Package 'BayesianPower'

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Type Package

Title Sample Size and Power for Comparing Inequality Constrained
Hypotheses

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Description A collection of methods to determine the required sample size for
the evaluation of inequality constrained hypotheses by means of a Bayes
factor. Alternatively, for a given sample size, the unconditional error
probabilities or the expected conditional error probabilities can be
determined. Additional material on the methods in this package is
available in Klaassen, F., Hoijtink, H. & Gu, X. (2019)
<doi:10.31219/osf.io/d5kf3>.

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RoxygenNote 7.1.0

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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R topics documented:

bayes_error	*Determine the unconditional error probabilities for a set of simulated Bayes factors.*

Description

Determine the unconditional error probabilities for a set of simulated Bayes factors.

Usage

```
bayes_error(BFs1, BFs2, bound1 = 1, bound2 = 1/bound1)
```

Arguments

BFs1	A vector. Simulated BF12 under H1 for a given n
BFs2	A vector. Simulated BF12 under H2 for a given n
bound1	A number. The boundary above which BF12 favors H1
bound2	A number. The boundary below which BF12 favors H2

Value

A named vector. The Type 1, Type 2, Decision error and Area of Indecision probabilities and the median Bayes factors under H1 and H2

bayes_power	*Determine the 'power' for a Bayesian hypothesis test*

Description

Determine the 'power' for a Bayesian hypothesis test

Usage

```
bayes_power(
  n,
  h1,
  h2,
  m1,
  m2,
  sd1 = 1,
  sd2 = 1,
  scale = 1000,
  bound1 = 1,
  bound2 = 1/bound1,
```

```
      datasets = 1000,
      nsamp = 1000,
      seed = 31
    )
```

Arguments

n	A number. The sample size
h1	A constraint matrix defining H1
h2	A constraint matrix defining H2
m1	A vector of expected population means under H1
m2	A vector of expected populations means under H2 `m2` must be of same length as `m1`
sd1	A vector of standard deviations under H1. Must be a single number (equal standard deviation under all populations), or a vector of the same length as `m1`
sd2	A vector of standard deviations under H2. Must be a single number (equal standard deviation under all populations), or a vector of the same length as `m2`
scale	A number specifying the prior scale
bound1	A number. The boundary above which BF12 favors H1
bound2	A number. The boundary below which BF12 favors H2
datasets	A number. The number of datasets to compute the error probabilities
nsamp	A number. The number of prior or posterior samples to determine the fit and complexity
seed	A number. The random seed to be set

Value

The Type 1, Type 2, Decision error and Area of Indecision probability and the median BF12s under H1 and H2

Examples

```
# Short example WITH SMALL AMOUNT OF SAMPLES
h1 <- matrix(c(1,-1,0,0,1,-1), nrow= 2, byrow= TRUE)
h2 <- "c"
m1 <- c(.4,.2,0)
m2 <- c(.2,0,.1)
bayes_power(40, h1, h2, m1, m2, datasets = 50, nsamp = 50)
```

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bayes_sampsize   *Determine the required sample size for a Bayesian hypothesis test*

Description

Determine the required sample size for a Bayesian hypothesis test

Usage

```
bayes_sampsize(
  h1,
  h2,
  m1,
  m2,
  sd1 = 1,
  sd2 = 1,
  scale = 1000,
  type = 1,
  cutoff,
  bound1 = 1,
  bound2 = 1/bound1,
  datasets = 1000,
  nsamp = 1000,
  minss = 2,
  maxss = 1000,
  seed = 31
)
```

