

Package ‘metaBMA’

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Title Bayesian Model Averaging for Random and Fixed Effects
Meta-Analysis

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Description Computes the posterior model probabilities for four meta-analysis models (null model vs. alternative model assuming either fixed- or random-effects, respectively). These posterior probabilities are used to estimate the overall mean effect size as the weighted average of the mean effect size estimates of the random- and fixed-effect model as proposed by Gronau, Van Erp, Heck, Cesario, Jonas, & Wagenmakers (2017, <doi:10.1080/23743603.2017.1326760>). The user can define a wide range of noninformative or informative priors for the mean effect size and the heterogeneity coefficient. Funding for this research was provided by the Berkeley Initiative for Transparency in the Social Sciences, a program of the Center for Effective Global Action (CEGA), with support from the Laura and John Arnold Foundation.

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Imports mvtnorm, logspline, coda, runjags, LaplacesDemon

Suggests testthat, knitr

VignetteBuilder knitr

SystemRequirements JAGS (<http://mcmc-jags.sourceforge.net>)

URL <https://github.com/danheck/metaBMA>

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metaBMA-package	<i>metaBMA: Bayesian Model Averaging for Random and Fixed Effects Meta-Analysis</i>
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Description

Fixed-effects meta-analyses assume that the effect size d is identical in all studies. In contrast, random-effects meta-analyses assume that effects vary according to a normal distribution with mean d and standard deviation τ . Both models can be compared in a Bayesian framework by assuming specific prior distribution for d and τ (see [prior](#)). Given the posterior model probabilities, the evidence for or against an effect (i.e., whether $d = 0$) and the evidence for or against random effects can be evaluated (i.e., whether $\tau = 0$). By using Bayesian model averaging, both tests can be performed by integrating over the other model. This allows to test whether an effect exists while accounting for uncertainty whether study heterogeneity exists (so-called inclusion Bayes factors).

Details

The most general functions in metaBMA are `meta_bma` and `meta_default`, which fit random- and fixed-effects models, compute the inclusion Bayes factor for the presence of an effect and the averaged posterior distribution of the mean effect d (which accounts for uncertainty regarding study heterogeneity). Prior distributions can be specified and plotted using the function `prior`.

Moreover, `meta_fixed` and `meta_random` fit a single meta-analysis models. The model-specific posteriors for d can be averaged by `bma` and inclusion Bayes factors be computed by `inclusion`.

Results can be visualized with the functions `plot_posterior`, which compares the prior and posterior density for a fitted meta-analysis, and `plot_forest`, which plots study and overall effect sizes.

For more details, see the vignette: `vignette("metaBMA")`

Author(s)

Heck, D. W., Gronau, Q. F., & Wagenmakers, E.-J.

References

Gronau, Q. F., Erp, S. V., Heck, D. W., Cesario, J., Jonas, K. J., & Wagenmakers, E.-J. (2017). A Bayesian model-averaged meta-analysis of the power pose effect with informed and default priors: the case of felt power. *Comprehensive Results in Social Psychology*, 2(1), 123-138. <https://doi.org/10.1080/23743603.2017.1326760>

Heck, D. W., Gronau, Q. F., & Wagenmakers, E.-J. (2017). metaBMA: Bayesian model averaging for random and fixed effects meta-analysis. R package version 0.3.9. <https://github.com/danheck/metaBMA>. doi:10.5281/zenodo.835494

See Also

Useful links:

- <https://github.com/danheck/metaBMA>

bma

Bayesian Model Averaging

Description

Model averaging of meta-analysis models according to their posterior model probability.

