Package ‘RProbSup’

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Title Calculates Probability of Superiority
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Description The A() function calculates the A statistic, a nonparametric measure of effect size for two independent groups that’s also known as the probability of superiority (Ruscio, 2008), along with its standard error and a confidence interval constructed using bootstrap methods (Ruscio & Mullen, 2012). Optional arguments can be specified to calculate variants of the A statistic developed for other research designs (e.g., related samples, more than two independent groups or related samples; Ruscio & Gera, 2013).
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Description

Calculates probability of superiority (A), its standard error, and a confidence interval.

Usage

\[ A(data, design = 1, statistic = 1, weights = FALSE, \]
\[ w = 0, w1 = 0, w2 = 0, increase = FALSE, ref = 1, r = 0, \]
\[ n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1) \]

Arguments

- **data**: For a between subjects design, a matrix of cases (rows) by scores (column 1) and group codes (column 2). For a within subjects design, a matrix of scores with each sample in its own column (matrix).
- **design**: Design of experiment (scalar, default = 1 (for between subjects design), user can also call 2 (for within subjects design)).
- **statistic**: Statistic to be calculated (scalar, default = 1 (A), user can also call 2 (A.AAD), 3 (A.AAPD), 4 (A.IK), or 5 (A.Ord)).
- **weights**: Whether to assign weights to cases (default = FALSE); if set to TRUE, data contains case weights in final column.
- **w**: Weights for cases (vector; default = 0).
- **w1**: Weights for cases in group 1 (vector; default = 0).
- **w2**: Weights for cases in group 2 (vector; default = 0).
increase: Set to TRUE if scores are predicted to increase with group codes (default = FALSE).
ref: Reference group (to compare to all others) (scalar, default = 1).
r: Vector of proportions (vector, default = 0, represents equal proportions).
n.bootstrap: Number of bootstrap samples (scalar, default = 1999).
conf.level: Confidence level (default = .95).
ci.method: Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile)).
seed: Random number seed (scalar, default = 1).

Value

Author(s)
John Ruscio

References

Examples
x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
data <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
A(data, 1, 2)

Description
Calculates the standard error and constructs a confidence interval for the A statistic using bootstrap methods.

Usage
A1(y1, y2, weights = FALSE, w1 = 0, w2 = 0, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)
Arguments

y1       Scores for group 1 (vector).
y2       Scores for group 2 (vector).
weights  Whether to weight cases (default = FALSE).
w1       Weights for cases in group 1 (optional) (vector, default is 0).
w2       Weights for cases in group 2 (optional) (vector, default is 0).
n.bootstrap Number of bootstrap samples (scalar, default = 1999).
conf.level Confidence level (scalar, default = .95).
ci.method Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile).
seed     Random number seed (scalar, default = 1).

Value

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

Author(s)

John Ruscio

References


Examples

# Example used in Ruscio and Mullen (2012)
y1 <- c(6, 7, 8, 7, 9, 6, 5, 4, 7, 8, 7, 6, 9, 5, 4)
y2 <- c(4, 3, 5, 3, 6, 2, 2, 1, 6, 7, 4, 3, 2, 4, 3)
A1(y1, y2)

Description

Calculates the standard error and constructs a confidence interval for the A statistic for two correlated samples using bootstrap methods.

Usage

A2(y1, y2, weights = FALSE, w = 0, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)
Arguments

- `y1` Scores for group 1 (vector).
- `y2` Scores for group 2 (vector).
- `weights` Whether to weight cases (default = FALSE).
- `w` Weights for cases in group 1 (optional) (vector, default is 0).
- `n.bootstrap` Number of bootstrap samples (scalar, default = 1999).
- `conf.level` Confidence level (scalar, default = .95).
- `ci.method` Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile).
- `seed` Random number seed (scalar, default = 1).

Value

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

Author(s)

John Ruscio

References


Examples

```r
y1 <- c(6, 7, 8, 7, 9, 6, 5, 4, 7, 8, 7, 6, 9, 5, 4)
y2 <- c(7, 5, 6, 7, 6, 4, 3, 5, 4, 5, 4, 5, 7, 4, 5)
A2(y1, y2)
```

Description

Calculates the confidence interval for the A statistic for the average absolute deviation for two or more groups.

Usage

```r
AAD1(y, r = 0, weights = FALSE, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)
```
Arguments

- **y**: Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
- **r**: Vector of proportions (default = 0, represents equal proportions) (vector).
- **weights**: Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).
- **n.bootstrap**: Number of bootstrap samples (scalar, default = 1999).
- **conf.level**: Confidence level (scalar, default = .95).
- **ci.method**: Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile)).
- **seed**: Random number seed (scalar, default = 1).

Value

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

Author(s)

John Ruscio

References


Examples

```r
x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
AAD1(y)
```

Description

Calculates the confidence interval for the A statistic for the average absolute deviation for two or more correlated samples.

Usage

```r
AAD2(y, r = 0, weights = FALSE, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)
```
Arguments

- **y**
  Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).

