Package 'BayesRep'

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Title Bayesian Analysis of Replication Studies

Description Provides tools for the analysis of replication studies using Bayes factors (Pawel and Held, 2022) <doi:10.1111/rssb.12491>.

License GPL-3

Encoding UTF-8

Imports lamW, hypergeo

Suggests roxygen2, tinytest

NeedsCompilation no

RoxygenNote 7.2.3

URL `https://github.com/SamCH93/BayesRep`

BugReports `https://github.com/SamCH93/BayesRep/issues`

Repository CRAN

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Contents

`BayesRep` *BayesRep package*

Description

The BayesRep package provides various tools for Bayesian analysis of replication studies.

`repPosterior` visualizes the posterior distribution of the effect size based on both studies. `BFs` computes the sceptical Bayes factor (Pawel and Held, 2022), `BFr` computes the replication Bayes factor (Verhagen and Wagenmakers, 2014), and `BFe` computes the equality of effect size Bayes factor (Bayarri and Mayorall, 2002).

These functions take effect estimates and their standard errors from original and replication study as inputs. Throughout, original effect estimate and standard error are denoted by `to` and `so` and replication effect estimate and standard error are denoted `tr` and `sr`. It is assumed that each effect estimate is normally distributed around its true underlying effect size with variance equal to its squared standard error

$$\texttt{to} \,|\, \theta_o \sim \mathrm{N}(\theta_o, \texttt{so}^2) \text{ and } \texttt{tr} \,|\, \theta_r \sim \mathrm{N}(\theta_r, \texttt{sr}^2).$$

These assumptions may be inadequate for studies with small sample size (there are special functions for data with continuous outcomes and standardized mean difference effect size, `BFsSMD` and `BFrSMD`, and binary outcomes with log odds ratio effects, `BFslogOR` and `BFrlogOR`, which are based on the exact distribution of the data). If not specified otherwise, it is assumed that the true effect sizes from both studies are the same ($\theta_o = \theta_r$).

References

Bayarri, M. and Mayorall, A. (2002). Bayesian Design of "Successful" Replications. The American Statistician, 56(3): 207-214. doi:10.1198/000313002155

Verhagen, J. and Wagenmakers, E. J. (2014). Bayesian tests to quantify the result of a replication attempt. Journal of Experimental Psychology: General, 145:1457-1475. doi:10.1037/a0036731

Pawel, S. and Held, L. (2022). The sceptical Bayes factor for the assessment of replication success. Journal of the Royal Statistical Society Series B: Statistical Methodology, 84(3): 879-911. doi:10.1111/rssb.12491

`BFe` *Equality of effect size Bayes factor*

Description

Computes the equality of effect size Bayes factor

Usage

```
BFe(to, so, tr, sr, tau, log = FALSE)
```

Arguments

`to`	Original effect estimate
`so`	Standard error of the original effect estimate
`tr`	Replication effect estimate
`sr`	Standard error of the replication effect estimate
`tau`	The heterogeneity standard deviation τ under the hypothesis of unequal effect sizes H_1
`log`	Logical indicating whether the natural logarithm of the Bayes factor should be returned. Defaults to `FALSE`

Details

The equality of effect size Bayes factor is the Bayes factor contrasting the hypothesis of equal original and replication effect sizes $H_0 : \theta_o = \theta_r$ to the hypothesis of unequal effect sizes $H_1 : \theta_o \neq \theta_r$. Under the hypothesis of unequal effect sizes H_1 the study specific effect sizes are assumed to be normally distributed around an overall effect size with heterogeneity standard deviation `tau`.

Value

The equality of effect size Bayes factor BF_{01}. $\mathrm{BF}_{01} > 1$ indicates that the data favour the hypothesis of equal effect sizes H_0 (replication success), whereas $\mathrm{BF}_{01} < 1$ indicates that the data favour the hypothesis of unequal effect sizes H_1 (replication failure).