Usage

```
bma(meta, prior = 1, parameter = "d", summarize = "integrate")
```

Arguments

meta	list of meta-analysis models (fitted via <code>meta_random</code> or <code>meta_fixed</code>)
prior	prior probabilities over models (possibly unnormalized). For instance, if the first model is as likely as models 2, 3 and 4 together: <code>prior = c(3,1,1,1)</code> . The default is a discrete uniform distribution over models.
parameter	either the mean effect "d" or the heterogeneity across studies "tau"
summarize	whether and to compute parameter summaries (mean, median, SD, 95% quantile interval, HPD interval). If <code>summarize = "integrate"</code> , numerical integration is used (which is precise but can require some seconds of computing time), <code>summarize = "jags"</code> summarizes the JAGS samples, and <code>summarize = "none"</code> suppresses parameter summaries.

Examples

```

data(towels)
fix1 <- meta_fixed(towels$logOR, towels$SE, towels$study,
                  d = "halfnorm", d.par = c(mean=0, sd=.2))
fix2 <- meta_fixed(towels$logOR, towels$SE, towels$study,
                  d = "beta", d.par = c(alpha=1, beta=1))
fix3 <- meta_fixed(towels$logOR, towels$SE, towels$study,
                  d = "triangular",
                  d.par = c(min=0, peak=.3, max=1))

averaged <- bma(list(Halfnormal = fix1, Uniform = fix2,
                   Triangular = fix3))

averaged
plot_posterior(averaged)
plot_forest(averaged, mar = c(4.5,20,4,.3))

```

dtriangular

Triangular Distribution

Description

Distribution with a triangular density function.

Usage

```

dtriangular(x, min, peak, max, log = FALSE)

rtriangular(n, min, peak, max)

```

Arguments

x	vector of quantiles
min	lower bound of distribution

peak	peak of triangle density
max	upper bound of distribution
log	logical; if TRUE, probabilities p are given as log(p)
n	number of samples

Examples

```
plot(prior("triangular", c(.2, .6, 1.3)), 0, 2)

samples <- rtriangular(1e5, .2, .5, 1)
hist(samples, 200, FALSE)
curve(dtriangular(x, .2, .5, 1), col = 2,
      add = TRUE, lwd = 2)
```

dtruncnorm	<i>Truncated Normal Distribution</i>
------------	--------------------------------------

Description

Normal distribution truncated to the interval [a,b]

Usage

```
dtruncnorm(x, a = -Inf, b = Inf, mean = 0, sd = 1, log = FALSE)

rtruncnorm(n, a = -Inf, b = Inf, mean = 0, sd = 1)
```

Arguments

x	vector of quantiles
a	lower bound
b	upper bound
mean	vector of means
sd	vector of standard deviations
log	if TRUE, probabilities are given as log(p)
n	number of samples

Examples

```
samples <- rtruncnorm(1e5, -.5, 3, 1, 1)
hist(samples, 200, freq = FALSE)
curve(dtruncnorm(x, -.5, 3, 1, 1), -2,4,
      col = 2, lwd = 2, add = TRUE, n = 301)
```

`facial_feedback`*Data Set: Facial Feedback*

Description

Preregistered replication (Wagenmakers et al., 2016) that investigated the facial feedback hypothesis (Strack, Martin, & Stepper, 1988).

Usage`facial_feedback`**Format**

A data frame with three variables:

`study` Authors of original study (see Wagenmakers et. al, 2016)

`d` Measure of effect size: Cohen's d (difference between smile vs. pout condition)

`SE` Measure of precision: standard error of Cohen's d

Details

The facial-feedback hypothesis states that people's affective responses can be influenced by their own facial expression (e.g., smiling, pouting), even when their expression did not result from their emotional experiences (Strack, Martin, & Stepper, 1988).