- **r**
  Vector of proportions (default = 0, represents equal proportions) (vector).

- **weights**
  Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).

- **n.bootstrap**
  Number of bootstrap samples (scalar, default = 1999).

- **conf.level**
  Confidence level (scalar, default = .95).

- **ci.method**
  Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile).

- **seed**
  Random number seed (scalar, default = 1).

Value

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

Author(s)

John Ruscio

References


Examples

```r
x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(x1, x2, x3)
AAD2(y)
```

Description

Calculates the confidence interval for the A statistic for the average absolute paired deviation for two or more groups.

Usage

```r
AAD1(y, weights = FALSE, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)
```
Arguments

**y**
Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).

**weights**
Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).

**n.bootstrap**
Number of bootstrap samples (scalar, default = 1999).

**conf.level**
Confidence level (scalar, default = .95).

**ci.method**
Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile).

**seed**
Random number seed (scalar, default = 1).

Value

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

Author(s)

John Ruscio

References


Examples

```r
x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
AAPD1(y)
```

Description

Calculates the confidence interval for the A statistic for the average absolute paired deviation for two or more correlated samples.

Usage

```r
AAPD2(y, weights = FALSE, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)
```
**Arguments**

- **y**
  - Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
- **weights**
  - Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).
- **n.bootstrap**
  - Number of bootstrap samples (scalar, default = 1999).
- **conf.level**
  - Confidence level (scalar, default = 0.95).
- **ci.method**
  - Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile)).
- **seed**
  - Random number seed (scalar, default = 1).

**Value**

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

**Author(s)**

John Ruscio

**References**


**Examples**

```r
x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(x1, x2, x3)
AAPD2(y)
```

---

**Description**

Calculates the A statistic for 2 groups.

**Usage**

```r
CalcA1(y1, y2, weights = FALSE, w1 = 0, w2 = 0)
```
Arguments

- **y1**: Scores for group 1 (vector).
- **y2**: Scores for group 2 (vector).
- **weights**: Whether to weight cases (default = FALSE).
- **w1**: Weights for cases in group 1 (optional) (vector, default is 0).
- **w2**: Weights for cases in group 2 (optional) (vector, default is 0).

Value

- **a**: The A statistic.

Author(s)

John Ruscio

References


Examples

#Example used in Ruscio and Mullen (2012)
y1 <- c(6, 7, 8, 7, 9, 6, 5, 4, 7, 8, 7, 6, 9, 5, 4)
y2 <- c(4, 3, 5, 3, 6, 2, 2, 1, 6, 7, 4, 3, 2, 4, 3)
CalcA1(y1, y2)
Author(s)

John Ruscio

References


Examples

\[
y_1 \leftarrow c(6, 7, 8, 7, 9, 6, 5, 4, 7, 8, 7, 6, 9, 5, 4) \\
y_2 \leftarrow c(7, 5, 6, 7, 6, 4, 3, 5, 4, 5, 4, 5, 7, 4, 5) \\
CalcA2(y_1, y_2)
\]

Description

Calculates the A statistic for the average absolute deviation for two or more groups. Note: This function is not meant to be called by the user, but it is called by AAD1.

Usage

CalcAAD1(y, r = 0, weights = FALSE)

Arguments

- **y**: Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
- **r**: Vector of proportions (default = 0, represents equal proportions) (vector).
- **weights**: Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).

Value

- **a**: The A statistic.

Author(s)

John Ruscio

References

Examples

```r
x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
CalcAAD1(y)
```

Description

Calculates the A statistic for the average absolute deviation for two or more correlated samples. 
Note: This function is not meant to be called by the user, but it is called by AAD2.

Usage

```r
CalcAAD2(y, r = 0, weights = FALSE)
```

Arguments

- **y**: Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
- **r**: Vector of proportions (default = 0, represents equal proportions) (vector).
- **weights**: Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).

Value

- **a**: The A statistic.

Author(s)

John Ruscio

References


Examples

```r
x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(x1, x2, x3)
CalcAAD2(y)
```
CalcAAPD1

Description

Calculates the A statistic for the average absolute paired deviation for two or more groups. Note: This function is not meant to be called by the user, but it is called by AAPD1.

Usage

CalcAAPD1(y, weights = FALSE)

Arguments

y Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
weights Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).

Value

a The A statistic.

Author(s)

John Ruscio

References


Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
AAPD1(y)
Description

Calculates the A statistic for the average absolute paired deviation for two or more correlated samples. Note: This function is not meant to be called by the user, but it is called by AAPD2.

Usage

CalcAAPD2(y, weights = FALSE)

Arguments

y            Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
weights      Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).

Value

a            The A statistic.

Author(s)

John Ruscio

References


Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(x1, x2, x3)
AAPD2(y)
Description

Calculates the A statistic while singling out one group for two or more groups. Note: This function is not meant to be called by the user, but it is called by IK1.

Usage

CalcIK1(y, ref = 1, weights = FALSE)

Arguments

y Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
ref Reference group (to compare to all others) (scalar, default = 1).
weights Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).