Author(s)

Samuel Pawel

References

Bayarri, M. and Mayorall, A. (2002). Bayesian Design of "Successful" Replications. The American Statistician, 56(3): 207-214. doi:10.1198/000313002155

Verhagen, J. and Wagenmakers, E. J. (2014). Bayesian tests to quantify the result of a replication attempt. Journal of Experimental Psychology: General, 145:1457-1475. doi:10.1037/a0036731

Examples

```
## strong evidence for unequal effect sizes
BFe(to = 1, tr = 0.5, so = sqrt(1/100), sr = sqrt(1/100), tau = 0.3)

## some evidence for equal effect sizes
BFe(to = 1, tr = 1, so = sqrt(1/200), sr = sqrt(1/200), tau = 0.3)
```

`BFr` *Generalized replication Bayes factor*

Description

Computes the generalized replication Bayes factor

Usage

```
BFr(
  to,
  so,
  tr,
  sr,
  ss = 0,
  truncate = FALSE,
  log = FALSE,
  zo = NULL,
  zr = NULL,
  c = NULL,
  g = 0
)
```

Arguments

`to`	Original effect estimate
`so`	Standard error of the original effect estimate
`tr`	Replication effect estimate
`sr`	Standard error of the replication effect estimate
`ss`	Standard devation of the sceptical prior under H_{S}. Defaults to `0`
`truncate`	Logical indicating whether advocacy prior should be truncated to direction of the original effect estimate (i.e., a one-sided test). Defaults to `FALSE`
`log`	Logical indicating whether the natural logarithm of the Bayes factor should be returned. Defaults to `FALSE`
`zo`	Original z-value `zo` = `to`/`so` (alternative parametrization for `to` and `so`)
`zr`	Replication z-value `zr` = `tr`/`sr` (alternative parametrization for `tr` and `sr`)
`c`	Relative variance `c` = `so^2/sr^2` (alternative parametrization for `so` and `sr`)
`g`	Relative prior variance `g` = `ss^2/so^2`. Defaults to `0` (alternative parametrization for `ss`)

Details

The generalized replication Bayes factor is the Bayes factor contrasting the sceptic's hypothesis that the effect size is about zero

$$H_{\mathrm{S}} : \theta \sim \mathrm{N}(0, \texttt{ss}^2)$$

to the advocate's hypothesis that the effect size is compatible with its posterior distribution based on the original study and a uniform prior

$$H_{\mathrm{A}} : \theta \sim f(\theta \,|\, \text{original study}).$$

The standard replication Bayes factor from Verhagen and Wagenmakers (2014) is obtained by specifying a point-null hypothesis `ss = 0` (the default).

The function can be used with two input parametrizations, either on the absolute effect scale (`to`, `so`, `tr`, `sr`, `ss`) or alternatively on the relative *z*-scale (`zo`, `zr`, `c`, `g`). If an argument on the effect scale is missing, the *z*-scale is automatically used and the other non-missing arguments on the effect scale ignored.

Value

The generalized replication Bayes factor $\mathrm{BF}_{\mathrm{SA}}$. $\mathrm{BF}_{\mathrm{SA}} < 1$ indicates that the data favour the advocate's hypothesis H_{A} (replication success), whereas $\mathrm{BF}_{\mathrm{SA}} > 1$ indicates that the data favour the sceptic's hypothesis H_{S} (replication failure).

Author(s)

Samuel Pawel

References

Verhagen, J. and Wagenmakers, E. J. (2014). Bayesian tests to quantify the result of a replication attempt. Journal of Experimental Psychology: General, 145:1457-1475. doi:10.1037/a0036731

Ly, A., Etz, A., Marsman, M., Wagenmakers, E. J. (2019). Replication Bayes factors from evidence updating. Behavior Research Methods, 51(6):2498-2508. doi:10.3758/s134280181092x

Pawel, S. and Held, L. (2022). The sceptical Bayes factor for the assessment of replication success. Journal of the Royal Statistical Society Series B: Statistical Methodology, 84(3): 879-911. doi:10.1111/rssb.12491

See Also

`BFrSMD`, `BFrlogOR`

Examples

```
to <- 2
tr <- 2.5
so <- 1
sr <- 1
BFr(to = to, so = so, tr = tr, sr = sr)
BFr(zo = to/so, zr = tr/sr, c = so^2/sr^2)
```

