Package ‘metarep’

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Title Replicability-Analysis Tools for Meta-Analysis

Version 1.0.1

Depends R (>= 3.5)

Imports meta (>= 4.9.10),

Suggests metafor (>= 1.9.9), lme4, numDeriv, BiasedUrn, knitr, markdown

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URL https://github.com/IJaljuli/metarep

Description User-friendly package for reporting replicability-analysis methods, affixed to meta-analyses summary. The replicability-analysis output provides an assessment of the investigated intervention, where it offers quantification of effect replicability and assessment of the consistency of findings.
- Replicability-analysis for fixed-effects and random-effect meta analysis:
  - $r(u)$-value;
  - lower bounds on the number of studies with replicated positive and/or negative effect;
  - Allows detecting inconsistency of signals;
  - forest plots with the summary of replicability analysis results;
  - Allows Replicability-analysis with or without the common-effect assumption.

License GPL (>= 2)

NeedsCompilation yes

RoxygenNote 7.0.2

VignetteBuilder knitr

LazyData true

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A dataset containing the meta-data of the the intervention 'Invitation letter' (CMP001), in the review "PStrategies for increasing the participation of women in community breast cancer screening" (CD002943) the results were reported by 5 studies, and analysed by Fixed-Effects meta-analysis.

Format

A data frame with 5 rows of 12 variables:

- **STUDY** Name of the study.
- **STUDY_WEIGHT** Study weight in meta-analysis as reported in the review.
- **N_EVENTS1** Number of events in the first group tested.
- **N_EVENTS2** Number of events in the second group tested.
- **N_TOTAL1** Number of patients in the first group tested.
- **N_TOTAL2** Number of patients in the second group tested.
- **GROUP1** Names of the first group in each study.
- **GROUP2** Names of the second group in each study.
- **N_STUDIES** Overall number of studies in the meta-analysis
- **CMP_ID** Cochrane Database review number
- **SM** A character string indicating which summary measure ("RR", "OR", "RD", or "ASD") is to be used for pooling of studies.
- **RANDOM** "YES" or "NO" indicating whether random-effects meta-analysis was performed.
CD003366_CMP005

Source

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**CD003366_CMP005**

*Data in meta-analysis reported in review CD003366, ‘Cochrane library’.*

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**Description**

A dataset containing the meta-data of the outcome 'Leukopaenia' (CMP005), in the review ”Texane-containing regimins for metastatic breast cancer" (CD003366) the results were reported by 28 studies, and analysed by Random-Effects meta-analysis.

**Usage**

CD003366_CMP005

**Format**

A data frame with 28 rows and 12 variables:

- **STUDY** Name of the study.
- **STUDY_WEIGHT** Study weight in meta-analysis as reported in the review.
- **N_EVENTS1** Number of events in the first group tested.
- **N_EVENTS2** Number of events in the second group tested.
- **N_TOTAL1** Number of patients in the first group tested.
- **N_TOTAL2** Number of patients in the second group tested.
- **GROUP1** Names of the first group in each study.
- **GROUP2** Names of the second group in each study.
- **N_STUDIES** Overall number of studies in the meta-analysis.
- **CMP_ID** Cochrane Database review number.
- **SM** A character string indicating which summary measure ("RR", "OR", "RD", or "ASD") is to be used for pooling of studies.
- **RANDOM** "YES" or "NO" indicating whether random-effects meta-analysis was performed.

Source
Data in meta-analysis reported in review CD006823, 'Cochrane library'.

Description

A dataset containing the meta-data of the outcome 'Seroma formation' (CMP001), in the review "Wound drainage after axillary dissection for carcinoma of the breast" (CD006823) the results were reported by 7 studies, and analysed by Random-Effects meta-analysis.

