Package 'bayestestR'

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Type Package

Title Understand and Describe Bayesian Models and Posterior Distributions

Version 0.11.0

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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).

Depends R (>= 3.4)

Imports insight (>= 0.14.1), datawizard (>= 0.2.0), methods, stats, utils

Suggests BayesFactor, bayesQR, blavaan, bridgesampling, brms, dplyr, effectsize, emmeans, GGally, ggdist, ggplot2, ggridges, httr, KernSmooth, knitr, lavaan, lme4, logspline, MASS, mclust, mediation, modelbased, parameters, performance, rmarkdown, rstan, rstanarm, see, spelling, stringr, testthat, tidyr, tweedie

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R topics documented:

`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 compte 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 = c("fixed", "random", "all"),
  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 results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
`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

```
library(bayestestR)

if (require("logspline")) {
  prior <- distribution_normal(1000, mean = 0, sd = 1)
```

```
  posterior <- distribution_normal(1000, mean = .5, sd = .3)

  bayesfactor(posterior, prior = prior)
}
## Not run:
# rstanarm models
# ---------------
if (require("rstanarm")) {
  model <- stan_lmer(extra ~ group + (1 | ID), data = sleep)
  bayesfactor(model)
}

## End(Not run)

if (require("logspline")) {
  # 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)
}
```

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

Description

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 containe the main effect terms from which the interaction term is comprised.

Value

a data frame containing the prior and posterior probabilities, and log(BF) for each effect.

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) (*Wetzels et al. 2011*).

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

- 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
- 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.

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)
bayesfactor_inclusion(BFmodels)
## Not run:
# BayesFactor
# ------------------------------
library(BayesFactor)

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

bayesfactor_inclusion(BF)

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

## End(Not run)
```

---

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.

Usage

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

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

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

## S3 method for class 'bayesfactor_models'
as.matrix(x, ...)
```

Arguments

...	Fitted models (see details), all fit on the same data, or a single BFBayesFactor object (see 'Details'). Ignored in as.matrix(), update().
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.
object, x	A bayesfactor_models() object.
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.

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 mostly a wraparound BayesFactor::extractBF().
- BIC approximations are used to compute Bayes factors for all other model types (with a BIC method).
  - **Note** that BICs are extracted from models as-is. So if for example you want to compare mixed-models bases on ML instead of REML, you must supply models fit with ML.

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. How many? 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, bayesfactor_models() gives a warning.

See also the Bayes factors vignette.

Value

A data frame containing the models' formulas (reconstructed fixed and random effects) and their log(BF)s, that prints nicely.

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) (*Wetzels et al. 2011*).

Note

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

Author(s)

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References

- Gronau, Q. F., Singmann, H., & Wagenmakers, E. J. (2017). Bridgesampling: An R package for estimating normalizing constants. arXiv preprint arXiv:1710.08162.
- Kass, R. E., and Raftery, A. E. (1995). Bayes Factors. Journal of the American Statistical Association, 90(430), 773-795.
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Examples

```
# With lm objects:
# ----------------
lm1 <- lm(Sepal.Length ~ 1, data = iris)
lm2 <- lm(Sepal.Length ~ Species, data = iris)
lm3 <- lm(Sepal.Length ~ Species + Petal.Length, data = iris)
lm4 <- lm(Sepal.Length ~ Species * Petal.Length, data = iris)
bayesfactor_models(lm1, lm2, lm3, lm4, denominator = 1)
bayesfactor_models(lm2, lm3, lm4, denominator = lm1) # same result
BFM <- bayesfactor_models(lm1, lm2, lm3, lm4, denominator = lm1) # same result

update(BFM, reference = "bottom")
as.matrix(BFM)
## Not run:
# With lmerMod objects:
# ---------------------
if (require("lme4")) {
  lmer1 <- lmer(Sepal.Length ~ Petal.Length + (1 | Species), data = iris)
  lmer2 <- lmer(Sepal.Length ~ Petal.Length + (Petal.Length | Species), data = iris)
  lmer3 <- lmer(
    Sepal.Length ~ Petal.Length + (Petal.Length | Species) + (1 | Petal.Width),
    data = iris
  )
  bayesfactor_models(lmer1, lmer2, lmer3, denominator = 1)
  bayesfactor_models(lmer1, lmer2, lmer3, denominator = lmer1)
}

# rstanarm models
```

```
# ---------------------
# (note that a unique diagnostic_file MUST be specified in order to work)
if (require("rstanarm")) {
  stan_m0 <- stan_glm(Sepal.Length ~ 1,
    data = iris,
    family = gaussian(),
    diagnostic_file = file.path(tempdir(), "df0.csv")
  )
  stan_m1 <- stan_glm(Sepal.Length ~ Species,
    data = iris,
    family = gaussian(),
    diagnostic_file = file.path(tempdir(), "df1.csv")
  )
  stan_m2 <- 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)
}


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

  bayesfactor_models(brm1, brm2, brm3, denominator = 1)
}


# BayesFactor
# ---------------------------
if (require("BayesFactor")) {
  data(puzzles)
  BF <- anovaBF(RT ~ shape * color + ID,
    data = puzzles,
    whichRandom = "ID", progress = FALSE
  )
  BF
  bayesfactor_models(BF) # basically the same
}

## End(Not run)
```

`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 further 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).

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

`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). Aliases of the main functions are prefixed with bf_*, like `bf_parameters()` or `bf_pointnull()`.

For more info, in particular on specifying correct priors for factors with more than 2 levels, 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 = 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 = 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,
  verbose = TRUE,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "location", "smooth_terms", "sigma", "zi",
    "zero_inflated", "all"),
  parameters = NULL,
  ...
)

## S3 method for class 'brmsfit'
bayesfactor_parameters(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = 0,
  verbose = TRUE,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "location", "smooth_terms", "sigma", "zi",
    "zero_inflated", "all"),
  parameters = NULL,
  ...
)

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

## S3 method for class 'data.frame'
bayesfactor_parameters(
  posterior,
  prior = NULL,
  direction = "two-sided",
  null = 0,
  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).
verbose	Toggle off warnings.
...	Arguments passed to and from other methods. (Can be used to pass arguments to internal logspline::logspline().)
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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

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

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)).

Value

A data frame containing the (log) Bayes factor representing evidence *against* the null.

Setting the correct prior

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*); As the priors for the alternative get wider, the likelihood of the null value(s) increases, to the extreme that for completely flat priors

the null is infinitely more favorable than the alternative (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.

(Note that by default, `brms::brm()` uses flat priors for fixed-effects; See example below.)

It is important to provide the correct `prior` for meaningful results.

- When `posterior` is a numerical vector, `prior` should also be a numerical vector.
- When `posterior` is a `data.frame`, `prior` should also be a `data.frame`, with matching column order.
- When `posterior` is a `stanreg` or `brmsfit` model:
  - `prior` can be set to `NULL`, in which case prior samples are drawn internally.
  - `prior` can also be a model equivalent to `posterior` but with samples from the priors *only*. See `unupdate()`.
  - **Note:** When `posterior` is a `brmsfit_multiple` model, `prior` **must** be provided.
- When `posterior` is an `emmGrid` object:
  - `prior` should be the `stanreg` or `brmsfit` model used to create the `emmGrid` objects.
  - `prior` can also be an `emmGrid` object equivalent to `posterior` but created with a model of priors samples *only*.
  - **Note:** When the `emmGrid` has undergone any transformations (`"log"`, `"response"`, etc.), or `regriding`, then `prior` must be an `emmGrid` object, as stated above.

