

Package ‘baymedr’

March 28, 2021

Title Computation of Bayes Factors for Common Biomedical Designs

Version 0.1.1

Date 2021-03-26

Description BAYesian inference for MEDical designs in R. Functions for the computation of Bayes factors for common biomedical research designs. Implemented are functions to test the equivalence (`equiv_bf`), non-inferiority (`infer_bf`), and superiority (`super_bf`) of an experimental group compared to a control group on a continuous outcome measure. Bayes factors for these three tests can be computed based on raw data (`x`, `y`) or summary statistics (`n_x`, `n_y`, `mean_x`, `mean_y`, `sd_x`, `sd_y` [or `ci_margin` and `ci_level`]).

Depends R ($\geq 3.2.0$)

Imports methods, rlang, stats, stringr

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

RoxygenNote 7.1.1

License GPL-3

Encoding UTF-8

Language en-US

URL <https://github.com/maxlinde/baymedr>

BugReports <https://github.com/maxlinde/baymedr/issues>

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-03-28 03:20:02 UTC

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baymedr-package	<i>baymedr: Computation of Bayes Factors for Common Biomedical Designs</i>
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Description

baymedr provides functions for the computation of Bayes factors for common biomedical research designs.

Details

Package:	baymedr
Type:	Package
Version:	0.1.1
License:	GPL-3
Date:	2021-03-26

At this point in time, baymedr entails tests for the following research designs with a continuous outcome measure:

- Equivalence: [equiv_bf](#)
- Non-Inferiority: [infer_bf](#)
- Superiority: [super_bf](#)

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See Also

Useful links:

- <https://github.com/maxlinde/baymedr>
- Report bugs at <https://github.com/maxlinde/baymedr/issues>

equiv_bf

Bayes factor for equivalence designs

Description

`equiv_bf` computes a Bayes factor for equivalence designs with a continuous dependent variable.

Usage

```
equiv_bf(  
  x = NULL,  
  y = NULL,  
  n_x = NULL,  
  n_y = NULL,  
  mean_x = NULL,  
  mean_y = NULL,  
  sd_x = NULL,  
  sd_y = NULL,  
  ci_margin = NULL,  
  ci_level = NULL,  
  interval = 0,  
  interval_std = TRUE,  
  prior_scale = 1/sqrt(2)  
)
```

Arguments

<code>x</code>	A numeric vector of observations for the control group.
<code>y</code>	A numeric vector of observations for the experimental group.
<code>n_x</code>	A numeric vector of length one, specifying the sample size of the control group.
<code>n_y</code>	A numeric vector of length one, specifying the sample size of the experimental group.
<code>mean_x</code>	A numeric vector of length one, specifying the mean of the dependent variable in the control group.
<code>mean_y</code>	A numeric vector of length one, specifying the mean of the dependent variable in the experimental group.
<code>sd_x</code>	A numeric vector of length one, specifying the standard deviation of the dependent variable in the control group. Only <code>sd_x</code> and <code>sd_y</code> OR <code>ci_margin</code> and <code>ci_level</code> should be defined (see Details).

sd_y	A numeric vector of length one, specifying the standard deviation of the dependent variable in the experimental group. Only sd_x and sd_y OR ci_margin and ci_level should be defined (see Details).
ci_margin	A numeric vector of length one, specifying the margin of the confidence interval (i.e., the width of the confidence interval divided by 2) of the mean difference on the dependent variable between the experimental and control groups. The value should be a positive number Only sd_x and sd_y OR ci_margin and ci_level should be defined (see Details).
ci_level	A numeric vector of length one, specifying the confidence level of ci_margin. The value must be between 0 and 1 (e.g., 0.95 for a 95% confidence interval). Only sd_x and sd_y OR ci_margin and ci_level should be defined (see Details).
interval	A numeric vector of length one or two, specifying the boundaries of the equivalence interval. If a numeric vector of length one is specified, a symmetric equivalence interval will be used (e.g., a 0.1 is equivalent to c(-0.1, 0.1)). A numeric vector of length two provides the possibility to specify an asymmetric equivalence interval (e.g., c(-0.1, 0.2)). The default is 0, indicating a point null hypothesis rather than an interval (see Details).
interval_std	A logical vector of length one, specifying whether the equivalence interval (i.e., interval) is given in standardized (TRUE; the default) or unstandardized (FALSE) units.
prior_scale	A numeric vector of length one, specifying the scale of the Cauchy prior distribution for the effect size under the alternative hypothesis (see Details). The default value is $r = 1 / \sqrt{2}$.

