Package 'bayestestR'

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Type Package

Title Understand and Describe Bayesian Models and Posterior Distributions

Version 0.20.0

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Description Provides utilities to describe posterior distributions and Bayesian models. It includes point-estimates such as Maximum A Posteriori (MAP), measures of dispersion (Highest Density Interval - HDI; Kruschke, 2015 <doi:10.1016/C2012-0-00477-2>) and indices used for null-hypothesis testing (such as ROPE percentage, pd and Bayes factors). References: Makowski et al. (2021) <doi:10.21105/joss.01541>.

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`area_under_curve` *Area under the Curve (AUC)*

Description

Based on the DescTools `AUC` function. It can calculate the area under the curve with a naive algorithm or a more elaborated spline approach. The curve must be given by vectors of xy-coordinates. This function can handle unsorted x values (by sorting x) and ties for the x values (by ignoring duplicates).

Usage

```
area_under_curve(x, y, method = c("trapezoid", "step", "spline"), ...)

auc(x, y, method = c("trapezoid", "step", "spline"), ...)
```

Arguments

x	Vector of x values.
y	Vector of y values.
method	Method to compute the Area Under the Curve (AUC). Can be "trapezoid" (default), "step" or "spline". If "trapezoid", the curve is formed by connecting all points by a direct line (composite trapezoid rule). If "step" is chosen then a stepwise connection of two points is used. For calculating the area under a spline interpolation the splinefun function is used in combination with integrate.
...	Arguments passed to or from other methods.

See Also

DescTools

Examples

```
library(bayestestR)
posterior <- distribution_normal(1000)

dens <- estimate_density(posterior)
dens <- dens[dens$x > 0, ]
x <- dens$x
y <- dens$y

area_under_curve(x, y, method = "trapezoid")
area_under_curve(x, y, method = "step")
area_under_curve(x, y, method = "spline")
```

---

as.data.frame.density *Coerce to a Data Frame*

Description

Coerce to a Data Frame

Usage

```
## S3 method for class 'density'
as.data.frame(x, ...)
```

Arguments

x	any R object.
...	additional arguments to be passed to or from methods.

as.numeric.map_estimate *Convert to Numeric*

Description

Convert to Numeric

Usage

```
## S3 method for class 'map_estimate'
as.numeric(x, ...)

## S3 method for class 'p_direction'
as.numeric(x, ...)

## S3 method for class 'p_map'
as.numeric(x, ...)

## S3 method for class 'p_significance'
as.numeric(x, ...)
```

Arguments

x	object to be coerced or tested.
...	further arguments passed to or from other methods.

bayesfactor *Bayes Factors (BF)*

Description

This function computes the Bayes factors (BFs) that are appropriate to the input. For vectors or single models, it will compute BFs for single parameters, or is hypothesis is specified, BFs for restricted models. For multiple models, it will return the BF corresponding to comparison between models and if a model comparison is passed, it will compute the inclusion BF.

For a complete overview of these functions, read the Bayes factor vignette.

Usage

```
bayesfactor(
  ...,
  prior = NULL,
  direction = "two-sided",
  null = 0,
  hypothesis = NULL,
  effects = "fixed",
  verbose = TRUE,
  denominator = 1,
  match_models = FALSE,
  prior_odds = NULL
)
```

Arguments

`...`	A numeric vector, model object(s), or the output from `bayesfactor_models`.
`prior`	An object representing a prior distribution (see 'Details').
`direction`	Test type (see 'Details'). One of `0`, `"two-sided"` (default, two tailed), `-1`, `"left"` (left tailed) or `1`, `"right"` (right tailed).
`null`	Value of the null, either a scalar (for point-null) or a range (for a interval-null).
`hypothesis`	A character vector specifying the restrictions as logical conditions (see examples below).
`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.
`verbose`	Toggle off warnings.
`denominator`	Either an integer indicating which of the models to use as the denominator, or a model to be used as a denominator. Ignored for `BFBayesFactor`.
`match_models`	See details.
`prior_odds`	Optional vector of prior odds for the models. See `BayesFactor::priorOdds<-`.

Value

Some type of Bayes factor, depending on the input. See `bayesfactor_parameters()`, `bayesfactor_models()` or `bayesfactor_inclusion()`.

Note

There is also a `plot()`-method implemented in the **see**-package.

Examples

```
## Not run:
library(bayestestR)

prior <- distribution_normal(1000, mean = 0, sd = 1)
posterior <- distribution_normal(1000, mean = 0.5, sd = 0.3)

bayesfactor(posterior, prior = prior, verbose = FALSE)

# rstanarm models
# ---------------
model <- suppressWarnings(rstanarm::stan_lmer(extra ~ group + (1 | ID), data = sleep))
bayesfactor(model, verbose = FALSE)

# Frequentist models
# ---------------
m0 <- lm(extra ~ 1, data = sleep)
m1 <- lm(extra ~ group, data = sleep)
m2 <- lm(extra ~ group + ID, data = sleep)

comparison <- bayesfactor(m0, m1, m2)
comparison

bayesfactor(comparison)

## End(Not run)
```

`bayesfactor_inclusion` *Inclusion Bayes Factors for testing predictors across Bayesian models*

The `bf_*` *function is an alias of the main function.*

For more info, see Rhrefhttps://easystats.github.io/bayestestR/articles/bayes_factors.htmlthe Bayes factors vignette.

Description

Inclusion Bayes Factors for testing predictors across Bayesian models

The `bf_*` function is an alias of the main function.

For more info, see the Bayes factors vignette.

Usage

```
bayesfactor_inclusion(models, match_models = FALSE, prior_odds = NULL, ...)

bf_inclusion(models, match_models = FALSE, prior_odds = NULL, ...)
```

Arguments

models	An object of class bayesfactor_models() or BFBayesFactor.
match_models	See details.
prior_odds	Optional vector of prior odds for the models. See BayesFactor::priorOdds<-.
...	Arguments passed to or from other methods.

Details

Inclusion Bayes factors answer the question: Are the observed data more probable under models with a particular effect, than they are under models without that particular effect? In other words, on average - are models with effect X more likely to have produced the observed data than models without effect X?

Match Models:

If match_models=FALSE (default), Inclusion BFs are computed by comparing all models with a term against all models without that term. If TRUE, comparison is restricted to models that (1) do not include any interactions with the term of interest; (2) for interaction terms, averaging is done only across models that contain the main effect terms from which the interaction term is comprised.

Additional methods:

The resulting output is supported by the following methods:

- as.numeric(): Extract the (possibly log-)Bayes factor values.

See bayesfactor_methods.

Value

a data frame containing the prior and posterior probabilities, and log(BF) for each effect (Use as.numeric() to extract the non-log Bayes factors; see examples).

Interpreting Bayes Factors

A Bayes factor greater than 1 can be interpreted as evidence against the null, at which one convention is that a Bayes factor greater than 3 can be considered as "substantial" evidence against the null (and vice versa, a Bayes factor smaller than 1/3 indicates substantial evidence in favor of the null-model). See also effectsize::interpret_bf().

Note

Random effects in the lmer style are converted to interaction terms: i.e., (X|G) will become the terms 1:G and X:G.

Author(s)

Mattan S. Ben-Shachar

References

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- Clyde, M. A., Ghosh, J., & Littman, M. L. (2011). Bayesian adaptive sampling for variable selection and model averaging. Journal of Computational and Graphical Statistics, 20(1), 80-101.
- Mathot, S. (2017). Bayes like a Baws: Interpreting Bayesian Repeated Measures in JASP. Blog post.

See Also

`weighted_posteriors()` for Bayesian parameter averaging.

Other Bayes factors: `bayesfactor_models()`, `bayesfactor_parameters()`, `bayesfactor_restricted()`

Examples

```
library(bayestestR)

# Using bayesfactor_models:
# -----------------------------
mo0 <- lm(Sepal.Length ~ 1, data = iris)
mo1 <- lm(Sepal.Length ~ Species, data = iris)
mo2 <- lm(Sepal.Length ~ Species + Petal.Length, data = iris)
mo3 <- lm(Sepal.Length ~ Species * Petal.Length, data = iris)

BFmodels <- bayesfactor_models(mo1, mo2, mo3, denominator = mo0)
(bf_inc <- bayesfactor_inclusion(BFmodels))

as.numeric(bf_inc)


# BayesFactor
# -------------------------------
BF <- BayesFactor::generalTestBF(len ~ supp * dose, ToothGrowth, progress = FALSE)
bayesfactor_inclusion(BF)

# compare only matched models:
bayesfactor_inclusion(BF, match_models = TRUE)
```

bayesfactor_methods *Methods for Bayes factors*

Description

Methods for Bayes factors

Usage

```
## S3 method for class 'bayestestRBF'
as.matrix(x, log = TRUE, ...)

## S3 method for class 'bayesfactor_models'
update(object, subset = NULL, reference = NULL, ...)

## S3 method for class 'bayestestRBF'
as.numeric(x, log = FALSE, ...)

## S3 method for class 'bayesfactor_restricted'
as.logical(x, which = c("posterior", "prior"), ...)
```

Arguments

x, object	Bayes factor object
log	Return log(BF) (default), or BF values.
...	Additional arguments (currently not used).
subset	Vector of model indices to keep or remove.
reference	Index of model to reference to, or "top" to reference to the best model, or "bottom" to reference to the worst model.
which	Should the logical matrix be of the posterior or prior distribution(s)?

Value

- as.numeric() / as.double(): a numeric vector of (log) Bayes factors.
- as.logical(): a logical data frame with a column for each order-restricted hypothesis.
- as.matrix(): a square matrix of (log) Bayes factors, with rows as denominators and columns as numerators.
- update(): an updated bayesfactor_models object.

Interpreting Bayes Factors

A Bayes factor greater than 1 can be interpreted as evidence against the null, at which one convention is that a Bayes factor greater than 3 can be considered as "substantial" evidence against the null (and vice versa, a Bayes factor smaller than 1/3 indicates substantial evidence in favor of the null-model). See also effectsize::interpret_bf().

Transitivity of Bayes factors

For multiple inputs (models or hypotheses), the function will return multiple Bayes factors between each model and *the same* reference model (the `denominator` or un-restricted model). However, we can take advantage of the transitivity of Bayes factors - where if we have two Bayes factors for Model *A* and model *B* against the *same reference model C*, we can obtain a Bayes factor for comparing model *A* to model *B* by dividing them:

$$BF_{AB} = \frac{BF_{AC}}{BF_{BC}} = \frac{\frac{ML_A}{ML_C}}{\frac{ML_B}{ML_C}} = \frac{ML_A}{ML_B}$$

(Where *ML* is the *marginal likelihood*.)

A full matrix comparing all models can be obtained with `as.matrix()`.

Prior and posterior considerations

In order to correctly and precisely estimate Bayes factors, a rule of thumb are the 4 P's: **P**roper **P**riors and **P**lentiful **P**osteriors.

For the computation of Bayes factors, the model priors must be proper priors (at the very least they should be *not flat*, and it is preferable that they be *informative*) (Note that by default, `brms::brm()` uses flat priors for fixed-effects); Wide priors result in smaller marginal likelihoods, and thus models with wider priors are trivially less likely than models with narrower priors - where, at the extreme, that a model with completely flat priors is infinitely less favorable than a point null model (this is called *the Jeffreys-Lindley-Bartlett paradox*). Thus, you should only ever try (or want) to compute a Bayes factor when you have an informed prior.

Additionally, for models using MCMC estimation the number of posterior samples needed for testing is substantially larger than for estimation (the default of 4000 samples may not be enough in many cases). A conservative rule of thumb is to obtain 10 times more samples than would be required for estimation (*Gronau, Singmann, & Wagenmakers, 2017*). If less than 40,000 samples are detected, a warning is issued.

`bayesfactor_models` *Bayes Factors (BF) for model comparison*

Description

This function computes or extracts Bayes factors from fitted models.

The `bf_*` function is an alias of the main function.

For more info, see the Bayes factors vignette.

Usage

```
bayesfactor_models(..., denominator = 1, verbose = TRUE)

bf_models(..., denominator = 1, verbose = TRUE)

## Default S3 method:
bayesfactor_models(..., denominator = 1, verbose = TRUE)
```

Arguments

`...`	Fitted models (see details), all fit on the same data, or a single `BFBayesFactor` object (see 'Details'). Ignored in `as.matrix()`, `update()`. If the following named arguments are present, they are passed to `insight::get_loglikelihood()` (see details): • `estimator` (defaults to `"ML"`) • `check_response` (defaults to `FALSE`)
`denominator`	Either an integer indicating which of the models to use as the denominator, or a model to be used as a denominator. Ignored for `BFBayesFactor`.
`verbose`	Toggle off warnings.

Details

If the passed models are supported by **insight** the DV of all models will be tested for equality (else this is assumed to be true), and the models' terms will be extracted (allowing for follow-up analysis with bayesfactor_inclusion).

- For `brmsfit` or `stanreg` models, Bayes factors are computed using the **bridgesampling** package.
  - `brmsfit` models must have been fitted with `save_pars = save_pars(all = TRUE)`.
  - `stanreg` models must have been fitted with a defined `diagnostic_file`.
- For `BFBayesFactor`, `bayesfactor_models()` is a wraparound `BayesFactor::extractBF()`.
- For all other model types, Bayes factors are computed using the BIC approximation. Note that BICs are extracted from using insight::get_loglikelihood, see documentation there for options for dealing with transformed responses and REML estimation.

Additional methods:

The resulting output is supported by the following methods:

- `as.matrix()`: Extract a full matrix of (log-)Bayes factors between all models (using the transitivity of Bayes factors).
- `update()`: subset and/or re-reference the Bayes factors to a different model.
- `as.numeric()`: Extract the (possibly log-)Bayes factor values.

See examples and bayesfactor_methods.

Value

A data frame containing the models' formulas (reconstructed fixed and random effects) and their `log(BF)`s (Use `as.numeric()` to extract the non-log Bayes factors; see examples), that prints nicely.

For `as.matrix()` a square matrix of (log) Bayes factors, with rows as denominators and columns as numerators.

Prior and posterior considerations

In order to correctly and precisely estimate Bayes factors, a rule of thumb are the 4 P's: **P**roper **P**riors and **P**lentiful **P**osteriors.

For the computation of Bayes factors, the model priors must be proper priors (at the very least they should be *not flat*, and it is preferable that they be *informative*) (Note that by default, `brms::brm()` uses flat priors for fixed-effects); Wide priors result in smaller marginal likelihoods, and thus models with wider priors are trivially less likely than models with narrower priors - where, at the extreme, that a model with completely flat priors is infinitely less favorable than a point null model (this is called *the Jeffreys-Lindley-Bartlett paradox*). Thus, you should only ever try (or want) to compute a Bayes factor when you have an informed prior.

Additionally, for models using MCMC estimation the number of posterior samples needed for testing is substantially larger than for estimation (the default of 4000 samples may not be enough in many cases). A conservative rule of thumb is to obtain 10 times more samples than would be required for estimation (*Gronau, Singmann, & Wagenmakers, 2017*). If less than 40,000 samples are detected, a warning is issued.

Transitivity of Bayes factors

For multiple inputs (models or hypotheses), the function will return multiple Bayes factors between each model and *the same* reference model (the `denominator` or un-restricted model). However, we can take advantage of the transitivity of Bayes factors - where if we have two Bayes factors for Model *A* and model *B* against the *same reference model C*, we can obtain a Bayes factor for comparing model *A* to model *B* by dividing them:

$$BF_{AB} = \frac{BF_{AC}}{BF_{BC}} = \frac{\frac{ML_A}{ML_C}}{\frac{ML_B}{ML_C}} = \frac{ML_A}{ML_B}$$

(Where *ML* is the *marginal likelihood*.)

A full matrix comparing all models can be obtained with `as.matrix()`.

Interpreting Bayes Factors

A Bayes factor greater than 1 can be interpreted as evidence against the null, at which one convention is that a Bayes factor greater than 3 can be considered as "substantial" evidence against the

null (and vice versa, a Bayes factor smaller than 1/3 indicates substantial evidence in favor of the null-model). See also `effectsize::interpret_bf()`.

Note

There is also a `plot()`-method implemented in the **see**-package.

Author(s)

Mattan S. Ben-Shachar

References

- Gronau, Q. F., Singmann, H., & Wagenmakers, E. J. (2017). Bridgesampling: An R package for estimating normalizing constants. arXiv preprint arXiv:1710.08162.
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- Wetzels, R., Matzke, D., Lee, M. D., Rouder, J. N., Iverson, G. J., and Wagenmakers, E.-J. (2011). Statistical Evidence in Experimental Psychology: An Empirical Comparison Using 855 t Tests. Perspectives on Psychological Science, 6(3), 291–298. doi:10.1177/1745691611406923

See Also

`bayesfactor_inclusion()` for testing predictors across Bayesian models.

Other Bayes factors: `bayesfactor_inclusion()`, `bayesfactor_parameters()`, `bayesfactor_restricted()`

Examples

```
# With lm objects:
# ----------------
lm1 <- lm(mpg ~ 1, data = mtcars)
lm2 <- lm(mpg ~ hp, data = mtcars)
lm3 <- lm(mpg ~ hp + drat, data = mtcars)
lm4 <- lm(mpg ~ hp * drat, data = mtcars)
(BFM <- bayesfactor_models(lm1, lm2, lm3, lm4, denominator = 1))
# bayesfactor_models(lm2, lm3, lm4, denominator = lm1) # same result
# bayesfactor_models(lm1, lm2, lm3, lm4, denominator = lm1) # same result

update(BFM, reference = "bottom")
as.matrix(BFM)
as.numeric(BFM)

lm2b <- lm(sqrt(mpg) ~ hp, data = mtcars)
# Set check_response = TRUE for transformed responses
bayesfactor_models(lm2b, denominator = lm2, check_response = TRUE)
```

```
# With lmerMod objects:
# ---------------------
lmer1 <- lme4::lmer(Sepal.Length ~ Petal.Length + (1 | Species), data = iris)
lmer2 <- lme4::lmer(Sepal.Length ~ Petal.Length + (Petal.Length | Species), data = iris)
lmer3 <- lme4::lmer(
  Sepal.Length ~ Petal.Length + (Petal.Length | Species) + (1 | Petal.Width),
  data = iris
)
bayesfactor_models(lmer1, lmer2, lmer3,
  denominator = 1,
  estimator = "REML"
)

# rstanarm models
# ---------------------
# (note that a unique diagnostic_file MUST be specified in order to work)
stan_m0 <- suppressWarnings(rstanarm::stan_glm(Sepal.Length ~ 1,
  data = iris,
  family = gaussian(),
  diagnostic_file = file.path(tempdir(), "df0.csv")
))
stan_m1 <- suppressWarnings(rstanarm::stan_glm(Sepal.Length ~ Species,
  data = iris,
  family = gaussian(),
  diagnostic_file = file.path(tempdir(), "df1.csv")
))
stan_m2 <- suppressWarnings(rstanarm::stan_glm(Sepal.Length ~ Species + Petal.Length,
  data = iris,
  family = gaussian(),
  diagnostic_file = file.path(tempdir(), "df2.csv")
))
bayesfactor_models(stan_m1, stan_m2, denominator = stan_m0, verbose = FALSE)


# brms models
# --------------------
# (note the save_pars MUST be set to save_pars(all = TRUE) in order to work)
brm1 <- brms::brm(Sepal.Length ~ 1, data = iris, save_pars = save_pars(all = TRUE))
brm2 <- brms::brm(Sepal.Length ~ Species, data = iris, save_pars = save_pars(all = TRUE))
brm3 <- brms::brm(
  Sepal.Length ~ Species + Petal.Length,
  data = iris,
  save_pars = save_pars(all = TRUE)
)

bayesfactor_models(brm1, brm2, brm3, denominator = 1, verbose = FALSE)


# BayesFactor
# ---------------------------
data(puzzles)
BF <- BayesFactor::anovaBF(RT ~ shape * color + ID,
```

```
  data = puzzles,
  whichRandom = "ID", progress = FALSE
)
BF
bayesfactor_models(BF) # basically the same
```

`bayesfactor_parameters` *Bayes Factors (BF) for a Single Parameter*

Description

This method computes Bayes factors against the null (either a point or an interval), based on prior and posterior samples of a single parameter. This Bayes factor indicates the degree by which the mass of the posterior distribution has shifted away from or closer to the null value(s) (relative to the prior distribution), thus indicating if the null value has become less or more likely given the observed data.

