

Package ‘tidyBF’

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Type Package

Title Tidy Wrapper for 'BayesFactor' Package

Version 0.3.0

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Description Provides helper functions that make it easy to run 'BayesFactor' package tests on a data which is in a tidy format. Additionally, it provides a more consistent syntax and by default returns a dataframe with rich details. These functions can also return expressions containing results from Bayes Factor tests that can then be displayed on custom plots.

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URL <https://indrajeetpatil.github.io/tidyBF/>,
<https://github.com/IndrajeetPatil/tidyBF>

BugReports <https://github.com/IndrajeetPatil/tidyBF/issues>

Depends R (>= 3.6.0)

Imports broomExtra, BayesFactor, dplyr, ipmisc, metaBMA, rlang, tidyr

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bf_contingency_tab	<i>Bayesian contingency table analysis</i>
--------------------	--

Description

Bayesian contingency table analysis

Usage

```
bf_contingency_tab(
  data,
  x,
  y = NULL,
  counts = NULL,
  ratio = NULL,
  sampling.plan = "indepMulti",
  fixed.margin = "rows",
  prior.concentration = 1,
  caption = NULL,
  output = "results",
  k = 2L,
  ...
)
```

```
bf_onesample_proptest(
  data,
  x,
  y = NULL,
  counts = NULL,
  ratio = NULL,
  sampling.plan = "indepMulti",
  fixed.margin = "rows",
  prior.concentration = 1,
  caption = NULL,
```

```

    output = "results",
    k = 2L,
    ...
)

```

Arguments

data	A dataframe (or a tibble) from which variables specified are to be taken. A matrix or tables will not be accepted.
x	The variable to use as the rows in the contingency table.
y	The variable to use as the columns in the contingency table. Default is NULL. If NULL, one-sample proportion test (a goodness of fit test) will be run for the main variable. Otherwise an appropriate association test will be run.
counts	A string naming a variable in data containing counts, or NULL if each row represents a single observation (Default).
ratio	A vector of proportions: the expected proportions for the proportion test (should sum to 1). Default is NULL, which means the null is equal theoretical proportions across the levels of the nominal variable. This means if there are two levels this will be <code>ratio = c(0.5, 0.5)</code> or if there are four levels this will be <code>ratio = c(0.25, 0.25, 0.25, 0.25)</code> , etc.
sampling.plan	Character describing the sampling plan. Possible options are "indepMulti" (independent multinomial; default), "poisson", "jointMulti" (joint multinomial), "hypergeom" (hypergeometric). For more, see <code>?BayesFactor::contingencyTableBF()</code> .
fixed.margin	For the independent multinomial sampling plan, which margin is fixed ("rows" or "cols"). Defaults to "rows".
prior.concentration	Specifies the prior concentration parameter, set to 1 by default. It indexes the expected deviation from the null hypothesis under the alternative, and corresponds to Gunel and Dickey's (1974) "a" parameter.
caption	Text to display as caption (will be displayed on top of the Bayes Factor caption/message).
output	Can either be "null" (or "caption" or "H0" or "h0"), which will return expression with evidence in favor of the null hypothesis, or "alternative" (or "title" or "H1" or "h1"), which will return expression with evidence in favor of the alternative hypothesis, or "results", which will return a dataframe with results all the details).
k	Number of digits after decimal point (should be an integer) (Default: <code>k = 2L</code>).
...	further arguments to be passed to or from methods.

Note

Bayes Factor for goodness of fit test is based on gist provided by Richard Morey: <https://gist.github.com/richardmorey/a4cd3a2051f373db917550d67131dba4>.

See Also

[bf_corr_test](#), [bf_oneway_anova](#), [bf_ttest](#)

Examples

```
# for reproducibility
set.seed(123)
library(tidyBF)

# ----- association tests -----

# to get caption (in favor of null)
bf_contingency_tab(
  data = mtcars,
  x = am,
  y = cyl,
  fixed.margin = "cols"
)

# to see results
bf_contingency_tab(
  data = mtcars,
  x = am,
  y = cyl,
  sampling.plan = "jointMulti",
  fixed.margin = "rows",
  prior.concentration = 1
)

# ----- goodness of fit tests -----

bf_contingency_tab(
  data = mtcars,
  x = am,
  prior.concentration = 10
)
```

bf_corr_test

Bayesian correlation test.

Description

Bayesian correlation test.

