# Package ‘metaBMA’

January 8, 2021

**Type** Package

**Date** 2021-01-07

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

**Version** 0.6.6

**Description** Computes the posterior model probabilities for standard 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 non-informative or informative priors for the mean effect size and the heterogeneity coefficient. Moreover, using pre-compiled Stan models, meta-analysis with continuous and discrete moderators with Jeffreys-Zellner-Siow (JZS) priors can be fitted and tested. This allows to compute Bayes factors and perform Bayesian model averaging across random- and fixed-effects meta-analysis with and without moderators. For a primer on Bayesian model-averaged meta-analysis, see Gronau, Heck, Berkhout, Haaf, & Wagenmakers (2020, <doi:10.31234/osf.io/97qup>).

**Depends** R (>= 3.4.0), Rcpp (>= 1.0.0), methods

**Imports** bridgesampling, coda, LaplacesDemon, logspline, mvtnorm, RcppParallel (>= 5.0.1), rstan (>= 2.18.1), rstantools (>= 2.1.1)

**Suggests** testthat, knitr, rmarkdown

**LinkingTo** BH (>= 1.66.0), Rcpp (>= 1.0.0), RcppEigen (>= 0.3.3.3.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

**VignetteBuilder** knitr

**URL** https://github.com/danheck/metaBMA

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**NeedsCompilation** yes

**SystemRequirements** GNU make

**RoxygenNote** 7.1.1

**Biarch** true

**Author** Daniel W. Heck [aut, cre] (<https://orcid.org/0000-0002-6302-9252>),
Quentin F. Gronau [ctb],
Eric-Jan Wagenmakers [ctb]

**Maintainer** Daniel W. Heck <dheck@uni-marburg.de>

**Repository** CRAN

**Date/Publication** 2021-01-08 11:20:02 UTC

# R topics documented:



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`metaBMA-package` *metaBMA: Bayesian Model Averaging for Random and Fixed Effects Meta-Analysis*

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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 $\tau$. Both models can be compared in a Bayesian framework by assuming specific prior distribution for $d$ and $\tau$ (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). For a primer on Bayesian model-averaged meta-analysis, see Gronau, Heck, Berkhout, Haaf, and Wagenmakers (2020).

## Details

The most general functions in `metaBMA` is `meta_bma`, which fits 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 how to use the package, see the vignette: `vignette("metaBMA")`.

## Funding

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), Laura and John Arnold Foundation, and by the German Research Foundation (grant GRK-2277: Statistical Modeling in Psychology).

## Author(s)

Heck, D. W. & Gronau, Q. F.

## 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. doi: 10.1080/23743603.2017.1326760

Gronau, Q. F., Heck, D. W., Berkhout, S. W., Haaf, J. M., & Wagenmakers, E.-J. (2020). A primer on Bayesian model-averaged meta-analysis. doi: 10.31234/osf.io/97qup

Heck, D. W., Gronau, Q. F., & Wagenmakers, E.-J. (2019). metaBMA: Bayesian model averaging for random and fixed effects meta-analysis. https://CRAN.R-project.org/package=metaBMA

## See Also

Useful links:

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

bma *Bayesian Model Averaging*

## Description

Model averaging for different meta-analysis models (e.g., random-effects or fixed-effects with different priors) based on the posterior model probability.

## Usage

```
bma(
  meta,
  prior = 1,
  parameter = "d",
  summarize = "integrate",
  ci = 0.95,
  rel.tol = .Machine$double.eps^0.5
)
```

## Arguments

| | |
|---|---|
| `meta` | list of meta-analysis models (fitted via `meta_random` or `meta_fixed`) |
| `prior` | prior probabilities over models (possibly unnormalized). For instance, if the first model is as likely as models 2, 3 and 4 together: `prior = c(3,1,1,1)`. The default is a discrete uniform distribution over models. |
| `parameter` | either the mean effect `"d"` or the heterogeneity `"tau"` (i.e., the across-study standard deviation of population effect sizes). |
| `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). |

## Examples

```
# model averaging for fixed and random effects
data(towels)
fixed <- meta_fixed(logOR, SE, study, towels)
random <- meta_random(logOR, SE, study, towels)

averaged <- bma(list("fixed" = fixed, "random" = random))
averaged
plot_posterior(averaged)
plot_forest(averaged, mar = c(4.5,20,4,.3))
```