References

Strack, F., Martin, L. L., & Stepper, S. (1988). Inhibiting and facilitating conditions of the human smile: A nonobtrusive test of the facial feedback hypothesis. *Journal of Personality and Social Psychology*, 54, 768–777. <https://doi.org/10.1037/0022-3514.54.5.768>

Wagenmakers, E.-J., Beek, T., Dijkhoff, L., Gronau, Q. F., Acosta, A., Adams, R. B., ... Zwaan, R. A. (2016). Registered replication report: Strack, Martin, & Stepper (1988). *Perspectives on Psychological Science*, 11, 917-928. <https://doi.org/10.1177/1745691616674458>

Examples

```
data(facial_feedback)
head(facial_feedback)
```

inclusion	<i>Inclusion Bayes Factor</i>
-----------	-------------------------------

Description

Computes the inclusion Bayes factor for two sets of models (e.g., $A=\{M1,M2\}$ vs. $B=\{M3,M4\}$).

Usage

```
inclusion(logm1, include = 1, prior = 1)
```

Arguments

logm1	a vector with log-marginal likelihoods. Alternatively, a list with meta-analysis models (fitted via meta_random or meta_fixed)
include	integer vector which models to include in inclusion Bayes factor/posterior probability. If only two marginal likelihoods/meta-analyses are supplied, the Bayes factor $BF_{\{M1,M2\}}$ is computed by default.
prior	prior probabilities over models (possibly unnormalized). For instance, if the first model is as likely as models 2, 3 and 4 together: <code>prior = c(3,1,1,1)</code> . The default is a discrete uniform distribution over models.

Examples

```
#### Example with simple Normal-distribution models
# data:
x <- rnorm(50)

# Model 1: x ~ Normal(0,1)
logm1 <- sum(dnorm(x, log = TRUE))
# Model 2: x ~ Normal(1,1)
logm2 <-sum(dnorm(x, mean = 1, log = TRUE))
# Model 3: x ~ Student-t(df=2)
logm3 <-sum(dt(x, df=2, log = TRUE))

# BF: Correct (M1) vs. misspecified (M2, M3)
inclusion(c(logm1, logm2, logm3), include = 1)
```

meta_bma	<i>Model Averaging for Meta-Analysis</i>
----------	--

Description

Fits random- and fixed-effects meta-analyses and performs Bayesian model averaging for $H1$ ($d \neq 0$) vs. $H0$ ($d = 0$).

Usage

```
meta_bma(y, SE, labels = NULL, d = "norm", d.par = c(0, 0.3),
  tau = "halfcauchy", tau.par = 0.5, prior = c(1, 1, 1, 1),
  sample = 10000, summarize = "integrate", ...)
```

Arguments

y	mean in each study
SE	standard error in each study
labels	optional: character values with study labels
d	type of prior for mean effect d (see prior)
d.par	prior parameters for d
tau	type of prior for standard deviation of study effects τ in random-effects meta-analysis (i.e., the SD of d across studies; see prior)
tau.par	prior parameters for τ
prior	prior probabilities over models (possibly unnormalized) in the order <code>c(fixed.H0, fixed.H1, random.H0, random.H1)</code> . For instance, if we expect fixed effects to be two times as likely as random effects and H0 and H1 to be equally likely: <code>prior = c(2,2,1,1)</code>
sample	number of samples in JAGS after burn-in and thinning (see run.jags). Samples are used to get posterior estimates for each study effect (which will show shrinkage). Only works for priors defined in prior .
summarize	whether and to compute parameter summaries (mean, median, SD, 95% quantile interval, HPD interval). If <code>summarize = "integrate"</code> , numerical integration is used (which is precise but can require some seconds of computing time), <code>summarize = "jags"</code> summarizes the JAGS samples, and <code>summarize = "none"</code> suppresses parameter summaries.
...	arguments passed to run.jags (e.g., MCMC parameters such as <code>sample</code> , <code>burnin</code> , <code>n.chains</code> , <code>thin</code> or <code>method="parallel"</code>)

Details

Bayesian model averaging for four meta-analysis models: Fixed- vs. random-effects and H0 ($d = 0$) vs. H1 (e.g., $d > 0$).