Arguments

h1	A constraint matrix defining H1.
h2	A constraint matrix defining H2.
m1	A vector of expected population means under H1 (standardized).
m2	A vector of expected populations means under H2 (standardized). m2 must be of same length as m1
sd1	A vector of standard deviations under H1. Must be a single number (equal standard deviation under all populations), or a vector of the same length as m1
sd2	A vector of standard deviations under H2. Must be a single number (equal standard deviation under all populations), or a vector of the same length as m2
scale	A number specifying the prior scale
type	A character. The type of error to be controlled options are: "1", "2", "de", "aoi", "med.1", "med.2"
cutoff	A number. The cutoff criterion for type. If type is "1", "2", "de", "aoi", cutoff must be between 0 and 1 If type is "med.1" or "med.2", cutoff must be larger than 1

bound1	A number. The boundary above which BF12 favors H1
bound2	A number. The boundary below which BF12 favors H2
datasets	A number. The number of datasets to compute the error probabilities
nsamp	A number. The number of prior or posterior samples to determine the fit and complexity
minss	A number. The minimum sample size to consider
maxss	A number. The maximum sample size to consider
seed	A number. The random seed to be set

Value

The sample size for which the chosen type of error probability is at the set cutoff, and the according error probabilities and median Bayes factors

Examples

```
# Short computation example NOT SUFFICIENT SAMPLES
h1 <- matrix(c(1,-1), nrow= 1, byrow= TRUE)
h2 <- 'c'
m1 <- c(.4, 0)
m2 <- c(0, .1)
bayes_sampsize(h1, h2, m1, m2, sd1 = 1, sd2 = 1, scale = 1000,
type = "de", cutoff = .125, nsamp = 50, datasets = 50,
minss = 40, maxss = 70)
```

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calc_bf *Compute a Bayes factor*

Description

Compute a Bayes factor

Usage

```
calc_bf(data, h1, h2, scale, nsamp = 1000)
```

Arguments

data	A matrix. The dataset for which the BF must be computed
h1	A constraint matrix defining H1.
h2	A constraint matrix defining H2.
scale	A number specifying the prior scale.
nsamp	A number. The number of prior or posterior samples to determine the

Value

BF12, that is, the evidence for H1 relative to H2

---

calc_fc   *Compute the complexity or fit for two hypotheses.*

Description

Compute the complexity or fit for two hypotheses.

Usage

```
calc_fc(hyp, hyp2, means, sds, nsamp = 1000)
```

Arguments

hyp	A constraint matrix defining H1.
hyp2	A constraint matrix defining H2 OR a character `'u'` or `'c'` specifying an unconstrained or complement hypothesis
means	A vector of posterior or prior means
sds	A vector or posterior or prior standard deviation
nsamp	A number. The number of prior or posterior samples to determine the fit and complexity

Value

A vector. The proportion of posterior samples in agreement with H1 and with H2

---

eval_const   *Evaluate a constraint matrix for a set of prior/posterior samples*

Description

Evaluate a constraint matrix for a set of prior/posterior samples

Usage

```
eval_const(hyp, samples)
```

Arguments

hyp	A constraint matrix defining a hypothesis.
samples	A matrix. Prior or posterior samples, the number of columns corresponds to the number of groups, the number of rows the number of samples

Value

A number between 0 and 1. The proportion of samples in which the constraints are met.

---

samp_bf *Sample multiple datasets and compute the Bayes factor in each*

Description

Sample multiple datasets and compute the Bayes factor in each

Usage

```
samp_bf(datasets, n, ngroup, means, sds, h1, h2, scale, nsamp)
```

Arguments

datasets	A number. The number of datasets to simulate for each sample size `n`
n	A number. The group sample size to be used in data simulation
ngroup	A number. The number of groups.
means	A vector of expected population means.
sds	A vector of expected population standard deviations Note, when standardized, this is a vector of 1s
h1	A constraint matrix defining H1.
h2	A constraint matrix defining H2.
scale	A number specifying the prior scale.
nsamp	A number. The number of samples for the fit and complexity See `?BayesianPower::calc_fc`

Value

A vector of Bayes factors BF12 for each of the simulated datasets

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samp_dist *Sample from prior or posterior distribution*

Description

Sample from prior or posterior distribution

Usage

```
samp_dist(nsamp, means, sds)
```

Arguments

nsamp	A number. The number of prior or posterior samples to determine the fit and complexity
means	A vector. The prior or posterior means for each group
sds	A number or a vector. The standard deviations for each group If a number is used, the same prior or posterior standard deviation is used for each group.

Value

A matrix of nsamp rows and as many columns as the length of means.

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