Package 'insight'

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Type Package

Title Easy Access to Model Information for Various Model Objects

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 (>= 3.5)

Imports methods, stats, utils

Suggests AER, afex, aod, BayesFactor, bayestestR, betareg, BGGM, biglm, blavaan, blme, bbmle, brms, censReg, cgam, coxme, cplm, crch, effectsize, emmeans, estimatr, feisr, fixest, gam, gamm4, gamlss, gbm, gee, geepack, GLMMadaptive, glmmTMB, gmnl, httr, ivreg, JM, lavaan, lfe, logistf, MASS, Matrix, MCMCglmm, mice, mlogit, multgee, lme4, mgcv, nnet, nlme, ordinal, parameters, plm, pscl, quantreg, rms, robustbase, robustlmm, rstanarm, rstudioapi, speedglm, splines, statmod, survey, survival, tripack, truncreg, testthat, VGAM, knitr, rmarkdown, spelling

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R topics documented:

`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

```
library(lme4)
data(mtcars)
data(sleepstudy)

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

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

---

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()"
library(lme4)
m <- glmer(
  cbind(incidence, size - incidence) ~ period + (1 | herd),
  data = cbpp,
  family = binomial
)

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

---

clean_parameters *Get clean names of model parameters*

Description

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

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

Usage

```
clean_parameters(x, ...)
```

Arguments

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

Details

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

Value

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

Examples

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

## End(Not run)
```

---

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

The .

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)
```

`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")`. See the documentation for the specific objects' classes.

Usage

```
display(object, ...)

print_md(x, ...)
```

Arguments

`object, x`	A data frame.
`...`	Arguments passed to other methods.

Value

A data frame.

`download_model` *Download circus models*

Description

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

Usage

```
download_model(name, url = NULL)
```

Arguments

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

Details

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

Value

A model from the *circus*-repository.

References

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

---

export_table *Data frame and Tables Pretty Formatting*

Description

Data frame and Tables Pretty Formatting

Usage

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

format_table(
  x,
  sep = " | ",
```

```
  header = "-",
  digits = 2,
  protect_integers = TRUE,
  missing = "",
  width = NULL,
  format = NULL,
  caption = NULL,
  subtitle = NULL,
  align = NULL,
  footer = NULL,
  zap_small = FALSE
)
```

Arguments

x	A data frame.
sep	Column separator.
header	Header separator. Can be NULL.
digits	Number of significant digits.
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.
format	Name of output-format, as string. If NULL (or "text"), returned output is used for basic printing. Currently, only "markdown" is supported, or NULL (the default) resp. "text" for plain text.
caption, subtitle	Table caption and subtitle, as string. If NULL, no caption or subtitle is printed.
align	Column alignment. Only applies to markdown-formatted tables. By default align = NULL, numeric columns are right-aligned, and other columns are left-aligned. May be a string to indicate alignment rules for the complete table, like "left", "right", "center" or "firstleft" (to left-align first column, center remaining); or maybe a string with abbreviated alignment characters, where the length of the string must equal the number of columns, for instance, align = "lccrl" would left-align the first column, center the second and third, right-align column four and left-align the fifth column.
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.
zap_small	Logical, if TRUE, small values are rounded after digits decimal places. If FALSE, values with more decimal places than digits are printed in scientific notation.

Value

A data frame in character format.

Note

This function is going to be renamed in a future update. Please use its alias `export_table()`.

Examples

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

---

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

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

## End(Not run)
```

---

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, ...).

Usage

```
find_formula(x, ...)
```

Arguments

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

Value

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

- `conditional`, the "fixed effects" part from the model. One exception are `DirichletRegModel` models from **DirichletReg**, which has two or three components, depending on `model`.
- `random`, the "random effects" part from the model (or the `id` for gee-models and similar)
- `zero_inflated`, the "fixed effects" part from the zero-inflation component of the model
- `zero_inflated_random`, the "random effects" part from the zero-inflation component of the model
- `dispersion`, the dispersion formula
- `instruments`, for fixed-effects regressions like `ivreg`, `felm` or `plm`, the instrumental variables
- `cluster`, for fixed-effects regressions like `felm`, the cluster specification
- `correlation`, for models with correlation-component like `gls`, the formula that describes the correlation structure

- slopes, for fixed-effects individual-slope models like feis, the formula for the slope parameters
- precision, for DirichletRegModel models from **DirichletReg**, when parametrization (i.e. model) is "alternative".

Note

For models of class lme or gls the correlation-component is only returned, when it is explicitly defined as named argument (form), e.g. corAR1(form = ~1 | Mare)

Examples

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

---

find_interactions *Find interaction terms from models*

Description

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

Usage

```
find_interactions(
  x,
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion",
    "instruments"),
  flatten = FALSE
)
```

Arguments

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

Examples

```
data(mtcars)

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

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

---

find_offset *Find possible offset terms in a model*

Description

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

Usage

```
find_offset(x)
```

Arguments

x	A fitted model.

