Package ‘boutliers’

November 4, 2020

Type Package
Title Outlier Detection and Influence Diagnostics for Meta-Analysis
Version 1.1-1
Date 2020-10-27
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Description A R package for implementing outlier detection and influence diagnostics for meta-analysis. Bootstrap distributions of the influence statistics are calculated, and the thresholds to determine influential outliers are provided explicitly.
Depends R (>= 3.5.0)
Imports stats, metafor
License GPL-3
Encoding UTF-8
LazyData true
RoxygenNote 7.1.1
NeedsCompilation no
Repository CRAN
Date/Publication 2020-11-04 12:10:06 UTC

R topics documented:

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\textbf{boutliers-package} \hspace{1cm} \textit{The 'boutliers' package.}

\textbf{Description}

A R package for implementing outlier detection and influence diagnostics for meta-analysis. Bootstrap distributions of the influence statistics are calculated, and the thresholds to determine influential outliers are provided explicitly.

\textbf{References}


\textbf{convert_bin} \hspace{1cm} \textit{Converting binary data to summary statistics}

\textbf{Description}

Converting binary outcome data to the effect size estimates and the within studies variances vector

\textbf{Usage}

\begin{verbatim}
convert_bin(m1, n1, m2, n2, type = c("logOR", "logRR", "RD"))
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
\item \textbf{m1}: A vector of the number of successes in experimental group
\item \textbf{n1}: A vector of the number of patients in experimental group
\item \textbf{m2}: A vector of the number of successes in control group
\item \textbf{n2}: A vector of the number of patients in control group
\item \textbf{type}: the outcome measure for binary outcome data (default = "logOR").
\end{itemize}

- \textit{logOR}: logarithmic odds ratio, which is defined by $\log \left( \frac{(m_1+0.5)(n_2-m_2+0.5)}{(n_1-m_1+0.5)(m_2+0.5)} \right)$.
- \textit{logRR}: logarithmic relative risk, which is defined by $\log \left( \frac{m_1+0.5}{n_1+0.5} \cdot \frac{n_2+0.5}{m_2+0.5} \right)$.
- \textit{RD}: risk difference, which is defined by $\frac{m_1}{n_1} - \frac{m_2}{n_2}$.
**Details**

This function implements methods for logarithmic odds ratio, logarithmic relative risk, and risk difference described in Hartung & Knapp (2001).

**Value**

A data.frame of study data.

- **y**: A numeric vector of the effect size estimates.
- **v**: A numeric vector of the within studies variances.

**References**


**Examples**

```r
data(PPI)
attach(PPI)

dat1 <- convert_bin(d1, n1, d2, n2, type = "logOR")
print(dat1)

dat2 <- convert_bin(d1, n1, d2, n2, type = "logRR")
print(dat2)

dat3 <- convert_bin(d1, n1, d2, n2, type = "RD")
print(dat3)
```

---

**convert_mean**  
*Converting means and standard deviations to summary statistics*

**Description**

Converting estimated means and standard deviations in experimental and control groups to the effect size estimates and the within studies variances vector

**Usage**

```r
convert_mean(n1, m1, s1, n2, m2, s2, pooled = FALSE, type=c("MD", "SMD"))
```
Arguments

- `n1`: A vector of number of observations in experimental group
- `m1`: A vector of estimated mean in experimental group
- `s1`: A vector of standard deviation in experimental group
- `n2`: A vector of number of observations in experimental group
- `m2`: A vector of estimated mean in experimental group
- `s2`: A vector of standard deviation in experimental group

- `type`: the outcome measure for continuous outcome data (default = "MD").
  - MD: Mean difference.
  - SMD: Standardized mean difference.

- `pooled`: logical; if TRUE, a pooled variance is used. The default is FALSE.

Value

A data.frame of study data.

- `y`: A numeric vector of the effect size estimates.
- `v`: A numeric vector of the within studies variance estimates.

Examples

```r
data(SMT)
attach(SMT)

dat1 <- convert_mean(n1, m1, s1, n2, m2, s2, type="MD")
print(dat1)

dat2 <- convert_mean(n1, m1, s1, n2, m2, s2, type="SMD")
print(dat2)
```

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
Usage
data(PPI)

Format
A data frame with 29 rows and 7 variables

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>A vector of the outcome measure estimates (e.g., MD, SMD, log OR, log RR, RD)</td>
</tr>
<tr>
<td>v</td>
<td>A vector of the variance estimate of y</td>
</tr>
<tr>
<td>B</td>
<td>The number of bootstrap resampling (default: 2000)</td>
</tr>
<tr>
<td>alpha</td>
<td>The significance level (default: 0.05)</td>
</tr>
</tbody>
</table>

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 percentile for the bootstrap distribution of the likelihood ratio statistic.
- P: The bootstrap p-value for the likelihood ratio statistic.
Examples

```r
data(SMT)
attach(SMT)

dat <- convert_mean(n1, m1, s1, n2, m2, s2, type="MD")

LRT(dat$y, dat$v, B=100)
# For quick demonstration, B is set to 100.
# Practically, B should be set to >= 1000 (default is 2000).

detach(SMT)
```

---

**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

```r
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 percentile for the bootstrap distribution of the likelihood ratio statistic.
- `P`: The bootstrap p-value for the likelihood ratio statistic.
**Examples**

```r
data(SMT)
attach(SMT)

dat <- convert_mean(n1, m1, s1, n2, m2, s2, type="MD")

LRT_FE(dat$y, dat$v, B=100)
# For quick demonstration, B is set to 100.
# Practically, B should be set to >= 1000 (default is 2000).

detach(SMT)
```

---

**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**

**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
data(PPI)
attach(PPI)

dat <- convert_bin(d1, n1, d2, n2, type = "logOR")
print(dat)

STR(dat$y, dat$v, B=100)
# For quick demonstration, B is set to 100.
# Practically, B should be set to >= 1000 (default is 2000).

detach(PPI)
```

---

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
data(PPI)
attach(PPI)

dat <- convert_bin(d1, n1, d2, n2, type = "logOR")
print(dat)

STR_FE(dat$y, dat$v, B=100)
# For quick demonstration, B is set to 100.
# Practically, B should be set to >= 1000 (default is 2000).

detach(PPI)
```

**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**

`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
data(finasteride)
attach(finasteride)

dat <- convert_mean(n1, m1, s1, n0, m0, s0, type="MD")
print(dat)

VRATIO(dat$y, dat$v, B=100)
# For quick demonstration, B is set to 100.
# Practically, B should be set to >= 1000 (default is 2000).

detach(finasteride)
```
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