When the null is an interval, the Bayes factor is computed by comparing the prior and posterior odds of the parameter falling within or outside the null interval (Morey & Rouder, 2011; Liao et al., 2020); When the null is a point, a Savage-Dickey density ratio is computed, which is also an approximation of a Bayes factor comparing the marginal likelihoods of the model against a model in which the tested parameter has been restricted to the point null (Wagenmakers et al., 2010; Heck, 2019).

`bayesfactor_pointnull()` and `bayesfactor_rope()` are wrappers around `bayesfactor_parameters()` with different defaults for the null to be tested against (a point and a range, respectively; see details). The `bf_*` functions are aliases of the main functions.

For more info, see the Bayes factors vignette.

Usage

```
bayesfactor_parameters(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = 0,
  ...,
  verbose = TRUE
)

bayesfactor_pointnull(
  posterior,
  prior = NULL,
```

```
  direction = "two-sided",
  null = 0,
  ...,
  verbose = TRUE
)

bayesfactor_rope(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = rope_range(posterior, verbose = FALSE),
  ...,
  verbose = TRUE
)

bf_parameters(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = 0,
  ...,
  verbose = TRUE
)

bf_pointnull(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = 0,
  ...,
  verbose = TRUE
)

bf_rope(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = rope_range(posterior, verbose = FALSE),
  ...,
  verbose = TRUE
)

## S3 method for class 'numeric'
bayesfactor_parameters(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = 0,
```

```
  ...,
  verbose = TRUE
)

## S3 method for class 'stanreg'
bayesfactor_parameters(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = 0,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  ...,
  verbose = TRUE
)

## S3 method for class 'data.frame'
bayesfactor_parameters(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = 0,
  rvar_col = NULL,
  ...,
  verbose = TRUE
)
```

Arguments

posterior	A numerical vector, stanreg / brmsfit object, emmGrid or a data frame - representing a posterior distribution(s) from (see 'Details').
prior	An object representing a prior distribution (see 'Details').
direction	Test type (see 'Details'). One of 0, "two-sided" (default, two tailed), -1, "left" (left tailed) or 1, "right" (right tailed).
null	Value of the null, either a scalar (for point-null) or a range (for a interval-null).
...	Arguments passed to and from other methods. (Can be used to pass arguments to internal logspline::logspline().)
verbose	Toggle off warnings.
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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

rvar_col — A single character - the name of an rvar column in the data frame to be processed. See example in p_direction().

Details

This method is used to compute Bayes factors based on prior and posterior distributions.

Note that the logspline package is used for estimating densities and probabilities, and must be installed for the function to work.

One-sided & Dividing Tests (setting an order restriction)::

One sided tests (controlled by direction) are conducted by restricting the prior and posterior of the non-null values (the "alternative") to one side of the null only (*Morey & Wagenmakers, 2014*). For example, if we have a prior hypothesis that the parameter should be positive, the alternative will be restricted to the region to the right of the null (point or interval). For example, for a Bayes factor comparing the "null" of 0-0.1 to the alternative >0.1, we would set bayesfactor_parameters(null = c(0, 0.1), direction = ">").

It is also possible to compute a Bayes factor for **dividing** hypotheses - that is, for a null and alternative that are complementary, opposing one-sided hypotheses (*Morey & Wagenmakers, 2014*). For example, for a Bayes factor comparing the "null" of <0 to the alternative >0, we would set bayesfactor_parameters(null = c(-Inf, 0)).

Additional methods:

The resulting output is supported by the following methods:

- as.numeric(): Extract the (possibly log-)Bayes factor values.

See bayesfactor_methods.

Value

A data frame containing the (log) Bayes factor representing evidence *against* the null (Use `as.numeric()` to extract the non-log Bayes factors; see examples).

Obtaining prior samples

It is important to provide the correct `prior` for meaningful results, to match the `posterior`-type input:

- **A numeric vector** - `prior` should also be a *numeric vector*, representing the prior-distribution
- **A data frame** - `prior` should also be a *data frame*, representing the prior-estimates, in matching column order.
  - If `rvar_col` is specified, `prior` should be *the name of an* `rvar` *column* that represents the prior-estimates.
- **Supported Bayesian model (`stanreg`, `brmsfit`, etc.)**
  - `prior` should be *a model an equivalent model with MCMC samples from the priors* **only**. See `unupdate()`.
  - If `prior` is set to `NULL`, `unupdate()` is called internally (not supported for `brmsfit_multiple` model).
- **Output from a `{marginaleffects}` function** - `prior` should also be *an equivalent output* from a `{marginaleffects}` function based on a prior-model (See `unupdate()`).
- **Output from an `{emmeans}` function**
  - `prior` should also be *an equivalent output* from an `{emmeans}` function based on a prior-model (See `unupdate()`).
  - `prior` can also be *the original (posterior) model*, in which case the function will try to "unupdate" the estimates (not supported if the estimates have undergone any transformations – `"log"`, `"response"`, etc. – or any `regriding`).

Prior and posterior considerations

In order to correctly and precisely estimate Bayes factors, a rule of thumb are the 4 P's: **P**roper **P**riors and **P**lentiful **P**osteriors.

For the computation of Bayes factors, the model priors must be proper priors (at the very least they should be *not flat*, and it is preferable that they be *informative*) (Note that by default, `brms::brm()` uses flat priors for fixed-effects); Wide priors result in smaller marginal likelihoods, and thus models with wider priors are trivially less likely than models with narrower priors - where, at the extreme, that a model with completely flat priors is infinitely less favorable than a point null model (this is called *the Jeffreys-Lindley-Bartlett paradox*). Thus, you should only ever try (or want) to compute a Bayes factor when you have an informed prior.

Additionally, for models using MCMC estimation the number of posterior samples needed for testing is substantially larger than for estimation (the default of 4000 samples may not be enough in many cases). A conservative rule of thumb is to obtain 10 times more samples than would be required for estimation (*Gronau, Singmann, & Wagenmakers, 2017*). If less than 40,000 samples are detected, a warning is issued.

Interpreting Bayes Factors

A Bayes factor greater than 1 can be interpreted as evidence against the null, at which one convention is that a Bayes factor greater than 3 can be considered as "substantial" evidence against the null (and vice versa, a Bayes factor smaller than 1/3 indicates substantial evidence in favor of the null-model). See also `effectsize::interpret_bf()`.

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.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, or `smooth_terms` (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.

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. See also `?insight::find_parameters`.

Note

There is also a `plot()`-method implemented in the **see**-package.

Author(s)

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References

- Wagenmakers, E. J., Lodewyckx, T., Kuriyal, H., and Grasman, R. (2010). Bayesian hypothesis testing for psychologists: A tutorial on the Savage-Dickey method. Cognitive psychology, 60(3), 158-189.
- Heck, D. W. (2019). A caveat on the Savage–Dickey density ratio: The case of computing Bayes factors for regression parameters. British Journal of Mathematical and Statistical Psychology, 72(2), 316-333.
- Morey, R. D., & Wagenmakers, E. J. (2014). Simple relation between Bayesian order-restricted and point-null hypothesis tests. Statistics & Probability Letters, 92, 121-124.

- Morey, R. D., & Rouder, J. N. (2011). Bayes factor approaches for testing interval null hypotheses. Psychological methods, 16(4), 406.
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- Wetzels, R., Matzke, D., Lee, M. D., Rouder, J. N., Iverson, G. J., and Wagenmakers, E.-J. (2011). Statistical Evidence in Experimental Psychology: An Empirical Comparison Using 855 t Tests. Perspectives on Psychological Science, 6(3), 291–298. doi:10.1177/1745691611406923

See Also

Other Bayes factors: `bayesfactor_inclusion()`, `bayesfactor_models()`, `bayesfactor_restricted()`

Examples

```
library(bayestestR)
prior <- distribution_normal(1000, mean = 0, sd = 1)
posterior <- distribution_normal(1000, mean = .5, sd = .3)
(BF_pars <- bayesfactor_parameters(posterior, prior, verbose = FALSE))

as.numeric(BF_pars)



# rstanarm models
# ---------------
contrasts(sleep$group) <- contr.equalprior_pairs # see vingette
stan_model <- suppressWarnings(stan_lmer(
  extra ~ group + (1 | ID),
  data = sleep,
  refresh = 0
))
bayesfactor_parameters(stan_model, verbose = FALSE)
bayesfactor_parameters(stan_model, null = rope_range(stan_model))

# emmGrid objects
# ---------------
group_diff <- pairs(emmeans(stan_model, ~group, data = sleep))
bayesfactor_parameters(group_diff, prior = stan_model, verbose = FALSE)

# Or
# group_diff_prior <- pairs(emmeans(unupdate(stan_model), ~group))
# bayesfactor_parameters(group_diff, prior = group_diff_prior, verbose = FALSE)



# brms models
# -----------
## Not run:
contrasts(sleep$group) <- contr.equalprior_pairs # see vingette
my_custom_priors <-
```

```
  set_prior("student_t(3, 0, 1)", class = "b") +
  set_prior("student_t(3, 0, 1)", class = "sd", group = "ID")

brms_model <- suppressWarnings(brm(extra ~ group + (1 | ID),
  data = sleep,
  prior = my_custom_priors,
  refresh = 0
))
bayesfactor_parameters(brms_model, verbose = FALSE)

## End(Not run)
```

`bayesfactor_restricted` *Bayes Factors (BF) for Order Restricted Models*

Description

This method computes Bayes factors for comparing a model with an order restrictions on its parameters with the fully unrestricted model. *Note that this method should only be used for confirmatory analyses*.

The `bf_*` function is an alias of the main function.

For more info, see the Bayes factors vignette.

Usage

```
bayesfactor_restricted(posterior, ...)

bf_restricted(posterior, ...)

## S3 method for class 'stanreg'
bayesfactor_restricted(
  posterior,
  hypothesis,
  prior = NULL,
  verbose = TRUE,
  effects = "fixed",
  component = "conditional",
  ...
)

## S3 method for class 'brmsfit'
bayesfactor_restricted(
  posterior,
  hypothesis,
```

```
  prior = NULL,
  verbose = TRUE,
  effects = "fixed",
  component = "conditional",
  ...
)

## S3 method for class 'blavaan'
bayesfactor_restricted(
  posterior,
  hypothesis,
  prior = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'emmGrid'
bayesfactor_restricted(
  posterior,
  hypothesis,
  prior = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'matrix'
bayesfactor_restricted(
  posterior,
  hypothesis,
  prior = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'data.frame'
bayesfactor_restricted(
  posterior,
  hypothesis,
  prior = NULL,
  rvar_col = NULL,
  ...
)
```

Arguments

posterior	A stanreg / brmsfit object, emmGrid or a data frame - representing a posterior distribution(s) from (see Details).
...	Currently not used.

`hypothesis` A character vector specifying the restrictions as logical conditions (see examples below).

`prior` An object representing a prior distribution (see Details).

`verbose` Toggle off warnings.

`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.

`component` Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

`rvar_col` A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.

Details

This method is used to compute Bayes factors for order-restricted models vs un-restricted models by setting an order restriction on the prior and posterior distributions (*Morey & Wagenmakers, 2013*).

(Though it is possible to use `bayesfactor_restricted()` to test interval restrictions, it is more suitable for testing order restrictions; see examples).

Additional methods:

The resulting output is supported by the following methods:

- `as.matrix()`: Extract a full matrix of (log-)Bayes factors between all models (using the transitivity of Bayes factors).
- `as.logical()`: Extract boolean vectors indicating which (prior/posterior) samples are included in the hypothesized restriction.

- `as.numeric()`: Extract the (possibly log-)Bayes factor values.

See examples and bayesfactor_methods.

Value

A data frame containing the (log) Bayes factor representing evidence *against* the un-restricted model (Use `as.numeric()` to extract the non-log Bayes factors; see examples). (A `bool_results` attribute contains the results for each sample, indicating if they are included or not in the hypothesized restriction.)

Obtaining prior samples

It is important to provide the correct `prior` for meaningful results, to match the `posterior`-type input:

- **A numeric vector** - `prior` should also be a *numeric vector*, representing the prior-distribution
- **A data frame** - `prior` should also be a *data frame*, representing the prior-estimates, in matching column order.
  - If `rvar_col` is specified, `prior` should be *the name of an* `rvar` *column* that represents the prior-estimates.
- **Supported Bayesian model (`stanreg`, `brmsfit`, etc.)**
  - `prior` should be *a model an equivalent model with MCMC samples from the priors* **only**. See `unupdate()`.
  - If `prior` is set to `NULL`, `unupdate()` is called internally (not supported for `brmsfit_multiple` model).
- **Output from a `{marginaleffects}` function** - `prior` should also be *an equivalent output* from a `{marginaleffects}` function based on a prior-model (See `unupdate()`).
- **Output from an `{emmeans}` function**
  - `prior` should also be *an equivalent output* from an `{emmeans}` function based on a prior-model (See `unupdate()`).
  - `prior` can also be *the original (posterior) model*, in which case the function will try to "unupdate" the estimates (not supported if the estimates have undergone any transformations – `"log"`, `"response"`, etc. – or any `regriding`).

Transitivity of Bayes factors

For multiple inputs (models or hypotheses), the function will return multiple Bayes factors between each model and *the same* reference model (the `denominator` or un-restricted model). However, we can take advantage of the transitivity of Bayes factors - where if we have two Bayes factors for Model *A* and model *B* against the *same reference model C*, we can obtain a Bayes factor for comparing model *A* to model *B* by dividing them:

$$BF_{AB} = \frac{BF_{AC}}{BF_{BC}} = \frac{\frac{ML_A}{ML_C}}{\frac{ML_B}{ML_C}} = \frac{ML_A}{ML_B}$$

(Where *ML* is the *marginal likelihood*.)

A full matrix comparing all models can be obtained with `as.matrix()`.

Interpreting Bayes Factors

A Bayes factor greater than 1 can be interpreted as evidence against the null, at which one convention is that a Bayes factor greater than 3 can be considered as "substantial" evidence against the null (and vice versa, a Bayes factor smaller than 1/3 indicates substantial evidence in favor of the null-model). See also `effectsize::interpret_bf()`.

References

- Morey, R. D., & Wagenmakers, E. J. (2014). Simple relation between Bayesian order-restricted and point-null hypothesis tests. Statistics & Probability Letters, 92, 121-124.
- Morey, R. D., & Rouder, J. N. (2011). Bayes factor approaches for testing interval null hypotheses. Psychological methods, 16(4), 406.
- Morey, R. D. (Jan, 2015). Multiple Comparisons with BayesFactor, Part 2 – order restrictions. Retrieved from https://richarddmorey.org/category/order-restrictions/.

See Also

Other Bayes factors: `bayesfactor_inclusion()`, `bayesfactor_models()`, `bayesfactor_parameters()`

Examples

```
set.seed(444)
library(bayestestR)
prior <- data.frame(
  A = rnorm(500),
  B = rnorm(500),
  C = rnorm(500)
)

posterior <- data.frame(
  A = rnorm(500, .4, 0.7),
  B = rnorm(500, -.2, 0.4),
  C = rnorm(500, 0, 0.5)
)

hyps <- c(
  "A > B & B > C",
  "A > B & A > C",
  "C > A"
)


(b <- bayesfactor_restricted(posterior, hypothesis = hyps, prior = prior))

# See the matrix of BFs
as.matrix(b)
```

```
bool <- as.logical(b, which = "posterior")
head(bool)



see::plots(
  plot(estimate_density(posterior)),
  # distribution **conditional** on the restrictions
  plot(estimate_density(posterior[bool[, hyps[1]], ])) + ggplot2::ggtitle(hyps[1]),
  plot(estimate_density(posterior[bool[, hyps[2]], ])) + ggplot2::ggtitle(hyps[2]),
  plot(estimate_density(posterior[bool[, hyps[3]], ])) + ggplot2::ggtitle(hyps[3]),
  guides = "collect"
)



# rstanarm models
# ---------------
data("mtcars")

fit_stan <- rstanarm::stan_glm(mpg ~ wt + cyl + am,
  data = mtcars, refresh = 0
)
hyps <- c(
  "am > 0 & cyl < 0",
  "cyl < 0",
  "wt - cyl > 0"
)

bayesfactor_restricted(fit_stan, hypothesis = hyps)




# emmGrid objects
# ---------------
# replicating http://bayesfactor.blogspot.com/2015/01/multiple-comparisons-with-bayesfactor-2.html
data("disgust")
contrasts(disgust$condition) <- contr.equalprior_pairs # see vignette
fit_model <- rstanarm::stan_glm(score ~ condition, data = disgust, family = gaussian())

em_condition <- emmeans::emmeans(fit_model, ~condition, data = disgust)
hyps <- c("lemon < control & control < sulfur")

bayesfactor_restricted(em_condition, prior = fit_model, hypothesis = hyps)
# > # Bayes Factor (Order-Restriction)
# >
# >                           Hypothesis P(Prior) P(Posterior)   BF
# >  lemon < control & control < sulfur     0.17         0.75 4.49
# > ---
# > Bayes factors for the restricted model vs. the un-restricted model.
```

bci *Bias Corrected and Accelerated Interval (BCa)*

Description

Compute the **Bias Corrected and Accelerated Interval (BCa)** of posterior distributions.

Usage

```
bci(x, ...)

bcai(x, ...)

## S3 method for class 'numeric'
bci(x, ci = 0.95, verbose = TRUE, ...)

## S3 method for class 'data.frame'
bci(x, ci = 0.95, rvar_col = NULL, verbose = TRUE, ...)

## S3 method for class 'brmsfit'
bci(
  x,
  ci = 0.95,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'get_predicted'
bci(x, ci = 0.95, use_iterations = FALSE, verbose = TRUE, ...)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model. **bayestestR** supports a wide range of models (see, for example, `methods("hdi")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` or `.data.frame`methods.
...	Currently not used.
ci	Value or vector of probability of the (credible) interval - CI (between 0 and 1) to be estimated. Default to `.95` (95%).
verbose	Toggle off warnings.

`rvar_col` A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.

`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.

`component` Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

`parameters` Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like `lp__` or `prior_`) are filtered by default, so only parameters that typically appear in the `summary()` are returned. Use `parameters` to select specific parameters for the output.

`use_iterations` Logical, if `TRUE` and `x` is a `get_predicted` object, (returned by `insight::get_predicted()`), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., `brmsfit` models).

Details

Unlike equal-tailed intervals (see `eti()`) that typically exclude 2.5% from each tail of the distribution and always include the median, the HDI is *not* equal-tailed and therefore always includes the mode(s) of posterior distributions. While this can be useful to better represent the credibility mass of a distribution, the HDI also has some limitations. See `spi()` for details.

A 95% equal-tailed interval (ETI) has 2.5% of the distribution on either side of its limits. It indicates the 2.5th percentile and the 97.5th percentile. In symmetric distributions, the two methods of computing credible intervals, the ETI and the HDI, return similar results.

This is not the case for skewed distributions. Indeed, it is possible that parameter values in the ETI have lower credibility (are less probable) than parameter values outside the ETI. This property seems undesirable as a summary of the credible values in a distribution.

On the other hand, the ETI range does change when transformations are applied to the distribution (for instance, for a log odds scale to probabilities): the lower and higher bounds of the transformed distribution will correspond to the transformed lower and higher bounds of the original distribution. On the contrary, applying transformations to the distribution will change the resulting HDI.

The 95% or 89% Credible Intervals (CI) are two reasonable ranges to characterize the uncertainty related to the estimation (see here for a discussion about the differences between these two values).

Value

A data frame with following columns:

- `Parameter` The model parameter(s), if `x` is a model-object. If `x` is a vector, this column is missing.
- `CI` The probability of the credible interval.
- `CI_low`, `CI_high` The lower and upper credible interval limits for the parameters.

Draws-only approximation

Classical bootstrap BCa intervals use the original estimate (`t0`) for the bias correction and empirical influence or jackknife values for the acceleration. These quantities are not available when `x` contains only draws. In that case, `bci()` uses the mean of the draws as the reference estimate and one sixth of their standardized third moment as the acceleration. The resulting interval is therefore an approximation and can differ from `boot::boot.ci()`, which has access to `t0` and the original data.

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.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, or `smooth_terms` (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.

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. See also `?insight::find_parameters`.

References

DiCiccio, T. J. and B. Efron. (1996). Bootstrap Confidence Intervals. Statistical Science. 11(3): 189–212. 10.1214/ss/1032280214

See Also

Other ci: `ci()`, `eti()`, `hdi()`, `si()`, `spi()`

Examples

```
posterior <- rnorm(1000)
bci(posterior)
bci(posterior, ci = c(0.80, 0.89, 0.95))
```

`bic_to_bf` *Convert BIC indices to Bayes Factors via the BIC-approximation method.*

Description

The difference between two Bayesian information criterion (BIC) indices of two models can be used to approximate Bayes factors via:

$$BF_{10} = e^{(BIC_0 - BIC_1)/2}$$

Usage

```
bic_to_bf(bic, denominator, log = FALSE)
```

Arguments

`bic`	A vector of BIC values.
`denominator`	The BIC value to use as a denominator (to test against).
`log`	If `TRUE`, return the `log(BF)`.

Value

The Bayes Factors corresponding to the BIC values against the denominator.

References

Wagenmakers, E. J. (2007). A practical solution to the pervasive problems of p values. Psychonomic bulletin & review, 14(5), 779-804

Examples

```
bic1 <- BIC(lm(Sepal.Length ~ 1, data = iris))
bic2 <- BIC(lm(Sepal.Length ~ Species, data = iris))
bic3 <- BIC(lm(Sepal.Length ~ Species + Petal.Length, data = iris))
bic4 <- BIC(lm(Sepal.Length ~ Species * Petal.Length, data = iris))

bic_to_bf(c(bic1, bic2, bic3, bic4), denominator = bic1)
```

---

check_prior *Check if Prior is Informative*

Description

Performs a simple test to check whether the prior is informative to the posterior. This idea, and the accompanying heuristics, were discussed in *Gelman et al. 2017*. For a visual check of the prior predictive distribution, see `performance::check_priors()`.

Usage

```
check_prior(model, method = "gelman", simulate_priors = TRUE, ...)