Value

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

Examples

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

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

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

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

`find_parameters` *Find names of model parameters*

Description

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

Usage

```
find_parameters(x, ...)

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

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

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

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

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

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

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

## S3 method for class 'brmsfit'
find_parameters(
  x,
  effects = c("all", "fixed", "random"),
 component = c("all", "conditional", "zi", "zero_inflated", "dispersion", "simplex",
    "sigma", "smooth_terms"),
  flatten = FALSE,
  parameters = NULL,
  ...
)

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

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

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

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

Arguments

x	A fitted model.
...	Currently not used.
component	Should all parameters, parameters for the conditional model, the zero-inflated part of the model, the dispersion term, the instrumental variables or marginal effects be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variables (so called fixed-effects regressions), or models with marginal effects from **mfx**. May be abbreviated. Note that the *conditional* component is also called *count* or *mean* component, depending on the model.
flatten	Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.
effects	Should parameters for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
parameters	Regular expression pattern that describes the parameters that should be returned.

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. Not all model classes that support these arguments are listed here in the 'Usage' section.

Value

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

- `conditional`, the "fixed effects" part from the model
- `random`, the "random effects" part from the model
- `zero_inflated`, the "fixed effects" part from the zero-inflation component of the model
- `zero_inflated_random`, the "random effects" part from the zero-inflation component of the model
- `dispersion`, the dispersion parameters
- `simplex`, simplex parameters of monotonic effects (**brms** only)
- `smooth_terms`, the smooth parameters
- `marginal`, the marginal effects (for models from **mfx**)

Examples

```
data(mtcars)
m <- lm(mpg ~ wt + cyl + vs, data = mtcars)
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,
  effects = c("fixed", "random", "all"),
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion",
    "instruments", "correlation", "smooth_terms"),
  flatten = FALSE
)
```

Arguments

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

Value

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

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

Examples

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

---

find_random *Find names of random effects*

Description

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

Usage

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

Arguments

x	A fitted mixed model.
split_nested	Logical, if TRUE, terms from nested random effects will be returned as separated elements, not as single string with colon. See 'Examples'.
flatten	Logical, if TRUE, the values are returned as character vector, not as list. Duplicated values are removed.

Value

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

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

Examples

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

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

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

---

find_random_slopes *Find names of random slopes*

Description

Return the name of the random slopes from mixed effects models.

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

Examples

```
library(lme4)
data(sleepstudy)

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

---

find_response *Find name of the response variable*

Description

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

Usage

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

Arguments

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

Value

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

Examples

```
library(lme4)
data(cbpp)
cbpp$trials <- cbpp$size - cbpp$incidence
m <- glm(cbind(incidence, trials) ~ period, data = cbpp, family = binomial)

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

---

find_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.

Usage

```
find_terms(x, 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.

Value

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

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

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

Note

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

Examples

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

find_terms(m)
```

---

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 = c("all", "fixed", "random"),
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion",
    "instruments", "smooth_terms"),
  flatten = FALSE
)
```

Arguments

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

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

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

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

  m1 <- glmer(
    cbind(incidence, size - incidence) ~ period + (1 | herd),
    data = cbpp,
    family = binomial
  )
  find_variables(m1)

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

find_weights *Find names of model weights*

Description

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

Usage

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

Arguments

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

Value

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

Examples

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

fish *Sample data set*

Description

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

format_bf *Bayes Factor formatting*

Description

Bayes Factor formatting

Usage

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

Arguments

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

Value

A formatted string.