Usage

CD006823_CMP001

Format

A data frame with 7 rows and 12 variables:

STUDY  Name of the study.
STUDY_WEIGHT  Study weight in meta-analysis as reported in the review.
N_EVENTS1  Number of events in the first group tested.
N_EVENTS2  Number of events in the second group tested.
N_TOTAL1  Number of patients in the first group tested.
N_TOTAL2  Number of patients in the second group tested.
GROUP1  Names of the first group in each study.
GROUP2  Names of the second group in each study.
N_STUDIES  Overall number of studies in the meta-analysis
CMP_ID  Cochrane Database review number
SM  A character string indicating which summary measure ("RR", "OR", "RD", or "ASD") is to be used for pooling of studies.
RANDOM  "YES" or "NO" indicating whether random-effects meta-analysis was performed.

Source

Description

A dataset containing the meta-data of the outcome ‘cosmesis’ (CMP001), in the review "Partial breast irradiation for early breast cancer" (CD007077) the results were reported by 5 studies, and analysed by Fixed-Effects meta-analysis.

Usage

CD007077_CMP001

Format

A data frame with 5 rows and 12 variables:

- **STUDY**  Name of the study.
- **STUDY_WEIGHT**  Study weight in meta-analysis as reported in th review.
- **N_EVENTS1**  Number of events in the first group tested.
- **N_EVENTS2**  Number of events in the second group tested.
- **N_TOTAL1**  Number of patients in the first group tested.
- **N_TOTAL2**  Number of patients in the second group tested.
- **GROUP1**  Names of the first group in each study.
- **GROUP2**  Names of the second group in each study.
- **N_STUDIES**  Overall number of studies in the meta-analysis
- **CMP_ID**  Cochrane Database review number
- **SM**  A character string indicating which summary measure ("RR", "OR", "RD", or "ASD") is to be used for pooling of studies.
- **RANDOM**  "YES" or "NO" indicating whether random-effects meta-analysis was performed.

Source

find umax

Lower bounds on the number of studies with replicated effect

Description

lower bounds on the number of studies with increased and/or decreased effect.

Usage

find_umax(
  x,
  alternative = "two-sided",
  t = 0.05,
  confidence = 0.95,
  common.effect = FALSE
)

Arguments

x: Object of class 'meta'
alternative: ’less’, ’greater’ or ’two-sided’
t: truncation threshold for truncated-Pearson’s test (’t=0.05’ by default). t is ignored if ’common.effect = TRUE’.
confidence: Confidence level used in the computation of the lower bound(s) $u_{max}^L$ and/or $u_{max}^R$.
common.effect: Use common.effect = FALSE (default) for replicability-analysis combining with no assumptions (Pearson or truncated-Pearson test).

Value

An object of class list reporting the bounds on the number of studies with a positive or negative effect, as follows:

- worst.case: A character vector of the names of $n-u_{\max}+1$ studies at which the $r(u_{\max})$-value is computed.
- side: The direction of the replicated signal in the ‘worst.case’ studies. ’less’ if the effect is negative, ’greater’ if positive.
- u_max: The bound on the number of studies with either a positive or a negative effect.
- r-value: The ‘u-out-of-n’ $r(u)$-value calculated with $u=u_{\max}$.
- Replicability_Analysis: Report of the replicability lower bounds on the number of studies with negative effect and with positive effect.
Examples

```r
n.i.1 <- c(20, 208, 24, 190, 58, 36, 51)
a.i <- c(2,79,0,98,15,34,9)
n.i.2 <- c(20, 119, 22, 185, 29, 51, 47)
c.i <- c(9,106,14,98,12,49,9)
ml <- meta::metabin( event.e = a.i,n.e = n.i.1,
        event.c = c.i,n.c = n.i.2,
        studlab = paste('Study',1:7), sm = 'OR',
        comb.fixed = FALSE, comb.random = TRUE )
find_umax(ml , common.effect = FALSE, alternative = 'two-sided',
        t = 0.05 , confidence = 0.95 )
```

Description

Draws a forest plot in the active graphics window (using grid graphics system).

Usage

```r
forest(x, ...)
```

Arguments

- `x` An object of class `metarep`.
- `...` Arguments to be passed to methods, see `forest.meta`.

