Package ‘meta’

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Title  General Package for Meta-Analysis
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Depends R (>= 2.9.1)
Imports grid, metafor (>= 1.9-9), lme4
Suggests numDeriv, BiasedUrn
Description User-friendly general package providing standard methods for meta-
analysis and supporting Schwarzer, Carpenter, and Rücker <DOI:10.1007/978-3-319-21416-
0>, "Meta-Analysis with R" (2015):
- fixed effect and random effects meta-analysis;
- several plots (forest, funnel, Galbraith / radial, L’Abbe, Baujat, bubble);
- statistical tests and trim-and-fill method to evaluate bias in meta-analysis;
- import data from 'RevMan 5';
- prediction interval, Hartung-Knapp and Paule-Mandel method for random effects model;
- cumulative meta-analysis and leave-one-out meta-analysis;
- meta-regression;
- generalised linear mixed models;
- produce forest plot summarising several (subgroup) meta-analyses.
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Description


Details

R package **meta** (Schwarzer, 2007) provides the following statistical methods for meta-analysis.

1. Fixed effect and random effects model:
   - Meta-analysis of continuous outcome data (**metacont**)
   - Meta-analysis of binary outcome data (**metabin**)
   - Meta-analysis of incidence rates (**metainc**)
   - Generic inverse variance meta-analysis (**metagen**)
   - Meta-analysis of single correlations (**metacor**)
   - Meta-analysis of single means (**metamean**)
   - Meta-analysis of single proportions (**metaprop**)
   - Meta-analysis of single incidence rates (**metarate**)

2. Several plots for meta-analysis:
   - Forest plot (**forest**)
   - Funnel plot (**funnel**)
   - Galbraith plot / radial plot (**radial**)
   - L’Abbe plot for meta-analysis with binary outcome data (**labbe**)
   - Baujat plot to explore heterogeneity in meta-analysis (**baujat**)
   - Bubble plot to display the result of a meta-regression (**bubble**)

3. Statistical tests for funnel plot asymmetry (**metabias**) and trim-and-fill method (**trimfill**) to evaluate bias in meta-analysis

4. Import data from 'RevMan 5' (**read.rm5**): see also **metacr** to conduct meta-analysis for a single comparison and outcome from a Cochrane review

5. Prediction interval, Hartung-Knapp and Paule-Mandel method for random effects model (see arguments **prediction**, **hakn**, and **method.tau**, respectively, in meta-analysis functions listed under 1. Fixed effect and random effects model)

6. Cumulative meta-analysis (**metacum**) and leave-one-out meta-analysis (**metainf**)

7. Meta-regression (**metareg**): if R package **metafor** is installed

8. Generalised linear mixed models (**metabin**, **metainc**, **metaprop**, and **metarate**)

The following more advanced statistical methods are provided by add-on R packages:

- Frequentist methods for network meta-analysis (R package **netmeta**)
- Advanced methods to model and adjust for bias in meta-analysis (R package **metasens**)

---

**met-package**

**meta**: Brief overview of methods and general hints
Results of several meta-analyses can be combined with \texttt{metabind}. This is, for example, useful to generate a forest plot with results of subgroup analyses.

See \texttt{settings.meta} to learn how to print and specify default meta-analysis methods used during your R session. For example, the function can be used to specify general settings:

- \texttt{settings.meta("revman5")}
- \texttt{settings.meta("jama")}

The first command can be used to reproduce meta-analyses from Cochrane reviews conducted with \textit{Review Manager 5} (RevMan 5, \url{http://community.cochrane.org/tools/review-production-tools/revman-5}) and specifies to use a RevMan 5 layout in forest plots. The second command can be used to generate forest plots following instructions for authors of the \textit{Journal of the American Medical Association} (\url{http://jamanetwork.com/journals/jama/pages/instructions-for-authors}).

In addition, \texttt{settings.meta} can be used to change individual settings. For example, the following R command specifies the use of the Hartung-Knapp and Paule-Mandel methods, and the printing of prediction intervals in the current R session for any meta-analysis generated after execution of this command:

- \texttt{settings.meta(hakn=TRUE,method.tau="PM",prediction=TRUE)}

Type \texttt{help(package = "meta")} for a listing of R functions and datasets available in \texttt{meta}. Schwarzer (2007) is the preferred citation in publications for \texttt{meta}. Type \texttt{citation("meta")} for a BibTeX entry of this publication.

To report problems and bugs

- type \texttt{bug.report(package = "meta")} if you do not use RStudio,
- send an email to Guido Schwarzer <sc@imbi.uni-freiburg.de> if you use RStudio.

The development version of \texttt{meta} is available on GitHub \url{https://github.com/guido-s/meta}.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


Description

Meta-analysis on the effect of amlodipine on work capacity.

This meta-analysis is used as a data example in Hartung and Knapp (2001).

Format

A data frame with the following columns:

- **study**: study label
- **n.amlo**: number of observations in amlodipine group
- **mean.amlo**: estimated mean in amlodipine group
- **var.amlo**: variance in amlodipine group
- **n.plac**: number of observations in placebo group
- **mean.plac**: estimated mean in placebo group
- **var.plac**: variance in placebo group

Source


See Also

- metacont

Examples

```r
data(amlodipine)

m <- metacont(n.amlo, mean.amlo, sqrt(var.amlo),
              n.plac, mean.plac, sqrt(var.plac),
              data = amlodipine, studlab = study)
s1 <- summary(m)
s2 <- summary(update(m, hakn = TRUE))

vars <- c("TE", "lower", "upper")

# Same results for mean difference as in Table III in Hartung and Knapp (2001)
res.md <- rbind(data.frame(s1$fixed)[vars],
                data.frame(s1$random)[vars],
                data.frame(s2$random)[vars])
```
as.data.frame.meta

Additional functions for objects of class meta

Description

The as.data.frame method returns a data frame containing information on individual studies, e.g., estimated treatment effect and its standard error.

Usage

## S3 method for class 'meta'
as.data.frame(x, row.names = NULL, optional = FALSE, …)

Arguments

x  
An object of class meta.

row.names  
NULL or a character vector giving the row names for the data frame.

optional  
logical. If TRUE, setting row names and converting column names (to syntactic names) is optional.

…  
other arguments

Value

A data frame is returned by the function as.data.frame.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

See Also

metabin, metacont, metagen, forest.meta
Examples

data(Fleiss93cont)
# Generate additional variable with grouping information
# Fleiss93cont$group <- c(1, 2, 1, 1, 2)
# Do meta-analysis without grouping information
# m1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, study,
# data = Fleiss93cont, sm = "SMD")
# Update meta-analysis object and do subgroup analyses
# summary(update(m1, byvar = group))

# Same result using metacont function directly
# m2 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, study,
# data = Fleiss93cont, sm = "SMD", byvar = group)

# Compare printout of the following two commands
# as.data.frame(m1)
# m1$data

---

**baujat**  

Baujat plot to explore heterogeneity in meta-analysis

**Description**

Draw a Baujat plot to explore heterogeneity in meta-analysis.

**Usage**

baujat(x, ...)

## S3 method for class 'meta'
baujat(x, yscale = 1, xlim, ylim,
  xlab = "Contribution to overall heterogeneity",
  ylab = "Influence on overall result", pch = 21, cex = 1,
  col = "black", bg = "darkgray", studlab = TRUE,
  cex.studlab = 0.8, xmin = 0, ymin = 0, pos = 2, offset = 0.5,
  grid = TRUE, col.grid = "lightgray", lty.grid = "dotted",
  lwd.grid = par("lwd"), pty = "s", ...)
Arguments

- **x**: An object of class `meta`.
- **...**: Graphical arguments as in `par` may also be passed as arguments.
- **yscale**: Scaling factor for values on y-axis.
- **xlim**: The x limits (min,max) of the plot.
- **ylim**: The y limits (min,max) of the plot.
- **xlab**: A label for the x-axis.
- **ylab**: A label for the y-axis.
- **pch**: The plotting symbol used for individual studies.
- **cex**: The magnification to be used for plotting symbol.
- **col**: A vector with colour of plotting symbols.
- **bg**: A vector with background colour of plotting symbols (only used if `pch` in 21:25).
- **studlab**: A logical indicating whether study labels should be printed in the graph. A vector with study labels can also be provided (must be of same length as `x$TE` then).
- **cex.studlab**: The magnification for study labels.
- **xmin**: A numeric specifying minimal value to print study labels (on x-axis).
- **ymin**: A numeric specifying minimal value to print study labels (on y-axis).
- **pos**: A position specifier for study labels (see `text`).
- **offset**: Offset for study labels (see `text`).
- **grid**: A logical indicating whether a grid is printed in the plot.
- **col.grid**: Colour for grid lines.
- **lty.grid**: The line type for grid lines.
- **lwd.grid**: The line width for grid lines.
- **pty**: A character specifying type of plot region (see `par`).

Details

Baujat et al. (2002) introduced a scatter plot to explore heterogeneity in meta-analysis. On the x-axis the contribution of each study to the overall heterogeneity statistic (see list object `Q` of the meta-analysis object `x`) is plotted. On the y-axis the standardised difference of the overall treatment effect with and without each study is plotted; this quantity describes the influence of each study on the overall treatment effect.

Internally, the `metainf` function is used to calculate the values on the y-axis.

Value

A data.frame with the following variables:

- **x**: Coordinate on x-axis (contribution to heterogeneity statistic)
- **y**: Coordinate on y-axis (influence on overall treatment effect)
Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

metagen, metainf

Examples

data(Olkin95)

m1 <- metabin(event.e, n.e, event.c, n.c, data = Olkin95,
               studlab = author, sm = "OR", method = "I")

# Generate Baujat plot
baujat(m1)

# Do not print study labels if the x-value is smaller than 4 and
# the y-value is smaller than 1
baujat(m1, yscale = 10, xmin = 4, ymin = 1)

# Change position of study labels
baujat(m1, yscale = 10, xmin = 4, ymin = 1,
      pos = 1, xlim = c(0, 6.5))

# Generate Baujat plot and assign x- and y- coordinates to R object
# b1
b1 <- baujat(m1)

# Calculate overall heterogeneity statistic
sum(b1$x)
m1$Q

---

bubble  Bubble plot to display the result of a meta-regression

Description

Draw a bubble plot to display the result of a meta-regression.
Usage

bubble(x, ...)

## S3 method for class 'metareg'
bubble(x, xlim, ylim, xlab, ylab, cex, min.cex = 0.5,
        max.cex = 5, pch = 21, col = "black", bg = "darkgray", lty = 1,
        lwd = 1, col.line = "black", studlab = FALSE, cex.studlab = 0.8,
        pos = 2, offset = 0.5, regline = TRUE, axes = TRUE, box = TRUE,
        ...)
Details

A bubble plot can be used to display the result of a meta-regression. It is a scatter plot with the treatment effect for each study on the y-axis and the covariate used in the meta-regression on the x-axis. Typically, the size of the plotting symbol is inversely proportional to the variance of the estimated treatment effect (Thompson & Higgins, 2002).

Argument `cex` specifies the plotting size for each individual study. If this argument is missing the weights from the meta-regression model will be used (which typically is a random effects model). Use `weight="fixed"` in order to utilise weights from a fixed effect model to define the size of the plotted symbols (even for a random effects meta-regression). If a vector with individual study weights is provided, the length of this vector must be of the same length as the number of studies.

Arguments `min.cex` and `max.cex` can be used to define the size of the smallest and largest plotting symbol. The plotting size of the most precise study is set to `max.cex` whereas the plotting size of all studies with a plotting size smaller than `min.cex` will be set to `min.cex`.

For a meta-regression with more than one covariate. Only a scatter plot of the first covariate in the regression model is shown. In this case the effect of the first covariate adjusted for other covariates in the meta-regression model is shown.

For a factor or categorial covariate separate bubble plots for each group compared to the baseline group are plotted.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

`metagen, metainf`

Examples

data(Fleiss93cont)

# Add some (fictitious) grouping variables:
Fleiss93cont$age <- c(55, 65, 52, 65, 58)
Fleiss93cont$region <- c("Europe", "Europe", "Asia", "Asia", "Europe")

m1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c,
               data = Fleiss93cont, sm = "MD")

mr1 <- metareg(m1, region)
mr1

bubble(mr1)
bubble(mr1, lwd = 2, col.line = "blue")
```
mr2 <- metareg(m1, age)

bubble(mr2, lwd = 2, col.line = "blue", xlim = c(50, 70))
bubble(mr2, lwd = 2, col.line = "blue", xlim = c(50, 70), cex = "fixed")

# Do not print regression line
# bubble(mr2, lwd = 2, col.line = "blue", xlim = c(50, 70), regline = FALSE)
```

---

### Description

Calculation of confidence intervals; based on normal approximation or t-distribution.

### Usage

```r
.ci(TE, seTE, level = 0.95, df = NULL, null.effect = 0)
```

### Arguments

- **TE**: Estimated treatment effect.
- **seTE**: Standard error of treatment estimate.
- **level**: The confidence level required.
- **df**: Degrees of freedom (for confidence intervals based on t-distribution).
- **null.effect**: A numeric value specifying the effect under the null hypothesis.

### Value

List with components

<table>
<thead>
<tr>
<th>Component</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TE</td>
<td>Estimated treatment effect</td>
</tr>
<tr>
<td>seTE</td>
<td>Standard error of treatment estimate</td>
</tr>
<tr>
<td>lower</td>
<td>Lower confidence limits</td>
</tr>
<tr>
<td>upper</td>
<td>Upper confidence limits</td>
</tr>
<tr>
<td>z</td>
<td>Test statistic (either z-score or t-score)</td>
</tr>
<tr>
<td>p</td>
<td>P-value of test with null hypothesis TE=0</td>
</tr>
<tr>
<td>level</td>
<td>The confidence level required</td>
</tr>
<tr>
<td>df</td>
<td>Degrees of freedom (t-distribution)</td>
</tr>
</tbody>
</table>
Note
This function is primarily called from other functions of the library meta, e.g. forest.meta, summary.meta.

Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

Examples
data.frame(ci(170, 10))
data.frame(ci(170, 10, 0.99))
data.frame(ci(1.959964, 1))
data.frame(ci(2.2621571628, 1, df = 9))

cisapride  Cisapride in Non-Ulcer Dispepsia

Description
Meta-analysis on cisapride in non-ulcer dispepsia.
This meta-analysis is used as a data example in Hartung and Knapp (2001).

Format
A data frame with the following columns:

- study: study label
- event.cisa: number of events in cisapride group
- n.cisa: number of observations in cisapride group
- event.plac: number of events in placebo group
- n.plac: number of observations in placebo group

Source

See Also
metabin

Examples
data(cisapride)
m.or <- metabin(event.cisa, n.cisa, event.plac, n.plac,
data = cisapride, sm = "OR", method = "Inverse", studlab = study, addincr = TRUE)

s1 <- summary(update(m.or, sm = "RR"))
s2 <- summary(update(m.or, sm = "RR", hakn = TRUE))
#
s3 <- summary(m.or)
s4 <- summary(update(m.or, hakn = TRUE))

vars <- c("TE", "lower", "upper")

# Results for log risk ratio - see Table VII in Hartung and Knapp (2001)
#
res.rr <- rbind(data.frame(s1$fixed)[vars],
  data.frame(s1$random)[vars],
  data.frame(s2$random)[vars])
#
row.names(res.rr) <- c("FE", "RE", "RE (HaKn)"
names(res.rr) <- c("Log risk ratio", "CI lower", "CI upper")
#
res.rr

# Results for log odds ratio (Table VII in Hartung and Knapp 2001)
#
res.or <- rbind(data.frame(s3$fixed)[vars],
  data.frame(s3$random)[vars],
  data.frame(s4$random)[vars])
#
row.names(res.or) <- c("FE", "RE", "RE (HaKn)"
names(res.or) <- c("Log odds ratio", "CI lower", "CI upper")
#
res.or

Fleiss93  
**Aspirin after Myocardial Infarction**

Description

Meta-analysis on aspirin in preventing death after myocardial infarction.

Data example in Fleiss (1993) for meta-analysis with binary outcomes.

Format

A data frame with the following columns:

- **study**: study label
- **year**: year of publication
- **event.e**: number of deaths in aspirin group
\[ \text{n.e} \quad \text{number of observations in aspirin group} \\
\text{event.c} \quad \text{number of deaths in placebo group} \\
\text{n.c} \quad \text{number of observations in placebo group} \]

**Source**


**Examples**

```r
data(Fleiss93)
metabin(event.e, n.e, event.c, n.c,
data = Fleiss93,
studlab = paste(study, year),
sm = "OR", comb.random = FALSE)
```

---

**Fleiss93cont**  
*Mental Health Treatment*

**Description**

Meta-analysis on the Effect of Mental Health Treatment on Medical Utilisation. 
Data example in Fleiss (1993) for meta-analysis with continuous outcomes.

**Format**

A data frame with the following columns:

- **study** study label
- **year** year of publication
- **n.e** number of observations in psychotherapy group
- **mean.e** estimated mean in psychotherapy group
- **sd.e** standard deviation in psychotherapy group
- **n.c** number of observations in control group
- **mean.c** estimated mean in control group
- **sd.c** standard deviation in control group

**Source**


**See Also**

Fleiss93
Examples

```r
data(Fleiss93cont)
metacont(n.e, mean.e, sd.e,
n.c, mean.c, sd.c,
data = Fleiss93cont,
studlab = paste(study, year),
comb.random = FALSE)
```

---

forest

**Forest plot to display the result of a meta-analysis**

Description

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

Usage

`forest(x, ...)`

```r
## S3 method for class 'meta'
forest(x, sortvar, studlab = TRUE,
      layout = gs("layout"), comb.fixed = x$comb.fixed,
      comb.random = x$comb.random, overall = comb.fixed | comb.random,
      text.fixed = NULL, text.random = NULL, lty.fixed = 2,
      lty.random = 3, col.fixed = "black", col.random = "black",
      prediction = x$prediction, text.predict = NULL, subgroup = TRUE,
      print.subgroup.labels = TRUE, bylab = x$bylab,
      print.byvar = x$print.byvar, byseparator = x$byseparator,
      text.fixed.w = text.fixed, text.random.w = text.random,
      bysort = FALSE, pooled.totals = comb.fixed | comb.random,
      pooled.events = FALSE, pooled.times = FALSE, study.results = TRUE,
      xlab = "", xlab.pos, smlab = NULL, smlab.pos, xlim = "symmetric",
      allstudies = TRUE, weight.study, weight.subgroup, pscale = x$pscale,
      irscale = x$irscale, irunit = x$irunit, ref = ifelse(backtransf &
```
is.relative.effect(x$sm), 1, 0), lower.equi = NA, upper.equi = NA,
lty.equi = 1, col.equi = "blue", fill.equi = "transparent",
leftcols = NULL, rightcols = NULL, leftlabs = NULL,
rightlabs = NULL, lab.e = x$label.e, lab.c = x$label.c,
lab.e.attach.to.col = NULL, lab.c.attach.to.col = NULL,
label.right = x$label.right, label.left = x$label.left,
bottom.lr = TRUE, lab.NA = ",", lab.NA.weight = "--",
lwd = 1, at = NULL, lab = TRUE,
type.study = "square", type.fixed = "diamond",
type.random = type.fixed, type.subgroup = ifelse(study.results,
"diamond", "square"), type.subgroup.fixed = type.subgroup,
type.subgroup.random = type.subgroup, col.study = "black",
col.square = "gray", col.square.lines = col.square,
col.inside = "white", col.diamond = "gray",
col.diamond.fixed = col.diamond, col.diamond.random = col.diamond,
col.diamond.lines = "black",
col.diamond.lines.fixed = col.diamond.lines,
col.diamond.lines.random = col.diamond.lines,
col.inside.fixed = col.inside, col.inside.random = col.inside,
col.predict = "red", col.predict.lines = "black",
col.by = "darkgray", col.label.right = "black",
col.label.left = "black", hetstat = print.I2 | print.tau2 | print.Q |
print.pval.Q | print.Rb, overall.hetstat = overall &
(!is.character(hetstat) & hetstat), hetlab = "Heterogeneity: ",
resid.hetstat = overall & (is.character(hetstat) | hetstat),
resid.hetlab = "Residual heterogeneity: ", print.I2 = comb.fixed |
comb.random, print.I2.ci = FALSE, print.tau2 = comb.fixed |
comb.random, print.Q = FALSE, print.pval.Q = comb.fixed |
comb.random, print.Rb = FALSE, print.Rb.ci = FALSE,
text.subgroup.nohet = "not applicable",
text.overall = gs("test.overall"), test.overall.fixed = comb.fixed &
overall & test.overall, test.overall.random = comb.random & overall &
test.overall, label.test.overall.fixed, label.test.overall.random,
print.zval = TRUE, test.subgroup, test.subgroup.fixed,
test.subgroup.random, print.Q.subgroup = TRUE,
label.test.subgroup.fixed, label.test.subgroup.random,
test.effect.subgroup, test.effect.subgroup.fixed,
test.effect.subgroup.random, label.test.effect.subgroup.fixed,
label.test.effect.subgroup.random, fontsize = 12, fontfamily = NULL,
fs.heading = fontsize, fs.fixed, fs.random, fs.predict,
fs.fixed.labels, fs.random.labels, fs.predict.labels,
fs.study = fontsize, fs.study.labels = fs.study, fs.predict,
fs.axis = fontsize, fs.smlab = fontsize, fs.xlab = fontsize,
fs.lr = fontsize, ff.heading = "bold", ff.fixed, ff.random,
ff.predict, ff.fixed.labels, ff.predict.labels, ff.study = "plain",
ff.study.labels = ff.study, ff.hetstat,
ff.test.overall, ff.test.subgroup, ff.test.effect.subgroup,
Arguments

- **x**: An object of class `meta` or `metabind`.
- **...**: Additional graphical arguments.
- **leftcols**: A character vector specifying (additional) columns to be plotted on the left side of the forest plot or a logical value (see Details).
- **leftlabs**: A character vector specifying labels for (additional) columns on left side of the forest plot (see Details).
- **rightcols**: A character vector specifying (additional) columns to be plotted on the right side of the forest plot or a logical value (see Details).
- **rightlabs**: A character vector specifying labels for (additional) columns on right side of the forest plot (see Details).
- **overall**: A logical indicating whether overall summaries should be plotted. This argument is useful in a meta-analysis with subgroups if summaries should only be plotted on group level.
- **subgroup**: A logical indicating whether subgroup results should be shown in forest plot. This argument is useful in a meta-analysis with subgroups if summaries should not be plotted on group level.
- **hetstat**: Either a logical value indicating whether to print results for heterogeneity measures at all or a character string (see Details).
overall.hetstat
A logical value indicating whether to print heterogeneity measures for overall treatment comparisons. This argument is useful in a meta-analysis with subgroups if heterogeneity statistics should only be printed on subgroup level.

lab.NA
A character string to label missing values.

digits
Minimal number of significant digits for treatment effects, see print.default.
digits.se
Minimal number of significant digits for standard errors, see print.default.
digits.zval
Minimal number of significant digits for z- or t-statistic for test of overall effect, see print.default.
digits.pval
Minimal number of significant digits for p-value of overall treatment effect, see print.default.
digits.pval.Q
Minimal number of significant digits for p-value of heterogeneity test, see print.default.
digits.Q
Minimal number of significant digits for heterogeneity statistic Q, see print.default.
digits.tau2
Minimal number of significant digits for between-study variance, see print.default.
digits.I2
Minimal number of significant digits for I-squared statistic, see print.default.
scientific.pval
A logical specifying whether p-values should be printed in scientific notation, e.g., 1.2345e-01 instead of 0.12345.

big.mark
A character used as thousands separator.
smlab
A label for the summary measurex (printed at top of figure).
sortvar
An optional vector used to sort the individual studies (must be of same length as x$TE).

studlab
A logical indicating whether study labels should be printed in the graph. A vector with study labels can also be provided (must be of same length as x$TE then).

layout
A character string specifying the layout of the forest plot (see Details).
comb.fixed
A logical indicating whether fixed effect estimate should be plotted.
comb.random
A logical indicating whether random effects estimate should be plotted.
text.fixed
A character string used in the plot to label the pooled fixed effect estimate.
text.random
A character string used in the plot to label the pooled random effects estimate.
lty.fixed
Line type (pooled fixed effect estimate).
lty.random
Line type (pooled random effects estimate).
col.fixed
Line colour (pooled fixed effect estimate).
col.random
Line colour (pooled random effects estimate).
prediction
A logical indicating whether a prediction interval should be printed.
text.predict
A character string used in the plot to label the prediction interval.
print.subgroup.labels
A logical indicating whether subgroup label should be printed.
bylab
A character string with a label for the grouping variable.
print.byvar
A logical indicating whether the name of the grouping variable should be printed in front of the group labels.
byseparator: A character string defining the separator between label and levels of grouping variable.

text.fixed.w: A character string to label the pooled fixed effect estimate within subgroups, or a character vector of same length as number of subgroups with corresponding labels.

text.random.w: A character string to label the pooled random effect estimate within subgroups, or a character vector of same length as number of subgroups with corresponding labels.

bysort: A logical indicating whether groups should be ordered alphabetically.
pooled.totals: A logical indicating whether total number of observations should be given in the figure.
pooled.events: A logical indicating whether total number of events should be given in the figure.
pooled.times: A logical indicating whether total person time at risk should be given in the figure.

study.results: A logical indicating whether results for individual studies should be shown in the figure (useful to only plot subgroup results).

xlab: A label for the x-axis.
xlab.pos: A numeric specifying the center of the label on the x-axis.
smlab.pos: A numeric specifying the center of the label for the summary measure.
xlim: The x limits (min,max) of the plot, or the character "s" to produce symmetric forest plots.

allstudies: A logical indicating whether studies with inestimable treatment effects should be plotted.

weight.study: A character string indicating weighting used to determine size of squares or diamonds (argument type.study) to plot individual study results. One of missing, "same", "fixed", or "random", can be abbreviated. Plot symbols have the same size for all studies or represent study weights from fixed effect or random effects model.

weight.subgroup: A character string indicating weighting used to determine size of squares or diamonds (argument type.subgroup) to plot subgroup results. One of missing, "same", or "weight", can be abbreviated. Plot symbols have the same size for all subgroup results or represent subgroup weights from fixed effect or random effects model.

pscale: A numeric giving scaling factor for printing of single event probabilities or risk differences, i.e. if argument sm is equal to "PLOGIT", "PLN", "PRAW", "PAS", "PFT", or "RD".

irscale: A numeric defining a scaling factor for printing of single incidence rates or incidence rate differences, i.e. if argument sm is equal to "IR", "IRLN", "IRS", "IRFT", or "IRD".

irunit: A character specifying the time unit used to calculate rates, e.g., person-years.

ref: A numerical giving the reference value to be plotted as a line in the forest plot. No reference line is plotted if argument ref is equal to NA.
lower.equi  A numerical giving the lower limit of equivalence to be plotted as a line in the forest plot. No line is plotted if argument lower.equi is equal to NA.

upper.equi  A numerical giving the upper limit of equivalence to be plotted as a line in the forest plot. No line is plotted if argument upper.equi is equal to NA.

lty.equi     Line type (limits of equivalence).

col.equi     Line colour (limits of equivalence).

fill.equi    Colour of area between limits of equivalence.

lab.e        Label to be used for experimental group in table heading.

lab.c        Label to be used for control group in table heading.

lab.e.attach.to.col
             A character specifying the column name where label lab.e should be attached to in table heading.

lab.c.attach.to.col
               A character specifying the column name where label lab.c should be attached to in table heading.

label.right  Graph label on right side of forest plot.

label.left   Graph label on left side of forest plot.

bottom.lr    A logical indicating whether labels on right and left side should be printed at bottom or top of forest plot.

lab.NA.effect A character string to label missing values in individual treatment estimates and confidence intervals.

lab.NA.weight A character string to label missing weights.

lwd           The line width, see par.

at            The points at which tick-marks are to be drawn, see grid.xaxis.

label        A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. See grid.xaxis.

type.study    A character string or vector specifying how to plot treatment effects and confidence intervals for individual studies (see Details).

type.fixed    A character string specifying how to plot treatment effect and confidence interval for fixed effect meta-analysis (see Details).

type.random   A character string specifying how to plot treatment effect and confidence interval for random effects meta-analysis (see Details).

type.subgroup A character string specifying how to plot treatment effect and confidence interval for subgroup results (see Details).

type.subgroup.fixed
                     A character string specifying how to plot treatment effect and confidence interval for subgroup results (fixed effect model).

type.subgroup.random
                      A character string specifying how to plot treatment effect and confidence interval for subgroup results (random effects model).