Examples

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

format_ci *Confidence/Credible Interval (CI) Formatting*

Description

Confidence/Credible Interval (CI) Formatting

Usage

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

Arguments

CI_low	Lower CI bound.
CI_high	Upper CI bound.
ci	CI level in percentage.
digits	Number of significant digits.
brackets	Either a logical, and if TRUE (default), values are encompassed in square brackets. If FALSE or NULL, no brackets are used. Else, a character vector of length two, indicating the opening and closing brackets.
width	Minimum width of the returned string. If not NULL and width is larger than the string's length, leading whitespaces are added to the string. If width="auto", width will be set to the length of the longest string.
width_low, width_high	Like width, but only applies to the lower or higher confidence interval value. This can be used when the values for the lower and upper CI are of very different length.
missing	Value by which NA values are replaced. By default, an empty string (i.e. "") is returned for NA.

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(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_number *Convert number to words*

Description

Convert number to words. The code has been adapted from here https://github.com/ateucher/useful_code/blob/master/R/numb

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.

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,
  name = "p",
  missing = "",
  digits = 3,
  ...
)
```

Arguments

p	value or vector of p-values.
stars	Add significance stars (e.g., p < .001***).
stars_only	Return only significance stars.
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.
digits	Number of significant digits. May also be "scientific" to return exact p-values in scientific notation, or "apa" to use an APA-style for p-values.
...	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 = "scientific")
```

format_pd *Probability of direction (pd) formatting*

Description

Probability of direction (pd) formatting

Usage

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

Arguments

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

Value

A formatted string.

Examples

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

format_rope *Percentage in ROPE formatting*

Description

Percentage in ROPE formatting

Usage

```
format_rope(rope_percentage, name = "in ROPE")
```

Arguments

rope_percentage	Value or vector of percentages in ROPE.
name	Name prefixing the text. Can be NULL.

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_value` *Numeric Values Formatting*

Description

Numeric Values Formatting

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,
  ...
)

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

Arguments

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

Value

A formatted string.

Examples

```
format_value(1.20)
format_value(1.2)
format_value(1.2012313)
format_value(c(0.0045, 234, -23))
format_value(c(0.0045, .12, .34))
format_value(c(0.0045, .12, .34), as_percent = TRUE)

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

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

format_value(iris)
```

---

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, ...)

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

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

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

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

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

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

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

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

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

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

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

## S3 method for class 'MixMod'
get_data(
  x,
```

```
  effects = c("all", "fixed", "random"),
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion"),
  ...
)

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

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

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

Arguments

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

Value

The data that was used to fit the model.

Note

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

Examples

```
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_parameters *Get model parameters*

Description

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

Usage

```
get_parameters(x, ...)

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

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

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

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

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

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

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

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

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

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

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

```
  x,
  effects = c("fixed", "random"),
  component = c("all", "conditional", "zi", "zero_inflated", "dispersion"),
  ...
)

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

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

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

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

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

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

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

## S3 method for class 'BFBayesFactor'
```

```
get_parameters(
  x,
  effects = c("all", "fixed", "random"),
  component = c("all", "extra"),
  iterations = 4000,
  progress = FALSE,
  verbose = TRUE,
  ...
)

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

## S3 method for class 'brmsfit'
get_parameters(
  x,
  effects = c("fixed", "random", "all"),
 component = c("all", "conditional", "zi", "zero_inflated", "dispersion", "simplex",
    "sigma", "smooth_terms"),
  parameters = NULL,
  summary = FALSE,
  centrality = "mean",
  ...
)

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

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

```
  centrality = "mean",
  ...
)
```

Arguments

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

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 and 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**)
- for Bayesian models, the posterior samples from the requested parameters as data frame
- for Anova (`aov()`) with error term, a list of parameters for the conditional and the random effects parameters
- 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

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 `weighted_posteriors`.

Examples

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

---

get_predictors *Get the data from model predictors*

Description

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

Usage

```
get_predictors(x)
```

Arguments

`x`	A fitted model.

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

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

## End(Not run)
```

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

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

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

head(get_random(m))
```

---

get_response *Get the values from the response variable*

Description

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

Usage

```
get_response(x, select = NULL)
```

Arguments

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

Value

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

Examples

```
library(lme4)
data(cbpp)
data(mtcars)
cbpp$trials <- cbpp$size - cbpp$incidence

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

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

---

get_sigma *Get residual standard deviation from models*

Description

Returns the residual standard deviation from classical and mixed models.

Usage

```
get_sigma(x)
```

Arguments

x	A model.

Details

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.

Value

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

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_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, ...)