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) (*Wetzels et al. 2011*).

Note

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

Author(s)

Mattan S. Ben-Shachar

References

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Examples

```
library(bayestestR)
if (require("logspline")) {
  prior <- distribution_normal(1000, mean = 0, sd = 1)
  posterior <- distribution_normal(1000, mean = .5, sd = .3)
  bayesfactor_parameters(posterior, prior)
}
## Not run:
# rstanarm models
# ---------------
if (require("rstanarm") && require("emmeans") && require("logspline")) {
  contrasts(sleep$group) <- contr.orthonorm # see vingette
  stan_model <- stan_lmer(extra ~ group + (1 | ID), data = sleep)
  bayesfactor_parameters(stan_model)
  bayesfactor_parameters(stan_model, null = rope_range(stan_model))

  # emmGrid objects
  # ---------------
  group_diff <- pairs(emmeans(stan_model, ~group))
  bayesfactor_parameters(group_diff, prior = stan_model)
}

# brms models
# -----------
if (require("brms")) {
  contrasts(sleep$group) <- contr.orthonorm # 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 <- brm(extra ~ group + (1 | ID),
    data = sleep,
    prior = my_custom_priors
  )
  bayesfactor_parameters(brms_model)
}

## 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, in particular on specifying correct priors for factors with more than 2 levels, see the Bayes factors vignette.

Usage

```
bayesfactor_restricted(
  posterior,
  hypothesis,
  prior = NULL,
  verbose = TRUE,
  ...
)

bf_restricted(posterior, hypothesis, prior = NULL, verbose = TRUE, ...)

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

## S3 method for class 'brmsfit'
bayesfactor_restricted(
  posterior,
  hypothesis,
  prior = NULL,
  verbose = TRUE,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  ...
```

```
)

## 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,
  ...
)
```

Arguments

posterior	A stanreg / brmsfit object, emmGrid or a data frame - representing a posterior distribution(s) from (see Details).
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.
...	Currently not used.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.

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).

Value

A data frame containing the (log) Bayes factor representing evidence *against* the un-restricted model.

Setting the correct `prior`

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*); As the priors for the alternative get wider, the likelihood of the null value(s) increases, to the extreme that for completely flat priors the null is infinitely more favorable than the alternative (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.

(Note that by default, `brms::brm()` uses flat priors for fixed-effects; See example below.)

It is important to provide the correct `prior` for meaningful results.

- When `posterior` is a numerical vector, `prior` should also be a numerical vector.
- When `posterior` is a `data.frame`, `prior` should also be a `data.frame`, with matching column order.
- When `posterior` is a `stanreg` or `brmsfit` model:
  - `prior` can be set to `NULL`, in which case prior samples are drawn internally.
  - `prior` can also be a model equivalent to `posterior` but with samples from the priors *only*. See `unupdate()`.
  - **Note:** When `posterior` is a `brmsfit_multiple` model, `prior` **must** be provided.
- When `posterior` is an `emmGrid` object:
  - `prior` should be the `stanreg` or `brmsfit` model used to create the `emmGrid` objects.
  - `prior` can also be an `emmGrid` object equivalent to `posterior` but created with a model of priors samples *only*.
  - **Note:** When the `emmGrid` has undergone any transformations (`"log"`, `"response"`, etc.), or `regriding`, then `prior` must be an `emmGrid` object, as stated above.

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) (*Wetzels et al. 2011*).

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. Retrived from https://richarddmorey.org/category/order-restrictions/.

Examples

```
library(bayestestR)
prior <- data.frame(
  X = rnorm(100),
  X1 = rnorm(100),
  X3 = rnorm(100)
)

posterior <- data.frame(
  X = rnorm(100, .4),
  X1 = rnorm(100, -.2),
  X3 = rnorm(100)
)

hyps <- c(
  "X > X1 & X1 > X3",
  "X > X1"
)

bayesfactor_restricted(posterior, hypothesis = hyps, prior = prior)
## Not run:
# rstanarm models
# ---------------
if (require("rstanarm") && require("emmeans")) {
  fit_stan <- 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
 disgust_data <- read.table(url("http://www.learnbayes.org/disgust_example.txt"), header = TRUE)

  contrasts(disgust_data$condition) <- contr.orthonorm # see vignette
  fit_model <- stan_glm(score ~ condition, data = disgust_data, family = gaussian())

  em_condition <- emmeans(fit_model, ~condition)
  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.
```

```
}

## End(Not run)
```

---

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, verbose = TRUE, ...)

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

## S3 method for class 'sim.merMod'
bci(
  x,
  ci = 0.95,
  effects = c("fixed", "random", "all"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

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

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

## S3 method for class 'stanreg'
bci(
  x,
  ci = 0.95,
  effects = c("fixed", "random", "all"),
```

```
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

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

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

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model (stanreg, brmsfit, MCMCglmm, mcmc or bcplm) or a BayesFactor model.
...	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.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
parameters	Regular expression pattern that describes the parameters that should be returned. 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.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-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.

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). The 89% intervals (`ci = 0.89`) are deemed to be more stable than, for instance, 95% intervals (*Kruschke, 2014*). An effective sample size of at least 10.000 is recommended if one wants to estimate 95% intervals with high precision (*Kruschke, 2014, p. 183ff*). Unfortunately, the default number of posterior samples for most Bayes packages (e.g., `rstanarm` or `brms`) is only 4.000 (thus, you might want to increase it when fitting your model). Moreover, 89 indicates the arbitrariness of interval limits - its only remarkable property is being the highest prime number that does not exceed the already unstable 95% threshold (*McElreath, 2015*).
However, 95% has some advantages too. For instance, it shares (in the case of a normal posterior distribution) an intuitive relationship with the standard deviation and it conveys a more accurate image of the (artificial) bounds of the distribution. Also, because it is wider, it makes analyses more conservative (i.e., the probability of covering 0 is larger for the 95% CI than for lower ranges such as 89%), which is a good thing in the context of the reproducibility crisis.

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 97.5h 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.

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.

References

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

See Also

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

Examples

```
posterior <- rnorm(1000)
bci(posterior)
bci(posterior, ci = c(.80, .89, .95))
```

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

Description

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

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	Return the log(BF)?

Value

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

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 this blogpost.

Usage

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

Arguments

model	A stanreg, stanfit, or brmsfit 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.

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

https://statmodeling.stat.columbia.edu/2019/08/10/

Examples

```
## Not run:
library(bayestestR)
if (require("rstanarm")) {
  model <- 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 <- 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")
  plot(si(model)) # can provide visual confirmation to the Lakeland method
}

## End(Not run)
```

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", verbose = TRUE, BF = 1, ...)

## S3 method for class 'sim.merMod'
ci(
  x,
  ci = 0.95,
  method = "ETI",
  effects = c("fixed", "random", "all"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'sim'
ci(x, ci = 0.95, method = "ETI", parameters = NULL, verbose = TRUE, ...)

## S3 method for class 'stanreg'
ci(
  x,
  ci = 0.95,
  method = "ETI",
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  verbose = TRUE,
  BF = 1,
  ...
)

## S3 method for class 'brmsfit'
```

```
ci(
  x,
  ci = 0.95,
  method = "ETI",
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  parameters = NULL,
  verbose = TRUE,
  BF = 1,
  ...
)

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

## S3 method for class 'MCMCglmm'
ci(x, ci = 0.95, method = "ETI", verbose = TRUE, ...)
```

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 .95 (95%).
method	Can be 'ETI' (default), 'HDI', 'BCI' or 'SI'.
verbose	Toggle off warnings.
BF	The amount of support required to be included in the support interval.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
parameters	Regular expression pattern that describes the parameters that should be returned. 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.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.