col.study     The colour for individual study results and confidence limits.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>col.square</td>
<td>The colour for squares reflecting study’s weight in the meta-analysis.</td>
</tr>
<tr>
<td>col.square.lines</td>
<td>The colour for the outer lines of squares reflecting study’s weight in the meta-analysis.</td>
</tr>
<tr>
<td>col.inside</td>
<td>The colour for individual study results and confidence limits if confidence limits are completely within squares.</td>
</tr>
<tr>
<td>col.diamond</td>
<td>The colour of diamonds representing the results for fixed effect and random effects models.</td>
</tr>
<tr>
<td>col.diamond.fixed</td>
<td>The colour of diamonds for fixed effect estimates.</td>
</tr>
<tr>
<td>col.diamond.random</td>
<td>The colour of diamonds for random effects estimates.</td>
</tr>
<tr>
<td>col.diamond.lines</td>
<td>The colour of the outer lines of diamonds representing the results for fixed effect and random effects models.</td>
</tr>
<tr>
<td>col.diamond.lines.fixed</td>
<td>The colour of the outer lines of diamond for fixed effect estimate.</td>
</tr>
<tr>
<td>col.diamond.lines.random</td>
<td>The colour of the outer lines of diamond for random effects estimate.</td>
</tr>
<tr>
<td>col.inside.fixed</td>
<td>The colour for result of fixed effect meta-analysis if confidence limit lies completely within square.</td>
</tr>
<tr>
<td>col.inside.random</td>
<td>The colour for result of random effects meta-analysis if confidence limit lies completely within square.</td>
</tr>
<tr>
<td>col.predict</td>
<td>Background colour of prediction interval.</td>
</tr>
<tr>
<td>col.predict.lines</td>
<td>Colour of outer lines of prediction interval.</td>
</tr>
<tr>
<td>col.by</td>
<td>The colour to print information on subgroups.</td>
</tr>
<tr>
<td>col.label.right</td>
<td>The colour for label on right side of null effect.</td>
</tr>
<tr>
<td>col.label.left</td>
<td>The colour for label on left side of null effect.</td>
</tr>
<tr>
<td>hetlab</td>
<td>Label printed in front of results for heterogeneity measures.</td>
</tr>
<tr>
<td>resid.hetstat</td>
<td>A logical value indicating whether to print measures of residual heterogeneity in a meta-analysis with subgroups.</td>
</tr>
<tr>
<td>resid.hetlab</td>
<td>Label printed in front of results for residual heterogeneity measures.</td>
</tr>
<tr>
<td>print.I2</td>
<td>A logical value indicating whether to print the value of the I-squared statistic.</td>
</tr>
<tr>
<td>print.I2.ci</td>
<td>A logical value indicating whether to print the confidence interval of the I-squared statistic.</td>
</tr>
<tr>
<td>print.tau2</td>
<td>A logical value indicating whether to print the value of the between-study variance tau-squared.</td>
</tr>
<tr>
<td>print.Q</td>
<td>A logical value indicating whether to print the value of the heterogeneity statistic Q.</td>
</tr>
</tbody>
</table>
print.pval.Q A logical value indicating whether to print the p-value of the heterogeneity statistic Q.

print.Rb A logical value indicating whether to print the value of the I-squared statistic.

print.Rb.ci A logical value indicating whether to print the confidence interval of the I-squared statistic.

text.subgroup.nohet A logical value or character string which is printed to indicate subgroups with less than two studies contributing to meta-analysis (and thus without heterogeneity). If FALSE, heterogeneity statistics are printed (with NAs).

test.overall A logical value indicating whether to print results of test for overall effect.

test.overall.fixed A logical value indicating whether to print results of test for overall effect (based on fixed effect model).

test.overall.random A logical value indicating whether to print results of test for overall effect (based on random effects model).

label.test.overall.fixed Label printed in front of results of test for overall effect (based on fixed effect model).

label.test.overall.random Label printed in front of results of test for overall effect (based on random effects model).

print.zval A logical value indicating whether z-value for test of treatment effect should be printed.

test.subgroup A logical value indicating whether to print results of test for subgroup differences.

test.subgroup.fixed A logical value indicating whether to print results of test for subgroup differences (based on fixed effect model).

test.subgroup.random A logical value indicating whether to print results of test for subgroup differences (based on random effects model).

print.Q.subgroup A logical value indicating whether to print the value of the heterogeneity statistic Q (test for subgroup differences).

label.test.subgroup.fixed Label printed in front of results of test for subgroup differences (based on fixed effect model).

label.test.subgroup.random Label printed in front of results of test for subgroup differences (based on random effects model).

test.effect.subgroup A logical value indicating whether to print results of test for effect in subgroups.

test.effect.subgroup.fixed A logical value indicating whether to print results of test for effect in subgroups (based on fixed effect model).
test.effect.subgroup.random
   A logical value indicating whether to print results of test for effect in subgroups
   (based on random effects model).

label.test.effect.subgroup.fixed
   Label printed in front of results of test for effect in subgroups (based on fixed
effect model).

label.test.effect.subgroup.random
   Label printed in front of results of test for effect in subgroups (based on random
effects model).

fontsize
   The size of text (in points), see \texttt{gpar}.

fontfamily
   The font family, see \texttt{gpar}.

fs.heading
   The size of text for column headings, see \texttt{gpar}.

fs.fixed
   The size of text for results of fixed effect model, see \texttt{gpar}.

fs.random
   The size of text for results of random effects model, see \texttt{gpar}.

fs.predict
   The size of text for results of prediction interval, see \texttt{gpar}.

fs.fixed.labels
   The size of text for label of fixed effect model, see \texttt{gpar}.

fs.random.labels
   The size of text for label of random effects model, see \texttt{gpar}.

fs.predict.labels
   The size of text for label of prediction interval, see \texttt{gpar}.

fs.study
   The size of text for results of individual studies, see \texttt{gpar}.

fs.study.labels
   The size of text for labels of individual studies, see \texttt{gpar}.

fs.hetstat
   The size of text for heterogeneity measures, see \texttt{gpar}.

fs.test.overall
   The size of text of test for overall effect, see \texttt{gpar}.

fs.test.subgroup
   The size of text of test of subgroup differences, see \texttt{gpar}.

fs.test.effect.subgroup
   The size of text of test of effect in subgroups, see \texttt{gpar}.

fs.axis
   The size of text on x-axis, see \texttt{gpar}.

fs.smlab
   The size of text of label for summary measure, see \texttt{gpar}.

fs.xlab
   The size of text of label on x-axis, see \texttt{gpar}.

fs.lr
   The size of text of label on left and right side of forest plot, see \texttt{gpar}.

ff.heading
   The fontface for column headings, see \texttt{gpar}.

ff.fixed
   The fontface of text for results of fixed effect model, see \texttt{gpar}.

ff.random
   The fontface of text for results of random effects model, see \texttt{gpar}.

ff.predict
   The fontface of text for results of prediction interval, see \texttt{gpar}.

ff.fixed.labels
   The fontface of text for label of fixed effect model, see \texttt{gpar}.
ff.random.labels
   The fontface of text for label of random effects model, see gpar.
ff.predict.labels
   The fontface of text for label of prediction interval, see gpar.
ff.study
   The fontface of text for results of individual studies, see gpar.
ff.study.labels
   The fontface of text for labels of individual studies, see gpar.
ff.hetstat
   The fontface of text for heterogeneity measures, see gpar.
ff.test.overall
   The fontface of text of test for overall effect, see gpar.
ff.test.subgroup
   The fontface of text for test of subgroup differences, see gpar.
ff.test.effect.subgroup
   The fontface of text for test of effect in subgroups, see gpar.
ff.axis
   The fontface of text on x-axis, see gpar.
ff.smlab
   The fontface of text of label for summary measure, see gpar.
ff.xlab
   The fontface of text of label on x-axis, see gpar.
ff.lr
   The fontface of text of label on left and right side of forest plot, see gpar.
squaresize
   A numeric used to increase or decrease the size of squares in the forest plot.
plotwidth
   Either a character string, e.g., "8cm", "60mm", or "3inch", or a unit object
   specifying width of the forest plot.
colgap
   Either a character string or a unit object specifying gap between columns printed
   on left and right side of forest plot.
colgap.left
   Either a character string or a unit object specifying gap between columns printed
   on left side of forest plot.
colgap.right
   Either a character string or a unit object specifying gap between columns printed
   on right side of forest plot.
colgap.studlab
   Either a character string or a unit object specifying gap between column with
   study labels and subsequent column.
colgap.forest
   Either a character string or a unit object specifying gap between column adjacent
   to forest plot and the forest plot.
colgap.forest.left
   Either a character string or a unit object specifying gap between column on the
   left side of forest plot and the forest plot.
colgap.forest.right
   Either a character string or a unit object specifying gap between column on the
   right side of forest plot and the forest plot.
calcwidth.pooled
   A logical indicating whether text for fixed effect and random effects model
   should be considered to calculate width of the column with study labels.
calcwidth.fixed
   A logical indicating whether text given in arguments text.fixed and text.fixed.w
   should be considered to calculate width of the column with study labels.
calcwidth.random
A logical indicating whether text given in arguments text.random and text.random.w should be considered to calculate width of the column with study labels.

calcwidth.predict
A logical indicating whether text given in argument text.predict should be considered to calculate width of the column with study labels.

calcwidth.hetstat
A logical indicating whether text for heterogeneity statistics should be considered to calculate width of the column with study labels.

calcwidth.tests
A logical indicating whether text for tests of overall effect or subgroup differences should be considered to calculate width of the column with study labels.

calcwidth.subgroup
A logical indicating whether text with subgroup labels should be considered to calculate width of the column with study labels.

just
Justification of text in all columns but columns with study labels and additional variables (possible values: "left", "right", "center").

just.studlab
Justification of text for study labels (possible values: "left", "right", "center").

just.addcols
Justification of text for additional columns (possible values: "left", "right", "center").

just.addcols.left
Justification of text for additional columns on left side of forest plot (possible values: "left", "right", "center"). Can be of same length as number of additional columns on left side of forest plot.

just.addcols.right
Justification of text for additional columns on right side of forest plot (possible values: "left", "right", "center"). Can be of same length as number of additional columns on right side of forest plot.

spacing
A numeric determining line spacing in a forest plot.

addrow
A logical value indicating whether an empty row is printed above and below study results.

addrow.overall
A logical value indicating whether an empty row is printed above overall meta-analysis results.

addrow.subgroups
A logical value indicating whether an empty row is printed between results for subgroups.

new
A logical value indicating whether a new figure should be printed in an existing graphics window.

backtransf
A logical indicating whether results should be back transformed in forest plots. If backtransf = TRUE, results for sm = "OR" are presented as odds ratios rather than log odds ratios and results for sm = "ZCOR" are presented as correlations rather than Fisher's z transformed correlations, for example.

digits.weight
Minimal number of significant digits for weights, see print.default.

digits.mean
Minimal number of significant digits for means; only applies to metacont objects.
digits.sd  Minimal number of significant digits for standard deviations; only applies to `metacont` objects.
digits.cor  Minimal number of significant digits for correlations; only applies to `metacor` objects.
digits.time  Minimal number of significant digits for times; only applies to `metainc` and `metarate` objects.
digits.addcols  A vector or scalar with minimal number of significant digits for additional columns.
digits.addcols.right  A vector or scalar with minimal number of significant digits for additional columns on right side of forest plot.
digits.addcols.left  A vector or scalar with minimal number of significant digits for additional columns on left side of forest plot.
zero.pval  A logical specifying whether p-values should be printed with a leading zero.
col.i  Deprecated argument (replaced by `col.study`).
weight  Deprecated argument (replaced by `weight.study`).

details
A forest plot, also called confidence interval plot, is drawn in the active graphics window. The forest function is based on the grid graphics system. In order to print the forest plot, (i) resize the graphics window, (ii) either use `dev.copy2eps` or `dev.copy2pdf`.

By default, treatment estimates and confidence intervals are plotted in the following way:

- For an individual study, a square with treatment estimate in the center and confidence interval as line extending either side of the square (`type.study = "square"`)
- For meta-analysis results, a diamond with treatment estimate in the center and right and left side corresponding to lower and upper confidence limits (`type.fixed = "diamond"`, `type.random = "diamond"`, and `type.subgroup = "diamond"`)

In a forest plot, size of the squares typically reflects the precision of individual treatment estimates based either on the fixed effect (`weight.study = "fixed"`) or random effects meta-analysis (`weight.study = "random"`). Information from meta-analysis object x is utilised if argument `weight.study` is missing. Weights from the fixed effect model are used if argument `x$comb.fixed` is TRUE; weights from the random effects model are used if argument `x$comb.random` is TRUE and `x$comb.fixed` is FALSE. The same square sizes are used if `weight.study = "same"`.

Arguments `text.fixed`, `text.random`, and `text.predict` can be used to change the label to identify overall results (fixed effect and random effects model as well as prediction interval). By default the following text is printed:

- "Fixed effect model" (argument `text.fixed`)
- "Random effects model" (text.random)
- "Prediction interval" (text.predict)
If confidence interval levels are different for individual studies, meta-analysis, and prediction interval (arguments `level`, `level.comb`, `level.predict` in meta-analysis functions, e.g., `metabin`), additional information is printed, e.g., 

\[(99\%-CI)\]

for a 99% confidence interval in the meta-analysis.

The following arguments can be used to print results for various statistical tests:

<table>
<thead>
<tr>
<th>Argument</th>
<th>Statistical test</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>test.overall.fixed</code></td>
<td>Test for overall effect (fixed effect model)</td>
</tr>
<tr>
<td><code>test.overall.random</code></td>
<td>Test for overall effect (random effects model)</td>
</tr>
<tr>
<td><code>test.effect.subgroup.fixed</code></td>
<td>Test for effect in subgroup (FE model)</td>
</tr>
<tr>
<td><code>test.effect.subgroup.random</code></td>
<td>Test for effect in subgroup (RE model)</td>
</tr>
<tr>
<td><code>test.subgroup.fixed</code></td>
<td>Test for subgroup differences (FE model)</td>
</tr>
<tr>
<td><code>test.subgroup.random</code></td>
<td>Test for subgroup differences (RE model)</td>
</tr>
</tbody>
</table>

By default, these arguments are `FALSE`. R function `settings.meta` can be used to change this default for the entire R session. For example, use the following command to always print results of tests for an overall effect: `settings.meta(test.overall = TRUE)`

The arguments `leftcols` and `rightcols` can be used to specify columns which are plotted on the left and right side of the forest plot, respectively. If argument `rightcols` is `FALSE`, no columns will be plotted on the right side. By default, i.e. if arguments `leftcols` and `rightcols` are `NULL` and `layout = "meta"`, the following columns will be printed on the right side of the forest plot:

<table>
<thead>
<tr>
<th>Meta-analysis results</th>
<th>Value of argument rightcols</th>
</tr>
</thead>
<tbody>
<tr>
<td>No summary</td>
<td>c(&quot;effect&quot;, &quot;ci&quot;)</td>
</tr>
<tr>
<td>Only fixed effect model</td>
<td>c(&quot;effect&quot;, &quot;ci&quot;, &quot;w.fixed&quot;)</td>
</tr>
<tr>
<td>Only random effects model</td>
<td>c(&quot;effect&quot;, &quot;ci&quot;, &quot;w.random&quot;)</td>
</tr>
<tr>
<td>Both models</td>
<td>c(&quot;effect&quot;, &quot;ci&quot;, &quot;w.fixed&quot;, &quot;w.random&quot;)</td>
</tr>
</tbody>
</table>

By default, estimated treatment effect and corresponding confidence interval will be printed. Depending on arguments `comb.fixed` and `comb.random`, weights of the fixed effect and/or random effects model will be given too. For an object of class `metacum` or `metainf` only the estimated treatment effect with confidence interval are plotted.

Depending on the class of the meta-analysis object (which is defined by the R function used to generate the object) a different set of columns is printed on the left side of the forest plot:

<table>
<thead>
<tr>
<th>Function</th>
<th>Value of argument leftcols</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>metabin</code></td>
<td>c(&quot;studlab&quot;, &quot;event.e&quot;, &quot;n.e&quot;, &quot;event.c&quot;, &quot;n.c&quot;)</td>
</tr>
<tr>
<td><code>metacont</code></td>
<td>c(&quot;studlab&quot;, &quot;n.e&quot;, &quot;mean.e&quot;, &quot;sd.e&quot;, &quot;n.c&quot;, &quot;mean.c&quot;, &quot;sd.c&quot;)</td>
</tr>
<tr>
<td><code>metacor</code></td>
<td>c(&quot;studlab&quot;, &quot;n&quot;)</td>
</tr>
<tr>
<td><code>metagen</code></td>
<td>c(&quot;studlab&quot;, &quot;TE&quot;, &quot;seTE&quot;)</td>
</tr>
<tr>
<td><code>metainc</code></td>
<td>c(&quot;studlab&quot;, &quot;event.e&quot;, &quot;time.e&quot;, &quot;event.c&quot;, &quot;time.c&quot;)</td>
</tr>
<tr>
<td><code>metaprop</code></td>
<td>c(&quot;studlab&quot;, &quot;event&quot;, &quot;n&quot;)</td>
</tr>
<tr>
<td><code>metarate</code></td>
<td>c(&quot;studlab&quot;, &quot;event&quot;, &quot;time&quot;)</td>
</tr>
<tr>
<td><code>metacum</code></td>
<td>&quot;studlab&quot;</td>
</tr>
<tr>
<td><code>metainf</code></td>
<td>&quot;studlab&quot;</td>
</tr>
</tbody>
</table>

The arguments `leftlabs` and `rightlabs` can be used to specify column headings which are plotted.
on left and right side of the forest plot, respectively. For certain columns predefined labels exist. If
the arguments leftlabs and rightlabs are NULL, the following default labels will be used:

<table>
<thead>
<tr>
<th>Column</th>
<th>studlab</th>
<th>TE</th>
<th>seTE</th>
<th>n.e</th>
<th>n.c</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>Label</td>
<td>&quot;Study&quot;</td>
<td>&quot;TE&quot;</td>
<td>&quot;seTE&quot;</td>
<td>&quot;Total&quot;</td>
<td>&quot;Total&quot;</td>
<td>&quot;Total&quot;</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Column</th>
<th>event.e</th>
<th>event.c</th>
<th>event</th>
<th>mean.e</th>
<th>mean.c</th>
</tr>
</thead>
<tbody>
<tr>
<td>Label</td>
<td>&quot;Events&quot;</td>
<td>&quot;Events&quot;</td>
<td>&quot;Events&quot;</td>
<td>&quot;Mean&quot;</td>
<td>&quot;Mean&quot;</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Column</th>
<th>sd.e</th>
<th>sd.c</th>
<th>time.e</th>
<th>time.c</th>
<th>effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Label</td>
<td>&quot;SD&quot;</td>
<td>&quot;SD&quot;</td>
<td>&quot;Time&quot;</td>
<td>&quot;Time&quot;</td>
<td>x$sm</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Column</th>
<th>ci</th>
<th>effect.ci</th>
<th>w.fixed</th>
<th>w.random</th>
</tr>
</thead>
<tbody>
<tr>
<td>Label</td>
<td>x$level&quot;%-CI&quot;</td>
<td>effect+ci</td>
<td>&quot;W(fixed)&quot;</td>
<td>&quot;W(random)&quot;</td>
</tr>
</tbody>
</table>

For additional columns, the column name will be used as a label. It is possible to only provide
labels for new columns (see Examples). Otherwise the length of leftlabs and rightlabs must
be the same as the number of printed columns, respectively. The value NA can be used to specify
columns which should use default labels (see Examples).

If argument layout = "RevMan5" (and arguments leftcols and rightcols are NULL), the layout
for forest plots used for Cochrane reviews (which are generated with Review Manager 5, http://community.cochrane.org/tools/review-production-tools/revman-5) is reproduced:

1. All columns are printed on the left side of the forest plot (see arguments leftcols and
   rightcols)
2. Tests for overall effect and subgroup differences are printed (test.overall, test.effect.subgroup,
est.subgroup)
3. Diamonds representing meta-analysis results are printed in black (diamond.fixed, diamond.random)
4. Color of squares depends on the meta-analysis object (col.square, col.square.lines)
5. Information on effect measure and meta-analysis method is printed above the forest plot
   (smlab)
6. Label "Study or Subgroup" is printed for meta-analysis with subgroups (leftlabs)

If argument layout = "JAMA" (and arguments leftcols and rightcols are NULL), instructions
for authors of the Journal of the American Medical Association, see http://jamanetwork.com/
journals/jama/pages/instructions-for-authors, are taken into account:

1. Graph labels on right and left side are printed in bold font at top of forest plot (see arguments
   bottom.lr and ff.lr)
2. Information on effect measure and level of confidence interval is printed at bottom of forest
   plot (xlab)
3. Tests for overall effect are printed (test.overall)
4. Diamonds representing meta-analysis results are printed in lightblue (diamond.fixed, diamond.random)
5. Squares representing individual study results are printed in darkblue (col.square, col.square.lines)
6. Between-study variance $\tau^2$ is not printed
7. Empty rows are omitted (addrow)
8. Label "Source" is printed instead of "Study" (leftlabs)

The following changes are conducted if argument layout = "subgroup" (and arguments leftcols and rightcols are NULL) and a subgroup analysis was conducted:

1. Individual study results are omitted (see argument study.results)
2. Total number of observations is not printed (pooled.totals)
3. Label "Subgroup" is printed instead of "Study" (leftlabs)

If arguments lab.e and lab.c are NULL, "Experimental" and "Control" are used as labels for experimental and control group, respectively.

Argument pscale can be used to rescale single proportions or risk differences, e.g., pscale = 1000 means that proportions are expressed as events per 1000 observations. This is useful in situations with (very) low event probabilities.

Argument irscale can be used to rescale single rates or rate differences, e.g., irscale = 1000 means that rates are expressed as events per 1000 time units, e.g., person-years. This is useful in situations with (very) low rates. Argument irunit can be used to specify the time unit used in individual studies (default: "person-years"). This information is printed in summaries and forest plots if argument irscale is not equal to 1.

A prediction interval for treatment effect of a new study (Higgins et al., 2009) is given in the forest plot if arguments prediction and comb.random are TRUE. For graphical presentation of prediction intervals the approach by Guddat et al. (2012) is used.

Argument hetstat can be a character string to specify where to print heterogeneity information:

- row with results for fixed effect model (hetstat = "fixed"),
- row with results for random effects model (hetstat = "random"),
- rows with 'study' information (hetstat = "study") - only considered for metabind objects.

Otherwise, information on heterogeneity is printed in dedicated rows.

Note, in R package meta, version 3.0-0 the following arguments have been removed from R function forest.meta: byvar, level, level.comb, level.predict. This functionality is now provided by R function update.meta (or directly in R functions, e.g., metabin, metacont, metagen, metacor, and metaprop).

Author(s)

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References


See Also

metabin, metacont, metagen, metabind, settings.meta
Examples

data(Olkin95)
m1 <- metabin(event.e, n.e, event.c, n.c,
    data = Olkin95, subset = c(41, 47, 51, 59),
    sm = "RR", method = "I",
    studlab = paste(author, year))

## Not run:
# Do standard (symmetric) forest plot
#
forest(m1)
## End(Not run)

# Layout of forest plot similar to Review Manager 5
# (see http://community.cochrane.org/tools/review-production-tools/revman-5)
#
# Furthermore, add labels on both sides of forest plot and
# prediction interval
#
forest(m1, layout = "RevMan5", comb.fixed = FALSE,
     label.right = "Favours control", col.label.right = "red",
     label.left = "Favours experimental", col.label.left = "green",
     prediction = TRUE)

## Not run:
# Sort studies by decreasing treatment effect within year subgroups
#
ifelse(year < 1987, "Before 1987", "1987 and later")

m2 <- update(m1, byvar =

# Forest plot specifying argument xlim
#
forest(m1, xlim = c(0.01, 10))

# Print results of test for overall effect
#
forest(m1, test.overall.fixed = TRUE, test.overall.random = TRUE)

# Forest plot with 'classic' layout used in R package meta,
# version < 1.6-0
#
forest(m1, col.square = "black", hetstat = FALSE)

# Change set of columns printed on left side of forest plot
#
forest(m1, comb.random = FALSE, leftcols = "studlab")
# Do not print columns on right side of forest plot
# forest(m1, rightcols = FALSE)

# Change study label to "Author"
# forest(m1, comb.random = FALSE, leftlabs = c("Author", NA, NA, NA, NA))

# Just give effect estimate and 95% confidence interval on right
# side of forest plot (in one column)
# forest(m1, rightcols = c("effect.ci"))

# Just give effect estimate and 95% confidence interval on right
# side of forest plot
# forest(m1, rightcols = c("effect", "ci"))

# 1. Change order of columns on left side
# 2. Attach labels to columns 'event.e' and 'event.c' instead of
#    columns 'n.e' and 'n.c'
# forest(m1,
#      leftcols = c("studlab", "n.e", "event.e", "n.c", "event.c"),
#      lab.e.attach.to.col = "event.e",
#      lab.c.attach.to.col = "event.c")

# Specify column labels only for newly created variables 'year' and
# 'author' (which are part of dataset Olkin95)
# forest(m1,
#      leftcols = c("studlab", "event.e", "n.e", "event.c", "n.c",
#                    "author", "year"),
#      leftlabs = c("Author", "Year of Publ"))

# Center text in all columns
# forest(m1,
#      leftcols = c("studlab", "event.e", "n.e", "event.c", "n.c",
#                    "author", "year"),
#      leftlabs = c("Author", "Year of Publ"), hetstat = FALSE,
#      just = "center", just.addcols = "center", just.studlab = "center")

# Same result
# forest(m1,
#      leftcols = c("studlab", "event.e", "n.e", "event.c", "n.c",
#                    "author", "year"),
#      leftlabs = c("Author", "Year of Publ"), hetstat = FALSE,
#      just = "c", just.addcols = "c", just.studlab = "c")

# Change some fontsizes and fontfaces
#
forest(m1, 
  fs.study = 10, ff.study = "italic", 
  fs.study.label = 11, ff.study.label = "bold", 
  fs.axis = 5, ff.axis = "italic", 
  ff.smlab = "bold.italic", 
  ff.fixed = "plain", ff.hetstat = "plain")

# Change some colours
# forest(m1, 
  col.diamond = "green", col.diamond.lines = "red", 
  col.study = c("green", "blue", "red", "orange"), 
  col.square = "pink", col.square.lines = "black")

# Sort by weight in fixed effect model
# forest(m1, sortvar = 1 / w.fixed, comb.random = FALSE)

# Sort by decreasing weight in fixed effect model
# forest(m1, sortvar = -1 / w.fixed, comb.random = FALSE)

# Sort by size of treatment effect
# forest(m1, sortvar = TE, comb.random = FALSE)

# Sort by size of treatment effect
# forest(m1, sortvar = -TE, comb.random = FALSE)

# Sort by decreasing year of publication
# forest(m1, sortvar = -year, comb.random = FALSE)

# Print results of test for subgroup differences (random effects # model)
# forest(m2, 
  sortvar = -TE, comb.fixed = FALSE, 
  test.subgroup.random = TRUE)

# Print only subgroup results
# forest(m2, layout = "subgroup")

# Print only subgroup results (and consider text for heterogeneity # measures in width of subgroup column)
# forest(m2, layout = "subgroup", calcwidth.hetstat = TRUE)

## End(Not run)
funnel

Funnel plot

Description

Draw a funnel plot which can be used to assess small study effects in meta-analysis. A contour-enhanced funnel plot can also be produced to assess causes of funnel plot asymmetry.

Usage

funnel(x, ...)

## Default S3 method:
funnel(x, y, xlim = NULL, ylim = NULL, xlab = NULL,
ylab = NULL, comb.fixed = FALSE, comb.random = FALSE,
axes = TRUE, pch = 21, text = NULL, cex = 1, lty.fixed = 2,
lty.random = 9, lwd = 1, lwd.fixed = lwd, lwd.random = lwd,
col = "black", bg = "darkgray", col.fixed = "black",
col.random = "black", log = "", yaxis = "se", sm = "",
contour.levels = NULL, col.contour, ref = ifelse(backtransf &
is.relative.effect(sm), 1, 0), level = NULL, studlab = FALSE,
cex.studlab = 0.8, pos.studlab = 2, backtransf = TRUE, ...)

## S3 method for class 'meta'
funnel(x, xlim = NULL, ylim = NULL, xlab = NULL,
ylab = NULL, comb.fixed = x$comb.fixed,
comb.random = x$comb.random, axes = TRUE, pch = if (!inherits(x,
"trimfill")) 21 else ifelse(x$trimfill, 1, 21), text = NULL, cex = 1,
lty.fixed = 2, lty.random = 9, lwd = 1, lwd.fixed = lwd,
lwd.random = lwd, col = "black", bg = "darkgray",
col.fixed = "black", col.random = "black", log = "",
yaxis = "se", contour.levels = NULL, col.contour,
ref = ifelse(backtransf & is.relative.effect(x$sm), 1, 0),
level = x$level, studlab = FALSE, cex.studlab = 0.8,
pos.studlab = 2, ref.triangle = FALSE, lty.ref = 1,
lwd.ref = lwd, col.ref = "black", lty.ref.triangle = 5,
backtransf = x$backtransf, ...)

Arguments

x

An object of class meta, or estimated treatment effect in individual studies.

...  

Graphical arguments as in par may also be passed as arguments.

y

Standard error of estimated treatment effect.

xlim

The x limits (min,max) of the plot.

ylim

The y limits (min,max) of the plot.
funnel

xlab A label for the x-axis.
ylab A label for the y-axis.
comb.fixed A logical indicating whether the pooled fixed effect estimate should be plotted.
comb.random A logical indicating whether the pooled random effects estimate should be plotted.
axes A logical indicating whether axes should be drawn on the plot.
pch The plotting symbol used for individual studies.
text A character vector specifying the text to be used instead of plotting symbol.
cex The magnification to be used for plotting symbol.
lty.fixed Line type (pooled fixed effect estimate).
lty.random Line type (pooled random effects estimate).
lwd The line width for confidence intervals (if level is not NULL).
lwd.fixed The line width for fixed effect estimate (if comb.fixed is not NULL).
lwd.random The line width for random effects estimate (if comb.random is not NULL).
col A vector with colour of plotting symbols.
bg A vector with background colour of plotting symbols (only used if pch in 21:25).
col.fixed Color of line representing fixed effect estimate.
col.random Color of line representing random effects estimate.
log A character string which contains "x" if the x-axis is to be logarithmic, "y" if the y-axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic (applies only to function funnel).
yaxis A character string indicating which type of weights are to be used. Either "se", "invvar", "invse". or "size" (applies only to function funnel).
sm A character string indicating underlying summary measure, e.g., "RD", "RR", "OR", "ASD", "HR", "MD", "SMD", or "ROM" (applies only to function funnel).
contour.levels A numeric vector specifying contour levels to produce contour-enhanced funnel plot.
col.contour Colour of contours.
ref Reference value (null effect) used to produce contour-enhanced funnel plot.
level The confidence level utilised in the plot. For the funnel plot, confidence limits are not drawn if yaxis="size".
studlab A logical indicating whether study labels should be printed in the graph. A vector with study labels can also be provided (must be of same length as x$TE then).
cex.studlab Size of study labels, see argument cex in text.
pos.studlab Position of study labels, see argument pos in text.
backtransf A logical indicating whether results for relative summary measures (argument sm equal to "OR", "RR", "HR", or "IRR") should be back transformed in funnel plots. If backtransf=TRUE, results for sm="OR" are printed as odds ratios rather than log odds ratios, for example.
funnel

ref.triangle  A logical indicating whether reference value (null effect) should be printed.
lty.ref  Line type (reference value).
lwd.ref  The line width for the reference value and corresponding confidence intervals (if ref.triangle is TRUE and level is not NULL).
col.ref  Color of line representing reference value.
lty.ref.triangle  Line type (confidence intervals of reference value).