`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. doi: 10.1037/00223514.54.5.768

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. doi: 10.1177/1745691616674458

### Examples

```
data(facial_feedback)
head(facial_feedback)
mf <- meta_fixed(d, SE, study, facial_feedback)
mf
plot_posterior(mf)
```

inclusion *Inclusion Bayes Factor*

## Description

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

## Usage

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

## Arguments

| | |
|---|---|
| `logml` | 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 inclusion Bayes factor is identical to the usual Bayes factor BF_{M1,M2}. One can include models depending on the names of the models (such as `"random_H1"`) by providing a character value, for instance: `include="H1"` (all H1 vs. all H0 models) or `include="random"` (all random- vs. all fixed-effects models). |
| `prior` | prior probabilities over models (possibly unnormalized). For instance, if the first model is as likely as models 2, 3 and 4 together: `prior = c(3,1,1,1)`. The default is a discrete uniform distribution over models. |

## Examples

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

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

# BF: Correct (Model 1) vs. misspecified (2 & 3)
inclusion(c(logm1, logm2, logm3), include = 1)
```

meta_bma *Model Averaging for Meta-Analysis*

## Description

Fits random- and fixed-effects meta-anayses and performs Bayesian model averaging for H1 (d != 0) vs. H0 (d = 0).

## Usage

```
meta_bma(
  y,
  SE,
  labels,
  data,
  d = prior("cauchy", c(location = 0, scale = 0.707)),
  tau = prior("invgamma", c(shape = 1, scale = 0.15)),
  rscale_contin = 0.5,
  rscale_discrete = 0.707,
  centering = TRUE,
  prior = c(1, 1, 1, 1),
  logml = "integrate",
  summarize = "stan",
  ci = 0.95,
  rel.tol = .Machine$double.eps^0.3,
  logml_iter = 5000,
  silent_stan = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| `y` | effect size per study. Can be provided as (1) a numeric vector, (2) the quoted or unquoted name of the variable in `data`, or (3) a `formula` to include discrete or continuous moderator variables. |
| `SE` | standard error of effect size for each study. Can be a numeric vector or the quoted or unquoted name of the variable in `data` |
| `labels` | optional: character values with study labels. Can be a character vector or the quoted or unquoted name of the variable in `data` |
| `data` | data frame containing the variables for effect size `y`, standard error `SE`, `labels`, and moderators per study. |
| `d` | `prior` distribution on the average effect size `d`. The prior probability density function is defined via `prior`. |
| `tau` | `prior` distribution on the between-study heterogeneity `tau` (i.e., the standard deviation of the study effect sizes `dstudy` in a random-effects meta-analysis. A (nonnegative) prior probability density function is defined via `prior`. |

`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.

`prior` prior probabilities over models (possibly unnormalized) in the order `c(fixed_H0,fixed_H1,random_H0,` For instance, if we expect fixed effects to be two times as likely as random effects and H0 and H1 to be equally likely: `prior = c(2,2,1,1)`.

`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.

`...` further arguments passed to `rstan::sampling` (see `stanmodel-method-sampling`). Relevant MCMC settings concern the number of warmup samples that are discarded (`warmup=500`), the total number of iterations per chain (`iter=2000`), the number of MCMC chains (`chains=4`), whether multiple cores should be used (`cores=4`), and control arguments that make the sampling in Stan more robust, for instance: `control=list(adapt_delta=.97)`.

## Details

Bayesian model averaging for four meta-analysis models: Fixed- vs. random-effects and H0 ($d = 0$) vs. H1 (e.g., $d > 0$). For a primer on Bayesian model-averaged meta-analysis, see Gronau, Heck, Berkhout, Haaf, and Wagenmakers (2020).

By default, the log-marginal likelihood is computed by numerical integration (`logml="integrate"`). This is relatively fast and gives precise, reproducible results. However, for extreme priors or data (e.g., very small standard errors), numerical integration is not robust and might provide incorrect results. As an alternative, the log-marginal likelihood can be estimated using MCMC/Stan samples and bridge sampling (`logml="stan"`).