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.

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. doi: 10.1136/bmj.l5381

See Also

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

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(.80, .89, .95))
ci(df, method = "HDI", ci = c(.80, .89, .95))
## Not run:
if (require("rstanarm")) {
  model <- stan_glm(mpg ~ wt, data = mtcars, chains = 2, iter = 200, refresh = 0)
  ci(model, method = "ETI", ci = c(.80, .89))
  ci(model, method = "HDI", ci = c(.80, .89))
  ci(model, method = "SI")
}

if (require("brms")) {
  model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
  ci(model, method = "ETI")
  ci(model, method = "HDI")
  ci(model, method = "SI")
}

if (require("BayesFactor")) {
  bf <- ttestBF(x = rnorm(100, 1, 1))
  ci(bf, method = "ETI")
```

```
  ci(bf, method = "HDI")
}

if (require("emmeans")) {
  model <- emtrends(model, ~1, "wt")
  ci(model, method = "ETI")
  ci(model, method = "HDI")
  ci(model, method = "SI")
}

## End(Not run)
```

`contr.orthonorm` *Orthonormal Contrast Matrices for Bayesian Estimation*

Description

Returns a design or model matrix of orthonormal contrasts such that the marginal prior on all effects is identical. Implementation from Singmann & Gronau's `bfrms`, following the description in Rouder, Morey, Speckman, & Province (2012, p. 363).

Though using this factor coding scheme might obscure the interpretation of parameters, it is essential for 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.

Usage

```
contr.orthonorm(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 `dgCMatrix`), using package **Matrix**.

Details

When `contrasts = FALSE`, the returned contrasts are equivalent to `contr.treatment(,contrasts = FALSE)`, as suggested by McElreath (also known as one-hot encoding).

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

- McElreath, R. (2020). Statistical rethinking: A Bayesian course with examples in R and Stan. CRC press.
- 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.orthonorm(2) # Q_2 in Rouder et al. (2012, p. 363)

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

## check decomposition
Q3 <- contr.orthonorm(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)

bayesian_as_frequentist(model, data = NULL)
```

Arguments

model	A Bayesian model.
data	Data used by the model. If NULL, will try to extract it from the model.

Examples

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

```
## Not run:
if (require("rstanarm")) {
  model <- stan_glm(vs ~ mpg,
    family = "binomial",
    data = mtcars, chains = 2, refresh = 0
  )
  bayesian_as_frequentist(model)

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

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

## End(Not run)
```

`cwi` *Curve-wise Intervals (CWI)*

Description

Compute the **Curve-Wise Interval (CWI)** of posterior distributions using `ggdist::curve_interval()`. These are particularly useful for visualisation of model's predictions.

Usage

```
cwi(x, ...)

## S3 method for class 'data.frame'
cwi(x, ci = 0.95, ...)
```

Arguments

`x`	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model (`stanreg`, `brmsfit`, `MCMCglmm`, `mcmc` or `bcplm`) or a `BayesFactor` model.
`...`	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%).

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.

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). The 89% intervals (`ci = 0.89`) are deemed to be more stable than, for instance, 95% intervals (*Kruschke, 2014*). An effective sample size of at least 10.000 is recommended if one wants to estimate 95% intervals with high precision (*Kruschke, 2014, p. 183ff*). Unfortunately, the default number of posterior samples for most Bayes packages (e.g., `rstanarm` or `brms`) is only 4.000 (thus, you might want to increase it when fitting your model). Moreover, 89 indicates the arbitrariness of interval limits - its only remarkable property is being the highest prime number that does not exceed the already unstable 95% threshold (*McElreath, 2015*).
However, 95% has some advantages too. For instance, it shares (in the case of a normal posterior distribution) an intuitive relationship with the standard deviation and it conveys a more accurate image of the (artificial) bounds of the distribution. Also, because it is wider, it makes analyses more conservative (i.e., the probability of covering 0 is larger for the 95% CI than for lower ranges such as 89%), which is a good thing in the context of the reproducibility crisis.

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 97.5h 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.

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.

See Also

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

Examples

```
library(bayestestR)
```

```
if (require("ggplot2") && require("rstanarm") && require("ggdist")) {

# Generate data ================================================
k = 11 # number of curves (iterations)
n = 201 # number of rows
data <- data.frame(x = seq(-15,15,length.out = n))

# Simulate iterations as new columns
for(i in 1:k) {
 data[paste0("iter_", i)] <- dnorm(data$x, seq(-5,5, length.out = k)[i], 3)
}

# Note: first, we need to transpose the data to have iters as rows
iters <- datawizard::data_transpose(data[paste0("iter_", 1:k)])

# Compute Median
data$Median <- point_estimate(iters)[["Median"]]

# Compute Credible Intervals ===================================

# Compute ETI (default type of CI)
data[c("ETI_low", "ETI_high")] <- eti(iters, ci = 0.5)[c("CI_low", "CI_high")]

# Compute CWI
# ggdist::curve_interval(reshape_iterations(data), iter_value .width = c(.5))

# Visualization ================================================
ggplot(data, aes(x = x, y = Median)) +
 geom_ribbon(aes(ymin = ETI_low, ymax = ETI_high), fill = "red", alpha = 0.3) +
 geom_line(size = 1) +
 geom_line(data = reshape_iterations(data),
           aes(y = iter_value, group = iter_group),
           alpha = 0.3)
}
```

`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(
  posteriors,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "hdi",
  test = c("p_direction", "rope"),
  rope_range = "default",
  rope_ci = 0.95,
  keep_iterations = FALSE,
  ...
)

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

```
  keep_iterations = FALSE,
  bf_prior = NULL,
  BF = 1,
  ...
)

## S3 method for class 'stanreg'
describe_posterior(
  posteriors,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "hdi",
  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 = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  BF = 1,
  ...
)

## S3 method for class 'stanmvreg'
describe_posterior(
  posteriors,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "hdi",
  test = "p_direction",
  rope_range = "default",
  rope_ci = 0.95,
  keep_iterations = FALSE,
  bf_prior = NULL,
  diagnostic = c("ESS", "Rhat"),
  priors = FALSE,
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  ...
)
```

