Package ‘replicationInterval’

May 26, 2016

<table>
<thead>
<tr>
<th>Type</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>Title</td>
<td>Replication Interval Functions</td>
</tr>
<tr>
<td>Version</td>
<td>2.0.1</td>
</tr>
<tr>
<td>Date</td>
<td>2016-05-24</td>
</tr>
<tr>
<td>Author</td>
<td>David Stanley</td>
</tr>
<tr>
<td>Maintainer</td>
<td>David Stanley <a href="mailto:dstanley@uoguelph.ca">dstanley@uoguelph.ca</a></td>
</tr>
<tr>
<td>Description</td>
<td>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.</td>
</tr>
<tr>
<td>Imports</td>
<td>ggplot2, MBESS, MASS, stats, pbapply</td>
</tr>
<tr>
<td>License</td>
<td>MIT License + file LICENSE</td>
</tr>
<tr>
<td>RoxygenNote</td>
<td>5.0.1</td>
</tr>
<tr>
<td>NeedsCompilation</td>
<td>no</td>
</tr>
<tr>
<td>Repository</td>
<td>CRAN</td>
</tr>
<tr>
<td>Date/Publication</td>
<td>2016-05-26 09:21:07</td>
</tr>
</tbody>
</table>

**R topics documented:**

- replicationInterval-package ........................................ 2
- ri.d ................................................................. 3
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.

Package: replicationInterval
Type: Package
Version: 2.0.1
Date: 2016-05-24
License: MIT License + file LICENSE

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., $M$)

Author(s)
References

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

Also:


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

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 *d*-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
(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


Examples

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

Description

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

Usage

```r
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  Replication interval for the mean

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

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**

*Correlation replication interval*

**Description**

Correlation replication interval

**Usage**

```r
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**

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

---

**ri.r.demo**

*Simulation to demonstrate the meaning of the correlation replication interval*

**Description**

Simulation to demonstrate the meaning of the correlation replication interval

**Usage**

```r
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

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

*Topic **package**
  replicationInterval-package, 2

replicationInterval
  (replicationInterval-package), 2
replicationInterval-package, 2
ri.d, 2, 3
ri.d.demo, 2, 4
ri.m, 2, 5
ri.m.demo, 2, 6
ri.r, 2, 7
ri.r.demo, 2, 7