

Package ‘Replicate’

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Type Package

Title Statistical Metrics for Multisite Replication Studies

Version 1.1.0

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Description For a multisite replication project, computes metrics and confidence intervals representing: (1) the probability that the original study would observe an estimated effect size as extreme or more extreme than it actually did, if in fact the original study is statistically consistent with the replications; (2) the probability of a true effect of scientifically meaningful size in the same direction as the estimate the original study; and (3) the probability of a true effect of meaningful size in the direction opposite the original study's estimate. Additionally computes older metrics used in replication projects (namely expected agreement in "statistical significance" between an original study and replication studies as well as prediction intervals for the replication estimates). See Mathur and VanderWeele (2017; <<https://osf.io/apnjk/>>) for details.

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Imports metafor, stats

RoxygenNote 6.1.1

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R topics documented:

pred_int	2
prob_signif_agree	3
p_orig	4

Index	5
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 pred_int

Compute prediction interval for replication study given original

Description

Given effect estimates and their variances for one or multiple original studies and one or more replication studies, returns a vector stating whether each replication estimate is in its corresponding prediction interval. Assumes no heterogeneity.

Usage

```
pred_int(orig.y, orig.vy, rep.y = NULL, rep.vy, level = 0.95)
```

Arguments

orig.y	Effect estimate in the original study. Can be a vector for multiple original studies.
orig.vy	Estimated variance of effect estimate in the original study (i.e., its squared standard error). Can be a vector for multiple original studies.
rep.y	Effect estimate in the replication study. Can be a vector for multiple replication studies. Can be omitted, in which case function returns only the prediction interval.
rep.vy	Estimated variance of effect estimate in the replication study (i.e., its squared standard error). Can be a vector for multiple replication studies.
level	Coverage level of prediction interval. Typically 0.95.

Examples

```
# calculate prediction interval for a single replication study
pred_int( orig.y = 1, orig.vy = .5, rep.y = 0.6,
  rep.vy = .2 )

# calculate prediction intervals for a one-to-one design
pred_int( orig.y = c(1, 1.3), orig.vy = c(.01, .6),
  rep.y = c(.6, .7), rep.vy = c(.01,.3) )

# no need to pass rep.y if you only want the intervals
pred_int( orig.y = c(1, 1.3), orig.vy = c(.01, .6),
  rep.vy = c(.01,.3) )

# calculate prediction intervals for a many-to-one design
pred_int( orig.y = c(1), orig.vy = c(.01), rep.y = c(.6, .7), rep.vy = c(.01,.3) )
```

prob_signif_agree	<i>Compute probability of "significance agreement" between replication and original study</i>
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Description

Given effect estimates and their variances for one or multiple original studies and variances for one or more replication studies, returns a vector of probabilities that the replication estimate is "statistically significant" and in the same direction as the original. Can be computed assuming no heterogeneity or allowing for heterogeneity.

Usage

```
prob_signif_agree(orig.y, orig.vy, rep.vy, t2 = 0, null = 0,
  alpha = 0.05)
```

Arguments

orig.y	Effect estimate in the original study. Can be a vector for multiple original studies.
orig.vy	Estimated variance of effect estimate in the original study (i.e., its squared standard error). Can be a vector for multiple original studies.
rep.vy	Estimated variance of effect estimate in the replication study (i.e., its squared standard error). Can be a vector for multiple replication studies.
t2	Optionally (if allowing for heterogeneity), the estimated variance of true effects across replication studies.
null	Null value for the hypothesis tests.
alpha	Alpha level for the hypothesis tests.

Examples

```
# replication estimates (Fisher's z scale) and SEs
# from moral credential example in Mathur & VanderWeele
# (in preparation)
r.fis = c(0.303, 0.078, 0.113, -0.055, 0.056, 0.073,
  0.263, 0.056, 0.002, -0.106, 0.09, 0.024, 0.069, 0.074,
  0.107, 0.01, -0.089, -0.187, 0.265, 0.076, 0.082)

r.SE = c(0.111, 0.092, 0.156, 0.106, 0.105, 0.057,
  0.091, 0.089, 0.081, 0.1, 0.093, 0.086, 0.076,
  0.094, 0.065, 0.087, 0.108, 0.114, 0.073, 0.105, 0.04)

# how many do we expect to agree?
sum( prob_signif_agree( orig.y = 0.21, orig.vy = 0.004, rep.vy = r.SE^2 ) )
```

p_orig

*Statistical consistency of original study with replication***Description**

Given the original study's effect estimate and its variance, the estimated average true effect size in the replications, and the estimated heterogeneity in the replications, computes estimated probability that the original study would have an effect estimate at least as extreme as the observed value if the original and the replications in fact are statistically consistent. Allows for heterogeneity.

Usage

```
p_orig(orig.y, orig.vy, yr, t2, vyr)
```

Arguments

orig.y	Effect estimate in the original study.
orig.vy	Estimated variance of effect estimate in the original study (i.e., its squared standard error).
yr	Estimated average true effect size in the replications.
t2	Estimated heterogeneity of true effect sizes in the replications.
vyr	Estimated variance of yr (i.e., its squared standard error).

Details

yr, vyr, and t2 can be estimated through, for example, random-effects meta-analysis or a mixed model fit to the individual subject data. See Mathur & VanderWeele (Appendix) for details of how to specify such models.

Examples

```
# replication estimates (Fisher's z scale) and SEs
# from moral credential example in Mathur and VanderWeele
# (in preparation)
r.fis = c(0.303, 0.078, 0.113, -0.055, 0.056, 0.073,
0.263, 0.056, 0.002, -0.106, 0.09, 0.024, 0.069, 0.074,
0.107, 0.01, -0.089, -0.187, 0.265, 0.076, 0.082)

r.SE = c(0.111, 0.092, 0.156, 0.106, 0.105, 0.057,
0.091, 0.089, 0.081, 0.1, 0.093, 0.086, 0.076,
0.094, 0.065, 0.087, 0.108, 0.114, 0.073, 0.105, 0.04)

# meta-analyze the replications
library(metafor)
m = rma.uni( yi = r.fis, vi = r.SE^2, measure = "ZCOR" )

p_orig( orig.y = 0.210, orig.vy = 0.062^2,
yr = m$b, t2 = m$se.tau2^2, vyr = m$vb )
```

Index

p_orig, 4
pred_int, 2
prob_signif_agree, 3