To obtain posterior summary statistics for the average effect size `d` and the heterogeneity parameter `tau`, one can also choose between numerical integration (`summarize="integrate"`) or MCMC sampling in Stan (`summarize="stan"`). If any moderators are included in a model, both the marginal likelihood and posterior summary statistics can only be computed using Stan.

### 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. doi: 10.1080/23743603.2017.1326760

Gronau, Q. F., Heck, D. W., Berkhout, S. W., Haaf, J. M., & Wagenmakers, E.-J. (2020). A primer on Bayesian model-averaged meta-analysis. doi: 10.31234/osf.io/97qup

### See Also

meta_fixed, meta_random

### Examples

```
### Bayesian Model-Averaged Meta-Analysis (H1: d>0)
data(towels)
set.seed(123)
mb <- meta_bma(logOR, SE, study, towels,
               d = prior("norm", c(mean=0, sd=.3), lower=0),
               tau = prior("invgamma", c(shape = 1, scale = 0.15)))
mb
plot_posterior(mb, "d")
```

---

## meta_default — *Defaults for Model Averaging in Meta-Analysis*

---

### Description

Wrapper with default prior for Bayesian meta-analysis. Since version 0.6.6, the default priors for Cohen's d have been changed from a normal distribution with scale=0.3 to a Cauchy distribution with scale=0.707. Moreover, scale adjustments were implemented when using Fisher's z or log odds-ratios.

### Usage

```
meta_default(y, SE, labels, data, field = "psychology", effect = "d", ...)
```

### Arguments

| | |
|---|---|
| `y` | effect size per study. Can be provided as (1) a numeric vector, (2) the quoted or unquoted name of the variable in `data`, or (3) a `formula` to include discrete or continuous moderator variables. |
| `SE` | standard error of effect size for each study. Can be a numeric vector or the quoted or unquoted name of the variable in `data` |

| | |
|---|---|
| `labels` | optional: character values with study labels. Can be a character vector or the quoted or unquoted name of the variable in `data` |
| `data` | data frame containing the variables for effect size `y`, standard error `SE`, `labels`, and moderators per study. |
| `field` | either`"psychology"` or `"medicine"` |
| `effect` | the type of effect size used in the meta-analysis: either Cohen's d (`"d"`), Fisher's z-transformed correlation (`"z"`), or log-odds ratios (`"logOR"`). |
| `...` | further arguments passed to `meta_bma` |

## Details

The prior distribution depends on the scale of the effect size that is used in the meta-analysis (Cohen's d, Fisher's z, or log odds ratio). To ensure that the results are comparable when transforming between different effect sizes, it is necessary to adjust the scale of the prior distributions.

- The distribution of Fisher's z is approximately half as wide as the distribution of Cohen's d and hence the prior scale parameter is divided by two.
- The distribution of the log odds ratio is approximately twice as wide as the distribution of Cohen's d and hence the prior scale parameter is doubled.

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

- `effect = "d"`: Cauchy distribution with scale=0.707 on the overall effect size (parameter d) and inverse gamma distribution with shape=1 and scale=.15 on the standard deviation of effect sizes across studies (parameter tau).
- `effect = "z"`: Cauchy distribution with scale=0.3535 on d and inverse gamma with shape=1 and scale=.075 on tau.
- `effect = "logOR"`: Cauchy distribution with scale=1.414 on d and inverse gamma with shape=1 and scale=0.3 on tau.

Currently, the same priors are used when specifying `field = "medicine"`.

Default prior distributions can be plotted using `plot_default`.

## 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. doi: 10.1080/23743603.2017.1326760

## See Also

`meta_bma`, `plot_default`

## Examples

```
data(towels)
set.seed(123)
md <- meta_default(logOR, SE, study, towels,
                   field = "psychology", effect = "logOR")
md
plot_forest(md)
```

