Package 'boutliers'

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Title Outlier Detection and Influence Diagnostics for Meta-Analysis

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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.

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boutliers-package   *The 'boutliers' package.*

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.

References

Hedges, L. V., and Olkins, I. (1985). *Statistical Methods for Meta-Analysis.* New York: Academic Press.

Noma, H., Gosho, M., Ishii, R., Oba, K., and Furukawa, T. A. (2020+). Outlier detection and influence diagnostics in network meta-analysis. *Research Synthesis Methods.* https://doi.org/10.1002/jrsm.1455

Viechtbauer, W., and Cheung, M. W. (2010). Outlier and influence diagnostics for meta-analysis. *Research Synthesis Methods.* **1**(2): 112-125. https://doi.org/10.1002/jrsm.11

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convert_bin   *Converting binary data to summary statistics*

Description

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

Usage

```
convert_bin(m1, n1, m2, n2, type = c("logOR", "logRR", "RD"))
```

Arguments

m1	A vector of the number of successes in experimental group
n1	A vector of the number of patients in experimental group
m2	A vector of the number of successes in contorol group
n2	A vector of the number of patients in contorol group
type	the outcome measure for binary outcome data (default = "logOR").

- logOR: logarithmic odds ratio, which is defined by $= \log \frac{(m1+0.5)(n2-m2+0.5)}{(n1-m1+0.5)(m2+0.5)}$.
- logRR: logarithmic relative risk, which is defined by $= \log \frac{(m1+0.5)(n2+0.5)}{(n1+0.5)(m2+0.5)}$.
- RD: risk difference, which is defined by $= \frac{m1}{n1} - \frac{m2}{n2}$.

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

Hartung, J., and Knapp, G. (2001). A refined method for the meta-analysis of controlled clinical trials with binary outcome. *Stat Med.* **20**(24): 3875-3889. <https://doi.org/10.1002/sim.1009>

Examples

```
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)
```

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convert_mean	*Converting means and standard deviations to summary statistics*

Description

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

Usage

```
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 continous 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

```
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)
```

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finasteride	*A multicenter clinical trial data assessing the treatment effect of finasteride for benign prostatic hyperplasia*

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

Gormley, G. J., Stoner, E., Bruskewitz, R. C., et al. (1992). The effect of finasteride in men with benign prostatic hyperplasia. The Finasteride Study Group. *New England Journal of Medicine.* **327**: 1185-1191. https://www.nejm.org/doi/full/10.1056/NEJM199210223271701

Gould, A. L. (1998). Multi-centre trial analysis revisited. *Statistics in Medicine.* **17**: 1779-1797.

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 (defalt: 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

```
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

```
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 (defalt: 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

```
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

```
data(PPI)
```

Format

A data frame with 21 rows and 5 variables

References

Crocker, J. C., Ricci-Cabello, I., Parker, A., Hirst, J. A., Chant, A., Petit-Zeman, S., Evans, D., Rees, S. (2018). Impact of patient and public involvement on enrolment and retention in clinical trials: systematic review and meta-analysis. *BMJ*. **363**: k4738. https://doi.org/10.1136/bmj.k4738

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

Description

- `ID`: Study ID
- `Souce`: 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

```
data(SMT)
```

Format

A data frame with 23 rows and 8 variables

References

Rubinstein, S. M,, de Zoete, A., van Middelkoop, M., Assendelft, W. J. J., de Boer, M. R., van Tulder, M. W. (2019). Benefits and harms of spinal manipulative therapy for the treatment of chronic low back pain: systematic review and meta-analysis of randomised controlled trials. *BMJ*. **364**: l689. https://doi.org/10.1136/bmj.l689

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

```
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 (defalt: 2000)
alpha	The bootstrap percentiles to be outputted; 0.5(1-alpha)th and (1-0.5(1-alpha))th pecentiles. 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

```
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

```
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 (defalt: 2000)
alpha	The bootstrap percentiles to be outputted; 0.5(1-alpha)th and (1-0.5(1-alpha))th pecentiles. 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

```
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 (defalt: 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: alphath 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: alphath percentile for the bootstrap distribution of the TAU2RATIO statistic.

Examples

```
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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