	Variance-covariance matrix used to compute uncertainty estimates (e.g., for robust standard errors). This argument accepts a covariance matrix, a function which returns a covariance matrix, or a string which identifies the function to be used to compute the covariance matrix. • A covariance matrix • A function which returns a covariance matrix (e.g., stats::vcov()) • A string which indicates the kind of uncertainty estimates to return. – Heteroskedasticity-consistent: "HC", "HC0", "HC1", "HC2", "HC3", "HC4", "HC4m", "HC5". See ?sandwich::vcovHC – Cluster-robust: "CR", "CR0", "CR1", "CR1p", "CR1S", "CR2", "CR3". See ?clubSandwich::vcovCR – Bootstrap: "BS", "xy", "residual", "wild", "mammen", "fractional", "jackknife", "norm", "webb". See ?sandwich::vcovBS – Other sandwich package functions: "HAC", "PC", "CL", "OPG", "PL". – Kenward-Roger approximation: "kenward-roger". See ?pbkrtest::vcovAdj. – Finite Population Correction: "fpc" applies the finite population correction. Requires the population_size to be specified in vcov_args. For mixed models, FPC is based on *Lai et al. 2018*. When vcov = "fpc", at least one of population_size (size of the finite population, must be larger than the number of observations in the model) or cluster_size (the finite size of cluster groups in the population, must be larger than the number of groups of the random effects) in the vcov_args argument. You can additionally apply the Kenward-Roger approximation with the kr argument, e.g. vcov_args = list(cluster_size = 15, kr = TRUE). Exceptions are following models: • Model of class glmgee, which have pre-defined options for the variance-covariance matrix calculation. These are "robust", "df-adjusted", "model", "bias-corrected", and "jackknife". See ?glmtoolbox::vcov.glmgee for details. • Model of class glmmTMB currently only support the "HC0" option. • Models of class fixest use the vcov() method of the **fixest** package, so vcov accepts the types listed in ?fixest::vcov.fixest. Of the heteroskedasticity-consistent types, "HC0" to "HC3" are supported. "HC0" uses vcov = "hetero" without the small-sample adjustment (ssc = fixest::ssc(K.adj = FALSE)).

vcov_args — List of arguments to be passed to the function identified by the vcov argument. This function is typically supplied by the **sandwich** or **clubSandwich** packages. Please refer to their documentation (e.g., ?sandwich::vcovHAC) to see the list of available arguments. If no estimation type (argument type) is given, the default type for "HC" equals the default from the **sandwich** package; for type "CR", the default is set to "CR3". For vcov = "fpc", vcov_args must specify either population_size or cluster_size, depending on the model.

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 also refers to the *count* or *mean* component - names may differ, depending on the modeling package. See section *Model components* for details. For models of class glmmTMB, the component argument can also be "full", to return the full variance-covariance matrix (including random effects, called theta).

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

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 and MixMod.

Value

The variance-covariance matrix, as matrix-object.

Model components

Possible values for the component argument depend on the model class. Following are valid options:

- "all": returns all model components, applies to all models, but will only have an effect for models with more than just the conditional model component.
- "conditional": only returns the conditional component, i.e. "fixed effects" terms from the model. Will only have an effect for models with more than just the conditional model component.
- "smooth_terms": returns smooth terms, only applies to GAMs (or similar models that may contain smooth terms).
- "zero_inflated" (or "zi"): returns the zero-inflation component.
- "dispersion": returns the dispersion model component. This is common for models with zero-inflation or that can model the dispersion parameter.
- "instruments": for instrumental-variable or some fixed effects regression, returns the instruments.
- "nonlinear": for non-linear models (like models of class nlmerMod), returns the nonlinear parameters. Not available for functions that return variables, like find_predictors().

- "correlation": for models with correlation-component, like gls, the variables used to describe the correlation structure are returned. The grouping factor (like Subject in ~ age | Subject) is only returned for effects = "all".
- "location": returns location parameters such as conditional, zero_inflated, smooth_terms, or instruments (everything that are fixed or random effects - depending on the effects argument - but no auxiliary parameters).
- "distributional" (or "auxiliary"): components like sigma, dispersion, beta or precision (and other auxiliary parameters) are returned.

Special models

Some model classes also allow rather uncommon options. These are:

- **mhurdle**: "infrequent_purchase", "ip", and "auxiliary"
- **BGGM**: "correlation" and "intercept"
- **BFBayesFactor**, **glmx**: "extra"
- **averaging**:"conditional" and "full"
- **mjoint**: "survival"
- **mfx**: "precision", "marginal"
- **betareg**, **DirichletRegModel**: "precision"
- **mvord**: "thresholds" and "correlation"
- **clm2**: "scale"
- **selection**: "selection", "outcome", and "auxiliary"
- **lcmm**: "membership", "longitudinal", "beta", "splines", and "linear"

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. It can be any pre-defined or arbitrary distributional parameter, like mu, ndt, kappa, etc.

