

Package ‘replicationInterval’

October 14, 2022

Type Package

Title Replication Interval Functions

Version 2.0.1

Date 2016-05-24

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Description A common problem faced by journal reviewers and authors is the question of whether the results of a replication study are consistent with the original published study. One solution to this problem is to examine the effect size from the original study and generate the range of effect sizes that could reasonably be obtained (due to random sampling) in a replication attempt (i.e., calculate a replication interval). If a replication effect size falls outside the replication interval, then that effect likely did not occur due to the effects of sampling error alone. Alternatively, if a replication effect size falls within the replication interval, then the replication effect could have reasonably occurred due to the effects of sampling error alone. This package has functions that calculate the replication interval for the correlation (i.e., r), standardized mean difference (i.e., d -value), and mean. The calculations used in version 2.0.0 and onward differ from past calculations due to feedback during the journal review process. The new calculations allow for a more precise interpretation of the replication interval.

Imports ggplot2, MBESS, MASS, stats, pbapply

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RoxygenNote 5.0.1

NeedsCompilation no

Repository CRAN

Date/Publication 2016-05-26 09:21:07

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replicationInterval-package
Replication Interval Functions

Description

A common problem faced by journal reviewers and authors is the question of whether the results of a replication study are consistent with the original published study. One solution to this problem is to examine the effect size from the original study and generate the range of effect sizes that could reasonably be obtained (due to random sampling) in a replication attempt (i.e., calculate a replication interval). If a replication effect size falls outside the replication interval, then that effect likely did not occur due to the effects of sampling error alone. Alternatively, if a replication effect size falls within the replication interval, then the replication effect could have reasonably occurred due to the effects of sampling error alone. This package has functions that calculate the replication interval for the correlation (i.e., r), standardized mean difference (i.e., d -value), and mean. The calculations used in version 2.0.0 and onward differ from past calculations due to feedback during the journal review process. The new calculations allow for a more precise interpretation of the replication interval.

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Details

[ri.r](#) creates a replication interval for a correlation (i.e., r)
[ri.d](#) creates a replication interval for a standardized mean difference (i.e., d)
[ri.m](#) creates a replication interval for a mean (i.e., M)

[ri.r.demo](#) demonstrates RI capture percentage for a correlation (i.e., r)
[ri.d.demo](#) demonstrates RI capture percentage for a standardized mean difference (i.e., d)
[ri.m.demo](#) demonstrates RI capture percentage for a mean (i.e., M)

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References

Spence, J.R. & Stanley, D.J.(in prep). Replication Interval: What to expect when you're expecting a replication.

Also:

Cumming, G. & Maillardet, R. (2006). Confidence intervals and replication: where will the next mean fall? *Psychological Methods*, 11(3), 217-227.

Estes, W.K. (1997). On the communication of information by displays of standard error and confidence intervals. *Psychonomic Bulletin & Review*, 4(3), 330-341.

Zou, G.Y. (2007). Toward using a confidence intervals to compare correlations. *Psychological Methods*, 12(4), 399-413.

Examples

```
ri.r(r=.35,n=100,rep.n=200)
ri.d(d=.65,n1=50,n2=50,rep.n1=100,rep.n2=100)
ri.m(M=2.53,SD=1.02,n=40,rep.n=80)
```

ri.d	<i>d-value (i.e., standardized mean difference) Replication Interval</i>
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Description

d-value (i.e., standardized mean difference) Replication Interval

Usage

```
ri.d(d, n1, n2, rep.n1 = NA, rep.n2 = NA, prob.level = 0.95)
```

Arguments

d	Original study: Sample <i>d</i> -value (standardized mean difference) created with pooled variance denominator. See formulas 4.18 and 4.19 (p.26) in Borenstein, Hedges, Higgins, & Rothstein (2009).
n1	Original study: Sample size for group 1
n2	Original study: Sample size for group 2

rep.n1	(optional) Replication study: Sample size for group 1. If not specified, n1 is used.
rep.n2	(optional) Replication study: Sample size for group 2. If not specified, n2 is used.
prob.level	(optional 0 to 1 value) Probability level desired (0 to 1). If not specified .95 (i.e., 95 percent) will be used.

Value

A list of values (lower.replication.interval.d, upper.replication.interval.d) containing the replication interval (and related statistics if requested with the extended.output argument).

References

Borenstein, M., Hedges, L. V., Higgins, J. P., & Rothstein, H. R. (2009). *Introduction to meta-analysis*. John Wiley & Sons.

Cumming, G., & Finch, S. (2001). A primer on the understanding, use, and calculation of confidence intervals that are based on central and noncentral distributions. *Educational and Psychological Measurement*, *61*(4), 532-574.