Usage

```
bf_corr_test(
  data,
  x,
  y,
  bf.prior = 0.707,
  caption = NULL,
  output = "results",
```

```

    k = 2L,
    ...
  )

```

Arguments

data	A dataframe (or a tibble) from which variables specified are to be taken. A matrix or tables will not be accepted.
x	The column in data containing the explanatory variable to be plotted on the x-axis. Can be entered either as a character string (e.g., "x") or as a bare expression (e.g, x).
y	The column in data containing the response (outcome) variable to be plotted on the y-axis. Can be entered either as a character string (e.g., "y") or as a bare expression (e.g, y).
bf.prior	A number between 0.5 and 2 (default 0.707), the prior width to use in calculating Bayes factors.
caption	Text to display as caption (will be displayed on top of the Bayes Factor caption/message).
output	Can either be "null" (or "caption" or "H0" or "h0"), which will return expression with evidence in favor of the null hypothesis, or "alternative" (or "title" or "H1" or "h1"), which will return expression with evidence in favor of the alternative hypothesis, or "results", which will return a dataframe with results all the details).
k	Number of digits after decimal point (should be an integer) (Default: k = 2L).
...	Additional arguments passed to <code>parameters::model_parameters.BFBayesFactor()</code> .

See Also

[bf_contingency_tab](#), [bf_oneway_anova](#), [bf_ttest](#)

Examples

```

# for reproducibility
set.seed(123)

# to see results
bf_corr_test(
  data = anscombe,
  x = x1,
  y = y4,
  bf.prior = 1
)

# to get caption
bf_corr_test(
  data = anscombe,
  x = x1,
  y = y4,

```

```

  bf.prior = 0.8,
  output = "null"
)

```

bf_expr

Prepare caption with expression for Bayes Factor results

Description

Convenience function to create an expression with Bayes Factor results.

Usage

```

bf_expr(
  bf.object,
  k = 2L,
  conf.level = 0.95,
  conf.method = "hdi",
  centrality = "median",
  output = "null",
  caption = NULL,
  anova.design = FALSE,
  ...
)

```

Arguments

bf.object	An object from BayesFactor package.
k	Number of digits after decimal point (should be an integer) (Default: k = 2L).
conf.level	Value or vector of probability of the CI (between 0 and 1) to be estimated. Default to 0.95 (95%).
conf.method	The type of index used for Credible Interval. Can be "hdi" (default, see bayestestR::hdi()), "eti" (see bayestestR::eti()) or "si" (see bayestestR::si()).
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" or "all".
output	Can either be "null" (or "caption" or "H0" or "h0"), which will return expression with evidence in favor of the null hypothesis, or "alternative" (or "title" or "H1" or "h1"), which will return expression with evidence in favor of the alternative hypothesis, or "results", which will return a dataframe with results all the details).
caption	Text to display as caption (will be displayed on top of the Bayes Factor caption/message).
anova.design	Whether the object is from BayesFactor::anovaBF (default: FALSE). The expression is different for anova designs because not all details are available.
...	Additional arguments passed to parameters::model_parameters.BFBayesFactor() .

Examples

```
# for reproducibility
set.seed(123)
library(tidyBF)

# creating caption (for null)
bf_expr(
  BayesFactor::correlationBF(
    x = iris$Sepal.Length,
    y = iris$Petal.Length
  ),
  output = "null",
  k = 3,
  caption = "Note: Iris dataset"
)
```

bf_extractor

Extract Bayes Factors from BayesFactor model object.

Description

Extract Bayes Factors from BayesFactor model object.

Usage

```
bf_extractor(bf.object, ...)
```

Arguments

bf.object An object from BayesFactor package.
... Additional arguments passed to `parameters::model_parameters.BFBayesFactor()`.

Note

Important: don't enter `1/bf_obj` to extract results for null hypothesis; doing so will return wrong results.

Examples

```
set.seed(123)

# creating a `BayesFactor` object
bf_obj <-
  BayesFactor::anovaBF(
    formula = Sepal.Length ~ Species,
    data = iris,
    progress = FALSE
```

```

)

# extracting Bayes Factors in a dataframe
bf_extractor(bf_obj)

```

bf_meta

Bayes factor for random-effects meta-analysis

Description

Bayes factor for random-effects meta-analysis

Usage

```

bf_meta(
  data,
  d = prior("norm", c(mean = 0, sd = 0.3)),
  tau = prior("invgamma", c(shape = 1, scale = 0.15)),
  k = 2L,
  output = "results",
  caption = NULL,
  messages = TRUE,
  ...
)