Note

get_varcov() tries to return the nearest positive definite matrix in case of negative eigenvalues of the variance-covariance matrix. This ensures that it is still possible, for instance, to calculate standard errors of model parameters. A message is shown when the matrix is negative definite and a corrected matrix is returned.

References

Lai, M. H. C., Kwok, O.-m., Hsiao, Y.-Y., & Cao, Q. (2018). Finite population correction for two-level hierarchical linear models. Psychological Methods, 23(1), 94–112. doi:10.1037/met0000137

Examples

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

# vcov of zero-inflation component from hurdle-model
```

```
data("bioChemists", package = "pscl")
mod <- hurdle(art ~ phd + fem | ment, data = bioChemists, dist = "negbin")
get_varcov(mod, component = "zero_inflated")

# robust vcov of, count component from hurdle-model
data("bioChemists", package = "pscl")
mod <- hurdle(art ~ phd + fem | ment, data = bioChemists, dist = "negbin")
get_varcov(
  mod,
  component = "conditional",
  vcov = "BS",
  vcov_args = list(R = 50)
)
```

`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

```
get_variance(x, ...)

## S3 method for class 'merMod'
get_variance(
  x,
  component = "all",
  tolerance = 1e-08,
  null_model = NULL,
  approximation = "lognormal",
  verbose = TRUE,
  ...
)

## S3 method for class 'glmmTMB'
get_variance(
  x,
  component = "all",
  model_component = NULL,
  tolerance = 1e-08,
  null_model = NULL,
  approximation = "lognormal",
  verbose = TRUE,
```

```
  ...
)

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

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

get_variance_random(x, verbose = TRUE, tolerance = 1e-08, ...)

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

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

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

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

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

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

Arguments

x	A mixed effects model.
...	Currently not used.
component	Character value, indicating the variance component that should be returned. By default, all variance components are returned. Valid options are "all", "fixed", "random", "residual", "distribution", "dispersion", "intercept", "slope", "rho01", and "rho00", which are equivalent to calling the dedicated functions like get_variance_residual() etc. The distribution-specific ("distribution") and residual ("residual") variance are the most computational intensive components, and hence may take a few seconds to calculate.
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().
null_model	Optional, a null-model to be used for the calculation of random effect variances. If NULL, the null-model is computed internally.
approximation	Character string, indicating the approximation method for the distribution-specific (observation level, or residual) variance. Only applies to non-Gaussian models. Can be "lognormal" (default), "delta" or "trigamma". For binomial models, the default is the *theoretical* distribution specific variance, however, it can also be "observation_level". See *Nakagawa et al. 2017*, in particular supplement 2, for details.
verbose	Toggle off warnings.
model_component	For models that can have a zero-inflation component, specify for which component variances should be returned. If NULL or "full" (the default), both

the conditional and the zero-inflation component are taken into account. If "conditional", only the conditional component is considered.

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).

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-specific/observation level variance)
- var.distribution, distribution-specific (or observation level) variance
- var.dispersion, variance due to additive dispersion
- var.intercept, the random-intercept-variance, or between-subject-variance (τ_{00})
- var.slope, the random-slope-variance (τ_{11})
- cor.slope_intercept, the random-slope-intercept-correlation (ρ_{01})
- cor.slopes, the correlation between random slopes (ρ_{00})

Fixed effects variance

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

Random effects variance

The random effect variance, σ^2_i, represents the *mean* random effect variance of the model. Since this variance reflects 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 (observation level) variance

The distribution-specific variance, σ^2_d, is the conditional variance of the response given the predictors , Var[y|x], which depends on the model family.

- **Gaussian:** For Gaussian models, it is σ^2 (i.e. sigma(model)^2).
- **Bernoulli:** For models with binary outcome, it is $\pi^2/3$ for logit-link, 1 for probit-link, and $\pi^2/6$ for cloglog-links.
- **Binomial:** For other binomial models, the distribution-specific variance for Bernoulli models is used, divided by a weighting factor based on the number of trials and successes.
- **Gamma:** Models from Gamma-families use μ^2 (as obtained from family$variance()).

- For all other models, the distribution-specific variance is by default based on lognormal approximation, $log(1 + var(x)/\mu^2)$ (see *Nakagawa et al. 2017*). Other approximation methods can be specified with the `approximation` argument.
- **Zero-inflation models:** 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, σ_e^2, 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, σ_ϵ^2, is simply $\sigma_d^2 + \sigma_e^2$. It is also called *within-subject variance*.

Random intercept variance

The random intercept variance, or *between-subject* variance (τ_{00}), is obtained from `VarCorr()`. It indicates how much groups or subjects differ from each other, while the residual variance σ_ϵ^2 indicates the *within-subject variance*.

