Package ‘puniform’

May 9, 2026

Type Package

Title Meta-Analysis Methods Correcting for Publication Bias

Version 0.2.8

Date 2025-09-02

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Description Provides meta-analysis methods that correct for publication bias and outcome reporting bias. Four methods and a visual tool are currently included in the package. The p-uniform method as described in van Assen, van Aert, and Wicherts (2015) <doi:10.1037/met0000025> can be used for estimating the average effect size, testing the null hypothesis of no effect, and testing for publication bias using only the statistically significant effect sizes of primary studies. The second method in the package is the p-uniform* method as described in van Aert and van Assen (2023) <doi:10.31222/osf.io/zqjr9>. This method is an extension of the p-uniform method that allows for estimation of the average effect size and the between-study variance in a meta-analysis, and uses both the statistically significant and nonsignificant effect sizes. The third method in the package is the hybrid method as described in van Aert and van Assen (2018) <doi:10.3758/s13428-017-0967-6>. The hybrid method is a meta-analysis method for combining a conventional study and replication/preregistered study while taking into account statistical significance of the conventional study. This method was extended in van Aert (2025) <doi:10.1037/met0000719> such that it allows for the inclusion of multiple conventional and replication/preregistered studies. The p-uniform and hybrid method are based on the statistical theory that the distribution of p-values is uniform conditional on the population effect size. The fourth method in the package is the Snapshot Bayesian Hybrid Meta-Analysis Method as described in van Aert and van Assen (2018) <doi:10.1371/journal.pone.0175302>. This method computes posterior probabilities for four true effect sizes (no, small, medium, and large) based on an original study and replication while taking into account publication bias in the original study. The method can also be used for computing the required sample size of the replication akin to power analysis in null-hypothesis significance testing. The meta-plot is a visual tool for meta-analysis that provides information on the primary studies in the meta-analysis, the results of the meta-analysis, and characteristics of the research on the effect under study (van Assen et al., 2023). Helper functions to apply the Correcting for Outcome Reporting Bias (CORB) method to correct for outcome reporting bias in a meta-analysis (van Aert & Wicherts, 2023).

License GPL (>= 2)

Imports Rcpp (>= 0.12.15), ADGofTest (>= 0.3), stats, metafor, numDeriv

Suggests metadat

LinkingTo Rcpp, RcppArmadillo

RoxygenNote 7.3.2

Encoding UTF-8

URL `https://github.com/RobbievanAert/puniform`

BugReports `https://github.com/RobbievanAert/puniform/issues`

NeedsCompilation yes

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Repository CRAN

Date/Publication 2025-09-02 15:10:02 UTC

Contents

`data.mccall93` *Data from a meta-analysis infants' habituation to a give stimulus and their later cognitive ability (IQ)*

Description

Results from 12 studies on the association between infants' habituation to a give stimulus and their later cognitive ability (IQ).

Format

The data frame contains two columns: ri (raw correlation coefficients) and ni (sample sizes).

Author(s)

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Source

McCall, R. B., & Carriger, M. S. (1993). A meta-analysis of infant habituation and recognition memory performance as predictors of later IQ. Child Development, 64, 57-79. http://dx.doi.org/10.2307/1131437

`diffprior` *diffprior*

Description

Function for computing posterior probabilities based on the Snapshot Bayesian Hybrid Meta-Analysis Method or Snapshot Bayesian Meta-Analysis Method (uncorrected) for another than a uniform prior.

Usage

```
diffprior(prior, res.snap)
```

Arguments

`prior`	A vector of length four containing the prior probabilities for no, small, medium, and large true effect size.
`res.snap`	A data frame with posterior probabilities obtained with the `snapshot` or `uncor.snapshot` function.

Details

The function computes posterior probabilities for four true effect sizes (no, small, medium, and large) based on the `snapshot` or `uncor.snapshot` function for another than a uniform prior. For more information see van Aert and van Assen (2016).

Value

The `diffprior` function returns a data frame with posterior probabilities for no (`p.0`), small (`p.sm`), medium (`p.me`), and large (`p.la`) true effect size.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & van Assen, M.A.L.M. (2017). Bayesian evaluation of effect size after replicating an original study. PLoS ONE, 12(4), e0175302. doi:10.1371/journal.pone.0175302

Examples

```
### Example as presented on page 491 in Maxwell, Lau, and Howard (2015)
res.snap <- snapshot(ri=c(0.243, 0.114), ni=c(80, 172), alpha=.05)

### Prior probabilities with probablity for no effect twice as large as for the other true effects
prior <- c(0.4, 0.2, 0.2, 0.2)

### Compute posterior probabilities based on new prior
diffprior(prior = prior, res.snap = res.snap)
```

`escompute` *escompute*

Description

Function that computes Hedges' g and its sampling variance for an one-sample mean and a two-independent means, Fisher's r-to-z transformed correlation coefficient and its sampling variance for a raw correlation coefficient and computes a p-value as in the primary studies was done.

Usage

```
escompute(
  mi,
  ri,
  ni,
  sdi,
  m1i,
  m2i,
  n1i,
  n2i,
  sd1i,
  sd2i,
  tobs,
```

```
  yi,
  vi,
  alpha,
  side,
  measure
)
```

Arguments

`mi`	A vector of group means for one-sample mean
`ri`	A vector of raw correlation coefficients
`ni`	A vector of sample sizes for one-sample mean
`sdi`	A vector of standard deviations for one-sample mean
`m1i`	A vector of means in group 1 for two-independent means
`m2i`	A vector of means in group 2 for two-independent means
`n1i`	A vector of sample sizes in group 1 for two-independent means
`n2i`	A vector of sample sizes in group 2 for two-independent means
`sd1i`	A vector of standard deviations in group 1 for two-independent means
`sd2i`	A vector of standard deviations in group 2 for two-independent means
`tobs`	A vector of t-values
`yi`	A vector of standardized effect sizes
`vi`	A vector of sampling variances belonging to the standardized effect sizes (`yi`)
`alpha`	A numerical value specifying the alpha level as used in primary studies
`side`	A character indicating the direction of the tested hypothesis in the primary studies (either `"right"` or `"left"`)
`measure`	A character indicating what kind of effect size should be computed (Hedges' g or Fisher's r-to-z transformed correlation coefficients) and which arguments are used as input (`"M"`, `"MT"`, `"MD"`, `"MDT"`, or `"COR"`). See Details below.

Details

The `measure` argument has to be used to specify the desired effect size and what input parameters are used. There are six options:

`"M"` for one-sample mean with `mi`, `ni`, `sdi`, `alpha`, and `side` as input parameters

`"MT"` for one-sample mean with `tobs`, `ni`, `alpha`, and `side` as input parameters

`"MD"` for two-sample mean with `m1i`, `m2i`, `n1i`, `n2i`, `sd1i`, `sd2i`, `alpha`, and `side` as input parameters

`"MDT"` for two-sample mean with `tobs`, `n1i`, `n2i`, `alpha`, and `side` as input parameters

`"COR"` for raw correlation coefficients with `ri`, `ni`, `alpha`, and `side` as input parameters

`"SPE"` for user-specified standardized effect sizes and sampling variances with `yi`, `vi`, `alpha`, and `side` as input parameters

Value

Function returns a data frame with standardized effect sizes (yi), variances of these standardized effect sizes (vi), z-values (zval), p-values as computed in primary studies (pval), and critical z-values (zcv).