```

Arguments

data	A dataframe. It must contain columns named <code>estimate</code> (effect sizes or outcomes) and <code>std.error</code> (corresponding standard errors). These two columns will be used for <code>yi</code> and <code>sei</code> arguments in <code>metafor::rma</code> (for parametric analysis) or <code>metaplus::metaplus</code> (for robust analysis).
d	prior distribution on the average effect size <code>d</code> . The prior probability density function is defined via prior .
tau	prior distribution on the between-study heterogeneity <code>tau</code> (i.e., the standard deviation of the study effect sizes <code>dstudy</code> in a random-effects meta-analysis. A (nonnegative) prior probability density function is defined via prior .
k	Number of digits after decimal point (should be an integer) (Default: <code>k = 2L</code>).
output	Can either be <code>"null"</code> (or <code>"caption"</code> or <code>"H0"</code> or <code>"h0"</code>), which will return expression with evidence in favor of the null hypothesis, or <code>"alternative"</code> (or <code>"title"</code> or <code>"H1"</code> or <code>"h1"</code>), which will return expression with evidence in favor of the alternative hypothesis, or <code>"results"</code> , which will return a dataframe with results all the details).
caption	Text to display as caption (will be displayed on top of the Bayes Factor caption/message).
messages	Deprecated. Retained only for backward compatibility.

... Arguments passed on to `metaBMA::meta_random`

`labels` optional: character values with study labels. Can be a character vector or the quoted or unquoted name of the variable in data

`rscale_contin` scale parameter of the JZS prior for the continuous covariates.

`rscale_discrete` scale parameter of the JZS prior for discrete moderators.

`centering` whether continuous moderators are centered.

`logml` how to estimate the log-marginal likelihood: either by numerical integration ("integrate") or by bridge sampling using MCMC/Stan samples ("stan"). To obtain high precision with `logml="stan"`, many MCMC samples are required (e.g., `logml_iter=10000, warmup=1000`).

`summarize` how to estimate parameter summaries (mean, median, SD, etc.): Either by numerical integration (`summarize = "integrate"`) or based on MCMC/Stan samples (`summarize = "stan"`).

`ci` probability for the credibility/highest-density intervals.

`rel.tol` relative tolerance used for numerical integration using `integrate`. Use `rel.tol=.Machine$double.eps` for maximal precision (however, this might be slow).

`logml_iter` number of iterations (per chain) from the posterior distribution of `d` and `tau`. The samples are used for computing the marginal likelihood of the random-effects model with bridge sampling (if `logml="stan"`) and for obtaining parameter estimates (if `summarize="stan"`). Note that the argument `iter=2000` controls the number of iterations for estimation of the random-effect parameters per study in random-effects meta-analysis.

`silent_stan` whether to suppress the Stan progress bar.

Examples

```
# setup
set.seed(123)
library(metaBMA)

# creating a dataframe
(df <-
  structure(
    .Data = list(
      study = c("1", "2", "3", "4", "5"),
      estimate = c(
        0.382047603321706,
        0.780783111514665,
        0.425607573765058,
        0.558365541235078,
        0.956473848429961
      )
    ),
    std.error = c(
      0.0465576338644502,
      0.0330218199731529,
      0.0362834986178494,
```

```

      0.0480571500648261,
      0.062215818388157
    )
  ),
  row.names = c(NA, -5L),
  class = c("tbl_df", "tbl", "data.frame")
))

# getting Bayes factor in favor of null hypothesis
bf_meta(
  data = df,
  k = 3,
  iter = 1500,
  messages = TRUE,
  # customizing analysis with additional arguments
  control = list(max_treedepth = 15)
)

```

bf_oneway_anova

Bayesian one-way analysis of variance

Description

Bayesian one-way analysis of variance

Usage

```

bf_oneway_anova(
  data,
  x,
  y,
  bf.prior = 0.707,
  caption = NULL,
  output = "results",
  paired = FALSE,
  k = 2L,
  ...
)

```

Arguments

data	A dataframe (or a tibble) from which variables specified are to be taken. A matrix or tables will not be accepted.
x	The grouping variable from the dataframe data.
y	The response (a.k.a. outcome or dependent) variable from the dataframe data.

bf.prior	A number between 0.5 and 2 (default 0.707), the prior width to use in calculating Bayes factors.
caption	Text to display as caption (will be displayed on top of the Bayes Factor caption/message).
output	Can either be "null" (or "caption" or "H0" or "h0"), which will return expression with evidence in favor of the null hypothesis, or "alternative" (or "title" or "H1" or "h1"), which will return expression with evidence in favor of the alternative hypothesis, or "results", which will return a dataframe with results all the details).
paired	Decides whether the design is repeated measures or not (Default: FALSE).
k	Number of digits after decimal point (should be an integer) (Default: k = 2L).
...	Additional arguments passed to <code>parameters::model_parameters.BFBayesFactor()</code> .