Random slope variance

The random slope variance (τ_{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 (ρ_{01}) is obtained from `VarCorr()`. This measure is only available for mixed models with random intercepts and slopes.

Supported models and model families

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 not fully implemented or tested, and therefore may not work for all models of the aforementioned classes.

The results are validated against the solutions provided by *Nakagawa et al. (2017)*, in particular examples shown in the Supplement 2 of the paper. Other model families are validated against results from the **MuMIn** package. This means that the returned variance components should be accurate and reliable for following mixed models or model families:

- Bernoulli (logistic) regression
- Binomial regression (with other than binary outcomes)
- Poisson and Quasi-Poisson regression
- Negative binomial regression (including nbinom1, nbinom2 and nbinom12 families)
- Gaussian regression (linear models)

- Gamma regression
- Tweedie regression
- Beta regression
- Ordered beta regression

Following model families are not yet validated, but should work:

- Zero-inflated and hurdle models
- Beta-binomial regression
- Compound Poisson regression
- Generalized Poisson regression
- Log-normal regression
- Skew-normal regression

Extracting variance components for models with zero-inflation part is not straightforward, because it is not definitely clear how the distribution-specific variance should be calculated. Therefore, it is recommended to carefully inspect the results, and probably validate against other models, e.g. Bayesian models (although results may be only roughly comparable).

Log-normal regressions (e.g. `lognormal()` family in **glmmTMB** or `gaussian("log")`) often have a very low fixed effects variance (if they were calculated as suggested by *Nakagawa et al. 2017*). This results in very low ICC or r-squared values, which may not be meaningful (see `performance::icc()` or `performance::r2_nakagawa()`).

References

- Johnson, P. C. D. (2014). Extension of Nakagawa & Schielzeth's R2 GLMM to random slopes models. Methods in Ecology and Evolution, 5(9), 944–946. doi:10.1111/2041210X.12225
- Nakagawa, S., Johnson, P. C. D., & Schielzeth, H. (2017). The coefficient of determination R2 and intra-class correlation coefficient from generalized linear mixed-effects models revisited and expanded. Journal of The Royal Society Interface, 14(134), 20170213. doi:10.1098/rsif.2017.0213
- Zuur, A. F., Savel'ev, A. A., & Ieno, E. N. (2012). Zero inflated models and generalized linear mixed models with R. Newburgh, United Kingdom: Highland Statistics.

Examples

```
library(lme4)
data(sleepstudy)
m <- lmer(Reaction ~ Days + (1 + Days | Subject), data = sleepstudy)

get_variance(m)
get_variance_fixed(m)
get_variance_residual(m)
```

`get_weights` *Get the values from model weights*

Description

Returns weighting variable of a model.

Usage

```
get_weights(x, ...)

## Default S3 method:
get_weights(x, remove_na = FALSE, null_as_ones = FALSE, ...)
```

Arguments

`x`	A fitted model.
`...`	Used for objects from package **survey**, to pass the `source` argument to `get_data()`. See related documentation of that argument for further details.
`remove_na`	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. 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)

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

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

has_intercept *Checks if model has an intercept*

Description

Checks if model has an intercept.

Usage

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

Arguments

x	A model object.
verbose	Toggle warnings.
...	Currently not used.

Value

TRUE if x has an intercept, FALSE otherwise.

Examples

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

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


model <- lmer(Reaction ~ 0 + Days + (Days | Subject), data = sleepstudy)
has_intercept(model)

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

insight-options *Global options from the insight package*

Description

Global options from the insight package

Global options to set defaults for function arguments

- `options(easystats_display_format = <value>)` will set the default format for the `display()` methods. Can be one of `"markdown"`, `"html"`, or `"tt"`. See `display()` for details.
- `options(easystats_table_width = <value>)` sets the default width for tables printed to the console. Tables exceeding this width are wrapped into multiple parts to ensure clean formatting and avoid excessively long lines.
- `options(easystats_ci_separator = <value>)` defines the separator string used between the lower and upper CI limits. Defaults to `", "`, resulting in an output like `[0.3, 0.8]`.
- `options(easystats_ci_brackets = <value>)` determines whether brackets or parentheses are used to enclose formatted CIs. Can be `FALSE` to omit them, `TRUE` to include them (defaults to `[` and `]` for text output), or a character vector of length 2 to define custom opening and closing symbols (e.g., `c("(", ")")`).
- `options(insight_use_symbols = <value>)` accepts `TRUE` or `FALSE`. If `TRUE`, statistical symbols (e.g., eta-squared, omega) are rendered using their corresponding Unicode characters.
- `options(easystats_errors = <value>)` accepts `TRUE` or `FALSE`. If `TRUE`, functions that typically suppress errors (via `tryCatch()`) will instead halt execution and throw an error when an issue occurs.