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`fe_ma` *fe_ma*

Description

Function that conducts fixed-effect meta-analysis

Usage

```
fe_ma(yi, vi)
```

Arguments

`yi`	A vector of standardized effect sizes
`vi`	A vector of sampling variances belonging to the standardized effect sizes (`yi`)

Details

The `fe.ma` function can be used for conducting fixed-effect meta-analysis on a set of studies

Value

`est.fe`	effect size estimate of fixed-effect meta-analysis
`se.fe`	standard error of estimate of fixed-effect meta-analysis
`ci.lb.fe`	lower bound 95% confidence interval
`ci.ub.fe`	upper bound 95% confidence interval
`zval.fe`	z-value of test of no effect
`pval.fe`	two-tailed p-value of test of no effect
`pval.fe.one`	one-tailed p-value of test of no effect
`Qstat`	test statistic of the Q-test
`Qpval`	p-value of the Q-test

`fis_trans` *fis_trans*

Description

Function for transforming raw correlation coefficients to Fisher-z transformed correlation coefficients and vice versa.

Usage

```
fis_trans(r, fis)
```

Arguments

`r`	A numerical value being a raw correlation coefficient
`fis`	A numerical value being a Fisher-z transformed correlation coefficient

Author(s)

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`hybrid` *hybrid*

Description

Function to statistically combine conventional and preregistered/replications studies by means of the hybrid methods as described in van Aert and van Assen (2018) and van Aert (2023).

Usage

```
hybrid(
  m1i,
  m2i,
  mi,
  ri,
  sd1i,
  sd2i,
  sdi,
  n1i,
  n2i,
  ni,
  tobs,
  yi,
  vi,
```

```
  conventional,
  mods = NULL,
  alpha = 0.05,
  side,
  control
)
```

Arguments

`m1i`	A vector of means in group 1 for two-independent means
`m2i`	A vector of means in group 2 for two-independent means
`mi`	A vector of group means for one-sample means
`ri`	A vector of raw correlations
`sd1i`	A vector of standard deviations in group 1 for two-independent means
`sd2i`	A vector of standard deviations in group 2 for two-independent means
`sdi`	A vector of standard deviations for one-sample means
`n1i`	A vector of sample sizes in group 1 for two-independent means
`n2i`	A vector of sample sizes in group 2 for two-independent means
`ni`	A vector of sample sizes for one-sample means and correlations
`tobs`	A vector of t-values
`yi`	A vector of standardized effect sizes (see Details)
`vi`	A vector of sampling variances belonging to the standardized effect sizes (see Details)
`conventional`	A vector indicating whether a study is a conventional study (indicated with a 1) and therefore was susceptible to bias. Studies not susceptible to bias are indicated with a 0
`mods`	A one-sided formula to specify the moderators to include. For example `x1` can be included as moderator by specifying `mods = ~ x1`
`alpha`	A numerical value specifying the alpha level as used in the conventional study (default is 0.05, see Details)
`side`	A character indicating whether the observed effect size of the conventional studies are in the right-tail of the distribution (i.e., positive) or in the left-tail of the distribution (i.e., negative) (either `"right"` or `"left"`)
`control`	An optional list of elements that give the user more control over the estimation procedures (see Note)

Details

Three different effect sizes can be used as input for the `hybrid` function: one-sample means, two-independent means, and raw correlation coefficients. Analyzing one-sample means and two-independent means can be done by either providing the function group means (`mi` or `m1i` and `m2i`), standard deviations (`sdi` or `sd1i` and `sd2i`), and sample sizes (`ni` or `n1i` and `n2i`) or t-values (`tobs`) and sample sizes (`ni` or `n1i` and `n2i`). Pearson correlation coefficients can be analyzed by supplying `ri` and `ni` to the `hybrid` function. These correlation coefficients are internally transformed to

Fisher's z correlations before analyzing the data. The results in the output are those of the Fisher's z transformed correlations. It is also possible to specify the standardized effect sizes and its sampling variances directly via the `yi` and `vi` arguments.

Two other arguments that need to be specified are `side` and `conventional`. `side` indicates whether the effect size in the conventional study was expected to be in the right-tail (`side = "right"` or in the left-tail (`side = "left"`) of the distribution. The argument `conventional` has to be used to indicate which studies are conventional studies and expected to be susceptible to bias. A 1 indicates that a study was susceptible to bias and a 0 indicates that a study was not susceptible to bias.

It is assumed that two-tailed hypothesis tests were conducted in the conventional studies. In case one-tailed hypothesis tests were conducted in the conventional studies, the alpha level has to be multiplied by two. For example, if one-tailed hypothesis tests were conducted with an alpha level of .05, an alpha of 0.1 has to be supplied to the `hybrid` function.

Previous version

The usage of a previous version of the `hybrid` function was more restricted. Users could only apply the method to a single conventional study and replication. Before the addition of the extra functionality to also analyze multiple conventional studies and replications, data of the conventional study and replication were specified in vectors containing two elements with the first element being the data of the conventional study and the second one the data of the replication. In order to maintain backwards compatibility, it is still possible to analyze data like this by using the arguments `m1i, m2i, mi, ri, sd1i, sd2i, sdi,n1i, n2i, ni, tobs`. However, using the `hybrid` function in this way is now deprecated.

Value

`k`	total number of effect sizes
`k.conventional`	number of effect sizes of conventional studies
`est`	parameter estimates of the fixed effects of the hybrid method
`tau2`	estimate of the between-study variance in true effect size of hybrid method
`se`	standard error of the fixed effects and of the estimated between-study variance
`ci.lb`	lower bound of hybrid method's confidence interval of the average effect size
`ci.ub`	upper bound of hybrid method's confidence interval of the average effect size
`L.0`	test statistic of hybrid method's test of null-hypothesis of no effect. This is either a z-value (`zval` in the output) or a chi-square value (`LR` in the output) in case of a likelihood-ratio test
`pval.0`	p-value of hybrid method's test of null-hypothesis of no effect
`tau2`	estimate of the between-study variance in true effect size of hybrid method
`tau2.lb`	lower bound of hybrid method's confidence interval of the between-study variance
`tau2.ub`	upper bound of hybrid method's confidence interval of the between-study variance
`L.het`	test statistic of hybrid method's test of null-hypothesis of no heterogeneity This is either a z-value (`zval` in the output) or a chi-square value (`LR` in the output) in case of a likelihood-ratio test
`pval.het`	p-value of hybrid method's test of null-hypothesis of no heterogeneity

`optim.info`	model fitting results if the implementation of van Aert (2023) is used

The elements below are only returned if the deprecated implementation of van Aert and van Assen (2018) is used:

`est.hyr`	effect size estimate of hybridR method
`ci.lb.hyr`	lower bound of hybridR method's confidence interval of the effect size
`ci.ub.hyr`	upper bound of hybridR method's confidence interval of the effect size
`L.0.hyr`	test statistic of hybridR method's test of null-hypothesis of no effect
`pval.0.hyr`	p-value of hybridR method's test of null-hypothesis of no effect
`pval.o`	two-tailed p-value of conventional study
`est.hy0`	effect size estimate of hybrid0 method
`ci.lb.hy0`	lower bound of hybrid0 method's confidence interval of the effect size
`ci.ub.hy0`	upper bound of hybrid0 method's confidence interval of the effect size
`L.0.hy0`	test statistic of hybrid0 method's test of null-hypothesis of no effect
`pval.0.hy0`	two-tailed p-value of hybrid0 method's test of null-hypothesis of no effect
`est.fe`	effect size estimate based on fixed-effect meta-analysis
`se.fe`	standard error of effect size estimate based on traditional fixed-effect meta-analysis
`zval.fe`	test statistic of the null-hypothesis of no effect based on fixed-effect meta-analysis
`pval.fe`	two-tailed p-value of the null-hypothesis of no effect based on fixed-effect meta-analysis
`ci.lb.fe`	lower bound of confidence interval based on traditional fixed-effect meta-analysis
`ci.ub.fe`	upper bound of confidence interval based on fixed-effect meta-analysis
`est.repl`	effect size estimate of replication
`se.repl`	standard error of replication's effect size estimate
`ci.lb.repl`	lower bound of replication's confidence interval
`ci.ub.repl`	upper bound of replication's confidence interval
`stat.repl`	test statistic of replication for testing null-hypothesis of no effect
`pval.repl`	two-tailed p-value of replication for testing null-hypothesis of no effect

Note

The `control` argument in the `hybrid` function is an optional argument that gives the user more control over the estimation procedures. This can be especially useful if estimation of the method does not converge and NAs are returned by the function. The `control` argument should be specified as a list containing one or more elements. For example, `control = list(verbose = TRUE)` Default values are used if an element is not specified. The following elements can be specified by the user:

`int`: A vector of length two that indicates the lower and upper bound of the interval that is used for estimating the effect size. The effect size estimate should be included in this interval. Its default values are -10 for the first element and the maximum effect size of a study included in the analysis + 1 as the second element. This control argument is only applicable to the implementation of van Aert and van Assen (2018).