```
## S3 method for class 'brmsfit'
describe_posterior(
  posteriors,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "hdi",
  test = c("p_direction", "rope"),
  rope_range = "default",
  rope_ci = 0.95,
  keep_iterations = FALSE,
  bf_prior = NULL,
  diagnostic = c("ESS", "Rhat"),
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all", "location",
    "distributional", "auxiliary"),
  parameters = NULL,
  BF = 1,
  priors = FALSE,
  ...
)

## S3 method for class 'MCMCglmm'
describe_posterior(
  posteriors,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "hdi",
  test = c("p_direction", "rope"),
  rope_range = "default",
  rope_ci = 0.95,
  keep_iterations = FALSE,
  diagnostic = "ESS",
  parameters = NULL,
  ...
)

## S3 method for class 'BFBayesFactor'
describe_posterior(
  posteriors,
  centrality = "median",
  dispersion = FALSE,
  ci = 0.95,
  ci_method = "hdi",
  test = c("p_direction", "rope", "bf"),
  rope_range = "default",
```

```
  rope_ci = 0.95,
  keep_iterations = FALSE,
  priors = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

posteriors	A vector, data frame or model of posterior draws.
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" or "all".
dispersion	Logical, if TRUE, computes indices of dispersion related to the estimate(s) (SD and MAD for mean and median, respectively).
ci	Value or vector of probability of the CI (between 0 and 1) to be estimated. Default to .95 (95%).
ci_method	The type of index used for Credible Interval. Can be "HDI" (default, see hdi()), "ETI" (see eti()), "BCI" (see bci()) 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", "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 list of two values (e.g., c(-0.1,0.1)) or "default". 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().
...	Additional arguments to be passed to or from methods.
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.
diagnostic	Diagnostic metrics to compute. Character (vector) or list with one or more of these options: "ESS", "Rhat", "MCSE" or "all".
priors	Add the prior used for each parameter.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.

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.

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).

References

- Comparison of Point-Estimates
- Region of Practical Equivalence (ROPE)
- Bayes factors

Examples

```
library(bayestestR)

if (require("logspline")) {
  x <- rnorm(1000)
  describe_posterior(x)
  describe_posterior(x, centrality = "all", dispersion = TRUE, test = "all")
  describe_posterior(x, ci = c(0.80, 0.90))

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

  df <- data.frame(replicate(4, rnorm(20)))
  head(reshape_iterations(describe_posterior(df, keep_iterations = TRUE)))
}
## Not run:
# rstanarm models
# ---------------------------------------------
if (require("rstanarm") && require("emmeans")) {
  model <- 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))

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

# brms models
```

```
# ------------------------------------------------
if (require("brms")) {
  model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
  describe_posterior(model)
  describe_posterior(model, centrality = "all", dispersion = TRUE, test = "all")
  describe_posterior(model, ci = c(0.80, 0.90))
}

# BayesFactor objects
# ------------------------------------------------
if (require("BayesFactor")) {
  bf <- 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))
}

## End(Not run)
```

`describe_prior` *Describe Priors*

Description

Returns a summary of the priors used in the model.

Usage

```
describe_prior(model, ...)
```

Arguments

`model`	A Bayesian model.
`...`	Currently not used.

Examples

```
## Not run:
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)
}

## End(Not run)
```

`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(posteriors, ...)
```

Arguments

`posteriors`	A stanreg or brms model.
`...`	Currently not used.

Examples

```
## Not run:
set.seed(333)

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

## End(Not run)
```

diagnostic_posterior *Posteriors Sampling Diagnostic*

Description

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

Usage

```
diagnostic_posterior(posteriors, diagnostic = c("ESS", "Rhat"), ...)

## S3 method for class 'stanreg'
diagnostic_posterior(
  posteriors,
  diagnostic = "all",
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  ...
)

## S3 method for class 'stanmvreg'
diagnostic_posterior(
  posteriors,
  diagnostic = "all",
  effects = c("fixed", "random", "all"),
  parameters = NULL,
  ...
)

## S3 method for class 'brmsfit'
diagnostic_posterior(
  posteriors,
  diagnostic = "all",
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  parameters = NULL,
  ...
)
```

Arguments

posteriors	A stanreg or brms model.
diagnostic	Diagnostic metrics to compute. Character (vector) or list with one or more of these options: "ESS", "Rhat", "MCSE" or "all".

`...`	Currently not used.
`effects`	Should parameters for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
`component`	Which type of parameters to return, such as parameters for the conditional model, the zero-inflated part of the model, the dispersion term, the instrumental variables or marginal effects be returned? Applies to models with zero-inflated and/or dispersion formula, or to models with instrumental variables (so called fixed-effects regressions), or models with marginal effects from **mfx**. May be abbreviated. Note that the *conditional* component is also called *count* or *mean* component, depending on the model. There are three convenient shortcuts: `component = "all"` returns all possible parameters. If `component = "location"`, location parameters such as `conditional`, `zero_inflated`, `smooth_terms`, or `instruments` are returned (everything that are fixed or random effects - depending on the `effects` argument - but no auxiliary parameters). For `component = "distributional"` (or `"auxiliary"`), components like `sigma`, `dispersion`, `beta` or `precision` (and other auxiliary parameters) are returned.
`parameters`	Regular expression pattern that describes the parameters that should be returned.

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 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*).

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".

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., \& 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

```
## Not run:
```

```
# rstanarm models
# -----------------------------------------------
if (require("rstanarm", quietly = TRUE)) {
  model <- stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
  diagnostic_posterior(model)
}

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

## End(Not run)
```

`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, ...)

rnorm_perfect(n, mean = 0, sd = 1)
```

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	the number of observations
random	Generate near-perfect or random (simple wrappers for the base R r* functions) distributions.
shape1	non-negative parameters of the Beta distribution.
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	location and scale parameters.
scale	location and scale parameters.
df	degrees of freedom (non-negative, but can be non-integer).
shape	shape and scale parameters. Must be positive, scale strictly.
mean	vector of means.
sd	vector of standard deviations.
mu	the mean
phi	Corresponding to glmmTMB's implementation of nbinom distribution, where size=mu/phi.
lambda	vector of (non-negative) means.
xi	the value of ξ such that the variance is var$[Y] = \phi\mu^{\xi}$
power	a synonym for ξ
min	lower and upper limits of the distribution. Must be finite.
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

This function returns the effective sample size (ESS).

Usage

```
effective_sample(model, ...)

## S3 method for class 'brmsfit'
effective_sample(
  model,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  parameters = NULL,
  ...
)

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

## S3 method for class 'blavaan'
effective_sample(model, parameters = NULL, ...)

## S3 method for class 'MCMCglmm'
effective_sample(
  model,
  effects = c("fixed", "random", "all"),
  parameters = NULL,
  ...
)
```

Arguments

model	A stanreg, stanfit, or brmsfit object.
...	Currently not used.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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, altough 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*).

Value

A data frame with two columns: Parameter name and effective sample size (ESS).

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

Examples

```
## Not run:
library(rstanarm)
model <- stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
effective_sample(model)

## End(Not run)
```

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 'numeric'
equivalence_test(x, range = "default", ci = 0.95, verbose = TRUE, ...)