Examples

```
ri.d(d=.65,n1=50,n2=50,rep.n1=100,rep.n2=100)
```

ri.d.demo	<i>Simulation to demonstrate the meaning of the d-value replication interval</i>
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Description

Simulation to demonstrate the meaning of the d-value replication interval

Usage

```
ri.d.demo(n1 = 50, n2 = 50, rep.n1 = NA, rep.n2 = NA, pop.d = 0.5,
  number.trials = 10000, prob.level = 0.95, bias.correction = FALSE)
```

Arguments

n1	Original study: Cell size 1
n2	Original study: Cell size 2
rep.n1	(optional) Replication study: Cell size 1. If not specified, n is used.
rep.n2	(optional) Replication study: Cell size 2. If not specified, n is used.
pop.d	All samples are drawn from a common population. This specifies the population correlation.

number.trials	Indicate the number of pairs of sample (original, replication) that should be used. 10,000 or higher suggested for stable results.
prob.level	(optional 0 to 1 value) Probability level desired (0 to 1). If not specified .95 (i.e., 95 percent) will be used.
bias.correction	Apply bias correction formula to d-values.

Value

The replication interval and related statistics in list format.

Examples

```
ri.d.demo(n1=50,n2=50,rep.n1=100,rep.n2=100,pop.d=.50,number.trials=10)
```

ri.m	<i>Replication interval for the mean</i>
------	--

Description

Replication interval for the mean

Usage

```
ri.m(M, SD = NA, VAR = NA, n, rep.n = NA, prob.level = 0.95)
```

Arguments

M	Original study: Mean
SD	Original study: Standard deviation. Provide this or variance - not both.
VAR	Original study: Variance. Provide this or standard deviation - not both.
n	Original study: Sample size
rep.n	(optional) Replication study: Sample size. If not specified, n is used.
prob.level	(optional 0 to 1 value) Probability level desired (0 to 1). If not specified .95 (i.e., 95 percent) will be used.

Value

The replication interval and related statistics in list format.

Examples

```
ri.m(M=2.53,SD=1.02,n=40,rep.n=80)
```

ri.m.demo	<i>Simulation to demonstrate the meaning of the replication interval for the mean</i>
-----------	---

Description

Simulation to demonstrate the meaning of the replication interval for the mean

Usage

```
ri.m.demo(n = 10, rep.n = NA, mu = 0, sigma = 1,
          number.trials = 10000, prob.level = 0.95, show.all.trials = FALSE)
```

Arguments

n	Original study: Sample size
rep.n	(optional) Replication study: Sample size. If not specified, n is used.
mu	All samples are drawn from a common population. This specifies the population correlation.
sigma	All samples are drawn from a common population. This specifies the population standard deviation.
number.trials	Indicate the number of pairs of sample (original, replication) that should be used. 10,000 or higher suggested for stable results.
prob.level	(optional 0 to 1 value) Probability level desired (0 to 1). If not specified .95 (i.e., 95 percent) will be used.
show.all.trials	Show original correlation, replication interval, replication correlation, and whether replication effect is in the interval.

Value

The replication interval and related statistics in list format.

Examples

```
ri.m.demo(n=150,mu=0,sigma=1,number.trials=10)
```

ri.r	<i>Correlation replication interval</i>
------	---

Description

Correlation replication interval

Usage

```
ri.r(r, n, rep.n = NA, prob.level = 0.95)
```

Arguments

r	Original study: Correlation
n	Original study: Sample size
rep.n	(optional) Replication study: Sample size. If not specified, n is used.
prob.level	(optional 0 to 1 value) Probability level desired (0 to 1). If not specified .95 (i.e., 95 percent) will be used.

Value

The replication interval and related statistics in list format.

Examples

```
ri.r(r=.35,n=100,rep.n=200)
```

ri.r.demo	<i>Simulation to demonstrate the meaning of the correlation replication interval</i>
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Description

Simulation to demonstrate the meaning of the correlation replication interval

Usage

```
ri.r.demo(n = 100, rep.n = NA, rho = 0.5, number.trials = 10000,
  prob.level = 0.95, bias.correction = FALSE)
```

Arguments

n	Original study: Sample size
rep.n	(optional) Replication study: Sample size. If not specified, n is used.
rho	All samples are drawn from a common population. This specifies the population correlation.
number.trials	Indicate the number of pairs of sample (original, replication) that should be used. 10,000 or higher suggested for stable results.
prob.level	(optional 0 to 1 value) Probability level desired (0 to 1). If not specified .95 (i.e., 95 percent) will be used.
bias.correction	Apply bias correction formula to d-values.

Value

The replication interval and related statistics in list format.

Examples

```
ri.r.demo(n=100,rho=.50,number.trials=10)
```


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