`est.ci`: A vector of length two indicating the values that are subtracted from and added to the estimate of the effect size for computing the 95% confidence intervals. Its default values are (50, 1). To give an example, estimates for the lower and upper bound around the effect size estimate are searched on the interval (est-50, est) and (est, est+1), respectively.

`tau2.ci` A vector of length two indicating the values that are subtracted from and added to the estimate of the between-study variance for computing the 95% confidence intervals. Its default values are (0.5, 0.5). To give an example, estimates for the lower and upper bound around the effect size estimate are searched on the interval (tau2-0.5, tau2) and (tau2, tau2+0.5), respectively.

`tol`: A number indicating the desired accuracy of the estimates. Its default value is .Machine$double.eps^0.25. This control argument is only applicable to the implementation of van Aert and van Assen (2018).

`verbose`: A logical indicating whether information should be printed about the estimation procedure. Its default value is FALSE.

`par`: Starting values for the optimization procedure in case of the implementation of van Aert (2023). The default values are zeros.

`implementation`: A character indicating whether the implementation of van Aert and van Assen (2018) based on a single conventional and single replication should be used (`implementation = "two"`) or whether the implementation of van Aert (2023) should be used that allows for including more than two studies (`implementation = "multiple"`).

`optimizer`: A character indicating the optimizer that is used if the implementation of van Aert (2023) is used. The default value is "Nelder-Mead". The `optim` function is used for optimization, so the optimization methods implemented in the `optim` function can be used. See the documentation of the `optim` function for more information.

`type`: A character vector indicating whether Wald-based hypothesis tests and confidence intervals are preferred (`type = "Wald"`) or likelihood-ratio tests and profile likelihood confidence intervals (`type = "profile"`). The default is "Wald/profile" which implies that Wald tests and confidence intervals are computed for the fixed effects and likelihood-ratio tests and profile likelihood confidence intervals for the between-study variance.

Author(s)

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References

van Aert, R. C. M., & van Assen, M. A. L. M. (2018). Examining reproducibility in psychology: A hybrid method for statistically combining a biased original study and replication. Behavior Research Methods, 50(4): 1515-1539. doi:10.3758/s13428-017-0967-6

van Aert, R.C.M. (2023). Empowering meta-analysis by taking advantage of preregistered studies: The extended hybrid meta-analysis method. Manuscript in preparation.

Examples

```
### Application using the implementation of van Aert (2023) with more than two studies.
# Note that these data come from the "metadat" R package that needs to be loaded.
# The data come from the meta-analyses by Lehmann et al. (2018). See the help
```

```
# file of dat.lehmann2018 for more information about this meta-analysis.
library(metadat)
dat <- dat.lehmann2018

### Create a new object to indicate which studies were conventional studies and
# which ones were preregistered
dat$conventional <- ifelse(dat$Preregistered == "Not Pre-Registered", 1, 0)

### Lehmann et al. split the analyses for males and females. We only use the data
# of females for this example.
red_romance_femalep <- dat[dat$Gender == "Females", ]

### Prepare data for the analysis
yi <- red_romance_femalep$yi
vi <- red_romance_femalep$vi
conventional <- red_romance_femalep$conventional

### Apply the hybrid method with Wald-type hypothesis tests and confidence intervals
hybrid(yi = yi, vi = vi, conventional = conventional, side = "right")

### Apply the hybrid method with likelihood ratio hypothesis tests and profile
# likelihood confidence intervals
hybrid(yi = yi, vi = vi, conventional = conventional, side = "right",
control = list(type = "profile"))

### Include Color_Match as moderator
Color_Match <- red_romance_femalep$Color_Match

### Apply the hybrid method with Wald-type hypothesis tests and confidence intervals
hybrid(yi = yi, vi = vi, conventional = conventional, side = "right", mods = ~ Color_Match)

### Apply the hybrid method with likelihood ratio hypothesis tests and profile
# likelihood confidence intervals
hybrid(yi = yi, vi = vi, conventional = conventional, side = "right", mods = ~ Color_Match,
control = list(type = "profile"))

### Application using the implementation of van Aert and van Assen (2018).
# The hybrid method is applied to example on page 5 of van Aert and van Assen
# (2018).

pval <- c(0.03, 0.3) # p-value conventional study and replication
n1i <- n2i <- c(40, 80) # Sample sizes per group
tobs <- qt(pval/2, df = n1i+n2i-2, lower.tail = FALSE) # Observed t-values

### Apply hybrid method using the implementation of van Aert and van Assen (2018)
hybrid(tobs = tobs, n1i = n1i, n2i = n2i, side = "right",
control = list(implementation = "two"))
```

`meta_plot` *Meta-plot*

Description

Function to create meta-plots for two-independent means, raw correlations, and odds ratios. See van Assen et al. (2023) for more information.

Usage

```
meta_plot(
  m1i,
  m2i,
  sd1i,
  sd2i,
  n1i,
  n2i,
  gi,
  vgi,
  ri,
  ni,
  ai,
  bi,
  ci,
  di,
  alpha = 0.05,
  method_tau2 = "PM",
  nr_lines = "all",
  pub_bias = TRUE,
  main = "",
  cex.pch = 1
)
```

Arguments

`m1i`	A vector of means in group 1 for two-independent means
`m2i`	A vector of means in group 2 for two-independent means
`sd1i`	A vector of standard deviations in group 1 for two-independent means
`sd2i`	A vector of standard deviations in group 2 for two-independent means
`n1i`	A vector of sample sizes in group 1 for two-independent means
`n2i`	A vector of sample sizes in group 2 for two-independent means
`gi`	A vector of Hedges' g values for two-independent means if group means and standard deviations are not available
`vgi`	A vector of Hedges' g sampling variances for two-independent means if group means and standard deviations are not available
`ri`	A vector of raw correlations
`ni`	A vector of sample sizes if raw correlations are the effect size measure
`ai`	A vector of frequencies in upper left cell of 2x2 frequency table (see Details)
`bi`	A vector of frequencies in upper right cell of 2x2 frequency table (see Details)

`ci`	A vector of frequencies in lower left cell of 2x2 frequency table (see Details)
`di`	A vector of frequencies in lower right cell of 2x2 frequency table (see Details)
`alpha`	A numerical value specifying the alpha level as used in primary studies (default is 0.05 but see Details)
`method_tau2`	A character indicating the estimation method for the between-study variance in true effect size in the meta-analysis (default is `"PM"`, but see Details)
`nr_lines`	A character indicating whether all primary study's effect sizes (`"all"`, default) or a selection of primary study's effect sizes (`"summary"`) are plotted (see Details)
`pub_bias`	A logical indicating whether the expected results of the cumulative meta-analysis based on a zero true effect in combination with extreme publication bias should be plotted. The default value is NA implying that these results are only included if at least 80% of the primary studies is statistically significant. These results are always included if this argument is set to TRUE and never included if this argument is set to FALSE
`main`	A character indicating the title of the plot (default is no title)
`cex.pch`	A numerical value to control the size of the points in the plot

Details

The `meta_plot` function assumes that two-tailed hypothesis tests were conducted in the primary studies. In case one-tailed hypothesis tests were conducted in the primary studies, the submitted `alpha` argument to the `meta_plot` function has to be multiplied by two. For example, if one-tailed hypothesis tests were conducted with an alpha level of .05, an alpha of 0.1 has to be submitted to the `meta_plot` function.

