Package ‘predictionInterval’

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Type Package
Title Prediction Interval Functions for Assessing Replication Study Results
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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 prediction interval). This package has functions that calculate the prediction interval for the correlation (i.e., r), standardized mean difference (i.e., d-value), and mean.
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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 prediction interval). This package has functions that calculate the prediction interval for the correlation (i.e., r), standardized mean difference (i.e., d-value), and mean.

Details

Package: predictionInterval
Type: Package
Version: 1.0.0
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License: MIT License + file LICENSE

\texttt{pi.r} creates a prediction interval for a correlation (i.e., r)
\texttt{pi.d} creates a prediction interval for a standardized mean difference (i.e., d)
\texttt{pi.m} creates a prediction interval for a mean (i.e., M)

\texttt{pi.r.demo} demonstrates PI capture percentage for a correlation (i.e., r)
\texttt{pi.d.demo} demonstrates PI capture percentage for a standardized mean difference (i.e., d)
\texttt{pi.m.demo} demonstrates PI capture percentage for a mean (i.e., M)

Author(s)

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Also:


**Examples**

\[
\pi.d(r=.35, n=100, rep.n=200) \\
\pi.d(d=.65, n1=50, n2=50, rep.n1=100, rep.n2=100) \\
\pi.m(M=2.53, SD=1.02, n=40, rep.n=80)
\]

<table>
<thead>
<tr>
<th>pi.d</th>
<th>d-value (i.e., standardized mean difference) Prediction Interval</th>
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**Description**

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

**Usage**

\[
\pi.d(d, n1, n2, rep.n1 = NA, rep.n2 = NA, prob.level = 0.95)
\]

**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
- **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**

The prediction interval and related statistics in list format.
References


Examples

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

<table>
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<tr>
<th>Argument</th>
<th>Description</th>
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<tbody>
<tr>
<td><code>n1</code></td>
<td>Original study: Cell size 1</td>
</tr>
<tr>
<td><code>n2</code></td>
<td>Original study: Cell size 2</td>
</tr>
<tr>
<td><code>rep.n1</code></td>
<td>(optional) Replication study: Cell size 1. If not specified, n is used.</td>
</tr>
<tr>
<td><code>rep.n2</code></td>
<td>(optional) Replication study: Cell size 2. If not specified, n is used.</td>
</tr>
<tr>
<td><code>pop.d</code></td>
<td>All samples are drawn from a common population. This specifies the population correlation.</td>
</tr>
<tr>
<td><code>number.trials</code></td>
<td>Indicate the number of pairs of sample (original, replication) that should be used. 10,000 or higher suggested for stable results.</td>
</tr>
<tr>
<td><code>prob.level</code></td>
<td>(optional 0 to 1 value) Probability level desired (0 to 1). If not specified .95 (i.e., 95 percent) will be used.</td>
</tr>
<tr>
<td><code>bias.correction</code></td>
<td>Apply bias correction formula to d-values.</td>
</tr>
</tbody>
</table>

Value

The prediction interval capture percentage and related statistics in list format.

Examples

```r
pi.d.demo(n1=50,n2=50,rep.n1=100,rep.n2=100,pop.d=.50,number.trials=10)
```
**pi.m**

*Prediction interval for the mean*

**Description**

Prediction interval for the mean

**Usage**

\[ \text{pi.m}(M, SD = \text{NA}, VAR = \text{NA}, n, rep.n = \text{NA}, \text{prob.level} = 0.95) \]

**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 prediction interval and related statistics in list format.

**Examples**

\[ \text{pi.m}(M=2.53, SD=1.02, n=40, rep.n=80) \]

**pi.m.demo**

*Simulation to demonstrate the meaning of the prediction interval for the mean*

**Description**

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

**Usage**

\[ \text{pi.m.demo}(n = 10, \text{rep.n} = \text{NA}, \text{mu} = 0, \text{sigma} = 1, \text{number.trials} = 10000, \text{prob.level} = 0.95, \text{show.all.trials} = \text{FALSE}) \]
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, prediction interval, replication correlation, and whether replication effect is in the interval.

Value

The prediction interval capture percentage and related statistics in list format.

Examples

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

---

**Description**

Correlation prediction interval

**Usage**

```r
pi.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 prediction interval and related statistics in list format.
Examples

pi.r(r=.35, n=100, rep.n=200)

pi.r.demo Simulation to demonstrate the meaning of the correlation prediction interval

Description
Simulation to demonstrate the meaning of the correlation prediction interval

Usage

pi.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 prediction interval capture percentage and related statistics in list format.

Examples

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