Details

A funnel plot (Light & Pillemer, 1984) is drawn in the active graphics window. If comb.fixed is TRUE, the pooled estimate of the fixed effect model is plotted. If level is not NULL, the corresponding confidence limits are drawn.

In the funnel plot, if yaxis is "se", the standard error of the treatment estimates is plotted on the y-axis which is likely to be the best choice (Sterne & Egger, 2001). Other possible choices for yaxis are "invvar" (inverse of the variance), "invse" (inverse of the standard error), and "size" (study size).

For yaxis!="size", contour-enhanced funnel plots can be produced (Peters et al., 2008) by specifying the contour levels (argument contour.levels). By default (argument col.contour missing), suitable gray levels will be used to distinguish the contours. Different colours can be chosen by argument col.contour.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>, Petra Graham <pgraham@efs.mq.edu.au>

References


See Also

metabias, metabin, metagen, radial

Examples

data(Olkin95)
ml <- metabin(event.e, n.e, event.c, n.c,
data = Olkin95, subset = c(41, 47, 51, 59),
studlab = paste(author, year),
sm = "RR", method = "I")
oldpar <- par(mfrow = c(2, 2))

# Standard funnel plot
# funnel(m1)
# Same result as code above:
funnel(m1$TE, m1$seTE, sm = "RR",
     comb.fixed = TRUE, level = 0.95)

# Funnel plot with confidence intervals, fixed effect estimate and
# contours
# cc <- funnel(m1, comb.fixed = TRUE,
# level = 0.95, contour = c(0.9, 0.95, 0.99))$col.contour
legend(0.05, 0.05,
       c("0.1 > p > 0.05", "0.05 > p > 0.01", "< 0.01"), fill = cc)

# Contour-enhanced funnel plot with user-chosen colours
# funnel(m1, comb.fixed = TRUE,
#       level = 0.95, contour = c("darkgreen", "green", "lightgreen"),
#       lwd = 2, cex = 2, pch = 16, studlab = TRUE, cex.studlab = 1.25)
legend(0.05, 0.05,
       c("0.1 > p > 0.05", "0.05 > p > 0.01", "< 0.01"),
       fill = c("darkgreen", "green", "lightgreen"))
par(oldpar)

---

**gs**

*Get default for a meta-analysis setting.*

**Description**

Get default for a meta-analysis setting in R package *meta*.

**Usage**

`gs(x)`

**Arguments**

- **x**  
  A character string holding a settings name.

**Details**

This function can be used to get the default for a meta-analysis setting defined using *settings.meta*.

This function is primarily used to define default settings in meta-analysis functions, e.g., *metabin* or *metacont*. A list of all arguments with current settings is printed using the command *settings.meta(“print”).*
Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

See Also
settings.meta

Examples

```# Get default setting for Hartung-Knapp method
#
gs("hakn")

# Get default setting for summary measure in metabin()
#
gs("smbin")```

---

**labbe**  
L’Abbé plot for meta-analysis with binary outcomes

Description

Draw a L’Abbé plot for meta-analysis with binary outcomes.

Usage

`labbe(x, ...)`

## Default S3 method:
labbe(x, y, xlim, ylim, xlab = NULL, ylab = NULL,  
TE.fixed = NULL, TE.random = NULL, comb.fixed = !is.null(TE.fixed),  
comb.random = !is.null(TE.random), backtransf = TRUE, axes = TRUE,  
pch = 21, text = NULL, cex = 1, col = "black",  
bg = "lightgray", lwd = 1, lwd.fixed = lwd, lwd.random = lwd,  
lty.fixed = 2, lty.random = 9, col.fixed = col, col.random = col,  
nulleffect = TRUE, lwd.nulleffect = lwd,  
col.nulleffect = "lightgray", sm = "", weight, studlab = FALSE,  
cex.studlab = 0.8, label.e = NULL, label.c = NULL, ...)

## S3 method for class 'metabin'
labbe(x, xlim, ylim, xlab = NULL, ylab = NULL,  
TE.fixed = x$TE.fixed, TE.random = x$TE.random,  
comb.fixed = x$comb.fixed, comb.random = x$comb.random,  
backtransf = x$backtransf, axes = TRUE, pch = 21, text = NULL,  
cex = 1, col = "black", bg = "lightgray", lwd = 1,  
lwd.fixed = lwd, lwd.random = lwd, lty.fixed = 2, lty.random = 9,  
...)

---

## Default S3 method:

```r
## S3 method for class 'metabin'
```
labbe

col.fixed = col, col.random = col, nulleffect = TRUE,
lwd.nulleffect = lwd, col.nulleffect = "lightgray", sm = x$sm,
weight, studlab = FALSE, cex.studlab = 0.8, label.e = x$label.e,
label.c = x$label.c, ...)

Arguments

x An object of class `metabin`. Alternatively, the x coordinates of points of the
L’Abbé plot.

y The y coordinates of the L’Abbé plot, if argument x is not an object of class
`metabin`.

xlim The x limits (min, max) of the plot.

ylim The y limits (min, max) of the plot.

xlab A label for the x-axis.

ylab A label for the y-axis.

TE.fixed A numeric or vector specifying combined fixed effect estimate(s).

TE.random A numeric or vector specifying combined random effects estimate(s).

comb.fixed A logical indicating whether the pooled fixed effect estimate should be plotted.

comb.random A logical indicating whether the pooled random effects estimate should be plotted.

backtransf A logical indicating which values should be printed on x- and y-axis (see De-
tails).

axes A logical indicating whether axes should be drawn on the plot.

cex The magnification to be used for plotting symbol.

col A vector with colour of plotting symbols.

bg A vector with background colour of plotting symbols (only used if pch in 21:25).

lwd The line width.

lwd.fixed The line width(s) for fixed effect estimate(s) (if `comb.fixed` is not NULL or
FALSE).

lwd.random The line width(s) for random effects estimate(s) (if `comb.random` is not NULL or
FALSE).

lty.fixed Line type(s) for fixed effect estimate(s).

lty.random Line type(s) for random effects estimate(s).

col.fixed Color of line(s) for fixed effect estimate(s).

col.random Color of line(s) for random effects estimate(s).

nulleffect A logical indicating whether line for null effect should be added to the plot.

lwd.nulleffect Width of line for null effect.
col.nulleffect  Color of line for null effect.

sm          A character string indicating underlying summary measure, i.e., "RD", "RR", "OR", or "ASD".

weight      Either a numeric vector specifying relative sizes of plotting symbols or a character string indicating which type of plotting symbols is to be used for individual treatment estimates. One of missing (see Details), "same", "fixed", or "random", can be abbreviated. Plot symbols have the same size for all studies or represent study weights from fixed effect or random effects model.

studlab     A logical indicating whether study labels should be printed in the graph. A vector with study labels can also be provided (must be of same length as x$event.e then).

cex.studlab Size of study labels.

label.e     Label for experimental group.

label.c     Label for control group.

Details

A L’Abbé plot is a scatter plot with the risk in the control group on the x-axis and the risk in the experimental group on the y-axis (L’Abbé et al., 1987). It can be used to evaluate heterogeneity in meta-analysis. Furthermore, this plot can aid to choose a summary measure (odds ratio, risk ratio, risk difference) that will result in more consistent results (Jiménez et al., 1997; Deeks, 2002).

If argument backtransf is TRUE (default), event probabilities will be printed on x- and y-axis. Otherwise, transformed event probabilities will be printed as defined by the summary measure, i.e., log odds of probabilities for odds ratio as summary measure (sm = "OR"), log probabilities for sm = "RR", and arcsine-transformed probabilities for sm = "ASD".

If comb.fixed is TRUE, the pooled estimate of the fixed effect model is plotted as a line. If comb.random is TRUE, the pooled estimate of the random effects model is plotted as a line.

Information from object x is utilised if argument weight is missing. Weights from the fixed effect model are used (weight = "fixed") if argument x$comb.fixed is TRUE; weights from the random effects model are used (weight = "random") if argument x$comb.random is TRUE and x$comb.fixed is FALSE.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

`metabin`

Examples

data(Olkin95)
m1 <- metabin(event.e, n.e, event.c, n.c,
    data = Olkin95,
    studlab = paste(author, year),
    sm = "RR", method = "I")

# L'Abbe plot for risk ratio
#
# labbe(m1)

# L'Abbe plot for odds ratio
#
# labbe(m1, sm = "OR")
# same plot
# labbe(update(m1, sm = "OR"))

# L'Abbe plot for risk difference
#
# labbe(m1, sm = "RD")

# L'Abbe plot on log odds scale
#
# labbe(m1, sm = "OR", backtransf = FALSE)

# L'Abbe plot for odds ratio with coloured lines for various
# treatment effects (defined as log odds ratios)
#
# mycols <- c("blue", "yellow", "green", "red",
#            "green", "yellow", "blue")
# labbe(m1, sm = "OR",
#      comb.random = FALSE,
#      TE.fixed = log(c(1 / 10, 1 / 5, 1 / 2,
#                       1, 2, 5, 10)),
#      col.fixed = mycols, lwd.fixed = 2)

# L'Abbe plot on log odds scale with coloured lines for various
# treatment effects (defined as log odds ratios)
#
# labbe(m1, sm = "OR",
#      comb.random = FALSE,
#      TE.fixed = log(c(1 / 10, 1 / 5, 1 / 2,
#                       1, 2, 5, 10)),
#      col.fixed = mycols, lwd.fixed = 2,
#      backtransf = FALSE)
metabias

Test for funnel plot asymmetry

Description

Test for funnel plot asymmetry, based on rank correlation or linear regression method.

Usage

metabias(x, ...)

## Default S3 method:
metabias(x, seTE, method.bias = "linreg",
         plotit = FALSE, correct = FALSE, k.min = 10, ...)

## S3 method for class 'meta'
metabias(x, method.bias = x$method.bias, plotit = FALSE,
         correct = FALSE, k.min = 10, ...)

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

Arguments

x An object of class meta or estimated treatment effect in individual studies.
...
seTE Standard error of estimated treatment effect (mandatory if x not of class meta).
method.bias A character string indicating which test is to be used. Either "rank", "linreg",
             "mm", "count", "score", or "peters", can be abbreviated.
plotit A logical indicating whether a plot should be produced for method.bias "rank",
        "linreg", "mm", or "score".
correct A logical indicating whether a continuity corrected statistic is used for rank cor-
         relation methods "rank" and "count".
k.min Minimum number of studies to perform test for funnel plot asymmetry.

Details

Functions to conduct rank correlation or linear regression tests for funnel plot asymmetry.

Following recommendations by Sterne et al. (2011), by default, a test for funnel plot asymmetry is
only conducted if the number of studies is ten or larger (argument k.min = 10). This behaviour can
be changed by setting a smaller value for argument k.min. Note, the minimum number of studies
is three.

If argument method.bias is "rank", the test statistic is based on the rank correlation between
standardised treatment estimates and variance estimates of estimated treatment effects; Kendall’s
tau is used as correlation measure (Begg & Mazumdar, 1994). The test statistic follows a standard
normal distribution. By default (if correct is FALSE), no continuity correction is utilised (Kendall & Gibbons, 1990).

If argument method.bias is "linreg", the test statistic is based on a weighted linear regression of the treatment effect on its standard error (Egger et al., 1997). The test statistic follows a t distribution with number of studies -2 degrees of freedom.

If argument method.bias is "mm", the test statistic is based on a weighted linear regression of the treatment effect on its standard error using the method of moments estimator for the additive between-study variance component (method 3a in Thompson, Sharp, 1999). The test statistic follows a t distribution with number of studies -2 degrees of freedom.

If argument method.bias is "peters", the test statistic is based on a weighted linear regression of the treatment effect on the inverse of the total sample size using the variance of the average event rate as weights (Peters et al., 2006). The test statistic follows a t distribution with number of studies -2 degrees of freedom. This test is available for meta-analyses comparing two binary outcomes or combining single proportions, i.e. generated with functions metabin and metaprop.

The following tests for funnel plot asymmetry are only available for meta-analyses comparing two binary outcomes, i.e. meta-analyses generated with the metabin function.

If argument method.bias is "count", the test statistic is based on the rank correlation between a standardised cell frequency and the inverse of the variance of the cell frequency: Kendall’s tau is used as correlation measure (Schwarzer et al., 2007). The test statistic follows a standard normal distribution. By default (if correct is FALSE), no continuity correction is utilised (Kendall & Gibbons, 1990).

If argument method.bias is "score", the test statistic is based on a weighted linear regression utilising efficient score and score variance (Harbord et al., 2006, 2009). The test statistic follows a t distribution with number of studies -2 degrees of freedom.

In order to calculate an arcsine test for funnel plot asymmetry (Rücker et al., 2008), one has to use the metabin function with argument sm = "ASD" as input to the metabias command. The three arcsine tests described in Rücker et al. (2008) can be calculated by setting method.bias to "rank", "linreg" and "mm", respectively.

If argument method.bias is missing, the Harbord test (method.bias = "score") is used for the odds ratio as effect measure and the Egger test (method.bias = "linreg") for other effect measures (Sterne et al., 2011).

No test for funnel plot asymmetry is conducted in meta-analyses with subgroups.

**Value**

A list with class htest containing the following components if a test for funnel plot asymmetry is conducted:

- **estimate**
  - The estimated degree of funnel plot asymmetry, with name "ks" or "bias" corresponding to the method employed, i.e., rank correlation or regression method.

- **statistic**
  - The value of the test statistic.

- **parameters**
  - The degrees of freedom of the test statistic in the case that it follows a t distribution.

- **p.value**
  - The p-value for the test.

- **alternative**
  - A character string describing the alternative hypothesis.
metabias

method A character string indicating what type of test was used.
data.name A character string giving the names of the data.
title Title of Cochrane review.
complab Comparison label.
outclab Outcome label.
version Version of R package meta used to create object.

Or a list with the following elements if test is not conducted due to the number of studies:
k Number of studies in meta-analysis.
k.min Minimum number of studies to perform test for funnel plot asymmetry.
version Version of R package meta used to create object.

Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


Schwarzer G, Antes G & Schumacher M (2007): A test for publication bias in meta-analysis with sparse binary data. Statistics in Medicine, 26, 721–33

Sterne, JAC et al. (2011): Recommendations for examining and interpreting funnel plot asymmetry in meta-analyses of randomised controlled trials. BMJ (Clinical research ed.), 343, 1

Thompson SG & Sharp, SJ (1999): Explaining heterogeneity in meta-analysis: a comparison of methods, Statistics in Medicine, 18, 2693–708

See Also

funnel, funnel.meta, metabin, metacont, metagen
Examples

data(Olkin95)
m1 <- metabin(event.e, n.e, event.c, n.c,
data = Olkin95, subset = 1:10,
sm = "RR", method = "I")

metabias(m1)
metabias(m1, plotit = TRUE)

metabias(m1, method.bias = "rank")
metabias(m1, method.bias = "rank", correct = TRUE)

metabias(m1, method.bias = "count")
metabias(m1, method.bias = "linreg")$p.value

# Arcsine test (based on linear regression)
#
m1.as <- update(m1, sm = "ASD")
metabias(m1.as)
# Same result (using function metabias.default)
metabias(m1.as$TE, m1.as$seTE)

# No test for funnel plot asymmetry calculated
#
m2 <- update(m1, subset = 1:5)
metabias(m2)

m3 <- update(m1, subset = 1:2)
metabias(m3)

# Test for funnel plot asymmetry calculated (use of argument k.min)
#
metabias(m2, k.min = 5)

metabias.rm5

Cochrane review: Test for funnel plot asymmetry

Description

Conduct a test for funnel plot asymmetry for all outcomes in a Cochrane review

Usage

## S3 method for class 'rm5'
metabias(x, comp.no, outcome.no, method.bias = "linreg",
method.bias.binary = method.bias, method.bias.or = "score",
k.min = 10, ... )
Arguments

x An object of class rm5.
comp.no Comparison number.
outcome.no Outcome number.
method.bias A character string indicating which test for small-study effects is to be used for all outcomes. Either "rank", "linreg", or "mm", can be abbreviated. See function metabias
method.bias.binary A character string indicating which test is to be used for binary outcomes. Either "rank", "linreg", "mm", "count", "score", or "peters", can be abbreviated. See function metabias
method.bias.or A character string indicating which test is to be used for binary outcomes with odds ratio as summary measure. Either "rank", "linreg", "mm", "count", "score", or "peters", can be abbreviated. See function metabias
k.min Minimum number of studies to perform test for small-study effects.
... Additional arguments (ignored at the moment)

Details

This function can be used to conduct a test for funnel plot asymmetry for all or selected meta-analyses in a Cochrane Review.

Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://community.cochrane.org/tools/review-production-tools/revman-5). In RevMan 5, subgroup analyses can be defined and data from a Cochrane review can be imported to R using the function read.rm5.

The R function metacr is called internally.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

metabias, metacr, read.rm5, summary.rm5

Examples

# Locate export data file "Fleiss93_CR.csv" in sub-directory of
# package "meta"
# filename <- system.file("extdata", "Fleiss93_CR.csv", package = "meta")
Fleiss93.CR <- read.rm5(filename)
metabin

Meta-analysis of binary outcome data

Description
Calculation of fixed effect and random effects estimates (risk ratio, odds ratio, risk difference, or arcsine difference) for meta-analyses with binary outcome data. Mantel-Haenszel, inverse variance, Peto method, and generalised linear mixed model (GLMM) are available for pooling. For GLMMs, the \texttt{rma.glmm} function from R package \texttt{metafor} (Viechtbauer 2010) is called internally.

Usage

\begin{verbatim}
metabin(event.e, n.e, event.c, n.c, studlab, data = NULL, 
subset = NULL, exclude = NULL, method = ifelse(tau.common, 
"Inverse", gs("method")), sm = ifelse(is.na(charmatch(tolower(method), 
c("peto", "glm"), nomatch = NA)), "OR", gs("smbin")), 
incr = gs("incr"), allincr = gs("allincr"), 
addincr = gs("addincr"), allstudies = gs("allstudies"), 
MH.exact = gs("MH.exact"), RR.cochrane = gs("RR.cochrane"), 
model.glmm = "UM.FS", level = gs("level"), 
level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"), 
comb.random = gs("comb.random"), hakn = gs("hakn"), 
method.tau = ifelse(is.na(charmatch(tolower(method), "glm", nomatch = 
NA)), "ML", gs("method.tau")), tau.preset = NULL, 
TE.tau = NULL, tau.common = gs("tau.common"), prediction = gs("prediction"), 
level.predict = gs("level.predict"), method.bias = ifelse(sm == "OR", 
"score", gs("method.bias")), backtransf = gs("backtransf"), 
pscale = 1, title = gs("title"), complab = gs("complab"), 
outclab = ", label.e = gs("label.e"), label.c = gs("label.c"), 
label.left = gs("label.left"), label.right = gs("label.right"), 
byvar, bylab, print.byvar = gs("print.byvar"), 
byseparator = gs("byseparator"), print.CMH = gs("print.CMH"), 
keepdata = gs("keepdata"), warn = gs("warn"), control = NULL, ...)
\end{verbatim}
Arguments

- **event.e**: Number of events in experimental group.
- **n.e**: Number of observations in experimental group.
- **event.c**: Number of events in control group.
- **n.c**: Number of observations in control group.
- **studlab**: An optional vector with study labels.
- **data**: An optional data frame containing the study information, i.e., event.e, n.e, event.c, and n.c.
- **subset**: An optional vector specifying a subset of studies to be used.
- **exclude**: An optional vector specifying studies to exclude from meta-analysis, however, to include in printouts and forest plots.
- **method**: A character string indicating which method is to be used for pooling of studies. One of "Inverse", "MH", "Peto", or "GLMM", can be abbreviated.
- **sm**: A character string indicating which summary measure ("RR", "OR", "RD", or "ASD") is to be used for pooling of studies, see Details.
- **incr**: Could be either a numerical value which is added to each cell frequency for studies with a zero cell count or the character string "TACC" which stands for treatment arm continuity correction, see Details.
- **allincr**: A logical indicating if incr is added to each cell frequency of all studies if at least one study has a zero cell count. If FALSE (default), incr is added only to each cell frequency of studies with a zero cell count.
- **addincr**: A logical indicating if incr is added to each cell frequency of all studies irrespective of zero cell counts.
- **allstudies**: A logical indicating if studies with zero or all events in both groups are to be included in the meta-analysis (applies only if sm is equal to "RR" or "OR").
- **MH.exact**: A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.
- **RR.cochrane**: A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.
- **model.glmm**: A character string indicating which GLMM should be used. One of "UM.FS", "UM.RS", "CM.EL", and "CM.AL", see Details.
- **level**: The level used to calculate confidence intervals for individual studies.
- **level.comb**: The level used to calculate confidence intervals for pooled estimates.
- **comb.fixed**: A logical indicating whether a fixed effect meta-analysis should be conducted.
- **comb.random**: A logical indicating whether a random effects meta-analysis should be conducted.
- **hakn**: A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.
method.tau  A character string indicating which method is used to estimate the between-study variance $\tau^2$. Either "DL", "PM", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.

tau.preset  Prespecified value for the square-root of the between-study variance $\tau^2$.

TE.tau  Overall treatment effect used to estimate the between-study variance $\tau^2$.

tau.common  A logical indicating whether tau-squared should be the same across subgroups.

prediction  A logical indicating whether a prediction interval should be printed.

level.predict  The level used to calculate prediction interval for a new study.

method.bias  A character string indicating which test for funnel plot asymmetry is to be used. Either "rank", "linreg", "mm", "count", "score", or "peters", can be abbreviated. See function metabias

backtransf  A logical indicating whether results for odds ratio (sm="OR") and risk ratio (sm="RR") should be back transformed in printouts and plots. If TRUE (default), results will be presented as odds ratios and risk ratios; otherwise log odds ratios and log risk ratios will be shown.

pscale  A numeric defining a scaling factor for printing of risk differences.

title  Title of meta-analysis / systematic review.

complab  Comparison label.

outclab  Outcome label.

label.e  Label for experimental group.

label.c  Label for control group.

label.left  Graph label on left side of forest plot.

label.right  Graph label on right side of forest plot.

byvar  An optional vector containing grouping information (must be of same length as event.e).

bylab  A character string with a label for the grouping variable.

print.byvar  A logical indicating whether the name of the grouping variable should be printed in front of the group labels.

byseparator  A character string defining the separator between label and levels of grouping variable.

print.CMH  A logical indicating whether result of the Cochran-Mantel-Haenszel test for overall effect should be printed.

keepdata  A logical indicating whether original data (set) should be kept in meta object.

warn  A logical indicating whether warnings should be printed (e.g., if incr is added to studies with zero cell frequencies).

control  An optional list to control the iterative process to estimate the between-study variance $\tau^2$. This argument is passed on to rma.uni or rma.glmm, respectively.

...  Additional arguments passed on to rma.glmm function.
Details

Treatment estimates and standard errors are calculated for each study. The following measures of
treatment effect are available:

- Risk ratio (sm = "RR")
- Odds ratio (sm = "OR")
- Risk difference (sm = "RD")
- Arcsine difference (sm = "ASD")

For several arguments defaults settings are utilised (assignments using gs function). These defaults
can be changed using the settings.meta function.

Internally, both fixed effect and random effects models are calculated regardless of values chosen
for arguments comb.fixed and comb.random. Accordingly, the estimate for the random effects
model can be extracted from component TE.random of an object of class "meta" even if argument
comb.random = FALSE. However, all functions in R package meta will adequately consider the
values for comb.fixed and comb.random. E.g. function print.meta will not print results for the
random effects model if comb.random = FALSE.

By default, both fixed effect and random effects models are considered (see arguments comb.fixed
and comb.random). If method is "MH" (default), the Mantel-Haenszel method is used to calculate
the fixed effect estimate; if method is "Inverse", inverse variance weighting is used for pooling;
if method is "Peto", the Peto method is used for pooling. For the Peto method, Peto's log odds
ratio, i.e. \((O - E) / V\) and its standard error \(\sqrt{1 / V}\) with \(O - E\) and \(V\) denoting "Observed minus
Expected" and "V", are utilised in the random effects model. Accordingly, results of a random
effects model using sm = "Peto" can be (slightly) different to results from a random effects model
using sm = "MH" or sm = "Inverse".

A distinctive and frequently overlooked advantage of binary endpoints is that individual patient
data (IPD) can be extracted from a two-by-two table. Accordingly, statistical methods for IPD, i.e.,
logistic regression and generalised linear mixed models, can be utilised in a meta-analysis of binary
outcomes (Stijnen et al., 2010; Simmonds et al., 2016). These methods are available (argument
method = "GLMM") for the odds ratio as summary measure by calling the rma.glmm function from R
package metafor internally.

Four different GLMMs are available for meta-analysis with binary outcomes using argument model.glmm
(which corresponds to argument model in the rma.glmm function):

1. Logistic regression model with fixed study effects (default)
   (model.glmm = "UM.FS", i.e., Unconditional Model - Fixed Study effects)
2. Mixed-effects logistic regression model with random study effects
   (model.glmm = "UM.RS", i.e., Unconditional Model - Random Study effects)
3. Generalised linear mixed model (conditional Hypergeometric-Normal)
   (model.glmm = "CM.EL", i.e., Conditional Model - Exact Likelihood)
4. Generalised linear mixed model (conditional Binomial-Normal)
   (model.glmm = "CM.UL", i.e., Conditional Model - Approximate Likelihood)

Details on these four GLMMs as well as additional arguments which can be provided using argu-
ment `...{}` in metabin are described in rma.glmm where you can also find information on
the iterative algorithms used for estimation. Note, regardless of which value is used for argument
model.glmm, results for two different GLMMs are calculated: fixed effect model (with fixed treatment effect) and random effects model (with random treatment effects).

For studies with a zero cell count, by default, 0.5 is added to all cell frequencies of these studies; if inc r is "TACC" a treatment arm continuity correction is used instead (Sweeting et al., 2004; Diamond et al., 2007). For odds ratio and risk ratio, treatment estimates and standard errors are only calculated for studies with zero or all events in both groups if allstudies is TRUE. This continuity correction is used both to calculate individual study results with confidence limits and to conduct meta-analysis based on the inverse variance method. For Peto method and GLMMs no continuity correction is used. For the Mantel-Haenszel method, by default (if MH.exact is FALSE), inc r is added to all cell frequencies of a study with a zero cell count in the calculation of the pooled risk ratio or odds ratio as well as the estimation of the variance of the pooled risk difference, risk ratio or odds ratio. This approach is also used in other software, e.g., RevMan 5 and the Stata procedure metan. According to Fleiss (in Cooper & Hedges, 1994), there is no need to add 0.5 to a cell frequency of zero to calculate the Mantel-Haenszel estimate and he advocates the exact method (MH.exact = TRUE). Note, estimates based on exact Mantel-Haenszel method or GLMM are not defined if the number of events is zero in all studies either in the experimental or control group.

Argument byvar can be used to conduct subgroup analysis for all methods but GLMMs. Instead use the metareg function for GLMMs which can also be used for continuous covariates.

A prediction interval for the treatment effect of a new study is calculated (Higgins et al., 2009) if arguments prediction and comb.random are TRUE.

R function update.meta can be used to redo the meta-analysis of an existing metabin object by only specifying arguments which should be changed.

For the random effects, the method by Hartung and Knapp (2001) is used to adjust test statistics and confidence intervals if argument hakn = TRUE. For GLMMs, a method similar to Knapp and Hartung (2003) is implemented, see description of argument tdist in rma.glmm.

The DerSimonian-Laird estimate (1986) is used in the random effects model if method.tau = "DL". The iterative Paule-Mandel method (1982) to estimate the between-study variance is used if argument method.tau = "PM". Internally, R function paulemandel is called which is based on R function mpaule.default from R package metRology from S.L.R. Ellison <s.ellison at lgc.co.uk>.

If R package metafor (Viechtbauer 2010) is installed, the following methods to estimate the between-study variance \( \tau^2 \) (argument method.tau) are also available:

- Restricted maximum-likelihood estimator (method.tau = "REML")
- Maximum-likelihood estimator (method.tau = "ML")
- Hunter-Schmidt estimator (method.tau = "HS")
- Sidik-Jonkman estimator (method.tau = "SJ")
- Hedges estimator (method.tau = "HE")
- Empirical Bayes estimator (method.tau = "EB")

For these methods the R function rma.uni of R package metafor is called internally. See help page of R function rma.uni for more details on these methods to estimate between-study variance.

Value

An object of class c("metabin", "meta") with corresponding print, summary, and forest functions. The object is a list containing the following components:
event.e, n.e, event.c, n.c, studlab, exclude,
   As defined above.
sm, method, incr, allincr, addincr,
   As defined above.
allstudies, MH.exact, RR.cochrane, model.glmm, warn,
   As defined above.
level, level.comb, comb.fixed, comb.random,
   As defined above.
hakn, method.tau, tau.preset, TE.tau, method.bias,
   As defined above.
tau.common, title, complab, outclab,
   As defined above.
label.e, label.c, label.left, label.right,
   As defined above.
byvar, bylab, print.byvar, byseparator
   As defined above.
TE, seTE  Estimated treatment effect and standard error of individual studies.
lower, upper  Lower and upper confidence interval limits for individual studies.
zval, pval  z-value and p-value for test of treatment effect for individual studies.
w.fixed, w.random  Weight of individual studies (in fixed and random effects model).
TE.fixed, seTE.fixed  Estimated overall treatment effect, e.g., log risk ratio or risk difference, and standard error (fixed effect model).
lower.fixed, upper.fixed  Lower and upper confidence interval limits (fixed effect model).
zval.fixed, pval.fixed  z-value and p-value for test of overall treatment effect (fixed effect model).
TE.random, seTE.random  Estimated overall treatment effect, e.g., log risk ratio or risk difference, and standard error (random effects model).
lower.random, upper.random  Lower and upper confidence interval limits (random effects model).
zval.random, pval.random  z-value or t-value and corresponding p-value for test of overall treatment effect (random effects model).
prediction, level.predict  As defined above.
seTE.predict  Standard error utilised for prediction interval.
lower.predict, upper.predict  Lower and upper limits of prediction interval.
k  Number of studies combined in meta-analysis.
Q  Heterogeneity statistic Q.
df.Q  Degrees of freedom for heterogeneity statistic.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pval.Q</td>
<td>P-value of heterogeneity test.</td>
</tr>
<tr>
<td>Q.LRT</td>
<td>Heterogeneity statistic for likelihood-ratio test (only if method = &quot;GLMM&quot;).</td>
</tr>
<tr>
<td>df.Q.LRT</td>
<td>Degrees of freedom for likelihood-ratio test.</td>
</tr>
<tr>
<td>pval.Q.LRT</td>
<td>P-value of likelihood-ratio test.</td>
</tr>
<tr>
<td>tau</td>
<td>Square-root of between-study variance.</td>
</tr>
<tr>
<td>se.tau</td>
<td>Standard error of square-root of between-study variance.</td>
</tr>
<tr>
<td>C</td>
<td>Scaling factor utilised internally to calculate common tau-squared across subgroups.</td>
</tr>
<tr>
<td>Q.CMH</td>
<td>Cochran-Mantel-Haenszel test statistic for overall effect.</td>
</tr>
<tr>
<td>df.Q.CMH</td>
<td>Degrees of freedom for Cochran-Mantel-Haenszel test statistic.</td>
</tr>
<tr>
<td>incr.e, incr.c</td>
<td>Increment added to cells in the experimental and control group, respectively.</td>
</tr>
<tr>
<td>sparse</td>
<td>Logical flag indicating if any study included in meta-analysis has any zero cell frequencies.</td>
</tr>
<tr>
<td>doublezeros</td>
<td>Logical flag indicating if any study has zero cell frequencies in both treatment groups.</td>
</tr>
<tr>
<td>df.hakn</td>
<td>Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn = TRUE).</td>
</tr>
<tr>
<td>k.MH</td>
<td>Number of studies combined in meta-analysis using Mantel-Haenszel method.</td>
</tr>
<tr>
<td>bylevs</td>
<td>Levels of grouping variable - if byvar is not missing.</td>
</tr>
<tr>
<td>TE.fixed.w, seTE.fixed.w</td>
<td>Estimated treatment effect and standard error in subgroups (fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>lower.fixed.w, upper.fixed.w</td>
<td>Lower and upper confidence interval limits in subgroups (fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>zval.fixed.w, pval.fixed.w</td>
<td>z-value and p-value for test of treatment effect in subgroups (fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>TE.random.w, seTE.random.w</td>
<td>Estimated treatment effect and standard error in subgroups (random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>lower.random.w, upper.random.w</td>
<td>Lower and upper confidence interval limits in subgroups (random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>zval.random.w, pval.random.w</td>
<td>z-value or t-value and corresponding p-value for test of treatment effect in subgroups (random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>w.fixed.w, w.random.w</td>
<td>Weight of subgroups (in fixed and random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>df.hakn.w</td>
<td>Degrees of freedom for test of treatment effect for Hartung-Knapp method in subgroups - if byvar is not missing and hakn = TRUE.</td>
</tr>
</tbody>
</table>
n.harmonic.mean.w  Harmonic mean of number of observations in subgroups (for back transformation of Freeman-Tukey Double arcsine transformation) - if byvar is not missing.

event.e.w  Number of events in experimental group in subgroups - if byvar is not missing.
n.e.w  Number of observations in experimental group in subgroups - if byvar is not missing.

event.c.w  Number of events in control group in subgroups - if byvar is not missing.
n.c.w  Number of observations in control group in subgroups - if byvar is not missing.
k.w  Number of studies combined within subgroups - if byvar is not missing.
k.all.w  Number of all studies in subgroups - if byvar is not missing.

Q.w.fixed  Overall within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

Q.w.random  Overall within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing (only calculated if argument tau.common is TRUE).

df.Q.w  Degrees of freedom for test of overall within subgroups heterogeneity - if byvar is not missing.

pval.Q.w.fixed  P-value of within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

pval.Q.w.random  P-value of within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

Q.b.fixed  Overall between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

Q.b.random  Overall between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

df.Q.b  Degrees of freedom for test of overall between subgroups heterogeneity - if byvar is not missing.

pval.Q.b.fixed  P-value of between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

pval.Q.b.random  P-value of between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

tau.w  Square-root of between-study variance within subgroups - if byvar is not missing.

C.w  Scaling factor utilised internally to calculate common tau-squared across subgroups - if byvar is not missing.

H.w  Heterogeneity statistic H within subgroups - if byvar is not missing.

lower.H.w, upper.H.w  Lower and upper confidence limits for heterogeneity statistic H within subgroups - if byvar is not missing.

I2.w  Heterogeneity statistic I2 within subgroups - if byvar is not missing.
metabin

lower.I2.w, upper.I2.w
Lower and upper confidence limit for heterogeneity statistic I2 within subgroups - if byvar is not missing.

keepdata
As defined above.
data
Original data (set) used in function call (if keepdata = TRUE).
subset
Information on subset of original data used in meta-analysis (if keepdata = TRUE).
.glmm.fixed
GLMM object generated by call of \texttt{rma.glmm} function (fixed effect model).
.glmm.random
GLMM object generated by call of \texttt{rma.glmm} function (random effects model).
call
Function call.
version
Version of R package \texttt{meta} used to create object.
version.metafor
Version of R package \texttt{metafor} used for GLMMs.

Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


StataCorp. 2011. *Stata Statistical Software: Release 12*. College Station, TX: StataCorp LP.


**See Also**

`update.meta`, `forest`, `funnel`, `metabias`, `metacont`, `metagen`, `metareg`, `print.meta`

**Examples**

