Package ‘metarep’

October 13, 2022

Title Replicability-Analysis Tools for Meta-Analysis
Version 1.1
Depends R (>= 4.1)
Imports meta (>= 4.9.10),
Suggests metafor (>= 1.9.9), lme4, numDeriv, BiasedUrn, knitr, rmarkdown
Date 2022-03-10

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

Description User-friendly package for reporting replicability-analysis methods, affixed to meta-analyses summary. This package implements the methods introduced in Jaljuli et. al. (2022) <doi:10.1080/19466315.2022.2050291>. 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)
Encoding UTF-8
NeedsCompilation yes
RoxygenNote 7.0.2
VignetteBuilder knitr
LazyData true

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Repository CRAN
Date/Publication 2022-03-14 08:30:02 UTC
Data in meta-analysis reported in review CD002943, 'Cochrane library'.

Description
A dataset containing the meta-data of 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.

Usage
CD002943_CMP001

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 participants in the first group tested.
- **N_TOTAL2** Number of participants 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


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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 regimes 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

CD006823_CMP001

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 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

Descirption

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-Pearsons' 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) \( u_{max} \) 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

```
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 = paste('Study',1:7), sm = 'OR',
                   comb.fixed = FALSE, comb.random = TRUE )
find_umax(m1 , 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

```
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

```
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 = paste('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)
forest(mr1, layout = "RevMan5", comb.fixed = FALSE,
```

---

**Forest plot to display the result of a meta-analysis with replicability analysis results**
metarep

Replicability-analysis of a meta-analysis

Description

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

Usage

```r
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-Pearsons' 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) $u_{\text{max}}^L$ and/or $u_{\text{max}}^R$.
- **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 \( r(u) \)-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)
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)
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

```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)print(mr1, digits = 2)
```
Summary of meta-analysis with replicability-analysis results

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

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  
truncartion threshold for truncated-Pearson test. Use alpha.tilde = 1 for ordinary Pearsons’ test for combining p-values.

Value

A 'list' containing the following quantities:

A list containing results of truncated-Pearson’s test, as follows:

• chisq: Pearson test statistic
• df: degrees of freedom of truncated-Pearson statistic
• rvalue: p-value of the test
• validp: p-values used in the test.

Examples

truncatedPearson( p = c( 0.001 , 0.01 , 0.1 ) , alpha.tilde = 1 )
truncatedPearson( p = c( 0.001 , 0.01 , 0.1 ) , alpha.tilde = 0.05 )
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