## S3 method for class 'brmsfit'
check_prior(
  model,
  method = "gelman",
  simulate_priors = TRUE,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

`model`	A `stanreg`, `stanfit`, `brmsfit`, `blavaan`, or `MCMCglmm` object.
`method`	Can be `"gelman"` or `"lakeland"`. For the `"gelman"` method, if the SD of the posterior is more than 0.1 times the SD of the prior, then the prior is considered as informative. For the `"lakeland"` method, the prior is considered as informative if the posterior falls within the 95% HDI of the prior.
`simulate_priors`	Should prior distributions be simulated using `simulate_prior()` (default; faster) or sampled via `unupdate()` (slower, more accurate).
`...`	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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

verbose — Toggle off warnings.

Value

A data frame with two columns: The parameter names and the quality of the prior (which might be "informative", "uninformative") or "not determinable" if the prior distribution could not be determined).

References

Gelman, A., Simpson, D., and Betancourt, M. (2017). The Prior Can Often Only Be Understood in the Context of the Likelihood. Entropy, 19(10), 555. doi:10.3390/e19100555

See Also

performance::check_priors()

Examples

```
library(bayestestR)
```

```
model <- rstanarm::stan_glm(mpg ~ wt + am, data = mtcars, chains = 1, refresh = 0)
check_prior(model, method = "gelman")
check_prior(model, method = "lakeland")

# An extreme example where both methods diverge:
model <- rstanarm::stan_glm(mpg ~ wt,
  data = mtcars[1:3, ],
  prior = normal(-3.3, 1, FALSE),
  prior_intercept = normal(0, 1000, FALSE),
  refresh = 0
)
check_prior(model, method = "gelman")
check_prior(model, method = "lakeland")
# can provide visual confirmation to the Lakeland method
plot(si(model, verbose = FALSE))
```

---

ci *Confidence/Credible/Compatibility Interval (CI)*

Description

Compute Confidence/Credible/Compatibility Intervals (CI) or Support Intervals (SI) for Bayesian and frequentist models. The Documentation is accessible for:

Usage

```
ci(x, ...)

## S3 method for class 'numeric'
ci(x, ci = 0.95, method = "ETI", verbose = TRUE, BF = 1, ...)

## S3 method for class 'data.frame'
ci(x, ci = 0.95, method = "ETI", BF = 1, rvar_col = NULL, verbose = TRUE, ...)

## S3 method for class 'brmsfit'
ci(
  x,
  ci = 0.95,
  method = "ETI",
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  BF = 1,
  ...
)
```

Arguments

x	A stanreg or brmsfit model, or a vector representing a posterior distribution.
...	Currently not used.
ci	Value or vector of probability of the CI (between 0 and 1) to be estimated. Default to 0.95 (95%).
method	Can be "ETI" (default), "HDI", "BCI", "SPI" or "SI".
verbose	Toggle off warnings.
BF	The amount of support required to be included in the support interval.
rvar_col	A single character - the name of an rvar column in the data frame to be processed. See example in p_direction().
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.
component	Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.
parameters	Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

Details

- Bayesian models
- Frequentist models

Value

A data frame with following columns:

- `Parameter` The model parameter(s), if `x` is a model-object. If `x` is a vector, this column is missing.
- `CI` The probability of the credible interval.
- `CI_low`, `CI_high` The lower and upper credible interval limits for the 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.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, or `smooth_terms` (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.

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. See also `?insight::find_parameters`.

Note

When it comes to interpretation, we recommend thinking of the CI in terms of an "uncertainty" or "compatibility" interval, the latter being defined as "Given any value in the interval and the background assumptions, the data should not seem very surprising" (*Gelman & Greenland 2019*).

There is also a `plot()`-method implemented in the **see**-package.

References

Gelman A, Greenland S. Are confidence intervals better termed "uncertainty intervals"? BMJ 2019;l5381. 10.1136/bmj.l5381

See Also

Other ci: `bci()`, `eti()`, `hdi()`, `si()`, `spi()`

Examples

```
library(bayestestR)

posterior <- rnorm(1000)
ci(posterior, method = "ETI")
ci(posterior, method = "HDI")

df <- data.frame(replicate(4, rnorm(100)))
ci(df, method = "ETI", ci = c(0.80, 0.89, 0.95))
ci(df, method = "HDI", ci = c(0.80, 0.89, 0.95))

model <- suppressWarnings(rstanarm::stan_glm(
  mpg ~ wt,
  data = mtcars, chains = 2, iter = 200, refresh = 0
))
ci(model, method = "ETI", ci = c(0.80, 0.89, 0.95))
ci(model, method = "HDI", ci = c(0.80, 0.89, 0.95))


bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
ci(bf, method = "ETI")
ci(bf, method = "HDI")


model <- emmeans::emtrends(model, ~1, "wt", data = mtcars)
ci(model, method = "ETI")
ci(model, method = "HDI")
```

---

contr.equalprior *Contrast Matrices for Equal Marginal Priors in Bayesian Estimation*

Description

Build contrasts for factors with equal marginal priors on all levels. The 3 functions give the same orthogonal contrasts, but are scaled differently to allow different prior specifications (see 'Details'). Implementation from Singmann & Gronau's bfrms, following the description in Rouder, Morey, Speckman, & Province (2012, p. 363).

Usage

```
contr.equalprior(n, contrasts = TRUE, sparse = FALSE)

contr.equalprior_pairs(n, contrasts = TRUE, sparse = FALSE)

contr.equalprior_deviations(n, contrasts = TRUE, sparse = FALSE)
```

Arguments

n	a vector of levels for a factor, or the number of levels.
contrasts	a logical indicating whether contrasts should be computed.
sparse	Logical, indicating if the result should be sparse (of class Matrix::dgCMatrix), using package **Matrix**.

Details

When using stats::contr.treatment, each dummy variable is the difference between each level and the reference level. While this is useful if setting different priors for each coefficient, it should not be used if one is trying to set a general prior for differences between means, as it (as well as stats::contr.sum and others) results in unequal marginal priors on the means the the difference between them.

```
library(brms)

data <- data.frame(
  group = factor(rep(LETTERS[1:4], each = 3)),
  y = rnorm(12)
)

contrasts(data$group) # R's default contr.treatment
#>   B C D
#> A 0 0 0
#> B 1 0 0
#> C 0 1 0
#> D 0 0 1

model_prior <- brm(
  y ~ group, data = data,
  sample_prior = "only",
  # Set the same priors on the 3 dummy variable
  # (Using an arbitrary scale)
  prior = set_prior("normal(0, 10)", coef = c("groupB", "groupC", "groupD"))
)

est <- emmeans::emmeans(model_prior, pairwise ~ group)

point_estimate(est, centr = "mean", disp = TRUE)
#> Point Estimate
#>
#> Parameter |  Mean |    SD
#> ------------------------
#> A         | -0.01 |  6.35
#> B         | -0.10 |  9.59
#> C         |  0.11 |  9.55
#> D         | -0.16 |  9.52
#> A - B     |  0.10 |  9.94
```

```
#> A - C     | -0.12 |  9.96
#> A - D     |  0.15 |  9.87
#> B - C     | -0.22 | 14.38
#> B - D     |  0.05 | 14.14
#> C - D     |  0.27 | 14.00
```

We can see that the priors for means aren't all the same (A having a more narrow prior), and likewise for the pairwise differences (priors for differences from A are more narrow).

The solution is to use one of the methods provided here, which *do* result in marginally equal priors on means differences between them. Though this will obscure the interpretation of parameters, setting equal priors on means and differences is important for they are useful for specifying equal priors on all means in a factor and their differences correct estimation of Bayes factors for contrasts and order restrictions of multi-level factors (where k>2). See info on specifying correct priors for factors with more than 2 levels in the Bayes factors vignette.

NOTE: When setting priors on these dummy variables, always:

1. Use priors that are **centered on 0**! Other location/centered priors are meaningless!
2. Use **identically-scaled priors** on all the dummy variables of a single factor!

`contr.equalprior` returns the original orthogonal-normal contrasts as described in Rouder, Morey, Speckman, & Province (2012, p. 363). Setting `contrasts = FALSE` returns the $I_n - \frac{1}{n}$ matrix.

`contr.equalprior_pairs`**:**

Useful for setting priors in terms of pairwise differences between means - the scales of the priors defines the prior distribution of the pair-wise differences between all pairwise differences (e.g., A - B, B - C, etc.).

```
contrasts(data$group) <- contr.equalprior_pairs
contrasts(data$group)
#>         [,1]       [,2]       [,3]
#> A  0.0000000  0.6123724  0.0000000
#> B -0.1893048 -0.2041241  0.5454329
#> C -0.3777063 -0.2041241 -0.4366592
#> D  0.5670111 -0.2041241 -0.1087736

model_prior <- brm(
  y ~ group, data = data,
  sample_prior = "only",
  # Set the same priors on the 3 dummy variable
  # (Using an arbitrary scale)
  prior = set_prior("normal(0, 10)", coef = c("group1", "group2", "group3"))
)

est <- emmeans(model_prior, pairwise ~ group)

point_estimate(est, centr = "mean", disp = TRUE)
#> Point Estimate
#>
#> Parameter |  Mean |    SD
```

```
#> -------------------------
#> A         | -0.31 |  7.46
#> B         | -0.24 |  7.47
#> C         | -0.34 |  7.50
#> D         | -0.30 |  7.25
#> A - B     | -0.08 | 10.00
#> A - C     |  0.03 | 10.03
#> A - D     | -0.01 |  9.85
#> B - C     |  0.10 | 10.28
#> B - D     |  0.06 |  9.94
#> C - D     | -0.04 | 10.18
```

All means have the same prior distribution, and the distribution of the differences matches the prior we set of "normal(0, 10)". Success!

contr.equalprior_deviations:

Useful for setting priors in terms of the deviations of each mean from the grand mean - the scales of the priors defines the prior distribution of the distance (above, below) the mean of one of the levels might have from the overall mean. (See examples.)

Value

A matrix with n rows and k columns, with k=n-1 if contrasts is TRUE and k=n if contrasts is FALSE.

References

Rouder, J. N., Morey, R. D., Speckman, P. L., & Province, J. M. (2012). Default Bayes factors for ANOVA designs. *Journal of Mathematical Psychology*, 56(5), 356-374. https://doi.org/10.1016/j.jmp.2012.08.001

Examples

```
contr.equalprior(2) # Q_2 in Rouder et al. (2012, p. 363)

contr.equalprior(5) # equivalent to Q_5 in Rouder et al. (2012, p. 363)

## check decomposition
Q3 <- contr.equalprior(3)
Q3 %*% t(Q3) ## 2/3 on diagonal and -1/3 on off-diagonal elements
```

---

convert_bayesian_as_frequentist

Convert (refit) a Bayesian model to frequentist

Description

Refit Bayesian model as frequentist. Can be useful for comparisons.

Usage

```
convert_bayesian_as_frequentist(model, data = NULL, REML = TRUE, resp = NULL)

bayesian_as_frequentist(model, data = NULL, REML = TRUE, resp = NULL)
```

Arguments

model	A Bayesian model.
data	Data used by the model. If NULL, will try to extract it from the model.
REML	For mixed effects, should models be estimated using restricted maximum likelihood (REML) (TRUE, default) or maximum likelihood (FALSE)?
resp	For multivariate *brms* models, the name of the one response to convert, as returned by names(insight::find_formula(model)). Other models ignore resp.

Details

Linear models from *BayesFactor* with random factors (see whichRandom in BayesFactor::lmBF()) are refit with lme4::lmer(). A random term with only factors, such as cyl:gear, becomes (1 | cyl:gear). A random term with a continuous variable, such as Days:Subject, becomes (0 + Days | Subject).

Examples

```
# Rstanarm ----------------------
# Simple regressions
model <- rstanarm::stan_glm(Sepal.Length ~ Species,
  data = iris, chains = 2, refresh = 0
)
bayesian_as_frequentist(model)

model <- rstanarm::stan_glm(vs ~ mpg,
  family = "binomial",
  data = mtcars, chains = 2, refresh = 0
)
bayesian_as_frequentist(model)

# Mixed models
model <- rstanarm::stan_glmer(
  Sepal.Length ~ Petal.Length + (1 | Species),
  data = iris, chains = 2, refresh = 0
)
bayesian_as_frequentist(model)

model <- rstanarm::stan_glmer(vs ~ mpg + (1 | cyl),
  family = "binomial",
  data = mtcars, chains = 2, refresh = 0
)
bayesian_as_frequentist(model)
```

density_at *Density Probability at a Given Value*

Description

Compute the density value at a given point of a distribution (i.e., the value of the y axis of a value x of a distribution).

Usage

```
density_at(posterior, x, precision = 2^10, method = "kernel", ...)
```

Arguments

posterior	Vector representing a posterior distribution.
x	The value of which to get the approximate probability.
precision	Number of points of density data. See the n parameter in density.
method	Density estimation method. Can be "kernel" (default), "logspline" or "KernSmooth".
...	Currently not used.

Examples

```
library(bayestestR)
posterior <- distribution_normal(n = 10)
density_at(posterior, 0)
density_at(posterior, c(0, 1))
```

describe_posterior *Describe Posterior Distributions*

Description

Compute indices relevant to describe and characterize the posterior distributions.

Usage

```
describe_posterior(posterior, ...)

## S3 method for class 'numeric'
describe_posterior(
  posterior,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "eti",
  test = c("p_direction", "rope"),
  rope_range = "default",
  rope_ci = 0.95,
  keep_iterations = FALSE,
  bf_prior = NULL,
  BF = 1,
  verbose = TRUE,
  ...
)

## S3 method for class 'data.frame'
describe_posterior(
  posterior,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "eti",
  test = c("p_direction", "rope"),
  rope_range = "default",
  rope_ci = 0.95,
  keep_iterations = FALSE,
  bf_prior = NULL,
  BF = 1,
  rvar_col = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'stanreg'
describe_posterior(
  posterior,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "eti",
  test = c("p_direction", "rope"),
  rope_range = "default",
  rope_ci = 0.95,
```

```
  keep_iterations = FALSE,
  bf_prior = NULL,
  diagnostic = c("ESS", "Rhat"),
  priors = FALSE,
  effects = "fixed",
  component = "location",
  parameters = NULL,
  BF = 1,
  verbose = TRUE,
  ...
)
```

Arguments

posterior	A vector, data frame or model of posterior draws. **bayestestR** supports a wide range of models (see `methods("describe_posterior")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` method.
...	Additional arguments to be passed to or from methods.
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: `"median"`, `"mean"`, `"MAP"` (see `map_estimate()`), `"trimmed"` (which is just `mean(x, trim = threshold)`), `"mode"` or `"all"`.
dispersion	Logical, if `TRUE`, computes indices of dispersion related to the estimate(s) (`SD` and `MAD` for `mean` and `median`, respectively). Dispersion is not available for `"MAP"` or `"mode"` centrality indices.
ci	Value or vector of probability of the CI (between 0 and 1) to be estimated. Default to `0.95` (95%).
ci_method	The type of index used for Credible Interval. Can be `"ETI"` (default, see `eti()`), `"HDI"` (see `hdi()`), `"BCI"` (see `bci()`), `"SPI"` (see `spi()`), or `"SI"` (see `si()`).
test	The indices of effect existence to compute. Character (vector) or list with one or more of these options: `"p_direction"` (or `"pd"`), `"rope"`, `"p_map"`, `"p_significance"` (or `"ps"`), `"p_rope"`, `"equivalence_test"` (or `"equitest"`), `"bayesfactor"` (or `"bf"`) or `"all"` to compute all tests. For each "test", the corresponding **bayestestR** function is called (e.g. `rope()` or `p_direction()`) and its results included in the summary output.
rope_range	ROPE's lower and higher bounds. Should be a vector of two values (e.g., `c(-0.1, 0.1)`), `"default"` or a list of numeric vectors of the same length as numbers of parameters. If `"default"`, the bounds are set to `x +- 0.1*SD(response)`.
rope_ci	The Credible Interval (CI) probability, corresponding to the proportion of HDI, to use for the percentage in ROPE.
keep_iterations	If `TRUE`, will keep all iterations (draws) of bootstrapped or Bayesian models. They will be added as additional columns named `iter_1, iter_2, ...`. You can reshape them to a long format by running `reshape_iterations()`.
bf_prior	Distribution representing a prior for the computation of Bayes factors / SI. Used if the input is a posterior, otherwise (in the case of models) ignored.

BF — The amount of support required to be included in the support interval.

verbose — Toggle off warnings.

rvar_col — A single character - the name of an rvar column in the data frame to be processed. See example in p_direction().

diagnostic — Diagnostic metrics to compute. Character (vector) or list with one or more of these options: "ESS", "ESS_bulk", "Rhat", "MCSE" or "all". "ESS" returns the **tail-ESS** (the minimum of the effective sample sizes for the 5% and 95% quantiles), which is the most relevant diagnostic for assessing the reliability of credible intervals and other tail-based quantities. "ESS_bulk" additionally returns the **bulk-ESS** (the effective sample size for the bulk of the posterior, useful for assessing the reliability of central tendency estimates such as the mean or median). "all" includes both tail and bulk "ESS", "Rhat", and "MCSE".

priors — Add the prior used for each parameter.

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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

Details

One or more components of point estimates (like posterior mean or median), intervals and tests can be omitted from the summary output by setting the related argument to `NULL`. For example, `test = NULL` and `centrality = NULL` would only return the HDI (or CI).

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.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, or `smooth_terms` (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.

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. See also `?insight::find_parameters`.

References

- Makowski, D., Ben-Shachar, M. S., Chen, S. H. A., and Lüdecke, D. (2019). *Indices of Effect Existence and Significance in the Bayesian Framework*. Frontiers in Psychology 2019;10:2767. doi:10.3389/fpsyg.2019.02767
- Region of Practical Equivalence (ROPE)
- Bayes factors

Examples

```
library(bayestestR)

x <- rnorm(1000)
describe_posterior(x, verbose = FALSE)
describe_posterior(x,
  centrality = "all",
  dispersion = TRUE,
  test = "all",
  verbose = FALSE
)
describe_posterior(x, ci = c(0.80, 0.90), verbose = FALSE)
```

```
df <- data.frame(replicate(4, rnorm(100)))
describe_posterior(df, verbose = FALSE)
describe_posterior(
  df,
  centrality = "all",
  dispersion = TRUE,
  test = "all",
  verbose = FALSE
)
describe_posterior(df, ci = c(0.80, 0.90), verbose = FALSE)

df <- data.frame(replicate(4, rnorm(20)))
head(reshape_iterations(
  describe_posterior(df, keep_iterations = TRUE, verbose = FALSE)
))


# rstanarm models
# ---------------------------------------------
model <- suppressWarnings(
  rstanarm::stan_glm(
    mpg ~ wt + gear,
    data = mtcars, chains = 2, iter = 200,
    refresh = 0
  )
)
describe_posterior(model)
describe_posterior(model, centrality = "all", dispersion = TRUE, test = "all")
describe_posterior(model, ci = c(0.80, 0.90))
describe_posterior(model, rope_range = list(c(-10, 5), c(-0.2, 0.2), "default"))

# emmeans estimates
# ---------------------------------------------
describe_posterior(emmeans::emtrends(model, ~1, "wt"))

# BayesFactor objects
# ---------------------------------------------
bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
describe_posterior(bf)
describe_posterior(bf, centrality = "all", dispersion = TRUE, test = "all")
describe_posterior(bf, ci = c(0.80, 0.90))
```

`describe_prior` *Describe Priors*

Description

Returns a summary of the priors used in the model.