```r
# Calculate odds ratio and confidence interval for a single study
#
metabin(10, 20, 15, 20, sm = "OR")

# Different results (due to handling of studies with double zeros)
#
metabin(0, 10, 0, 10, sm = "OR")
metabin(0, 10, 0, 10, sm = "OR", allstudies = TRUE)

# Use subset of Olkin (1995) to conduct meta-analysis based on
# inverse variance method (with risk ratio as summary measure)
#
data(Olkin95)
m1 <- metabin(event.e, n.e, event.c, n.c,
data = Olkin95, subset = c(41, 47, 51, 59),
method = "Inverse")
summary(m1)

# Use different subset of Olkin (1995)
#
m2 <- metabin(event.e, n.e, event.c, n.c,
data = Olkin95, subset = year < 1970,
method = "Inverse", studlab = author)
summary(m2)
forest(m2)

# Meta-analysis with odds ratio as summary measure
#
m3 <- metabin(event.e, n.e, event.c, n.c,
data = Olkin95, subset = year < 1970,
sm = "OR", method = "Inverse", studlab = author)
# Same meta-analysis result using 'update.meta' function
m3 <- update(m2, sm = "OR")
```

summary(m3)

# Meta-analysis based on Mantel-Haenszel method (with odds ratio as
# summary measure)
#
m4 <- update(m3, method = "MH")
summary(m4)

# Meta-analysis based on Peto method (only available for odds ratio
# as summary measure)
#
m5 <- update(m3, method = "Peto")
summary(m5)

## Not run:
# Meta-analysis using generalised linear mixed models (only if R
# packages 'metafor' and 'lme4' are available)
#
if (suppressMessages(require(metafor, quietly = TRUE, warn = FALSE)) &
    require(lme4, quietly = TRUE)) {
    # Logistic regression model with (k = 4) fixed study effects
    # (default: model.glmm = "UM.FS")
    #
m6 <- metabin(event.e, n.e, event.c, n.c,
                   data = Olkin95, subset = year < 1970,
                   method = "GLMM")
    # Same results:
    m6 <- update(m2, method = "GLMM")
    summary(m6)

    # Mixed-effects logistic regression model with random study effects
    # (warning message printed due to argument 'nAGQ')
    #
m7 <- update(m6, model.glmm = "UM.RS")
    #
    # Use additional argument 'nAGQ' for internal call of 'rma.glmm'
    # function
    #
m7 <- update(m6, model.glmm = "UM.RS", nAGQ = 1)
summary(m7)

    # Generalised linear mixed model (conditional
    # Hypergeometric-Normal) (R package 'BiasedUrn' must be available)
    #
    if (require(BiasedUrn, quietly = TRUE)) {
        m8 <- update(m6, model.glmm = "CM.EL")
        summary(m8)
    }

    # Generalised linear mixed model (conditional Binomial-Normal)
    #
m9 <- update(m6, model.glmm = "CM.AL")
summary(m9)

# Logistic regression model with (k = 70) fixed study effects
# (about 18 seconds with Intel Core i7-3667U, 2.0GHz)
#
m10 <- metabin(event.e, n.e, event.c, n.c,
    data = Olkin95, method = "GLMM")
summary(m10)

# Mixed-effects logistic regression model with random study effects
# - about 50 seconds with Intel Core i7-3667U, 2.0GHz
# - several warning messages, e.g. "failure to converge, ...
# summary(update(m10, model.glmm = "UM.RS"))

# Conditional Hypergeometric-Normal GLMM
# - long computation time (about 12 minutes with Intel Core
#   i7-3667U, 2.0GHz)
# - estimation problems for this very large dataset:
#   * warning that Choleski factorization of Hessian failed
#   * confidence interval for treatment effect smaller in random
#   effects model compared to fixed effect model
# if (require(BiasedUrn, quietly = TRUE)) {
#    system.time(m11 <- update(m10, model.glmm = "CM.EL"))
#    summary(m11)
# }

# Generalised linear mixed model (conditional Binomial-Normal)
# (less than 1 second with Intel Core i7-3667U, 2.0GHz)
# summary(update(m10, model.glmm = "CM.AL"))
#
## End(Not run)

---

**metabind**  
*Combine meta-analysis objects*

**Description**

This function can be used to combine meta-analysis objects and is, for example, useful to generate a forest plot with results of subgroup analyses.

**Usage**

metabind(...)
Arguments

... Any number of meta-analysis objects (see Details).

name An optional character vector providing descriptive names for the meta-analysis objects.

pooled A character string indicating whether results of a fixed effect or random effects model should be considered. Either "fixed" or "random", can be abbreviated.

backtransf A logical indicating whether results should be back transformed in printouts and plots. If backtransf=TRUE (default), results for sm="OR" are printed as odds ratios rather than log odds ratios, for example.

outclab Outcome label for all meta-analysis objects.

Details

This function can be used to combine meta-analysis objects and is, for example, useful to generate a forest plot with results of subgroup analyses.

Value

An object of class c("metabind","meta") with corresponding print, summary, and forest functions. See metagen for more information on list elements.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

See Also

metagen, forest.metabind

Examples

data(Fleiss93cont)

# Add some (fictitious) grouping variables:
#
Fleiss93cont$age <- c(55, 65, 55, 65, 55)
Fleiss93cont$region <- c("Europe", "Europe", "Asia", "Asia", "Europe")

m1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c,
data = Fleiss93cont, sm = "MD")

# Conduct two subgroup analyses
#
m1 <- update(m1, byvar = age, bylab = "Age group")
m2 <- update(m1, byvar = region, bylab = "Region")

# Combine subgroup meta-analyses and show forest plot with subgroup results
#
metacont <- metabind(mu1, mu2)
mb1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, studlab, data = NULL, subset = NULL, exclude = NULL, sm = gs("smcont"), pooledvar = gs("pooledvar"), method.smd = gs("method.smd"), sd.glass = gs("sd.glass"), exact.smd = gs("exact.smd"), level = gs("level"), level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"), comb.random = gs("comb.random"), hakn = gs("hakn"), method.tau = gs("method.tau"), tau.preset = NULL, TE.tau = NULL, tau.common = gs("tau.common"), prediction = gs("prediction"), level.predict = gs("level.predict"), method.bias = gs("method.bias"), backtransf = gs("backtransf"), title = gs("title"), complab = gs("complab"), outclab = "", label.e = gs("label.e"), label.c = gs("label.c"), label.left = gs("label.left"), label.right = gs("label.right"), byvar, bylab, print.byvar = gs("print.byvar"), byseparator = gs("byseparator"), keepdata = gs("keepdata"), warn = gs("warn"), control = NULL)

Description

Calculation of fixed and random effects estimates for meta-analyses with continuous outcome data; inverse variance weighting is used for pooling.

Usage

```
metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, studlab, data = NULL, subset = NULL, exclude = NULL, sm = gs("smcont"), pooledvar = gs("pooledvar"), method.smd = gs("method.smd"), sd.glass = gs("sd.glass"), exact.smd = gs("exact.smd"), level = gs("level"), level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"), comb.random = gs("comb.random"), hakn = gs("hakn"), method.tau = gs("method.tau"), tau.preset = NULL, TE.tau = NULL, tau.common = gs("tau.common"), prediction = gs("prediction"), level.predict = gs("level.predict"), method.bias = gs("method.bias"), backtransf = gs("backtransf"), title = gs("title"), complab = gs("complab"), outclab = "", label.e = gs("label.e"), label.c = gs("label.c"), label.left = gs("label.left"), label.right = gs("label.right"), byvar, bylab, print.byvar = gs("print.byvar"), byseparator = gs("byseparator"), keepdata = gs("keepdata"), warn = gs("warn"), control = NULL)
```

Arguments

- `n.e`: Number of observations in experimental group.
- `mean.e`: Estimated mean in experimental group.
- `sd.e`: Standard deviation in experimental group.
- `n.c`: Number of observations in control group.
- `mean.c`: Estimated mean in control group.
- `sd.c`: Standard deviation in control group.
- `studlab`: An optional vector with study labels.
- `data`: An optional data frame containing the study information.
- `subset`: An optional vector specifying a subset of studies to be used.
- `exclude`: An optional vector specifying studies to exclude from meta-analysis, however, to include in printouts and forest plots.
sm  A character string indicating which summary measure ("MD", "SMD", or "ROM") is to be used for pooling of studies.

pooledvar  A logical indicating if a pooled variance should be used for the mean difference (sm="MD").

method.smd  A character string indicating which method is used to estimate the standardised mean difference (sm="SMD"). Either "Hedges" for Hedges’ g (default), "Cohen" for Cohen’s d, or "Glass" for Glass’ delta, can be abbreviated.

sd.glass  A character string indicating which standard deviation is used in the denominator for Glass’ method to estimate the standardised mean difference. Either "control" using the standard deviation in the control group (sd.c) or "experimental" using the standard deviation in the experimental group (sd.e), can be abbreviated.

exact.smd  A logical indicating whether exact formulae should be used in estimation of the standardised mean difference and its standard error (see Details).

level  The level used to calculate confidence intervals for individual studies.

level.comb  The level used to calculate confidence intervals for pooled estimates.

comb.fixed  A logical indicating whether a fixed effect meta-analysis should be conducted.

comb.random  A logical indicating whether a random effects meta-analysis should be conducted.

hakn  A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.

method.tau  A character string indicating which method is used to estimate the between-study variance $\tau^2$. Either "DL", "PM", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.

tau.preset  Prespecified value for the square-root of the between-study variance $\tau^2$.

TE.tau  Overall treatment effect used to estimate the between-study variance tau-squared.

tau.common  A logical indicating whether tau-squared should be the same across subgroups.

prediction  A logical indicating whether a prediction interval should be printed.

level.predict  The level used to calculate prediction interval for a new study.

method.bias  A character string indicating which test is to be used. Either "rank", "linreg", or "mm", can be abbreviated. See function metabias.

backtransf  A logical indicating whether results for ratio of means (sm="ROM") should be back transformed in printouts and plots. If TRUE (default), results will be presented as ratio of means; otherwise log ratio of means will be shown.

title  Title of meta-analysis / systematic review.

complab  Comparison label.

outclab  Outcome label.

label.e  Label for experimental group.

label.c  Label for control group.

label.left  Graph label on left side of forest plot.

label.right  Graph label on right side of forest plot.
byvar An optional vector containing grouping information (must be of same length as n.e).
bylab A character string with a label for the grouping variable.
print.byvar A logical indicating whether the name of the grouping variable should be printed in front of the group labels.
byseparator A character string defining the separator between label and levels of grouping variable.
keepdata A logical indicating whether original data (set) should be kept in meta object.
warn A logical indicating whether warnings should be printed (e.g., if studies are excluded from meta-analysis due to zero standard deviations).
control An optional list to control the iterative process to estimate the between-study variance tau^2. This argument is passed on to rma.uni.

Details

Calculation of fixed and random effects estimates for meta-analyses with continuous outcome data; inverse variance weighting is used for pooling.

Three different types of summary measures are available for continuous outcomes:

• mean difference (argument sm = "MD")
• standardised mean difference (sm = "SMD")
• ratio of means (sm = "ROM")

Meta-analysis of ratio of means – also called response ratios – is described in Hedges et al. (1999) and Friedrich et al. (2008).

For the standardised mean difference three methods are implemented:

• Hedges’ g (default, method.smd = "Hedges") - see Hedges (1981)
• Cohen’s d (method.smd = "Cohen") - see Cohen (1988)
• Glass’ delta (method.smd = "Glass") - see Glass (1976)

Hedges (1981) calculated the exact bias in Cohen’s d which is a ratio of gamma distributions with the degrees of freedom, i.e. total sample size minus two, as argument. By default (argument exact.smd = FALSE), an accurate approximation of this bias provided in Hedges (1981) is utilised for Hedges’ g as well as its standard error; these approximations are also used in RevMan 5. Following Borenstein et al. (2009) these approximations are not used in the estimation of Cohen’s d. White and Thomas (2005) argued that approximations are unnecessary with modern software and accordingly promote to use the exact formulae; this is possible using argument exact.smd = TRUE.

For Hedges’ g the exact formulae are used to calculate the standardised mean difference as well as the standard error; for Cohen’s d the exact formula is only used to calculate the standard error. In typical applications (with sample sizes above 10), the differences between using the exact formulae and the approximation will be minimal.

For Glass’ delta, by default (argument sd.glass = "control"), the standard deviation in the control group (sd.c) is used in the denominator of the standard mean difference. The standard deviation in the experimental group (sd.e) can be used by specifying sd.glass = "experimental".
Calculations are conducted on the log scale for ratio of means (sm = "ROM"). Accordingly, list elements TE, TE.fixed, and TE.random contain the logarithm of ratio of means. In printouts and plots these values are back transformed if argument backtransf = TRUE.

For several arguments defaults settings are utilised (assignments using gs function). These defaults can be changed using the settings.meta function.

Internally, both fixed effect and random effects models are calculated regardless of values choosen for arguments comb.fixed and comb.random. Accordingly, the estimate for the random effects model can be extracted from component TE.random of an object of class "meta" even if argument comb.random = FALSE. However, all functions in R package meta will adequately consider the values for comb.fixed and comb.random. E.g. function print.meta will not print results for the random effects model if comb.random = FALSE.

The function metagen is called internally to calculate individual and overall treatment estimates and standard errors.

A prediction interval for the treatment effect of a new study is calculated (Higgins et al., 2009) if arguments prediction and comb.random are TRUE.

R function update.meta can be used to redo the meta-analysis of an existing metacont object by only specifying arguments which should be changed.

For the random effects, the method by Hartung and Knapp (2003) is used to adjust test statistics and confidence intervals if argument hakn = TRUE.

The DerSimonian-Laird estimate (1986) is used in the random effects model if method.tau = "DL". The iterative Paule-Mandel method (1982) to estimate the between-study variance is used if argument method.tau = "PM". Internally, R function paulemandel is called which is based on R function mpaule.default from R package metRology from S.L.R. Ellison <s.ellison at lgc.co.uk>.

If R package metafor (Viechtbauer 2010) is installed, the following methods to estimate the between-study variance $\tau^2$ (argument method.tau) are also available:

- Restricted maximum-likelihood estimator (method.tau = "REML")
- Maximum-likelihood estimator (method.tau = "ML")
- Hunter-Schmidt estimator (method.tau = "HS")
- Sidik-Jonkman estimator (method.tau = "SJ")
- Hedges estimator (method.tau = "HE")
- Empirical Bayes estimator (method.tau = "EB")

For these methods the R function rma.uni of R package metafor is called internally. See help page of R function rma.uni for more details on these methods to estimate between-study variance.

**Value**

An object of class c("metacont","meta") with corresponding print, summary, and forest functions. The object is a list containing the following components:

- n.e, mean.e, sd.e,  
  As defined above.
- n.c, mean.c, sd.c,  
  As defined above.
studlab, exclude, sm, level, level.comb,
   As defined above.
comb.fixed, comb.random,
   As defined above.
pooledvar, method.smd, sd.glass,
   As defined above.
hakn, method.tau, tau.preset, TE.tau, method.bias,
   As defined above.
tau.common, title, complab, outclab,
   As defined above.
label.e, label.c, label.left, label.right,
   As defined above.
byvar, bylab, print.byvar, byseparator
   As defined above.
TE, seTE 
   Estimated treatment effect and standard error of individual studies.
lower, upper 
   Lower and upper confidence interval limits for individual studies.
zval, pval 
   z-value and p-value for test of treatment effect for individual studies.
w.fixed, w.random
   Weight of individual studies (in fixed and random effects model).
TE.fixed, seTE.fixed
   Estimated overall treatment effect and standard error (fixed effect model).
lower.fixed, upper.fixed 
   Lower and upper confidence interval limits (fixed effect model).
zval.fixed, pval.fixed 
   z-value and p-value for test of overall treatment effect (fixed effect model).
TE.random, seTE.random
   Estimated overall treatment effect and standard error (random effects model).
lower.random, upper.random 
   Lower and upper confidence interval limits (random effects model).
zval.random, pval.random 
   z-value or t-value and corresponding p-value for test of overall treatment effect 
   (random effects model).
prediction, level.predict
   As defined above.
seTE.predict 
   Standard error utilised for prediction interval.
lower.predict, upper.predict
   Lower and upper limits of prediction interval.
k 
   Number of studies combined in meta-analysis.
Q 
   Heterogeneity statistic Q.
df.Q 
   Degrees of freedom for heterogeneity statistic.
pval.Q 
   P-value of heterogeneity test.
tau 
   Square-root of between-study variance.
se.tau 
   Standard error of square-root of between-study variance.
C

df.hakn

method

bylevs

TE.fixed.w, seTE.fixed.w

lower.fixed.w, upper.fixed.w

zval.fixed.w, pval.fixed.w

TE.random.w, seTE.random.w

lower.random.w, upper.random.w

zval.random.w, pval.random.w

w.fixed.w, w.random.w

df.hakn.w

n.e.w

n.c.w

k.w

k.all.w

Q.w.fixed

Q.w.random

df.Q.w

pval.Q.w.fixed

Scaling factor utilised internally to calculate common tau-squared across subgroups.

Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn = TRUE).

Pooling method: "Inverse".

Levels of grouping variable - if byvar is not missing.

Estimated treatment effect and standard error in subgroups (fixed effect model) - if byvar is not missing.

Lower and upper confidence interval limits in subgroups (fixed effect model) - if byvar is not missing.

z-value and p-value for test of treatment effect in subgroups (fixed effect model) - if byvar is not missing.

Estimated treatment effect and standard error in subgroups (random effects model) - if byvar is not missing.

Lower and upper confidence interval limits in subgroups (random effects model) - if byvar is not missing.

z-value or t-value and corresponding p-value for test of treatment effect in subgroups (random effects model) - if byvar is not missing.

Weight of subgroups (in fixed and random effects model) - if byvar is not missing.

Degrees of freedom for test of treatment effect for Hartung-Knapp method in subgroups - if byvar is not missing and hakn = TRUE.

Number of observations in experimental group in subgroups - if byvar is not missing.

Number of observations in control group in subgroups - if byvar is not missing.

Number of studies combined within subgroups - if byvar is not missing.

Number of all studies in subgroups - if byvar is not missing.

Overall within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

Overall within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing (only calculated if argument tau.common is TRUE).

Degrees of freedom for test of overall within subgroups heterogeneity - if byvar is not missing.

P-value of within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.
pval.Q.w.random

P-value of within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

Q.b.fixed

Overall between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

Q.b.random

Overall between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

df.Q.b

Degrees of freedom for test of overall between subgroups heterogeneity - if byvar is not missing.

pval.Q.b.fixed

P-value of between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

pval.Q.b.random

P-value of between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

tau.w

Square-root of between-study variance within subgroups - if byvar is not missing.

C.w

Scaling factor utilised internally to calculate common tau-squared across subgroups - if byvar is not missing.

H.w

Heterogeneity statistic H within subgroups - if byvar is not missing.

lower.H.w, upper.H.w

Lower and upper confidence limits for heterogeneity statistic H within subgroups - if byvar is not missing.

I2.w

Heterogeneity statistic I2 within subgroups - if byvar is not missing.

lower.I2.w, upper.I2.w

Lower and upper confidence limit for heterogeneity statistic I2 within subgroups - if byvar is not missing.

keepdata

As defined above.

data

Original data (set) used in function call (if keepdata = TRUE).

subset

Information on subset of original data used in meta-analysis (if keepdata = TRUE).

call

Function call.

version

Version of R package meta used to create object.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


Friedrich JO, Adhikari NK, Beyene J (2008): The ratio of means method as an alternative to mean differences for analyzing continuous outcome variables in meta-analysis: A simulation study. *BMC Medical Research Methodology, 8*, 32


White IR, Thomas J (2005): Standardized mean differences in individually-randomized and cluster-randomized trials, with applications to meta-analysis. *Clinical Trials, 2*, 141–51

See Also

update.meta, metabin, metagen

Examples

data(Fleiss93cont)

# Meta-analysis with Hedges' g as effect measure
#
ml <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c,
data = Fleiss93cont, sm = "SMD")

ml

forest(ml)

# Use Cohen's d instead of Hedges' g as effect measure
#
update(ml, method.smd = "Cohen")
# Use Glass' delta instead of Hedges' g as effect measure
#
update(m1, method.smd = "Glass")

# Use Glass' delta based on the standard deviation in the experimental group
#
update(m1, method.smd = "Glass", sd.glass = "experimental")

# Calculate Hedges' g based on exact formulae
#
update(m1, exact.smd = TRUE)

data(amlodipine)

m2 <- metacont(n.amlo, mean.amlo, sqrt(var.amlo),
               n.plac, mean.plac, sqrt(var.plac),
               data = amlodipine, studlab = study)

summary(m2)

# Use pooled variance
#
summary(update(m2, pooledvar = TRUE))

# Meta-analysis of response ratios (Hedges et al., 1999)
#
data(woodyplants)

m3 <- metacont(n.elev, mean.elev, sd.elev,
               n.amb, mean.amb, sd.amb,
               data = woodyplants, sm = "ROM")

summary(m3)

summary(m3, backtransf = FALSE)

---

**metacor**  
*Meta-analysis of correlations*

**Description**

Calculation of fixed and random effects estimates for meta-analyses with correlations; inverse variance weighting is used for pooling.

**Usage**