Different estimators can be used for estimating the between-study variance in true effect size. The default estimator is the Paule-Mandel estimator (Paule & Mandel, 1982), because this estimator was recommended in Veroniki et al. (2016) and Langan, Higgins, and Simmonds (2016). However, all estimators that are included in the `rma.uni` function of the `metafor` package can be used, because this function is called in the `meta_plot` function.

When `nr_lines = "summary"` is specified, the estimates of meta-analyses based on primary studies with sufficient statistical power are displayed. Next to the estimate and 95% confidence interval of the meta-analysis including all studies (leftmost), it shows these results for studies with sufficient statistical power (80%) to detect a large true effect size (left vertical line), medium true effect size (middle), and small true effect size (right). Note that the summary meta-plot is just the meta-plot with many meta-analyses and confidence intervals left out, and keeping the leftmost meta-analysis and those just immediately to the right of the vertical lines.

The meta-plot can be created for standardized mean differences by providing the function with the sample means (`m1i` and `m21`), the sample sizes (`n1i` and `n2i`), and the standard deviations (`sd1i` and `sd2i`) or by specifying the standardized mean differences (i.e., Hedges' g; `gi`) together with the corresponding sampling variances (`vgi`) and the sample sizes (`n1i` and `n2i`). Hedges' g standardized mean differences and corresponding sampling variances are computed in the function if the sample means, sample sizes, and standard deviations are provided.

For creating a meta-plot based on odds ratios as effect size measure, the 2x2 frequency table should follow a specific format. The reason for this is that the probability for the outcome of interest in the control conditions has to be estimated. Hence, the 2x2 frequency table should look like this:

	Outcome 1	**Outcome 2**
Group 1	ai	bi
Group 2	ci	di

Value

An invisibly returned data frame consisting of the submitted data and

`yi`	Standardized effect sizes used in the analyses
`vi`	Sampling variances of the standardized effect sizes used in the analyses
`est_cum`	Estimates of the cumulative meta-analyses
`lb_cum`	Lower bounds of the 95% confidence intervals of the cumulative meta-analyses
`ub_cum`	Upper bounds of the 95% confidence intervals of the cumulative meta-analyses
`pub_est`	Estimates of cumulative meta-analyses based on Mill's ratios
`info`	Information of a primary study (only for two-independent means)
`stand_info`	Standardized information of a primary study (only for two-independent means)
`preci`	Precision of a primary study (only for odds ratios)

Author(s)

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References

Langan, D., Higgins, J. P. T., & Simmonds, M. (2016). Comparative performance of heterogeneity variance estimators in meta-analysis: A review of simulation studies. Research Synthesis Methods, 8(2), 181-198. doi:10.1002/jrsm.1198

Paule, R. C., & Mandel, J. (1982). Consensus values and weighting factors. Journal of Research of the National Bureau of Standards, 87(5), 377-385.

van Assen, ..., & van Aert (2023). The meta-plot: A graphical tool for interpreting the results of a meta-analysis. Zeitschrift fur Psychologie, 231(1), 65-78. doi:10.1027/2151-2604/a000513

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Examples

```
### Load data from meta-analysis by McCall and Carriger (1993)
data(data.mccall93)

### Create meta-plot
meta_plot(ri = data.mccall93$ri, ni = data.mccall93$ni)

### Create summary meta-plot
meta_plot(ri = data.mccall93$ri, ni = data.mccall93$ni, nr_lines = "summary")
```

`puniform` *p-uniform*

Description

Function to apply the p-uniform method for one-sample mean, two-independent means, and one raw correlation coefficient as described in van Assen, van Aert, and Wicherts (2015) and van Aert, Wicherts, and van Assen (2016).

Usage

```
puniform(
  mi,
  ri,
  ni,
  sdi,
  m1i,
  m2i,
  n1i,
  n2i,
  sd1i,
  sd2i,
  tobs,
  yi,
  vi,
  alpha = 0.05,
  side,
  method = "P",
  plot = FALSE
)
```

Arguments

`mi`	A vector of group means for one-sample means
`ri`	A vector of raw correlations
`ni`	A vector of sample sizes for one-sample means and correlations
`sdi`	A vector of standard deviations for one-sample means
`m1i`	A vector of means in group 1 for two-independent means
`m2i`	A vector of means in group 2 for two-independent means
`n1i`	A vector of sample sizes in group 1 for two-independent means
`n2i`	A vector of sample sizes in group 2 for two-independent means
`sd1i`	A vector of standard deviations in group 1 for two-independent means
`sd2i`	A vector of standard deviations in group 2 for two-independent means
`tobs`	A vector of t-values

`yi`	A vector of standardized effect sizes (see Details)
`vi`	A vector of sampling variances belonging to the standardized effect sizes (see Details)
`alpha`	A numerical value specifying the alpha level as used in primary studies (default is 0.05, see Details).
`side`	A character indicating whether the effect sizes in the primary studies are in the right-tail of the distribution (i.e., positive) or in the left-tail of the distribution (i.e., negative) (either `"right"` or `"left"`)
`method`	A character indicating the method to be used `"P"` (default), `"LNP"`, `"LN1MINP"`, `"KS"`, `"AD"`, or `"ML"`
`plot`	A logical indicating whether a plot showing the relation between observed and expected p-values has to be rendered (default is `TRUE`)

Details

Three different effect size measures can be used as input for the `puniform` function: one-sample means, two-independent means, and raw correlation coefficients. Analyzing one-sample means and two-independent means can be done by either providing the function group means (`mi` or `m1i` and `m2i`), standard deviations (`sdi` or `sd1i` and `sd2i`), and sample sizes (`ni` or `n1i` and `n2i`) or t-values (`tobs`) and sample sizes (`ni` or `n1i` and `n2i`). Both options should be accompanied with input for the arguments `side`, `method`, and `alpha`. See the Example section for examples. Raw correlation coefficients can be analyzed by supplying the raw correlation coefficients `ri` and sample sizes and `ni` to the `puni_star` function next to input for the arguments `side`, `method`, and `alpha`. Note that the method internally transforms the raw correlation coefficients to Fisher's z correlation coefficients. The output of the function also shows the results for the Fisher's z correlation coefficient. Hence, the results need to be transformed to raw correlation coefficients if this is preferred by the user.

It is also possible to specify the standardized effect sizes and its sampling variances directly via the `yi` and `vi` arguments. However, extensive knowledge about computing standardized effect sizes and its sampling variances is required and specifying standardized effect sizes and sampling variances is not recommended to be used if the p-values in the primary studies are not computed with a z-test. In case the p-values in the primary studies were computed with, for instance, a t-test, the p-values of a z-test and t-test do not exactly coincide and studies may be incorrectly included in the analyses. Furthermore, critical values in the primary studies cannot be transformed to critical z-values if `yi` and `vi` are used as input. This yields less accurate results.

