

# Package ‘metarep’

July 22, 2025

**Title** Replicability-Analysis Tools for Meta-Analysis

**Version** 1.2.0

**Depends** R (>= 4.1), meta (>= 6.0-0)

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

**Date** 2023-12-15

**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)

**Encoding** UTF-8

**NeedsCompilation** yes

**RoxygenNote** 7.2.3

**VignetteBuilder** knitr

**LazyData** true

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**Repository** CRAN

**Date/Publication** 2023-12-15 18:20:02 UTC

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CD002943_CMP001	<i>Data in meta-analysis reported in review CD002943, 'Cochrane library'.</i>
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## 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** 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 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	<i>Data in meta-analysis reported in review CD003366, 'Cochrane library'.</i>
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**Description**

A dataset containing the meta-data of the outcome 'Leukopaenia' (CMP005), in the review "Taxane-containing regimens 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**

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

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CD006823_CMP001	<i>Data in meta-analysis reported in review CD006823, 'Cochrane library'.</i>
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## 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

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

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CD007077_CMP001	<i>Data in meta-analysis reported in review CD007077, 'Cochrane library'.</i>
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## 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

<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) $u_{max}^L$ 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 charachter vector of the names of $n-u_{\{max\}}+1$ studies at which the 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 <- 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',
               common = FALSE, random = TRUE )
find_umax(m1 , common.effect = FALSE, alternative = 'two-sided',
          t = 0.05 , confidence = 0.95 )

```

---

forest.metarep	<i>Forest plot to display the result of a meta-analysis with replicability analysis results</i>
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---

**Description**

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

**Usage**

```

## S3 method for class 'metarep'
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 <- 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' ,
               common = FALSE, random = TRUE )
mr1 <- metarep( m1 , u = 2, common.effect = FALSE , t = 0.05 ,

```

```

        alternative = 'two-sided', report.u.max = TRUE)
forest(mr1, layout = "RevMan5", common = 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 common- 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-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) $u_{max}^L$ and/or $u_{max}^R$ .
common.effect	Use common.effect = FALSE (default) for replicability-analysis combining with no assumptions (Pearson or truncated-Pearson test). Replicability-analysis based on the test-statistic of common-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**

```
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 <- 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' ,
               common = FALSE, random = TRUE )
mr1 <- metarep( m1 , u = 2, common.effect = FALSE , t = 0.05 ,
               alternative = 'two-sided', report.u.max = TRUE)
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,
  common = FALSE,
  random = TRUE,
  alternative = "less",
  do.truncated.umax = TRUE,
  alpha.tilde = 0.05
)
```

**Arguments**

x	object of class 'meta'
u	integer between 2-n
common	logical
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.metarep	<i>Print meta-analysis with replicability-analysis results</i>
---------------	--

---

**Description**

Print method for objects of class 'metarep'.

**Usage**

```
## S3 method for class 'metarep'
print(x, details.methods = TRUE, ...)
```

**Arguments**

x	An object of class 'metarep'
details.methods	A logical specifying whether details on statistical methods should be printed
...	Arguments to be passed to methods, see print.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 <- 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' ,
               common = FALSE, random = TRUE )
mr1 <- metarep( m1 , u = 2, common.effect = FALSE , t = 0.05 ,
               alternative = 'two-sided', report.u.max = TRUE)
print(mr1, digits = 2)

```

---

```
print.summary.metarep
```

*Print detailed meta-analysis with replicability-analysis results*


---

**Description**

Print method for objects of class 'summary.metarep'.

**Usage**

```
## S3 method for class 'summary.metarep'
print(x, details.methods = TRUE, ...)
```

**Arguments**

x	An object of class 'summary.metarep'
details.methods	A logical specifying whether details on statistical methods should be printed
...	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 <- 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' ,
               common = FALSE, random = TRUE )
mr1 <- metarep( m1 , u = 2, common.effect = FALSE , t = 0.05 ,
               alternative = 'two-sided', report.u.max = TRUE)
print(summary(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 <- 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' ,
               common = FALSE, random = TRUE )
mr1 <- metarep( m1 , u = 2, common.effect = FALSE , t = 0.05 ,
               alternative = 'two-sided', report.u.max = TRUE)
summary(mr1)
```

---

truncatedPearson	<i>Truncated-Pearsons' test</i>
------------------	---------------------------------

---

**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	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:

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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