`BFrlogOR` *Generalized replication Bayes factor for logOR effect sizes*

Description

Computes the generalized replication Bayes factor for log odds ratio (logOR) effect sizes

Usage

```
BFrlogOR(
  ao,
  bo,
  nTo = ao + bo,
  co,
  do,
  nCo = co + do,
  ar,
  br,
  nTr = ar + br,
  cr,
  dr,
  nCr = cr + dr,
  ss,
  method = c("integration", "hypergeo")
)
```

Arguments

`ao`	Number of cases in original study treatment group
`bo`	Number of non-cases in original study treatment group
`nTo`	Number of participants in original study treatment group (specify alternatively to `b`)
`co`	Number of cases in original study control group
`do`	Number of non-cases in original study control group
`nCo`	Number of participants in original study control group (specify alternatively to `d`)
`ar`	Number of cases in replication study treatment group
`br`	Number of non-cases in replication study treatment group
`nTr`	Number of participants in replication study treatment group (specify alternatively to `b`)
`cr`	Number of cases in replication study control group
`dr`	Number of non-cases in replication study control group
`nCr`	Number of participants in replication study control group (specify alternatively to `d`)

`ss`	Standard deviation of the sceptical prior under H_{S}. Defaults to `0`
`method`	Method to compute posterior density. Either `"integration"` (default) or `"hypergeo"`

Details

This function computes the generalized replication Bayes factor for log odds ratio (logOR) effect sizes using an exact binomial likelihood for the data instead of the normal approximation used in `BFr` (for details, see Section 4 in Pawel and Held, 2022).

Value

The generalized replication Bayes factor $\mathrm{BF}_{\mathrm{SA}}$. $\mathrm{BF}_{\mathrm{SA}} < 1$ indicates that the data favour the advocate's hypothesis H_{A} (replication success), whereas $\mathrm{BF}_{\mathrm{SA}} > 1$ indicates that the data favour the sceptic's hypothesis H_{S} (replication failure).

Author(s)

Samuel Pawel

References

Verhagen, J. and Wagenmakers, E. J. (2014). Bayesian tests to quantify the result of a replication attempt. Journal of Experimental Psychology: General, 145:1457-1475. doi:10.1037/a0036731

Pawel, S. and Held, L. (2022). The sceptical Bayes factor for the assessment of replication success. Journal of the Royal Statistical Society Series B: Statistical Methodology, 84(3): 879-911. doi:10.1111/rssb.12491

Examples

```
data("SSRPexact")
balafoutas2012 <- subset(SSRPexact, study == "Balafoutas and Sutter (2012), Science")
with(balafoutas2012,
     BFrlogOR(ao = ao, bo = bo, co = co, do = do, ar = ar, br = br, cr = cr, dr = dr,
              ss = 0))
```

`BFrSMD` *Generalized replication Bayes factor for SMD effect sizes*

Description

Computes the generalized replication Bayes factor for standardized mean difference (SMD) effect sizes

Usage

```
BFrSMD(
  to,
  no,
  n1o = no,
  n2o = no,
  tr,
  nr,
  n1r = nr,
  n2r = nr,
  ss,
  type = c("two.sample", "one.sample", "paired")
)
```

Arguments

`to`	t-statistic from the original study
`no`	Sample size of the original study (per group)
`n1o`	Sample size in group 1 of the original study (only required for two-sample t-test with unequal group sizes)
`n2o`	Sample size in group 2 of the original study (only specify if unequal group sizes)
`tr`	t-statistic from the replication study
`nr`	Sample size of the replication study (per group)
`n1r`	Sample size in group 1 of the replication study (only required for two-sample t-test with unequal group sizes)
`n2r`	Sample size in group 2 of the replication study (only required for two-sample t-test with unequal group sizes)
`ss`	Standard devation of the sceptical prior under H_S. Defaults to `0`
`type`	Type of t-test associated with t-statistic. Can be `"two.sample"`, `"one.sample"`, `"paired"`. Defaults to `"two.sample"`

Details

This function computes the generalized replication Bayes factor for standardized mean difference (SMD) effect sizes using an exact t-likelihood for the data instead of the normal approximation used in `BFr` (for details, see Section 4 in Pawel and Held, 2022). Data from both studies are summarized by t-statistics and sample sizes. The following types of t-tests are accepted:

- Two-sample t-test where the SMD represents the standardized mean difference between two group means (assuming equal variances in both groups).
- One-sample t-test where the SMD represents the standardized mean difference to the null value.
- Paired t-test where the SMD represents the standardized mean difference score.