---

is_bayesian_model *Checks if a model is a Bayesian model*

Description

Small helper that checks if a model is a Bayesian model.

Usage

```
is_bayesian_model(x, exclude = NULL)
```

Arguments

x	A model object.
exclude	Optional character vector, indicating classes that should not be included in the check. E.g., `exclude = "stanreg"` would return `FALSE` for models from package **rstanarm**.

Value

A logical, `TRUE` if `x` is a Bayesian model.

Examples

```
library(rstanarm)
model <- stan_glm(Sepal.Width ~ Species * Petal.Length, data = iris)
is_bayesian_model(model)
```

is_converged *Convergence test for mixed effects, Stan and Cox models*

Description

is_converged() provides an alternative convergence test for merMod-objects. For models fitted with Stan (stanfit, brmsfit, stanreg and CmdStanMCMC), it checks the diagnostics of the sampler. For coxph models, it recomputes the checks of the *survival* package.

Usage

```
is_converged(x, tolerance = 0.001, ...)

## S3 method for class 'merMod'
is_converged(x, tolerance = 0.001, verbose = TRUE, ...)

## S3 method for class 'stanfit'
is_converged(x, tolerance = 0.001, verbose = TRUE, ...)

## S3 method for class 'coxph'
is_converged(x, tolerance = 0.001, verbose = TRUE, ...)
```

Arguments

x	A model object from class merMod, glmmTMB, glm, lavaan, _glm, stanfit, brmsfit, stanreg, CmdStanMCMC or coxph.
tolerance	Indicates up to which value the convergence result is accepted. The smaller tolerance is, the stricter the test will be. Not used for Stan and coxph models.
...	Currently not used.
verbose	Toggle messages and warnings.

Value

TRUE if convergence is fine and FALSE if convergence is suspicious or cannot be assessed. For merMod models, the convergence value is returned as attribute gradient. If the model is singular, convergence is determined by the optimizer's convergence code. For non-singular models where derivatives are unavailable, FALSE is returned and a message is printed to indicate that convergence cannot be assessed through the usual gradient-based checks.

For Stan models, the attribute diagnostics is a data frame with the value, the threshold and the result of each check. For Stan models whose convergence cannot be assessed, FALSE is returned without this attribute, and a message gives the reason: models without MCMC draws from the NUTS sampler (for example, models fitted with variational inference or optimization), models without draws after warmup, and models fitted with brms::brm_multiple(), whose chains come from different data sets (such as imputed ones).

For coxph models, the attribute diagnostics is a data frame with the result of each check. If convergence cannot be assessed, FALSE is returned without this attribute, and, if verbose = TRUE, a message gives the reason.

Stan models

For models fitted with Stan, `is_converged()` returns `FALSE` if at least one of the checks below fails. The checks and thresholds are those of the warnings that *rstan* gives after sampling. For `stanfit`, `brmsfit` and `stanreg` models, the values are computed with functions from *rstan*:

- Divergent transitions after warmup (`rstan::get_num_divergent()`): the check fails if there is at least one.
- Transitions after warmup that reach the maximum treedepth stored in the model (`rstan::get_sampler_params()`): the check fails if there is at least one. The maximum is read from the `control` settings. Models from `rstan::read_stan_csv()` store it outside `control`, and `is_converged()` reads it from there. For these models, `rstan::get_num_max_treedepth()` counts against the default maximum of 10. If the model stores no maximum, 10 is used.
- E-BFMI (`rstan::get_bfmi()`): the check fails if at least one chain has a value below 0.2. This is the E-BFMI of `rstan::check_hmc_diagnostics()`, which can differ from the warning that *rstan* prints after sampling.
- R-hat (`rstan::Rhat()`): the check fails if the largest value over all parameters is above 1.05.
- Bulk and tail effective sample size (`rstan::ess_bulk()` and `rstan::ess_tail()`): each check fails if the smallest value over all parameters is below 100 times the number of chains with draws after warmup.

For `CmdStanMCMC` models from *cmdstanr*, the same checks and thresholds are used. Divergent transitions, transitions at the maximum treedepth and E-BFMI come from the `$diagnostic_summary()` method of the model, and R-hat and effective sample size from its `$summary()` method. The E-BFMI warning of *cmdstanr* uses a threshold of 0.3, not 0.2.

Missing values (for example, R-hat of a constant parameter) are ignored. Stan also prints messages about rejected proposals ("exception thrown") during sampling. These messages are not checked, because the model object does not store them.

Convergence and log-likelihood

Convergence problems typically arise when the model hasn't converged to a solution where the log-likelihood has a true maximum. This may result in unreliable and overly complex (or non-estimable) estimates and standard errors.