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

## S3 method for class 'emmGrid'
equivalence_test(x, range = "default", ci = 0.95, verbose = TRUE, ...)

## S3 method for class 'BFBayesFactor'
equivalence_test(x, range = "default", ci = 0.95, verbose = TRUE, ...)

## S3 method for class 'stanreg'
equivalence_test(
  x,
  range = "default",
  ci = 0.95,
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'brmsfit'
equivalence_test(
  x,
  range = "default",
  ci = 0.95,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  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. In models with one response, range should be a vector of length two (e.g., c(-0.1,0.1)). In multivariate models, range should be a list with a numeric vectors for each response variable. 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.
ci	The Credible Interval (CI) probability, corresponding to the proportion of HDI, to use for the percentage in ROPE.
verbose	Toggle off warnings.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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 89% HDI 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 HDI, *Kruschke (2018)* suggests using the percentage of the 95% (or 89%, considered more stable) HDI that falls within the ROPE as a decision rule. If the HDI is completely outside the ROPE, the "null hypothesis" for this parameter is "rejected". If the ROPE completely covers the HDI, i.e., all most credible values of a parameter are inside the region of practical equivalence, the null hypothesis is accepted. Else, it's undecided whether to accept or reject the null hypothesis. If the full ROPE is used (i.e., 100% of the HDI), 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).

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 HDI.
- `ROPE_low`, `ROPE_high` The limits of the ROPE. These values are identical for all parameters.
- `ROPE_Percentage` The proportion of the HDI that lies inside the ROPE.
- `ROPE_Equivalence` The "test result", as character. Either "rejected", "accepted" or "undecided".
- `HDI_low` , `HDI_high` The lower and upper HDI limits for the 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)
## Not run:
library(rstanarm)
model <- rstanarm::stan_glm(mpg ~ wt + cyl, data = mtcars)
equivalence_test(model)
equivalence_test(model, ci = c(.50, 1))

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

library(emmeans)
equivalence_test(emtrends(model, ~1, "wt"))

library(brms)
model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
equivalence_test(model)
equivalence_test(model, ci = c(.50, .99))

library(BayesFactor)
bf <- ttestBF(x = rnorm(100, 1, 1))
equivalence_test(bf)
equivalence_test(bf, ci = c(.50, .99))

## End(Not run)
```

---

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 \& Wickham suggest that `method = "KernSmooth"` is the fastest and the most accurate.

Usage

```
estimate_density(
```

```
  x,
  method = "kernel",
  precision = 2^10,
  extend = FALSE,
  extend_scale = 0.1,
  bw = "SJ",
  ...
)

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

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model (stanreg, brmsfit, MCMCglmm, mcmc or bcplm) or a BayesFactor model.
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.
...	Currently not used.
ci	The confidence interval threshold. Only used when method = "kernel".
group_by	Optional character vector. If not NULL and x is a data frame, density estimation is performed for each group (subset) indicated by group_by.

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
df <- data.frame(replicate(4, rnorm(100)))
head(estimate_density(df))

# Grouped data
estimate_density(iris, group_by = "Species")
estimate_density(iris$Petal.Width, group_by = iris$Species)
## Not run:
# rstanarm models
# -----------------------------------------------
library(rstanarm)
model <- 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")))

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

## End(Not run)
```

---

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, verbose = TRUE, ...)

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

## S3 method for class 'sim.merMod'
eti(
  x,
  ci = 0.95,
  effects = c("fixed", "random", "all"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

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

## S3 method for class 'emmGrid'
```

```
eti(x, ci = 0.95, verbose = TRUE, ...)

## S3 method for class 'stanreg'
eti(
  x,
  ci = 0.95,
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

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

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

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model (stanreg, brmsfit, MCMCglmm, mcmc or bcplm) or a BayesFactor model.
...	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.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
parameters	Regular expression pattern that describes the parameters that should be returned. 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.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-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.

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). The 89% intervals (`ci = 0.89`) are deemed to be more stable than, for instance, 95% intervals (*Kruschke, 2014*). An effective sample size of at least 10.000 is recommended if one wants to estimate 95% intervals with high precision (*Kruschke, 2014, p. 183ff*). Unfortunately, the default number of posterior samples for most Bayes packages (e.g., `rstanarm` or `brms`) is only 4.000 (thus, you might want to increase it when fitting your model). Moreover, 89 indicates the arbitrariness of interval limits - its only remarkable property is being the highest prime number that does not exceed the already unstable 95% threshold (*McElreath, 2015*).
However, 95% has some advantages too. For instance, it shares (in the case of a normal posterior distribution) an intuitive relationship with the standard deviation and it conveys a more accurate image of the (artificial) bounds of the distribution. Also, because it is wider, it makes analyses more conservative (i.e., the probability of covering 0 is larger for the 95% CI than for lower ranges such as 89%), which is a good thing in the context of the reproducibility crisis.

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 97.5h 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.

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.

See Also

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

Examples

```
library(bayestestR)
```

```
posterior <- rnorm(1000)
eti(posterior)
eti(posterior, ci = c(.80, .89, .95))

df <- data.frame(replicate(4, rnorm(100)))
eti(df)
eti(df, ci = c(.80, .89, .95))
## Not run:
library(rstanarm)
model <- stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
eti(model)
eti(model, ci = c(.80, .89, .95))

library(emmeans)
eti(emtrends(model, ~1, "wt"))

library(brms)
model <- brms::brm(mpg ~ wt + cyl, data = mtcars)
eti(model)
eti(model, ci = c(.80, .89, .95))

library(BayesFactor)
bf <- ttestBF(x = rnorm(100, 1, 1))
eti(bf)
eti(bf, ci = c(.80, .89, .95))

## End(Not run)
```

---

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

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

## S3 method for class 'sim.merMod'
hdi(
  x,
  ci = 0.95,
  effects = c("fixed", "random", "all"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

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

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

## S3 method for class 'stanreg'
hdi(
  x,
  ci = 0.95,
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

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

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

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model (stanreg, brmsfit, MCMCglmm, mcmc or bcplm) or a

	BayesFactor model.
...	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.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
parameters	Regular expression pattern that describes the parameters that should be returned. 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.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-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.

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). The 89% intervals (ci = 0.89) are deemed to be more stable than, for instance, 95% intervals (*Kruschke, 2014*). An effective sample size of at least 10.000 is recommended if one wants to estimate 95% intervals with high precision (*Kruschke, 2014, p. 183ff*). Unfortunately, the default number of posterior samples for most Bayes packages (e.g., rstanarm or brms) is only 4.000 (thus, you might want to increase it when fitting your model). Moreover, 89 indicates the arbitrariness of interval limits - its only remarkable property is being the highest prime number that does not exceed the already unstable 95% threshold (*McElreath, 2015*).
However, 95% has some advantages too. For instance, it shares (in the case of a normal posterior distribution) an intuitive relationship with the standard deviation and it conveys a more accurate image of the (artificial) bounds of the distribution. Also, because it is wider, it makes analyses more conservative (i.e., the probability of covering 0 is larger for the 95% CI than for lower ranges such as 89%), which is a good thing in the context of the reproducibility crisis.

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 97.5h 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.

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

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()`, `si()`, `cwi()`.

Other ci: `bci()`, `ci()`, `cwi()`, `eti()`, `si()`

Examples

```
library(bayestestR)

posterior <- rnorm(1000)
hdi(posterior, ci = .89)
hdi(posterior, ci = c(.80, .90, .95))

df <- data.frame(replicate(4, rnorm(100)))
hdi(df)
hdi(df, ci = c(.80, .90, .95))
## Not run:
library(rstanarm)
model <- stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
hdi(model)
hdi(model, ci = c(.80, .90, .95))

library(emmeans)
hdi(emtrends(model, ~1, "wt"))

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

```
hdi(model)
hdi(model, ci = c(.80, .90, .95))

library(BayesFactor)
bf <- ttestBF(x = rnorm(100, 1, 1))
hdi(bf)
hdi(bf, ci = c(.80, .90, .95))

## End(Not run)
```

`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, precision = 2^10, method = "kernel", ...)

