

Package ‘puniform’

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Description Provides meta-analysis methods that correct for publication bias. Four methods 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 Chapter 5 of van Aert (2018) <doi:10.31222/osf.io/eqhjd>. 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 (2017) <doi:10.3758/s13428-017-0967-6>. The hybrid method is a meta-analysis method for combining an original study and replication and while taking into account statistical significance of the original study. 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 (2017) <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.

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data.mccall93	<i>Data from a meta-analysis infants' habituation to a give stimulus and their later cognitive ability (IQ)</i>
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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).

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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

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

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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)
res.snap <- snapshot(ri=c(0.243, 0.114), ni=c(80, 172), alpha=.05)
```

```
### Prior probabilities with probability 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

<code>mi</code>	A vector of group means for one-sample mean
<code>ri</code>	A vector of raw correlation coefficients
<code>ni</code>	A vector of sample sizes for one-sample mean
<code>sdi</code>	A vector of standard deviations for one-sample mean
<code>m1i</code>	A vector of means in group 1 for two-independent means
<code>m2i</code>	A vector of means in group 2 for two-independent means
<code>n1i</code>	A vector of sample sizes in group 1 for two-independent means
<code>n2i</code>	A vector of sample sizes in group 2 for two-independent means
<code>sd1i</code>	A vector of standard deviations in group 1 for two-independent means
<code>sd2i</code>	A vector of standard deviations in group 2 for two-independent means
<code>tobs</code>	A vector of t -values
<code>yi</code>	A vector of standardized effect sizes
<code>vi</code>	A vector of sampling variances belonging to the standardized effect sizes (y_i)
<code>alpha</code>	An integer specifying the alpha level as used in primary studies
<code>side</code>	A character indicating the direction of the tested hypothesis in the primary studies (either "right" or "left")
<code>measure</code>	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

<code>r</code>	An integer being a raw correlation coefficient
<code>fis</code>	An integer being a Fisher-z transformed correlation coefficient

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hybrid	<i>hybrid</i>
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Description

Function to statistically combine an original study and replication by means of the hybrid methods and fixed-effect meta-analysis as described in van Aert and van Assen (2018).

Usage

```
hybrid(m1i, m2i, mi, ri, sd1i, sd2i, sdi, n1i, n2i, ni, tobs,
       alpha = 0.05, side)
```

Arguments

<code>m1i</code>	A vector of means in group 1 for two-independent means
<code>m2i</code>	A vector of means in group 2 for two-independent means
<code>mi</code>	A vector of group means for one-sample means
<code>ri</code>	A vector of raw correlations
<code>sd1i</code>	A vector of standard deviations in group 1 for two-independent means
<code>sd2i</code>	A vector of standard deviations in group 2 for two-independent means
<code>sdi</code>	A vector of standard deviations for one-sample means
<code>n1i</code>	A vector of sample sizes in group 1 for two-independent means
<code>n2i</code>	A vector of sample sizes in group 2 for two-independent means
<code>ni</code>	A vector of sample sizes for one-sample means and correlations
<code>tobs</code>	A vector of t-values
<code>alpha</code>	A integer specifying the alpha level as used in the original study (default is 0.05, see Details).
<code>side</code>	A character indicating whether the observed effect size of the original study is 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")

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`). Both options should be accompanied with input for the arguments `side` and `method`. See the Example section for an example. Raw correlation coefficients can be analyzed by supplying `ri` and `ni` to the `puniform` function next to input for the arguments `side` and `method`. The vectors containing data of the original study and replication should always be of length two; the first element should contain information about the original study and the second element should contain information about the replication.

The hybrid methods assume that the original study is statistically significant and a two-tailed hypothesis test was conducted in the original study. In case a 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 entered into the hybrid function.