Inspect model convergence

lme4 performs a convergence-check (see `?lme4::convergence`), however, as discussed here and suggested by one of the lme4-authors in this comment, this check can be too strict. `is_converged()` (and its wrapper function, `performance::check_convergence()`) thus provides an alternative convergence test for `merMod`-objects.

Resolving convergence issues

Convergence issues are not easy to diagnose. The help page on `?lme4::convergence` provides most of the current advice about how to resolve convergence issues. In general, convergence issues may be addressed by one or more of the following strategies: 1. Rescale continuous predictors; 2. try a different optimizer; 3. increase the number of iterations; or, if everything else fails, 4. simplify the model. Another clue might be large parameter values, e.g. estimates (on the scale of the

linear predictor) larger than 10 in (non-identity link) generalized linear model *might* indicate complete separation, which can be addressed by regularization, e.g. penalized regression or Bayesian regression with appropriate priors on the fixed effects.

Cox proportional hazards models

survival warns about convergence problems when a `coxph` model is fitted, but does not store the warnings in the model object. For `coxph` models, `is_converged()` therefore computes the two checks of *survival* again, with the `iter.max`, `eps` and `toler.inf` values of the model call:

- Iterations: the check fails if the model did not converge within `iter.max` iterations ("Ran out of iterations and did not converge").
- Infinite coefficient: the check fails for a coefficient if the log-likelihood converged before the coefficient did ("Loglik converged before variable ...; coefficient may be infinite", or "beta may be infinite" for counting-process data). This happens, for example, if a factor level has no events. As in *survival*, this check runs only if the first check passed.

`is_converged()` returns `FALSE` if a check fails. The attribute `diagnostics` is a data frame with the value, the threshold and the result of each check, with one row for each coefficient for the second check. The `tolerance` argument is not used for `coxph` models.

Convergence cannot be assessed, and `FALSE` is returned, for penalized models (with `frailty()`, `ridge()` or `pspline()` terms), for models with `ties = "exact"`, for models with `tt()` terms, for models with `iter.max` of 1 or less, for right-censored and multi-state models fitted with `y = FALSE`, for models without events, for model objects without a call, and if the control arguments of the model call or the score residuals cannot be computed. Convergence also cannot be assessed if the model call does not write the formula as a `~` expression, for example `coxph(f, data = d, iter.max = n)`, and a control argument refers to a variable. The control arguments are evaluated in the environment of the formula, which can differ from the environment in which the model was fitted, for example inside a function. This also applies to models fitted in top-level code, where the two environments are usually the same. Single-state counting-process models fitted with `y = FALSE` are assessed, because their checks use only the stored score vector and convergence flag. A model without events and without predictors returns `TRUE`, as other null models.

Models from `survival::clogit()` are assessed as other `coxph` models. The default method of `clogit()` is `"exact"`, so convergence can only be assessed for models fitted with `method = "efron"` or `method = "breslow"` (or `"approximate"`). Objects of other classes that inherit from `coxph`, for example from `survey::svycoxph()`, are not supported: `NULL` is returned with a message (no message if `verbose = FALSE`).

For models with right-censored data, the score residuals are computed from the data of the model call, unless the model was fitted with `model = TRUE`, or with `x = TRUE` for single-state models. If these data were removed after the model was fitted, convergence cannot be assessed. If the predictor data were changed, so that the linear predictor computed from them differs from the one of the model, convergence cannot be assessed either. For single-state models with a `strata()` term, the log-likelihood and the martingale residuals at the coefficients of the model are also computed again from these data and the stored response and weights. If they differ from those of the model, for example because observations were moved to other strata, or if they cannot be computed, convergence cannot be assessed. Strata that are relabeled without a change of grouping are not detected, but they leave the result the same. For multi-state models, the linear predictor is compared within each transition. A change that adds the same constant to all values of a predictor is not detected,

but it leaves the score residuals the same. The check is not done for multi-state models in which transitions share a baseline hazard, or that were fitted with `x = TRUE`. Other changes that stay undetected can give a wrong result: a change of several predictors that leaves the linear predictor the same, changes to a `strata()` or `istate` variable of a multi-state model, and changes to the data of models without the check. In these cases, refit the model, or fit it with `model = TRUE`, which avoids them.

Convergence versus Singularity

Note the different meaning between singularity and convergence: singularity indicates an issue with the "true" best estimate, i.e. whether the maximum likelihood estimation for the variance-covariance matrix of the random effects is positive definite or only semi-definite. Convergence is a question of whether we can assume that the numerical optimization has worked correctly or not. A convergence failure means the optimizer (the algorithm) could not find a stable solution (*Bates et. al 2015*).

For singular models (see `?lme4::isSingular`), convergence is determined based on the optimizer's convergence code. If the optimizer reports successful convergence (convergence code 0) for a singular model, `is_converged()` returns `TRUE`. For non-singular models, in cases where the gradient and Hessian are not available, `is_converged()` returns `FALSE` and prints a message to indicate that convergence cannot be assessed through the usual gradient-based checks. Note that `performance::check_convergence()` is a wrapper around `insight::is_converged()`.