Details

The equivalence design has the following hypotheses: The null hypothesis (i.e., H0) states that the population means of the experimental group (e.g., a new medication) and the control group (e.g., a placebo or an already existing medication) are (practically) equivalent; the alternative hypothesis (i.e., H1) states that the population means of the two groups are not equivalent. The dependent variable must be continuous.

Since the main goal of `equiv_bf` is to establish equivalence, the resulting Bayes factor quantifies evidence in favor of the null hypothesis (i.e., BF01). Evidence for the alternative hypothesis can easily be calculated by taking the reciprocal of the original Bayes factor (i.e., $BF10 = 1 / BF01$). Quantification of evidence in favor of the null hypothesis is logically sound and legitimate within the Bayesian framework (see e.g., van Ravenzwaaij et al., 2019).

`equiv_bf` can be utilized to calculate a Bayes factor based on raw data (i.e., if arguments `x` and `y` are defined) or summary statistics (i.e., if arguments `n_x`, `n_y`, `mean_x`, and `mean_y` are defined). In the latter case, either values for the arguments `sd_x` and `sd_y` **OR** `ci_margin` and `ci_level` can be supplied. Arguments with 'x' as a name or suffix correspond to the control group, whereas arguments with 'y' as a name or suffix correspond to the experimental group.

The equivalence interval can be specified with the argument `interval`. However, it is not compulsory to specify an equivalence interval (see van Ravenzwaaij et al., 2019). The default value of the argument `interval` is 0, indicating a point null hypothesis. If an interval is preferred, the argument `interval` can be set in two ways: A *symmetric* interval can be defined by either specifying a numeric vector of length one (e.g., 0.1, which is converted to c(-0.1, 0.1)) or a numeric

vector of length two (e.g., `c(-0.1, 0.1)`); an *asymmetric* interval can be defined by specifying a numeric vector of length two (e.g., `c(-0.1, 0.2)`). It can be specified whether the equivalence interval (i.e., `interval`) is given in standardized or unstandardized units with the `interval_std` argument, where `TRUE`, corresponding to standardized units, is the default.

For the calculation of the Bayes factor, a Cauchy prior density centered on 0 is chosen for the effect size under the alternative hypothesis. The standard Cauchy distribution, with a location parameter of 0 and a scale parameter of 1, resembles a standard Normal distribution, except that the Cauchy distribution has less mass at the center but heavier tails (Liang et al., 2008; Rouder et al., 2009). The argument `prior_scale` specifies the width of the Cauchy prior, which corresponds to half of the interquartile range. Thus, by adjusting the Cauchy prior scale with `prior_scale`, different ranges of expected effect sizes can be emphasized. The default prior scale is set to $r = 1 / \sqrt{2}$.

`equiv_bf` creates an S4 object of class `baymedrEquivalence`, which has multiple slots/entries (e.g., type of data, prior scale, Bayes factor, etc.; see `Value`). If it is desired to store or extract solely the Bayes factor, the user can do this with `get_bf`, by setting the S4 object as an argument (see `Examples`).

Value

An S4 object of class `baymedrEquivalence` is returned. Contained are a description of the model and the resulting Bayes factor:

- `test`: The type of analysis
- `hypotheses`: A statement of the hypotheses
 - `h0`: The null hypothesis
 - `h1`: The alternative hypothesis
- `interval`: Specification of the equivalence interval in standardized and unstandardized units
 - `lower_std`: The standardized lower boundary of the equivalence interval
 - `upper_std`: The standardized upper boundary of the equivalence interval
 - `lower_unstd`: The unstandardized lower boundary of the equivalence interval
 - `upper_unstd`: The unstandardized upper boundary of the equivalence interval
- `data`: A description of the data
 - `type`: The type of data ('raw' when arguments `x` and `y` are used or 'summary' when arguments `n_x`, `n_y`, `mean_x`, `mean_y`, `sd_x`, and `sd_y` (or `ci_margin` and `ci_level` instead of `sd_x` and `sd_y`) are used)
 - ...: values for the arguments used, depending on 'raw' or 'summary'
- `prior_scale`: The width of the Cauchy prior distribution
- `bf`: The resulting Bayes factor

A summary of the model is shown by printing the object.