---

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,
  data,
  d = prior("cauchy", c(location = 0, scale = 0.707)),
  rscale_contin = 1/2,
  rscale_discrete = 0.707,
  centering = TRUE,
  logml = "integrate",
  summarize = "integrate",
  ci = 0.95,
  rel.tol = .Machine$double.eps^0.3,
  silent_stan = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| `y` | effect size per study. Can be provided as (1) a numeric vector, (2) the quoted or unquoted name of the variable in `data`, or (3) a `formula` to include discrete or continuous moderator variables. |
| `SE` | standard error of effect size for each study. Can be a numeric vector or the quoted or unquoted name of the variable in `data` |
| `labels` | optional: character values with study labels. Can be a character vector or the quoted or unquoted name of the variable in `data` |

| | |
|---|---|
| data | data frame containing the variables for effect size y, standard error SE, labels, and moderators per study. |
| d | prior distribution on the average effect size d. The prior probability density function is defined via prior. |
| 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). |
| silent_stan | whether to suppress the Stan progress bar. |
| ... | further arguments passed to rstan::sampling (see stanmodel-method-sampling). Relevant MCMC settings concern the number of warmup samples that are discarded (warmup=500), the total number of iterations per chain (iter=2000), the number of MCMC chains (chains=4), whether multiple cores should be used (cores=4), and control arguments that make the sampling in Stan more robust, for instance: control=list(adapt_delta=.97). |

## Examples

```
### Bayesian Fixed-Effects Meta-Analysis (H1: d>0)
data(towels)
mf <- meta_fixed(logOR, SE, study, data = towels,
                 d = prior("norm", c(mean=0, sd=.3), lower=0))
mf
plot_posterior(mf)
plot_forest(mf)
```

---

meta_ordered *Meta-Analysis with Order-Constrained Study Effects*

---

## Description

Computes the Bayes factor for the hypothesis that the true study effects in a random-effects meta-anaysis are all positive or negative.

### Usage

```
meta_ordered(
  y,
  SE,
  labels,
  data,
  d = prior("norm", c(mean = 0, sd = 0.3), lower = 0),
  tau = prior("invgamma", c(shape = 1, scale = 0.15)),
  prior = c(1, 1, 1, 1),
  logml = "integrate",
  summarize = "stan",
  ci = 0.95,
  rel.tol = .Machine$double.eps^0.3,
  logml_iter = 5000,
  iter = 5000,
  silent_stan = TRUE,
  ...
)
```

### Arguments

| | |
|---|---|
| `y` | effect size per study. Can be provided as (1) a numeric vector, (2) the quoted or unquoted name of the variable in `data`, or (3) a `formula` to include discrete or continuous moderator variables. |
| `SE` | standard error of effect size for each study. Can be a numeric vector or the quoted or unquoted name of the variable in `data` |
| `labels` | optional: character values with study labels. Can be a character vector or the quoted or unquoted name of the variable in `data` |
| `data` | data frame containing the variables for effect size `y`, standard error `SE`, `labels`, and moderators per study. |
| `d` | `prior` distribution on the average effect size `d`. The prior probability density function is defined via `prior`. |
| `tau` | `prior` distribution on the between-study heterogeneity `tau` (i.e., the standard deviation of the study effect sizes `dstudy` in a random-effects meta-analysis. A (nonnegative) prior probability density function is defined via `prior`. |
| `prior` | prior probabilities over models (possibly unnormalized) in the order `c(fixed_H0,fixed_H1,ordered_H1` Note that the model `random_H0` is not included in the comparison. |
| `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. |
| `iter` | number of MCMC iterations for the random-effects meta-analysis. Needs to be larger than usual to estimate the probability of all random effects being ordered (i.e., positive or negative). |
| `silent_stan` | whether to suppress the Stan progress bar. |
| `...` | further arguments passed to `rstan::sampling` (see `stanmodel-method-sampling`). Relevant MCMC settings concern the number of warmup samples that are discarded (`warmup=500`), the total number of iterations per chain (`iter=2000`), the number of MCMC chains (`chains=4`), whether multiple cores should be used (`cores=4`), and control arguments that make the sampling in Stan more robust, for instance: `control=list(adapt_delta=.97)`. |

## Details

Usually, in random-effects meta-analysis,the study-specific random-effects are allowed to be both negative or positive even when the prior on the overall effect size `d` is truncated to be positive). In contrast, the function `meta_ordered` fits and tests a model in which the random effects are forced to be either all positive or all negative. The direction of the study-specific random-effects is defined via the prior on the mode of the truncated normal distribution `d`. For instance, `d=prior("norm",c(0,.5),lower=0)` means that all random-effects are positive (not just the overall mean effect size).