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

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

## S3 method for class 'stanreg'
map_estimate(
  x,
  precision = 2^10,
  method = "kernel",
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  ...
)

## S3 method for class 'brmsfit'
map_estimate(
  x,
  precision = 2^10,
  method = "kernel",
```

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

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

## S3 method for class 'emmGrid'
map_estimate(x, precision = 2^10, method = "kernel", ...)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model (stanreg, brmsfit, MCMCglmm, mcmc or bcplm) or a BayesFactor model.
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.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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.

Value

A numeric value if posterior is a vector. If posterior 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.

Examples

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

posterior <- rnorm(10000)
map_estimate(posterior)

plot(density(posterior))
```

```
abline(v = map_estimate(posterior), col = "red")

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

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

## End(Not run)
```

---

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 = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  ...
)
```

Arguments

model	A stanreg, stanfit, or brmsfit object.
...	Currently not used.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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

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".

References

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

Examples

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

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

## End(Not run)
```

`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",
  ...
)

## S3 method for class 'stanmvreg'
```

```
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 should match the names of the model formulas, 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" or "all".
ci	Value or vector of probability of the CI (between 0 and 1) to be estimated. Default to .95 (95%).
method	Can be 'ETI' (default), 'HDI', 'BCI' 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 89% 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 different **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

```
## Not run:
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, cores = 4, refresh = 0)

# Fit Bayesian mediation model in rstanarm
m3 <- stan_mvmer(
  list(
    job_seek ~ treat + econ_hard + sex + age + (1 | occp),
    depress2 ~ treat + job_seek + econ_hard + sex + age + (1 | occp)
  ),
  data = jobs,
  cores = 4,
  refresh = 0
)

summary(m1)
mediation(m2, centrality = "mean", ci = .95)
mediation(m3, centrality = "mean", ci = .95)

## End(Not run)
```

`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

```
## Not run:
# 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)
}

## End(Not run)
```

`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, direction = "two-sided", ...)

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

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

convert_pd_to_p(pd, direction = "two-sided", ...)
```

Arguments

pd	A Probability of Direction (pd) value (between 0 and 1).
direction	What type of p-value is requested or provided. Can be "two-sided" (default, two tailed) or "one-sided" (one tailed).
...	Arguments passed to or from other methods.
p	A p-value.

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, centrality = "all", dispersion = FALSE, ...)

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

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

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

## S3 method for class 'BFBayesFactor'
point_estimate(x, centrality = "all", dispersion = FALSE, ...)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model (stanreg, brmsfit, MCMCglmm, mcmc or bcplm) or a BayesFactor model.

centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" or "all".
dispersion	Logical, if TRUE, computes indices of dispersion related to the estimate(s) (SD and MAD for mean and median, respectively).
...	Additional arguments to be passed to or from methods.
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.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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.

Note

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

References

Vignette In-Depth 1: Comparison of Point-Estimates

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"))
## Not run:
# rstanarm models
# -----------------------------------------------
library(rstanarm)
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
# -----------------------------------------------
library(emmeans)
```

```
point_estimate(emtrends(model, ~1, "wt"), centrality = c("median", "MAP"))

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

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

## End(Not run)
```

`p_direction` *Probability of Direction (pd)*

Description

Compute the **Probability of Direction** (**pd**, also known as the Maximum Probability of Effect - *MPE*). It varies between 50% and 100% (*i.e.*, `0.5` and 1) and can be interpreted as the probability (expressed in percentage) that a parameter (described by its posterior distribution) is strictly positive or negative (whichever is the most probable). It is mathematically defined as the proportion of the posterior distribution that is of the median's sign. Although differently expressed, this index is fairly similar (*i.e.*, is strongly correlated) to the frequentist **p-value**.

Note that in some (rare) cases, especially when used with model averaged posteriors (see `weighted_posteriors()` or `brms::posterior_average`), pd can be smaller than `0.5`, reflecting high credibility of `0`.

Usage

```
p_direction(x, ...)

pd(x, ...)

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

## S3 method for class 'data.frame'
p_direction(x, method = "direct", null = 0, ...)

## S3 method for class 'MCMCglmm'
p_direction(x, method = "direct", null = 0, ...)
```

```
## S3 method for class 'emmGrid'
p_direction(x, method = "direct", null = 0, ...)

## S3 method for class 'stanreg'
p_direction(
  x,
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  method = "direct",
  null = 0,
  ...
)

## S3 method for class 'brmsfit'
p_direction(
  x,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  parameters = NULL,
  method = "direct",
  null = 0,
  ...
)

## S3 method for class 'BFBayesFactor'
p_direction(x, method = "direct", null = 0, ...)
```

Arguments

x	Vector representing a posterior distribution. Can also be a Bayesian model (stanreg, brmsfit or BayesFactor).
...	Currently not used.
method	Can be "direct" or one of methods of density estimation, such as "kernel", "logspline" or "KernSmooth". If "direct" (default), the computation is based on the raw ratio of samples superior and inferior to 0. Else, the result is based on the Area under the Curve (AUC) of the estimated density function.
null	The value considered as a "null" effect. Traditionally 0, but could also be 1 in the case of ratios.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.

`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

What is the *pd*?: The Probability of Direction (pd) is an index of effect existence, ranging from 50% to 100%, representing the certainty with which an effect goes in a particular direction (*i.e.*, is positive or negative). Beyond its simplicity of interpretation, understanding and computation, this index also presents other interesting properties:

- It is independent from the model: It is solely based on the posterior distributions and does not require any additional information from the data or the model.
- 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.

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 $p_{onesided} = 1 - \frac{p_d}{100}$ and to the two-sided p-value (the most commonly reported one) through the formula $p_{twosided} = 2 * (1 - \frac{p_d}{100})$. 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 also `pd_to_p()`.

Methods of computation: The most simple and direct way to compute the *pd* is to 1) look at the median's sign, 2) select the portion of the posterior of the same sign and 3) compute the percentage that this portion represents. 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 density function (for which many methods are available), and then computing the area under the curve (AUC) of the density curve on the other side of 0.