References

- Gronau, Q. F., Ly, A., & Wagenmakers, E.-J. (2020). Informed Bayesian t-tests. *The American Statistician*, 74(2), 137-143.
- Liang, F., Paulo, R., Molina, G., Clyde, M. A., & Berger, J. O. (2008). Mixtures of g priors for Bayesian variable selection. *Journal of the American Statistical Association*, 103(481), 410-423.

Rouder, J. N., Speckman, P. L., Sun, D., Morey, R. D., & Iverson, G. (2009). Bayesian t tests for accepting and rejecting the null hypothesis. *Psychonomic Bulletin & Review*, 16(2), 225-237.

van Ravenzwaaij, D., Monden, R., Tendeiro, J. N., & Ioannidis, J. P. A. (2019). Bayes factors for superiority, non-inferiority, and equivalence designs. *BMC Medical Research Methodology*, 19(1), 71.

Examples

```
## equiv_bf using raw data:

# Assign model to variable.
equiv_raw <- equiv_bf(x = rnorm(100, 10, 15),
                     y = rnorm(130, 13, 10))

# Extract Bayes factor from variable.
get_bf(equiv_raw)

# -----
# -----

## equiv_bf using summary statistics with data from Steiner et al. (2015).
## With a point null hypothesis:

# Assign model to variable.
equiv_sum_point <- equiv_bf(n_x = 560,
                           n_y = 538,
                           mean_x = 8.683,
                           mean_y = 8.516,
                           sd_x = 3.6,
                           sd_y = 3.6)

# Extract Bayes factor from model.
get_bf(equiv_sum_point)

# -----
# -----

## equiv_bf using summary statistics with data from Steiner et al. (2015).
## With an interval null hypothesis:

# Assign model to variable.
equiv_sum_interval <- equiv_bf(n_x = 560,
                              n_y = 538,
                              mean_x = 8.683,
                              mean_y = 8.516,
                              sd_x = 3.6,
                              sd_y = 3.6,
                              interval = 0.05)

# Extract Bayes factor from model.
get_bf(equiv_sum_interval)
```

`get_bf`*Extract Bayes factor from S4 object*

Description

`get_bf` extracts the Bayes factor from an S4 object (i.e., `baymedrSuperiority`, `baymedrEquivalence`, `baymedrNonInferiority`), created from the functions `super_bf`, `equiv_bf`, or `infer_bf`.

Usage

```
get_bf(object)
```

Arguments

`object` An S4 object of class `baymedrSuperiority`, `baymedrEquivalence`, or `baymedrNonInferiority`.

Value

A numeric scalar, providing the Bayes factor from an S4 object.

Examples

```
# Extract Bayes factor from a baymedrSuperiority object using raw data:
mod_super <- super_bf(x = rnorm(100, 10, 15),
                    y = rnorm(130, 13, 10))

get_bf(object = mod_super)

# Extract Bayes factor from a baymedrEquivalence object using raw data:
mod_equiv <- equiv_bf(x = rnorm(100, 10, 15),
                    y = rnorm(130, 13, 10))

get_bf(object = mod_equiv)

# Extract Bayes factor from a baymedrNonInferiority object using raw data:
mod_infer <- infer_bf(x = rnorm(100, 10, 15),
                    y = rnorm(130, 13, 10),
                    ni_margin = 1)

get_bf(object = mod_infer)
```

infer_bf

*Bayes factor for non-inferiority designs***Description**

`infer_bf` computes a Bayes factor for non-inferiority designs with a continuous dependent variable.

Usage

```
infer_bf(
  x = NULL,
  y = NULL,
  n_x = NULL,
  n_y = NULL,
  mean_x = NULL,
  mean_y = NULL,
  sd_x = NULL,
  sd_y = NULL,
  ci_margin = NULL,
  ci_level = NULL,
  ni_margin = NULL,
  ni_margin_std = TRUE,
  prior_scale = 1/sqrt(2),
  direction = "high"
)
```

Arguments

<code>x</code>	A numeric vector of observations for the control group.
<code>y</code>	A numeric vector of observations for the experimental group.
<code>n_x</code>	A numeric vector of length one, specifying the sample size of the control group.
<code>n_y</code>	A numeric vector of length one, specifying the sample size of the experimental group.
<code>mean_x</code>	A numeric vector of length one, specifying the mean of the dependent variable in the control group.
<code>mean_y</code>	A numeric vector of length one, specifying the mean of the dependent variable in the experimental group.
<code>sd_x</code>	A numeric vector of length one, specifying the standard deviation of the dependent variable in the control group. Only <code>sd_x</code> and <code>sd_y</code> OR <code>ci_margin</code> and <code>ci_level</code> should be defined (see Details).
<code>sd_y</code>	A numeric vector of length one, specifying the standard deviation of the dependent variable in the experimental group. Only <code>sd_x</code> and <code>sd_y</code> OR <code>ci_margin</code> and <code>ci_level</code> should be defined (see Details).