Value

est.hy	effect size estimate of hybrid method
ci.lb.hy	lower bound of hybrid method's confidence interval
ci.ub.hy	upper bound of hybrid method's confidence interval
x.hy	test statistic of hybrid method's test of null-hypothesis of no effect
pval.hy	two-tailed p-value of hybrid method's test of null-hypothesis of no effect
measure	effect size measure
est.hyr	effect size estimate of hybridR method
ci.lb.hyr	lower bound of hybridR method's confidence interval
ci.ub.hyr	upper bound of hybridR method's confidence interval
stat.hyr	test statistic of hybridR method's test of null-hypothesis of no effect
pval.hyr	two-tailed p-value of hybridR method's test of null-hypothesis of no effect
pval.o	two-tailed p-value of original study
est.hy0	effect size estimate of hybrid0 method
ci.lb.hy0	lower bound of hybrid0 method's confidence interval
ci.ub.hy0	upper bound of hybrid0 method's confidence interval
x.hy0	test statistic of hybrid0 method's test of null-hypothesis of no effect
pval.hy0	two-tailed p-value of hybrid0 method's test of null-hypothesis of no effect
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	two-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	upper bound of confidence interval based on traditional 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

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

Examples

```
### Apply hybrid function to example on page 5 of van Aert and van Assen (2018).
hybrid(tobs = c(2.211,1.04), n1i = c(40,80), n2i = c(40,80), side = "right")
```

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

<code>mi</code>	A vector of group means for one-sample means
<code>ri</code>	A vector of raw correlations
<code>ni</code>	A vector of sample sizes for one-sample means and correlations
<code>sdi</code>	A vector of standard deviations for one-sample means
<code>m1i</code>	A vector of means in group 1 for two-independent means
<code>m2i</code>	A vector of means in group 2 for two-independent means
<code>n1i</code>	A vector of sample sizes in group 1 for two-independent means
<code>n2i</code>	A vector of sample sizes in group 2 for two-independent means
<code>sd1i</code>	A vector of standard deviations in group 1 for two-independent means
<code>sd2i</code>	A vector of standard deviations in group 2 for two-independent means
<code>tobs</code>	A vector of t-values
<code>yi</code>	A vector of standardized effect sizes (see Details)

<code>vi</code>	A vector of sampling variances belonging to the standardized effect sizes (see Details)
<code>alpha</code>	A integer specifying the alpha level as used in primary studies (default is 0.05, see Details).
<code>side</code>	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")
<code>method</code>	A character indicating the method to be used "P" (default), "LNP", "LN1MINP", "KS", or "AD")
<code>plot</code>	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 (`sd1i` 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 `ri` and `ni` to the `puniform` function next to input for the arguments `side`, `method`, and `alpha`.

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.mccall193)

### Apply p-uniform method
puniform(ri = data.mccall193$ri, ni = data.mccall193$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 (2019).

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

<code>mi</code>	A vector of group means for one-sample means
<code>ri</code>	A vector of raw correlations
<code>ni</code>	A vector of sample sizes for one-sample means and correlations
<code>sdi</code>	A vector of standard deviations for one-sample means
<code>m1i</code>	A vector of means in group 1 for two-independent means
<code>m2i</code>	A vector of means in group 2 for two-independent means
<code>n1i</code>	A vector of sample sizes in group 1 for two-independent means
<code>n2i</code>	A vector of sample sizes in group 2 for two-independent means
<code>sd1i</code>	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 integer 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 "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 (m_i or m_{1i} and m_{2i}), standard deviations (s_{d1} or s_{d1i} and s_{d2i}), and sample sizes (n_i or n_{1i} and n_{2i}) or t-values ($tobs$) and sample sizes (n_i or n_{1i} and n_{2i}). 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 r_i and n_i to the `puni_star` function next to input for the arguments `side`, `method`, and `alpha`.

It is also possible to specify the standardized effect sizes and its sampling variances directly via the y_i and v_i 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 y_i and v_i 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 the publication bias test and 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

<code>est</code>	p-uniform*'s effect size estimate
<code>ci.lb</code>	lower bound of p-uniform*'s 95% confidence interval of the effect size
<code>ci.ub</code>	upper bound of p-uniform*'s 95% confidence interval of the effect size
<code>L.0</code>	test statistic of p-uniform*'s test of the null hypothesis of no effect
<code>pval.0</code>	one-tailed p-value of p-uniform*'s test of null hypothesis of no effect
<code>tau2</code>	p-uniform*'s estimate of the between-study variance
<code>tau2.lb</code>	lower bound of p-uniform*'s 95% confidence interval of the between-study variance
<code>tau2.ub</code>	upper bound of p-uniform*'s 95% confidence interval of the between-study variance
<code>L.het</code>	test statistic of p-uniform*'s test of the null hypothesis of no between-study variance
<code>pval.het</code>	one-tailed p-value of p-uniform*'s test of null hypothesis of no between-study variance
<code>pval.boot</code>	one-tailed p-value of p-uniform*'s test of null hypothesis of no between-study variance obtained with a parametric bootstrap
<code>L.pb</code>	test statistic of p-uniform*'s publication bias test
<code>pval.pb</code>	one-tailed p-value of p-uniform*'s publication bias test
<code>...</code>	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:

- `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 and its default value is 0.
- `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 y_i . The lower bound is the minimum y_i minus 1 and the upper bound is the maximum y_i 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 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.
- `max.iter`: 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.
- `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. (2019). Correcting for publication bias in a meta-analysis with the p-uniform* method. Manuscript submitted for publication. Preprint: <https://osf.io/preprints/bits/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, side = "right")

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

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

<code>ri.o</code>	An integer containing the raw correlation coefficient of the original study
<code>ni.o</code>	An integer containing the sample size for the raw correlation coefficient
<code>m1i.o</code>	An integer containing the mean in group 1 of the original study for two-independent means
<code>m2i.o</code>	An integer containing the mean in group 2 of the original study for two-independent means
<code>n1i.o</code>	An integer containing the sample size in group 1 of the original study for two-independent means
<code>n2i.o</code>	An integer containing the sample size in group 2 of the original study for two-independent means
<code>sd1i.o</code>	An integer containing the standard deviation in group 1 of the original study for two-independent means
<code>sd2i.o</code>	An integer containing the standard deviation in group 2 of the original study for two-independent means

tobs.o	An integer containing the t-value of the original study
alpha	An integer specifying the alpha level as used in the original study
des.pprob	An integer specifying the posterior probability that an user desires to obtain for one of the four true effect sizes
des.pow	An integer 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	An integer specifying the lower bound of the search interval that is used for the optimization procedure (default is 4)
hi	An integer 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)

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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

<code>ri</code>	A vector of length two containing the raw correlation coefficients of the original study and replication
<code>ni</code>	A vector of length two containing the sample size of the original study and replication for the raw correlation coefficient
<code>m1i</code>	A vector of length two containing the means in group 1 for the original study and replication for two-independent means
<code>m2i</code>	A vector of length two containing the means in group 2 for the original and replication for two-independent means
<code>n1i</code>	A vector of length two containing the sample sizes in group 1 for the original study and replication for two-independent means
<code>n2i</code>	A vector of length two containing the sample sizes in group 2 for the original study and replication for two-independent means
<code>sd1i</code>	A vector of length two containing the standard deviations in group 1 for the original study and replication for two-independent means
<code>sd2i</code>	A vector of length two containing the standard deviations in group 2 for the original study and replication for two-independent means
<code>tobs</code>	A vector of length two containing the t-values of the original study and replication
<code>alpha</code>	An integer 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 (n_{1i} and n_{2i}) or t-values (t_{obs}) and sample sizes (n_{1i} and n_{2i}). Both options should be accompanied with input for the argument α . See the Example section for an example. Raw correlation coefficients can be analyzed by supplying r_i and n_i to the snapshot function next to input for the argument α .

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 ($p.\emptyset$), small ($p.sm$), medium ($p.me$), and large ($p.la$) true effect size.

Author(s)

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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	<i>snapshot_naive</i>
----------------	-----------------------

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

r_i	A vector of length two containing the raw correlation coefficients of the original study and replication
n_i	A vector of length two containing the sample size of the original study and replication for the raw correlation coefficient

<code>m1i</code>	A vector of length two containing the means in group 1 for the original study and replication for two-independent means
<code>m2i</code>	A vector of length two containing the means in group 2 for the original and replication for two-independent means
<code>n1i</code>	A vector of length two containing the sample sizes in group 1 for the original study and replication for two-independent means
<code>n2i</code>	A vector of length two containing the sample sizes in group 2 for the original study and replication for two-independent means
<code>sd1i</code>	A vector of length two containing the standard deviations in group 1 for the original study and replication for two-independent means
<code>sd2i</code>	A vector of length two containing the standard deviations in group 2 for the original study and replication for two-independent means
<code>tobs</code>	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)

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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))
```

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