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

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

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

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

## 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, ...)

## S3 method for class 'betareg'
```

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

## S3 method for class 'DirichletRegModel'
get_statistic(x, component = c("all", "conditional", "precision"), ...)
```

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.
component	Should all parameters, parameters for the conditional model, or for the zero-inflated part of the model be returned? Applies to models with zero-inflated component. component may be one of "conditional", "zi", "zero-inflated" or "all" (default). For models with smooth terms, component = "smooth_terms" is also possible. May be abbreviated. Note that the *conditional* component is also called *count* or *mean* component, depending on the model.
ci	Confidence Interval (CI) level. Default to 0.95 (95%). Currently only applies to objects of class emmGrid.
adjust	Character value naming the method used to adjust p-values or confidence 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.

Examples

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

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, ...)

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

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

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

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

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

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

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

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

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

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

## S3 method for class 'betamfx'
```

```
get_varcov(x, component = c("conditional", "precision", "all"), ...)

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

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

Arguments

x	A model.
...	Currently not used.
component	Should the complete variance-covariance matrix of the model be returned, or only for specific model components only (like count or zero-inflated model parts)? Applies to models with zero-inflated component, or models with precision (e.g. betareg) component. component may be one of "conditional", "zi", "zero-inflated", "dispersion", "precision", or "all". May be abbreviated. Note that the *conditional* component is also called *count* or *mean* component, depending on the model.
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.

Value

The variance-covariance matrix, as matrix-object.

Note

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

Examples

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

---

get_variance *Get variance components from random effects models*

Description

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

Usage

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

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

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

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

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, ...)
```

Arguments

x	A mixed effects model.
component	Character value, indicating the variance component that should be returned. By default, all variance components are returned. The distribution-specific ("distribution") and residual ("residual") variance are the most computational intensive components, and hence may take a few seconds to calculate.
verbose	Toggle off warnings.
...	Currently not used.

Details

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

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

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

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

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

Residual variance: The residual variance, σ^2_ϵ, is simply $\sigma^2_d + \sigma^2_e$.

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^2_ϵ 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.

Value

A list with following elements:

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

Note

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

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

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

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

## End(Not run)
```

---

get_weights *Get the values from model weights*

Description

Returns weighting variable of a model.

Usage

```
get_weights(x, na_rm = FALSE, ...)
```

Arguments

x	A fitted model.
na_rm	Logical, if TRUE, removes possible missing values.
...	Currently not used.

Value

The weighting variable, or NULL if no weights were specified (or if all weights were 1).

Examples

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

`has_intercept` *Checks if model has an intercept*

Description

Checks if model has an intercept.

Usage

```
has_intercept(x)
```

Arguments

`x`	A model object.

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)

library(lme4)
model <- lmer(Reaction ~ 0 + Days + (Days | Subject), data = sleepstudy)
has_intercept(model)

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

is_model — *Checks if an object is a regression model object*

Description

Small helper that checks if a model is a regression model object.

Usage

```
is_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)
```

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

Description

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

Usage

```
is_model_supported(x)

supported_models()
```

Arguments

x	An object.

Details

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

Value

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

Examples

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

is_model_supported(m)
is_model_supported(mtcars)
```

---

is_multivariate *Checks if an object stems from a multivariate response model*

Description

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

Usage

```
is_multivariate(x)
```

Arguments

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

Value

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

Examples

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

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

## End(Not run)
```

---

is_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)

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

```
is_nullmodel(model)

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

`link_function` *Get link-function from model object*

Description

Returns the link-function from a model object.

Usage

```
link_function(x, ...)

## S3 method for class '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)(.3)
# same as
log(.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)(.3)
# same as
exp(.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, ...)
```

Arguments

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

Details

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

- `is_binomial`: family is binomial (but not negative binomial)
- `is_poisson`: family is poisson
- `is_negbin`: family is negative binomial
- `is_count`: model is a count model (i.e. family is either poisson or negative binomial)
- `is_beta`: family is beta
- `is_betabinomial`: family is beta-binomial
- `is_dirichlet`: family is dirichlet
- `is_exponential`: family is exponential (e.g. Gamma or Weibull)
- `is_logit`: model has logit link
- `is_probit`: model has probit link
- `is_linear`: family is gaussian
- `is_tweedie`: family is tweedie
- `is_ordinal`: family is ordinal or cumulative link

- is_cumulative: family is ordinal or cumulative link
- is_multinomial: family is multinomial or categorical link
- is_categorical: family is categorical link
- is_censored: model is a censored model (has a censored response, including survival models)
- is_truncated: model is a truncated model (has a truncated response)
- is_survival: model is a survival model
- is_zero_inflated: model has zero-inflation component
- is_hurdle: model has zero-inflation component and is a hurdle-model (truncated family distribution)
- is_dispersion: model has dispersion component
- is_mixed: model is a mixed effects model (with random effects)
- is_multivariate: model is a multivariate response model (currently only works for *brmsfit* objects)
- is_trial: model response contains additional information about the trials
- is_bayesian: model is a Bayesian model
- is_anova: model is an Anova object
- is_ttest: model is an an object of class htest, returned by t.test()
- is_correlation: model is an an object of class htest, returned by cor.test()
- is_onewaytest: model is an an object of class htest, returned by oneway.test()
- is_proptest: model is an an object of class htest, returned by prop.test()
- is_binomtest: model is an an object of class htest, returned by binom.test()
- is_chi2test: model is an an object of class htest, returned by chisq.test()
- link_function: the link-function
- family: the family-object
- n_obs: number of observations
- model_terms: a list with all model terms, including terms such as random effects or from zero-inflated model parts.

Value

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

Examples