ci_margin	A numeric vector of length one, specifying the margin of the confidence interval (i.e., the width of the confidence interval divided by 2) of the mean difference on the dependent variable between the experimental and control groups. The value should be a positive number Only sd_x and sd_y OR ci_margin and ci_level should be defined (see Details).
ci_level	A numeric vector of length one, specifying the confidence level of ci_margin. The value must be between 0 and 1 (e.g., 0.95 for a 95% confidence interval). Only sd_x and sd_y OR ci_margin and ci_level should be defined (see Details).
ni_margin	A numeric vector of length one, specifying the non-inferiority margin. The value should be a positive number.
ni_margin_std	A logical vector of length one, specifying whether the non-inferiority margin (i.e., ni_margin) is given in standardized (TRUE; the default) or unstandardized (FALSE) units.
prior_scale	A numeric vector of length one, specifying the scale of the Cauchy prior distribution for the effect size under the alternative hypothesis (see Details). The default value is $r = 1 / \sqrt{2}$.
direction	A character vector of length one, specifying the direction of non-inferior scores. 'low' indicates that low scores on the measure of interest correspond to a non-inferior outcome and 'high' (the default) indicates that high scores on the measure of interest correspond to a non-inferior outcome (see Details).

Details

The formulation of the null and alternative hypotheses for the non-inferiority design differs depending on whether high or low scores on the dependent variable represent non-inferiority. In the case where high scores correspond to non-inferiority, the hypotheses are as follows: The null hypothesis states that the population mean of the experimental group (e.g., a new medication) is lower than the population mean of the control group (e.g., a placebo or an already existing medication) minus the non-inferiority margin. The alternative hypothesis states that the population mean of the experimental group is higher than the population mean of the control group minus the non-inferiority margin. Thus, the null hypothesis goes in the negative direction (i.e., H-) and the alternative hypothesis in the positive direction (i.e., H+). In turn, in the case where low scores correspond to non-inferiority, the hypotheses are as follows: The null hypothesis states that the population mean of the experimental group is higher than the population mean of the control group plus the non-inferiority margin. The alternative hypothesis states that the population mean of the experimental group is lower than the population mean of the control group plus the non-inferiority margin. Thus, the null hypothesis goes in the positive direction (i.e., H+) and the alternative hypothesis in the negative direction (i.e., H-). The dependent variable must be continuous.

Since the main goal of `infer_bf` is to establish non-inferiority, the resulting Bayes factor quantifies evidence in favor of the alternative hypothesis. In the case where high values represent non-inferiority we have BF+- and in the case where low values represent non-inferiority we have BF-+. Evidence for the null hypothesis can easily be calculated by taking the reciprocal of the original Bayes factor (i.e., $BF+- = 1 / BF+-$ and vice versa). Quantification of evidence in favor of the null hypothesis is logically sound and legitimate within the Bayesian framework (see e.g., van Ravenzwaaij et al., 2019).

`infer_bf` can be utilized to calculate a Bayes factor based on raw data (i.e., if arguments `x` and `y` are defined) or summary statistics (i.e., if arguments `n_x`, `n_y`, `mean_x`, and `mean_y` (or `ci_margin` and `ci_level` instead of `sd_x` and `sd_y`) are defined). Arguments with 'x' as a name or suffix correspond to the control group, whereas arguments with 'y' as a name or suffix correspond to the experimental group.

Since sometimes high scores on the dependent variable are considered non-inferior (e.g., amount of social interactions) and sometimes rather the low scores (e.g., severity of symptoms), the direction of non-inferiority can be specified with the argument `direction`. For the case where high values on the dependent variable indicate non-inferiority, 'high' (the default) should be specified for the argument `direction`; if low values on the dependent variable indicate non-inferiority, 'low' should be specified for the argument `direction`.