Usage

```
describe_prior(model, ...)

## S3 method for class 'brmsfit'
describe_prior(model, parameters = NULL, ...)
```

Arguments

model	A Bayesian model.
...	Currently not used.
parameters	Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

Examples

```
library(bayestestR)

# rstanarm models
# ---------------------------------------------
if (require("rstanarm")) {
  model <- rstanarm::stan_glm(mpg ~ wt + cyl, data = mtcars)
  describe_prior(model)
}

# brms models
# ---------------------------------------------
if (require("brms")) {
  model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
  describe_prior(model)
}

# BayesFactor objects
# ---------------------------------------------
if (require("BayesFactor")) {
  bf <- ttestBF(x = rnorm(100, 1, 1))
  describe_prior(bf)
}
```

---

diagnostic_draws *Diagnostic values for each iteration*

Description

Returns the accumulated log-posterior, the average Metropolis acceptance rate, divergent transitions, treedepth rather than terminated its evolution normally.

Usage

```
diagnostic_draws(posterior, ...)
```

Arguments

posterior	A stanreg, stanfit, brmsfit, or blavaan object; a list of data frames or matrices representing MCMC chains (rows as samples, columns as parameters); or a 3D array (dimensions: samples, chains, parameters)
...	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)).

Examples

```
set.seed(333)

if (require("brms", quietly = TRUE)) {
  model <- suppressWarnings(brm(mpg ~ wt * cyl * vs,
    data = mtcars,
    iter = 100, control = list(adapt_delta = 0.80),
    refresh = 0
  ))
  diagnostic_draws(model)
}
```

---

diagnostic_posterior *Posteriors Sampling Diagnostic*

Description

Extract diagnostic metrics (Effective Sample Size (ESS), Rhat and Monte Carlo Standard Error MCSE).

Usage

```
diagnostic_posterior(posterior, ...)

## Default S3 method:
diagnostic_posterior(posterior, diagnostic = "all", ...)

## S3 method for class 'stanreg'
diagnostic_posterior(
  posterior,
  diagnostic = "all",
  effects = "fixed",
```

```
  component = "location",
  parameters = NULL,
  centrality = "median",
  ...
)
```

Arguments

posterior	A stanreg, stanfit, brmsfit, or blavaan object; a list of data frames or matrices representing MCMC chains (rows as samples, columns as parameters); or a 3D array (dimensions: samples, chains, parameters)
...	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)).
diagnostic	Diagnostic metrics to compute. Character (vector) or list with one or more of these options: "ESS", "ESS_bulk", "Rhat", "MCSE" or "all". "ESS" returns the **tail-ESS** (the minimum of the effective sample sizes for the 5% and 95% quantiles), which is the most relevant diagnostic for assessing the reliability of credible intervals and other tail-based quantities. "ESS_bulk" additionally returns the **bulk-ESS** (the effective sample size for the bulk of the posterior, useful for assessing the reliability of central tendency estimates such as the mean or median). "all" includes both tail and bulk "ESS", "Rhat", and "MCSE".
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.
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.

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

centrality — The point-estimate (centrality index) for which to compute the MCSE. Can be "median" (default) or "mean". To not break other functions like describe_posterior() or diagnostic_posterior(), all other values are silently converted to "median".

Details

Effective Sample (ESS) should be as large as possible, although for most applications, an effective sample size greater than 1000 is sufficient for stable estimates (*Bürkner, 2017*). The ESS returned by diagnostic_posterior() is the **tail-ESS**: it corresponds to the minimum of the effective sample sizes for the 5% and 95% quantiles, and is a diagnostic for the sampling efficiency in the tails of the posterior distribution. It is more relevant than the bulk-ESS for assessing the reliability of credible intervals, probabilities of direction, and other tail-based quantities. Note that the tail-ESS may differ from the ESS reported by brms (Bulk_ESS) or other tools; use "ESS_bulk" to also retrieve the bulk-ESS.

Rhat should be the closest to 1. It should not be larger than 1.1 (*Gelman and Rubin, 1992*) or 1.01 (*Vehtari et al., 2019*). The split Rhat statistic quantifies the consistency of an ensemble of Markov chains.

Monte Carlo Standard Error (MCSE) is another measure of accuracy of the chains. It is defined as standard deviation of the chains divided by their effective sample size (the formula for mcse() is from Kruschke 2015, p. 187). The MCSE "provides a quantitative suggestion of how big the estimation noise is".

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.
- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

References

- Gelman, A., & Rubin, D. B. (1992). Inference from iterative simulation using multiple sequences. Statistical science, 7(4), 457-472.
- Vehtari, A., Gelman, A., Simpson, D., Carpenter, B., and Bürkner, P. C. (2019). Rank-normalization, folding, and localization: An improved Rhat for assessing convergence of MCMC. arXiv preprint arXiv:1903.08008.
- Kruschke, J. (2014). Doing Bayesian data analysis: A tutorial with R, JAGS, and Stan. Academic Press.

Examples

```
# rstanarm models
# -----------------------------------------------
model <- suppressWarnings(
  rstanarm::stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
)
diagnostic_posterior(model)

# brms models
# -----------------------------------------------
model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
diagnostic_posterior(model)



set.seed(101)
mkdata <- function(nrow = 1000, ncol = 2, parnm = LETTERS[1:ncol]) {
  x <- as.data.frame(replicate(ncol, rnorm(nrow)))
  names(x) <- parnm
  x
}
dd <- replicate(5, mkdata(), simplify = FALSE)
diagnostic_posterior(dd)
```

---

disgust *Moral Disgust Judgment*

Description

A sample (simulated) dataset, used in tests and some examples.

Format

A data frame with 500 rows and 5 variables:

score Score on the questionnaire, which ranges from 0 to 50 with higher scores representing harsher moral judgment

condition one of three conditions, differing by the odor present in the room: a pleasant scent associated with cleanliness (lemon), a disgusting scent (sulfur), and a control condition in which no unusual odor is present

```
data("disgust")
head(disgust, n = 5)
#>   score condition
#> 1    13   control
#> 2    26   control
#> 3    30   control
#> 4    23   control
#> 5    34   control
```

Author(s)

Richard D. Morey

`display.describe_posterior`

Print tables in different output formats

Description

Prints tables (i.e. data frame) in different output formats.

Usage

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

## S3 method for class 'describe_posterior'
print(x, digits = 2, caption = "Summary of Posterior Distribution", ...)

## S3 method for class 'describe_posterior'
print_html(x, digits = 2, caption = "Summary of Posterior Distribution", ...)

## S3 method for class 'describe_posterior'
print_md(x, digits = 2, caption = "Summary of Posterior Distribution", ...)
```

Arguments

`object`, `x`	An object returned by one of the package's function, for example `describe_posterior()`, `point_estimate()`, or `eti()`.
`format`	String, indicating the output format. Can be `"markdown"` `"html"`, or `"tt"`. `format = "tt"` creates a `tinytable` object, which is either printed as markdown or HTML table, depending on the environment. See `insight::export_table()` for details.

...	Arguments passed down to print_html() or print_md() (e.g., digits), or to insight::export_table().
digits	Integer, number of digits to round the table output. Defaults to 2.
caption	Character, caption for the table. If NULL, no caption is added. By default, a caption is created based on the object type.

Details

display() is useful when the table-output from functions, which is usually printed as formatted text-table to console, should be formatted for pretty table-rendering in markdown documents, or if knitted from rmarkdown to PDF or Word files. See vignette for examples.

Value

If format = "markdown", the return value will be a character vector in markdown-table format. If format = "html", an object of class gt_tbl. If format = "tt", an object of class tinytable.

Examples

```
d <- data.frame(replicate(4, rnorm(20)))
result <- describe_posterior(d)

# markdown format
display(result)

# gt HTML
display(result, format = "html")

# tinytable
display(result, format = "tt")
```

---

distribution *Empirical Distributions*

Description

Generate a sequence of n-quantiles, i.e., a sample of size n with a near-perfect distribution.

Usage

```
distribution(type = "normal", ...)

distribution_custom(n, type = "norm", ..., random = FALSE)

distribution_beta(n, shape1, shape2, ncp = 0, random = FALSE, ...)
```

```
distribution_binomial(n, size = 1, prob = 0.5, random = FALSE, ...)

distribution_binom(n, size = 1, prob = 0.5, random = FALSE, ...)

distribution_cauchy(n, location = 0, scale = 1, random = FALSE, ...)

distribution_chisquared(n, df, ncp = 0, random = FALSE, ...)

distribution_chisq(n, df, ncp = 0, random = FALSE, ...)

distribution_gamma(n, shape, scale = 1, random = FALSE, ...)

distribution_mixture_normal(n, mean = c(-3, 3), sd = 1, random = FALSE, ...)

distribution_normal(n, mean = 0, sd = 1, random = FALSE, ...)

distribution_gaussian(n, mean = 0, sd = 1, random = FALSE, ...)

distribution_nbinom(n, size, prob, mu, phi, random = FALSE, ...)

distribution_poisson(n, lambda = 1, random = FALSE, ...)

distribution_student(n, df, ncp, random = FALSE, ...)

distribution_t(n, df, ncp, random = FALSE, ...)

distribution_student_t(n, df, ncp, random = FALSE, ...)

distribution_tweedie(n, xi = NULL, mu, phi, power = NULL, random = FALSE, ...)

distribution_uniform(n, min = 0, max = 1, random = FALSE, ...)
```

Arguments

type	Can be any of the names from base R's Distributions, like "cauchy", "pois" or "beta".
...	Arguments passed to or from other methods.
n	number of observations.
random	Generate near-perfect or random (simple wrappers for the base R r* functions) distributions. When random = FALSE, these function return q*(ppoints(n), ...).
shape1, shape2	non-negative parameters of the Beta distribution.
ncp	non-centrality parameter.
size	number of trials (zero or more).
prob	probability of success on each trial.
location, scale	location and scale parameters.

df	degrees of freedom (non-negative, but can be non-integer).
shape	Shape parameter.
mean	vector of means.
sd	vector of standard deviations.
mu	vector of mean μ.
phi	Corresponding to glmmTMB's implementation of nbinom distribution, where size=mu/phi.
lambda	vector of (non-negative) means.
xi	For tweedie distributions, the value of xi such that the variance is var(Y) = phi * mu^xi.
power	Alias for xi.
min, max	lower and upper limits of the distribution. Must be finite.

Examples

```
library(bayestestR)
x <- distribution(n = 10)
plot(density(x))

x <- distribution(type = "gamma", n = 100, shape = 2)
plot(density(x))
```

---

effective_sample *Effective Sample Size (ESS)*

Description

Effective Sample Size (ESS) is a measure of how much independent information there is in autocorrelated chains. It is used to assess the quality of MCMC samples. A higher ESS indicates more reliable estimates. For most applications, an effective sample size greater than 1,000 is sufficient for stable estimates (Bürkner, 2017). This function returns the effective sample size (ESS) for various Bayesian model objects. For brmsfit, stanreg, and stanfit objects, both **bulk-ESS** and **tail-ESS** are returned.

Usage

```
effective_sample(model, ...)

## S3 method for class 'brmsfit'
effective_sample(
  model,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  ...
)
```

Arguments

model	A stanreg, stanfit, brmsfit, blavaan, or MCMCglmm object.
...	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.
component	Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.
parameters	Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

Details

- **Effective Sample (ESS)** should be as large as possible, although for most applications, an effective sample size greater than 1,000 is sufficient for stable estimates (Bürkner, 2017). The ESS corresponds to the number of independent samples with the same estimation power as the N autocorrelated samples. It is is a measure of "how much independent information there is in autocorrelated chains" (*Kruschke 2015, p182-3*).
- **Bulk-ESS** is useful as a diagnostic for the sampling efficiency in the bulk of the posterior. It is defined as the effective sample size for rank normalized values using split chains. It can be interpreted as the reliability of indices of central tendency (mean, median, etc.).

- **Tail-ESS** is useful as a diagnostic for the sampling efficiency in the tails of the posterior. It is defined as the minimum of the effective sample sizes for 5% and 95% quantiles. It can be interpreted as the reliability of indices that depend on the tails of the distribution (e.g., credible intervals, tail probabilities, etc.).

Value

A data frame with columns for the parameter name, bulk ESS (`ESS`), and (where available) tail ESS (`ESS_tail`).

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.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, or `smooth_terms` (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.

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. See also `?insight::find_parameters`.

References

- Kruschke, J. (2014). Doing Bayesian data analysis: A tutorial with R, JAGS, and Stan. Academic Press.
- Bürkner, P. C. (2017). brms: An R package for Bayesian multilevel models using Stan. Journal of Statistical Software, 80(1), 1-28
- Vehtari, A., Gelman, A., Simpson, D., Carpenter, B., & Bürkner, P.-C. (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC. Bayesian Analysis, 16(2), 667-718.

Examples

```
model <- suppressWarnings(rstanarm::stan_glm(
  mpg ~ wt + gear,
  data = mtcars,
```

```
  chains = 2,
  iter = 200,
  refresh = 0
))
effective_sample(model)

model <- suppressWarnings(brms::brm(
  mpg ~ wt,
  data = mtcars,
  chains = 2,
  iter = 200,
  refresh = 0
))
effective_sample(model)
```

`equivalence_test` *Test for Practical Equivalence*

Description

Perform a **Test for Practical Equivalence** for Bayesian and frequentist models.

Usage

```
equivalence_test(x, ...)

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

## S3 method for class 'data.frame'
equivalence_test(
  x,
  range = "default",
  ci = 0.95,
  ci_method = "ETI",
  rvar_col = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'brmsfit'
equivalence_test(
  x,
  range = "default",
  ci = 0.95,
  ci_method = "ETI",
```

```
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

x	Vector representing a posterior distribution. Can also be a stanreg or brmsfit model.
...	Currently not used.
range	ROPE's lower and higher bounds. Should be "default" or depending on the number of outcome variables a vector or a list. For models with one response, range can be: • a vector of length two (e.g., c(-0.1, 0.1)), • a list of numeric vector of the same length as numbers of parameters (see 'Examples'). • a list of *named* numeric vectors, where names correspond to parameter names. In this case, all parameters that have no matching name in range will be set to "default". In multivariate models, range should be a list with another list (one for each response variable) of numeric vectors . Vector names should correspond to the name of the response variables. If "default" and input is a vector, the range is set to c(-0.1, 0.1). If "default" and input is a Bayesian model, rope_range() is used. See 'Examples'.
ci	The Credible Interval (CI) probability, corresponding to the proportion of HDI, to use for the percentage in ROPE.
ci_method	The type of interval to use to quantify the percentage in ROPE. Can be 'HDI' or 'ETI' (default). See ci().
rvar_col	A single character - the name of an rvar column in the data frame to be processed. See example in p_direction().
verbose	Toggle off warnings.
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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like `lp__` or `prior_`) are filtered by default, so only parameters that typically appear in the `summary()` are returned. Use `parameters` to select specific parameters for the output.

Details

Documentation is accessible for:

- Bayesian models
- Frequentist models

For Bayesian models, the **Test for Practical Equivalence** is based on the *"HDI+ROPE decision rule"* (*Kruschke, 2014, 2018*) to check whether parameter values should be accepted or rejected against an explicitly formulated "null hypothesis" (i.e., a ROPE). In other words, it checks the percentage of the 95% CI that is the null region (the ROPE). If this percentage is sufficiently low, the null hypothesis is rejected. If this percentage is sufficiently high, the null hypothesis is accepted.

Using the ROPE and the CI, *Kruschke (2018)* suggests using the percentage of the 95% CI that falls within the ROPE as a decision rule. If the CI is completely outside the ROPE, the "null hypothesis" for this parameter is "rejected". If the ROPE completely covers the CI, i.e., all most credible values of a parameter are inside the region of practical equivalence, the null hypothesis is accepted. Else, it is undecided whether to accept or reject the null hypothesis. If the full ROPE is used (i.e., 100% of the CI), then the null hypothesis is rejected or accepted if the percentage of the posterior within the ROPE is smaller than to 2.5% or greater than 97.5%. Desirable results are low proportions inside the ROPE (the closer to zero the better).

While Kruschke suggested using the 95% *HDI*, any CI can be used. Here we default to the 95% *ETI* (can be changed by setting the `ci_method` argument).

Some attention is required for finding suitable values for the ROPE limits (argument `range`). See 'Details' in `rope_range()` for further information.

Multicollinearity: Non-independent covariates

When parameters show strong correlations, i.e. when covariates are not independent, the joint parameter distributions may shift towards or away from the ROPE. In such cases, the test for practical equivalence may have inappropriate results. Collinearity invalidates ROPE and hypothesis

testing based on univariate marginals, as the probabilities are conditional on independence. Most problematic are the results of the "undecided" parameters, which may either move further towards "rejection" or away from it (*Kruschke 2014, 340f*).

`equivalence_test()` performs a simple check for pairwise correlations between parameters, but as there can be collinearity between more than two variables, a first step to check the assumptions of this hypothesis testing is to look at different pair plots. An even more sophisticated check is the projection predictive variable selection (*Piironen and Vehtari 2017*).

Value

A data frame with following columns:

- `Parameter` The model parameter(s), if `x` is a model-object. If `x` is a vector, this column is missing.
- `CI` The probability of the CI.
- `ROPE_low`, `ROPE_high` The limits of the ROPE. These values are identical for all parameters.
- `ROPE_Percentage` The proportion of the CI that lies inside the ROPE.
- `ROPE_Equivalence` The "test result", as character. Either "rejected", "accepted" or "undecided".
- `CI_low` , `CI_high` The lower and upper CI limits for the 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.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, or `smooth_terms` (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.

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. See also `?insight::find_parameters`.

Note

There is a `print()`-method with a `digits`-argument to control the amount of digits in the output, and there is a `plot()`-method to visualize the results from the equivalence-test (for models only).

References

- Kruschke, J. K. (2018). Rejecting or accepting parameter values in Bayesian estimation. Advances in Methods and Practices in Psychological Science, 1(2), 270-280. doi:10.1177/2515245918771304
- Kruschke, J. K. (2014). Doing Bayesian data analysis: A tutorial with R, JAGS, and Stan. Academic Press
- Piironen, J., & Vehtari, A. (2017). Comparison of Bayesian predictive methods for model selection. Statistics and Computing, 27(3), 711–735. doi:10.1007/s112220169649y

Examples

```
library(bayestestR)

equivalence_test(x = rnorm(1000, 0, 0.01), range = c(-0.1, 0.1))
equivalence_test(x = rnorm(1000, 0, 1), range = c(-0.1, 0.1))
equivalence_test(x = rnorm(1000, 1, 0.01), range = c(-0.1, 0.1))
equivalence_test(x = rnorm(1000, 1, 1), ci = c(.50, .99))

# print more digits
test <- equivalence_test(x = rnorm(1000, 1, 1), ci = c(.50, .99))
print(test, digits = 4)

model <- rstanarm::stan_glm(mpg ~ wt + cyl, data = mtcars, refresh = 0)
equivalence_test(model)
# multiple ROPE ranges - asymmetric, symmetric, default
equivalence_test(model, range = list(c(10, 40), c(-5, -4), "default"))
# named ROPE ranges
equivalence_test(model, range = list(wt = c(-5, -4), `(Intercept)` = c(10, 40)))

# plot result
test <- equivalence_test(model)
plot(test)

equivalence_test(emmeans::emtrends(model, ~1, "wt", data = mtcars))

model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
equivalence_test(model)

bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
# equivalence_test(bf)
```

`estimate_density` *Density Estimation*

Description

This function is a wrapper over different methods of density estimation. By default, it uses the base R `density` with by default uses a different smoothing bandwidth (`"SJ"`) from the legacy default implemented the base R `density` function (`"nrd0"`). However, Deng and Wickham suggest that `method = "KernSmooth"` is the fastest and the most accurate.

Usage

```
estimate_density(x, ...)

## S3 method for class 'data.frame'
estimate_density(
  x,
  method = "kernel",
  precision = 2^10,
  extend = FALSE,
  extend_scale = 0.1,
  bw = "SJ",
  ci = NULL,
  select = NULL,
  by = NULL,
  rvar_col = NULL,
  ...
)

## S3 method for class 'brmsfit'
estimate_density(
  x,
  method = "kernel",
  precision = 2^10,
  extend = FALSE,
  extend_scale = 0.1,
  bw = "SJ",
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  ...
)
```

Arguments

`x`	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model. **bayestestR** supports a wide range of models (see, for example, `methods("hdi")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` or `.data.frame`methods.
`...`	Currently not used.
`method`	Density estimation method. Can be `"kernel"` (default), `"logspline"` or `"KernSmooth"`.