Value

a The A statistic.

Author(s)

John Ruscio

References


Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
CalcIK1(y)
Description

Calculates the A statistic while singling out one group for two or more correlated samples. Note: This function is not meant to be called by the user, but it is called by IK2.

Usage

CalcIK2(y, ref = 1, weights = FALSE)

Arguments

y Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
ref Reference group (to compare to all others) (scalar, default = 1).
weights Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).

Value

a The A statistic.

Author(s)

John Ruscio

References


Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(x1, x2, x3)
CalcIK2(y)
Description

Calculates the ordinal comparison of the A statistic for two or more groups. Note: This function is not meant to be called by the user, but it is called by AOrd1.

Usage

CalcOrd1(y, weights = FALSE, increase = FALSE)

Arguments

y Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
weights Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).
increase Set to TRUE if scores are predicted to increase with group codes (default = FALSE).

Value

a The A statistic.

Author(s)

John Ruscio

References


Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
CalcOrd1(y)
Description

Calculates the ordinal comparison of the A statistic for two or more correlated samples. Note: This function is not meant to be called by the user, but it is called by AOrd2.

Usage

CalcOrd2(y, weights = FALSE, increase = FALSE)

Arguments

y Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
weights Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).
increase Set to TRUE if scores are predicted to increase with group codes (default = FALSE).

Value

a The A statistic.

Author(s)

John Ruscio

References


Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(x1, x2, x3)
CalcOrd2(y)
Description

Calculates the confidence interval for the A statistic while singling out one group for two or more groups.

Usage

IK1(y, ref = 1, weights = FALSE, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)

Arguments

y Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
ref Reference group (to compare to all others) (scalar, default = 1).
weights Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).
n.bootstrap Number of bootstrap samples (scalar, default = 1999).
conf.level Confidence level (scalar, default = .95).
ci.method Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile).
seed Random number seed (scalar, default = 1).

Value

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

Author(s)

John Ruscio

References


Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
IK1(y)
Description

Calculates the confidence interval for the A statistic while singling out one group for two or more correlated samples.

Usage

IK2(y, ref = 1, weights = FALSE, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)

Arguments

y Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
ref Reference group (to compare to all others) (scalar, default = 1).
weights Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).
n.bootstrap Number of bootstrap samples (scalar, default = 1999).
conf.level Confidence level (scalar, default = .95).

Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(x1, x2, x3)
IK2(y)
Description

Calculates the confidence interval for the ordinal comparison of the A statistic for two or more groups.

Usage

```r
Ord1(y, weights = FALSE, increase = FALSE, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)
```

Arguments

- **y**: Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
- **weights**: Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).
- **increase**: Set to TRUE if scores are predicted to increase with group codes (default = FALSE).
- **n.bootstrap**: Number of bootstrap samples (scalar, default = 1999).
- **conf.level**: Confidence level (scalar, default = .95).
- **ci.method**: Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile).
- **seed**: Random number seed (scalar, default = 1).

Value

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

Author(s)

John Ruscio

References


Examples

```r
x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(c(x1, x2, x3), c(rep(1, 25), rep(2, 25), rep(3, 25)))
Ord1(y)
```
Description

Calculates the confidence interval for the ordinal comparison of the A statistic for two or more correlated samples.

Usage

Ord2(y, weights = FALSE, increase = FALSE, n.bootstrap = 1999, conf.level = .95, ci.method = 1, seed = 1)

Arguments

y Matrix of cases (rows) by scores (column 1) and group codes (column 2) (matrix).
weights Weight of each case. Set to TRUE to weight cases; if so, column 3 contains case weights (default = FALSE).
increase Set to TRUE if scores are predicted to increase with group codes (default = FALSE).
n.bootstrap Number of bootstrap samples (scalar, default = 1999).
c.conf.level Confidence level (scalar, default = .95).
ci.method Method used to construct confidence interval (scalar, default = 1 (for BCA), user can also call 2 (for percentile).
seed Random number seed (scalar, default = 1).

Value

A vector containing the A statistic, its estimated standard error, and the upper and lower bounds of the confidence interval.

Author(s)

John Ruscio

References


Examples

x1 <- rnorm(25)
x2 <- x1 - rnorm(25, mean = 1)
x3 <- x2 - rnorm(25, mean = 1)
y <- cbind(x1, x2, x3)
Ord2(y)
Description

Checks for missing data and performs listwise deletion if any is detected.

Usage

RemoveMissing(data)

Arguments

data  For a between subjects design, a matrix of cases (rows) by scores (column 1) and group codes (column 2). For a within subjects design, a matrix of scores with each sample in its own column (matrix).

Value

Data matrix with any missing data removed using listwise deletion of cases.

Author(s)

John Ruscio

References


Examples

x1 <- c(rnorm(25), NA)
x2 <- x1 - rnorm(26, mean = 1)
x3 <- x2 - rnorm(26, mean = 1)
data <- cbind(c(x1, x2, x3), c(rep(1, 26), rep(2, 26), rep(3, 26)))
A(data, 1, 2)
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