With the argument `ni_margin`, the non-inferiority margin can be specified. `ni_margin` should be a positive number. It can be declared whether the non-inferiority margin is specified in standardized or unstandardized units with the `ni_margin_std` argument, where `TRUE`, corresponding to standardized units, is the default.

For the calculation of the Bayes factor, a Cauchy prior density centered on 0 is chosen for the effect size under the alternative hypothesis. The standard Cauchy distribution, with a location parameter of 0 and a scale parameter of 1, resembles a standard Normal distribution, except that the Cauchy distribution has less mass at the center but heavier tails (Liang et al., 2008; Rouder et al., 2009). The argument `prior_scale` specifies the width of the Cauchy prior, which corresponds to half of the interquartile range. Thus, by adjusting the Cauchy prior scale with `prior_scale`, different ranges of expected effect sizes can be emphasized. The default prior scale is set to $r = 1 / \sqrt{2}$.

`infer_bf` creates an S4 object of class `baymedrNonInferiority`, which has multiple slots/entries (e.g., type of data, prior scale, Bayes factor, etc.; see Value). If it is desired to store or extract solely the Bayes factor, the user can do this with `get_bf`, by setting the S4 object as an argument (see Examples).

Value

An S4 object of class `baymedrNonInferiority` is returned. Contained are a description of the model and the resulting Bayes factor:

- `test`: The type of analysis
- `hypotheses`: A statement of the hypotheses
 - `h0`: The null hypothesis
 - `h1`: The alternative hypothesis
- `ni_margin`: The value for `ni_margin` in standardized and unstandardized units
 - `ni_mar_std`: The standardized non-inferiority margin
 - `ni_mar_unstd`: The unstandardized non-inferiority margin
- `data`: A description of the data
 - `type`: The type of data ('raw' when arguments `x` and `y` are used or 'summary' when arguments `n_x`, `n_y`, `mean_x`, `mean_y`, `sd_x`, and `sd_y` (or `ci_margin` and `ci_level` instead of `sd_x` and `sd_y`) are used)
 - ...: values for the arguments used, depending on 'raw' or 'summary'
- `prior_scale`: The width of the Cauchy prior distribution

- bf: The resulting Bayes factor

A summary of the model is shown by printing the object.

References

Gronau, Q. F., Ly, A., & Wagenmakers, E.-J. (2020). Informed Bayesian t-tests. *The American Statistician*, 74(2), 137-143.

Liang, F., Paulo, R., Molina, G., Clyde, M. A., & Berger, J. O. (2008). Mixtures of g priors for Bayesian variable selection. *Journal of the American Statistical Association*, 103(481), 410-423.

Rouder, J. N., Speckman, P. L., Sun, D., Morey, R. D., & Iverson, G. (2009). Bayesian t tests for accepting and rejecting the null hypothesis. *Psychonomic Bulletin & Review*, 16(2), 225-237.

van Ravenzwaaij, D., Monden, R., Tendeiro, J. N., & Ioannidis, J. P. A. (2019). Bayes factors for superiority, non-inferiority, and equivalence designs. *BMC Medical Research Methodology*, 19(1), 71.

Examples

```
## infer_bf using raw data:

# Assign model to variable.
infer_raw <- infer_bf(x = rnorm(100, 10, 15),
                    y = rnorm(130, 13, 10),
                    ni_margin = 1.5,
                    ni_margin_std = FALSE)

# Extract Bayes factor from model.
get_bf(infer_raw)

# -----
# -----

## infer_bf using summary statistics with data from Andersson et al. (2013).
## Test at timepoint 1:

# Assign model to variable.
infer_sum_t1 <- infer_bf(n_x = 33,
                       n_y = 32,
                       mean_x = 17.1,
                       mean_y = 13.6,
                       sd_x = 8,
                       sd_y = 9.8,
                       ni_margin = 2,
                       ni_margin_std = FALSE,
                       direction = "low")

# Extract Bayes factor from model
get_bf(infer_sum_t1)

# -----
# -----
```

```
## infer_bf using summary statistics with data from Andersson et al. (2013).  
## Test at timepoint 2:  
  
# Assign model to variable.  
infer_sum_t2 <- infer_bf(n_x = 30,  
                        n_y = 32,  
                        mean_x = 13.5,  
                        mean_y = 9.2,  
                        sd_x = 8.7,  
                        sd_y = 7.6,  
                        ni_margin = 2,  
                        ni_margin_std = FALSE,  
                        direction = "low")  
  
# Extract Bayes factor from model  
get_bf(infer_sum_t2)
```

model-classes

S4 classes to represent different models

Description

The S4 classes [baymedrSuperiority](#), [baymedrEquivalence](#), and [baymedrNonInferiority](#) represent models for the superiority ([super_bf](#)), equivalence ([equiv_bf](#)), and non-inferiority ([infer_bf](#)) tests, respectively.