References

Gronau, Q. F., Erp, S. V., Heck, D. W., Cesario, J., Jonas, K. J., & Wagenmakers, E.-J. (2017). A Bayesian model-averaged meta-analysis of the power pose effect with informed and default priors: the case of felt power. *Comprehensive Results in Social Psychology*, 2(1), 123-138. <https://doi.org/10.1080/23743603.2017.1326760>

See Also

[meta_default](#), [meta_fixed](#), [meta_random](#)

Examples

```

data(towels)
mb <- meta_bma(towels$logOR, towels$SE, towels$study,
               d = "norm", d.par = c(0,.3),
               tau = "halfcauchy", tau.par = .5,
               sample = 0, summarize = "none")
               # (no summary: only for CRAN checks)

mb
plot_posterior(mb, "d")

```

meta_default

*Defaults for Model Averaging in Meta-Analysis***Description**

Wrapper with default prior for Bayesian meta-analysis based on a literature review. Currently, the same default is used in all cases.

Usage

```

meta_default(y, SE, labels = NULL, field = "psychology", effect = "ttest",
            ...)

```

Arguments

y	mean in each study
SE	standard error in each study
labels	optional: character values with study labels
field	either "psychology" or "medicine" (uses partial matching, so "p" and "m" are sufficient)
effect	the type of effect size: either means ("ttest"), log-odds ratios ("logOR") or (Fisher's z-transformed) correlations ("corr") (also uses partial matching)
...	further arguments passed to meta_bma

Details

Default prior distributions can be plotted using [plot_default](#).

For field = "psychology", the following defaults are used:

- effect = "ttest": Half-normal with SD=0.3 on mean effect and half-Cauchy with scale=.5 on standard deviation of effects.
- effect = "logOR": Half-normal with SD=0.3 on mean effect and half-Cauchy with scale=.5 on standard deviation of effects.
- effect = "corr": Half-normal with SD=0.3 on mean effect and half-Cauchy with scale=.5 on standard deviation of effects.

For field = "medicine", the following defaults are used:

- effect = "ttest": Half-normal with SD=0.3 on mean effect and half-Cauchy with scale=.5 on standard deviation of effects.
- effect = "logOR": Half-normal with SD=0.3 on mean effect and half-Cauchy with scale=.5 on standard deviation of effects.
- effect = "corr": Half-normal with SD=0.3 on mean effect and half-Cauchy with scale=.5 on standard deviation of effects.

References

Gronau, Q. F., Erp, S. V., Heck, D. W., Cesario, J., Jonas, K. J., & Wagenmakers, E.-J. (2017). A Bayesian model-averaged meta-analysis of the power pose effect with informed and default priors: the case of felt power. *Comprehensive Results in Social Psychology*, 2(1), 123-138. <https://doi.org/10.1080/23743603.2017.1326760>

See Also

[meta_bma](#), [plot_default](#)

Examples

```
## Not run:
data(towels)
d1 <- meta_default(towels$logOR, towels$SE, towels$study,
                  field = "psych", effect = "logOR",
                  sample = 5000)

d1
plot_forest(d1)

## End(Not run)
```

meta_fixed

Bayesian Fixed-Effects Meta-Analysis

Description

Runs a Bayesian meta-analysis assuming that the mean effect d in each study is identical (i.e., a fixed-effects analysis).

Usage

```
meta_fixed(y, SE, labels = NULL, d = "halfnorm", d.par = c(mean = 0, sd =
0.3), sample = 0, summarize = "integrate", ...)
```

Arguments

y	mean in each study
SE	standard error in each study
labels	optional: character values with study labels
d	type of prior for mean effect d (see prior)
d.par	prior parameters for d
sample	number of samples in JAGS after burn-in and thinning (see run.jags). Samples are used to get posterior estimates for each study effect (which will show shrinkage). Only works for priors defined in prior .
summarize	whether and to compute parameter summaries (mean, median, SD, 95% quantile interval, HPD interval). If <code>summarize = "integrate"</code> , numerical integration is used (which is precise but can require some seconds of computing time), <code>summarize = "jags"</code> summarizes the JAGS samples, and <code>summarize = "none"</code> suppresses parameter summaries.
...	arguments passed to run.jags (e.g., MCMC parameters such as <code>sample</code> , <code>burnin</code> , <code>n.chains</code> , <code>thin</code> or <code>method="parallel"</code>)