```r
metacor(cor, n, studlab, data = NULL, subset = NULL, exclude = NULL,
         sm = gs("smcor"), level = gs("level"),
         level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"),
         comb.random = gs("comb.random"), hakn = gs("hakn"),
         method.tau = gs("method.tau"), tau.preset = NULL, TE.tau = NULL,
         tau.common = gs("tau.common"), prediction = gs("prediction"),
         level.predict = gs("level.predict"), null.effect = 0,
```

method.bias = gs("method.bias"), backtransf = gs("backtransf"),
title = gs("title"), complab = gs("complab"), outclab = "", byvar,
bylab, print.byvar = gs("print.byvar"),
byseparator = gs("byseparator"), keepdata = gs("keepdata"),
control = NULL)

Arguments

  cor  Correlation.
  n    Number of observations.
  studlab An optional vector with study labels.
  data An optional data frame containing the study information, i.e., cor and n.
  subset An optional vector specifying a subset of studies to be used.
  exclude An optional vector specifying studies to exclude from meta-analysis, however,
to include in printouts and forest plots.
  sm    A character string indicating which summary measure ("ZCOR" or "COR") is to
        be used for pooling of studies.
  level The level used to calculate confidence intervals for individual studies.
  level.comb The level used to calculate confidence intervals for pooled estimates.
  comb.fixed A logical indicating whether a fixed effect meta-analysis should be conducted.
  comb.random A logical indicating whether a random effects meta-analysis should be con-
             conducted.
  hakn  A logical indicating whether the method by Hartung and Knapp should be used
        to adjust test statistics and confidence intervals.
  method.tau A character string indicating which method is used to estimate the between-
             study variance $\tau^2$. Either "DL", "PM", "REML", "ML", "HS", "SJ", "HE",
             or "EB", can be abbreviated.
  tau.preset Prespecified value for the square-root of the between-study variance $\tau^2$.
  TE.tau Overall effect used to estimate the between-study variance tau-squared.
  tau.common A logical indicating whether tau-squared should be the same across subgroups.
  prediction A logical indicating whether a prediction interval should be printed.
  level.predict The level used to calculate prediction interval for a new study.
  null.effect A numeric value specifying the effect under the null hypothesis.
  method.bias A character string indicating which test is to be used. Either "rank", "linreg",
             or "mm", can be abbreviated. See function metabias
  backtransf A logical indicating whether results for Fisher’s z transformed correlations (sm
             = "ZCOR") should be back transformed in printouts and plots. If TRUE (default),
             results will be presented as correlations; otherwise Fisher’s z transformed corre-
             lations will be shown.
  title  Title of meta-analysis / systematic review.
  complab Comparison label.
  outclab Outcome label.
byvar  An optional vector containing grouping information (must be of same length as event.e).
bylab  A character string with a label for the grouping variable.
print.byvar  A logical indicating whether the name of the grouping variable should be printed in front of the group labels.
byseparator  A character string defining the separator between label and levels of grouping variable.
keepdata  A logical indicating whether original data (set) should be kept in meta object.
control  An optional list to control the iterative process to estimate the between-study variance $\tau^2$. This argument is passed on to rma.uni.

Details

Fixed effect and random effects meta-analysis of correlations based either on Fisher's z transformation of correlations (sm = "ZCOR") or direct combination of correlations (sm = "COR") (see Cooper et al., p264-5 and p273-4).

Only few statisticians would advocate the use of untransformed correlations unless sample sizes are very large (see Cooper et al., p265). The artificial example given below shows that the smallest study gets the largest weight if correlations are combined directly because the correlation is closest to 1.

For several arguments defaults settings are utilised (assignments using gs function). These defaults can be changed using the settings.meta function.

Internally, both fixed effect and random effects models are calculated regardless of values chosen for arguments comb.fixed and comb.random. Accordingly, the estimate for the random effects model can be extracted from component TE.random of an object of class "meta" even if argument comb.random = FALSE. However, all functions in R package meta will adequately consider the values for comb.fixed and comb.random. E.g. function print.meta will not print results for the random effects model if comb.random = FALSE.

A prediction interval for the correlation in a new study is calculated (Higgins et al., 2009) if arguments prediction and comb.random are TRUE.

R function update.meta can be used to redo the meta-analysis of an existing metacor object by only specifying arguments which should be changed.

For the random effects, the method by Hartung and Knapp (2003) is used to adjust test statistics and confidence intervals if argument hakn = TRUE.

The DerSimonian-Laird estimate (1986) is used in the random effects model if method.tau = "DL". The iterative Paule-Mandel method (1982) to estimate the between-study variance is used if argument method.tau = "PM". Internally, R function paulemandel is called which is based on R function mpaule.default from R package metRology from S.L.R. Ellison <s.ellison at lgc.co.uk>.

If R package metafor (Viechtbauer 2010) is installed, the following methods to estimate the between-study variance $\tau^2$ (argument method.tau) are also available:

- Restricted maximum-likelihood estimator (method.tau = "REML")
- Maximum-likelihood estimator (method.tau = "ML")
- Hunter-Schmidt estimator (method.tau = "HS")
- Sidik-Jonkman estimator \( \text{method.tau = "SJ"} \)
- Hedges estimator \( \text{method.tau = "HE"} \)
- Empirical Bayes estimator \( \text{method.tau = "EB"} \)

For these methods the R function `rma.uni` of R package `metafor` is called internally. See help page of R function `rma.uni` for more details on these methods to estimate between-study variance.

**Value**

An object of class `c("metacor","meta")` with corresponding `print`, `summary`, and `forest` functions. The object is a list containing the following components:

- `cor`, `n`, `studlab`, `exclude`,
  - As defined above.
- `sm`, `level`, `level.comb`,
  - As defined above.
- `comb.fixed`, `comb.random`,
  - As defined above.
- `hakn`, `method.tau`, `tau.preset`, `TE.tau`, `null.effect`,
  - As defined above.
- `method.bias`, `tau.common`, `title`, `complab`, `outclab`,
  - As defined above.
- `byvar`, `bylab`, `print.byvar`, `byseparator`
  - As defined above.
- `TE`, `seTE`
  - Either Fisher's z transformation of correlations \( \text{sm = "ZCOR"} \) or correlations \( \text{sm="COR"} \) for individual studies.
- `lower`, `upper`
  - Lower and upper confidence interval limits for individual studies.
- `zval`, `pval`
  - z-value and p-value for test of effect in individual studies.
- `w.fixed`, `w.random`
  - Weight of individual studies (in fixed and random effects model).
- `TE.fixed`, `seTE.fixed`
  - Estimated overall effect (Fisher's z transformation of correlation or correlation) and standard error (fixed effect model).
- `lower.fixed`, `upper.fixed`
  - Lower and upper confidence interval limits (fixed effect model).
- `zval.fixed`, `pval.fixed`
  - z-value and p-value for test of overall effect (fixed effect model).
- `TE.random`, `seTE.random`
  - Estimated overall effect (Fisher's z transformation of correlation or correlation) and standard error (random effects model).
- `lower.random`, `upper.random`
  - Lower and upper confidence interval limits (random effects model).
- `zval.random`, `pval.random`
  - z-value or t-value and corresponding p-value for test of overall effect (random effects model).
- `prediction`, `level.predict`
  - As defined above.
seTE.predict  Standard error utilised for prediction interval.
lower.predict, upper.predict
   Lower and upper limits of prediction interval.
k  Number of studies combined in meta-analysis.
Q  Heterogeneity statistic Q.
df.Q  Degrees of freedom for heterogeneity statistic.
pval.Q  P-value of heterogeneity test.
tau  Square-root of between-study variance.
se.tau  Standard error of square-root of between-study variance.
C  Scaling factor utilised internally to calculate common tau-squared across subgroups.
df.hakn  Degrees of freedom for test of effect for Hartung-Knapp method (only if hakn = TRUE).
method  Pooling method: "Inverse".
bylevs  Levels of grouping variable - if byvar is not missing.
TE.fixed.w, seTE.fixed.w
   Estimated effect and standard error in subgroups (fixed effect model) - if byvar is not missing.
lower.fixed.w, upper.fixed.w
   Lower and upper confidence interval limits in subgroups (fixed effect model) - if byvar is not missing.
zval.fixed.w, pval.fixed.w
   z-value and p-value for test of effect in subgroups (fixed effect model) - if byvar is not missing.
TE.random.w, seTE.random.w
   Estimated effect and standard error in subgroups (random effects model) - if byvar is not missing.
lower.random.w, upper.random.w
   Lower and upper confidence interval limits in subgroups (random effects model) - if byvar is not missing.
zval.random.w, pval.random.w
   z-value or t-value and corresponding p-value for test of effect in subgroups (random effects model) - if byvar is not missing.
w.fixed.w, w.random.w
   Weight of subgroups (in fixed and random effects model) - if byvar is not missing.
df.hakn.w  Degrees of freedom for test of effect for Hartung-Knapp method in subgroups - if byvar is not missing and hakn = TRUE.
n.e.w  Number of observations in experimental group in subgroups - if byvar is not missing.
n.c.w  Number of observations in control group in subgroups - if byvar is not missing.
k.w  Number of studies combined within subgroups - if byvar is not missing.
<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>k.all.w</td>
<td>Number of all studies in subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>Q.w.fixed</td>
<td>Overall within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>Q.w.random</td>
<td>Overall within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>df.Q.w</td>
<td>Degrees of freedom for test of overall within subgroups heterogeneity - if byvar is not missing.</td>
</tr>
<tr>
<td>pval.Q.w.fixed</td>
<td>P-value of within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>pval.Q.w.random</td>
<td>P-value of within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>Q.b.fixed</td>
<td>Overall between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>Q.b.random</td>
<td>Overall between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>df.Q.b</td>
<td>Degrees of freedom for test of overall between subgroups heterogeneity - if byvar is not missing.</td>
</tr>
<tr>
<td>pval.Q.b.fixed</td>
<td>P-value of between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>pval.Q.b.random</td>
<td>P-value of between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>tau.w</td>
<td>Square-root of between-study variance within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>C.w</td>
<td>Scaling factor utilised internally to calculate common tau-squared across subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>H.w</td>
<td>Heterogeneity statistic H within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>lower.H.w, upper.H.w</td>
<td>Lower and upper confidence limits for heterogeneity statistic H within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>I2.w</td>
<td>Heterogeneity statistic I2 within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>lower.I2.w, upper.I2.w</td>
<td>Lower and upper confidence limit for heterogeneity statistic I2 within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>keepdata</td>
<td>As defined above.</td>
</tr>
<tr>
<td>data</td>
<td>Original data (set) used in function call (if keepdata = TRUE).</td>
</tr>
<tr>
<td>subset</td>
<td>Information on subset of original data used in meta-analysis (if keepdata = TRUE).</td>
</tr>
<tr>
<td>call</td>
<td>Function call.</td>
</tr>
<tr>
<td>version</td>
<td>Version of R package meta used to create object.</td>
</tr>
</tbody>
</table>
Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

References
Cooper H, Hedges LV, Valentine JC (2009): The Handbook of Research Synthesis and Meta-
Higgins JPT, Thompson SG, Spiegelhalter DJ (2009): A re-evaluation of random-effects meta-
Knapp G & Hartung J (2003): Improved tests for a random effects meta-regression with a single
_covariate. Statistics in Medicine, 22, 2693–710
National Bureau of Standards, 87, 377–85
Viechtbauer W (2010): Conducting Meta-Analyses in R with the Metafor Package. Journal of
Statistical Software, 36, 1–48

See Also
update.meta, metacont, metagen, print.meta

Examples
m1 <- metacor(c(0.85, 0.7, 0.95), c(20, 40, 10))

# Print correlations (back transformed from Fisher's z
# transformation)
#
# m1

# Print Fisher's z transformed correlations
# print(m1, backtransf = FALSE)

# Forest plot with back transformed correlations
# forest(m1)

# Forest plot with Fisher's z transformed correlations
# forest(m1, backtransf = FALSE)

m2 <- update(m1, sm = "cor")
m2

# Identical forest plots (as back transformation is the identity
# transformation)
# forest(m2)
Description

Wrapper function to perform meta-analysis for a single outcome of a Cochrane Intervention review.

Usage

```r
metacr(x, comp.no = 1, outcome.no = 1, method, sm,
       level = gs("level"), level.comb = gs("level.comb"), comb.fixed,
       comb.random, hakn = FALSE, method.tau = "DL", tau.common = FALSE,
       prediction = gs("prediction"), level.predict = gs("level.predict"),
       swap.events, logscale, backtransf = gs("backtransf"), title, complab,
       outclab, keepdata = gs("keepdata"), warn = FALSE)
```

Arguments

- `x`: An object of class `rm5` created by R function `read.rm5`.
- `comp.no`: Comparison number.
- `outcome.no`: Outcome number.
- `method`: A character string indicating which method is to be used for pooling of studies. One of “Inverse”, “MH”, or “Peto”, can be abbreviated.
- `sm`: A character string indicating which summary measure (“RR”, “OR”, “RD”, “ASD”, “HR”, “MD”, or “SMD”, or “ROM”) is to be used for pooling of studies.
- `level`: The level used to calculate confidence intervals for individual studies.
- `level.comb`: The level used to calculate confidence intervals for pooled estimates.
- `comb.fixed`: A logical indicating whether a fixed effect meta-analysis should be conducted.
- `comb.random`: A logical indicating whether a random effects meta-analysis should be conducted.
- `hakn`: A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.
- `method.tau`: A character string indicating which method is used to estimate the between-study variance \( \tau^2 \). Either “DL”, “PM”, “REML”, “ML”, “HS”, “SJ”, “HE”, or “EB”, can be abbreviated.
- `tau.common`: A logical indicating whether tau-squared should be the same across subgroups.
- `prediction`: A logical indicating whether a prediction interval should be printed.
- `level.predict`: The level used to calculate prediction interval for a new study.
- `swap.events`: A logical indicating whether events and non-events should be interchanged.
- `logscale`: A logical indicating whether effect estimates are entered on log-scale.
backtransf A logical indicating whether results should be back transformed in printouts and plots. If backtransf=TRUE (default), results for sm="OR" are printed as odds ratios rather than log odds ratios and results for sm="ZCOR" are printed as correlations rather than Fisher's z transformed correlations, for example.

title Title of meta-analysis / systematic review.
complab Comparison label.
outclab Outcome label.
keepdata A logical indicating whether original data (set) should be kept in meta object.
warn A logical indicating whether warnings should be printed (e.g., if incr is added to studies with zero cell frequencies).

Details

Cochrane Intervention reviews are based on the comparison of two interventions. Each Cochrane Intervention review can have a variable number of comparisons. For each comparison, a variable number of outcomes can be define. For each outcome, a separate meta-analysis is conducted. Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://community.cochrane.org/tools/review-production-tools/revman-5).

This wrapper function can be used to perform meta-analysis for a single outcome of a Cochrane Intervention review. Internally, R functions metabin, metacont, and metagen are called - depending on the definition of the outcome in RevMan 5.

Note, it is recommended to choose the RevMan 5 settings before executing metacr, i.e., settings.meta("revman5").

Value

An object of class "meta" and "metabin", "metacont", or "metagen" depending on outcome type utilised in Cochrane Intervention review for selected outcome.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

metabin, metacont, metagen, read.rm5, settings.meta

Examples

# Locate export data file "Fleiss93_CR.csv"
# in sub-directory of package "meta"
#
filename <- system.file("extdata", "Fleiss93_CR.csv", package = "meta")
#

Fleiss93_CR <- read.rm5(filename)

# Choose RevMan 5 settings and store old settings
#
oldset <- settings.meta("revman5")

# Same result as R command example(Fleiss93)
#
metacr(Fleiss93_CR)

# Same result as R command example(Fleiss93cont)
#
metacr(Fleiss93_CR, 1, 2)
forest(metacr(Fleiss93_CR, 1, 2))

# Change summary measure to RR
#
ml <- metacr(Fleiss93_CR)
update(ml, sm="RR")

# Use old settings
#
settings.meta(oldset)

---

**metacum**

*Cumulative meta-analysis*

**Description**

Performs a cumulative meta-analysis.

**Usage**

metacum(x, pooled, sortvar)

**Arguments**

- **x**
  An object of class meta.

- **pooled**
  A character string indicating whether a fixed effect or random effects model is used for pooling. Either missing (see Details), "fixed", or "random", can be abbreviated.

- **sortvar**
  An optional vector used to sort the individual studies (must be of same length as x$TE).
Details

A cumulative meta-analysis is performed. Studies are included sequentially as defined by sortvar. Information from object x is utilised if argument pooled is missing. A fixed effect model is assumed (pooled = "fixed") if argument x$comb.fixed is TRUE; a random effects model is assumed (pooled = "random") if argument x$comb.random is TRUE and x$comb.fixed is FALSE.

Value

An object of class c("metacum","meta") with corresponding print, and forest functions. The object is a list containing the following components:

<table>
<thead>
<tr>
<th>Component</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TE, seTE</td>
<td>Estimated treatment effect and standard error of pooled estimate in cumulative meta-analyses.</td>
</tr>
<tr>
<td>lower, upper</td>
<td>Lower and upper confidence interval limits.</td>
</tr>
<tr>
<td>studlab</td>
<td>Study label describing addition of studies.</td>
</tr>
<tr>
<td>p.value</td>
<td>P-value for test of overall effect.</td>
</tr>
<tr>
<td>w</td>
<td>Sum of weights from fixed effect or random effects model.</td>
</tr>
<tr>
<td>I2</td>
<td>Heterogeneity statistic I2.</td>
</tr>
<tr>
<td>Rb</td>
<td>Heterogeneity statistic Rb.</td>
</tr>
<tr>
<td>tau</td>
<td>Square-root of between-study variance.</td>
</tr>
<tr>
<td>df.hakn</td>
<td>Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn = TRUE).</td>
</tr>
<tr>
<td>sm</td>
<td>Summary measure.</td>
</tr>
<tr>
<td>method</td>
<td>Method used for pooling.</td>
</tr>
<tr>
<td>k</td>
<td>Number of studies combined in meta-analysis.</td>
</tr>
<tr>
<td>pooled</td>
<td>As defined above.</td>
</tr>
<tr>
<td>comb.fixed</td>
<td>A logical indicating whether analysis is based on fixed effect model.</td>
</tr>
<tr>
<td>comb.random</td>
<td>A logical indicating whether analysis is based on random effects model.</td>
</tr>
<tr>
<td>TE.fixed, seTE.fixed</td>
<td>Value is NA.</td>
</tr>
<tr>
<td>TE.random, seTE.random</td>
<td>Value is NA.</td>
</tr>
<tr>
<td>Q</td>
<td>Value is NA.</td>
</tr>
<tr>
<td>level.comb</td>
<td>The level used to calculate confidence intervals for pooled estimates.</td>
</tr>
<tr>
<td>hakn</td>
<td>A logical indicating whether the method by Hartung and Knapp is used to adjust test statistics and confidence intervals.</td>
</tr>
<tr>
<td>method.tau</td>
<td>A character string indicating which method is used to estimate the between-study variance $\tau^2$.</td>
</tr>
<tr>
<td>tau.preset</td>
<td>Prespecified value for the square-root of the between-study variance $\tau^2$.</td>
</tr>
<tr>
<td>TE.tau</td>
<td>Overall treatment effect used to estimate the between-study variance $\tau^2$.</td>
</tr>
<tr>
<td>n.harmonic.mean</td>
<td>Harmonic mean of number of observations (for back transformation of Freeman-Tukey Double arcsine transformation).</td>
</tr>
<tr>
<td>version</td>
<td>Version of R package meta used to create object.</td>
</tr>
</tbody>
</table>
**metagen**

Generic inverse variance meta-analysis

---

**Description**

Fixed effect and random effects meta-analysis based on estimates (e.g. log hazard ratios) and their standard errors. The inverse variance method is used for pooling.
Usage

metagen(TE, seTE, studlab, data = NULL, subset = NULL,
    exclude = NULL, sm = "", level = gs("level"),
    level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"),
    comb.random = gs("comb.random"), hakn = gs("hakn"),
    method.tau = gs("method.tau"), tau.preset = NULL, TE.tau = NULL,
    tau.common = gs("tau.common"), prediction = gs("prediction"),
    level.predict = gs("level.predict"), null.effect = 0,
    method.bias = gs("method.bias"), n.e = NULL, n.c = NULL, pval, df,
    lower, upper, level.ci = 0.95, median, q1, q3, min, max, approx.TE,
    approx.seTE, backtransf = gs("backtransf"), pscale = 1,
    irscale = 1, irunit = "person-years", title = gs("title"),
    complab = gs("complab"), outclab = ", label.e = gs("label.e"),
    label.c = gs("label.c"), label.left = gs("label.left"),
    label.right = gs("label.right"), byvar, bylab,
    print.byvar = gs("print.byvar"), byseparator = gs("byseparator"),
    keepdata = gs("keepdata"), warn = gs("warn"), control = NULL)

Arguments

TE | Estimate of treatment effect, e.g., log hazard ratio or risk difference.
seTE | Standard error of treatment estimate.
studlab | An optional vector with study labels.
data | An optional data frame containing the study information.
subset | An optional vector specifying a subset of studies to be used.
exclude | An optional vector specifying studies to exclude from meta-analysis, however, to include in printouts and forest plots.
sm | A character string indicating underlying summary measure, e.g., "RD", "RR", "OR", "ASD", "HR", "MD", "SMD", or "ROM".
level | The level used to calculate confidence intervals for individual studies.
level.comb | The level used to calculate confidence intervals for pooled estimates.
comb.fixed | A logical indicating whether a fixed effect meta-analysis should be conducted.
comb.random | A logical indicating whether a random effects meta-analysis should be conducted.
hakn | A logical indicating whether method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.
method.tau | A character string indicating which method is used to estimate the between-study variance $\tau^2$. Either "DL", "PM", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.
tau.preset | Prespecified value for the square-root of the between-study variance $\tau^2$.
TE.tau | Overall treatment effect used to estimate the between-study variance tau-squared.
tau.common | A logical indicating whether tau-squared should be the same across subgroups.
prediction | A logical indicating whether a prediction interval should be printed.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>level.predict</td>
<td>The level used to calculate prediction interval for a new study.</td>
</tr>
<tr>
<td>null.effect</td>
<td>A numeric value specifying the effect under the null hypothesis.</td>
</tr>
<tr>
<td>method.bias</td>
<td>A character string indicating which test is to be used. Either &quot;rank&quot;, &quot;linreg&quot;, or &quot;mm&quot;, can be abbreviated. See function metabias</td>
</tr>
<tr>
<td>n.e</td>
<td>Number of observations in experimental group.</td>
</tr>
<tr>
<td>n.c</td>
<td>Number of observations in control group.</td>
</tr>
<tr>
<td>pval</td>
<td>P-value (used to estimate the standard error).</td>
</tr>
<tr>
<td>df</td>
<td>Degrees of freedom (used in test or to construct confidence interval).</td>
</tr>
<tr>
<td>lower</td>
<td>Lower limit of confidence interval (used to estimate the standard error).</td>
</tr>
<tr>
<td>upper</td>
<td>Upper limit of confidence interval (used to estimate the standard error).</td>
</tr>
<tr>
<td>level.ci</td>
<td>Level of confidence interval.</td>
</tr>
<tr>
<td>median</td>
<td>Median (used to estimate the treatment effect and standard error).</td>
</tr>
<tr>
<td>q1</td>
<td>First quartile (used to estimate the treatment effect and standard error).</td>
</tr>
<tr>
<td>q3</td>
<td>Third quartile (used to estimate the treatment effect and standard error).</td>
</tr>
<tr>
<td>min</td>
<td>Minimum (used to estimate the treatment effect and standard error).</td>
</tr>
<tr>
<td>max</td>
<td>Maximum (used to estimate the treatment effect and standard error).</td>
</tr>
<tr>
<td>approx.TE</td>
<td>Approximation method to estimate treatment estimate (see Details).</td>
</tr>
<tr>
<td>approx.seTE</td>
<td>Approximation method to estimate standard error (see Details).</td>
</tr>
<tr>
<td>backtransf</td>
<td>A logical indicating whether results should be back transformed in printouts and plots. If backtransf = TRUE (default), results for sm = &quot;OR&quot; are printed as odds ratios rather than log odds ratios and results for sm = &quot;ZCOR&quot; are printed as correlations rather than Fisher's z transformed correlations, for example.</td>
</tr>
<tr>
<td>pscale</td>
<td>A numeric giving scaling factor for printing of single event probabilities or risk differences, i.e. if argument sm is equal to &quot;PLOGIT&quot;, &quot;PLN&quot;, &quot;PRAW&quot;, &quot;PAS&quot;, &quot;PFT&quot;, or &quot;RD&quot;.</td>
</tr>
<tr>
<td>irscale</td>
<td>A numeric defining a scaling factor for printing of single incidence rates or incidence rate differences, i.e. if argument sm is equal to &quot;IR&quot;, &quot;IRLN&quot;, &quot;IRS&quot;, &quot;IRFT&quot;, or &quot;IRD&quot;.</td>
</tr>
<tr>
<td>irunit</td>
<td>A character specifying the time unit used to calculate rates, e.g. person-years.</td>
</tr>
<tr>
<td>title</td>
<td>Title of meta-analysis/systematic review.</td>
</tr>
<tr>
<td>complab</td>
<td>Comparison label.</td>
</tr>
<tr>
<td>outclab</td>
<td>Outcome label.</td>
</tr>
<tr>
<td>label.e</td>
<td>Label for experimental group.</td>
</tr>
<tr>
<td>label.c</td>
<td>Label for control group.</td>
</tr>
<tr>
<td>label.left</td>
<td>Graph label on left side of forest plot.</td>
</tr>
<tr>
<td>label.right</td>
<td>Graph label on right side of forest plot.</td>
</tr>
<tr>
<td>byvar</td>
<td>An optional vector containing grouping information (must be of same length as TE).</td>
</tr>
<tr>
<td>bylab</td>
<td>A character string with a label for the grouping variable.</td>
</tr>
</tbody>
</table>
print.byvar A logical indicating whether the name of the grouping variable should be printed in front of the group labels.

byseparator A character string defining the separator between label and levels of grouping variable.

keepdata A logical indicating whether original data (set) should be kept in meta object.

warn A logical indicating whether warnings should be printed (e.g., if studies are excluded from meta-analysis due to zero standard errors).

control An optional list to control the iterative process to estimate the between-study variance tau^2. This argument is passed on to rma.uni.

Details

This function provides the generic inverse variance method for meta-analysis which requires treatment estimates and their standard errors (Borenstein et al., 2010). The method is useful, e.g., for pooling of survival data (using log hazard ratio and standard errors as input). Arguments TE and seTE can be used to provide treatment estimates and standard errors directly. However, it is possible to derive these quantities from other information.

For several arguments defaults settings are utilised (see assignments with gs under Usage). These defaults can be changed using settings.meta.

Furthermore, R function update.meta can be used to rerun a meta-analysis with different settings.

Approximate treatment estimates:

Missing treatment estimates can be derived from

1. confidence limits provided by arguments lower and upper;
2. median, interquartile range and range (arguments median, q1, q3, min, and max);
3. median and interquartile range (arguments median, q1 and q3);
4. median and range (arguments median, min and max).

For confidence limits, the treatment estimate is defined as the center of the confidence interval (on the log scale for relative effect measures like the odds ratio or hazard ratio). For median, interquartile range and range, equation (10) in Wan et al. (2014) is used to approximate the treatment effect (i.e., mean). Similarly, equations (14) and (2) in Wan et al. (2014) are used if median and interquartile range or range, respectively, are provided.

By default, missing treatment estimates are replaced successively using these method, e.g., confidence limits are utilised before interquartile ranges. Argument approx.TE can be used to overwrite this default for each individual study:

- Use treatment estimate directly (entry "" in argument approx.TE);
- confidence limits ("ci" in argument approx.TE);
- median, interquartile range and range ("iqr.range");
- median and interquartile range ("iqr");
- median and range ("range").

Approximate standard errors:

Missing standard errors can be derived from

1. p-value provided by arguments pval and (optional) df;
2. confidence limits (arguments lower, upper, and (optional) df);
3. sample size, median, interquartile range and range (arguments n.e and / or n.c, median, q1, q3, min, and max);
4. sample size, median and interquartile range (arguments n.e and / or n.c, median, q1 and q3);
5. sample size, median and range (arguments n.e and / or n.c, median, min and max).

For p-values and confidence limits, calculations are either based on the standard normal or $t$ distribution if argument df is provided. Furthermore, argument level.ci can be used to provide the level of the confidence interval. For median, interquartile range and range, depending on the sample size, equation (12) or (13) in Wan et al. (2014) is used to approximate the standard error. Similarly, equations (15) / (16) and (7) / (9) in Wan et al. (2014) are used if median and interquartile range or range, respectively, are provided. The sample size of individual studies must be provided with arguments n.e and / or n.c. The total sample size is calculated as n.e + n.c if both arguments are provided.

By default, missing standard errors are replaced successively using these method, e.g., p-value before confidence limits before interquartile range and range. Argument approx.seTE can be used to overwrite this default for each individual study:

- Use standard error directly (entry "" in argument approx.seTE);
- p-value ("pval" in argument approx.seTE);
- confidence limits ("ci");
- median, interquartile range and range ("iqr.range");
- median and interquartile range ("iqr");
- median and range ("range").

**Estimation of between-study variance:**

The following methods are available to estimate the between-study variance $\tau^2$.

<table>
<thead>
<tr>
<th>Argument</th>
<th>Method</th>
</tr>
</thead>
<tbody>
<tr>
<td>method.tau = &quot;DL&quot;</td>
<td>DerSimonian-Laird estimator (DerSimonian and Laird, 1986)</td>
</tr>
<tr>
<td>method.tau = &quot;PM&quot;</td>
<td>Paule-Mandel estimator (Paule and Mandel, 1982)</td>
</tr>
<tr>
<td>method.tau = &quot;REML&quot;</td>
<td>Restricted maximum-likelihood estimator (Viechtbauer, 2005)</td>
</tr>
<tr>
<td>method.tau = &quot;ML&quot;</td>
<td>Maximum-likelihood estimator (Viechtbauer, 2005)</td>
</tr>
<tr>
<td>method.tau = &quot;HS&quot;</td>
<td>Hunter-Schmidt estimator (Hunter and Schmidt, 2015)</td>
</tr>
<tr>
<td>method.tau = &quot;SJ&quot;</td>
<td>Sidik-Jonkman estimator (Sidik and Jonkman, 2005)</td>
</tr>
<tr>
<td>method.tau = &quot;HE&quot;</td>
<td>Hedges estimator (Hedges and Olkin, 1985)</td>
</tr>
<tr>
<td>method.tau = &quot;EB&quot;</td>
<td>Empirical Bayes estimator (Morris, 1983)</td>
</tr>
</tbody>
</table>

Historically, the DerSimonian-Laird method was the de facto standard to estimate the between-study variance $\tau^2$ and is still the default in many software packages including Review Manager 5 (RevMan 5) and R package meta. However, its role has been challenged and especially the Paule-Mandel and REML estimators have been recommended (Veroniki et al., 2016). Accordingly, the following R command can be used to use the Paule-Mandel estimator in all meta-analyses of the R session: settings.meta(method.tau = "PM")

The DerSimonian-Laird and Paule-Mandel estimators are implemented in R package meta. The other estimators are available if R package metafor (Viechtbauer 2010) is installed by internally calling R function rma.uni.
Hartung-Knapp method:
Hartung and Knapp (2001a,b) proposed an alternative method for random effects meta-analysis based on a refined variance estimator for the treatment estimate. Simulation studies (Hartung and Knapp, 2001a,b; IntHout et al., 2014; Langen et al., 2018) show improved coverage probabilities compared to the classic random effects method. However, in rare settings with very homogeneous treatment estimates, the Hartung-Knapp method can be anti-conservative (Wiksten et al., 2016). The Hartung-Knapp method is used if argument hakn = TRUE.

Prediction interval:
A prediction interval for the treatment effect of a new study (Higgins et al., 2009) is calculated if arguments prediction and comb.random are TRUE. Note, the definition of prediction intervals varies in the literature. This function implements equation (12) of Higgins et al., (2009) which proposed a t distribution with \( K-2 \) degrees of freedom where \( K \) corresponds to the number of studies in the meta-analysis.

Presentation of meta-analysis results:
Internally, both fixed effect and random effects models are calculated regardless of values choosen for arguments comb.fixed and comb.random. Accordingly, the estimate for the random effects model can be extracted from component TE.random of an object of class "meta" even if argument comb.random = FALSE. However, all functions in R package meta will adequately consider the values for comb.fixed and comb.random. For example, functions print.meta and forest.meta will not show results for the random effects model if comb.random = FALSE.

Argument pscale can be used to rescale single proportions or risk differences, e.g. pscale = 1000 means that proportions are expressed as events per 1000 observations. This is useful in situations with (very) low event probabilities.

Argument irscale can be used to rescale single rates or rate differences, e.g. irscale = 1000 means that rates are expressed as events per 1000 time units, e.g. person-years. This is useful in situations with (very) low rates. Argument irunit can be used to specify the time unit used in individual studies (default: "person-years"). This information is printed in summaries and forest plots if argument irscale is not equal to 1.

Default settings for comb.fixed, comb.random, pscale, irscale, irunit and several other arguments can be set for the whole R session using settings.meta.

Value
An object of class c("metagen","meta") with corresponding print, summary, and forest functions. The object is a list containing the following components:

- TE, seTE, studLab, exclude, n.e, n.c
  As defined above.
- sm, level, level.comb
  As defined above.
- comb.fixed, comb.random
  As defined above.
- hakn, method.tau, tau.preset, TE.tau, method.bias
  As defined above.
- tau.common, title, complab, outclab
  As defined above.
label.e, label.c, label.left, label.right,
As defined above.
byvar, bylab, print.byvar, byseparator, warn
As defined above.
lower, upper
Lower and upper confidence interval limits for individual studies.
zval, pval
z-value and p-value for test of treatment effect for individual studies.
w.fixed, w.random
Weight of individual studies (in fixed and random effects model).
TE.fixed, seTE.fixed
Estimated overall treatment effect and standard error (fixed effect model).
lower.fixed, upper.fixed
Lower and upper confidence interval limits (fixed effect model).
zval.fixed, pval.fixed
z-value and p-value for test of overall treatment effect (fixed effect model).
TE.random, seTE.random
Estimated overall treatment effect and standard error (random effects model).
lower.random, upper.random
Lower and upper confidence interval limits (random effects model).
zval.random, pval.random
z-value or t-value and corresponding p-value for test of overall treatment effect
(random effects model).
prediction, level.predict
As defined above.
seTE.predict
Standard error utilised for prediction interval.
lower.predict, upper.predict
Lower and upper limits of prediction interval.
null.effect
As defined above.
k
Number of studies combined in meta-analysis.
Q
Heterogeneity statistic.
df.Q
Degrees of freedom for heterogeneity statistic.
pval.Q
P-value of heterogeneity test.
tau
Square-root of between-study variance.
se.tau
Standard error of square-root of between-study variance.
C
Scaling factor utilised internally to calculate common tau-squared across sub-
groups.
method
Pooling method: "Inverse".
df.hakn
Degrees of freedom for test of treatment effect for Hartung-Knapp method (only
if hakn = TRUE).
bylevs
Levels of grouping variable - if byvar is not missing.
TE.fixed.w, seTE.fixed.w
Estimated treatment effect and standard error in subgroups (fixed effect model)
- if byvar is not missing.
lower.fixed.w, upper.fixed.w
  Lower and upper confidence interval limits in subgroups (fixed effect model) - if byvar is not missing.

zval.fixed.w, pval.fixed.w
  z-value and p-value for test of treatment effect in subgroups (fixed effect model) - if byvar is not missing.

TE.random.w, seTE.random.w
  Estimated treatment effect and standard error in subgroups (random effects model) - if byvar is not missing.

lower.random.w, upper.random.w
  Lower and upper confidence interval limits in subgroups (random effects model) - if byvar is not missing.

zval.random.w, pval.random.w
  z-value or t-value and corresponding p-value for test of treatment effect in subgroups (random effects model) - if byvar is not missing.

w.fixed.w, w.random.w
  Weight of subgroups (in fixed and random effects model) - if byvar is not missing.

df.hakn.w
  Degrees of freedom for test of treatment effect for Hartung-Knapp method in subgroups - if byvar is not missing and hakn = TRUE.

n.harmonic.mean.w
  Harmonic mean of number of observations in subgroups (for back transformation of Freeman-Tukey Double arcsine transformation) - if byvar is not missing.

n.e.w
  Number of observations in experimental group in subgroups - if byvar is not missing.

n.c.w
  Number of observations in control group in subgroups - if byvar is not missing.

k.w
  Number of studies combined within subgroups - if byvar is not missing.

k.all.w
  Number of all studies in subgroups - if byvar is not missing.

Q.w.fixed
  Overall within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

Q.w.random
  Overall within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing (only calculated if argument tau.common is TRUE).

df.Q.w
  Degrees of freedom for test of overall within subgroups heterogeneity - if byvar is not missing.

pval.Q.w.fixed
  P-value of within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

pval.Q.w.random
  P-value of within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

Q.b.fixed
  Overall between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

Q.b.random
  Overall between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.
df.Q.b  Degrees of freedom for test of overall between subgroups heterogeneity - if byvar is not missing.
pval.Q.b.fixed  P-value of between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.
pval.Q.b.random  P-value of between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.
tau.w  Square-root of between-study variance within subgroups - if byvar is not missing.
C.w  Scaling factor utilised internally to calculate common tau-squared across subgroups - if byvar is not missing.
H.w  Heterogeneity statistic H within subgroups - if byvar is not missing.
lower.H.w, upper.H.w  Lower and upper confidence limits for heterogeneity statistic H within subgroups - if byvar is not missing.
I2.w  Heterogeneity statistic I2 within subgroups - if byvar is not missing.
lower.I2.w, upper.I2.w  Lower and upper confidence limits for heterogeneity statistic I2 within subgroups - if byvar is not missing.
keepdata  As defined above.
data  Original data (set) used in function call (if keepdata = TRUE).
subset  Information on subset of original data used in meta-analysis (if keepdata = TRUE).
call  Function call.
version  Version of R package meta used to create object.

Author(s)
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References

**See Also**

`update.meta, metabin, metacont, print.meta, settings.meta`

**Examples**

data(Fleiss93)
m1 <- metabin(event.e, n.e, event.c, n.c, 
  data = Fleiss93, sm = "RR", method = "I")
m1
# Identical results by using the generic inverse variance method
metagen(m1$TE, m1$seTE, sm = "RR")
#
forest(metagen(m1$TE, m1$seTE, sm = "RR"))
# Meta-analysis with prespecified between-study variance
# summary(metagen(m1$TE, m1$seTE, sm = "RR", tau.preset = sqrt(0.1)))

# Meta-analysis of survival data:
# logHR <- log(c(0.95, 1.5))
# selogHR <- c(0.25, 0.35)
# metagen(logHR, selogHR, sm = "HR")

# Paule-Mandel method to estimate between-study variance for data
# from Paule & Mandel (1982)
# average <- c(27.044, 26.022, 26.340, 26.787, 26.796)
# variance <- c(0.003, 0.076, 0.464, 0.003, 0.014)
# summary(metagen(average, sqrt(variance), sm = "MD", method.tau = "PM"))

# Conduct meta-analysis using hazard ratios and 95% confidence intervals
# Data from Steurer et al. (2006), Analysis 1.1 Overall survival
# HR <- c(0.55, 0.92, 0.79, 1.18)
# lower.HR <- c(0.28, 0.79, 0.59, 0.64)
# upper.HR <- c(1.09, 1.08, 1.05, 2.17)
# metagen(log(HR), lower = log(lower.HR), upper = log(upper.HR),
# studlab = study, sm = "HR")

---

**Description**

Calculation of fixed effect and random effects estimates (incidence rate ratio or incidence rate difference) for meta-analyses with event counts. Mantel-Haenszel, Cochran, inverse variance method, and generalised linear mixed model (GLMM) are available for pooling. For GLMMs, the rma.glmm function from R package metafor (Viechtbauer 2010) is called internally.
Usage