Slots

`test` Type of test that was conducted.

`hypotheses` The hypotheses that are tested.

`data` The type of data that was used.

`prior_scale` The Cauchy prior scale that was used.

`bf` The resulting Bayes factor.

`interval` The equivalence interval in case of [equiv_bf](#).

`ni_margin` The non-inferiority margin in case of [infer_bf](#).

 super_bf

Bayes factor for superiority designs

Description

`super_bf` computes a Bayes factor for superiority designs with a continuous dependent variable.

Usage

```
super_bf(
  x = NULL,
  y = NULL,
  n_x = NULL,
  n_y = NULL,
  mean_x = NULL,
  mean_y = NULL,
  sd_x = NULL,
  sd_y = NULL,
  ci_margin = NULL,
  ci_level = NULL,
  prior_scale = 1/sqrt(2),
  direction = "high"
)
```

Arguments

<code>x</code>	A numeric vector of observations for the control group.
<code>y</code>	A numeric vector of observations for the experimental group.
<code>n_x</code>	A numeric vector of length one, specifying the sample size of the control group.
<code>n_y</code>	A numeric vector of length one, specifying the sample size of the experimental group.
<code>mean_x</code>	A numeric vector of length one, specifying the mean of the dependent variable in the control group.
<code>mean_y</code>	A numeric vector of length one, specifying the mean of the dependent variable in the experimental group.
<code>sd_x</code>	A numeric vector of length one, specifying the standard deviation of the dependent variable in the control group. Only <code>sd_x</code> and <code>sd_y</code> OR <code>ci_margin</code> and <code>ci_level</code> should be defined (see Details).
<code>sd_y</code>	A numeric vector of length one, specifying the standard deviation of the dependent variable in the experimental group. Only <code>sd_x</code> and <code>sd_y</code> OR <code>ci_margin</code> and <code>ci_level</code> should be defined (see Details).
<code>ci_margin</code>	A numeric vector of length one, specifying the margin of the confidence interval (i.e., the width of the confidence interval divided by 2) of the mean difference on the dependent variable between the experimental and control groups. The value should be a positive number Only <code>sd_x</code> and <code>sd_y</code> OR <code>ci_margin</code> and <code>ci_level</code> should be defined (see Details).

ci_level	A numeric vector of length one, specifying the confidence level of ci_margin. The value must be between 0 and 1 (e.g., 0.95 for a 95% confidence interval). Only sd_x and sd_y OR ci_margin and ci_level should be defined (see Details).
prior_scale	A numeric vector of length one, specifying the scale of the Cauchy prior distribution for the effect size under the alternative hypothesis (see Details). The default value is $r = 1 / \sqrt{2}$.
direction	A character vector of length one, specifying the direction of superior scores. 'low' indicates that low scores on the measure of interest correspond to a superior outcome and 'high' (the default) indicates that high scores on the measure of interest correspond to a superior outcome (see Details).

Details

The formulation of the null and alternative hypotheses for the superiority design differs depending on whether high or low scores on the dependent variable represent superiority. In both cases, the null hypothesis (i.e., H_0) states that the population means of the experimental group and the control group are equivalent. In the case where high scores correspond to superiority, the alternative hypothesis states that the population mean of the experimental group is higher than the population mean of the control group. Thus, the alternative hypothesis goes in the positive direction (i.e., H_+). In turn, in the case where low scores correspond to superiority, the alternative hypothesis states that the population mean of the experimental group is lower than the population mean of the control group. Thus, the alternative hypothesis goes in the negative direction (i.e., H_-). The dependent variable must be continuous.

Since the main goal of `super_bf` is to establish superiority, the resulting Bayes factor quantifies evidence in favor of the alternative hypothesis. In the case where low values represent superiority we have BF_0 , whereas in the case where high values represent superiority we have BF_+ . Evidence for the null hypothesis can easily be calculated by taking the reciprocal of the original Bayes factor (i.e., $BF_0^- = 1 / BF_0$ and $BF_+ = 1 / BF_+$). Quantification of evidence in favor of the null hypothesis is logically sound and legitimate within the Bayesian framework (see e.g., van Ravenzwaaij et al., 2019).

