**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**

```r
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

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**bayes_power**

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

**Description**

Determine the 'power' for a Bayesian hypothesis test

**Usage**

```r
bayes_power(n, h1, h2, m1, m2, ngroup = NULL, comp = NULL,
             bound1 = 1, bound2 = 1/bound1, datasets = 1000, nsamp = 1000,
             seed = NULL)
```
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 (standardized)
m2      A vector of expected populations means under H2 (standardized) m2 must be of same length as m1
ngroup  A number or NULL. The number of groups If NULL the number of groups is determined from the length of m1
comp    A vector or NULL. The complexity of H1 and H2. If NULL the complexity is also estimated
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)

# Example 1 H1 vs Hc
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 = 500, nsamp = 500)

# Example 2 H1 vs H2
h1 <- matrix(c(1,-1,0,0,1,-1,0,0,0,1,-1), nrow= 3, byrow= TRUE)
h2 <- matrix(c(0,1,1,0,0,1,0,-1,0,0,1), nrow = 3, byrow= TRUE)
m1 <- c(.7,.3,.1,0)
m2 <- c(.4,.5,.1)
bayes_power(40, h1, h2, m1, m2, datasets = 500, nsamp = 500)
bayes_sampsize

Determine the required sample size for a Bayesian hypothesis test

Usage

bayes_sampsize(h1, h2, m1, m2, 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.
- **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_samps(h1, h2, m1, m2, "de", .125, nsamp = 50, datasets = 50, minss = 40, maxss = 70)

# Example 1 Decision error and Hc
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_samps(h1, h2, m1, m2, "de", .125)

# Example 2 Indecision error and H2
h1 <- matrix(c(1,-1,0,0,0,1,-1,0,0,1,-1), nrow= 3, byrow= TRUE)
h2 <- matrix(c(0,-1,1,0,0,1,0,-1,0,0,1), nrow= 3, byrow= TRUE)
m1 <- c(.7,.3,.1,0)
m2 <- c(.0,.4,.5,.1)
bayes_samps(h1, h2, m1, m2, type = "aoi", cutoff = .2, minss = 2, maxss = 500)

---

calc_bf  

Compute a Bayes factor

description

Compute a Bayes factor

Usage

calc_bf(data, h1, h2, comp, 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.
comp  
A vector with the complexity of H1 and H2
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, comp, 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 (standardized).
sds A vector of expected population effect sizes. Note, when standardized, this is a vector of 1s
h1 A constraint matrix defining H1.
h2 A constraint matrix defining H2.
comp A vector of the complexities of H1 and H2.
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

 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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