Package ‘boutliers’

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Description Computational tools for outlier detection and influence diagnostics of meta-analysis. Bootstrap distributions of the influence statistics are calculated, and the thresholds to determine outliers are explicitly provided.
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R topics documented:

boutliers-package .................................................. 2
finasteride ........................................................... 2
LRT ................................................................. 3
LRT_FE ............................................................ 4
PPI ................................................................. 5
SMT ............................................................... 5
STR ............................................................... 6
STR_FE .......................................................... 7
VRATIO ......................................................... 8

Index 10
Description

Computational tools for implementing outlier detection and influence diagnostics for meta-analysis. Bootstrap distributions of the influence statistics are calculated, and the thresholds to determine outliers are provided.

References


Usage

data(PPI)

Format

A data frame with 29 rows and 7 variables

Description

- center: Center ID
- n1: Number of observations in finasteride group
- m1: Mean of the change of Boyarsky score from baseline in finasteride group
- s1: SD of the change of Boyarsky score from baseline in finasteride group
- n0: Number of observations in placebo group
- m0: Mean of the change of Boyarsky score from baseline in placebo group
- s0: SD of the change of Boyarsky score from baseline in placebo group
References


LRT

Likelihood ratio test using a mean-shifted model

Description

Implementing the likelihood ratio tests using the mean-shifted model for the DerSimonian-Laird-type random-effects model. The bootstrap p-values are provided.

Usage

LRT(y, v, B=2000, alpha=0.05)

Arguments

y: A vector of the outcome measure estimates (e.g., MD, SMD, log OR, log RR, RD)
v: A vector of the variance estimate of y
B: The number of bootstrap resampling (default: 2000)
alpha: The significance level (default: 0.05)

Value

Results of the likelihood ratio tests involving bootstrap p-values. The outputs are ordered by the p-values.

• id: ID of the study.
• LR: The likelihood ratio statistic for based on the mean-shifted model.
• Q: 1-alphath percentile for the bootstrap distribution of the likelihood ratio statistic.
• P: The bootstrap p-value for the likelihood ratio statistic.

Examples

require(metafor)
data(SMT)
edat2 <- escalc(m1i=m1, sd1i=s1, n1i=n1, m2i=m2, sd2i=s2, n2i=n2, measure="MD", data=SMT)
LRT(edat2$yi, edat2$vi, B=10) # This is an example command for illustration. B should be >= 1000.
**LRT_FE**

*Likelihood ratio test using a mean-shifted model by the fixed-effect model*

### Description
Implementing the likelihood ratio tests using the mean-shifted model for the fixed-effect model. The bootstrap p-values are provided.

### Usage
```
LRT_FE(y, v, B=2000, alpha=0.05)
```

### Arguments
- **y**: A vector of the outcome measure estimates (e.g., MD, SMD, log OR, log RR, RD)
- **v**: A vector of the variance estimate of y
- **B**: The number of bootstrap resampling (default: 2000)
- **alpha**: The significance level (default: 0.05)

### Value
Results of the likelihood ratio tests involving bootstrap p-values. The outputs are ordered by the p-values.

- **id**: ID of the study.
- **LR**: The likelihood ratio statistic for based on the mean-shifted model.
- **Q**: 1-\(\alpha\)th percentile for the bootstrap distribution of the likelihood ratio statistic.
- **P**: The bootstrap p-value for the likelihood ratio statistic.

### Examples
```r
require(metafor)
data(SMT)
edat2 <- escalc(m1i=m1,sd1i=s1,n1i=n1,m2i=m2,sd2i=s2,n2i=n2,measure="MD",data=SMT)
LRT_FE(edat2$yi, edat2$vi, B=10)
# This is an example command for illustration. B should be \(\geq 1000\).
**PPI**

*Crocker et al. (2018)*’s patient and public involvement (PPI) intervention data

**Description**

- **ID**: Study ID
- **d1**: Number of events in PPI intervention group
- **n1**: Number of observations in PPI intervention group
- **d2**: Number of events in non-PPI intervention group
- **n2**: Number of observations in non-PPI intervention group

**Usage**

```r
data(PPI)
```

**Format**

A data frame with 21 rows and 5 variables

**References**


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**SMT**

*Rubinstein et al. (2019)*’s chronic low back pain data

**Description**

- **ID**: Study ID
- **Source**: First author name and year of publication
- **m1**: Estimated mean in experimental group
- **s1**: Standard deviation in experimental group
- **n1**: Number of observations in experimental group
- **m2**: Estimated mean in control group
- **s2**: Standard deviation in control group
- **n2**: Number of observations in control group

**Usage**