The posterior summary statistics of the overall effect size in the model `ordered` refer to the the *average/mean* of the study-specific effect sizes (as implied by the fitted truncated normal distribution) and *not* to the location parameter `d` of the truncated normal distribution (which is only the mode, not the expected value of a truncated normal distribution).

The Bayes factor for the order-constrained model is computed using the encompassing Bayes factor. Since many posterior samples are required for this approach, the default number of MCMC iterations for `meta_ordered` is `iter=5000` per chain.

## References

Haaf, J. M., & Rouder, J. N. (2018). Some do and some don't? Accounting for variability of individual difference structures. Psychonomic Bulletin & Review, 26, 772–789. doi: 10.3758/s134230181522x

## See Also

meta_bma, meta_random

## Examples

```
### Bayesian Meta-Analysis with Order Constraints (H1: d>0)
data(towels)
set.seed(123)
mo <- meta_ordered(logOR, SE, study, towels,
                   d = prior("norm", c(mean=0, sd=.3), lower=0))
mo
plot_posterior(mo)
```

---

meta_random *Bayesian Random-Effects Meta-Analysis*

---

## Description

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

## Usage

```
meta_random(
  y,
  SE,
  labels,
  data,
  d = prior("cauchy", c(location = 0, scale = 0.707)),
  tau = prior("invgamma", c(shape = 1, scale = 0.15)),
  rscale_contin = 0.5,
  rscale_discrete = 0.707,
  centering = TRUE,
  logml = "integrate",
  summarize = "stan",
  ci = 0.95,
  rel.tol = .Machine$double.eps^0.3,
  logml_iter = 5000,
  silent_stan = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| y | effect size per study. Can be provided as (1) a numeric vector, (2) the quoted or unquoted name of the variable in `data`, or (3) a `formula` to include discrete or continuous moderator variables. |
| SE | standard error of effect size for each study. Can be a numeric vector or the quoted or unquoted name of the variable in `data` |

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

data
: data frame containing the variables for effect size y, standard error SE, labels, and moderators per study.

d
: prior distribution on the average effect size d. The prior probability density function is defined via prior.

tau
: prior distribution on the between-study heterogeneity tau (i.e., the standard deviation of the study effect sizes dstudy in a random-effects meta-analysis. A (nonnegative) prior probability density function is defined via prior.

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.

...
: further arguments passed to rstan::sampling (see stanmodel-method-sampling). Relevant MCMC settings concern the number of warmup samples that are discarded (warmup=500), the total number of iterations per chain (iter=2000), the number of MCMC chains (chains=4), whether multiple cores should be used (cores=4), and control arguments that make the sampling in Stan more robust, for instance: control=list(adapt_delta=.97).

## Examples

```
### Bayesian Random-Effects Meta-Analysis (H1: d>0)
data(towels)
set.seed(123)
mr <- meta_random(logOR, SE, study, data = towels,
                  d = prior("norm", c(mean=0, sd=.3), lower = 0),
```

```
                  tau = prior("invgamma", c(shape = 1, scale = 0.15)))
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 objct 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", "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.prior *Plot Prior Distribution*

---

## Description

Plot the probability density function of a prior distribution.

## Usage

```
## S3 method for class 'prior'
plot(x, from, to, ...)
```

## Arguments

| | |
|---|---|
| x | prior probability density function defined via prior. |
| from | lower boundary |
| to | upper boundary |
| ... | further arguments passed to plot |

### Examples

```
p1 <- prior("t", c(location=0, scale=0.707, nu=1), 0, 3)
plot(p1, 0, 2)

# define custom prior pdf up to a constant:
p2 <- prior("custom", function(x) x^.5, 0, .5)
plot(p2)
```

---

## plot_default *Plot Default Priors*

---

### Description

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

### Usage

```
plot_default(field = "psychology", effect = "d", ...)
```

### Arguments

| | |
|---|---|
| `field` | either"psychology" or "medicine" |
| `effect` | the type of effect size used in the meta-analysis: either Cohen's d ("d"), Fisher's z-transformed correlation ("z"), or log-odds ratios ("logOR"). |
| `...` | further arguments passed to `plot` (e.g., `from`, `to`) |

### See Also

`meta_default` for details on standard priors.