References

Bates, D., Mächler, M., Bolker, B., and Walker, S. (2015). Fitting Linear Mixed-Effects Models Using lme4. Journal of Statistical Software, 67(1), 1-48. doi:10.18637/jss.v067.i01

Examples

```
library(lme4)
data(cbpp)
set.seed(1)
cbpp$x <- rnorm(nrow(cbpp))
cbpp$x2 <- runif(nrow(cbpp))

model <- glmer(
  cbind(incidence, size - incidence) ~ period + x + x2 + (1 + x | herd),
  data = cbpp,
  family = binomial()
)

is_converged(model)



library(glmmTMB)
model <- glmmTMB(
  Sepal.Length ~ poly(Petal.Width, 4) * poly(Petal.Length, 4) +
    (1 + poly(Petal.Width, 4) | Species),
  data = iris
)
```

```
is_converged(model)
```

```
# a model fitted with brms
model <- download_model("brms_1")
result <- is_converged(model)
result
attributes(result)$diagnostics
```

`is_empty_object` *Check if object is empty*

Description

Check if object is empty

Usage

```
is_empty_object(x)
```

Arguments

`x`	A list, a vector, or a dataframe.

Value

A logical indicating whether the entered object is empty.

Examples

```
is_empty_object(c(1, 2, 3, NA))
is_empty_object(list(NULL, c(NA, NA)))
is_empty_object(list(NULL, NA))
```

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

```
is_gam_model(x)
```

Arguments

x	A model object.

Value

A logical, TRUE if x is a generalized additive model *and* has smooth-terms

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

```
data(iris)
model1 <- lm(Petal.Length ~ Petal.Width + Sepal.Length, data = iris)
model2 <- mgcv::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.

Examples

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

data(sleepstudy, package = "lme4")
model <- lme4::lmer(Reaction ~ Days + (1 | Subject), data = sleepstudy)
is_mixed_model(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)
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 a regression model object is supported by the 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)

# to see all supported models
supported_models()
```

`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)
```

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

```
library(rstanarm)
data("pbcLong")
model <- suppressWarnings(stan_mvmer(
  formula = list(
    logBili ~ year + (1 | id),
    albumin ~ sex + year + (year | id)
  ),
  data = pbcLong,
  chains = 1, cores = 1, seed = 12345, iter = 1000,
  show_messages = FALSE, refresh = 0
))

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

`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.

Details

The term "nested" here means that all the fixed predictors of a model are contained within the fixed predictors of a larger model (sometimes referred to as the encompassing model). Currently, `is_nested_models()` ignores random effects parameters.

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)

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

model <- lme4::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 'betamfx'
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)(0.3)
# same as
log(0.3)
```

---

link_inverse *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)(0.3)
# same as
exp(0.3)
```

---

model_info *Access information from model objects*

Description

Retrieve information from model objects.

Usage

```
model_info(x, ...)

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

## S3 method for class 'brmsfit'
model_info(x, response = NULL, ...)
```

Arguments

x	A fitted model.
...	Currently not used.
verbose	Toggle off warnings.
response	If x is a multivariate response model, model_info() returns a list of information for each response variable. Set response to the number of a specific response variable, or provide the name of the response variable in response, to return the information for only one response.

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.

Common families and distributions:

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

- is_poisson: family is poisson
- is_probit: model has probit link
- is_tweedie: family is tweedie

Special model types:

- is_anova: model is an Anova object
- is_bayesian: model is a Bayesian model
- is_dispersion: model has dispersion component (not only dispersion *parameter*)
- is_gam: model is a generalized additive model
- is_meta: model is a meta-analysis object
- is_mixed: model is a mixed effects model (with random effects)
- is_mixture: model is a finite mixture model (currently only recognized for package *brms*).
- is_multivariate: model is a multivariate response model (currently only works for *brmsfit* and *vglm/vgam* objects)
- is_hurdle: model has zero-inflation component and is a hurdle-model (truncated family distribution)
- is_rtchoice: model is a *brms* decision-making (sequential sampling) model, which models outcomes that consists of two components (reaction times and choice). This currently covers the ddm(), lba(), lnr() and rdm() custom families from package *cogmod*.
- is_survival: model is a survival model
- is_trial: model response contains additional information about the trials
- is_truncated: model is a truncated model (has a truncated response)
- is_wiener: model is a *brms* decision-making (sequential sampling) model with Wiener process (also called drift diffusion model)
- is_zero_inflated: model has zero-inflation component

Hypotheses tests:

- 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_correlation: model is an an object of class htest, returned by cor.test()
- is_ftest: model is an an object of class htest, and test-statistic is an F-statistic.
- 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_ranktest: model is an an object of class htest, returned by cor.test() (if Spearman's rank correlation), wilcox.text() or kruskal.test().
- is_ttest: model is an an object of class htest, returned by t.test()
- is_variancetest: model is an an object of class htest, returned by bartlett.test(), shapiro.test() or car::leveneTest().