Strengths and Limitations: **Strengths:** Straightforward computation and interpretation. Objective property of the posterior distribution. 1:1 correspondence with the frequentist p-value.

Limitations: Limited information favoring the null hypothesis.

Value

Values between 0.5 and 1 corresponding to the probability of direction (pd).

Note that in some (rare) cases, especially when used with model averaged posteriors (see `weighted_posteriors()` or `brms::posterior_average`), `pd` can be smaller than `0.5`, reflecting high credibility of `0`. To detect such cases, the `method = "direct"` must be used.

Note

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

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

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")
## Not run:
# rstanarm models
# ---------------------------------------------
if (require("rstanarm")) {
  model <- rstanarm::stan_glm(mpg ~ wt + cyl,
    data = mtcars,
    chains = 2, refresh = 0
  )
  p_direction(model)
  p_direction(model, method = "kernel")
}

# emmeans
# ---------------------------------------------
if (require("emmeans")) {
  p_direction(emtrends(model, ~1, "wt"))
}

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

# BayesFactor objects
# -------------------------------------------
```

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

## End(Not run)
```

---

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 0 divided by the density at the Maximum A Posteriori (MAP).

Usage

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

p_pointnull(x, precision = 2^10, method = "kernel", ...)

## S3 method for class 'stanreg'
p_map(
  x,
  precision = 2^10,
  method = "kernel",
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  ...
)

## S3 method for class 'brmsfit'
p_map(
  x,
  precision = 2^10,
  method = "kernel",
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  parameters = NULL,
  ...
)
```

Arguments

x	Vector representing a posterior distribution, or a data frame of such vectors. Can also be a Bayesian model (stanreg, brmsfit, MCMCglmm, mcmc or bcplm) or a BayesFactor model.
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.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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.

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))
## Not run:
```

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

library(emmeans)
p_map(emtrends(model, ~1, "wt"))

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

library(BayesFactor)
bf <- 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" = p_map(x, method = "kernel"),
    "KernSmooth" = p_map(x, method = "KernSmooth"),
    "logspline" = 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")])

## End(Not run)
```

---

p_rope *Probability of being in the ROPE*

Description

Compute the proportion of the whole posterior distribution that doesn't lie within a region of practical equivalence (ROPE). It is equivalent to running `rope(...,ci = 1)`.

Usage

```
p_rope(x, ...)

## Default S3 method:
```

```
p_rope(x, ...)

## S3 method for class 'numeric'
p_rope(x, range = "default", ...)

## S3 method for class 'data.frame'
p_rope(x, range = "default", ...)

## S3 method for class 'emmGrid'
p_rope(x, range = "default", ...)

## S3 method for class 'BFBayesFactor'
p_rope(x, range = "default", ...)

## S3 method for class 'MCMCglmm'
p_rope(x, range = "default", ...)

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

## S3 method for class 'brmsfit'
p_rope(
  x,
  range = "default",
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  parameters = NULL,
  ...
)
```

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. In models with one response, `range` should be a vector of length two (e.g., `c(-0.1,0.1)`). In multivariate models, `range` should be a list with a numeric vectors for each response variable. 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.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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)

p_rope(x = rnorm(1000, 0, 0.01), range = c(-0.1, 0.1))
p_rope(x = mtcars, range = c(-0.1, 0.1))
```

---

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 'emmGrid'
p_significance(x, threshold = "default", ...)

## S3 method for class 'stanreg'
p_significance(
  x,
  threshold = "default",
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
```

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

## S3 method for class 'brmsfit'
p_significance(
  x,
  threshold = "default",
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  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. If "default", the range is set to 0.1 if input is a vector, and based on rope_range() if a Bayesian model is provided.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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.

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).

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)
## Not run:
# rstanarm models
# -----------------------------------------------
if (require("rstanarm")) {
  model <- rstanarm::stan_glm(mpg ~ wt + cyl,
    data = mtcars,
    chains = 2, refresh = 0
  )
  p_significance(model)
}

## End(Not run)
```

---

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

Description

Reshape a wide data.frame of iterations (such as posterior draws or bootsrapped 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)*

Description

Compute the proportion of the HDI (default to the 89% HDI) of a posterior distribution that lies within a region of practical equivalence.

Usage

```
rope(x, ...)

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

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

## S3 method for class 'data.frame'
rope(x, range = "default", ci = 0.95, ci_method = "HDI", verbose = TRUE, ...)

## S3 method for class 'emmGrid'
rope(x, range = "default", ci = 0.95, ci_method = "HDI", verbose = TRUE, ...)

## S3 method for class 'BFBayesFactor'
rope(x, range = "default", ci = 0.95, ci_method = "HDI", verbose = TRUE, ...)
```

```
## S3 method for class 'MCMCglmm'
rope(x, range = "default", ci = 0.95, ci_method = "HDI", verbose = TRUE, ...)

## S3 method for class 'stanreg'
rope(
  x,
  range = "default",
  ci = 0.95,
  ci_method = "HDI",
  effects = c("fixed", "random", "all"),
  component = c("location", "all", "conditional", "smooth_terms", "sigma",
    "distributional", "auxiliary"),
  parameters = NULL,
  verbose = TRUE,
  ...
)

## S3 method for class 'brmsfit'
rope(
  x,
  range = "default",
  ci = 0.95,
  ci_method = "HDI",
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  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. In models with one response, range should be a vector of length two (e.g., c(-0.1,0.1)). In multivariate models, range should be a list with a numeric vectors for each response variable. 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.
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' (default) or 'ETI'. See ci().

verbose	Toggle off warnings.
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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

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 the 95% (or 89%, considered more stable) 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.

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(.90, .95))
## Not run:
library(rstanarm)
model <- stan_glm(mpg ~ wt + gear, data = mtcars, chains = 2, iter = 200, refresh = 0)
rope(model)
rope(model, ci = c(.90, .95))

library(emmeans)
rope(emtrends(model, ~1, "wt"), ci = c(.90, .95))

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

```
rope(model, ci = c(.90, .95))

library(brms)
model <- brms::brm(brms::mvbind(mpg, disp) ~ wt + cyl, data = mtcars)
rope(model)
rope(model, ci = c(.90, .95))

library(BayesFactor)
bf <- ttestBF(x = rnorm(100, 1, 1))
rope(bf)
rope(bf, ci = c(.90, .95))

## End(Not run)
```

`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.
`...`	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 $[-0.1 * SD_y, 0.1 * SD_y]$.

```
\item For **logistic models**, the parameters expressed in log odds
ratio can be converted to standardized difference through the formula
\ifelse{html}{\out{&pi;/&radic;(3)}}{\eqn{\pi/\sqrt{3}}}, resulting in a
range of `-0.18` to `0.18`.

\item 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.

\item 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!

\item For **t-tests**, the standard deviation of the response is
used, similarly to linear models (see above).

\item 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.

