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

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R topics documented:

`CD002943_CMP001` *Data in meta-analysis reported in review CD002943, 'Cochrane library'.*

Description

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.

Usage

```
CD002943_CMP001
```

Format

A data frame with 5 rows of 12 variables:

STUDY Name of the study.

STUDY_WEIGHT Stydy 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 patirnts in the first group tested.

N_TOTAL2 Number of patirnts 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

https://www.cochranelibrary.com/cdsr/doi/10.1002/14651858.CD002943/full

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`CD003366_CMP005` *Data in meta-analysis reported in review CD003366, 'Cochrane library'.*

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 Stydy 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 patirnts in the first group tested.

N_TOTAL2 Number of patirnts 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

https://www.cochranelibrary.com/cdsr/doi/10.1002/14651858.CD003366.pub3/full

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`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 Stydy 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 patirnts in the first group tested.

N_TOTAL2 Number of patirnts 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

`https://www.cochranelibrary.com/cdsr/doi/10.1002/14651858.CD006823.pub2/full`

`CD007077_CMP001` *Data in meta-analysis reported in review CD007077, 'Cochrane library'.*

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 Stydy 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 patirnts in the first group tested.

N_TOTAL2 Number of patirnts 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

`https://www.cochranelibrary.com/cdsr/doi/10.1002/14651858.CD007077.pub3/full`

`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-Pearsons' test ('t=0.05' by default). t is ignored if 'common.effect = TRUE'.
`confidence`	Confidence level used in the computaion of the lower bound(s) u^L_{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).

Value

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

- worst.caseA charachter vector of the names of `n-u_{max}+1` studies at which the the `r(u_{max})`-value is computed.
- sideThe direction of the replicated signal in the 'worst.case' studies. 'less' if the effect is negative, 'greater' if positive.
- u_maxThe bound on the number of studies with either a positive or a negative effect.
- r-valueThe 'u-out-of-n' `r(u)`-value calculated with u=u_max.
- Replicability_AnalysisReport 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 )
```

`forest` *Forest plot to display the result of a meta-analysis with replicability analysis resuls*

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

```
        label.right = "Favours control", col.label.right = "red",
        label.left = "Favours experimental", col.label.left = "green",
        prediction = TRUE)
```

`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 intiger between 2 and `n` (nmber 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 computaion of the lower bound(s) u^L_{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.studiesA charachter 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 specied u.
- sideThe 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 simultinualsly only when performing replicability analysis for two-sided alternative with no assumptions

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)
meta::forest(mr1, layout='revman5',digits.pval = 4 , test.overall = TRUE )
```

`metaRvalue.onesided.U` *One-sided replicability analysis*

Description

One-sided replicability analysis

Usage

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

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)
```

`summary.metarep` *Summary of meta-analysis with replicability-analysis results*

Description

Summary method for objects of class ’metarep’.

Usage

```
## 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

```
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)
```

`truncatedPearson` *Truncated-Pearsons' test*

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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