```r
data(SMT)
```
Format

A data frame with 23 rows and 8 variables

References


---

**STR**

*Studentized residuals by leave-one-out analysis*

---

Description

Calculating the studentized residuals by leave-one-out analysis (studentized deleted residuals) and the percentiles of their bootstrap distributions.

Usage

```r
STR(y, v, B=2000, alpha=0.95)
```

Arguments

- **y**: A vector of the outcome measure estimates (e.g., MD, SMD, log OR, log RR, RD)
- **v**: A vector of the variance estimate of `y`
- **B**: The number of bootstrap resampling (default: 2000)
- **alpha**: The bootstrap percentiles to be outputted; 0.5(1-alpha)th and (1-0.5(1-alpha))th percentiles. Default is 0.95; 2.5th and 97.5th percentiles are calculated.

Value

The studentized residuals by leave-one-out analysis. The outputs are ordered by the sizes of the studentized residuals.

- **id**: ID of the study.
- **psi**: The studentized residuals by leave-one-out analysis (studentized deleted residuals).
- **Q1**: 0.5(1-alpha)th percentile for the bootstrap distribution of the studentized residual (default: 2.5th percentile).
- **Q2**: 1-0.5(1-alpha)th percentile for the bootstrap distribution of the studentized residual (default: 97.5th percentile).
Examples

```r
require(metafor)
data(PPI)
edat1 <- escalc(ai=d1,n1i=n1,ci=d2,n2i=n2,measure="OR",data=PPI)
STR(edat1$yi,edat1$vi,B=10) # This is an example command for illustration. B should be >= 1000.
```

---

**STR_FE**

*Studentized residuals by leave-one-out analysis for the fixed-effect model*

---

**Description**

Calculating the studentized residuals by leave-one-out analysis (studentized deleted residuals) for the fixed-effect model and the percentiles of their bootstrap distributions.

**Usage**

```r
STR_FE(y, v, B=2000, alpha=0.95)
```

**Arguments**

- `y`: A vector of the outcome measure estimates (e.g., MD, SMD, log OR, log RR, RD)
- `v`: A vector of the variance estimate of `y`
- `B`: The number of bootstrap resampling (default: 2000)
- `alpha`: The bootstrap percentiles to be outputted; 0.5(1-alpha)th and (1-0.5(1-alpha))th percentiles. Default is 0.95; 2.5th and 97.5th percentiles are calculated.

**Value**

The studentized residuals by leave-one-out analysis. The outputs are ordered by the sizes of the studentized residuals.

- `id`: ID of the study.
- `psi`: The studentized residuals by leave-one-out analysis (studentized deleted residuals).
- `Q1`: 0.5(1-alpha)th percentile for the bootstrap distribution of the studentized residual (default: 2.5th percentile).
- `Q2`: 1-0.5(1-alpha)th percentile for the bootstrap distribution of the studentized residual (default: 97.5th percentile).
Examples

```r
require(metafor)
data(PPI)
edat1 <- escalc(ai=d1,n1i=n1,ci=d2,n2i=n2,measure="OR",data=PPI)
STR_FE(edat1$yi,edat1$vi)
```

---

**VRATIO**

*Variance ratio influential statistics*

Description

Calculating the variance ratio influential statistics by leave-one-out analysis and the percentiles of their bootstrap distributions.

Usage

```r
VRATIO(y, v, B=2000, alpha=0.05)
```

Arguments

- **y**: A vector of the outcome measure estimates (e.g., MD, SMD, log OR, log RR, RD)
- **v**: A vector of the variance estimate of `y`
- **B**: The number of bootstrap resampling (default: 2000)
- **alpha**: The bootstrap percentile to be outputted (default: 0.05)

Value

The variance ratio influential statistics by leave-one-out analysis and their bootstrap percentiles. The outputs are ordered by the sizes of the variance ratio statistics.

- **id**: ID of the study.
- **VR**: The VRATIO statistic (relative change of the variance of the overall estimator) by leave-one-out analysis.
- **Q1**: alpha percentile for the bootstrap distribution of the VRATIO statistic.
- **TR**: The TAU2RATIO statistic (relative change of the heterogeneity variance) by leave-one-out analysis.
- **Q2**: alpha percentile for the bootstrap distribution of the TAU2RATIO statistic.
Examples

```r
require(metafor)
data(finasteride)
edat3 <- escalc(m1i=m1, sd1i=s1, n1i=n1, m2i=m0, sd2i=s0, n2i=n0, measure="MD", data=finasteride)

VRATIO(edat3$yi, edat3$vi, B=10)
# This is an example command for illustration. B should be >= 1000.
```
Index

* datasets
  - finasteride, 2
  - PPI, 5
  - SMT, 5

boutliers-package, 2

finasteride, 2

LRT, 3
LRT_FE, 4

PPI, 5

SMT, 5

STR, 6
STR_FE, 7

VRATIO, 8