Value

The generalized replication Bayes factor $\mathrm{BF}_{\mathrm{SA}}$. $\mathrm{BF}_{\mathrm{SA}} < 1$ indicates that the data favour the advocate's hypothesis H_{A} (replication success), whereas $\mathrm{BF}_{\mathrm{SA}} > 1$ indicates that the data favour the sceptic's hypothesis H_{S} (replication failure).

Author(s)

Samuel Pawel

References

Verhagen, J. and Wagenmakers, E. J. (2014). Bayesian tests to quantify the result of a replication attempt. Journal of Experimental Psychology: General, 145:1457-1475. doi:10.1037/a0036731

Pawel, S. and Held, L. (2022). The sceptical Bayes factor for the assessment of replication success. Journal of the Royal Statistical Society Series B: Statistical Methodology, 84(3): 879-911. doi:10.1111/rssb.12491

See Also

`BFr`, `BFrlogOR`

Examples

```
data("SSRPexact")
morewedge2010 <- subset(SSRPexact, study == "Morewedge et al. (2010), Science")
with(morewedge2010,
     BFrSMD(to = to, n1o = n1o, n2o = n2o, tr = tr, n1r = n1r, n2r = n2r, ss = 0))
```

`BFs` *Sceptical Bayes factor*

Description

Computes the sceptical Bayes factor

Usage

```
BFs(to, so, tr, sr, truncate = FALSE, zo = NULL, zr = NULL, c = NULL)
```

Arguments

`to`	Original effect estimate
`so`	Standard error of the original effect estimate
`tr`	Replication effect estimate
`sr`	Standard error of the replication effect estimate

`truncate`	Logical indicating whether advocacy prior should be truncated to direction of the original effect estimate (i.e., a one-sided test). Defaults to `FALSE`
`zo`	Original z-value `zo = to/so` (alternative parametrization for `to` and `so`)
`zr`	Replication z-value `zr = tr/sr` (alternative parametrization for `tr` and `sr`)
`c`	Relative variance `c = so^2/sr^2` (alternative parametrization for `so` and `sr`)

Details

The sceptical Bayes factor is a summary measure of the following two-step reverse-Bayes procedure for assessing replication success:

1. Use the data from the original study to determine the standard deviation τ_γ of a sceptical normal prior $\theta \sim \mathrm{N}(0, \tau_\gamma^2)$ such that the Bayes factor contrasting the null hypothesis $H_0 : \theta = 0$ to the sceptic's hypothesis $H_\mathrm{S} : \theta \sim \mathrm{N}(0, \tau_\gamma^2)$ equals a specified level $\gamma \in (0, 1]$. This prior represents a sceptic who remains unconvinced about the presence of an effect at level γ.
2. Use the data from the replication study to compare the sceptic's hypothesis $H_\mathrm{S} : \theta \sim \mathrm{N}(0, \tau_\gamma^2)$ to the advocate's hypothesis $H_\mathrm{A} : \theta \sim f(\theta \,|\, \mathrm{original\ study})$. The prior of the effect size under H_A is its posterior based on the original study and a uniform prior, thereby representing the position of an advocate of the original study. Replication success at level γ is achieved if the Bayes factor contrasting H_S to H_A is smaller than γ, which means that the replication data favour the advocate over the sceptic at a higher level than the sceptic's initial objection. The sceptical Bayes factor BF_S is the smallest level γ at which replication success can be established.

The function can be used with two input parametrizations, either on the absolute effect scale (`to`, `so`, `tr`, `sr`) or alternatively on the relative z-scale (`zo`, `zr`, `c`). If an argument on the effect scale is missing, the z-scale is automatically used and the other non-missing arguments on the effect scale ignored.