`precision` Number of points of density data. See the `n` parameter in `density`.

`extend` Extend the range of the x axis by a factor of `extend_scale`.

`extend_scale` Ratio of range by which to extend the x axis. A value of `0.1` means that the x axis will be extended by `1/10` of the range of the data.

`bw` See the eponymous argument in `density`. Here, the default has been changed for `"SJ"`, which is recommended.

`ci` The confidence interval threshold. Only used when `method = "kernel"`. This feature is experimental, use with caution.

`select` Character vector of column names. If `NULL` (the default), all numeric variables will be selected. Other arguments from `datawizard::extract_column_names()` (such as `exclude`) can also be used.

`by` Optional character vector. If not `NULL` and input is a data frame, density estimation is performed for each group (subsets) indicated by `by`. See examples.

`rvar_col` A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.

`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.

`component` Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

`parameters` Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like `lp__` or `prior_`) are filtered by default, so only parameters that typically appear in the `summary()` are returned. Use `parameters` to select specific parameters for the output.

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.
- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

Note

There is also a plot()-method implemented in the **see**-package.

References

Deng, H., & Wickham, H. (2011). Density estimation in R. Electronic publication.

Examples

```
library(bayestestR)

set.seed(1)
x <- rnorm(250, mean = 1)

# Basic usage
density_kernel <- estimate_density(x) # default method is "kernel"

hist(x, prob = TRUE)
lines(density_kernel$x, density_kernel$y, col = "black", lwd = 2)
lines(density_kernel$x, density_kernel$CI_low, col = "gray", lty = 2)
lines(density_kernel$x, density_kernel$CI_high, col = "gray", lty = 2)
legend("topright",
  legend = c("Estimate", "95% CI"),
  col = c("black", "gray"), lwd = 2, lty = c(1, 2)
)

# Other Methods
```

```
density_logspline <- estimate_density(x, method = "logspline")
density_KernSmooth <- estimate_density(x, method = "KernSmooth")
density_mixture <- estimate_density(x, method = "mixture")

hist(x, prob = TRUE)
lines(density_kernel$x, density_kernel$y, col = "black", lwd = 2)
lines(density_logspline$x, density_logspline$y, col = "red", lwd = 2)
lines(density_KernSmooth$x, density_KernSmooth$y, col = "blue", lwd = 2)
lines(density_mixture$x, density_mixture$y, col = "green", lwd = 2)

# Extension
density_extended <- estimate_density(x, extend = TRUE)
density_default <- estimate_density(x, extend = FALSE)

hist(x, prob = TRUE)
lines(density_extended$x, density_extended$y, col = "red", lwd = 3)
lines(density_default$x, density_default$y, col = "black", lwd = 3)

# Multiple columns
head(estimate_density(iris))
head(estimate_density(iris, select = "Sepal.Width"))

# Grouped data
head(estimate_density(iris, by = "Species"))
head(estimate_density(iris$Petal.Width, by = iris$Species))

# rstanarm models
# ---------------------------------------------
library(rstanarm)
model <- suppressWarnings(
  stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
)
head(estimate_density(model))

library(emmeans)
head(estimate_density(emtrends(model, ~1, "wt", data = mtcars)))

# brms models
# ---------------------------------------------
library(brms)
model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
estimate_density(model)
```

---

eti *Equal-Tailed Interval (ETI)*

Description

Compute the **Equal-Tailed Interval (ETI)** of posterior distributions using the quantiles method. The probability of being below this interval is equal to the probability of being above it. The ETI can be used in the context of uncertainty characterisation of posterior distributions as **Credible Interval (CI)**.

Usage

```
eti(x, ...)

## S3 method for class 'numeric'
eti(x, ci = 0.95, verbose = TRUE, ...)

## S3 method for class 'data.frame'
eti(x, ci = 0.95, rvar_col = NULL, verbose = TRUE, ...)

## S3 method for class 'brmsfit'
eti(
  x,
  ci = 0.95,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'get_predicted'
eti(x, ci = 0.95, use_iterations = FALSE, verbose = TRUE, ...)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model. **bayestestR** supports a wide range of models (see, for example, `methods("hdi")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` or `.data.frame`methods.
...	Currently not used.
ci	Value or vector of probability of the (credible) interval - CI (between 0 and 1) to be estimated. Default to `.95` (95%).
verbose	Toggle off warnings.
rvar_col	A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.
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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

use_iterations — Logical, if TRUE and x is a get_predicted object, (returned by insight::get_predicted()), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., brmsfit models).

Details

Unlike equal-tailed intervals (see eti()) that typically exclude 2.5% from each tail of the distribution and always include the median, the HDI is *not* equal-tailed and therefore always includes the mode(s) of posterior distributions. While this can be useful to better represent the credibility mass of a distribution, the HDI also has some limitations. See spi() for details.

A 95% equal-tailed interval (ETI) has 2.5% of the distribution on either side of its limits. It indicates the 2.5th percentile and the 97.5th percentile. In symmetric distributions, the two methods of computing credible intervals, the ETI and the HDI, return similar results.

This is not the case for skewed distributions. Indeed, it is possible that parameter values in the ETI have lower credibility (are less probable) than parameter values outside the ETI. This property seems undesirable as a summary of the credible values in a distribution.

On the other hand, the ETI range does change when transformations are applied to the distribution (for instance, for a log odds scale to probabilities): the lower and higher bounds of the transformed distribution will correspond to the transformed lower and higher bounds of the original distribution. On the contrary, applying transformations to the distribution will change the resulting HDI.

The 95% or 89% Credible Intervals (CI) are two reasonable ranges to characterize the uncertainty related to the estimation (see here for a discussion about the differences between these two values).

Value

A data frame with following columns:

- `Parameter` The model parameter(s), if `x` is a model-object. If `x` is a vector, this column is missing.
- `CI` The probability of the credible interval.
- `CI_low`, `CI_high` The lower and upper credible interval limits for the 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.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, or `smooth_terms` (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.

For models of class `brmsfit` (package **brms**), even more options are possible for the `component` argument, which are not all documented in detail here. See also `?insight::find_parameters`.

See Also

Other ci: `bci()`, `ci()`, `hdi()`, `si()`, `spi()`

Examples

```
library(bayestestR)

posterior <- rnorm(1000)
eti(posterior)
eti(posterior, ci = c(0.80, 0.89, 0.95))

df <- data.frame(replicate(4, rnorm(100)))
eti(df)
eti(df, ci = c(0.80, 0.89, 0.95))
```

```
model <- suppressWarnings(
  rstanarm::stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
)
eti(model)
eti(model, ci = c(0.80, 0.89, 0.95))

eti(emmeans::emtrends(model, ~1, "wt", data = mtcars))

model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
eti(model)
eti(model, ci = c(0.80, 0.89, 0.95))

bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
eti(bf)
eti(bf, ci = c(0.80, 0.89, 0.95))
```

---

hdi *Highest Density Interval (HDI)*

Description

Compute the **Highest Density Interval (HDI)** of posterior distributions. All points within this interval have a higher probability density than points outside the interval. The HDI can be used in the context of uncertainty characterisation of posterior distributions as **Credible Interval (CI)**.

Usage

```
hdi(x, ...)

## S3 method for class 'numeric'
hdi(x, ci = 0.95, verbose = TRUE, ...)

## S3 method for class 'data.frame'
hdi(x, ci = 0.95, rvar_col = NULL, verbose = TRUE, ...)

## S3 method for class 'brmsfit'
hdi(
  x,
  ci = 0.95,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)
```

```
## S3 method for class 'get_predicted'
hdi(x, ci = 0.95, use_iterations = FALSE, verbose = TRUE, ...)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model. **bayestestR** supports a wide range of models (see, for example, `methods("hdi")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` or `.data.frame`methods.
...	Currently not used.
ci	Value or vector of probability of the (credible) interval - CI (between 0 and 1) to be estimated. Default to `.95` (95%).
verbose	Toggle off warnings.
rvar_col	A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.
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.
component	Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.
parameters	Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like `lp__` or `prior_`) are filtered by default, so only parameters that typically appear in the `summary()` are returned. Use `parameters` to select specific parameters for the output.

use_iterations Logical, if TRUE and x is a get_predicted object, (returned by insight::get_predicted()), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., brmsfit models).

Details

Unlike equal-tailed intervals (see eti()) that typically exclude 2.5% from each tail of the distribution and always include the median, the HDI is *not* equal-tailed and therefore always includes the mode(s) of posterior distributions. While this can be useful to better represent the credibility mass of a distribution, the HDI also has some limitations. See spi() for details.

A 95% equal-tailed interval (ETI) has 2.5% of the distribution on either side of its limits. It indicates the 2.5th percentile and the 97.5th percentile. In symmetric distributions, the two methods of computing credible intervals, the ETI and the HDI, return similar results.

This is not the case for skewed distributions. Indeed, it is possible that parameter values in the ETI have lower credibility (are less probable) than parameter values outside the ETI. This property seems undesirable as a summary of the credible values in a distribution.

On the other hand, the ETI range does change when transformations are applied to the distribution (for instance, for a log odds scale to probabilities): the lower and higher bounds of the transformed distribution will correspond to the transformed lower and higher bounds of the original distribution. On the contrary, applying transformations to the distribution will change the resulting HDI.

The 95% or 89% Credible Intervals (CI) are two reasonable ranges to characterize the uncertainty related to the estimation (see here for a discussion about the differences between these two values).

Value

A data frame with following columns:

- Parameter The model parameter(s), if x is a model-object. If x is a vector, this column is missing.
- CI The probability of the credible interval.
- CI_low, CI_high The lower and upper credible interval limits for the 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.

- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

Note

There is also a plot()-method implemented in the **see**-package.

Author(s)

Credits go to **ggdistribute** and **HDInterval**.

References

- Kruschke, J. (2014). Doing Bayesian data analysis: A tutorial with R, JAGS, and Stan. Academic Press.
- McElreath, R. (2015). Statistical rethinking: A Bayesian course with examples in R and Stan. Chapman and Hall/CRC.

See Also

Other interval functions, such as hdi(), eti(), bci(), spi(), si().

Other ci: bci(), ci(), eti(), si(), spi()

Examples

```
library(bayestestR)

posterior <- rnorm(1000)
hdi(posterior, ci = 0.89)
hdi(posterior, ci = c(0.80, 0.90, 0.95))

hdi(iris[1:4])
hdi(iris[1:4], ci = c(0.80, 0.90, 0.95))

model <- suppressWarnings(
  rstanarm::stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
)
hdi(model)
hdi(model, ci = c(0.80, 0.90, 0.95))

hdi(emmeans::emtrends(model, ~1, "wt", data = mtcars))

model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
hdi(model)
hdi(model, ci = c(0.80, 0.90, 0.95))
```

```
bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
hdi(bf)
hdi(bf, ci = c(0.80, 0.90, 0.95))
```

`map_estimate` *Maximum A Posteriori probability estimate (MAP)*

Description

Find the **Highest Maximum A Posteriori probability estimate (MAP)** of a posterior, i.e., the value associated with the highest probability density (the "peak" of the posterior distribution). In other words, it is an estimation of the *mode* for continuous parameters. Note that this function relies on `estimate_density()`, which by default uses a different smoothing bandwidth (`"SJ"`) compared to the legacy default implemented the base R `density()` function (`"nrd0"`).

Usage

```
map_estimate(x, ...)

## S3 method for class 'numeric'
map_estimate(x, precision = 2^10, method = "kernel", verbose = TRUE, ...)

## S3 method for class 'brmsfit'
map_estimate(
  x,
  precision = 2^10,
  method = "kernel",
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'data.frame'
map_estimate(
  x,
  precision = 2^10,
  method = "kernel",
  rvar_col = NULL,
  verbose = TRUE,
  ...
)
```

```
## S3 method for class 'get_predicted'
map_estimate(
  x,
  precision = 2^10,
  method = "kernel",
  use_iterations = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model. **bayestestR** supports a wide range of models (see, for example, `methods("hdi")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` or `.data.frame`methods.
...	Currently not used.
precision	Number of points of density data. See the `n` parameter in `density`.
method	Density estimation method. Can be `"kernel"` (default), `"logspline"` or `"KernSmooth"`.
verbose	Toggle off warnings.
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.
component	Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters	Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.
rvar_col	A single character - the name of an rvar column in the data frame to be processed. See example in p_direction().
use_iterations	Logical, if TRUE and x is a get_predicted object, (returned by insight::get_predicted()), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., brmsfit models).

Value

A numeric value if x is a vector. If x is a model-object, returns a data frame with following columns:

- Parameter: The model parameter(s), if x is a model-object. If x is a vector, this column is missing.
- MAP_Estimate: The MAP estimate for the posterior or each model 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.
- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

Examples

```
library(bayestestR)

posterior <- rnorm(10000)
map_estimate(posterior)
```

```
plot(density(posterior))
abline(v = as.numeric(map_estimate(posterior)), col = "red")

model <- rstanarm::stan_glm(mpg ~ wt + cyl, data = mtcars)
map_estimate(model)

model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
map_estimate(model)
```

---

mcse *Monte-Carlo Standard Error (MCSE)*

Description

This function returns the Monte Carlo Standard Error (MCSE).

Usage

```
mcse(model, ...)

## S3 method for class 'stanreg'
mcse(
  model,
  effects = "fixed",
  component = "location",
  parameters = NULL,
  centrality = "median",
  ...
)
```

Arguments

model	A stanreg, stanfit, brmsfit, blavaan, or MCMCglmm object.
...	Additional arguments to be passed to or from methods.
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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

centrality — The point-estimate (centrality index) for which to compute the MCSE. Can be "median" (default) or "mean". To not break other functions like describe_posterior() or diagnostic_posterior(), all other values are silently converted to "median".

Details

Monte Carlo Standard Error (MCSE) is another measure of accuracy of the chains. It is defined as standard deviation of the chains divided by their effective sample size (the formula for mcse() is from Kruschke 2015, p. 187). The MCSE "provides a quantitative suggestion of how big the estimation noise is".

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.
- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

References

Kruschke, J. (2014). Doing Bayesian data analysis: A tutorial with R, JAGS, and Stan. Academic Press.

Examples

```
library(bayestestR)

model <- suppressWarnings(
  rstanarm::stan_glm(mpg ~ wt + am, data = mtcars, chains = 1, refresh = 0)
)
mcse(model)
```

---

mediation *Summary of Bayesian multivariate-response mediation-models*

Description

mediation() is a short summary for multivariate-response mediation-models, i.e. this function computes average direct and average causal mediation effects of multivariate response models.

Usage

```
mediation(model, ...)

## S3 method for class 'brmsfit'
mediation(
  model,
  treatment,
  mediator,
  response = NULL,
  centrality = "median",
  ci = 0.95,
  method = "ETI",
  ...
)
```

Arguments

model	A brmsfit or stanmvreg object.
...	Not used.
treatment	Character, name of the treatment variable (or direct effect) in a (multivariate response) mediator-model. If missing, mediation() tries to find the treatment variable automatically, however, this may fail.
mediator	Character, name of the mediator variable in a (multivariate response) mediator-model. If missing, mediation() tries to find the treatment variable automatically, however, this may fail.
response	A named character vector, indicating the names of the response variables to be used for the mediation analysis. Usually can be NULL, in which case these variables are retrieved automatically. If not NULL, names must match the names of the model formulas. For *brms* models, these are names(insight::find_formula(model)), one name per formula, and the values are the left side of each formula without addition terms such as cens(). For other models, they are names(insight::find_response(model, combine = TRUE)). This can be useful if, for instance, the mediator variable used as predictor has a different name from the mediator variable used as response. This might occur when the mediator is transformed in one model, but used "as is" as response variable in the other model. Example: The mediator m is used as response variable, but the centered version m_center is used as mediator variable. The second response variable (for the treatment model, with the mediator as additional predictor), y, is not transformed. Then we could use response like this: mediation(model, response = c(m = "m_center", y = "y")).
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" (see map_estimate()), "trimmed" (which is just mean(x, trim = threshold)), "mode" or "all".
ci	Value or vector of probability of the CI (between 0 and 1) to be estimated. Default to 0.95 (95%).
method	Can be "ETI" (default), "HDI", "BCI", "SPI" or "SI".

Details

mediation() returns a data frame with information on the *direct effect* (mean value of posterior samples from treatment of the outcome model), *mediator effect* (mean value of posterior samples from mediator of the outcome model), *indirect effect* (mean value of the multiplication of the posterior samples from mediator of the outcome model and the posterior samples from treatment of the mediation model) and the total effect (mean value of sums of posterior samples used for the direct and indirect effect). The *proportion mediated* is the indirect effect divided by the total effect.

For all values, the 95% credible intervals are calculated by default. Use ci to calculate a different interval.

The arguments treatment and mediator do not necessarily need to be specified. If missing, mediation() tries to find the treatment and mediator variable automatically. If this does not work, specify these variables.

The direct effect is also called *average direct effect* (ADE), the indirect effect is also called *average causal mediation effects* (ACME). See also *Tingley et al. 2014* and *Imai et al. 2010*.

Value

A data frame with direct, indirect, mediator and total effect of a multivariate-response mediation-model, as well as the proportion mediated. The effect sizes are median values of the posterior samples (use `centrality` for other centrality indices).

Note

There is an `as.data.frame()` method that returns the posterior samples of the effects, which can be used for further processing in the **bayestestR** package.

References

- Imai, K., Keele, L. and Tingley, D. (2010) A General Approach to Causal Mediation Analysis, Psychological Methods, Vol. 15, No. 4 (December), pp. 309-334.
- Tingley, D., Yamamoto, T., Hirose, K., Imai, K. and Keele, L. (2014). mediation: R package for Causal Mediation Analysis, Journal of Statistical Software, Vol. 59, No. 5, pp. 1-38.

See Also

The **mediation** package for a causal mediation analysis in the frequentist framework.

Examples

```
library(mediation)
library(brms)
library(rstanarm)

# load sample data
data(jobs)
set.seed(123)

# linear models, for mediation analysis
b1 <- lm(job_seek ~ treat + econ_hard + sex + age, data = jobs)
b2 <- lm(depress2 ~ treat + job_seek + econ_hard + sex + age, data = jobs)
# mediation analysis, for comparison with Stan models
m1 <- mediate(b1, b2, sims = 1000, treat = "treat", mediator = "job_seek")

# Fit Bayesian mediation model in brms
f1 <- bf(job_seek ~ treat + econ_hard + sex + age)
f2 <- bf(depress2 ~ treat + job_seek + econ_hard + sex + age)
m2 <- brm(f1 + f2 + set_rescor(FALSE), data = jobs, refresh = 0)

# Fit Bayesian mediation model in rstanarm
m3 <- suppressWarnings(stan_mvmer(
  list(
    job_seek ~ treat + econ_hard + sex + age + (1 | occp),
    depress2 ~ treat + job_seek + econ_hard + sex + age + (1 | occp)
  ),
  data = jobs,
  refresh = 0
```

```
))

summary(m1)
mediation(m2, centrality = "mean", ci = 0.95)
mediation(m3, centrality = "mean", ci = 0.95)
```

`model_to_priors` *Convert model's posteriors to priors (EXPERIMENTAL)*

Description

Convert model's posteriors to (normal) priors.

Usage

```
model_to_priors(model, scale_multiply = 3, ...)
```

Arguments

`model`	A Bayesian model.
`scale_multiply`	The SD of the posterior will be multiplied by this amount before being set as a prior to avoid overly narrow priors.
`...`	Other arguments for `insight::get_prior()` or `describe_posterior`.

Examples

```
# brms models
# -----------------------------------------------
if (require("brms")) {
  formula <- brms::brmsformula(mpg ~ wt + cyl, center = FALSE)

  model <- brms::brm(formula, data = mtcars, refresh = 0)
  priors <- model_to_priors(model)
  priors <- brms::validate_prior(priors, formula, data = mtcars)
  priors

  model2 <- brms::brm(formula, data = mtcars, prior = priors, refresh = 0)
}
```

overlap *Overlap Coefficient*

Description

A method to calculate the overlap coefficient between two empirical distributions (that can be used as a measure of similarity between two samples).

Usage

```
overlap(
  x,
  y,
  method_density = "kernel",
  method_auc = "trapezoid",
  precision = 2^10,
  extend = TRUE,
  extend_scale = 0.1,
  ...
)
```

Arguments

x	Vector of x values.
y	Vector of x values.
method_density	Density estimation method. See estimate_density().
method_auc	Area Under the Curve (AUC) estimation method. See area_under_curve().
precision	Number of points of density data. See the n parameter in density.
extend	Extend the range of the x axis by a factor of extend_scale.
extend_scale	Ratio of range by which to extend the x axis. A value of 0.1 means that the x axis will be extended by 1/10 of the range of the data.
...	Currently not used.

Examples

```
library(bayestestR)

x <- distribution_normal(1000, 2, 0.5)
y <- distribution_normal(1000, 0, 1)

overlap(x, y)
plot(overlap(x, y))
```

pd_to_p *Convert between Probability of Direction (pd) and p-value.*

Description

Enables a conversion between Probability of Direction (pd) and p-value.

Usage

```
pd_to_p(pd, ...)