- 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()).

Other model information:

- link_function: the link-function
- family: name of the distributional family of the model. For some exceptions (like some htest objects), can also be the name of the test.
- n_obs: number of observations
- n_grouplevels: for mixed models, returns names and numbers of random effect groups

Value

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

Examples

```
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 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)

# logistic regression
model_info(m)

# t-test
m <- t.test(1:10, y = c(7:20))
model_info(m)
```

---

model_name *Name the model*

Description

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

Usage

```
model_name(x, ...)

## Default S3 method:
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).

Examples

```
m <- lm(Sepal.Length ~ Petal.Width, data = iris)
model_name(m)
model_name(m, include_formula = TRUE)
model_name(m, include_call = TRUE)

model_name(lme4::lmer(Sepal.Length ~ Sepal.Width + (1 | Species), data = iris))
```

---

n_grouplevels *Count number of random effect levels in a mixed model*

Description

Returns the number of group levels of random effects from mixed models.

Usage

```
n_grouplevels(x, ...)
```

Arguments

x	A mixed model.
...	Additional arguments that can be passed to the function. Currently, you can use data to provide the model data, if available, to avoid retrieving model data multiple times.

Value

The number of group levels in the model.

Examples

```
data(sleepstudy, package = "lme4")
set.seed(12345)
sleepstudy$grp <- sample(1:5, size = 180, replace = TRUE)
sleepstudy$subgrp <- NA
for (i in 1:5) {
  filter_group <- sleepstudy$grp == i
  sleepstudy$subgrp[filter_group] <-
    sample(1:30, size = sum(filter_group), replace = TRUE)
}
model <- lme4::lmer(
  Reaction ~ Days + (1 | grp / subgrp) + (1 | Subject),
  data = sleepstudy
)
n_grouplevels(model)
```

---

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

```
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'). For *brms* models with a `trials()` term in the response (e.g., `y | trials(size) ~ x`), the values of `trials()` are summed.
`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

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


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 = "fixed", remove_nonestimable = FALSE, ...)

## S3 method for class 'glmmTMB'
```

```
n_parameters(
  x,
  effects = "fixed",
  component = "all",
  remove_nonestimable = FALSE,
  ...
)
```

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 variables for fixed effects ("fixed"), random effects ("random") or both ("all") be returned? Only applies to mixed models. May be abbreviated. For find_predictors() and find_variables(), it also applies to the correlation part of models from *nlme* (like gls).
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**). See details in section *Model Components* .May be abbreviated. Note that the *conditional* component also refers to the *count* or *mean* component - names may differ, depending on the modeling package. There are three convenient shortcuts (not applicable to *all* model classes): • 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

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)
```

`null_model` *Compute intercept-only model for regression models*

Description

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

Usage

```
null_model(model, ...)

## Default S3 method:
null_model(model, verbose = TRUE, ...)
```

Arguments

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

Value

The null-model of `x`

Examples

```
data(sleepstudy)
m <- lmer(Reaction ~ Days + (1 + Days | Subject), data = sleepstudy)
summary(m)
summary(null_model(m))
```

object_has_names *Check names and rownames*

Description

`object_has_names()` checks if specified names are present in the given object. `object_has_rownames()` checks if rownames are present in a dataframe.

Usage

```
object_has_names(x, names)

object_has_rownames(x)
```

Arguments

x	A named object (an atomic vector, a list, a dataframe, etc.).
names	A single character or a vector of characters.

Value

A logical or a vector of logicals.

Examples

```
# check if specified names are present in the given object
object_has_names(mtcars, "am")
object_has_names(anscombe, c("x1", "z1", "y1"))
object_has_names(list("x" = 1, "y" = 2), c("x", "a"))

# check if a dataframe has rownames
object_has_rownames(mtcars)
```

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 "white", "black", "red", "yellow", "green", "blue", "violet", "cyan" or "grey". Bright variants of colors are available by adding the prefix "b" (or "br_" or "bright_"), e.g. "bred" (or "br_red" resp. "bright_red"). Background colors can be set by adding the prefix "bg_" (e.g. "bg_red"). Formatting is also possible with "bold" or "italic". Note that "bright_black" is equivalent to "grey", and "bg_grey" has no effect (it is equivalent to the IDE's default background).