Value

The sceptical Bayes factor BF_S. $\mathrm{BF}_\mathrm{S} < 1$ indicates replication success, the smaller the value of BF_S the higher the degree of replication success. It is possible that the result of the replication is so inconclusive that replication success cannot be established at any level. In this case, the sceptical Bayes factor does not exist and the function returns `NaN`.

Author(s)

Samuel Pawel

References

Pawel, S. and Held, L. (2022). The sceptical Bayes factor for the assessment of replication success. Journal of the Royal Statistical Society Series B: Statistical Methodology, 84(3): 879-911. doi:10.1111/rssb.12491

See Also

`BFsSMD`, `BFslogOR`

Examples

```
to <- 2
tr <- 2.5
so <- 1
sr <- 1
BFs(to = to, so = so, tr = tr, sr = sr)
BFs(zo = to/so, zr = tr/sr, c = so^2/sr^2)
```

`BFslogOR` *Sceptical Bayes factor for logOR effect sizes*

Description

Computes the sceptical Bayes factor for logOR effect sizes

Usage

```
BFslogOR(
  ao,
  bo,
  nTo = ao + bo,
  co,
  do,
  nCo = co + do,
  ar,
  br,
  nTr = ar + br,
  cr,
  dr,
  nCr = cr + dr,
  method = c("integration", "hypergeo")
)
```

Arguments

`ao`	Number of cases in original study treatment group
`bo`	Number of non-cases in original study treatment group
`nTo`	Number of participants in original study treatment group (specify alternatively to `b`)
`co`	Number of cases in original study control group
`do`	Number of non-cases in original study control group
`nCo`	Number of participants in original study control group (specify alternatively to `d`)
`ar`	Number of cases in replication study treatment group

`br`	Number of non-cases in replication study treatment group
`nTr`	Number of participants in replication study treatment group (specify alternatively to `b`)
`cr`	Number of cases in replication study control group
`dr`	Number of non-cases in replication study control group
`nCr`	Number of participants in replication study control group (specify alternatively to `d`)
`method`	Method to compute posterior density. Either `"integration"` (default) or `"hypergeo"`

Details

This function computes the sceptical Bayes factor for log odds ratio (logOR) effect sizes using an exact binomial likelihood for the data instead of the normal approximation used in `BFs` (for details, see Section 4 in Pawel and Held, 2022).

Value

The sceptical Bayes factor BF_{S}. $\mathrm{BF}_{\mathrm{S}} < 1$ indicates replication success, the smaller the value of BF_{S} the higher the degree of replication success. It is possible that the result of the replication is so inconclusive that replication success cannot be established at any level. In this case, the sceptical Bayes factor does not exist and the function returns `NaN`.

Author(s)

Samuel Pawel

References

Pawel, S. and Held, L. (2022). The sceptical Bayes factor for the assessment of replication success. Journal of the Royal Statistical Society Series B: Statistical Methodology, 84(3): 879-911. doi:10.1111/rssb.12491

See Also

`BFs`, `BFslogOR`

Examples

```
data("SSRPexact")
balafoutas2012 <- subset(SSRPexact, study == "Balafoutas and Sutter (2012), Science")
with(balafoutas2012,
     BFslogOR(ao = ao, bo = bo, co = co, do = do, ar = ar, br = br, cr = cr, dr = dr))
```

`BFsSMD` *Sceptical Bayes factor for SMD effect sizes*

Description

Computes the sceptical Bayes factor for standardized mean difference (SMD) effect sizes

Usage

```
BFsSMD(
  to,
  no,
  n1o = no,
  n2o = no,
  tr,
  nr,
  n1r = nr,
  n2r = nr,
  type = c("two.sample", "one.sample", "paired")
)
```

Arguments

`to`	t-statistic from the original study
`no`	Sample size of the original study (per group)
`n1o`	Sample size in group 1 of the original study (only required for two-sample t-test with unequal group sizes)
`n2o`	Sample size in group 2 of the original study (only specify if unequal group sizes)
`tr`	t-statistic from the replication study
`nr`	Sample size of the replication study (per group)
`n1r`	Sample size in group 1 of the replication study (only required for two-sample t-test with unequal group sizes)
`n2r`	Sample size in group 2 of the replication study (only required for two-sample t-test with unequal group sizes)
`type`	Type of t-test associated with t-statistic. Can be `"two.sample"`, `"one.sample"`, `"paired"`. Defaults to `"two.sample"`.