Examples

```
data(towels)
### Bayesian Fixed-Effects Meta-Analysis (H1:  $d > 0$  Cauchy)
mf <- meta_fixed(towels$logOR, towels$SE, towels$study,
                d = "halfnorm", d.par = c(0, .3))
mf
plot_posterior(mf)
plot_forest(mf)
```

 meta_random

Bayesian Random-Effects Meta-Analysis

Description

Runs a Bayesian meta-analysis assuming that the effect size d varies across studies with standard deviation τ (i.e., a random-effects analysis).

Usage

```
meta_random(y, SE, labels, d = "norm", d.par = c(0, 0.3),
            tau = "halfcauchy", tau.par = 0.5, sample = 10000,
            summarize = "integrate", ...)
```

Arguments

y	mean in each study
SE	standard error in each study
labels	optional: character values with study labels
d	type of prior for mean effect d (see prior)
d.par	prior parameters for d
tau	type of prior for standard deviation of study effects τ in random-effects meta-analysis (i.e., the SD of d across studies; see prior)
tau.par	prior parameters for τ
sample	number of samples in JAGS after burn-in and thinning (see run.jags). Samples are used to get posterior estimates for each study effect (which will show shrinkage). Only works for priors defined in prior .
summarize	whether and to compute parameter summaries (mean, median, SD, 95% quantile interval, HPD interval). If <code>summarize = "integrate"</code> , numerical integration is used (which is precise but can require some seconds of computing time), <code>summarize = "jags"</code> summarizes the JAGS samples, and <code>summarize = "none"</code> suppresses parameter summaries.
...	arguments passed to run.jags (e.g., MCMC parameters such as <code>sample</code> , <code>burnin</code> , <code>n.chains</code> , <code>thin</code> or <code>method="parallel"</code>)

Examples

```
data(towels)
### Bayesian Random-Effects Meta-Analysis
mr <- meta_random(towels$logOR, towels$SE, towels$study,
                 d = "norm", d.par = c(0,.3),
                 tau = "halfcauchy", tau.par = .5,
                 sample = 0, summarize = "none")
# (no summary: only for CRAN checks)

mr
plot_posterior(mr)
```

plot.meta_pred

Plot Predicted Bayes Factors

Description

Plot Predicted Bayes Factors

Usage

```
## S3 method for class 'meta_pred'
plot(x, which = "d_10_averaged", scale = "BF", ...)
```

Arguments

x	an object of the class "prediction" which contains observed and predicted Bayes factors
which	a character value defining which Bayes factor to plot (one of "d_10_fixed", "d_10_random", "d_10_averaged", "tau_10_random", "H1_fixed_vs_random")
scale	either plots Bayes factors ("BF"), inverse Bayes factors ("1/BF"), log Bayes factors ("log"), or the log-inverse Bayes factor ("1/log")
...	arguments passed to plot

plot_default

Plot Default Priors

Description

Plots default priors for the mean effect d and the standard deviation of effects τ .

Usage

```
plot_default(field, effect, ...)
```

Arguments

field	either "psychology" or "medicine" (uses partial matching, so "p" and "m" are sufficient)
effect	the type of effect size: either means ("ttest"), log-odds ratios ("logOR") or (Fisher's z-transformed) correlations ("corr") (also uses partial matching)
...	further arguments passed to plot (e.g., from, to)

See Also

[meta_default](#) for details on standard priors.

Examples

```
plot_default("psychology", "ttest", 0, 2)
plot_default("medicine", "logOR", 0, 2)
```

plot_forest	<i>Forest Plot for Meta-Analysis</i>
-------------	--------------------------------------

Description

Plots estimated effect sizes for all studies.