The `puniform` function assumes that two-tailed hypothesis tests were conducted in the primary studies. In case one-tailed hypothesis tests were conducted in the primary studies, the alpha level has to be multiplied by two. For example, if one-tailed hypothesis tests were conducted with an alpha level of .05, an alpha of 0.1 has to be submitted to p-uniform.

Note that only one effect size measure can be specified at a time. A combination of effect size measures usually causes true heterogeneity among effect sizes and including different effect size measures is therefore not recommended.

Six different estimators can be used when applying p-uniform. The `P` method is based on the distribution of the sum of independent uniformly distributed random variables (Irwin-Hall distribution) and is the recommended estimator (van Aert et al., 2016). The `ML` estimator refers to effect size estimation with maximum likelihood. Profile likelihood confidence intervals are computed, and likelihood ratio tests are used for the test of no effect and publication bias test if `ML` is used. The `LNP` estimator refers to Fisher's method (1950, Chapter 4) for combining p-values and the `LN1MINP` estimator first computes 1 - p-value in each study before applying Fisher's method on these transformed p-values (van Assen et al., 2015). `KS` and `AD` respectively use the Kolmogorov-Smirnov test (Massey, 1951) and the Anderson-Darling test (Anderson & Darling, 1954) for testing whether the (conditional) p-values follow a uniform distribution.

Value

`est`	p-uniform's effect size estimate
`ci.lb`	lower bound of p-uniform's confidence interval
`ci.ub`	upper bound of p-uniform's confidence interval
`ksig`	number of significant studies
`L.0`	test statistic of p-uniform's test of null-hypothesis of no effect (for method `"P"` a z-value)
`pval.0`	one-tailed p-value of p-uniform's test of null-hypothesis of no effect
`L.pb`	test statistic of p-uniform's publication bias test
`pval.pb`	one-tailed p-value of p-uniform's publication bias test
`est.fe`	effect size estimate based on traditional fixed-effect meta-analysis
`se.fe`	standard error of effect size estimate based on traditional fixed-effect meta-analysis
`zval.fe`	test statistic of the null-hypothesis of no effect based on traditional fixed-effect meta-analysis
`pval.fe`	one-tailed p-value of the null-hypothesis of no effect based on traditional fixed-effect meta-analysis
`ci.lb.fe`	lower bound of confidence interval based on traditional fixed-effect meta-analysis
`ci.ub.fe`	ci.ub.fe upper bound of confidence interval based on traditional fixed-effect meta-analysis
`Qstat`	test statistic of the Q-test for testing the null-hypothesis of homogeneity
`Qpval`	one-tailed p-value of the Q-test

Author(s)

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References

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Van Aert, R. C. M., Wicherts, J. M., & van Assen, M. A. L. M. (2016). Conducting meta-analyses on p-values: Reservations and recommendations for applying p-uniform and p-curve. Perspectives on Psychological Science, 11(5), 713-729. doi:10.1177/1745691616650874

Van Assen, M. A. L. M., van Aert, R. C. M., & Wicherts, J. M. (2015). Meta-analysis using effect size distributions of only statistically significant studies. Psychological Methods, 20(3), 293-309. doi: http://dx.doi.org/10.1037/met0000025

Examples

```
### Load data from meta-analysis by McCall and Carriger (1993)
data(data.mccall93)

### Apply p-uniform method
puniform(ri = data.mccall93$ri, ni = data.mccall93$ni, side = "right",
method = "LNP", plot = TRUE)

### Generate example data for one-sample means design
set.seed(123)
ni <- 100
sdi <- 1
mi <- rnorm(8, mean = 0.2, sd = sdi/sqrt(ni))
tobs <- mi/(sdi/sqrt(ni))

### Apply p-uniform method based on sample means
puniform(mi = mi, ni = ni, sdi = sdi, side = "right", plot = FALSE)

### Apply p-uniform method based on t-values
puniform(ni = ni, tobs = tobs, side = "right", plot = FALSE)
```

`puni_star` *p-uniform**

Description

Function to apply the p-uniform* method for one-sample mean, two-independent means, and one raw correlation coefficient as described in van Aert and van Assen (2023).

Usage

```
puni_star(
  mi,
  ri,
  ni,
  sdi,
  m1i,
  m2i,
  n1i,
```

```
  n2i,
  sd1i,
  sd2i,
  tobs,
  yi,
  vi,
  alpha = 0.05,
  side,
  method = "ML",
  boot = FALSE,
  control
)
```

Arguments

`mi`	A vector of group means for one-sample means
`ri`	A vector of raw correlations
`ni`	A vector of sample sizes for one-sample means and correlations
`sdi`	A vector of standard deviations for one-sample means
`m1i`	A vector of means in group 1 for two-independent means
`m2i`	A vector of means in group 2 for two-independent means
`n1i`	A vector of sample sizes in group 1 for two-independent means
`n2i`	A vector of sample sizes in group 2 for two-independent means
`sd1i`	A vector of standard deviations in group 1 for two-independent means
`sd2i`	A vector of standard deviations in group 2 for two-independent means
`tobs`	A vector of t-values
`yi`	A vector of standardized effect sizes (see Details)
`vi`	A vector of sampling variances belonging to the standardized effect sizes (see Details)
`alpha`	A numerical value specifying the alpha level as used in primary studies (default is 0.05 but see Details).
`side`	A character indicating whether the effect sizes in the primary studies are in the right-tail of the distribution (i.e., positive) or in the left-tail of the distribution (i.e., negative) (either `"right"` or `"left"`)
`method`	A character indicating the method to be used `"ML"` (default), `"P"`, or `"LNP"`
`boot`	A logical indicating whether the p-value of testing whether the between-study variance is zero for methods `P` and `LNP` should be obtained by means of a parametric bootstrap. The default value is FALSE.
`control`	An optional list of elements that give the user more control over the optimization and root-finding algorithms (see Note)

Details

Three different effect size measures can be used as input for the `puni_star` function: one-sample means, two-independent means, and raw correlation coefficients. Analyzing one-sample means and two-independent means can be done by either providing the function group means (`mi` or `m1i` and `m2i`), standard deviations (`sdi` or `sd1i` and `sd2i`), and sample sizes (`ni` or `n1i` and `n2i`) or t-values (`tobs`) and sample sizes (`ni` or `n1i` and `n2i`). Both options should be accompanied with input for the arguments `side`, `method`, and `alpha`. See the Example section for examples. Raw correlation coefficients can be analyzed by supplying the raw correlation coefficients `ri` and sample sizes and `ni` to the `puni_star` function next to input for the arguments `side`, `method`, and `alpha`. Note that the method internally transforms the raw correlation coefficients to Fisher's z correlation coefficients. The output of the function also shows the results for the Fisher's z correlation coefficient. Hence, the results need to be transformed to raw correlation coefficients if this is preferred by the user.

It is also possible to specify the standardized effect sizes and its sampling variances directly via the `yi` and `vi` arguments. However, extensive knowledge about computing standardized effect sizes and its sampling variances is required and specifying standardized effect sizes and sampling variances is not recommended to be used if the p-values in the primary studies are not computed with a z-test. In case the p-values in the primary studies were computed with, for instance, a t-test, the p-values of a z-test and t-test do not exactly coincide and studies may be incorrectly included as a statistically significant or nonsignificant effect size. Furthermore, critical values in the primary studies are not transformed to critical z-values if `yi` and `vi` are used as input. This yields less accurate results.

The `puni_star` function assumes that two-tailed hypothesis tests were conducted in the primary studies. In case one-tailed hypothesis tests were conducted in the primary studies, the submitted `alpha` argument to the `puni_star` function has to be multiplied by two. For example, if one-tailed hypothesis tests were conducted with an alpha level of .05, an alpha of 0.1 has to be submitted to the `puni_star` function.