```r
metainc(event.e, time.e, event.c, time.c, studlab, data = NULL,
subset = NULL, exclude = NULL, method = "MH", sm = gs("sminc"),
inincr = gs("incr"), allinincr = gs("allinincr"),
addinincr = gs("addinincr"), model.glmm = "UM.FS", level = gs("level"),
level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"),
comb.random = gs("comb.random"), hakn = gs("hakn"),
method.tau = ifelse(!is.na(charmatch(tolower(method), "glmm", nomatch =
NA)), "ML", gs("method.tau")), tau.preset = NULL, TE.tau = NULL,
tau.common = gs("tau.common"), prediction = gs("prediction"),
level.predict = gs("level.predict"), method.bias = gs("method.bias"),
n.e = NULL, n.c = NULL, backtransf = gs("backtransf"),
irscale = 1, irunit = "person-years", title = gs("title"),
complab = gs("complab"), outclab = "", label.e = gs("label.e"),
label.c = gs("label.c"), label.left = gs("label.left"),
label.right = gs("label.right"), byvar, bylab,
print.byvar = gs("print.byvar"), byseparator = gs("byseparator"),
keepdata = gs("keepdata"), warn = gs("warn"), control = NULL, ...)
```

Arguments

- **event.e**  Number of events in experimental group.
- **time.e**  Person time at risk in experimental group.
- **event.c**  Number of events in control group.
- **time.c**  Person time at risk in control group.
- **studlab**  An optional vector with study labels.
- **data**  An optional data frame containing the study information, i.e., event.e, time.e, event.c, and time.c.
- **subset**  An optional vector specifying a subset of studies to be used.
- **exclude**  An optional vector specifying studies to exclude from meta-analysis, however, to include in printouts and forest plots.
- **method**  A character string indicating which method is to be used for pooling of studies. One of "MH", "Inverse", "Cochran", or "GLMM" can be abbreviated.
- **sm**  A character string indicating which summary measure ("IRR" or "IRD") is to be used for pooling of studies, see Details.
- **incr**  A numerical value which is added to each cell frequency for studies with a zero cell count, see Details.
- **allinincr**  A logical indicating if incr is added to each cell frequency of all studies if at least one study has a zero cell count. If FALSE (default), incr is added only to each cell frequency of studies with a zero cell count.
- **addinincr**  A logical indicating if incr is added to each cell frequency of all studies irrespective of zero cell counts.
- **model.glmm**  A character string indicating which GLMM should be used. One of "UM.FS", "UM.RS", and "CM.EL", see Details.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>level</code></td>
<td>The level used to calculate confidence intervals for individual studies.</td>
</tr>
<tr>
<td><code>level.comb</code></td>
<td>The level used to calculate confidence intervals for pooled estimates.</td>
</tr>
<tr>
<td><code>comb.fixed</code></td>
<td>A logical indicating whether a fixed effect meta-analysis should be conducted.</td>
</tr>
<tr>
<td><code>comb.random</code></td>
<td>A logical indicating whether a random effects meta-analysis should be conducted.</td>
</tr>
<tr>
<td><code>hakn</code></td>
<td>A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.</td>
</tr>
<tr>
<td><code>method.tau</code></td>
<td>A character string indicating which method is used to estimate the between-study variance $\tau^2$. Either &quot;DL&quot;, &quot;PM&quot;, &quot;REML&quot;, &quot;ML&quot;, &quot;HS&quot;, &quot;SJ&quot; , &quot;HE&quot;, or &quot;EB&quot;, can be abbreviated.</td>
</tr>
<tr>
<td><code>tau.preset</code></td>
<td>Prespecified value for the square-root of the between-study variance $\tau^2$.</td>
</tr>
<tr>
<td><code>TE.tau</code></td>
<td>Overall treatment effect used to estimate the between-study variance $\tau^2$.</td>
</tr>
<tr>
<td><code>tau.common</code></td>
<td>A logical indicating whether tau-squared should be the same across subgroups.</td>
</tr>
<tr>
<td><code>prediction</code></td>
<td>A logical indicating whether a prediction interval should be printed.</td>
</tr>
<tr>
<td><code>level.predict</code></td>
<td>The level used to calculate prediction interval for a new study.</td>
</tr>
<tr>
<td><code>method.bias</code></td>
<td>A character string indicating which test for funnel plot asymmetry is to be used. Either &quot;linreg&quot; or &quot;rank&quot;, can be abbreviated. See function <code>metabias</code></td>
</tr>
<tr>
<td><code>n.e</code></td>
<td>Number of observations in experimental group (optional).</td>
</tr>
<tr>
<td><code>n.c</code></td>
<td>Number of observations in control group (optional).</td>
</tr>
<tr>
<td><code>backtransf</code></td>
<td>A logical indicating whether results for incidence rate ratio (sm = &quot;IRR&quot;) should be back transformed in printouts and plots. If TRUE (default), results will be presented as incidence rate ratios; otherwise log incidence rate ratios will be shown.</td>
</tr>
<tr>
<td><code>irscale</code></td>
<td>A numeric defining a scaling factor for printing of incidence rate differences.</td>
</tr>
<tr>
<td><code>irunit</code></td>
<td>A character string specifying the time unit used to calculate rates, e.g. person-years.</td>
</tr>
<tr>
<td><code>title</code></td>
<td>Title of meta-analysis / systematic review.</td>
</tr>
<tr>
<td><code>complab</code></td>
<td>Comparison label.</td>
</tr>
<tr>
<td><code>outclab</code></td>
<td>Outcome label.</td>
</tr>
<tr>
<td><code>label.e</code></td>
<td>Label for experimental group.</td>
</tr>
<tr>
<td><code>label.c</code></td>
<td>Label for control group.</td>
</tr>
<tr>
<td><code>label.left</code></td>
<td>Graph label on left side of forest plot.</td>
</tr>
<tr>
<td><code>label.right</code></td>
<td>Graph label on right side of forest plot.</td>
</tr>
<tr>
<td><code>byvar</code></td>
<td>An optional vector containing grouping information (must be of same length as <code>event.e</code>).</td>
</tr>
<tr>
<td><code>bylab</code></td>
<td>A character string with a label for the grouping variable.</td>
</tr>
<tr>
<td><code>print.byvar</code></td>
<td>A logical indicating whether the name of the grouping variable should be printed in front of the group labels.</td>
</tr>
<tr>
<td><code>byseparator</code></td>
<td>A character string defining the separator between label and levels of grouping variable.</td>
</tr>
</tbody>
</table>
keepdata A logical indicating whether original data (set) should be kept in meta object.

warn A logical indicating whether warnings should be printed (e.g., if incr is added to studies with zero cell frequencies).

control An optional list to control the iterative process to estimate the between-study variance tau^2. This argument is passed on to rma.uni or rma.glmm, respectively.

... Additional arguments passed on to rma.glmm function.

Details

Treatment estimates and standard errors are calculated for each study. The following measures of treatment effect are available:

- Incidence Rate Ratio (sm = "IRR")
- Incidence Rate Difference (sm = "IRD")

For several arguments defaults settings are utilised (assignments using gs function). These defaults can be changed using the settings.meta function.

Internally, both fixed effect and random effects models are calculated regardless of values chosen for arguments comb.fixed and comb.random. Accordingly, the estimate for the random effects model can be extracted from component TE.random of an object of class "meta" even if argument comb.random = FALSE. However, all functions in R package meta will adequately consider the values for comb.fixed and comb.random. E.g. function print.meta will not print results for the random effects model if comb.random = FALSE.

By default, both fixed effect and random effects models are considered (see arguments comb.fixed and comb.random). If method is "MH" (default), the Mantel-Haenszel method is used to calculate the fixed effect estimate (Greenland & Robbins, 1985); if method is "Inverse", inverse variance weighting is used for pooling; if method is "Cochran", the Cochran method is used for pooling (Bayne-Jones, 1964, Chapter 8).

A distinctive and frequently overlooked advantage of incidence rates is that individual patient data (IPD) can be extracted from count data. Accordingly, statistical methods for IPD, i.e., generalised linear mixed models, can be utilised in a meta-analysis of incidence rate ratios (Stijnen et al., 2010). These methods are available (argument method = "GLMM") by calling the rma.glmm function from R package metafor internally.

Three different GLMMs are available for meta-analysis of incidence rate ratios using argument model.glmm (which corresponds to argument model in the rma.glmm function):

1. Poisson regression model with fixed study effects (default)
   (model.glmm = "UM.FS", i.e., Unconditional Model - Fixed Study effects)
2. Mixed-effects Poisson regression model with random study effects
   (model.glmm = "UM.RS", i.e., Unconditional Model - Random Study effects)
3. Generalised linear mixed model (conditional Poisson-Normal)
   (model.glmm = "CM.EL", i.e., Conditional Model - Exact Likelihood)

Details on these three GLMMs as well as additional arguments which can be provided using argument "...{}" in metaine are described in rma.glmm where you can also find information on the iterative algorithms used for estimation. Note, regardless of which value is used for argument
model.glmm, results for two different GLMMs are calculated: fixed effect model (with fixed treatment effect) and random effects model (with random treatment effects).

For studies with a zero cell count, by default, 0.5 is added to all cell frequencies of these studies (argument incr). This continuity correction is used both to calculate individual study results with confidence limits and to conduct meta-analysis based on the inverse variance method. For Mantel-Haenszel method, Cochran method, and GLMMs, nothing is added to zero cell counts. Accordingly, estimates for these methods are not defined if the number of events is zero in all studies either in the experimental or control group.

Argument byvar can be used to conduct subgroup analysis for all methods but GLMMs. Instead use the metareg function for GLMMs which can also be used for continuous covariates.

A prediction interval for the treatment effect of a new study is calculated (Higgins et al., 2009) if arguments prediction and comb.random are TRUE.

R function update.meta can be used to redo the meta-analysis of an existing metainc object by only specifying arguments which should be changed.

For the random effects, the method by Hartung and Knapp (2003) is used to adjust test statistics and confidence intervals if argument hakn = TRUE.

The DerSimonian-Laird estimate (1986) is used in the random effects model if method.tau = "DL". The iterative Paule-Mandel method (1982) to estimate the between-study variance is used if argument method.tau = "PM". Internally, R function paulemandel is called which is based on R function mpaule.default from R package metRology from S.L.R. Ellison <s.ellison at lgc.co.uk>.

If R package metafor (Viechtbauer 2010) is installed, the following methods to estimate the between-study variance $\tau^2$ (argument method.tau) are also available:

- Restricted maximum-likelihood estimator (method.tau = "REML")
- Maximum-likelihood estimator (method.tau = "ML")
- Hunter-Schmidt estimator (method.tau = "HS")
- Sidik-Jonkman estimator (method.tau = "SJ")
- Hedges estimator (method.tau = "HE")
- Empirical Bayes estimator (method.tau = "EB")

For these methods the R function rma.uni of R package metafor is called internally. See help page of R function rma.uni for more details on these methods to estimate between-study variance.

### Value

An object of class c("metainc","meta") with corresponding print, summary, and forest functions. The object is a list containing the following components:

- event.e, time.e, event.c, time.c, studlab, exclude, As defined above.
- sm, method, incr, allincr, addincr, model.glmm, warn, As defined above.
- level, level.comb, comb.fixed, comb.random, As defined above.
- hakn, method.tau, tau.preset, TE.tau, method.bias, As defined above.
tau.common, title, complab, outclab,
   As defined above.
label.e, label.c, label.left, label.right,
   As defined above.
byvar, bylab, print.byvar, byseparator
   As defined above.
TE, seTE
   Estimated treatment effect and standard error of individual studies.
lower, upper
   Lower and upper confidence interval limits for individual studies.
zval, pval
   z-value and p-value for test of treatment effect for individual studies.
w.fixed, w.random
   Weight of individual studies (in fixed and random effects model).
TE.fixed, seTE.fixed
   Estimated overall treatment effect and standard error (fixed effect model).
lower.fixed, upper.fixed
   Lower and upper confidence interval limits (fixed effect model).
zval.fixed, pval.fixed
   z-value and p-value for test of overall treatment effect (fixed effect model).
TE.random, seTE.random
   Estimated overall treatment effect and standard error (random effects model).
lower.random, upper.random
   Lower and upper confidence interval limits (random effects model).
zval.random, pval.random
   z-value or t-value and corresponding p-value for test of overall treatment effect
   (random effects model).
prediction, level.predict
   As defined above.
seTE.predict
   Standard error utilised for prediction interval.
lower.predict, upper.predict
   Lower and upper limits of prediction interval.
k
   Number of studies combined in meta-analysis.
Q
   Heterogeneity statistic Q.
df.Q
   Degrees of freedom for heterogeneity statistic.
pval.Q
   P-value of heterogeneity test.
Q.LRT
   Heterogeneity statistic for likelihood-ratio test (only if method = "GLMM").
df.Q.LRT
   Degrees of freedom for likelihood-ratio test
pval.Q.LRT
   P-value of likelihood-ratio test.
tau
   Square-root of between-study variance.
se.tau
   Standard error of square-root of between-study variance.
C
   Scaling factor utilised internally to calculate common tau-squared across sub-
groups.
sparse
   Logical flag indicating if any study included in meta-analysis has any zero cell
   frequencies.
incr.event: Increment added to number of events.
df.hakn: Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn = TRUE).
k.MH: Number of studies combined in meta-analysis using Mantel-Haenszel method.
bylevs: Levels of grouping variable - if byvar is not missing.
TE.fixed.w, seTE.fixed.w: Estimated treatment effect and standard error in subgroups (fixed effect model) - if byvar is not missing.
lower.fixed.w, upper.fixed.w: Lower and upper confidence interval limits in subgroups (fixed effect model) - if byvar is not missing.
zval.fixed.w, pval.fixed.w: z-value and p-value for test of treatment effect in subgroups (fixed effect model) - if byvar is not missing.
TE.random.w, seTE.random.w: Estimated treatment effect and standard error in subgroups (random effects model) - if byvar is not missing.
lower.random.w, upper.random.w: Lower and upper confidence interval limits in subgroups (random effects model) - if byvar is not missing.
zval.random.w, pval.random.w: z-value or t-value and corresponding p-value for test of treatment effect in subgroups (random effects model) - if byvar is not missing.
w.fixed.w, w.random.w: Weight of subgroups (in fixed and random effects model) - if byvar is not missing.
df.hakn.w: Degrees of freedom for test of treatment effect for Hartung-Knapp method in subgroups - if byvar is not missing and hakn = TRUE.
n.harmonic.mean.w: Harmonic mean of number of observations in subgroups (for back transformation of Freeman-Tukey Double arcsine transformation) - if byvar is not missing.
event.e.w: Number of events in experimental group in subgroups - if byvar is not missing.
time.e.w: Total person time in subgroups (experimental group) - if byvar is not missing.
n.e.w: Number of observations in experimental group in subgroups - if byvar is not missing.
event.c.w: Number of events in control group in subgroups - if byvar is not missing.
time.c.w: Total person time in subgroups (control group) - if byvar is not missing.
n.c.w: Number of observations in control group in subgroups - if byvar is not missing.
k.w: Number of studies combined within subgroups - if byvar is not missing.
k.all.w: Number of all studies in subgroups - if byvar is not missing.
Q.w.fixed: Overall within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.
Q.w.random Overall within subgroups heterogeneity statistic $Q$ (based on random effects model) - if byvar is not missing (only calculated if argument tau.common is TRUE).

df.Q.w Degrees of freedom for test of overall within subgroups heterogeneity - if byvar is not missing.

pval.Q.w.fixed P-value of within subgroups heterogeneity statistic $Q$ (based on fixed effect model) - if byvar is not missing.

pval.Q.w.random P-value of within subgroups heterogeneity statistic $Q$ (based on random effects model) - if byvar is not missing.

Q.b.fixed Overall between subgroups heterogeneity statistic $Q$ (based on fixed effect model) - if byvar is not missing.

Q.b.random Overall between subgroups heterogeneity statistic $Q$ (based on random effects model) - if byvar is not missing.

df.Q.b Degrees of freedom for test of overall between subgroups heterogeneity - if byvar is not missing.

pval.Q.b.fixed P-value of between subgroups heterogeneity statistic $Q$ (based on fixed effect model) - if byvar is not missing.

pval.Q.b.random P-value of between subgroups heterogeneity statistic $Q$ (based on random effects model) - if byvar is not missing.

tau.w Square-root of between-study variance within subgroups - if byvar is not missing.

C.w Scaling factor utilised internally to calculate common tau-squared across subgroups - if byvar is not missing.

H.w Heterogeneity statistic $H$ within subgroups - if byvar is not missing.

lower.H.w, upper.H.w Lower and upper confidence limits for heterogeneity statistic $H$ within subgroups - if byvar is not missing.

I2.w Heterogeneity statistic $I^2$ within subgroups - if byvar is not missing.

lower.I2.w, upper.I2.w Lower and upper confidence limits for heterogeneity statistic $I^2$ within subgroups - if byvar is not missing.

keepdata As defined above.

data Original data (set) used in function call (if keepdata = TRUE).

subset Information on subset of original data used in meta-analysis (if keepdata = TRUE).

.glmm.fixed GLMM object generated by call of rma.glmm function (fixed effect model).

.glmm.random GLMM object generated by call of rma.glmm function (random effects model).

call Function call.

version Version of R package meta used to create object.

version.metafor Version of R package metafor used for GLMMs.
Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

`metabin`, `update.meta`, `print.meta`

Examples

data(smoking)
m1 <- metainc(d.smokers, py.smokers, d.nonsmokers, py.nonsmokers, 
data = smoking, studlab = study)
print(m1, digits = 2)

m2 <- update(m1, method = "Cochran")
print(m2, digits = 2)

data(lungcancer)
m3 <- metainc(d.smokers, py.smokers, 
d.nonsmokers, py.nonsmokers, 
data = lungcancer, studlab = study)
print(m3, digits = 2)
# Redo Cochran meta-analysis with inflated standard errors
#
# All cause mortality
#
TEa <- log((smoking$d.smokers/smoking$py.smokers) /
           (smoking$d.nonsmokers/smoking$py.nonsmokers))
seTEa <- sqrt(1 / smoking$d.smokers + 1 / smoking$d.nonsmokers +
              2.5 / smoking$d.nonsmokers)
metagen(TEa, seTEa, sm = "IRR", studlab = smoking$study)

# Lung cancer mortality
#
TEl <- log((lungcancer$d.smokers/lungcancer$py.smokers) /
           (lungcancer$d.nonsmokers/lungcancer$py.nonsmokers))
seTEl <- sqrt(1 / lungcancer$d.smokers + 1 / lungcancer$d.nonsmokers +
              2.25 / lungcancer$d.nonsmokers)
metagen(TEl, seTEl, sm = "IRR", studlab = lungcancer$study)

## Not run:
# Meta-analysis using generalised linear mixed models
# (only if R packages 'metafor' and 'lme4' are available)
#
# Poisson regression model (fixed study effects)
#
m4 <- metainc(d.smokers, py.smokers, d.nonsmokers, py.nonsmokers,
              data = smoking, studlab = study, method = "GLMM")
m4

# Mixed-effects Poisson regression model (random study effects)
#
update(m4, model.glmm = "UM.RS", nAGQ = 1)
#
# Generalised linear mixed model (conditional Poisson-Normal)
#
update(m4, model.glmm = "CM.EL")

## End(Not run)

---

### metainf

**Influence analysis in meta-analysis using leave-one-out method**

**Description**

Performs an influence analysis. Pooled estimates are calculated omitting one study at a time.

**Usage**

metainf(x, pooled, sortvar)
Arguments

x | An object of class meta.
pooled | A character string indicating whether a fixed effect or random effects model is used for pooling. Either missing (see Details), "fixed" or "random", can be abbreviated.
sortvar | An optional vector used to sort the individual studies (must be of same length as x$TE).

Details

Performs a influence analysis; pooled estimates are calculated omitting one study at a time. Studies are sorted according to sortvar.

Information from object x is utilised if argument pooled is missing. A fixed effect model is assumed (pooled="fixed") if argument x$comb.fixed is TRUE; a random effects model is assumed (pooled="random") if argument x$comb.random is TRUE and x$comb.fixed is FALSE.

Value

An object of class c("metainf", "meta") with corresponding print, and forest functions. The object is a list containing the following components:

- TE, seTE: Estimated treatment effect and standard error of pooled estimate in influence analysis.
- lower, upper: Lower and upper confidence interval limits.
- studlab: Study label describing omission of studies.
- p.value: P-value for test of overall effect.
- w: Sum of weights from fixed effect or random effects model.
- I2: Heterogeneity statistic I2.
- Rb: Heterogeneity statistic Rb.
- tau: Square-root of between-study variance.
- df.hakn: Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn = TRUE).
- sm: Summary measure.
- method: Method used for pooling.
- k: Number of studies combined in meta-analysis.
- pooled: As defined above.
- comb.fixed: A logical indicating whether analysis is based on fixed effect model.
- comb.random: A logical indicating whether analysis is based on random effects model.
- TE.fixed, seTE.fixed: Value is NA.
- TE.random, seTE.random: Value is NA.
- Q: Value is NA.
level.comb  The level used to calculate confidence intervals for pooled estimates.
hakn  A logical indicating whether the method by Hartung and Knapp is used to adjust test statistics and confidence intervals.
method.tau  A character string indicating which method is used to estimate the between-study variance $\tau^2$.
tau.preset  Prespecified value for the square-root of the between-study variance $\tau^2$.
TE.tau  Overall treatment effect used to estimate the between-study variance $\tau^2$.
n.harmonic.mean  Harmonic mean of number of observations (for back transformation of Freeman-Tukey Double arcsine transformation).
version  Version of R package meta used to create object.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

metabin, metacont, print.meta

Examples

data(Fleiss93)
m1 <- metabin(event.e, n.e, event.c, n.c,
data = Fleiss93, studlab = study,
sm = "RR", method = "I")
m1
metainf(m1)
m1, pooled = "random")
forest(metainf(m1))
forest(metainf(m1), layout = "revman5")
forest(metainf(m1, pooled = "random"))
metainf(m1, sortvar = study)
metainf(m1, sortvar = 7:1)
m2 <- update(m1, title = "Fleiss93 meta-analysis",
backtransf = FALSE)
m2
metainf(m2)
data(Fleiss93cont)
m3 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c,
data = Fleiss93cont, sm = "SMD")
m3
Description

Calculation of an overall mean from studies reporting a single mean using the inverse variance method for pooling; inverse variance weighting is used for pooling.

Usage

metamean(n, mean, sd, studlab, data = NULL, subset = NULL, exclude = NULL, sm = gs("smmean"), level = gs("level"), level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"), comb.random = gs("comb.random"), hakn = gs("hakn"), method.tau = gs("method.tau"), tau.preset = NULL, TE.tau = NULL, tau.common = gs("tau.common"), prediction = gs("prediction"), level.predict = gs("level.predict"), null.effect = NA, method.bias = gs("method.bias"), backtransf = gs("backtransf"), title = gs("title"), complab = gs("complab"), outclab = "", byvar, bylab, print.byvar = gs("print.byvar"), byseparator = gs("byseparator"), keepdata = gs("keepdata"), warn = gs("warn"), control = NULL)

Arguments

n Number of observations.
mean Estimated mean.
sd Standard deviation.
studlab An optional vector with study labels.
data An optional data frame containing the study information.
subset An optional vector specifying a subset of studies to be used.
exclude An optional vector specifying studies to exclude from meta-analysis, however, to include in printouts and forest plots.
sm A character string indicating which summary measure ("MRAW" or "MLN") is to be used for pooling of studies.
level The level used to calculate confidence intervals for individual studies.
level.comb The level used to calculate confidence intervals for pooled estimates.
comb.fixed A logical indicating whether a fixed effect meta-analysis should be conducted.
comb.random A logical indicating whether a random effects meta-analysis should be conducted.
hakn A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.
metamean

method.tau A character string indicating which method is used to estimate the between-study variance $\tau^2$. Either "DL", "PM", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.

tau.preset Prespecified value for the square-root of the between-study variance $\tau^2$.

TE.tau Overall treatment effect used to estimate the between-study variance tau-squared.

tau.common A logical indicating whether tau-squared should be the same across subgroups.

prediction A logical indicating whether a prediction interval should be printed.

level.predict The level used to calculate prediction interval for a new study.

null.effect A numeric value specifying the effect under the null hypothesis.

method.bias A character string indicating which test is to be used. Either "rank", "linreg", or "mm", can be abbreviated. See function metabias

backtransf A logical indicating whether results should be back transformed in printouts and plots for sm = "MLN". If TRUE (default), results will be presented as means; otherwise logarithm of means will be shown.

title Title of meta-analysis / systematic review.

complab Comparison label.

outclab Outcome label.

byvar An optional vector containing grouping information (must be of same length as n).

bylab A character string with a label for the grouping variable.

print.byvar A logical indicating whether the name of the grouping variable should be printed in front of the group labels.

byseparator A character string defining the separator between label and levels of grouping variable.

keepdata A logical indicating whether original data (set) should be kept in meta object.

warn A logical indicating whether warnings should be printed (e.g., if studies are excluded from meta-analysis due to zero standard deviations).

control An optional list to control the iterative process to estimate the between-study variance tau^2. This argument is passed on to rma.uni.

Details

Fixed effect and random effects meta-analysis of single means to calculate an overall mean; inverse variance weighting is used for pooling. The following transformations of means are implemented to calculate an overall mean:

- Raw, i.e. untransformed, means (sm = "MRAW", default)
- Log transformed means (sm = "MLN")

Note, you should use R function metacont to compare means of pairwise comparisons instead of using metamean for each treatment arm separately which will break randomisation in randomised controlled trials.