```
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)
```

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

## End(Not run)

model_info(m)
```

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

Arguments

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

Value

The null-model of `x`

Examples

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

n_obs *Get number of observations from a model*

Description

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

Usage

```
n_obs(x, ...)

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

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

Arguments

x	A fitted model.
...	Currently not used.
weighted	For survey designs, returns the weighted sample size.
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)
```

parameters_table *Parameter table formatting*

Description

This functions takes a data frame with model parameters as input and formats certain columns into a more readable layout (like collapsing separate columns for lower and upper confidence interval values). Furthermore, column names are formatted as well.

Usage

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

Arguments

x	A data frame of model's parameters, as returned by various functions of the **easystats**-packages. May also be a result from `broom::tidy()`.
pretty_names	Return "pretty" (i.e. more human readable) parameter names.
stars	Add significance stars (e.g., p < .001***).
digits	Number of decimal places for numeric values (except confidence intervals and p-values).
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_digits	Number of decimal places for confidence intervals.
p_digits	Number of decimal places for p-values. May also be `"scientific"` for scientific notation of p-values.
preserve_attributes	Logical, if `TRUE`, preserves all attributes from the input data frame.
...	Arguments passed to or from other methods.

Value

A data frame.

Examples

```
if (require("parameters")) {
  x <- model_parameters(lm(Sepal.Length ~ Species * Sepal.Width, data = iris))
  as.data.frame(parameters_table(x))
  as.data.frame(parameters_table(x, p_digits = "scientific"))
}
```

```
if (require("rstanarm") && require("parameters")) {
  model <- stan_glm(Sepal.Length ~ Species, data = iris, refresh = 0, seed = 123)
  x <- model_parameters(model, ci = c(0.69, 0.89, 0.95))
  as.data.frame(parameters_table(x))
}
```

`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)
```

Arguments

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

Details

This function prints `text` directly to the console using `cat()`, so no string is returned.

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 hdi or equivalence_test, as input and splits this information into several parts, depending on the model. See details below.

Usage

```
print_parameters(
  x,
  ...,
  split_by = c("Effects", "Component", "Group", "Response"),
  format = "text",
  keep_parameter_column = TRUE
)
```

Arguments

x	A fitted model, or a data frame returned by clean_parameters.
...	One or more objects (data frames), which contain information about the model parameters and related statistics (like confidence intervals, HDI, ROPE, ...).
split_by	split_by should be a character vector with one or more of the following elements: "Effects", "Component", "Response" and "Group". These are the column names returned by clean_parameters, which is used to extract the information from which the group or component model parameters belong. If NULL, the merged data frame is returned. Else, the data frame is split into a list, split by the values from those columns defined in split_by.
format	Name of output-format, as string. If NULL (or "text"), assumed use for output is basic printing. If "markdown", markdown-format is assumed. This only affects the style of title- and table-caption attributes, which are used in export_table.
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".

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 hdi, where we have a) a Parameters column and b) columns with the HDI values.

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 statistic of interest (in our example: the HDI) is also associated with the different model components. The data frame is split into a list, so for a clear printing. Users can loop over this list and print each component for a better overview. Further, parameter names are "cleaned", if necessary, also for a cleaner print. See also 'Examples'.

Value

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

Examples

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

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

# Based on the "split_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

## End(Not run)
```

`standardize_names` *Standardize column names*

Description

Standardize column names from data frames, in particular objects returned from `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 `model_parameters()` or `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., `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

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

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

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