Value

No return value, called for side effects.

See Also

`forest.meta`, `metarep`.

Examples

```r
n.i.1 <- c( 20, 208, 24, 190, 58, 36, 51)
a.i <- c( 2,79,0,98,15,34,9)
n.i.2 <- c( 20, 119, 22, 185, 29, 51, 47)
c.i <- c(9,106,14,98,12,49,9)
ml <- meta::metabin( event.e = a.i,n.e = n.i.1,
        event.c = c.i,n.c = n.i.2,
        studlab = paste('Study',1:7), sm = 'OR',
        comb.fixed = FALSE, comb.random = TRUE )
mr1 <- metarep( ml , u = 2, common.effect = FALSE , t = 0.05 ,
        alternative = 'two-sided', report.u.max = TRUE)
forest(mr1, layout = "RevMan5", comb.fixed = FALSE,
```
metarep

Replicability-analysis of a meta-analysis

Description

Add results of replicability-analysis to a meta-analysis, whether fixed- or random-effects.

Usage

metarep(
  x,
  u = 2,
  t = 0.05,
  alternative = "two-sided",
  report.u.max = FALSE,
  confidence = 0.95,
  common.effect = FALSE
)

Arguments

x object of class 'meta'

u replicability requirement. u must be an integer between 2 and \( n \) (number of studies in the meta-analysis).

t truncation threshold for truncated-Pearson's test ('t=0.05' by default). t is ignored if 'common.effect = TRUE'.

alternative use 'less', 'greater' or 'two-sided'

report.u.max use TREU to report the lower bounds on number of studies with replicated effect.

confidence Confidence level used in the computation of the lower bound(s) \( u_{max} \) and/or \( u_{R_{max}} \).

common.effect Use common.effect = FALSE (default) for replicability-analysis combining with no assumptions (Pearson or truncated-Pearson test). Replicability-analysis based on the test-statistic of fixed-effects model can be applied using common.effect = TRUE.
Value

An object of class list containing meta-analysis and replicability analysis results, as follows:

- **worst.case.studies** A character vector of the names of $n-u+1$ studies at which the the $r(u)$-value is computed.
- **r.value** $r(u)$-value for the specified $u$.
- **side** The direction of the effect with the lower one-sided $r(u)$-value
- **u_L, u_R** Lower bounds of the number of studies with decreased or increased effect, respectively. Both bounds are reported simultaneously only when performing replicability analysis for two-sided alternative with no assumptions.

Examples

```r
n.i.1 <- c(20, 208, 24, 190, 58, 36, 51)
a.i <- c(2, 79, 0, 98, 15, 34, 9)
n.i.2 <- c(20, 119, 22, 185, 29, 51, 47)
c.i <- c(9, 106, 14, 98, 12, 49, 9)
ml <- meta::metabin(event.e = a.i, n.e = n.i.1, event.c = c.i, n.c = n.i.2,
  studlab = paste0('Study ', 1:7), sm = 'OR',
  comb.fixed = FALSE, comb.random = TRUE)
mr1 <- metarep(ml, u = 2, common.effect = FALSE, t = 0.05,
  alternative = 'two-sided', report.u.max = TRUE)
meta::forest(mr1, layout='revman5',digits.pval = 4, test.overall = TRUE)
```

metaRvalue.onesided.U  One-sided replicability analysis

Description

One-sided replicability analysis

Usage

```r
metaRvalue.onesided.U(
  x,
  u = 2,
  comb.fixed = F,
  comb.random = T,
  alternative = "less",
  do.truncated.umax = T,
  alpha.tilde = 0.05
)
```
print.summary.metarep

Arguments

x
object of class 'meta'

u
integer between 2-n
comb.fixed
logical
comb.random
logical
alternative
'less' or 'greater' only.
do.truncated.umax
logical.
alpha.tilde
between (0,1)

Value

No return value, called for internal use only.

print.summary.metarep  Print meta-analysis with replicability-analysis results

Description

Print method for objects of class 'metarep'.