\item 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

```
## Not run:
if (require("rstanarm")) {
  model <- stan_glm(
    mpg ~ wt + gear,
    data = mtcars,
    chains = 2,
    iter = 200,
    refresh = 0
  )
  rope_range(model)

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

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

if (require("BayesFactor")) {
  model <- ttestBF(mtcars[mtcars$vs == 1, "mpg"], mtcars[mtcars$vs == 0, "mpg"])
  rope_range(model)

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

```
## End(Not run)
```

`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, index = "Median", magnitude = 10, ...)
```

Arguments

`model`	A Bayesian model (`stanreg` or `brmsfit`).
`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 wil be updated with a prior located at 10 standard deviations from its original location.
`...`	Arguments passed to or from other methods.

See Also

DescTools

Examples

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

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

## End(Not run)
```

`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`	Vector representing a posterior distribution. Can also be a Bayesian model (`stanreg`, `brmsfit` or `BayesFactor`).
`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 \& 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 centred 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

```
## Not run:
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 <- rstanarm::stan_glm(mpg ~ wt * cyl,
    data = mtcars,
    iter = 400, refresh = 0
  )
  s <- sexit(model)
  s
  print(s, summary = TRUE)
}

## End(Not run)
```

`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))
## Not run:
if (require("rstanarm")) {
  model <- stan_glm(
    mpg ~ wt + gear,
    data = mtcars,
    chains = 2,
    iter = 200,
    refresh = 0
  )
  sexit_thresholds(model)

  model <- 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)
}

## End(Not run)
```

`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, in particular on specifying correct priors for factors with more than 2 levels, see the Bayes factors vignette.

Usage

```
si(posterior, prior = NULL, BF = 1, verbose = TRUE, ...)

## 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 = c("fixed", "random", "all"),
  component = c("conditional", "location", "zi", "zero_inflated", "all",
    "smooth_terms", "sigma", "distributional", "auxiliary"),
  parameters = NULL,
  ...
)

## S3 method for class 'brmsfit'
si(
  posterior,
  prior = NULL,
  BF = 1,
  verbose = TRUE,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "location", "zi", "zero_inflated", "all",
    "smooth_terms", "sigma", "distributional", "auxiliary"),
  parameters = NULL,
  ...
)
```

```
## S3 method for class 'blavaan'
si(
  posterior,
  prior = NULL,
  BF = 1,
  verbose = TRUE,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "location", "zi", "zero_inflated", "all",
    "smooth_terms", "sigma", "distributional", "auxiliary"),
  parameters = NULL,
  ...
)

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

## S3 method for class 'data.frame'
si(posterior, prior = NULL, BF = 1, 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').
BF	The amount of support required to be included in the support interval.
verbose	Toggle off warnings.
...	Arguments passed to and from other methods. (Can be used to pass arguments to internal logspline::logspline().)
effects	Should results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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

This method is used to compute support intervals based on prior and posterior distributions. For the computation of support intervals, 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; see example below).

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.

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].

Setting the correct `prior`

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*); As the priors for the alternative get wider, the likelihood of the null value(s) increases, to the extreme that for completely flat priors the null is infinitely more favorable than the alternative (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.

(Note that by default, `brms::brm()` uses flat priors for fixed-effects; See example below.)

It is important to provide the correct `prior` for meaningful results.

- When `posterior` is a numerical vector, `prior` should also be a numerical vector.
- When `posterior` is a `data.frame`, `prior` should also be a `data.frame`, with matching column order.
- When `posterior` is a `stanreg` or `brmsfit` model:
  - `prior` can be set to `NULL`, in which case prior samples are drawn internally.
  - `prior` can also be a model equivalent to `posterior` but with samples from the priors *only*. See `unupdate()`.
  - **Note:** When `posterior` is a `brmsfit_multiple` model, `prior` **must** be provided.
- When `posterior` is an `emmGrid` object:
  - `prior` should be the `stanreg` or `brmsfit` model used to create the `emmGrid` objects.
  - `prior` can also be an `emmGrid` object equivalent to `posterior` but created with a model of priors samples *only*.
  - **Note:** When the `emmGrid` has undergone any transformations (`"log"`, `"response"`, etc.), or `regriding`, then `prior` must be an `emmGrid` object, as stated above.

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(), cwi(), eti(), hdi()

Examples

```
library(bayestestR)

prior <- distribution_normal(1000, mean = 0, sd = 1)
posterior <- distribution_normal(1000, mean = .5, sd = .3)

si(posterior, prior)
## Not run:
# rstanarm models
# ---------------
library(rstanarm)
contrasts(sleep$group) <- contr.orthonorm # see vingette
stan_model <- stan_lmer(extra ~ group + (1 | ID), data = sleep)
si(stan_model)
si(stan_model, BF = 3)

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

# brms models
# -----------
library(brms)
contrasts(sleep$group) <- contr.orthonorm # 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 <- brm(extra ~ group + (1 | ID),
  data = sleep,
  prior = my_custom_priors
)
si(brms_model)

## End(Not run)
```

---

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, ...)
```

Arguments

`model`	A `stanreg`, `stanfit`, or `brmsfit` object.
`n`	Size of the simulated prior distributions.
`...`	Currently not used.

See Also

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

Examples

```
## Not run:
library(bayestestR)
if (require("rstanarm")) {
  model <- stan_glm(mpg ~ wt + am, data = mtcars, chains = 1, refresh = 0)
  simulate_prior(model)
}

## End(Not run)
```

`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")
}
```

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 = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  parameters = NULL
)

## S3 method for class 'brmsfit'
weighted_posteriors(
  ...,
  prior_odds = NULL,
  missing = 0,
  verbose = TRUE,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  parameters = NULL
)

## S3 method for class 'blavaan'
weighted_posteriors(
  ...,
  prior_odds = NULL,
  missing = 0,
  verbose = TRUE,
  effects = c("fixed", "random", "all"),
  component = c("conditional", "zi", "zero_inflated", "all"),
  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.frames, 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 results for fixed effects, random effects or both be returned? Only applies to mixed models. May be abbreviated.
component	Should results for all parameters, parameters for the conditional model or the zero-inflated part of the model be returned? May be abbreviated. Only applies to **brms**-models.
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.orthonorm() 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")) {
  stan_m0 <- stan_glm(extra ~ 1,
    data = sleep,
    family = gaussian(),
    refresh = 0,
    diagnostic_file = file.path(tempdir(), "df0.csv")
  )

  stan_m1 <- stan_glm(extra ~ group,
    data = sleep,
    family = gaussian(),
    refresh = 0,
    diagnostic_file = file.path(tempdir(), "df1.csv")
  )


  res <- weighted_posteriors(stan_m0, stan_m1)

  plot(eti(res))
}

## With BayesFactor
if (require("BayesFactor")) {
```

```
  extra_sleep <- ttestBF(formula = extra ~ group, data = sleep)

  wp <- weighted_posteriors(extra_sleep)

  describe_posterior(extra_sleep, test = NULL)
  describe_posterior(wp$delta, test = NULL) # also considers the null
}


## weighted prediction distributions via data.frames
if (require("rstanarm")) {
  m0 <- stan_glm(
    mpg ~ 1,
    data = mtcars,
    family = gaussian(),
    diagnostic_file = file.path(tempdir(), "df0.csv"),
    refresh = 0
  )

  m1 <- 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)

  wp <- weighted_posteriors(pred_m0, pred_m1,
    prior_odds = BFmods$BF[2]
  )

  # 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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