## S3 method for class 'numeric'
pd_to_p(pd, direction = "two-sided", verbose = TRUE, ...)

p_to_pd(p, direction = "two-sided", ...)

convert_p_to_pd(p, direction = "two-sided", ...)

convert_pd_to_p(pd, ...)
```

Arguments

pd	A Probability of Direction (pd) value (between 0 and 1). Can also be a data frame with a column named pd, p_direction, or PD, as returned by p_direction(). In this case, the column is converted to p-values and the new data frame is returned.
...	Arguments passed to or from other methods.
direction	What type of p-value is requested or provided. Can be "two-sided" (default, two tailed) or "one-sided" (one tailed).
verbose	Toggle off warnings.
p	A p-value.

Details

Conversion is done using the following equation (see *Makowski et al., 2019*):

When direction = "two-sided"

$p = 2 \times (1 - p_d)$

When direction = "one-sided"

$p = 1 - p_d$

Note that this conversion is only valid when the lowest possible values of pd is 0.5 - i.e., when the posterior represents continuous parameter space (see p_direction()). If any pd < 0.5 are detected, they are converted to a p of 1, and a warning is given.

Value

A p-value or a data frame with a p-value column.

References

Makowski, D., Ben-Shachar, M. S., Chen, S. H. A., and Lüdecke, D. (2019). *Indices of Effect Existence and Significance in the Bayesian Framework*. Frontiers in Psychology 2019;10:2767. doi:10.3389/fpsyg.2019.02767

Examples

```
pd_to_p(pd = 0.95)
pd_to_p(pd = 0.95, direction = "one-sided")
```

---

point_estimate *Point-estimates of posterior distributions*

Description

Compute various point-estimates, such as the mean, the median or the MAP, to describe posterior distributions.

Usage

```
point_estimate(x, ...)

## S3 method for class 'numeric'
point_estimate(x, centrality = "all", dispersion = FALSE, threshold = 0.1, ...)

## S3 method for class 'data.frame'
point_estimate(
  x,
  centrality = "all",
  dispersion = FALSE,
  threshold = 0.1,
  rvar_col = NULL,
  ...
)

## S3 method for class 'brmsfit'
point_estimate(
  x,
  centrality = "all",
  dispersion = FALSE,
  effects = "fixed",
  component = "conditional",
```

```
  parameters = NULL,
  ...
)

## S3 method for class 'get_predicted'
point_estimate(
  x,
  centrality = "all",
  dispersion = FALSE,
  use_iterations = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model. **bayestestR** supports a wide range of models (see, for example, `methods("hdi")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` or `.data.frame`methods.
...	Additional arguments to be passed to or from methods.
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: `"median"`, `"mean"`, `"MAP"` (see `map_estimate()`), `"trimmed"` (which is just `mean(x, trim = threshold)`), `"mode"` or `"all"`.
dispersion	Logical, if `TRUE`, computes indices of dispersion related to the estimate(s) (`SD` and `MAD` for `mean` and `median`, respectively). Dispersion is not available for `"MAP"` or `"mode"` centrality indices.
threshold	For `centrality = "trimmed"` (i.e. trimmed mean), indicates the fraction (0 to 0.5) of observations to be trimmed from each end of the vector before the mean is computed.
rvar_col	A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.
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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

use_iterations — Logical, if TRUE and x is a get_predicted object, (returned by insight::get_predicted()), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., brmsfit models).

verbose — Toggle off warnings.

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.
- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

Note

There is also a plot()-method implemented in the **see**-package.

References

Makowski, D., Ben-Shachar, M. S., Chen, S. H. A., and Lüdecke, D. (2019). *Indices of Effect Existence and Significance in the Bayesian Framework*. Frontiers in Psychology 2019;10:2767. doi:10.3389/fpsyg.2019.02767

Examples

```
library(bayestestR)

point_estimate(rnorm(1000))
point_estimate(rnorm(1000), centrality = "all", dispersion = TRUE)
point_estimate(rnorm(1000), centrality = c("median", "MAP"))

df <- data.frame(replicate(4, rnorm(100)))
point_estimate(df, centrality = "all", dispersion = TRUE)
point_estimate(df, centrality = c("median", "MAP"))

# rstanarm models
# ---------------------------------------------
model <- rstanarm::stan_glm(mpg ~ wt + cyl, data = mtcars)
point_estimate(model, centrality = "all", dispersion = TRUE)
point_estimate(model, centrality = c("median", "MAP"))


# emmeans estimates
# ---------------------------------------------
point_estimate(
  emmeans::emtrends(model, ~1, "wt", data = mtcars),
  centrality = c("median", "MAP")
)

# brms models
# ---------------------------------------------
model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
point_estimate(model, centrality = "all", dispersion = TRUE)
point_estimate(model, centrality = c("median", "MAP"))

# BayesFactor objects
# ---------------------------------------------
bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
point_estimate(bf, centrality = "all", dispersion = TRUE)
point_estimate(bf, centrality = c("median", "MAP"))
```

---

p_direction *Probability of Direction (pd)*

Description

Compute the **Probability of Direction** (**pd**, also known as the Maximum Probability of Effect - *MPE*). This can be interpreted as the probability that a parameter (described by its posterior distribution) is strictly positive or negative (whichever is the most probable). Although differently expressed, this index is fairly similar (*i.e.*, is strongly correlated) to the frequentist **p-value** (see details).

Usage

```
p_direction(x, ...)

pd(x, ...)

## S3 method for class 'numeric'
p_direction(
  x,
  method = "direct",
  null = 0,
  as_p = FALSE,
  remove_na = TRUE,
  ...
)

## S3 method for class 'data.frame'
p_direction(
  x,
  method = "direct",
  null = 0,
  as_p = FALSE,
  remove_na = TRUE,
  rvar_col = NULL,
  ...
)

## S3 method for class 'brmsfit'
p_direction(
  x,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  method = "direct",
  null = 0,
  as_p = FALSE,
  remove_na = TRUE,
  ...
)

## S3 method for class 'get_predicted'
```

```
p_direction(
  x,
  method = "direct",
  null = 0,
  as_p = FALSE,
  remove_na = TRUE,
  use_iterations = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

x	A vector representing a posterior distribution, a data frame of posterior draws (samples be parameter). Can also be a Bayesian model.
...	Currently not used.
method	Can be "direct" or one of methods of estimate_density(), such as "kernel", "logspline" or "KernSmooth". See details.
null	The value considered as a "null" effect. Traditionally 0, but could also be 1 in the case of ratios of change (OR, IRR, ...).
as_p	If TRUE, the p-direction (pd) values are converted to a frequentist p-value using pd_to_p().
remove_na	Should missing values be removed before computation? Note that Inf (infinity) are *not* removed.
rvar_col	A single character - the name of an rvar column in the data frame to be processed. See example in p_direction().
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.
component	Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

use_iterations — Logical, if TRUE and x is a get_predicted object, (returned by insight::get_predicted()), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., brmsfit models).

verbose — Toggle off warnings.

Value

Values between 0.5 and 1 *or* between 0 and 1 (see above) corresponding to the probability of direction (pd).

What is the *pd*?

The Probability of Direction (pd) is an index of effect existence, representing the certainty with which an effect goes in a particular direction (i.e., is positive or negative / has a sign), typically ranging from 0.5 to 1 (but see next section for cases where it can range between 0 and 1). Beyond its simplicity of interpretation, understanding and computation, this index also presents other interesting properties:

- Like other posterior-based indices, *pd* is solely based on the posterior distributions and does not require any additional information from the data or the model (e.g., such as priors, as in the case of Bayes factors).
- It is robust to the scale of both the response variable and the predictors.
- It is strongly correlated with the frequentist p-value, and can thus be used to draw parallels and give some reference to readers non-familiar with Bayesian statistics (Makowski et al., 2019).

Relationship with the p-value

In most cases, it seems that the *pd* has a direct correspondence with the frequentist one-sided p-value through the formula (for two-sided p): $p = 2 \times (1 - p_d)$ Thus, a two-sided p-value of respectively .1, .05, .01 and .001 would correspond approximately to a *pd* of 95%, 97.5%, 99.5% and 99.95%. See pd_to_p() for details.

Possible Range of Values

The largest value *pd* can take is 1 - the posterior is strictly directional. However, the smallest value *pd* can take depends on the parameter space represented by the posterior.

For a continuous parameter space, exact values of 0 (or any point null value) are not possible, and so 100% of the posterior has *some* sign, some positive, some negative. Therefore, the smallest the *pd* can be is 0.5 - with an equal posterior mass of positive and negative values. Values close to 0.5 *cannot* be used to support the null hypothesis (that the parameter does *not* have a direction) is a similar why to how large p-values cannot be used to support the null hypothesis (see `pd_to_p()`; Makowski et al., 2019).

For a discrete parameter space or a parameter space that is a mixture between discrete and continuous spaces, exact values of 0 (or any point null value) *are* possible! Therefore, the smallest the *pd* can be is 0 - with 100% of the posterior mass on 0. Thus values close to 0 can be used to support the null hypothesis (see van den Bergh et al., 2021).

Examples of posteriors representing discrete parameter space:

- When a parameter can only take discrete values.
- When a mixture prior/posterior is used (such as the spike-and-slab prior; see van den Bergh et al., 2021).
- When conducting Bayesian model averaging (e.g., `weighted_posteriors()` or `brms::posterior_average`).

Methods of computation

The *pd* is defined as:

$$p_d = max(Pr(\hat{\theta} < \theta_{null}), Pr(\hat{\theta} > \theta_{null}))$$

The most simple and direct way to compute the *pd* is to compute the proportion of positive (or larger than `null`) posterior samples, the proportion of negative (or smaller than `null`) posterior samples, and take the larger of the two. This "simple" method is the most straightforward, but its precision is directly tied to the number of posterior draws.

The second approach relies on density estimation: It starts by estimating the continuous-smooth density function (for which many methods are available), and then computing the area under the curve (AUC) of the density curve on either side of `null` and taking the maximum between them. Note the this approach assumes a continuous density function, and so **when the posterior represents a (partially) discrete parameter space, only the direct method *must* be used** (see above).

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.
- `"location"`: returns location parameters such as `conditional`, `zero_inflated`, or `smooth_terms` (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

Note

There is also a plot()-method implemented in the **see**-package.

References

- Makowski, D., Ben-Shachar, M. S., Chen, S. A., & Lüdecke, D. (2019). Indices of effect existence and significance in the Bayesian framework. Frontiers in psychology, 10, 2767. doi:10.3389/fpsyg.2019.02767
- van den Bergh, D., Haaf, J. M., Ly, A., Rouder, J. N., & Wagenmakers, E. J. (2021). A cautionary note on estimating effect size. Advances in Methods and Practices in Psychological Science, 4(1). doi:10.1177/2515245921992035

See Also

pd_to_p() to convert between Probability of Direction (pd) and p-value.

Examples

```
library(bayestestR)

# Simulate a posterior distribution of mean 1 and SD 1
# ----------------------------------------------------
posterior <- rnorm(1000, mean = 1, sd = 1)
p_direction(posterior)
p_direction(posterior, method = "kernel")

# Simulate a dataframe of posterior distributions
# -----------------------------------------------
df <- data.frame(replicate(4, rnorm(100)))
p_direction(df)
p_direction(df, method = "kernel")


# rstanarm models
# ---------------------------------------------
model <- rstanarm::stan_glm(mpg ~ wt + cyl,
  data = mtcars,
  chains = 2, refresh = 0
)
p_direction(model)
p_direction(model, method = "kernel")

# emmeans
# ---------------------------------------------
p_direction(emmeans::emtrends(model, ~1, "wt", data = mtcars))
```

```
# brms models
# -----------------------------------------------
model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
p_direction(model)
p_direction(model, method = "kernel")

# BayesFactor objects
# -----------------------------------------------
bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
p_direction(bf)
p_direction(bf, method = "kernel")



# Using "rvar_col"
x <- data.frame(mu = c(0, 0.5, 1), sigma = c(1, 0.5, 0.25))
x$my_rvar <- posterior::rvar_rng(rnorm, 3, mean = x$mu, sd = x$sigma)
x
p_direction(x, rvar_col = "my_rvar")
```

---

p_map *Bayesian p-value based on the density at the Maximum A Posteriori (MAP)*

Description

Compute a Bayesian equivalent of the *p*-value, related to the odds that a parameter (described by its posterior distribution) has against the null hypothesis (*h0*) using Mills' (2014, 2017) *Objective Bayesian Hypothesis Testing* framework. It corresponds to the density value at the null (e.g., 0) divided by the density at the Maximum A Posteriori (MAP).

Usage

```
p_map(x, ...)

p_pointnull(x, ...)

## S3 method for class 'numeric'
p_map(x, null = 0, precision = 2^10, method = "kernel", ...)

## S3 method for class 'get_predicted'
p_map(
  x,
  null = 0,
  precision = 2^10,
  method = "kernel",
  use_iterations = FALSE,
```

```
  verbose = TRUE,
  ...
)

## S3 method for class 'data.frame'
p_map(x, null = 0, precision = 2^10, method = "kernel", rvar_col = NULL, ...)

## S3 method for class 'brmsfit'
p_map(
  x,
  null = 0,
  precision = 2^10,
  method = "kernel",
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  ...
)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model. **bayestestR** supports a wide range of models (see, for example, `methods("hdi")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` or `.data.frame`methods.
...	Currently not used.
null	The value considered as a "null" effect. Traditionally 0, but could also be 1 in the case of ratios of change (OR, IRR, ...).
precision	Number of points of density data. See the `n` parameter in `density`.
method	Density estimation method. Can be `"kernel"` (default), `"logspline"` or `"KernSmooth"`.
use_iterations	Logical, if `TRUE` and `x` is a `get_predicted` object, (returned by `insight::get_predicted()`), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., `brmsfit` models).
verbose	Toggle off warnings.
rvar_col	A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.
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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

Details

Note that this method is sensitive to the density estimation method (see the section in the examples below).

Strengths and Limitations:

Strengths: Straightforward computation. Objective property of the posterior distribution.

Limitations: Limited information favoring the null hypothesis. Relates on density approximation. Indirect relationship between mathematical definition and interpretation. Only suitable for weak / very diffused priors.

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.

- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

References

- Makowski D, Ben-Shachar MS, Chen SHA, Lüdecke D (2019) Indices of Effect Existence and Significance in the Bayesian Framework. Frontiers in Psychology 2019;10:2767. doi:10.3389/fpsyg.2019.02767
- Mills, J. A. (2018). Objective Bayesian Precise Hypothesis Testing. University of Cincinnati.

See Also

Jeff Mill's talk

Examples

```
library(bayestestR)

p_map(rnorm(1000, 0, 1))
p_map(rnorm(1000, 10, 1))

model <- suppressWarnings(
  rstanarm::stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
)
p_map(model)

p_map(suppressWarnings(
  emmeans::emtrends(model, ~1, "wt", data = mtcars)
))

model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
p_map(model)

bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
p_map(bf)

# ----------------------------------------
# Robustness to density estimation method
set.seed(333)
data <- data.frame()
for (iteration in 1:250) {
  x <- rnorm(1000, 1, 1)
  result <- data.frame(
    Kernel = as.numeric(p_map(x, method = "kernel")),
    KernSmooth = as.numeric(p_map(x, method = "KernSmooth")),
```

```
    logspline = as.numeric(p_map(x, method = "logspline"))
  )
  data <- rbind(data, result)
}
data$KernSmooth <- data$Kernel - data$KernSmooth
data$logspline <- data$Kernel - data$logspline

summary(data$KernSmooth)
summary(data$logspline)
boxplot(data[c("KernSmooth", "logspline")])
```

---

p_significance *Practical Significance (ps)*

Description

Compute the probability of **Practical Significance** (**ps**), which can be conceptualized as a unidirectional equivalence test. It returns the probability that effect is above a given threshold corresponding to a negligible effect in the median's direction. Mathematically, it is defined as the proportion of the posterior distribution of the median sign above the threshold.

Usage

```
p_significance(x, ...)

## S3 method for class 'numeric'
p_significance(x, threshold = "default", ...)

## S3 method for class 'get_predicted'
p_significance(
  x,
  threshold = "default",
  use_iterations = FALSE,
  verbose = TRUE,
  ...
)

## S3 method for class 'data.frame'
p_significance(x, threshold = "default", rvar_col = NULL, ...)

## S3 method for class 'brmsfit'
p_significance(
  x,
  threshold = "default",
  effects = "fixed",
  component = "conditional",
```

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

Arguments

x	Vector representing a posterior distribution. Can also be a stanreg or brmsfit model.
...	Currently not used.
threshold	The threshold value that separates significant from negligible effect, which can have following possible values: • "default", in which case the range is set to 0.1 if input is a vector, and based on rope_range() if a (Bayesian) model is provided. • a single numeric value (e.g., 0.1), which is used as range around zero (i.e. the threshold range is set to -0.1 and 0.1, i.e. reflects a symmetric interval) • a numeric vector of length two (e.g., c(-0.2, 0.1)), useful for asymmetric intervals • a list of numeric vectors, where each vector corresponds to a parameter • a list of *named* numeric vectors, where names correspond to parameter names. In this case, all parameters that have no matching name in threshold will be set to "default".
use_iterations	Logical, if TRUE and x is a get_predicted object, (returned by insight::get_predicted()), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., brmsfit models).
verbose	Toggle off warnings.
rvar_col	A single character - the name of an rvar column in the data frame to be processed. See example in p_direction().
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.
component	Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

Details

p_significance() returns the proportion of a probability distribution (x) that is outside a certain range (the negligible effect, or ROPE, see argument threshold). If there are values of the distribution both below and above the ROPE, p_significance() returns the higher probability of a value being outside the ROPE. Typically, this value should be larger than 0.5 to indicate practical significance. However, if the range of the negligible effect is rather large compared to the range of the probability distribution x, p_significance() will be less than 0.5, which indicates no clear practical significance.

Value

Values between 0 and 1 corresponding to the probability of practical significance (ps).

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.
- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

Note

There is also a plot()-method implemented in the **see**-package.

Examples

```
library(bayestestR)

# Simulate a posterior distribution of mean 1 and SD 1
# ----------------------------------------------------
posterior <- rnorm(1000, mean = 1, sd = 1)
p_significance(posterior)

# Simulate a dataframe of posterior distributions
# -----------------------------------------------
df <- data.frame(replicate(4, rnorm(100)))
p_significance(df)

# rstanarm models
# ---------------------------------------------
model <- rstanarm::stan_glm(mpg ~ wt + cyl,
  data = mtcars,
  chains = 2, refresh = 0
)
p_significance(model)
# multiple thresholds - asymmetric, symmetric, default
p_significance(model, threshold = list(c(-10, 5), 0.2, "default"))
# named thresholds
p_significance(model, threshold = list(wt = 0.2, `(Intercept)` = c(-10, 5)))
```

---

p_to_bf *Convert p-values to (pseudo) Bayes Factors*

Description

Convert p-values to (pseudo) Bayes Factors. This transformation has been suggested by Aust, Pawel, and Wagenmakers (2026), but is based on a vast amount of assumptions. It might therefore be not reliable. Use at your own risks.

Usage

```
p_to_bf(x, ...)

## S3 method for class 'numeric'
p_to_bf(x, n_obs = NULL, log = FALSE, ...)

## Default S3 method:
p_to_bf(x, n_obs = NULL, log = FALSE, ...)
```

Arguments

x	A (frequentist) model object, or a (numeric) vector of p-values. p-values must come from a *two-tailed* z- or t-test or from an F- or a χ^2-test with a single degree of freedom. p-values must not be corrected for multiple testing.
...	Arguments passed to `parameters::p_value()` if x is a model object.
n_obs	(Effective) number of observations. For mixed models this must be supplied and generally corresponds to the number of clusters. Either length 1, or same length as p.
log	Whether to return log Bayes Factors. **Note:** The `print()` method always shows BF - the "log_BF" column is only accessible from the returned data frame.

Value

A data frame with the p-values and pseudo-Bayes factors (against the null).