See Also

[bf_contingency_tab](#), [bf_corr_test](#), [bf_ttest](#)

Examples

```
# setup
set.seed(123)

# between-subjects -----
bf_oneway_anova(
  data = iris,
  x = Species,
  y = Sepal.Length,
  bf.prior = 0.8
)

# within-subjects -----
bf_oneway_anova(
  data = bugs_long,
  x = condition,
  y = desire,
  paired = TRUE
)

# expression -----
bf_oneway_anova(
  data = bugs_long,
  x = condition,
  y = desire,
  paired = TRUE,
  output = "null"
)
```

`bf_ttest`*Bayes Factor for t-test*

DescriptionBayes Factor for *t*-test**Usage**

```
bf_ttest(  
  data,  
  x,  
  y = NULL,  
  test.value = 0,  
  paired = FALSE,  
  bf.prior = 0.707,  
  caption = NULL,  
  output = "results",  
  k = 2L,  
  ...  
)
```

```
bf_one_sample_ttest(  
  data,  
  x,  
  y = NULL,  
  test.value = 0,  
  paired = FALSE,  
  bf.prior = 0.707,  
  caption = NULL,  
  output = "results",  
  k = 2L,  
  ...  
)
```

```
bf_two_sample_ttest(  
  data,  
  x,  
  y = NULL,  
  test.value = 0,  
  paired = FALSE,  
  bf.prior = 0.707,  
  caption = NULL,  
  output = "results",  
  k = 2L,  
  ...  
)
```

Arguments

data	A dataframe (or a tibble) from which variables specified are to be taken. A matrix or tables will not be accepted.
x	Either the grouping variable from the dataframe data if it's a two-sample <i>t</i> -test or a numeric variable if it's a one-sample <i>t</i> -test.
y	The column in data containing the response (outcome) variable to be plotted on the y-axis. Can be entered either as a character string (e.g., "y") or as a bare expression (e.g, y).
test.value	A number specifying the value of the null hypothesis (Default: 0).
paired	Decides whether the design is repeated measures or not (Default: FALSE).
bf.prior	A number between 0.5 and 2 (default 0.707), the prior width to use in calculating Bayes factors.
caption	Text to display as caption (will be displayed on top of the Bayes Factor caption/message).
output	Can either be "null" (or "caption" or "H0" or "h0"), which will return expression with evidence in favor of the null hypothesis, or "alternative" (or "title" or "H1" or "h1"), which will return expression with evidence in favor of the alternative hypothesis, or "results", which will return a dataframe with results all the details).
k	Number of digits after decimal point (should be an integer) (Default: k = 2L).
...	Additional arguments passed to <code>parameters::model_parameters.BFBayesFactor()</code> .

Details

If y is NULL, a one-sample *t*-test will be carried out, otherwise a two-sample *t*-test will be carried out.

See Also

[bf_contingency_tab](#), [bf_corr_test](#), [bf_oneway_anova](#)

Examples

```
# ----- two-samples tests -----

# for reproducibility
set.seed(123)
library(tidyBF)

# to get dataframe
bf_ttest(
  data = mtcars,
  x = am,
  y = wt,
  paired = FALSE,
  bf.prior = 0.880
```

```
)  
  
# ----- one-samples test -----  
  
# to get dataframe  
bf_ttest(  
  data = iris,  
  x = Sepal.Length,  
  test.value = 5.85  
)
```

bugs_long

Tidy version of the "Bugs" dataset.

Description

Tidy version of the "Bugs" dataset.

Usage

bugs_long

Format

A data frame with 372 rows and 6 variables

- subject. Dummy identity number for each participant.
- gender. Participant's gender (Female, Male).
- region. Region of the world the participant was from.
- education. Level of education.
- condition. Condition of the experiment the participant gave rating for (**LDLF**: low frighteningness and low disgustingness; **LFHD**: low frighteningness and high disgustingness; **HFHD**: high frighteningness and low disgustingness; **HFHD**: high frighteningness and high disgustingness).
- desire. The desire to kill an arthropod was indicated on a scale from 0 to 10.

Details

This data set, "Bugs", provides the extent to which men and women want to kill arthropods that vary in frighteningness (low, high) and disgustingness (low, high). Each participant rates their attitudes towards all arthropods. Subset of the data reported by Ryan et al. (2013).

Source

<https://www.sciencedirect.com/science/article/pii/S0747563213000277>

Examples

```
dim(bugs_long)
head(bugs_long)
dplyr::glimpse(bugs_long)
```

meta_data_check	<i>Helper function to check column names for meta-analysis.</i>
-----------------	---

Description

Helper function to check column names for meta-analysis.

Usage

```
meta_data_check(data)
```

Arguments

data	A dataframe. It must contain columns named estimate (effect sizes or outcomes) and std.error (corresponding standard errors). These two columns will be used for yi and sei arguments in metafor::rma (for parametric analysis) or metaplus::metaplust (for robust analysis).
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