Note that only one effect size measure can be specified at a time. A combination of effect size measures usually causes true heterogeneity among effect sizes and including different effect size measures is therefore not recommended.

Selecting a method

Three different methods are currently implemented in the `puni_star` function. The `ML` method refers to maximum likelihood estimation of the effect size and the between-study variance. Profile likelihood confidence intervals around the estimates are computed by means of inverting the likelihood-ratio test. Likelihood-ratio tests are used for testing the null hypotheses of no effect and no between-study variance. The `ML` method is the recommended method for applying p-uniform*.

The two other methods (`P` and `LNP`) are moment based estimators. The method `P` is based on the distribution of the sum of independent uniformly distributed random variables (Irwin-Hall distribution) and the `LNP` method refers to Fisher's method (1950, Chapter 4). For these methods, a p-value for testing the null hypothesis of no between-study variance can also be obtained by means of a parametric bootstrap. This is necessary since the data is otherwise first used for estimating the effect size in the procedure for testing the null hypothesis of no between-study variance and then also used for computing a p-value. The test of no effect is not available for the methods `P` and `LNP` and the publication bias test for these methods is not yet implemented.

Value

`est`	p-uniform*'s effect size estimate

`ci.lb`	lower bound of p-uniform*'s 95% confidence interval of the effect size
`ci.ub`	upper bound of p-uniform*'s 95% confidence interval of the effect size
`L.0`	test statistic of p-uniform*'s test of the null hypothesis of no effect
`pval.0`	one-tailed p-value of p-uniform*'s test of null hypothesis of no effect
`tau2`	p-uniform*'s estimate of the between-study variance
`tau2.lb`	lower bound of p-uniform*'s 95% confidence interval of the between-study variance
`tau2.ub`	upper bound of p-uniform*'s 95% confidence interval of the between-study variance
`L.het`	test statistic of p-uniform*'s test of the null hypothesis of no between-study variance
`pval.het`	one-tailed p-value of p-uniform*'s test of null hypothesis of no between-study variance
`pval.boot`	one-tailed p-value of p-uniform*'s test of null hypothesis of no between-study variance obtained with a parametric bootstrap
`...`	a number of additional elements

Note

The `control` argument in the `puni_star` function is an optional argument that gives the user more control over the optimization and root-finding algorithms. This can be especially useful if estimation of the method does not converge and NAs are returned by the function. The `control` argument should be specified as a list containing one or more elements. For example, `control = list(verbose = TRUE)` Default values are used if an element is not specified. The following elements can be specified by the user:

`proc.ml`: A character indicating with optimization procedure should be used for the method `ML`. The initial implementation of p-uniform* iteratively optimized the profile log-likelihood functions. As of version 0.2.6 of this package, the default optimization routine estimates both parameters at the same time. The old optimization procedure can be used by specifying `proc.ml = "prof"`.

`stval.d`: An integer that is the starting value of the effect size for estimation. This starting value is used for the method `ML` and is only needed when both parameters are estimated at the same time. See argument `proc.ml` for more information. The default value is the mean of the effect sizes in the meta-analysis.

`stval.tau`: An integer that is the starting value of tau for estimation. This starting value is used for the methods `ML`, `P`, and `LNP`. The default value is the standard deviation of the effect sizes in the meta-analysis.

`int`: A vector of length two that indicates the lower and upper bound of the interval that is used for estimating the effect size. The effect size estimate should be included in this interval. This interval is used for the methods `ML`, `P`, and `LNP` and its default values are (-2, 2).

`bounds.int` A vector of length two that is used for determining the bounds for estimating the effect size with `P` and `LNP`. The default values are a function of the `yi`. The lower bound is the minimum `yi` minus 1 and the upper bound is the maximum `yi` plus 1. The effect size has to be between the lower and upper bound.

`tau.int`: A vector of length two that indicates the lower and upper bound of the interval that is used for estimating the between-study variance. The estimate of the between-study variance should be included in this interval. This interval is used for the methods `ML`, `P`, and `LNP` and its default values are (0, 2).

`est.ci`: A vector of length two indicating the values that are subtracted from and added to the estimate of the effect size for computing the 95% confidence intervals. This vector is used for the methods `ML`, `P`, and `LNP` and its default values are (3, 3). To give an example, estimates for the lower and upper bound around the effect size estimate are searched on the interval (est-3, est) and (est, est+3), respectively.

`tau.ci`: A vector of length two indicating the values that are added to the estimate of the between-study variance for computing the 95% confidence intervals. This vector is used for the methods `ML`, `P`, and `LNP` and its default values are (3, 1).

`tol`: A number indicating the desired accuracy of the estimates. This number is used for the methods `ML`, `P`, and `LNP` and its default value is 0.001.

`maxit`: An integer indicating the maximum number of iterations that is used for estimating the effect size and between-study variance. This number is used for the methods `ML`, `P`, and `LNP` and its default value is 300.

`fnscale`: An integer that can be used for scaling the log-likelihood value in the optimization. `fnscale` is one of the control arguments of the `optim()` function that is internally used for optimization when the `ML` method is used and both parameters are estimated at the same time. See the argument `proc.ml` above and the documentation of the `optim()` function for more information.

`verbose`: A logical indicating whether information should be printed about the algorithm for estimating the effect size and between-study variance. This logical is used for the methods `ML`, `P`, and `LNP` and its default value is FALSE.

`reps`: An integer indicating the number of bootstrap replications for computing the bootstrapped p-value for the test of no between-study variance. This integer is used for the methods `P` and `LNP` and its default value is 1000.

Author(s)

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References

Fisher, R.A. (1950). Statistical methods for research workers (11th ed.). London: Oliver & Boyd.

van Aert, R.C.M., & van Assen, M.A.L.M. (2023). Correcting for publication bias in a meta-analysis with the p-uniform* method. Manuscript submitted for publication. Preprint: https://osf.io/preprints/bitss/zqjr9/

Examples

```
### Generate data for one-sample mean with mu = 0.2 and tau^2 = 0.01
set.seed(123)
ni <- rep(50, 25)
sdi <- rep(1, 25)
ui <- rnorm(25, mean = 0.2, sd = 0.1)
mi <- rnorm(25, mean = ui, sd = sdi/sqrt(ni))
```

```
tobs <- mi/(sdi/sqrt(ni))

### Apply p-uniform* method using sample means
puni_star(mi = mi, ni = ni, sdi = sdi, alpha = 0.05, side = "right", method = "ML")

### Apply p-uniform* method using t-values
puni_star(tobs = tobs, ni = ni, alpha = 0.05, side = "right", method = "ML")
```

`req_ni_r` *req_ni_r*

Description

Function for computing the required sample size for a replication based on the Snapshot Bayesian Hybrid Meta-Analysis Method for two-independent means and raw correlation coefficients.