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")
```

---

print_parameters *Prepare summary statistics of model parameters for printing*

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

```
print_parameters(
  x,
  ...,
  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, ...).
by	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 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 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

```
library(bayestestR)
model <- download_model("brms_zi_2")
if (!is.null(model)) {
  x <- hdi(model, effects = "all", component = "all")

  # hdi() returns a data frame; here we use only the
  # information on parameter names and HDI values
  tmp <- as.data.frame(x)[, 1:4]
  tmp

  # Based on the "by" argument, we get a list of data frames that
  # is split into several parts that reflect the model components.
  print_parameters(model, tmp)

  # This is the standard print()-method for "bayestestR::hdi"-objects.
  # For printing methods, it is easy to print complex summary statistics
  # in a clean way to the console by splitting the information into
  # different model components.
  x
}
```

`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 = "easystats", ...)
```

Arguments

`data`	A data frame. In particular, objects from *easystats* package functions like `parameters::model_paramete` 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

```
# 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

```
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_paramete` 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

```
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)
```

---

trim_ws *Small helper functions*

Description

Collection of small helper functions. trim_ws() is an efficient function to trim leading and trailing whitespaces from character vectors or strings. n_unique() returns the number of unique values in a vector. has_single_value() is equivalent to n_unique() == 1 but is faster (note the different default for the remove_na argument). safe_deparse() is comparable to deparse1(), i.e. it can safely deparse very long expressions into a single string. safe_deparse_symbol() only deparses a substituted expressions when possible, which can be much faster than deparse(substitute()) for those cases where substitute() returns no valid object name.

Usage

```
trim_ws(x, ...)

## S3 method for class 'data.frame'
trim_ws(x, character_only = TRUE, ...)

n_unique(x, ...)

## Default S3 method:
n_unique(x, remove_na = TRUE, ...)

safe_deparse(x, ...)

safe_deparse_symbol(x)

has_single_value(x, remove_na = FALSE, ...)
```

Arguments

x	A (character) vector, or for some functions may also be a data frame.
...	Currently not used.
character_only	Logical, if TRUE and x is a data frame or list, only processes character vectors.
remove_na	Logical, if missing values should be removed from the input.

Value

- n_unique(): For a vector, n_unique always returns an integer value, even if the input is NULL (the return value will be 0 then). For data frames or lists, n_unique() returns a named numeric vector, with the number of unique values for each element.
- has_single_value(): TRUE if x has only one unique value, FALSE otherwise.
- trim_ws(): A character vector, where trailing and leading white spaces are removed.
- safe_deparse(): A character string of the unevaluated expression or symbol.
- safe_deparse_symbol(): A character string of the unevaluated expression or symbol, if x was a symbol. If x is no symbol (i.e. if is.name(x) would return FALSE), NULL is returned.

Examples

```
trim_ws("  no space!  ")
n_unique(iris$Species)
has_single_value(c(1, 1, 2))

# safe_deparse_symbol() compared to deparse(substitute())
safe_deparse_symbol(as.name("test"))
deparse(substitute(as.name("test")))
```

validate_argument *Validate arguments against a given set of options*

Description

This is a replacement for `match.arg()`, however, the error string should be more informative for users. The name of the affected argument is shown, and possible typos as well as remaining valid options. Note that the argument `several.ok` is always `FALSE` in `validate_argument()`, i.e. this function - unlike `match.arg()` - does *not* allow evaluating several valid options at once.

Usage

```
validate_argument(argument, options)
```

Arguments

`argument`	The bare name of the argument to be validated.
`options`	Valid options, usually a character vector.

Value

`argument` if it is a valid option, else an error is thrown.

Examples

```
foo <- function(test = "small") {
  validate_argument(test, c("small", "medium", "large"))
}
foo("small")
# errors:
# foo("masll")
```

vcovFPC *Obtain finite-population-adjusted variance-covariance matrix*

Description

This function returns the variance-covariance matrix as returned by `vcov()`, but with finite population correction (FPC) applied.

Usage

```
vcovFPC(model, ...)

## S3 method for class 'merMod'
vcovFPC(model, population_size = NULL, cluster_size = NULL, kr = FALSE, ...)
```

Arguments

model	A model inheriting from lm, glm, merMod or glmmTMB (2-level only).
...	Not used.
population_size	The finite population size (for mixed models: for level-1).
cluster_size	The finite population size for level-2 (cluster groups).
kr	Logical, if TRUE, also applies Kenward-Roger adjustment to the returned variance-covariance matrix.

Details

The FPC is defined as:

$$FPC = \frac{N - n}{N - 1}$$

FPC for multilevel models is based on the method described by Lai et al. (2018).

Value

The variance-covariance matrix of the fixed effect estimates, as returned by vcov(), but with FPC applied.

References

Lai, M. H., Kwok, O. M., Hsiao, Y. Y., & Cao, Q. (2018). Finite population correction for two-level hierarchical linear models. *Psychological methods, 23*(1), 94.

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