References

- Aust, F., Pawel, S., & Wagenmakers, E.J. (2026). Extracting Bayesian Evidence from Frequentist p-Values. Preprint available on ArXiv: https://arxiv.org/abs/2607.12132

See Also

`bic_to_bf()` for approximate Bayes factors based on BICs.

Examples

```
# Compare to BIC-approximated and pseudo BF
# ------------------------------------------
m0 <- lm(mpg ~ 1, data = mtcars)
m1 <- lm(mpg ~ am, data = mtcars)
m2 <- lm(mpg ~ factor(cyl), data = mtcars)

# BIC-approximated BF, m1 against null model
bayesfactor_models(m1, denominator = m0)
# bic_to_bf(BIC(m1), denominator = BIC(m0)) # equivalent

# pseudo-BF based on p-values
p_to_bf(m1)[-1, ] # dropping intercept

# When using a p-value from an F/chisq-test with more than one degree of
# freedom, the pseudo-BF is not reliable:
bayesfactor_models(m2, denominator = m0)
p_to_bf(anova(m2), n_obs = nrow(mtcars))



# Mixed models
# ------------------
```

```
data("sleepstudy", package = "lme4")
mixed0 <- lmerTest::lmer(Reaction ~ 1 + (Days | Subject), data = sleepstudy)
mixed1 <- lmerTest::lmer(Reaction ~ Days + (Days | Subject), data = sleepstudy)

bayesfactor_models(mixed1, denominator = mixed0)

p_to_bf(
  mixed1,
  n_obs = nlevels(lme4::sleepstudy$Subject), # *effective* sample size here
  method = "S" # make sure to get the correct p-values for the fixed effects
)[-1, ] # dropping intercept
```

`reshape_iterations` *Reshape estimations with multiple iterations (draws) to long format*

Description

Reshape a wide data.frame of iterations (such as posterior draws or bootstrapped samples) as columns to long format. Instead of having all iterations as columns (e.g., `iter_1, iter_2, ...`), will return 3 columns with the `\*_index` (the previous index of the row), the `\*_group` (the iteration number) and the `\*_value` (the value of said iteration).

Usage

```
reshape_iterations(x, prefix = c("draw", "iter", "iteration", "sim"))

reshape_draws(x, prefix = c("draw", "iter", "iteration", "sim"))
```

Arguments

`x`	A data.frame containing posterior draws obtained from `estimate_response` or `estimate_link`.
`prefix`	The prefix of the draws (for instance, `"iter_"` for columns named as `iter_1, iter_2, iter_3`). If more than one are provided, will search for the first one that matches.

Value

Data frame of reshaped draws in long format.

Examples

```
if (require("rstanarm")) {
  model <- stan_glm(mpg ~ am, data = mtcars, refresh = 0)
  draws <- insight::get_predicted(model)
  long_format <- reshape_iterations(draws)
  head(long_format)
}
```

rope *Region of Practical Equivalence (ROPE) Analysis*

Description

Compute the proportion of the CI (default to the 95% ETI) of a posterior distribution that lies within a region of practical equivalence. `p_rope()` is an alias for `rope(ci = 1)` convenient for computing the posterior probability of the ROPE.

Usage

```
rope(x, ...)

p_rope(
  x,
  range = "default",
  ci_method = "ETI",
  complement = FALSE,
  verbose = TRUE,
  ...
)

## S3 method for class 'numeric'
rope(
  x,
  range = "default",
  ci = 0.95,
  ci_method = "ETI",
  complement = FALSE,
  verbose = TRUE,
  ...
)

## S3 method for class 'data.frame'
rope(
  x,
  range = "default",
  ci = 0.95,
  ci_method = "ETI",
  complement = FALSE,
  rvar_col = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'stanreg'
rope(
```

```
  x,
  range = "default",
  ci = 0.95,
  ci_method = "ETI",
  complement = FALSE,
  effects = "fixed",
  component = "location",
  parameters = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'brmsfit'
rope(
  x,
  range = "default",
  ci = 0.95,
  ci_method = "ETI",
  complement = FALSE,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

x	Vector representing a posterior distribution. Can also be a stanreg or brmsfit model.
...	Currently not used.
range	ROPE's lower and higher bounds. Should be "default" or depending on the number of outcome variables a vector or a list. For models with one response, range can be: • a vector of length two (e.g., c(-0.1, 0.1)), • a list of numeric vector of the same length as numbers of parameters (see 'Examples'). • a list of *named* numeric vectors, where names correspond to parameter names. In this case, all parameters that have no matching name in range will be set to "default". In multivariate models, range should be a list with another list (one for each response variable) of numeric vectors . Vector names should correspond to the name of the response variables. If "default" and input is a vector, the range is set to c(-0.1, 0.1). If "default" and input is a Bayesian model, rope_range() is used. See 'Examples'.
ci_method	The type of interval to use to quantify the percentage in ROPE. Can be 'HDI' or 'ETI' (default). See ci().

`complement` Should the probabilities above/below the ROPE (the *complementary* probabilities) be returned as well? See `equivalence_test()` as well.

`verbose` Toggle off warnings.

`ci` The Credible Interval (CI) probability, corresponding to the proportion of HDI, to use for the percentage in ROPE.

`rvar_col` A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.

`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.

`component` Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

`parameters` Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like `lp__` or `prior_`) are filtered by default, so only parameters that typically appear in the `summary()` are returned. Use `parameters` to select specific parameters for the output.

ROPE

Statistically, the probability of a posterior distribution of being different from 0 does not make much sense (the probability of a single value null hypothesis in a continuous distribution is 0). Therefore, the idea underlining ROPE is to let the user define an area around the null value enclosing values that are *equivalent to the null* value for practical purposes (*Kruschke 2010, 2011, 2014*).

Kruschke (2018) suggests that such null value could be set, by default, to the -0.1 to 0.1 range of a standardized parameter (negligible effect size according to Cohen, 1988). This could be generalized: For instance, for linear models, the ROPE could be set as `0 +/- .1 * sd(y)`. This ROPE range can be automatically computed for models using the `rope_range()` function.

Kruschke (2010, 2011, 2014) suggests using the proportion of HDI that falls within the ROPE as an index for "null-hypothesis" testing (as understood under the Bayesian framework, see `equivalence_test()`).

Sensitivity to parameter's scale

It is important to consider the unit (i.e., the scale) of the predictors when using an index based on the ROPE, as the correct interpretation of the ROPE as representing a region of practical equivalence to zero is dependent on the scale of the predictors. Indeed, the percentage in ROPE depend on the unit of its parameter. In other words, as the ROPE represents a fixed portion of the response's scale, its proximity with a coefficient depends on the scale of the coefficient itself.

Multicollinearity - Non-independent covariates

When parameters show strong correlations, i.e. when covariates are not independent, the joint parameter distributions may shift towards or away from the ROPE. Collinearity invalidates ROPE and hypothesis testing based on univariate marginals, as the probabilities are conditional on independence. Most problematic are parameters that only have partial overlap with the ROPE region. In case of collinearity, the (joint) distributions of these parameters may either get an increased or decreased ROPE, which means that inferences based on `rope()` are inappropriate (*Kruschke 2014, 340f*).

`rope()` performs a simple check for pairwise correlations between parameters, but as there can be collinearity between more than two variables, a first step to check the assumptions of this hypothesis testing is to look at different pair plots. An even more sophisticated check is the projection predictive variable selection (*Piironen and Vehtari 2017*).

Strengths and Limitations

Strengths: Provides information related to the practical relevance of the effects.

Limitations: A ROPE range needs to be arbitrarily defined. Sensitive to the scale (the unit) of the predictors. Not sensitive to highly significant effects.

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.

- "location": returns location parameters such as conditional, zero_inflated, or smooth_terms (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.

For models of class brmsfit (package **brms**), even more options are possible for the component argument, which are not all documented in detail here. See also ?insight::find_parameters.

Note

There is also a plot()-method implemented in the **see**-package.

References

- Cohen, J. (1988). Statistical power analysis for the behavioural sciences.
- Kruschke, J. K. (2010). What to believe: Bayesian methods for data analysis. Trends in cognitive sciences, 14(7), 293-300. doi:10.1016/j.tics.2010.05.001.
- Kruschke, J. K. (2011). Bayesian assessment of null values via parameter estimation and model comparison. Perspectives on Psychological Science, 6(3), 299-312. doi:10.1177/1745691611406925.
- Kruschke, J. K. (2014). Doing Bayesian data analysis: A tutorial with R, JAGS, and Stan. Academic Press. doi:10.1177/2515245918771304.
- Kruschke, J. K. (2018). Rejecting or accepting parameter values in Bayesian estimation. Advances in Methods and Practices in Psychological Science, 1(2), 270-280. doi:10.1177/2515245918771304.
- Makowski D, Ben-Shachar MS, Chen SHA, Lüdecke D (2019) Indices of Effect Existence and Significance in the Bayesian Framework. Frontiers in Psychology 2019;10:2767. doi:10.3389/fpsyg.2019.02767
- Piironen, J., & Vehtari, A. (2017). Comparison of Bayesian predictive methods for model selection. Statistics and Computing, 27(3), 711–735. doi:10.1007/s112220169649y

Examples

```
library(bayestestR)

rope(x = rnorm(1000, 0, 0.01), range = c(-0.1, 0.1))
rope(x = rnorm(1000, 0, 1), range = c(-0.1, 0.1))
rope(x = rnorm(1000, 1, 0.01), range = c(-0.1, 0.1))
rope(x = rnorm(1000, 1, 1), ci = c(0.90, 0.95))

model <- suppressWarnings(
  rstanarm::stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
)
rope(model)
rope(model, ci = c(0.90, 0.95))

# multiple ROPE ranges
rope(model, range = list(c(-10, 5), c(-0.2, 0.2), "default"))
```

```
# named ROPE ranges
rope(model, range = list(gear = c(-3, 2), wt = c(-0.2, 0.2)))

rope(emmeans::emtrends(model, ~1, "wt"), ci = c(0.90, 0.95))

model <- brms::brm(mpg ~ wt + cyl, data = mtcars, refresh = 0)
rope(model)
rope(model, ci = c(0.90, 0.95))

model <- brms::brm(
  brms::bf(brms::mvbind(mpg, disp) ~ wt + cyl) + brms::set_rescor(rescor = TRUE),
  data = mtcars,
  refresh = 0
)
rope(model)
rope(model, ci = c(0.90, 0.95))

# different ROPE ranges for model parameters. For each response, a named
# list (with the name of the response variable) is required as list-element
# for the `range` argument.
rope(
  model,
  range = list(
    mpg = list(b_mpg_wt = c(-1, 1), b_mpg_cyl = c(-2, 2)),
    disp = list(b_disp_wt = c(-5, 5), b_disp_cyl = c(-4, 4))
  )
)

bf <- BayesFactor::ttestBF(x = rnorm(100, 1, 1))
rope(bf)
rope(bf, ci = c(0.90, 0.95))
```

---

rope_range *Find Default Equivalence (ROPE) Region Bounds*

Description

This function attempts at automatically finding suitable "default" values for the Region Of Practical Equivalence (ROPE).

Usage

```
rope_range(x, ...)

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

Arguments

x	A stanreg, brmsfit or BFBayesFactor object, or a frequentist regression model.
...	Currently not used.
verbose	Toggle warnings.

Details

Kruschke (2018) suggests that the region of practical equivalence could be set, by default, to a range from -0.1 to 0.1 of a standardized parameter (negligible effect size according to *Cohen, 1988*).

- For **linear models (lm)**, this can be generalised to $[-0.1 * SD_y, 0.1 * SD_y]$.
- For **logistic models**, the parameters expressed in log odds ratio can be converted to standardized difference through the formula $\pi/\sqrt{3}$, resulting in a range of -0.18 to 0.18.
- For other models with **binary outcome**, it is strongly recommended to manually specify the rope argument. Currently, the same default is applied that for logistic models.
- For models from **count data**, the residual variance is used. This is a rather experimental threshold and is probably often similar to -0.1, 0.1, but should be used with care!
- For **t-tests**, the standard deviation of the response is used, similarly to linear models (see above).
- For **correlations**, -0.05, 0.05 is used, i.e., half the value of a negligible correlation as suggested by Cohen's (1988) rules of thumb.
- For all other models, -0.1, 0.1 is used to determine the ROPE limits, but it is strongly advised to specify it manually.

References

Kruschke, J. K. (2018). Rejecting or accepting parameter values in Bayesian estimation. Advances in Methods and Practices in Psychological Science, 1(2), 270-280. doi:10.1177/2515245918771304.

Examples

```
model <- suppressWarnings(rstanarm::stan_glm(
  mpg ~ wt + gear,
  data = mtcars,
  chains = 2,
  iter = 200,
  refresh = 0
))
rope_range(model)

model <- suppressWarnings(
  rstanarm::stan_glm(vs ~ mpg, data = mtcars, family = "binomial", refresh = 0)
)
rope_range(model)

model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
rope_range(model)
```

```
model <- BayesFactor::ttestBF(mtcars[mtcars$vs == 1, "mpg"], mtcars[mtcars$vs == 0, "mpg"])
rope_range(model)

model <- lmBF(mpg ~ vs, data = mtcars)
rope_range(model)
```

`sensitivity_to_prior` *Sensitivity to Prior*

Description

Computes the sensitivity to priors specification. This represents the proportion of change in some indices when the model is fitted with an antagonistic prior (a prior of same shape located on the opposite of the effect).

Usage

```
sensitivity_to_prior(model, ...)

## S3 method for class 'stanreg'
sensitivity_to_prior(model, index = "Median", magnitude = 10, ...)

## S3 method for class 'brmsfit'
sensitivity_to_prior(model, index = "Median", magnitude = 10, ...)
```

Arguments

`model`	A Bayesian model (`stanreg` or `brmsfit`).
`...`	Arguments passed to or from other methods.
`index`	The indices from which to compute the sensitivity. Can be one or multiple names of the columns returned by `describe_posterior`. The case is important here (e.g., write 'Median' instead of 'median').
`magnitude`	This represent the magnitude by which to shift the antagonistic prior (to test the sensitivity). For instance, a magnitude of 10 (default) means that the mode will be updated with a prior located at 10 standard deviations from zero, on the opposite side of the effect.

Details

For `brmsfit` models, all slopes must have a normal, student_t, or cauchy prior, because only these priors are supported for moving to an antagonistic location. The default flat priors of **brms** are not supported, so set the priors with `brms::set_prior()` when fitting the model. Multivariate models are not supported. Only regular slopes of the main formula get a new prior. Other parameters, such as non-linear parameters or monotonic effects, give an error, and so do bounded slope priors. Intercepts, including the thresholds of ordinal models, are not changed.

Value

A data frame with a `Parameter` column and one `Sensitivity_*` column for `Median` and for each other index.

See Also

DescTools

Examples

```
library(bayestestR)

# rstanarm models
# ---------------------------------------------
model <- rstanarm::stan_glm(mpg ~ wt, data = mtcars)
sensitivity_to_prior(model)

model <- rstanarm::stan_glm(mpg ~ wt + cyl, data = mtcars)
sensitivity_to_prior(model, index = c("Median", "MAP"))




# brms models
# ---------------------------------------------
model <- brms::brm(
  mpg ~ wt + cyl,
  data = mtcars,
  prior = brms::set_prior("normal(0, 5)", class = "b"),
  chains = 2,
  iter = 1000,
  refresh = 0
)
sensitivity_to_prior(model)
```

`sexit` *Sequential Effect eXistence and sIgnificance Testing (SEXIT)*

Description

The SEXIT is a new framework to describe Bayesian effects, guiding which indices to use. Accordingly, the `sexit()` function returns the minimal (and optimal) required information to describe models' parameters under a Bayesian framework. It includes the following indices:

- Centrality: the median of the posterior distribution. In probabilistic terms, there is `50%` of probability that the effect is higher and lower. See `point_estimate()`.

- Uncertainty: the 95% Highest Density Interval (HDI). In probabilistic terms, there is 95% of probability that the effect is within this confidence interval. See ci().
- Existence: The probability of direction allows to quantify the certainty by which an effect is positive or negative. It is a critical index to show that an effect of some manipulation is not harmful (for instance in clinical studies) or to assess the direction of a link. See p_direction().
- Significance: Once existence is demonstrated with high certainty, we can assess whether the effect is of sufficient size to be considered as significant (i.e., not negligible). This is a useful index to determine which effects are actually important and worthy of discussion in a given process. See p_significance().
- Size: Finally, this index gives an idea about the strength of an effect. However, beware, as studies have shown that a big effect size can be also suggestive of low statistical power (see details section).

Usage

```
sexit(x, significant = "default", large = "default", ci = 0.95, ...)
```

Arguments

x	A vector representing a posterior distribution, a data frame of posterior draws (samples be parameter). Can also be a Bayesian model.
significant, large	The threshold values to use for significant and large probabilities. If left to 'default', will be selected through sexit_thresholds(). See the details section below.
ci	Value or vector of probability of the (credible) interval - CI (between 0 and 1) to be estimated. Default to .95 (95%).
...	Currently not used.

Details

Rationale: The assessment of "significance" (in its broadest meaning) is a pervasive issue in science, and its historical index, the p-value, has been strongly criticized and deemed to have played an important role in the replicability crisis. In reaction, more and more scientists have tuned to Bayesian methods, offering an alternative set of tools to answer their questions. However, the Bayesian framework offers a wide variety of possible indices related to "significance", and the debate has been raging about which index is the best, and which one to report.

This situation can lead to the mindless reporting of all possible indices (with the hopes that with that the reader will be satisfied), but often without having the writer understanding and interpreting them. It is indeed complicated to juggle between many indices with complicated definitions and subtle differences.

SEXIT aims at offering a practical framework for Bayesian effects reporting, in which the focus is put on intuitiveness, explicitness and usefulness of the indices' interpretation. To that end, we suggest a system of description of parameters that would be intuitive, easy to learn and apply, mathematically accurate and useful for taking decision.

Once the thresholds for significance (i.e., the ROPE) and the one for a "large" effect are explicitly defined, the SEXIT framework does not make any interpretation, i.e., it does not label the effects, but just sequentially gives 3 probabilities (of direction, of significance and of being large, respectively) as-is on top of the characteristics of the posterior (using the median and HDI for centrality and uncertainty description). Thus, it provides a lot of information about the posterior distribution (through the mass of different 'sections' of the posterior) in a clear and meaningful way.

Threshold selection: One of the most important thing about the SEXIT framework is that it relies on two "arbitrary" thresholds (i.e., that have no absolute meaning). They are the ones related to effect size (an inherently subjective notion), namely the thresholds for significant and large effects. They are set, by default, to `0.05` and `0.3` of the standard deviation of the outcome variable (tiny and large effect sizes for correlations according to Funder and Ozer, 2019). However, these defaults were chosen by lack of a better option, and might not be adapted to your case. Thus, they are to be handled with care, and the chosen thresholds should always be explicitly reported and justified.

- For **linear models (lm)**, this can be generalised to $[0.05 * SD_y]$ and $[0.3 * SD_y]$ for significant and large effects, respectively.
- For **logistic models**, the parameters expressed in log odds ratio can be converted to standardized difference through the formula $\pi/\sqrt{3}$, resulting a threshold of `0.09` and `0.54`.
- For other models with **binary outcome**, it is strongly recommended to manually specify the rope argument. Currently, the same default is applied that for logistic models.
- For models from **count data**, the residual variance is used. This is a rather experimental threshold and is probably often similar to `0.05` and `0.3`, but should be used with care!
- For **t-tests**, the standard deviation of the response is used, similarly to linear models (see above).
- For **correlations**,`0.05` and `0.3` are used.
- For all other models, `0.05` and `0.3` are used, but it is strongly advised to specify it manually.

Examples: The three values for existence, significance and size provide a useful description of the posterior distribution of the effects. Some possible scenarios include:

- The probability of existence is low, but the probability of being large is high: it suggests that the posterior is very wide (covering large territories on both side of 0). The statistical power might be too low, which should warrant any confident conclusion.
- The probability of existence and significance is high, but the probability of being large is very small: it suggests that the effect is, with high confidence, not large (the posterior is mostly contained between the significance and the large thresholds).
- The 3 indices are very low: this suggests that the effect is null with high confidence (the posterior is closely centered around 0).

Value

A dataframe and text as attribute.