Usage

```
req_ni_r(
  ri.o,
  ni.o,
  m1i.o,
  m2i.o,
  n1i.o,
  n2i.o,
  sd1i.o,
  sd2i.o,
  tobs.o,
  alpha,
  des.pprob,
  des.pow,
  lo = 4,
  hi = 1e+05
)
```

Arguments

`ri.o`	A numeric value containing the raw correlation coefficient of the original study
`ni.o`	An integer containing the sample size for the raw correlation coefficient
`m1i.o`	A numeric value containing the mean in group 1 of the original study for two-independent means
`m2i.o`	A numeric value containing the mean in group 2 of the original study for two-independent means
`n1i.o`	A numeric value containing the sample size in group 1 of the original study for two-independent means

`n2i.o`	A numeric value containing the sample size in group 2 of the original study for two-independent means
`sd1i.o`	A numeric value containing the standard deviation in group 1 of the original study for two-independent means
`sd2i.o`	A numeric value containing the standard deviation in group 2 of the original study for two-independent means
`tobs.o`	A numeric value containing the t-value of the original study
`alpha`	A numeric value specifying the alpha level as used in the original study
`des.pprob`	A numeric value specifying the posterior probability that an user desires to obtain for one of the four true effect sizes
`des.pow`	A numeric value specifying the probability of observing a posterior probability larger than des.pprob that an user desires to obtain for one of the four true effect sizes
`lo`	A numeric value specifying the lower bound of the search interval that is used for the optimization procedure (default is 4)
`hi`	A numeric value specifying the upper bound of the search interval that is used for the optimization procedure (default is 100,000)

Details

The function computes the required sample size for the replication based on the Snapshot Bayesian Hybrid Meta-Analysis Method for four true effect sizes (no, small, medium, and large). The required sample size is computed by optimizing $P(\pi_x \geq a) = b$ with π_x being the posterior probability with x referring to no (0), small (S), medium (M), and large (L) true effect size and a the desired posterior probability, and b the desired probability of observing a posterior probability larger than a. The required sample size for the replication is computed with and without including information of the original study. Computing the required sample size with the Snapshot Bayesian Hybrid Meta-Analysis Method is akin to computing the required sample size with a power analysis in null hypothesis significance testing. For more information see van Aert and van Assen (2016).

The `req.ni.r` function assumes that a two-tailed hypothesis test was conducted in the original study. In case one-tailed hypothesis tests was conducted in the original study, the alpha level has to be multiplied by two. For example, if a one-tailed hypothesis test was conducted with an alpha level of .05, an alpha of 0.1 has to be submitted to `req.ni.r`.

Value

The `req.ni.r` function returns a 4x2 matrix with in the first column the required total sample size of the replication when information of the original study is taken into account and in the second column the required sample size if information of the original study is ignored.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & van Assen, M.A.L.M. (2016). Bayesian evaluation of effect size after replicating an original study. Manuscript submitted for publication.

Examples

```
### Example as presented on page 491 in Maxwell, Lau, and Howard (2015)
req_ni_r(ri.o = 0.243, ni.o = 80, alpha = .05, des.pprob = 0.75, des.pow = 0.8)
```

`snapshot` *snapshot*

Description

Function for applying Snapshot Bayesian Hybrid Meta-Analysis Method for two-independent means and raw correlation coefficients.

Usage

```
snapshot(ri, ni, m1i, m2i, n1i, n2i, sd1i, sd2i, tobs, alpha = 0.05)
```

Arguments

`ri`	A vector of length two containing the raw correlation coefficients of the original study and replication
`ni`	A vector of length two containing the sample size of the original study and replication for the raw correlation coefficient
`m1i`	A vector of length two containing the means in group 1 for the original study and replication for two-independent means
`m2i`	A vector of length two containing the means in group 2 for the original and replication for two-independent means
`n1i`	A vector of length two containing the sample sizes in group 1 for the original study and replication for two-independent means
`n2i`	A vector of length two containing the sample sizes in group 2 for the original study and replication for two-independent means
`sd1i`	A vector of length two containing the standard deviations in group 1 for the original study and replication for two-independent means
`sd2i`	A vector of length two containing the standard deviations in group 2 for the original study and replication for two-independent means
`tobs`	A vector of length two containing the t-values of the original study and replication
`alpha`	A numerical value specifying the alpha level as used in the original study (default is 0.05, see Details)

Details

The function computes posterior probabilities (assuming a uniform prior distribution) for four true effect sizes (no, small, medium, and large) based on an original study and replication while taking into account statistical significance in the original study. For more information see van Aert and van Assen (2016).

Two different effect size measures can be used as input for the `snapshot` function: two-independent means and raw correlation coefficients. Analyzing two-independent means can be done by either providing the function group means (`m1i` and `m2i`), standard deviations (`sd1i` and `sd2i`), and sample sizes (`n1i` and `n2i`) or t-values (`tobs`) and sample sizes (`n1i` and `n2i`). Both options should be accompanied with input for the argument `alpha`. See the Example section for an example. Raw correlation coefficients can be analyzed by supplying `ri` and `ni` to the `snapshot` function next to input for the argument `alpha`.

The `snapshot` function assumes that a two-tailed hypothesis test was conducted in the original study. In case a one-tailed hypothesis test was conducted in the original study, the alpha level has to be multiplied by two. For example, if a one-tailed hypothesis test was conducted with an alpha level of .05, an alpha of 0.1 has to be submitted to `snapshot`.

Value

The `snapshot` function returns a data frame with posterior probabilities for no (`p.0`), small (`p.sm`), medium (`p.me`), and large (`p.la`) true effect size.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & van Assen, M.A.L.M. (2017). Bayesian evaluation of effect size after replicating an original study. PLoS ONE, 12(4), e0175302. doi:10.1371/journal.pone.0175302

Examples

```
### Example as presented on page 491 in Maxwell, Lau, and Howard (2015)
snapshot(ri = c(0.243, 0.114), ni = c(80, 172))
```

`snapshot_naive` *snapshot_naive*

Description

Function for applying Snapshot Bayesian Meta-Analysis Method (snapshot naive) for two-independent means and raw correlation coefficients.

Usage

```
snapshot_naive(ri, ni, m1i, m2i, n1i, n2i, sd1i, sd2i, tobs)
```

Arguments

`ri`	A vector of length two containing the raw correlation coefficients of the original study and replication
`ni`	A vector of length two containing the sample size of the original study and replication for the raw correlation coefficient
`m1i`	A vector of length two containing the means in group 1 for the original study and replication for two-independent means
`m2i`	A vector of length two containing the means in group 2 for the original and replication for two-independent means
`n1i`	A vector of length two containing the sample sizes in group 1 for the original study and replication for two-independent means
`n2i`	A vector of length two containing the sample sizes in group 2 for the original study and replication for two-independent means
`sd1i`	A vector of length two containing the standard deviations in group 1 for the original study and replication for two-independent means
`sd2i`	A vector of length two containing the standard deviations in group 2 for the original study and replication for two-independent means
`tobs`	A vector of length two containing the t-values of the original study and replication

Details

The function computes posterior probabilities (assuming a uniform prior distribution) for four true effect sizes (no, small, medium, and large) based on an original study and replication. For more information see van Aert and van Assen (2016).

Two different effect size measures can be used as input for the `snapshot.naive` function: two-independent means and raw correlation coefficients. Analyzing two-independent means can be done by either providing the function group means (`m1i` and `m2i`), standard deviations (`sd1i` and `sd2i`), and sample sizes (`n1i` and `n2i`) or t-values (`tobs`) and sample sizes (`n1i` and `n2i`).See the Example section for an example. Raw correlation coefficients can be analyzed by supplying `ri` and `ni` to the `snapshot.naive`.

Value

The `snapshot.naive` function returns a data frame with posterior probabilities for no (`p.0`), small (`p.sm`), medium (`p.me`), and large (`p.la`) true effect size.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & van Assen, M.A.L.M. (2017). Bayesian evaluation of effect size after replicating an original study. PLoS ONE, 12(4), e0175302. doi:10.1371/journal.pone.0175302

Examples

```
### Example as presented on page 491 in Maxwell, Lau, and Howard (2015)
snapshot_naive(ri = c(0.243, 0.114), ni = c(80, 172))
```

`var_boot_fis` *var_boot_fis*

Description

Function for parametric bootstrapping procedure to estimate the variability in outcomes' effect size in case of Fisher-z transformed correlations as effect size measure.