Usage

```
plot_forest(meta, from = 0, to = 1, shrinked = "Random Effects",
            summary = c("Mean", "HPD"), mar = c(4.5, 12, 4, 0.3), ...)
```

Arguments

meta	fitted meta-analysis model
from	lower limit of the x-axis
to	upper limit of the x-axis
shrinked	which meta-analysis model should be used to show (shrinked) estimates of the study effect sizes. The name must match the corresponding name in the list meta. Can be suppressed by shrinked = ""
summary	character vector with two values: first, either "Mean" or "Median"; and second, either highest-probability-density interval ("HPD") or the quantile interval ("quantile"); function resets margin to default after plotting)
mar	margin of the plot in the order c(bottom, left, top, right) (see par)
...	arguments passed to plot (e.g., from, to)

See Also

[meta_default](#), [meta_bma](#), [meta_fixed](#), [meta_random](#)

Examples

```
data(towels)
mf <- meta_fixed(towels$logOR, towels$SE, towels$study)
plot_forest(mf, mar = c(4.5,20,4,.2), xlab="Log Odds Ratio")
```

plot_posterior	<i>Plot Posterior Distribution</i>
----------------	------------------------------------

Description

Plot Posterior Distribution

Usage

```
plot_posterior(meta, parameter = "d", from = 0, to = 1,
  summary = c("Mean", "HPD"), ...)
```

Arguments

meta	fitted meta-analysis model
parameter	only for random-effects model: whether to plot "d" or "tau"
from	lower limit of the x-axis
to	upper limit of the x-axis
summary	character vector with two values: first, either "Mean" or "Median"; and second, either highest-probability-density interval ("HPD") or the quantile interval ("quantile"; function resets margin to default after plotting)
...	arguments passed to plot

See Also

[meta_default](#), [meta_bma](#), [meta_fixed](#), [meta_random](#)

power_pose	<i>Data Set: Power Pose Effect</i>
------------	------------------------------------

Description

Includes six pre-registered replication studies testing whether participants feel more powerful if they adopt expansive as opposed to constrictive body postures. In the data set `power_pose_unfamiliar`, only those participants are included who were unfamiliar with the power pose effect.

Usage

`power_pose`

`power_pose_unfamiliar`

Format

A data frame with three variables:

study Authors of original study

n_high_power number of participants in high-power condition

n_low_power number of participants in low-power condition

mean_high_power mean rating in high-power condition on a 5-point Likert scale

mean_low_power mean rating in low-power condition on a 5-point Likert scale

sd_high_power standard deviation of ratings in high-power condition

sd_low_power standard deviation of ratings in low-power condition

t_value t-value for two-sample t-test

df degrees of freedom for two-sample t-test

two_sided_p_value two-sided p-value of two-sample t-test

one_sided_p_value one-sided p-value of two-sample t-test

effectSize Cohen's d, the standardized effect size (high vs. low power)

SE Standard error of Cohen's d

Details

See Carney, Cuddy, and Yap (2010) for more details.

References

Carney, D. R., Cuddy, A. J. C., & Yap, A. J. (2010). Power posing: Brief nonverbal displays affect neuroendocrine levels and risk tolerance. *Psychological Science*, 21, 1363–1368.

Gronau, Q. F., Erp, S. V., Heck, D. W., Cesario, J., Jonas, K. J., & Wagenmakers, E.-J. (2017). A Bayesian model-averaged meta-analysis of the power pose effect with informed and default priors: the case of felt power. *Comprehensive Results in Social Psychology*, 2(1), 123-138. <https://doi.org/10.1080/23743603.2017.1326760>

Examples

```
data(power_pose)
head(power_pose)

# Simple fixed-effects meta-analysis
mfix <- meta_fixed(power_pose$effectSize, power_pose$SE,
                  power_pose$study)

mfix
plot_posterior(mfix)
```

predictive	<i>Predicted Bayes Factor for a New Study</i>
------------	---

Description

How much can be learned by an additional study? To judge this, this function samples the distribution of predicted Bayes factors for a new study given the current evidence.