Details

This function computes the sceptical Bayes factor for standardized mean difference (SMD) effect sizes using an exact t-likelihood for the data instead of the normal approximation used in `BFs` (for details, see Section 4 in Pawel and Held, 2022). Data from both studies are summarized by t-statistics and sample sizes. The following types of t-tests are accepted:

- Two-sample t-test where the SMD represents the standardized mean difference between two group means (assuming equal variances in both groups).

- One-sample t-test where the SMD represents the standardized mean difference to the null value.
- Paired t-test where the SMD represents the standardized mean difference score.

Value

The sceptical Bayes factor BF_{S}. $\mathrm{BF}_{\mathrm{S}} < 1$ indicates replication success, the smaller the value of BF_{S} the higher the degree of replication success. It is possible that the result of the replication is so inconclusive that replication success cannot be established at any level. In this case, the sceptical Bayes factor does not exist and the function returns `NaN`.

Author(s)

Samuel Pawel

References

Pawel, S. and Held, L. (2022). The sceptical Bayes factor for the assessment of replication success. Journal of the Royal Statistical Society Series B: Statistical Methodology, 84(3): 879-911. doi:10.1111/rssb.12491

See Also

`BFs`, `BFslogOR`

Examples

```
data("SSRPexact")
morewedge2010 <- subset(SSRPexact, study == "Morewedge et al. (2010), Science")
with(morewedge2010,
     BFsSMD(to = to, n1o = n1o, n2o = n2o, tr = tr, n1r = n1r, n2r = n2r))
```

`formatBF` *Formatting of Bayes factors*

Description

Formats Bayes factors such that Bayes factors smaller than 1 are represented as ratios $1/x$, where x is rounded to the specified number of digits, while Bayes factors larger than 1 are only rounded to the specified number of digits.

Usage

```
formatBF(BF, digits = "default")
```

Arguments

`BF`	Bayes factor
`digits`	either `"default"` (see Details) or a positive integer specifiying the number of decimal places to round the Bayes factor (for Bayes factors ≥ 1) or its inverse (for Bayes factors < 1)

Details

The default formatting, which is recommended in Held and Ott (2018), is as follows: For very small Bayes factors BF < 1/1000, "< 1/1000" is returned. Bayes factors BF with 1/1000 $\leq$ BF $\leq$ 1/10 are formatted as $1/x$ where x is an integer and Bayes factors BF with $1/10 <$ BF < 1 as $1/x$, where x is rounded to one decimal place. Accordingly, Bayes factors $\leq$ BF $<$ 10 are rounded to one decimal place, Bayes factors $10 \leq$ BF ≤ 1000 are rounded to the next integer and for larger Bayes factors, "> 1000" is returned.

If digits is specified, the Bayes factor (if it is ≥ 1) or its inverse (if the Bayes factor is < 1) is rounded to the number of decimal places specified and returned as a ratio if the Bayes factor is < 1.

Value

A character vector of ratios (for inputs < 1) or rounded numeric values (for inputs ≥ 1)).

Author(s)

Manuela Ott (creator of package `pCalibrate`), Leonhard Held (contributor of package `pCalibrate`), Samuel Pawel (made small changes to `pCalibrate::formatBF`)

References

Held, L. and Ott, M. (2018). On p-values and Bayes factors. Annual Review of Statistics and Its Application, 5, 393-419. doi:10.1146/annurevstatistics031017100307

Examples

```
(bf <- BFr(to = 2, so = 0.5, tr = 2.5, sr = 0.9))
formatBF(BF = bf)
```

`repPosterior` *Effect size posterior distribution*

Description

Computes the posterior distribution of the effect size based on the original and replication effect estimates and their standard errors, assuming a common underlying effect size and an initial flat prior.