References

- Makowski, D., Ben-Shachar, M. S., & Lüdecke, D. (2019). bayestestR: Describing Effects and their Uncertainty, Existence and Significance within the Bayesian Framework. Journal of Open Source Software, 4(40), 1541. doi:10.21105/joss.01541

- Makowski D, Ben-Shachar MS, Chen SHA, Lüdecke D (2019) Indices of Effect Existence and Significance in the Bayesian Framework. Frontiers in Psychology 2019;10:2767. doi:10.3389/fpsyg.2019.02767

Examples

```
library(bayestestR)

s <- sexit(rnorm(1000, -1, 1))
s
print(s, summary = TRUE)

s <- sexit(iris)
s
print(s, summary = TRUE)

if (require("rstanarm")) {
  model <- suppressWarnings(rstanarm::stan_glm(mpg ~ wt * cyl,
    data = mtcars,
    iter = 400, refresh = 0
  ))
  s <- sexit(model)
  s
  print(s, summary = TRUE)
}
```

---

sexit_thresholds *Find Effect Size Thresholds*

Description

This function attempts at automatically finding suitable default values for a "significant" (i.e., non-negligible) and "large" effect. This is to be used with care, and the chosen threshold should always be explicitly reported and justified. See the detail section in `sexit()` for more information.

Usage

```
sexit_thresholds(x, ...)
```

Arguments

`x`	Vector representing a posterior distribution. Can also be a `stanreg` or `brmsfit` model.
`...`	Currently not used.

References

Kruschke, J. K. (2018). Rejecting or accepting parameter values in Bayesian estimation. Advances in Methods and Practices in Psychological Science, 1(2), 270-280. doi:10.1177/2515245918771304.

Examples

```
sexit_thresholds(rnorm(1000))

if (require("rstanarm")) {
  model <- suppressWarnings(stan_glm(
    mpg ~ wt + gear,
    data = mtcars,
    chains = 2,
    iter = 200,
    refresh = 0
  ))
  sexit_thresholds(model)

  model <- suppressWarnings(
    stan_glm(vs ~ mpg, data = mtcars, family = "binomial", refresh = 0)
  )
  sexit_thresholds(model)
}

if (require("brms")) {
  model <- brm(mpg ~ wt + cyl, data = mtcars)
  sexit_thresholds(model)
}

if (require("BayesFactor")) {
  bf <- ttestBF(x = rnorm(100, 1, 1))
  sexit_thresholds(bf)
}
```

---

si *Compute Support Intervals*

Description

A support interval contains only the values of the parameter that predict the observed data better than average, by some degree *k*; these are values of the parameter that are associated with an updating factor greater or equal than *k*. From the perspective of the Savage-Dickey Bayes factor, testing against a point null hypothesis for any value within the support interval will yield a Bayes factor smaller than *1/k*.

For more info, see the Bayes factors vignette.

Usage

```
si(posterior, ...)

## S3 method for class 'numeric'
si(posterior, prior = NULL, BF = 1, verbose = TRUE, ...)
```

```
## S3 method for class 'stanreg'
si(
  posterior,
  prior = NULL,
  BF = 1,
  verbose = TRUE,
  effects = "fixed",
  component = "location",
  parameters = NULL,
  ...
)

## S3 method for class 'get_predicted'
si(
  posterior,
  prior = NULL,
  BF = 1,
  use_iterations = FALSE,
  verbose = TRUE,
  ...
)

## S3 method for class 'data.frame'
si(posterior, prior = NULL, BF = 1, rvar_col = NULL, verbose = TRUE, ...)
```

Arguments

posterior	A numerical vector, stanreg / brmsfit object, emmGrid or a data frame - representing a posterior distribution(s) from (see 'Details').
...	Arguments passed to and from other methods. (Can be used to pass arguments to internal logspline::logspline().)
prior	An object representing a prior distribution (see 'Details').
BF	The amount of support required to be included in the support interval.
verbose	Toggle off warnings.
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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

use_iterations — Logical, if TRUE and x is a get_predicted object, (returned by insight::get_predicted()), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., brmsfit models).

rvar_col — A single character - the name of an rvar column in the data frame to be processed. See example in p_direction().

Details

This method is used to compute support intervals based on prior and posterior distributions.

Value

A data frame containing the lower and upper bounds of the SI.

Note that if the level of requested support is higher than observed in the data, the interval will be [NA,NA].

Choosing a value of BF

The choice of BF (the level of support) depends on what we want our interval to represent:

- A BF = 1 contains values whose credibility is not decreased by observing the data.
- A BF > 1 contains values who received more impressive support from the data.
- A BF < 1 contains values whose credibility has *not* been impressively decreased by observing the data. Testing against values outside this interval will produce a Bayes factor larger than 1/BF in support of the alternative. E.g., if an SI (BF = 1/3) excludes 0, the Bayes factor against the point-null will be larger than 3.

Prior and posterior considerations

In order to correctly and precisely estimate Bayes factors, a rule of thumb are the 4 P's: **P**roper **P**riors and **P**lentiful **P**osteriors.

For the computation of Bayes factors, the model priors must be proper priors (at the very least they should be *not flat*, and it is preferable that they be *informative*) (Note that by default, `brms::brm()` uses flat priors for fixed-effects); Wide priors result in smaller marginal likelihoods, and thus models with wider priors are trivially less likely than models with narrower priors - where, at the extreme, that a model with completely flat priors is infinitely less favorable than a point null model (this is called *the Jeffreys-Lindley-Bartlett paradox*). Thus, you should only ever try (or want) to compute a Bayes factor when you have an informed prior.

Additionally, for models using MCMC estimation the number of posterior samples needed for testing is substantially larger than for estimation (the default of 4000 samples may not be enough in many cases). A conservative rule of thumb is to obtain 10 times more samples than would be required for estimation (*Gronau, Singmann, & Wagenmakers, 2017*). If less than 40,000 samples are detected, a warning is issued.

Obtaining prior samples

It is important to provide the correct `prior` for meaningful results, to match the `posterior`-type input:

- **A numeric vector** - `prior` should also be a *numeric vector*, representing the prior-distribution
- **A data frame** - `prior` should also be a *data frame*, representing the prior-estimates, in matching column order.
  - If `rvar_col` is specified, `prior` should be *the name of an* `rvar` *column* that represents the prior-estimates.
- **Supported Bayesian model (`stanreg`, `brmsfit`, etc.)**
  - `prior` should be *a model an equivalent model with MCMC samples from the priors* **only**. See `unupdate()`.
  - If `prior` is set to `NULL`, `unupdate()` is called internally (not supported for `brmsfit_multiple` model).
- **Output from a `{marginaleffects}` function** - `prior` should also be *an equivalent output* from a `{marginaleffects}` function based on a prior-model (See `unupdate()`).
- **Output from an `{emmeans}` function**
  - `prior` should also be *an equivalent output* from an `{emmeans}` function based on a prior-model (See `unupdate()`).
  - `prior` can also be *the original (posterior) model*, in which case the function will try to "unupdate" the estimates (not supported if the estimates have undergone any transformations – `"log"`, `"response"`, etc. – or any `regriding`).

Note

There is also a `plot()`-method implemented in the **see**-package.

References

Wagenmakers, E., Gronau, Q. F., Dablander, F., & Etz, A. (2018, November 22). The Support Interval. doi:10.31234/osf.io/zwnxb

See Also

Other ci: `bci()`, `ci()`, `eti()`, `hdi()`, `spi()`

Examples

```
library(bayestestR)

prior <- distribution_normal(1000, mean = 0, sd = 1)
posterior <- distribution_normal(1000, mean = 0.5, sd = 0.3)

si(posterior, prior, verbose = FALSE)

# rstanarm models
# ---------------
library(rstanarm)
contrasts(sleep$group) <- contr.equalprior_pairs # see vignette
stan_model <- stan_lmer(extra ~ group + (1 | ID), data = sleep)
si(stan_model, verbose = FALSE)
si(stan_model, BF = 3, verbose = FALSE)

# emmGrid objects
# ---------------
library(emmeans)
group_diff <- pairs(emmeans(stan_model, ~group))
si(group_diff, prior = stan_model, verbose = FALSE)

# brms models
# -----------
library(brms)
contrasts(sleep$group) <- contr.equalprior_pairs # see vingette
my_custom_priors <-
  set_prior("student_t(3, 0, 1)", class = "b") +
  set_prior("student_t(3, 0, 1)", class = "sd", group = "ID")

brms_model <- suppressWarnings(brm(extra ~ group + (1 | ID),
  data = sleep,
  prior = my_custom_priors,
  refresh = 0
))
si(brms_model, verbose = FALSE)
```

`simulate_correlation` *Data Simulation*

Description

Simulate data with specific characteristics.

Usage

```
simulate_correlation(n = 100, r = 0.5, mean = 0, sd = 1, names = NULL, ...)

simulate_ttest(n = 100, d = 0.5, names = NULL, ...)

simulate_difference(n = 100, d = 0.5, names = NULL, ...)
```

Arguments

`n`	The number of observations to be generated.
`r`	A value or vector corresponding to the desired correlation coefficients.
`mean`	A value or vector corresponding to the mean of the variables.
`sd`	A value or vector corresponding to the SD of the variables.
`names`	A character vector of desired variable names.
`...`	Arguments passed to or from other methods.
`d`	A value or vector corresponding to the desired difference between the groups.

Examples

```
# Correlation ------------------------------
data <- simulate_correlation(r = 0.5)
plot(data$V1, data$V2)
cor.test(data$V1, data$V2)
summary(lm(V2 ~ V1, data = data))

# Specify mean and SD
data <- simulate_correlation(r = 0.5, n = 50, mean = c(0, 1), sd = c(0.7, 1.7))
cor.test(data$V1, data$V2)
round(c(mean(data$V1), sd(data$V1)), 1)
round(c(mean(data$V2), sd(data$V2)), 1)
summary(lm(V2 ~ V1, data = data))

# Generate multiple variables
cor_matrix <- matrix(
  c(
    1.0, 0.2, 0.4,
    0.2, 1.0, 0.3,
    0.4, 0.3, 1.0
```

```
  ),
  nrow = 3
)

data <- simulate_correlation(r = cor_matrix, names = c("y", "x1", "x2"))
cor(data)
summary(lm(y ~ x1, data = data))

# t-test --------------------------------
data <- simulate_ttest(n = 30, d = 0.3)
plot(data$V1, data$V0)
round(c(mean(data$V1), sd(data$V1)), 1)
diff(t.test(data$V1 ~ data$V0)$estimate)
summary(lm(V1 ~ V0, data = data))
summary(glm(V0 ~ V1, data = data, family = "binomial"))

# Difference ----------------------------------
data <- simulate_difference(n = 30, d = 0.3)
plot(data$V1, data$V0)
round(c(mean(data$V1), sd(data$V1)), 1)
diff(t.test(data$V1 ~ data$V0)$estimate)
summary(lm(V1 ~ V0, data = data))
summary(glm(V0 ~ V1, data = data, family = "binomial"))
```

`simulate_prior` *Returns Priors of a Model as Empirical Distributions*

Description

Transforms priors information to actual distributions.

Usage

```
simulate_prior(model, n = 1000, ...)

## S3 method for class 'brmsfit'
simulate_prior(
  model,
  n = 1000,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

model	A stanreg, stanfit, brmsfit, blavaan, or MCMCglmm object.
n	Size of the simulated prior distributions.
...	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.
component	Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.
parameters	Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.
verbose	Toggle off warnings.

See Also

unupdate() for directly sampling from the prior distribution (useful for complex priors and designs).

Examples

```
library(bayestestR)
if (require("rstanarm")) {
  model <- suppressWarnings(
```

```
    stan_glm(mpg ~ wt + am, data = mtcars, chains = 1, refresh = 0)
  )
  simulate_prior(model)
}
```

`simulate_simpson` *Simpson's paradox dataset simulation*

Description

Simpson's paradox, or the Yule-Simpson effect, is a phenomenon in probability and statistics, in which a trend appears in several different groups of data but disappears or reverses when these groups are combined.

Usage

```
simulate_simpson(
  n = 100,
  r = 0.5,
  groups = 3,
  difference = 1,
  group_prefix = "G_"
)
```

Arguments

`n`	The number of observations for each group to be generated (minimum 4).
`r`	A value or vector corresponding to the desired correlation coefficients.
`groups`	Number of groups (groups can be participants, clusters, anything).
`difference`	Difference between groups.
`group_prefix`	The prefix of the group name (e.g., "G_1", "G_2", "G_3", ...).

Value

A dataset.

Examples

```
data <- simulate_simpson(n = 10, groups = 5, r = 0.5)

if (require("ggplot2")) {
  ggplot(data, aes(x = V1, y = V2)) +
    geom_point(aes(color = Group)) +
    geom_smooth(aes(color = Group), method = "lm") +
    geom_smooth(method = "lm")
}
```

spi *Shortest Probability Interval (SPI)*

Description

Compute the **Shortest Probability Interval (SPI)** of posterior distributions. The SPI is a more computationally stable HDI. The implementation is based on the algorithm from the **SPIn** package.

Usage

```
spi(x, ...)

## S3 method for class 'numeric'
spi(x, ci = 0.95, verbose = TRUE, ...)

## S3 method for class 'data.frame'
spi(x, ci = 0.95, rvar_col = NULL, verbose = TRUE, ...)

## S3 method for class 'brmsfit'
spi(
  x,
  ci = 0.95,
  effects = "fixed",
  component = "conditional",
  parameters = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'get_predicted'
spi(x, ci = 0.95, use_iterations = FALSE, verbose = TRUE, ...)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model. **bayestestR** supports a wide range of models (see, for example, `methods("hdi")`) and not all of those are documented in the 'Usage' section, because methods for other classes mostly resemble the arguments of the `.numeric` or `.data.frame`methods.
...	Currently not used.
ci	Value or vector of probability of the (credible) interval - CI (between 0 and 1) to be estimated. Default to `.95` (95%).
verbose	Toggle off warnings.
rvar_col	A single character - the name of an `rvar` column in the data frame to be processed. See example in `p_direction()`.

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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

use_iterations — Logical, if TRUE and x is a get_predicted object, (returned by insight::get_predicted()), the function is applied to the iterations instead of the predictions. This only applies to models that return iterations for predicted values (e.g., brmsfit models).

Details

The SPI is an alternative method to the HDI (hdi()) to quantify uncertainty of (posterior) distributions. The SPI is said to be more stable than the HDI, because, the *"HDI can be noisy (that is, have a high Monte Carlo error)"* (Liu et al. 2015). Furthermore, the HDI is sensitive to additional assumptions, in particular assumptions related to the different estimation methods, which can make the HDI less accurate or reliable.

Value

A data frame with following columns:

- Parameter The model parameter(s), if x is a model-object. If x is a vector, this column is missing.

- `CI` The probability of the credible interval.
- `CI_low`, `CI_high` The lower and upper credible interval limits for the parameters.

Note

The code to compute the SPI was adapted from the **SPIn** package, and slightly modified to be more robust for Stan models. Thus, credits go to Ying Liu for the original SPI algorithm and R implementation.

References

Liu, Y., Gelman, A., & Zheng, T. (2015). Simulation-efficient shortest probability intervals. Statistics and Computing, 25(4), 809–819. https://doi.org/10.1007/s11222-015-9563-8

See Also

Other ci: `bci()`, `ci()`, `eti()`, `hdi()`, `si()`

Examples

```
library(bayestestR)

posterior <- rnorm(1000)
spi(posterior)
spi(posterior, ci = c(0.80, 0.89, 0.95))

df <- data.frame(replicate(4, rnorm(100)))
spi(df)
spi(df, ci = c(0.80, 0.89, 0.95))

library(rstanarm)
model <- suppressWarnings(
  stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
)
spi(model)
```

---

weighted_posteriors *Generate posterior distributions weighted across models*

Description

Extract posterior samples of parameters, weighted across models. Weighting is done by comparing posterior model probabilities, via `bayesfactor_models()`.

Usage

```
weighted_posteriors(..., prior_odds = NULL, missing = 0, verbose = TRUE)

## S3 method for class 'data.frame'
weighted_posteriors(..., prior_odds = NULL, missing = 0, verbose = TRUE)

## S3 method for class 'stanreg'
weighted_posteriors(
  ...,
  prior_odds = NULL,
  missing = 0,
  verbose = TRUE,
  effects = "fixed",
  component = "conditional",
  parameters = NULL
)

## S3 method for class 'BFBayesFactor'
weighted_posteriors(
  ...,
  prior_odds = NULL,
  missing = 0,
  verbose = TRUE,
  iterations = 4000
)
```

Arguments

`...`	Fitted models (see details), all fit on the same data, or a single `BFBayesFactor` object.
`prior_odds`	Optional vector of prior odds for the models compared to the first model (or the denominator, for `BFBayesFactor` objects). For `data.frame`s, this will be used as the basis of weighting.
`missing`	An optional numeric value to use if a model does not contain a parameter that appears in other models. Defaults to 0.
`verbose`	Toggle off warnings.
`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.

component — Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, etc. 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.

parameters — Regular expression pattern that describes the parameters that should be returned. Meta-parameters (like lp__ or prior_) are filtered by default, so only parameters that typically appear in the summary() are returned. Use parameters to select specific parameters for the output.

iterations — For BayesFactor models, how many posterior samples to draw.

Details

Note that across models some parameters might play different roles. For example, the parameter A plays a different role in the model Y ~ A + B (where it is a main effect) than it does in the model Y ~ A + B + A:B (where it is a simple effect). In many cases centering of predictors (mean subtracting for continuous variables, and effects coding via contr.sum or orthonormal coding via contr.equalprior_pairs for factors) can reduce this issue. In any case you should be mindful of this issue.

See bayesfactor_models() details for more info on passed models.

Note that for BayesFactor models, posterior samples cannot be generated from intercept only models.

This function is similar in function to brms::posterior_average.

Value

A data frame with posterior distributions (weighted across models) .

Note

For BayesFactor < 0.9.12-4.3, in some instances there might be some problems of duplicate columns of random effects in the resulting data frame.

References

- Clyde, M., Desimone, H., & Parmigiani, G. (1996). Prediction via orthogonalized model mixing. Journal of the American Statistical Association, 91(435), 1197-1208.

- Hinne, M., Gronau, Q. F., van den Bergh, D., and Wagenmakers, E. (2019, March 25). A conceptual introduction to Bayesian Model Averaging. doi:10.31234/osf.io/wgb64
- Rouder, J. N., Haaf, J. M., & Vandekerckhove, J. (2018). Bayesian inference for psychology, part IV: Parameter estimation and Bayes factors. Psychonomic bulletin & review, 25(1), 102-113.
- van den Bergh, D., Haaf, J. M., Ly, A., Rouder, J. N., & Wagenmakers, E. J. (2019). A cautionary note on estimating effect size.

See Also

`bayesfactor_inclusion()` for Bayesian model averaging.

Examples

```
if (require("rstanarm") && require("see") && interactive()) {
  stan_m0 <- suppressWarnings(stan_glm(extra ~ 1,
    data = sleep,
    family = gaussian(),
    refresh = 0,
    diagnostic_file = file.path(tempdir(), "df0.csv")
  ))

  stan_m1 <- suppressWarnings(stan_glm(extra ~ group,
    data = sleep,
    family = gaussian(),
    refresh = 0,
    diagnostic_file = file.path(tempdir(), "df1.csv")
  ))

  res <- weighted_posteriors(stan_m0, stan_m1, verbose = FALSE)

  plot(eti(res))
}

## With BayesFactor
if (require("BayesFactor")) {
  extra_sleep <- ttestBF(formula = extra ~ group, data = sleep)

  wp <- weighted_posteriors(extra_sleep, verbose = FALSE)

  describe_posterior(extra_sleep, test = NULL, verbose = FALSE)
  # also considers the null
  describe_posterior(wp$delta, test = NULL, verbose = FALSE)
}


## weighted prediction distributions via data.frames
if (require("rstanarm") && interactive()) {
  m0 <- suppressWarnings(stan_glm(
    mpg ~ 1,
    data = mtcars,
    family = gaussian(),
```

```
  diagnostic_file = file.path(tempdir(), "df0.csv"),
  refresh = 0
))

m1 <- suppressWarnings(stan_glm(
  mpg ~ carb,
  data = mtcars,
  family = gaussian(),
  diagnostic_file = file.path(tempdir(), "df1.csv"),
  refresh = 0
))

# Predictions:
pred_m0 <- data.frame(posterior_predict(m0))
pred_m1 <- data.frame(posterior_predict(m1))

BFmods <- bayesfactor_models(m0, m1, verbose = FALSE)

wp <- weighted_posteriors(
  pred_m0, pred_m1,
  prior_odds = as.numeric(BFmods)[2],
  verbose = FALSE
)

# look at first 5 prediction intervals
hdi(pred_m0[1:5])
hdi(pred_m1[1:5])
hdi(wp[1:5]) # between, but closer to pred_m1
}
```

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