Usage

```
var_boot_fis(ri, n, r, dv = 10, reps = 1000)
```

Arguments

`ri`	A vector with Pearson correlation coefficients in a primary study (see Details)
`n`	A numerical value specifying the total sample size of a primary study
`r`	A numerical value specifying the Pearson correlation coefficient between variables h and m (see Details)
`dv`	An integer specifying the total number of dependent measures (default is 10, see Details)
`reps`	An integer specifying the number of bootstrap replications (default is 1,000)

Details

In case of three variables (l, h, and m), overlapping Fisher-z transformed correlation coefficients can be computed between variables l and h and variables l and m. The function computes the variance of the two overlapping Fisher-z transformed correlation coefficients using a parametric bootstrap procedure. For more information see van Aert & Wicherts (2023).

The vector `ri` can contain a single Pearson correlation coefficient or multiple coefficients if information on more than one outcome is available. The integer `dv` is an optional argument to specify the expected number of outcomes used in a primary study. This argument can be any value between 2 and infinity. Larger values yield more accurate estimates of the variance but slow down the bootstrap procedure.

The variance that is computed with this function can be used to correct for outcome reporting bias by including the variance as a moderator in a (multivariate) meta-analysis. Please see van Aert & Wicherts (2023) for more information.

Value

The `var_boot_fis` function returns a numerical value that is the variance of multiple correlated Fisher-z transformed correlations.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & Wicherts, J.M. (2023). Correcting for outcome reporting bias in a meta-analysis: A meta-regression approach. Behavior Research Methods.

Examples

```
### Compute variance for an artificial example
var_boot_fis(ri = 0, n = 100, r = 0.3)
```

`var_boot_rmd` *var_boot_rmd*

Description

Function for parametric bootstrapping procedure to estimate the variability in outcomes' effect size in case of raw mean difference as effect size measure.

Usage

```
var_boot_rmd(sd1i, sd2i, n1i, n2i, r, dv = 10, reps = 1000)
```

Arguments

`sd1i`	A vector of standard deviations of the outcomes in group 1 (see Details)
`sd2i`	A vector of standard deviations of the outcomes in group 2 (see Details)
`n1i`	An integer specifying the sample size of group 1
`n2i`	An integer specifying the sample size of group 2
`r`	A numerical value specifying the Pearson correlation coefficient between participants' scores on the different outcomes
`dv`	An integer specifying the total number of outcomes (default is 10, see Details)
`reps`	An integer specifying the number of bootstrap replications (default is 1,000)

Details

Multiple raw mean differences can be computed in case of two groups and multiple outcomes. The function estimates the variance of raw mean differences given a correlation among the outcomes using a parametric bootstrap procedure. For more information see van Aert & Wicherts (2023).

The vectors `sd1i` and `sd2i` can contain a single standard deviation or multiple standard deviations if information on more than one outcome is available. The integer `dv` is an optional argument to specify the expected number of outcomes used in a primary study. This argument can be any value between 2 and infinity. Larger values yield more accurate estimates of the variance but slow down the bootstrap procedure.

The variance that is estimated with this function can be used to correct for outcome reporting bias by including the variance as a moderator in a (multivariate) meta-analysis. Please see van Aert & Wicherts (2023) for more information.

Value

The `var_boot_rmd` function returns a numerical value that is an estimate of the variance of multiple correlated raw mean differences.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & Wicherts, J.M. (2023). Correcting for outcome reporting bias in a meta-analysis: A meta-regression approach. Behavior Research Methods.

Examples

```
### Compute variance for an artificial example
var_boot_rmd(sd1i = c(0.8, 1.2), sd2i = c(0.85, 1.15), n1i = 100, n2i = 95, r = 0.3)
```

`var_dif_fis` *var_dif_fis*

Description

Function for computing the variance of the difference between two overlapping Fisher-z transformed correlation coefficients.

Usage

```
var_dif_fis(n, r, rho)
```

Arguments

`n`	A numerical value specifying the total sample size of a primary study
`r`	A numerical value specifying the Pearson correlation coefficient between variables h and m (see Details)
`rho`	A numerical value specifying the Pearson correlation coefficient between variables l and h and variables h and m (see Details)

Details

In case of three variables (l, h, and m), overlapping Fisher-z transformed correlation coefficients can be computed between variables l and h and variables l and m. The function computes the variance of the difference between these two overlapping Fisher-z transformed correlations. For a derivation of this variance see van Aert & Wicherts (2023).

The variance that is computed with this function can be used to correct for outcome reporting bias by including the variance as a moderator in a (multivariate) meta-analysis. Please see van Aert & Wicherts (2023) for more information.

Value

The `var_dif_fis` function returns a numerical value that is the variance of the difference of two overlapping Fisher-z transformed correlations given n, r, and rho.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & Wicherts, J.M. (2023). Correcting for outcome reporting bias in a meta-analysis: A meta-regression approach. Behavior Research Methods.

Examples

```
### Compute variance for an artificial example
var_dif_fis(n = 100, r = 0.3, rho = 0.5)
```

`var_dif_rmd` *var_dif_rmd*

Description

Function for computing the variance of the difference between two raw mean differences.

Usage

```
var_dif_rmd(sd1i, sd2i, n1i, n2i, r)
```

Arguments

`sd1i`	A vector of standard deviations of the outcomes in group 1 (see Details)
`sd2i`	A vector of standard deviations of the outcomes in group 2 (see Details)
`n1i`	An integer specifying the sample size of group 1
`n2i`	An integer specifying the sample size of group 2
`r`	A numerical value specifying the Pearson correlation coefficient between participants' scores on the different outcomes

Details

Multiple raw mean differences can be computed in case of two groups and multiple outcomes. The function computes the variance of the difference of two raw mean differences given a correlation between the outcomes. For a derivation of this variance see the supplemental materials of van Aert & Wicherts (2023).

The vectors `sd1i` and `sd2i` can contain a single standard deviation or multiple standard deviations if information on more than one outcome measure is available.

The variance that is computed with this function can be used to correct for outcome reporting bias by including the variance as a moderator in a (multivariate) meta-analysis. Please see van Aert & Wicherts (2023) for more information.

Value

The `var_dif_rmd` function returns a numerical value that is the variance of the difference of two raw mean differences given r.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & Wicherts, J.M. (2023). Correcting for outcome reporting bias in a meta-analysis: A meta-regression approach. Behavior Research Methods.

Examples

```
### Compute variance for an artificial example
var_dif_rmd(sd1i = c(0.8, 1.2), sd2i = c(0.85, 1.15), n1i = 100, n2i = 95, r = 0.3)
```

`var_pop` *var_pop*

Description

Function for estimating the population variance of correlated outcomes' effect size within a primary study.

Usage

```
var_pop(v, r)
```

Arguments

`v`	A numerical value specifying the sampling variance of the effect size (see Details)
`r`	A numerical value specifying the Pearson correlation coefficient between the outcomes (see Details)

Details

This function estimates the population variance of the effect size of correlated outcomes within a study. That is, it estimates the population variance from a single draw of a multivariate normal distribution. The function assumes equal true effect size of all outcomes, equal sampling variances of the outcomes' effect size, and equal correlation (i.e., `r`) among the outcomes.

For a derivation of this estimator see van Aert & Wicherts (2023).

The variance that is computed with this function can be used to correct for outcome reporting bias by including the variance as a moderator in a (multivariate) meta-analysis. Please see van Aert & Wicherts (2023) for more information.

Value

The `var_pop` function returns a numerical value that is the estimate of the population variance of correlated outcomes' effect size given v and r.

Author(s)

Robbie C.M. van Aert <`R.C.M.vanAert@tilburguniversity.edu`>

References

van Aert, R.C.M. & Wicherts, J.M. (2023). Correcting for outcome reporting bias in a meta-analysis: A meta-regression approach. Behavior Research Methods.

Examples

```
### Compute variance for an artificial example
var_pop(v = 0.1, r = 0.3)
```

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