Usage

## S3 method for class 'summary.metarep'
print(x, ...)

Arguments

x
An object of class 'metarep'

...  Arguments to be passed to methods, see print.summary.meta

Value

No return value, called for side effects.

Examples

n.i.1 <- c( 20, 208, 24, 190, 58, 36, 51)
a.i <- c( 2,79,0,98,15,34,9)
n.i.2 <- c( 20, 119, 22, 185, 29, 51, 47)
c.i <- c(9,106,14,98,12,49,9)
m1 <- meta::metabin( event.e = a.i,n.e = n.i.1,event.c = c.i,n.c = n.i.2, studlab = paste0('Study ', 1:7) , sm = 'OR', comb.fixed = FALSE, comb.random = TRUE )

mr1 <- metarep( m1 , u = 2, common.effect = FALSE , t = 0.05 , alternative = 'two-sided', report.u.max = TRUE)

print(mr1, digits = 2)
Description

Summary method for objects of class 'metarep'.

Usage

```r
## S3 method for class 'metarep'
summary(object, ...)
```

Arguments

- `object`: An object of class 'metarep'.
- `...`: Arguments to be passed to methods, see `summary.meta`

Value

A list of the quantities for replicability analysis, as follows:

- meta-analysis results: Summary of the supplied 'meta' object.
- `r.value`: r-value of the tested alternative.
- `u.increased`: Maximal number of studies at which replicability of increasing effect can be claimed. It will be reported unless the alternative is 'less'.
- `u.decreased`: Maximal number of studies at which replicability of increasing effect can be claimed. It will be reported unless the alternative is 'greater'.

Examples

```r
n.i.1 <- c( 20, 208, 24, 190, 58, 36, 51)
a.i  <- c( 2,79,0,98,15,34,9)
n.i.2 <- c( 20, 119, 22, 185, 29, 51, 47)
c.i  <- c(9,106,14,98,12,49,9)
m1 <- meta::metabin( event.e = a.i,n.e = n.i.1,event.c = c.i,n.c = n.i.2,
    studlab = paste0('Study ', 1:7) , sm = 'OR',
    comb.fixed = FALSE, comb.random = TRUE )
mr1 <- metarep(  m1 , u = 2, common.effect = FALSE , t = 0.05 ,
    alternative = 'two-sided', report.u.max = TRUE)
summary(mr1)
```
Description

Apply Truncated-Pearsons’ test or ordinary Pearsons’ test on one-sided p-values.

Usage

\[ \text{truncatedPearson}(p, \alpha_{\tilde{}} = 1) \]

Arguments

- \( p \): one-sided p-values of the individual studies for testing one-sided alternative based on z-test.
- \( \alpha_{\tilde{}} \): truncation threshold for truncated-Pearson test. Use \( \alpha_{\tilde{}} = 1 \) for ordinary Pearsons’ test for combining p-values.

Value

A ‘list’ containing the following quantities:
- \( \text{chisq} \): Pearson test statistic
- \( \text{df} \): degrees of freedom of truncated-Pearson statistic
- \( rvalue \): p-value of the test
- \( \text{validp} \): p-values used in the test.

Examples

\[
\text{truncatedPearson(} p = c( 0.001, 0.01, 0.1 ) , \alpha_{\tilde{}} = 1 \text{)} \\
\text{truncatedPearson(} p = c( 0.001, 0.01, 0.1 ) , \alpha_{\tilde{}} = 0.05 \text{)}
\]
Index

*Topic datasets
    CD002943_CMP001, 2
    CD003366_CMP005, 3
    CD006823_CMP001, 4
    CD007077_CMP001, 5

    find_umax, 6
    forest, 7
    forest.meta, 7

    metarep, 7, 8
    metaRvalue.onesided.U, 9

    print.summary.metarep, 10
    summary.metarep, 11

    truncatedPearson, 12