Usage

```
predictive(meta, SE, resample = 100)
```

Arguments

meta	model-averaged meta-analysis (fitted with <code>meta_bma</code> or <code>meta_default</code>)
SE	expected standard error of future study. For instance, $SE = 1/\sqrt{N}$ for standardized effect sizes and $N = \text{sample size}$
resample	number of simulated Bayes factors

prior	<i>Prior Distributions</i>
-------	----------------------------

Description

Returns prior density function, e.g., for mean effect size d and heterogeneity of effect sizes τ

Usage

```
prior(family, param, label = "d", lower = -Inf, upper = Inf)
```

Arguments

family	a character value defining the distribution family
param	numeric parameters for the distribution
label	parameter label
lower	only for family = "custom": lower bound for prior density
upper	only for family = "custom": upper bound for prior density

Details

- "norm": Normal distribution with param = c(mean, sd) (see [dnorm](#))
- "halfnorm": Half-normal distribution (positive) with param = c(mean, sd) (see [dhalfnorm](#))
- "truncnorm": Truncated normal distribution with param = c(min, max, mean, sd) (see [dtruncnorm](#))
- "scaledt": Scaled Student-t with param = c(mean, sigma, nu) (see [dst](#))
- "halfst": Half-normal Student-t with param = c(scale, df) (see [dhalfst](#))
- "cauchy": Cauchy distribution with param = scale (see [dcauchy](#))
- "halfcauchy": Half-Cauchy distribution (positive) with param = scale (see [dhalfcauchy](#))
- "triangular": Triangular distribution with param = c(min, peak, max) (see [dtriangular](#))
- "beta": Beta distribution with param = c(alpha, beta) (see [dbeta](#))
- "custom": User-specified prior density function defined by param (see examples; the density must be nonnegative and vectorized, but is normalized internally). Integration is performed from (-Inf, Inf), which requires that the function returns zeros (and not NAs) for values not in the support of the distribution.

Value

an object of the class prior: a density function with the arguments x (parameter values) and log (whether to return density or log-density)

Examples

```
### Half-Normal Distribution
p1 <- prior("halfnorm", c(mean=0, sd=.3), "d")
p1
p1(c(-1,1,3))
plot(p1, -.1, 1)

### Half-Cauchy Distribution
p2 <- prior("halfcauchy", c(scale=.3))
plot(p2, -.5, 3)

### Custom Prior Distribution
p3 <- prior("custom", function(x) x^2, "d", 0, 1)
plot(p3, -.1, 1.2)
```

towels

Data Set: Reuse of Towels in Hotels

Description

Set of studies that investigated whether people reuse towels in hotels more often if they are provided with a descriptive norm (Scheibehenne, Jamil, & Wagenmakers, 2016).

Usage

```
towels
```

Format

A data frame with three variables:

study Authors of original study (see Scheibehenne et. al, 2016)

logOR Measure of effect size: log-odds ratio of towel reuse (descriptive-social-norm vs. control)

SE Measure of precision: standard error of log-odds ratio per study

Details

Two groups of hotel guests received different messages that encouraged them to reuse their towels. One message simply informed the guests about the benefits of environmental protection (the control condition), and the other message indicated that the majority of guests actually reused their towels in the past (the descriptive-social-norm condition). The results suggested that the latter message facilitated towel reuse.

References

Scheibehenne, B., Jamil, T., & Wagenmakers, E.-J. (2016). Bayesian Evidence Synthesis Can Reconcile Seemingly Inconsistent Results: The Case of Hotel Towel Reuse. *Psychological Science*, 27(7), 1043–1046. <https://doi.org/10.1177/0956797616644081>

Examples

```
data(towels)
head(towels)
```

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