Calculations are conducted on the log scale if \( sm = "ROM" \). Accordingly, list elements \( TE, TE\text{.fixed}, \) and \( TE\text{.random} \) contain the logarithm of means. In printouts and plots these values are back transformed if argument \( \text{backtransf} = \text{TRUE} \).

For several arguments defaults settings are utilised (assignments using \texttt{gs} function). These defaults can be changed using the \texttt{settings.meta} function.

Internally, both fixed effect and random effects models are calculated regardless of values chosen for arguments \( \text{comb\_fixed} \) and \( \text{comb\_random} \). Accordingly, the estimate for the random effects model can be extracted from component \( \text{TE\_random} \) of an object of class \texttt{"meta"} even if argument \( \text{comb\_random} = \text{FALSE} \). However, all functions in R package \texttt{meta} will adequately consider the values for \( \text{comb\_fixed} \) and \( \text{comb\_random} \). E.g. function \texttt{print.meta} will not print results for the random effects model if \( \text{comb\_random} = \text{FALSE} \).

The function \texttt{metagen} is called internally to calculate individual and overall treatment estimates and standard errors.

A prediction interval for the treatment effect of a new study is calculated (Higgins et al., 2009) if arguments \( \text{prediction} \) and \( \text{comb\_random} \) are \texttt{TRUE}.

R function \texttt{update.meta} can be used to redo the meta-analysis of an existing \texttt{metamean} object by only specifying arguments which should be changed.

For the random effects, the method by Hartung and Knapp (2001) / Knapp and Hartung (2003) is used to adjust test statistics and confidence intervals if argument \( \text{hakn} = \text{TRUE} \).

The DerSimonian-Laird estimate (1986) is used in the random effects model if \( \text{method\_tau} = \text{"DL"} \). The iterative Paule-Mandel method (1982) to estimate the between-study variance is used if argument \( \text{method\_tau} = \text{"PM"} \). Internally, R function \texttt{paulemandel} is called which is based on R function \texttt{mpaule.default} from R package \texttt{metRology} from S.L.R. Ellison <s.ellison at lgc.co.uk>.

If R package \texttt{metafor} (Viechtbauer 2010) is installed, the following methods to estimate the between-study variance \( \tau^2 \) (argument \( \text{method\_tau} \)) are also available:

- Restricted maximum-likelihood estimator (\( \text{method\_tau} = \text{"REML"} \))
- Maximum-likelihood estimator (\( \text{method\_tau} = \text{"ML"} \))
- Hunter-Schmidt estimator (\( \text{method\_tau} = \text{"HS"} \))
- Sidik-Jonkman estimator (\( \text{method\_tau} = \text{"SJ"} \))
- Hedges estimator (\( \text{method\_tau} = \text{"HE"} \))
- Empirical Bayes estimator (\( \text{method\_tau} = \text{"EB"} \))

For these methods the R function \texttt{rma.uni} of R package \texttt{metafor} is called internally. See help page of R function \texttt{rma.uni} for more details on these methods to estimate between-study variance.

**Value**

An object of class \texttt{c("metamean","meta")} with corresponding \texttt{print}, \texttt{summary}, and \texttt{forest} functions. The object is a list containing the following components:

- \( \text{n, mean, sd, } \) As defined above.
- \( \text{studlab, exclude, sm, level, level.comb, } \) As defined above.
- \( \text{comb\_fixed, comb\_random, } \) As defined above.
hakn, method.tau, tau.preset, TE.tau, method.bias,
   As defined above.
tau.common, title, complab, outclab,
   As defined above.
byvar, bylab, print.byvar, byseparator, warn
   As defined above.
TE, seTE
   Estimated effect (mean or log mean) and standard error of individual studies.
lower, upper
   Lower and upper confidence interval limits for individual studies.
zval, pval
   Z-value and p-value for test of overall effect for individual studies.
w.fixed, w.random
   Weight of individual studies (in fixed and random effects model).
TE.fixed, seTE.fixed
   Estimated overall effect (mean or log mean) and standard error (fixed effect model).
lower.fixed, upper.fixed
   Lower and upper confidence interval limits (fixed effect model).
zval.fixed, pval.fixed
   Z-value and p-value for test of overall effect (fixed effect model).
TE.random, seTE.random
   Estimated overall effect (mean or log mean) and standard error (random effects model).
lower.random, upper.random
   Lower and upper confidence interval limits (random effects model).
zval.random, pval.random
   Z-value or t-value and corresponding p-value for test of overall effect (random effects model).
prediction, level.predict
   As defined above.
seTE.predict
   Standard error utilised for prediction interval.
lower.predict, upper.predict
   Lower and upper limits of prediction interval.
k
   Number of studies combined in meta-analysis.
Q
   Heterogeneity statistic.
tau
   Square-root of between-study variance.
se.tau
   Standard error of square-root of between-study variance.
C
   Scaling factor utilised internally to calculate common tau-squared across subgroups.
method
   Pooling method: "Inverse".
df.hakn
   Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn = TRUE).
bylevs
   Levels of grouping variable - if byvar is not missing.
TE.fixed.w, seTE.fixed.w
   Estimated effect and standard error in subgroups (fixed effect model) - if byvar is not missing.
lower.fixed.w, upper.fixed.w
   Lower and upper confidence interval limits in subgroups (fixed effect model) -
   if byvar is not missing.

zval.fixed.w, pval.fixed.w
   z-value and p-value for test of treatment effect in subgroups (fixed effect model)
   - if byvar is not missing.

TE.random.w, seTE.random.w
   Estimated effect and standard error in subgroups (random effects model) - if
   byvar is not missing.

lower.random.w, upper.random.w
   Lower and upper confidence interval limits in subgroups (random effects model)
   - if byvar is not missing.

zval.random.w, pval.random.w
   z-value or t-value and corresponding p-value for test of effect in subgroups (random
   effects model) - if byvar is not missing.

w.fixed.w, w.random.w
   Weight of subgroups (in fixed and random effects model) - if byvar is not miss-
   ing.

df.hakn.w
   Degrees of freedom for test of effect for Hartung-Knapp method in subgroups -
   if byvar is not missing and hakn = TRUE.

n.e.w
   Number of observations in experimental group in subgroups - if byvar is not not
   missing.

n.c.w
   Number of observations in control group in subgroups - if byvar is not missing.

k.w
   Number of studies combined within subgroups - if byvar is not missing.

k.all.w
   Number of all studies in subgroups - if byvar is not missing.

Q.w.fixed
   Overall within subgroups heterogeneity statistic Q (based on fixed effect model)
   - if byvar is not missing.

Q.w.random
   Overall within subgroups heterogeneity statistic Q (based on random effects
   model) - if byvar is not missing (only calculated if argument tau.common is
   TRUE).

df.Q.w
   Degrees of freedom for test of overall within subgroups heterogeneity - if byvar
   is not missing.

pval.Q.w.fixed
   P-value of within subgroups heterogeneity statistic Q (based on fixed effect
   model) - if byvar is not missing.

pval.Q.w.random
   P-value of within subgroups heterogeneity statistic Q (based on random effects
   model) - if byvar is not missing.

Q.b.fixed
   Overall between subgroups heterogeneity statistic Q (based on fixed effect model)
   - if byvar is not missing.

Q.b.random
   Overall between subgroups heterogeneity statistic Q (based on random effects
   model) - if byvar is not missing.

df.Q.b
   Degrees of freedom for test of overall between subgroups heterogeneity - if byvar
   is not missing.
pval.Q.b.fixed  P-value of between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

pval.Q.b.random  P-value of between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

tau.w  Square-root of between-study variance within subgroups - if byvar is not missing.

C.w  Scaling factor utilised internally to calculate common tau-squared across subgroups - if byvar is not missing.

H.w  Heterogeneity statistic H within subgroups - if byvar is not missing.

lower.H.w, upper.H.w  Lower and upper confidence limits for heterogeneity statistic H within subgroups - if byvar is not missing.

I2.w  Heterogeneity statistic I2 within subgroups - if byvar is not missing.

lower.I2.w, upper.I2.w  Lower and upper confidence limits for heterogeneity statistic I2 within subgroups - if byvar is not missing.

keepdata  As defined above.

data  Original data (set) used in function call (if keepdata = TRUE).

subset  Information on subset of original data used in meta-analysis (if keepdata = TRUE).

call  Function call.

version  Version of R package meta used to create object.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


Knapp G & Hartung J (2003): Improved tests for a random effects meta-regression with a single covariate. Statistics in Medicine, 22, 2693–710


metaprop

Meta-analysis of single proportions

Description

Calculation of an overall proportion from studies reporting a single proportion. Inverse variance method and generalised linear mixed model (GLMM) are available for pooling. For GLMMs, the rma.glmm function from R package metafor (Viechtbauer 2010) is called internally.

Usage

metaprop(event, n, studlab, data = NULL, subset = NULL,
exclude = NULL, method, sm = gs("smprop"), incr = gs("incr"),
allincr = gs("allincr"), addincr = gs("addincr"),
method.ci = gs("method.ci"), level = gs("level"),
level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"),
comb.random = gs("comb.random"), hakn = gs("hakn"), method.tau,
tau.preset = NULL, TE.tau = NULL, tau.common = gs("tau.common"),
prediction = gs("prediction"), level.predict = gs("level.predict"),
null.effect = NA, method.bias = gs("method.bias"),
backtransf = gs("backtransf"), pscale = 1, title = gs("title"),
complab = gs("complab"), outclab = "", byvar, bylab,
print.byvar = gs("print.byvar"), byseparator = gs("byseparator"),
keepdata = gs("keepdata"), warn = gs("warn"), control = NULL, ...)
Arguments

**event**  
Number of events.

**n**  
Number of observations.

**studlab**  
An optional vector with study labels.

**data**  
An optional data frame containing the study information, i.e., event and n.

**subset**  
An optional vector specifying a subset of studies to be used.

**exclude**  
An optional vector specifying studies to exclude from meta-analysis, however, to include in printouts and forest plots.

**method**  
A character string indicating which method is to be used for pooling of studies. One of "Inverse" and "GLMM", can be abbreviated.

**sm**  
A character string indicating which summary measure ("PFT", "PAS", "PRAW", "PLN", or "PLOGIT") is to be used for pooling of studies, see Details.

**incr**  
A numeric which is added to event number and sample size of studies with zero or all events, i.e., studies with an event probability of either 0 or 1.

**allincr**  
A logical indicating if incr is considered for all studies if at least one study has either zero or all events. If FALSE (default), incr is considered only in studies with zero or all events.

**addincr**  
A logical indicating if incr is used for all studies irrespective of number of events.

**method.ci**  
A character string indicating which method is used to calculate confidence intervals for individual studies, see Details.

**level**  
The level used to calculate confidence intervals for individual studies.

**level.comb**  
The level used to calculate confidence intervals for pooled estimates.

**comb.fixed**  
A logical indicating whether a fixed effect meta-analysis should be conducted.

**comb.random**  
A logical indicating whether a random effects meta-analysis should be conducted.

**hakn**  
A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.

**method.tau**  
A character string indicating which method is used to estimate the between-study variance \( \tau^2 \), see Details.

**tau.preset**  
Prespecified value for the square-root of the between-study variance \( \tau^2 \).

**TE.tau**  
Overall treatment effect used to estimate the between-study variance tau-squared.

**tau.common**  
A logical indicating whether tau-squared should be the same across subgroups.

**prediction**  
A logical indicating whether a prediction interval should be printed.

**level.predict**  
The level used to calculate prediction interval for a new study.

**null.effect**  
A numeric value specifying the effect under the null hypothesis.

**method.bias**  
A character string indicating which test is to be used. Either "rank", "linreg", or "mm", can be abbreviated. See function metabias.

**backtransf**  
A logical indicating whether results for transformed proportions (argument sm != "PRAW") should be back transformed in printouts and plots. If TRUE (default), results will be presented as proportions; otherwise transformed proportions will be shown. See Details for presentation of confidence intervals.
**metaprop**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pscale</td>
<td>A numeric defining a scaling factor for printing of single event probabilities.</td>
</tr>
<tr>
<td>title</td>
<td>Title of meta-analysis / systematic review.</td>
</tr>
<tr>
<td>complab</td>
<td>Comparison label.</td>
</tr>
<tr>
<td>outclab</td>
<td>Outcome label.</td>
</tr>
<tr>
<td>byvar</td>
<td>An optional vector containing grouping information (must be of same length as event).</td>
</tr>
<tr>
<td>bylab</td>
<td>A character string with a label for the grouping variable.</td>
</tr>
<tr>
<td>print.byvar</td>
<td>A logical indicating whether the name of the grouping variable should be printed in front of the group labels.</td>
</tr>
<tr>
<td>byseparator</td>
<td>A character string defining the separator between label and levels of grouping variable.</td>
</tr>
<tr>
<td>keepdata</td>
<td>A logical indicating whether original data (set) should be kept in meta object.</td>
</tr>
<tr>
<td>warn</td>
<td>A logical indicating whether the addition of incr to studies with zero or all events should result in a warning.</td>
</tr>
<tr>
<td>control</td>
<td>An optional list to control the iterative process to estimate the between-study variance tau^2. This argument is passed on to rma.uni or rma.glmm, respectively.</td>
</tr>
<tr>
<td>...</td>
<td>Additional arguments passed on to rma.glmm function.</td>
</tr>
</tbody>
</table>

**Details**

This function provides methods for fixed effect and random effects meta-analysis of single proportions to calculate an overall proportion. Note, you should use R function metabin to compare proportions of pairwise comparisons instead of using metaprop for each treatment arm separately which will break randomisation in randomised controlled trials.

The following transformations of proportions are implemented to calculate an overall proportion:

- Logit transformation (sm = "PLOGIT", default)
- Log transformation (sm = "PLN")
- Freeman-Tukey Double arcsine transformation (sm = "PFT")
- Arcsine transformation (sm = "PAS")
- Raw, i.e. untransformed, proportions (sm = "PRAW")

Classic meta-analysis (Borenstein et al., 2010) utilises the transformed proportions and corresponding standard errors in the generic inverse variance method. A distinctive and frequently overlooked advantage of binary data is that individual patient data can be extracted. Accordingly, a generalised linear mixed model (GLMM) - more specific, a random intercept logistic regression model - can be utilised for the meta-analysis of proportions (Stijnen et al., 2010). This method - implicitly using the logit transformation - is available (argument method = "GLMM") by calling the rma.glmm function from R package metafor internally.

For the logit transformation, a random intercept logistic regression model is used by default, i.e., argument method = "GLMM". The classic meta-analysis model based on the inverse variance method can be used instead by setting argument method equal to "Inverse".
Contradictory recommendations on the use of transformations of proportions have been published in the literature. For example, Barendregt et al. (2013) recommend the use of the Freeman-Tukey double arcsine transformation instead of the logit transformation whereas Warton & Hui (2011) strongly advise to use generalised linear mixed models with the logit transformation instead of the arcsine transformation. Schwarzer et al. (2019) describe seriously misleading results in a meta-analysis with very different sample sizes due to problems with the back-transformation of the Freeman-Tukey transformation which requires a single sample size. Accordingly, Schwarzer et al. (2019) also recommend to use GLMMs for the meta-analysis of single proportions, however, admit that individual study weights are not available with this method. Meta-analysts which require individual study weights should consider the arcsine or logit transformation.

In order to prevent misleading conclusions for the Freeman-Tukey double arcsine transformation, sensitivity analyses using other transformations or using a range of sample sizes should be conducted (Schwarzer et al., 2019).

Various methods are available to calculate confidence intervals for individual study results (see Agresti & Coull 1998 and Newcombe 1988):

- Clopper-Pearson interval also called 'exact' binomial interval (method.ci = "CP", default)
- Wilson Score interval (method.ci = "WS")
- Wilson Score interval with continuity correction (method.ci = "WSCC")
- Agresti-Coull interval (method.ci = "AC")
- Simple approximation interval (method.ci = "SA")
- Simple approximation interval with continuity correction (method.ci = "SACC")
- Normal approximation interval based on summary measure, i.e. defined by argument sm (method.ci = "NAsm")

Note, with exception of the normal approximation based on the summary measure, i.e. method.ci = "NAsm", the same confidence interval is calculated for individual studies for any summary measure (argument sm) as only number of events and observations are used in the calculation disregarding the chosen summary measure. Results will be presented for transformed proportions if argument backtransf = FALSE in the print.meta, print.summary.meta, or forest.meta function. In this case, argument method.ci = "NAsm" is used, i.e. confidence intervals based on the normal approximation based on the summary measure.

Argument pscale can be used to rescale proportions, e.g. pscale = 1000 means that proportions are expressed as events per 1000 observations. This is useful in situations with (very) low event probabilities.

For several arguments defaults settings are utilised (assignments using gs function). These defaults can be changed using the settings.meta function.

Internally, both fixed effect and random effects models are calculated regardless of values choosen for arguments comb.fixed and comb.random. Accordingly, the estimate for the random effects model can be extracted from component TE.random of an object of class "meta" even if argument comb.random = FALSE. However, all functions in R package meta will adequately consider the values for comb.fixed and comb.random. E.g. function print.meta will not print results for the random effects model if comb.random = FALSE.

If the summary measure is equal to "PRAW", "PLN", or "PLOGIT", a continuity correction is applied if any study has either zero or all events, i.e., an event probability of either 0 or 1. By
default, 0.5 is used as continuity correction (argument incr). This continuity correction is used both to calculate individual study results with confidence limits and to conduct meta-analysis based on the inverse variance method. For GLMMs no continuity correction is used.

Argument byvar can be used to conduct subgroup analysis for all methods but GLMMs. Instead use the metareg function for GLMMs which can also be used for continuous covariates.

A prediction interval for the treatment effect of a new study is calculated (Higgins et al., 2009) if arguments prediction and comb.random are TRUE.

R function update.meta can be used to redo the meta-analysis of an existing metaprop object by only specifying arguments which should be changed.

For the random effects, the method by Hartung and Knapp (2003) is used to adjust test statistics and confidence intervals if argument hakn = TRUE.

The DerSimonian-Laird estimate (1986) is used in the random effects model if method.tau = "DL". The iterative Paule-Mandel method (1982) to estimate the between-study variance is used if argument method.tau = "PM". Internally, R function paulemandel is called which is based on R function mpaule.default from R package metRology from S.L.R. Ellison <s.ellison at lgc.co.uk>.

If R package metafor (Viechtbauer 2010) is installed, the following methods to estimate the between-study variance $\tau^2$ (argument method.tau) are also available:

- Restricted maximum-likelihood estimator (method.tau = "REML")
- Maximum-likelihood estimator (method.tau = "ML")
- Hunter-Schmidt estimator (method.tau = "HS")
- Sidik-Jonkman estimator (method.tau = "SJ")
- Hedges estimator (method.tau = "HE")
- Empirical Bayes estimator (method.tau = "EB")

For these methods the R function rma.uni of R package metafor is called internally. See help page of R function rma.uni for more details on these methods to estimate between-study variance.

Value

An object of class c("metaprop", "meta") with corresponding print, summary, and forest functions. The object is a list containing the following components:

- event, n, studlab, exclude,
  As defined above.
- sm, incr, allincr, addincr, method.ci,
  As defined above.
- level, level.comb,
  As defined above.
- comb.fixed, comb.random,
  As defined above.
- hakn, method.tau, tau.preset, TE.tau, null.hypothesis,
  As defined above.
- method.bias, tau.common, title, complab, outlab,
  As defined above.
byvar, bylab, print.byvar, byseparator, warn
As defined above.

TE, seTE
Estimated (un)transformed proportion and its standard error for individual studies.

lower, upper
Lower and upper confidence interval limits for individual studies.

zval, pval
z-value and p-value for test of treatment effect for individual studies.

w.fixed, w.random
Weight of individual studies (in fixed and random effects model).

TE.fixed, seTE.fixed
Estimated overall (un)transformed proportion and standard error (fixed effect model).

lower.fixed, upper.fixed
Lower and upper confidence interval limits (fixed effect model).

zval.fixed, pval.fixed
z-value and p-value for test of overall effect (fixed effect model).

TE.random, seTE.random
Estimated overall (un)transformed proportion and standard error (random effects model).

lower.random, upper.random
Lower and upper confidence interval limits (random effects model).

zval.random, pval.random
z-value or t-value and corresponding p-value for test of overall effect (random effects model).

prediction, level.predict
As defined above.

seTE.predict
Standard error utilised for prediction interval.

lower.predict, upper.predict
Lower and upper limits of prediction interval.

k
Number of studies combined in meta-analysis.

Q
Heterogeneity statistic Q.

df.Q
Degrees of freedom for heterogeneity statistic.

pval.Q
P-value of heterogeneity test.

Q.LRT
Heterogeneity statistic for likelihood-ratio test (only if method = "GLMM").

df.Q.LRT
Degrees of freedom for likelihood-ratio test

pval.Q.LRT
P-value of likelihood-ratio test.

tau
Square-root of between-study variance.

se.tau
Standard error of square-root of between-study variance.

C
Scaling factor utilised internally to calculate common tau-squared across subgroups.

method
A character string indicating method used for pooling: "Inverse"

df.hakn
Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn=TRUE).
bylevs

Levels of grouping variable - if `byvar` is not missing.

**TE.fixed.w, seTE.fixed.w**

Estimated treatment effect and standard error in subgroups (fixed effect model) - if `byvar` is not missing.

**lower.fixed.w, upper.fixed.w**

Lower and upper confidence interval limits in subgroups (fixed effect model) - if `byvar` is not missing.

**zval.fixed.w, pval.fixed.w**

z-value and p-value for test of treatment effect in subgroups (fixed effect model) - if `byvar` is not missing.

**TE.random.w, seTE.random.w**

Estimated treatment effect and standard error in subgroups (random effects model) - if `byvar` is not missing.

**lower.random.w, upper.random.w**

Lower and upper confidence interval limits in subgroups (random effects model) - if `byvar` is not missing.

**zval.random.w, pval.random.w**

z-value or t-value and corresponding p-value for test of treatment effect in subgroups (random effects model) - if `byvar` is not missing.

**w.fixed.w, w.random.w**

Weight of subgroups (in fixed and random effects model) - if `byvar` is not missing.

**df.hakn.w**

Degrees of freedom for test of treatment effect for Hartung-Knapp method in subgroups - if `byvar` is not missing and `hakn=TRUE`.

**n.harmonic.mean.w**

Harmonic mean of number of observations in subgroups (for back transformation of Freeman-Tukey Double arcsine transformation) - if `byvar` is not missing.

**event.w**

Number of events in subgroups - if `byvar` is not missing.

**n.w**

Number of observations in subgroups - if `byvar` is not missing.

**k.w**

Number of studies combined within subgroups - if `byvar` is not missing.

**k.all.w**

Number of all studies in subgroups - if `byvar` is not missing.

**Q.w.fixed**

Overall within subgroups heterogeneity statistic Q (based on fixed effect model) - if `byvar` is not missing.

**Q.w.random**

Overall within subgroups heterogeneity statistic Q (based on random effects model) - if `byvar` is not missing (only calculated if argument `tau.common` is `TRUE`).

**df.Q.w**

Degrees of freedom for test of overall within subgroups heterogeneity - if `byvar` is not missing.

**pval.Q.w.fixed**

P-value of within subgroups heterogeneity statistic Q (based on fixed effect model) - if `byvar` is not missing.

**pval.Q.w.random**

P-value of within subgroups heterogeneity statistic Q (based on random effects model) - if `byvar` is not missing.
Q.b.fixed  Overall between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

Q.b.random Overall between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

df.Q.b Degrees of freedom for test of overall between subgroups heterogeneity - if byvar is not missing.

pval.Q.b.fixed P-value of between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.

pval.Q.b.random P-value of between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.

tau.w Square-root of between-study variance within subgroups - if byvar is not missing.

C.w Scaling factor utilised internally to calculate common tau-squared across subgroups - if byvar is not missing.

H.w Heterogeneity statistic H within subgroups - if byvar is not missing.

lower.H.w, upper.H.w Lower and upper confidence limiti for heterogeneity statistic H within subgroups - if byvar is not missing.

I2.w Heterogeneity statistic I2 within subgroups - if byvar is not missing.

lower.I2.w, upper.I2.w Lower and upper confidence limiti for heterogeneity statistic I2 within subgroups - if byvar is not missing.

incr.event Increment added to number of events.

keepdata As defined above.

data Original data (set) used in function call (if keepdata=TRUE).

subset Information on subset of original data used in meta-analysis (if keepdata=TRUE).

.glmm.fixed GLMM object generated by call of rma.glmm function (fixed effect model).

.glmm.random GLMM object generated by call of rma.glmm function (random effects model).

call Function call.

version Version of R package meta used to create object.

version.metafor Version of R package metafor used for GLMMs.

Author(s)

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References


See Also

update.meta, metacont, metagen, print.meta

Examples