### Examples

```
plot_default(field = "psychology", effect = "d")
```

---

## plot_forest *Forest Plot for Meta-Analysis*

---

### Description

Plots estimated effect sizes for all studies.

## Usage

```
plot_forest(
  meta,
  from,
  to,
  shrinked = "random",
  summary = c("mean", "hpd"),
  mar = c(4.5, 12, 4, 0.3),
  cex.axis = 1,
  ...
)
```

## 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 `"50%"`; and second, either highest-probability-density interval `"hpd"` or the Bayesian credibility interval `"bci"`. |
| `mar` | margin of the plot in the order `c(bottom,left,top,right)` (see `par`) |
| `cex.axis` | size of the y-axis annotation for the labels of studies. |
| `...` | arguments passed to `plot` (e.g., `from`, `to`) |

## See Also

meta_bma, meta_fixed, meta_random

## Examples

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

---

# `plot_posterior` *Plot Posterior Distribution*

---

## Description

Plot Posterior Distribution

### Usage

```
plot_posterior(
  meta,
  parameter = "d",
  from,
  to,
  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 `"50%"`; and second, either highest-probability-density interval `"hpd"` or the Bayesian credibility interval `"bci"`. |
| `...` | arguments passed to `plot` |

### See Also

meta_bma, meta_fixed, meta_random

---

`power_pose` *Data Set: Power Pose Effect*

---

### 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

Data frame with 6 rows and 13 variables

An object of class `data.frame` with 6 rows and 13 columns.

## 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. doi: 10.1080/23743603.2017.1326760

## Examples

```
data(power_pose)
head(power_pose)

# Simple fixed-effects meta-analysis
mfix <- meta_fixed(effectSize, SE, study,
                   data = power_pose)
mfix
plot_posterior(mfix)
```

`predicted_bf` *Predicted Bayes Factors for a New Study*

## 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

```
predicted_bf(meta, SE, sample = 100, ...)
```

## Arguments

| | |
|---|---|
| `meta` | model-averaged meta-analysis (fitted with `meta_bma`). |
| `SE` | a scalar: the expected standard error of future study. For instance, SE = 1/sqrt(N) for standardized effect sizes and N = sample size) |
| `sample` | number of simulated Bayes factors |
| `...` | further arguments passed to rstan::sampling to draw posterior samples for d and tau. |

`prior` *Prior Distribution*

## Description

Defines a prior distribution/probability density function for the average effect size $d$ or for the heterogeneity of effect sizes $\tau$.

## Usage

```
prior(
  family,
  param,
  lower,
  upper,
  label = "d",
  rel.tol = .Machine$double.eps^0.5
)
```

## Arguments

| | |
|---|---|
| `family` | a character value defining the distribution family. |
| `param` | numeric parameters for the distribution. See details for the definition of the parameters of each family. |
| `lower` | lower boundary for truncatation of prior density. If `family="beta"`, the interval [0,1] is rescaled to the interval [lower,upper]. Must be specified if `family = "custom"`. |
| `upper` | See `lower`. |
| `label` | optional: parameter label. |
| `rel.tol` | relative tolerance used for integrating the density of `family="custom"`. |

## Details

The following prior distributions are currently implemented:

- `"norm"`: Normal distribution with `param = c(mean,sd)` (see `Normal`).
- `"t"`: Student's t-distribution with `param = c(location,scale,nu)` where `nu` are the degrees of freedom (see `dist.Student.t`).
- `"cauchy"`: Cauchy distribution with `param = c(location,scale)`. The Cauchy distribution is a special case of the t-distribution with degrees of freedom `nu=1`.
- `"invgamma"`: Inverse gamma distribution with `param = c(shape,scale)` (see `dist.Inverse.Gamma`).
- `"beta"`: (Scaled) beta distribution with `param = c(shape1,shape2)` (see `Beta`).
- `"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("norm", c(mean=0, sd=.3), lower = 0)
p1
p1(c(-1,1,3))
plot(p1, -.1, 1)

### Half-Cauchy Distribution
p2 <- prior("cauchy", c(location = 0, scale = .3), lower = 0)
plot(p2, -.5, 3)

### Custom Prior Distribution
p3 <- prior("custom", function(x) x^2, 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, 1043–1046. doi: 10.1177/0956797616644081

## Examples

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

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