`super_bf` can be utilized to calculate a Bayes factor based on raw data (i.e., if arguments `x` and `y` are defined) or summary statistics (i.e., if arguments `n_x`, `n_y`, `mean_x`, and `mean_y` are defined). In the latter case, the user has the freedom to supply values either for the arguments `sd_x` and `sd_y` **OR** `ci_margin` and `ci_level`. Arguments with 'x' as a name or suffix correspond to the control group, whereas arguments with 'y' as a name or suffix correspond to the experimental group (i.e., the group for which we seek to establish superiority).

For the calculation of the Bayes factor, a Cauchy prior density centered on 0 is chosen for the effect size under the alternative hypothesis. The standard Cauchy distribution, with a location parameter of 0 and a scale parameter of 1, resembles a standard Normal distribution, except that the Cauchy distribution has less mass at the center but heavier tails (Liang et al., 2008; Rouder et al., 2009). The argument `prior_scale` specifies the width of the Cauchy prior, which corresponds to half of the interquartile range. Thus, by adjusting the Cauchy prior scale with `prior_scale`, different ranges of expected effect sizes can be emphasized. The default prior scale is set to $r = 1 / \sqrt{2}$.

`super_bf` creates an S4 object of class `baymedrSuperiority`, which has multiple slots/entries (e.g., type of data, prior scale, Bayes factor, etc.; see Value). If it is desired to store or extract solely

the Bayes factor, the user can do this with `get_bf`, by setting the S4 object as an argument (see Examples).

Value

An S4 object of class `baymedrSuperiority` is returned. Contained are a description of the model and the resulting Bayes factor:

- test: The type of analysis
- hypotheses: A statement of the hypotheses
 - h0: The null hypothesis
 - h1: The alternative hypothesis
- data: A description of the data
 - type: The type of data ('raw' when arguments x and y are used or 'summary' when arguments n_x, n_y, mean_x, mean_y, sd_x, and sd_y (or ci_margin and ci_level instead of sd_x and sd_y) are used)
 - ...: values for the arguments used, depending on 'raw' or 'summary'
- prior_scale: The scale of the Cauchy prior distribution
- bf: The resulting Bayes factor

A summary of the model is shown by printing the object.

References

- Gronau, Q. F., Ly, A., & Wagenmakers, E.-J. (2020). Informed Bayesian t-tests. *The American Statistician*, 74(2), 137-143.
- Liang, F., Paulo, R., Molina, G., Clyde, M. A., & Berger, J. O. (2008). Mixtures of g priors for Bayesian variable selection. *Journal of the American Statistical Association*, 103(481), 410-423.
- Rouder, J. N., Speckman, P. L., Sun, D., Morey, R. D., & Iverson, G. (2009). Bayesian t tests for accepting and rejecting the null hypothesis. *Psychonomic Bulletin & Review*, 16(2), 225-237.
- van Ravenzwaaij, D., Monden, R., Tendeiro, J. N., & Ioannidis, J. P. A. (2019). Bayes factors for superiority, non-inferiority, and equivalence designs. *BMC Medical Research Methodology*, 19(1), 71.

Examples

```
## super_bf using raw data:

# Assign model to variable.
super_raw <- super_bf(x = rnorm(100, 10, 15),
                     y = rnorm(130, 13, 10))

# Extract Bayes factor from model.
get_bf(super_raw)

# -----
# -----
```

```
## super_bf using summary statistics with data from Skjerven et al. (2013).
## EXAMPLE 1

# Assign model to variable.
super_sum_ex1 <- super_bf(n_x = 201,
                        n_y = 203,
                        mean_x = 68.1,
                        mean_y = 63.6,
                        ci_margin = (15.5 - (-6.5)) / 2,
                        ci_level = 0.95,
                        direction = "low")

# Extract Bayes factor from model.
get_bf(super_sum_ex1)

# -----

## super_bf using summary statistics with data from Skjerven et al. (2013).
## EXAMPLE 2

# Assign model to variable.
super_sum_ex2 <- super_bf(n_x = 200,
                        n_y = 204,
                        mean_x = 47.6,
                        mean_y = 61.3,
                        ci_margin = (24.4 - 2.9) / 2,
                        ci_level = 0.95,
                        direction = "low")

# Extract Bayes factor from model.
get_bf(super_sum_ex2)
```

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