Usage

```
repPosterior(
  to,
  so,
  tr,
  sr,
  lower = min(c(to, tr)) - 4/sqrt(1/so^2 + 1/sr^2),
  upper = max(c(to, tr)) + 4/sqrt(1/so^2 + 1/sr^2),
  nGrid = 1000,
  plot = TRUE,
  CI = TRUE,
  ...
)
```

Arguments

`to`	Original effect estimate
`so`	Standard error of the original effect estimate
`tr`	Replication effect estimate
`sr`	Standard error of the replication effect estimate
`lower`	Lower bound of range for which distribution should computed. Defaults to minimum of `to` and `tr` minus four times the pooled standard error
`upper`	Upper bound of range for which distribution should computed. Defaults to maximum of `to` and `tr` plus four times the pooled standard error
`nGrid`	Number of grid points. Defaults to `1000`
`plot`	Logical indicating whether posterior distribution should be plotted. If `FALSE`, only data used for plotting are returned. Defaults to `TRUE`
`CI`	Logical indicating whether 95% highest posterior credible interval should be plotted. Defaults to `TRUE`
`...`	Additional arguments passed to `matplot`

Value

Plots posterior distribution of the effect size, invisibly returns a list with the data for the plot

Author(s)

Samuel Pawel

Examples

```
## Example from Reproducibility Project Cancer Biology
## Aird: Data from https://elifesciences.org/articles/21253 Fig4B
hro <- 25.93
lhro <- log(hro)
hroCI <- c(5.48, 122.58)
```

```
se_lhro <- diff(log(hroCI))/(2*qnorm(0.975))
hrr <- 3.75
lhrr <- log(hrr)
hrrCI <- c(1.19, 11.81)
se_lhrr <- diff(log(hrrCI))/(2*qnorm(0.975))
repPosterior(to = lhro, so = se_lhro, tr = lhrr, sr = se_lhrr)
```

`SSRPexact` *Data from the Social Sciences Replication Project*

Description

Data from the Social Sciences Replication Project. The variables are as follows:

`study`	Authors, year, and journal of the original study
`type`	Type of effect size. Either `"logOR"` for log oddds ratio effect size, `"SMD1"` for standardized mean difference from one-sample or paired t-test, or `"SMD2"` for standardized mean difference from two-sample t-test
`to`	t-statistic from the original study (only available for `"SMD1"` and `"SMD2"`)
`n1o`	Sample size in group 1 of the original study (only available for `"SMD1"` and `"SMD2"`)
`n2o`	Sample size in group 2 of the original study (only available for `"SMD2"`)
`tr`	t-statistic from the replication study (only available for `"SMD1"` and `"SMD2"`)
`n1r`	Sample size in group 1 of the replication study (only available for `"SMD1"` and `"SMD2"`)
`n2r`	Sample size in group 2 of the replication study (only available for `"SMD2"`)
`ao`	Number of cases in original study treatment group (only available for `"logOR"`)
`bo`	Number of non-cases in original study treatment group (only available for `"logOR"`)
`co`	Number of cases in original study control group (only available for `"logOR"`)
`do`	Number of non-cases in original study control group (only available for `"logOR"`)
`ar`	Number of cases in replication study treatment group (only available for `"logOR"`)
`br`	Number of cases in replication study control group (only available for `"logOR"`)
`cr`	Number of cases in replication study control group (only available for `"logOR"`)
`dr`	Number of non-cases in replication study control group (only available for `"logOR"`)

Usage

```
data(SSRPexact)
```

Format

A data frame with 21 rows and 16 variables

Author(s)

Samuel Pawel

Source

The data were manually extracted from the Bayesian supplement of the SSRP (`https://osf.io/nsxgj/`). The data are licensed under CC0 1.0 Universal.

References

Camerer, C. F., Dreber, A., Holzmeister, F., Ho, T.-H., Huber, J., Johannesson, M., ... Wu, H. (2018). Evaluating the replicability of social science experiments in Nature and Science between 2010 and 2015. Nature Human Behaviour, 2, 637-644. doi:10.1038/s415620180399z

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