```r
# Meta-analysis using generalised linear mixed model
#
metaprop(4:1, 10 * 1:4)

# Apply various classic meta-analysis methods to estimate
# proportions
#
ml <- metaprop(4:1, 10 * 1:4, method = "Inverse")
m2 <- update(ml, sm = "PAS")
```
m3 <- update(m1, sm = "PRAW")
m4 <- update(m1, sm = "PLN")
m5 <- update(m1, sm = "PFT")
#
m1
m2
m3
m4
m5
#
forest(m1)
## Not run:
forest(m2)
forest(m3)
forest(m3, pscale = 100)
forest(m4)
forest(m5)
## End(Not run)

# Do not back transform results, e.g. print logit transformed
# proportions if sm = "PLOGIT" and store old settings
#
oldset <- settings.meta(backtransf = FALSE)
#
m6 <- metaprop(4:1, c(10, 20, 30, 40), method = "Inverse")
m7 <- update(m6, sm = "PAS")
m8 <- update(m6, sm = "PRAW")
m9 <- update(m6, sm = "PLN")
m10 <- update(m6, sm = "PFT")
#
forest(m6)
## Not run:
forest(m7)
forest(m8)
forest(m8, pscale = 100)
forest(m9)
forest(m10)
## End(Not run)

# Use old settings
#
settings.meta(oldset)

# Examples with zero events
#
m1 <- metaprop(c(0, 0, 10, 10), rep(100, 4), method = "Inverse")
m2 <- metaprop(c(0, 0, 10, 10), rep(100, 4), incr = 0.1, method = "Inverse")
#
summary(m1)
summary(m2)
#
## Not run:
forest(m1)
forest(m2)

## End(Not run)

# Example from Miller (1978):

death <- c(3, 6, 10, 1)
animals <- c(11, 17, 21, 6)

m3 <- metaprop(death, animals, sm = "PFT")
forest(m3)

# Data examples from Newcombe (1998)
- apply various methods to estimate confidence intervals for
  individual studies

event <- c(81, 15, 0, 1)
n <- c(263, 148, 20, 29)

m1 <- metaprop(event, n, method.ci = "SA", method = "Inverse")
m2 <- update(m1, method.ci = "SACC")
m3 <- update(m1, method.ci = "WS")
m4 <- update(m1, method.ci = "WSCC")
m5 <- update(m1, method.ci = "CP")

lower <- round(rbind(NA, m1$lower, m2$lower, NA, m3$lower,
                      m4$lower, NA, m5$lower), 4)
upper <- round(rbind(NA, m1$upper, m2$upper, NA, m3$upper,
                      m4$upper, NA, m5$upper), 4)

#
# tab1 <- data.frame(
# scen1 = meta:::formatCI(lower[, 1], upper[, 1]),
# scen2 = meta:::formatCI(lower[, 2], upper[, 2]),
# scen3 = meta:::formatCI(lower[, 3], upper[, 3]),
# scen4 = meta:::formatCI(lower[, 4], upper[, 4]),
# stringsAsFactors = FALSE
# )
# names(tab1) <- c("r=81, n=263", "r=15, n=148",
# "r=0, n=20", "r=1, n=29")
# row.names(tab1) <- c("Simple", "- SA", "- SACC",
# "Score", "- WS", "- WSCC",
# "Binomial", "- CP")
# tab1[is.na(tab1)] <- ""
# Newcombe (1998), Table I, methods 1-5:
#
# # Same confidence interval, i.e. unaffected by choice of summary
# # measure
# print(metaprop(event, n, method.ci = "WS", method = "Inverse"), ma = FALSE)
print(metaprop(event, n, sm = "PLN", method.ci = "WS"), ma = FALSE)
Calculation of an overall incidence rate from studies reporting a single incidence rate. Inverse variance method and generalised linear mixed model (GLMM) are available for pooling. For GLMMs, the `rma.glmm` function from R package `metafor` (Viechtbauer 2010) is called internally.
Usage

metarate(event, time, studlab, data = NULL, subset = NULL,
exclude = NULL, method = "Inverse", sm = gs("smrate"),
incr = gs("incr"), allincr = gs("allincr"),
addincr = gs("addincr"), level = gs("level"),
level.comb = gs("level.comb"), comb.fixed = gs("comb.fixed"),
comb.random = gs("comb.random"), hakn = gs("hakn"),
method.tau = ifelse(is.na(charmatch(tolower(method), "glmm", nomatch =
NA)), "ML", gs("method.tau")), tau.preset = NULL, TE.tau = NULL,
tau.common = gs("tau.common"), prediction = gs("prediction"),
level.predict = gs("level.predict"), null.effect = NA,
method.bias = gs("method.bias"), backtransf = gs("backtransf"),
irscale = 1, irunit = "person-years", title = gs("title"),
complab = gs("complab"), outclab = ",", byvar, bylab,
print.byvar = gs("print.byvar"), byseparator = gs("byseparator"),
keepdata = gs("keepdata"), warn = gs("warn"), control = NULL, ...)

Arguments

event Number of events.
time Person time at risk.
studlab An optional vector with study labels.
data An optional data frame containing the study information, i.e., event and time.
subset An optional vector specifying a subset of studies to be used.
exclude An optional vector specifying studies to exclude from meta-analysis, however,
to include in printouts and forest plots.
method A character string indicating which method is to be used for pooling of studies.
One of "Inverse" and "GLMM", can be abbreviated.
sm A character string indicating which summary measure ("IR", "IRLN", "IRS", or
"IRFT") is to be used for pooling of studies, see Details.
incr A numeric which is added to the event number of studies with zero events, i.e.,
studies with an incidence rate of 0.
allincr A logical indicating if incr is considered for all studies if at least one study has
zero events. If FALSE (default), incr is considered only in studies with zero
events.
addincr A logical indicating if incr is used for all studies irrespective of number of
events.
level The level used to calculate confidence intervals for individual studies.
level.comb The level used to calculate confidence intervals for pooled estimates.
comb.fixed A logical indicating whether a fixed effect meta-analysis should be conducted.
comb.random A logical indicating whether a random effects meta-analysis should be con-
ducted.
hakn A logical indicating whether the method by Hartung and Knapp should be used
to adjust test statistics and confidence intervals.
method.tau  A character string indicating which method is used to estimate the between-study variance \( \tau^2 \), see Details.

tau.preset  Prespecified value for the square-root of the between-study variance \( \tau^2 \).

TE.tau  Overall treatment effect used to estimate the between-study variance tau-squared.

tau.common  A logical indicating whether tau-squared should be the same across subgroups.

prediction  A logical indicating whether a prediction interval should be printed.

level.predict  The level used to calculate prediction interval for a new study.

null.effect  A numeric value specifying the effect under the null hypothesis.

method.bias  A character string indicating which test is to be used. Either "rank", "linreg", or "mm", can be abbreviated. See function metabias.

backtransf  A logical indicating whether results for transformed rates (argument sm != "IR") should be back transformed in printouts and plots. If TRUE (default), results will be presented as incidence rates; otherwise transformed rates will be shown.

irscale  A numeric defining a scaling factor for printing of rates.

irunit  A character string specifying the time unit used to calculate rates, e.g. person-years.

title  Title of meta-analysis / systematic review.

complab  Comparison label.

outclab  Outcome label.

byvar  An optional vector containing grouping information (must be of same length as event).

bylab  A character string with a label for the grouping variable.

print.byvar  A logical indicating whether the name of the grouping variable should be printed in front of the group labels.

byseparator  A character string defining the separator between label and levels of grouping variable.

keepdata  A logical indicating whether original data (set) should be kept in meta object.

warn  A logical indicating whether the addition of incr to studies with zero events should result in a warning.

control  An optional list to control the iterative process to estimate the between-study variance tau^2. This argument is passed on to rma.uni or rma.glmm, respectively.

...  Additional arguments passed on to rma.glmm function.

Details

Fixed effect and random effects meta-analysis of single incidence rates to calculate an overall rate. The following transformations of incidence rates are implemented to calculate an overall rate:

- Log transformation (sm = "IRLN", default)
- Square root transformation (sm = "IRS")
- Freeman-Tukey Double arcsine transformation (sm = "IRFT")
• No transformation (sm = "IR")

Note, you should use R function `metainc` to compare incidence rates of pairwise comparisons instead of using `metarate` for each treatment arm separately which will break randomisation in randomised controlled trials.

Argument `irscale` can be used to rescale rates, e.g. `irscale = 1000` means that rates are expressed as events per 1000 time units, e.g. person-years. This is useful in situations with (very) low rates. Argument `irunit` can be used to specify the time unit used in individual studies (default: "person-years"). This information is printed in summaries and forest plots if argument `irscale` is not equal to 1.

For several arguments defaults settings are utilised (assignments using `gs` function). These defaults can be changed using the `settings.meta` function.

Internally, both fixed effect and random effects models are calculated regardless of values choosen for arguments `comb.fixed` and `comb.random`. Accordingly, the estimate for the random effects model can be extracted from component `TE.random` of an object of class "meta" even if argument `comb.random = FALSE`. However, all functions in R package `meta` will adequately consider the values for `comb.fixed` and `comb.random`. E.g. function `print.meta` will not print results for the random effects model if `comb.random = FALSE`.

A random intercept Poisson regression model can be utilised for the meta-analysis of incidence rates (Stijnen et al., 2010). This method is available (argument `method = "GLMM"`) by calling the `rma.glmm` function from R package `metafor` internally.

If the summary measure is equal to "IR" or "IRLN", a continuity correction is applied if any study has zero events, i.e., an incidence rate of 0. By default, 0.5 is used as continuity correction (argument `incr`). This continuity correction is used both to calculate individual study results with confidence limits and to conduct meta-analysis based on the inverse variance method. For Freeman-Tukey and square root transformation and GLMMs no continuity correction is used.

Argument `byvar` can be used to conduct subgroup analysis for all methods but GLMMs. Instead use the `metareg` function for GLMMs which can also be used for continuous covariates.

A prediction interval for the treatment effect of a new study is calculated (Higgins et al., 2009) if arguments `prediction` and `comb.random` are `TRUE`.

R function `update.meta` can be used to redo the meta-analysis of an existing `metarate` object by only specifying arguments which should be changed.

For the random effects, the method by Hartung and Knapp (2003) is used to adjust test statistics and confidence intervals if argument `hakn = TRUE`.

The DerSimonian-Laird estimate (1986) is used in the random effects model if `method.tau = "DL"`. The iterative Paule-Mandel method (1982) to estimate the between-study variance is used if argument `method.tau = "PM"`. Internally, R function `paulemandel` is called which is based on R function `mpaule.default` from R package `metRology` from S.L.R. Ellison <s.ellison at lgc.co.uk>.

If R package `metafor` (Viechtbauer 2010) is installed, the following methods to estimate the between-study variance $\tau^2$ (argument `method.tau`) are also available:

- Restricted maximum-likelihood estimator (`method.tau = "REML"`)
- Maximum-likelihood estimator (`method.tau = "ML"`)
- Hunter-Schmidt estimator (`method.tau = "HS"`)
• Hedges estimator (method.tau = "HE")
• Empirical Bayes estimator (method.tau = "EB")

For these methods the R function rma.uni of R package metafor is called internally. See help page of R function rma.uni for more details on these methods to estimate between-study variance.

Value

An object of class c("metarate", "meta") with corresponding print, summary, and forest functions. The object is a list containing the following components:

- event, n, studlab, exclude,
  As defined above.
- sm, incr, allincr, addincr, method.ci,
  As defined above.
- level, level.comb,
  As defined above.
- comb.fixed, comb.random,
  As defined above.
- hakn, method.tau, tau.preset, TE.tau, null.effect,
  As defined above.
- method.bias, tau.common, title, complab, outclab,
  As defined above.
- byvar, bylab, print.byvar, byseparator, warn
  As defined above.
- TE, seTE
  Estimated (un)transformed incidence rate and its standard error for individual studies.
- lower, upper
  Lower and upper confidence interval limits for individual studies.
- zval, pval
  z-value and p-value for test of treatment effect for individual studies.
- w.fixed, w.random
  Weight of individual studies (in fixed and random effects model).
- TE.fixed, seTE.fixed
  Estimated overall (un)transformed incidence rate and standard error (fixed effect model).
- lower.fixed, upper.fixed
  Lower and upper confidence interval limits (fixed effect model).
- zval.fixed, pval.fixed
  z-value and p-value for test of overall effect (fixed effect model).
- TE.random, seTE.random
  Estimated overall (un)transformed incidence rate and standard error (random effects model).
- lower.random, upper.random
  Lower and upper confidence interval limits (random effects model).
- zval.random, pval.random
  z-value or t-value and corresponding p-value for test of overall effect (random effects model).
prediction, level.predict
As defined above.

seTE.predict Standard error utilised for prediction interval.

lower.predict, upper.predict
Lower and upper limits of prediction interval.

k Number of studies combined in meta-analysis.

Q Heterogeneity statistic Q.
df.Q Degrees of freedom for heterogeneity statistic.
pval.Q P-value of heterogeneity test.

Q.LRT Heterogeneity statistic for likelihood-ratio test (only if method = "GLMM").
df.Q.LRT Degrees of freedom for likelihood-ratio test

pval.Q.LRT P-value of likelihood-ratio test.

tau Square-root of between-study variance.

se.tau Standard error of square-root of between-study variance.

C Scaling factor utilised internally to calculate common tau-squared across subgroups.

method A character string indicating method used for pooling: "Inverse"

df.hakn Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn = TRUE).

bylevs Levels of grouping variable - if byvar is not missing.

TE.fixed.w, seTE.fixed.w
Estimated treatment effect and standard error in subgroups (fixed effect model)
- if byvar is not missing.

lower.fixed.w, upper.fixed.w
Lower and upper confidence interval limits in subgroups (fixed effect model)
- if byvar is not missing.

zval.fixed.w, pval.fixed.w
z-value and p-value for test of treatment effect in subgroups (fixed effect model)
- if byvar is not missing.

TE.random.w, seTE.random.w
Estimated treatment effect and standard error in subgroups (random effects model)
- if byvar is not missing.

lower.random.w, upper.random.w
Lower and upper confidence interval limits in subgroups (random effects model)
- if byvar is not missing.

zval.random.w, pval.random.w
z-value or t-value and corresponding p-value for test of treatment effect in subgroups (random effects model) - if byvar is not missing.

w.fixed.w, w.random.w
Weight of subgroups (in fixed and random effects model) - if byvar is not missing.

df.hakn.w Degrees of freedom for test of treatment effect for Hartung-Knapp method in subgroups - if byvar is not missing and hakn = TRUE.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>n.harmonic.mean.w</td>
<td>Harmonic mean of number of observations in subgroups (for back transformation of Freeman-Tukey Double arcsine transformation) - if byvar is not missing.</td>
</tr>
<tr>
<td>event.w</td>
<td>Number of events in subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>n.w</td>
<td>Number of observations in subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>k.w</td>
<td>Number of studies combined within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>k.all.w</td>
<td>Number of all studies in subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>Q.w.fixed</td>
<td>Overall within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>Q.w.random</td>
<td>Overall within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing (only calculated if argument tau.common is TRUE).</td>
</tr>
<tr>
<td>df.Q.w</td>
<td>Degrees of freedom for test of overall within subgroups heterogeneity - if byvar is not missing.</td>
</tr>
<tr>
<td>pval.Q.w.fixed</td>
<td>P-value of within subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>pval.Q.w.random</td>
<td>P-value of within subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>Q.b.fixed</td>
<td>Overall between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>Q.b.random</td>
<td>Overall between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>df.Q.b</td>
<td>Degrees of freedom for test of overall between subgroups heterogeneity - if byvar is not missing.</td>
</tr>
<tr>
<td>pval.Q.b.fixed</td>
<td>P-value of between subgroups heterogeneity statistic Q (based on fixed effect model) - if byvar is not missing.</td>
</tr>
<tr>
<td>pval.Q.b.random</td>
<td>P-value of between subgroups heterogeneity statistic Q (based on random effects model) - if byvar is not missing.</td>
</tr>
<tr>
<td>tau.w</td>
<td>Square-root of between-study variance within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>C.w</td>
<td>Scaling factor utilised internally to calculate common tau-squared across subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>H.w</td>
<td>Heterogeneity statistic H within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>lower.H.w, upper.H.w</td>
<td>Lower and upper confidence limit for heterogeneity statistic H within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>I2.w</td>
<td>Heterogeneity statistic I2 within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>lower.I2.w, upper.I2.w</td>
<td>Lower and upper confidence limit for heterogeneity statistic I2 within subgroups - if byvar is not missing.</td>
</tr>
<tr>
<td>incr.event</td>
<td>Increment added to number of events.</td>
</tr>
</tbody>
</table>
**keepdata**

As defined above.

**data**

Original data (set) used in function call (if keepdata = TRUE).

**subset**

Information on subset of original data used in meta-analysis (if keepdata = TRUE).

**.glmm.fixed**

GLMM object generated by call of `rma.glmm` function (fixed effect model).

**.glmm.random**

GLMM object generated by call of `rma.glmm` function (random effects model).

**call**

Function call.

**version**

Version of R package `meta` used to create object.

**version.metafor**

Version of R package `metafor` used for GLMMs.

**Author(s)**

Guido Schwarzer <sc@imbi.uni-freiburg.de>

**References**


**See Also**

`update.meta`, `metacont`, `metagen`, `print.meta`

**Examples**

```r
# Apply various meta-analysis methods to estimate incidence rates
#
ml <- metarate(4:1, c(10, 20, 30, 40))
m2 <- update(ml, sm = "IR")
m3 <- update(ml, sm = "IRS")
m4 <- update(ml, sm = "IRFT")
#```
m1
m2
m3
m4
#
forest(m1)
forest(m1, irscale = 100)
forest(m1, irscale = 100, irunit = "person-days")
forest(m1, backtransf = FALSE)
## Not run:
forest(m2)
forest(m3)
forest(m4)
## End(Not run)

m5 <- metarate(40:37, c(100, 200, 300, 400), sm = "IRFT")
m5

---

**metareg**  
*Meta-regression*

**Description**

Meta-regression for objects of class `meta`. This is a wrapper function for the R function `rma.uni` in the R package `metafor` (Viechtbauer 2010).

**Usage**

```r
metareg(x, formula, method.tau = x$method.tau, hakn = x$hakn,
level.comb = x$level.comb, intercept = TRUE, ...)
```

**Arguments**

- `x`  
  An object of class `meta`.
- `formula`  
  Either a character string or a formula object.
- `method.tau`  
  A character string indicating which method is used to estimate the between-study variance tau-squared. Either "FE", "DL", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.
- `hakn`  
  A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.
- `level.comb`  
  The level used to calculate confidence intervals for parameter estimates in the meta-regression model.
- `intercept`  
  A logical indicating whether an intercept should be included in the meta-regression model.
- `...`  
  Additional arguments passed to R function `rma.uni`. 

---
Details

This R function is a wrapper function for R function \texttt{rma.uni} in the R package \texttt{metafor} (Viechtbauer 2010), i.e., function \texttt{metareg} can only be used if R package \texttt{metafor} is installed.

Note, results are not back-transformed in printouts of meta-analyses using summary measures with transformations, e.g., log risk ratios are printed instead of the risk ratio if argument \texttt{sm = "RR"} and logit transformed proportions are printed if argument \texttt{sm = "PLOGIT"}.

Argument ‘...’ can be used to pass additional arguments to R function \texttt{rma.uni}. For example, argument \texttt{control} to provide a list of control values for the iterative estimation algorithm. See help page of R function \texttt{rma.uni} for more details.

Value

An object of class c("metareg","rma.uni","rma"). Please look at the help page of R function \texttt{rma.uni} for more details on the output from this function.

In addition, a list \texttt{.meta} is added to the output containing the following components:

- \texttt{x}, \texttt{formula}, \texttt{method.tau}, \texttt{hakn}, \texttt{level.comb}, \texttt{intercept}
  - As defined above.
- \texttt{dots}
  - Information provided in argument ‘...’.
- \texttt{call}
  - Function call.
- \texttt{version}
  - Version of R package \texttt{meta} used to create object.
- \texttt{version.metafor}
  - Version of R package \texttt{metafor} used to create object.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

\texttt{bubble, summary.meta, metagen}

Examples

data(Fleiss93cont)
# Add some (fictitious) grouping variables:
Fleiss93cont$age <- c(55, 65, 55, 65, 55)
Fleiss93cont$region <- c("Europe", "Europe", "Asia", "Asia", "Europe")

m1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c,
  data = Fleiss93cont, sm = "MD")
## Not run:
# Warnings due to wrong ordering of arguments (order has changed
# with version 3.0-0 of R package meta)
#
mareg(~ region, m1)
mareg(~ region, data = m1)

# Warning as no information on covariate is available
#
mareg(m1)

## End(Not run)

# Do meta-regression for covariate region
#
mu2 <- update(m1, byvar = region, tau.common = TRUE, comb.fixed = FALSE)
mareg(mu2)

# Same result for
# - tau-squared
# - test of heterogeneity
# - test for subgroup differences
# (as argument 'tau.common' was used to create mu2)
#
mu2
mareg(mu2, intercept = FALSE)
mareg(m1, region)

# Different result for
# - tau-squared
# - test of heterogeneity
# - test for subgroup differences
# (as argument 'tau.common' is - by default - FALSE)
#
mu1 <- update(m1, byvar = region)
mu1

# Generate bubble plot
#
bubble(mareg(mu2))

# Do meta-regression with two covariates
#
mareg(mu1, region + age)

# Do same meta-regressions using formula notation
#
mareg(m1, ~ region)
mareg(mu1, ~ region + age)

# Do meta-regression using REML method and print intermediate
# results for iterative estimation algorithm; furthermore print
# results with three digits.
#
mareg(mu1, region, method.tau = "REML",


control = list(verbos = TRUE), digits = 3)

# Use Hartung-Knapp method
#
m3 <- update(m2, hakn = TRUE)
m3
metareg(m3, intercept = FALSE)

---

### nnt

*Calculate the number needed to treat (NNT)*

**Description**

Calculate the number needed to treat (NNT) from estimated risk difference, risk ratio, or odds ratio, and a baseline risk.

**Usage**

```r
nnt(x, ...)  
```

**Arguments**

- `x` An object of class `meta`, or estimated treatment effect, i.e., risk difference(s), risk ratio(s), or odds ratio(s).
- `...` Additional arguments (ignored at the moment).
- `p.c` Baseline risk (control group event probability).
- `comb.fixed` A logical indicating whether NNTs should be calculated based on fixed effect estimate.
- `comb.random` A logical indicating whether NNTs should be calculated based on random effects estimate.
- `sm` Summary measure.
- `lower` Lower confidence interval limit.
- `upper` Upper confidence interval limit.
digits Minimal number of significant digits, see print.default.
digits.prop Minimal number of significant digits for proportions, see print.default.
big.mark A character used as thousands separator.

Details

The number needed to treat (NNT) can be easily computed from an estimated risk difference (RD), risk ratio (RR), or odds ratio (OR) and a given baseline risk (Higgins & Green, 2011, section 12.5). Accordingly, this function can be used to calculate NNTs for meta-analyses generated with metabin or metagen if argument sm was equal to "RD", "RR", or "OR". It is also possible to directly provide estimated treatment effects without conducting a meta-analysis (see Examples).

The baseline risk can be specified using argument p.c. If this argument is missing, the minimum, mean, and maximum of the control event probabilities in the meta-analysis are used for metabin; otherwise the control event probabilities 0.1, 0.2, ..., 0.9 are used.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

metabin, metagen

Examples

# Calculate NNT for RD = -0.21
# (Cochrane Handbook, version 5.1, subsection 12.5.4.1)
nnt(-0.21, sm = "RD")

# Calculate NNT for RR = 0.92 and baseline risk p.c = 0.3
# (Cochrane Handbook, version 5.1, subsection 12.5.4.2)
nnt(0.92, p.c = 0.3, sm = "RR")

# Calculate NNT for OR = 0.73 and baseline risk p.c = 0.3
# (Cochrane Handbook, version 5.1, subsection 12.5.4.3)
nnt(0.73, p.c = 0.3, sm = "OR")

# Use Mantel-Haenszel odds ratio to calculate NNTs
data(Olkin95)
m1 <- metabin(event.e, n.e, event.c, n.c, data = Olkin95,
            comb.random = FALSE)
nnt(m1, comb.random = TRUE)
Description

Meta-analysis on Thrombolytic Therapy after Acute Myocardial Infarction

Format

A data frame with the following columns:

- **author**: first author
- **year**: year of publication
- **event.e**: number of events in experimental group
- **n.e**: number of observations in experimental group
- **event.c**: number of events in control group
- **n.c**: number of observations in control group

Source


Examples

data(Olkin95)
summary(metabin(event.e, n.e, event.c, n.c, data = Olkin95))

---

Conversion from log odds ratio to standardised mean difference

Description

Conversion from log odds ratio to standardised mean difference using method by Hasselblad & Hedges (1995) or Cox (1970).

Usage

```r
or2smd(lnOR, selnOR, studlab, data = NULL, subset = NULL,
exclude = NULL, method = "HH", ...)```

Arguments

\begin{itemize}
\item \texttt{lnOR} \quad Log odds ratio(s) or meta-analysis object.
\item \texttt{selnOR} \quad Standard error(s) of log odds ratio(s) (ignored if argument \texttt{lnOR} is a meta-analysis object).
\item \texttt{studlab} \quad An optional vector with study labels (ignored if argument \texttt{lnOR} is a meta-analysis object).
\item \texttt{data} \quad An optional data frame containing the study information (ignored if argument \texttt{lnOR} is a meta-analysis object).
\item \texttt{subset} \quad An optional vector specifying a subset of studies to be used (ignored if argument \texttt{lnOR} is a meta-analysis object).
\item \texttt{exclude} \quad An optional vector specifying studies to exclude from meta-analysis, however, to include in printouts and forest plots (ignored if argument \texttt{lnOR} is a meta-analysis object).
\item \texttt{method} \quad A character string indicating which method is used to convert log odds ratios to standardised mean differences. Either "HH" or "CS", can be abbreviated.
\item \ldots \quad Additional arguments passed on to \texttt{metagen} (ignored if argument \texttt{lnOR} is a meta-analysis object).
\end{itemize}

Details

This function implements the following methods for the conversion from log odds ratios to standardised mean difference:

\begin{itemize}
\item Hasselblad & Hedges (1995) assuming logistic distributions (method == "HH")
\item Cox (1970) and Cox & Snell (1989) assuming normal distributions (method == "CS")
\end{itemize}

Internally, \texttt{metagen} is used to conduct a meta-analysis with the standardised mean difference as summary measure.

Argument \texttt{lnOR} can be either a vector of log odds ratios or a meta-analysis object created with \texttt{metabin} or \texttt{metagen} and the odds ratio as summary measure.

Argument \texttt{selnOR} is mandatory if argument \texttt{lnOR} is a vector and ignored otherwise. Additional arguments in \ldots are only passed on to \texttt{metagen} if argument \texttt{lnOR} is a vector.

Value

An object of class "meta" and "metagen"; see \texttt{metagen}.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

`smd2or, metabin, metagen, metacont`

Examples

```r
# Example from Borenstein et al. (2009), Chapter 7
#
mb <- or2smd(0.9069, sqrt(0.0676))
# TE = standardised mean difference (SMD); seTE = standard error of SMD
data.frame(SMD = round(mb$TE, 4), varSMD = round(mb$seTE^2, 4))

# Use dataset from Fleiss (1993)
#
data(Fleiss93)
m1 <- metabin(event.e, n.e, event.c, n.c,
data = Fleiss93,
studlab = paste(study, year),
sm = "OR", comb.random = FALSE)
or2smd(m1)
```

print.meta

Print meta-analysis results

Description

Print method for objects of class `meta`.

Usage

```
## S3 method for class 'meta'
print(x, sortvar, comb.fixed = x$comb.fixed,
comb.random = x$comb.random, prediction = x$prediction,
details = FALSE, ma = TRUE, backtransf = x$backtransf,
pscale = x$pscale, irscale = x$irscale, irunit = x$irunit,
digits = gs("digits"), digits.se = gs("digits.se"),
digits.tau2 = gs("digits.tau2"), digits.I2 = gs("digits.I2"),
digits.prop = gs("digits.prop"), digits.weight = gs("digits.weight"),
big.mark = gs("big.mark"), warn.backtransf = FALSE, ...)
cilayout(bracket = "[", separator = "; ")
```
Arguments

x
sortvar
comb.fixed
comb.random
prediction
details
ma
backtransf
pscale
irscale
irunit
digits
digits.se
digits.tau2
digits.I2
digits.prop
digits.weight
big.mark
warn.backtransf
... 
bracket
separator

An object of class meta
An optional vector used to sort the individual studies (must be of same length as x$TE).
A logical indicating whether a fixed effect meta-analysis should be conducted.
A logical indicating whether a random effects meta-analysis should be conducted.
A logical indicating whether a prediction interval should be printed.
A logical indicating whether further details of individual studies should be printed.
A logical indicating whether the summary results of the meta-analysis should be printed.
A logical indicating whether printed results should be back transformed. If backtransf = TRUE, results for sm = "OR" are printed as odds ratios rather than log odds ratios and results for sm = "ZCOR" are printed as correlations rather than Fisher’s z transformed correlations, for example.
A numeric giving scaling factor for printing of single event probabilities or risk differences, i.e. if argument sm is equal to "PLOGIT", "PLN", "PRAW", "PAS", "PFT", or "RD".
A numeric defining a scaling factor for printing of single incidence rates or incidence rate differences, i.e. if argument sm is equal to "IR", "IRLN", "IRS", "IRFT", or "IRD".
A character specifying the time unit used to calculate rates, e.g. person-years.
Minimal number of significant digits, see print.default.
Minimal number of significant digits for standard deviations and standard errors, see print.default.
Minimal number of significant digits for between-study variance, see print.default.
Minimal number of significant digits for I-squared and Rb statistic, see print.default.
Minimal number of significant digits for proportions, see print.default.
Minimal number of significant digits for weights, see print.default.
A character used as thousands separator.
A logical indicating whether a warning should be printed if backtransformed proportions and rates are below 0 and backtransformed proportions are above 1.
Additional arguments (passed on to print.summary.meta called internally).
A character with bracket symbol to print lower confidence interval: ";", "(" , "{", "".
A character string with information on separator between lower and upper confidence interval.
Details

R function cilayout can be utilised to change the layout to print confidence intervals (both in printout from print.meta and print.summary.meta function as well as in forest plots). The default layout is "[lower; upper]". Another popular layout is "(lower - upper)" which is used throughout an R session by using R command cilayout("(", " -").

Argument pscale can be used to rescale single proportions or risk differences, e.g. pscale = 1000 means that proportions are expressed as events per 1000 observations. This is useful in situations with (very) low event probabilities.

Argument irscale can be used to rescale single rates or rate differences, e.g. irscale = 1000 means that rates are expressed as events per 1000 time units, e.g. person-years. This is useful in situations with (very) low rates. Argument irunit can be used to specify the time unit used in individual studies (default: "person-years"). This information is printed in summaries and forest plots if argument irscale is not equal to 1.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

summary.meta, update.meta, metabin, metacont, metagen

Examples

data(Fleiss93cont)
m1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, data = Fleiss93cont, sm = "SMD", studlab = paste(study, year))
m1

print(m1, digits = 2)

## Not run:
# Use unicode characters to print \tau^2 and I^2
print(m1, text.tau2 = "\u03c4\u00b2", text.I2 = "I\u00b2")

## End(Not run)
Radial plot

**Description**

Draw a radial plot (also called Galbraith plot) which can be used to assess bias in meta-analysis.

**Usage**

```r
radial(x, ...)  
## Default S3 method:  
radial(x, y, xlim = NULL, ylim = NULL,  
xlab = "Inverse of standard error",  
ylab = "Standardised treatment effect (z-score)", comb.fixed = TRUE,  
axes = TRUE, pch = 1, text = NULL, cex = 1, col = NULL,  
level = NULL, ...)  
## S3 method for class 'meta'  
radial(x, xlim = NULL, ylim = NULL,  
xlab = "Inverse of standard error",  
ylab = "Standardised treatment effect (z-score)", comb.fixed = TRUE,  
axes = TRUE, pch = 1, text = NULL, cex = 1, col = NULL,  
level = NULL, ...)  
```

**Arguments**

- `x`: An object of class `meta`, or estimated treatment effect in individual studies.
- `...`: Graphical arguments as in `par` may also be passed as arguments.
- `y`: Standard error of estimated treatment effect.
- `xlim`: The x limits (min, max) of the plot.
- `ylim`: The y limits (min, max) of the plot.
- `xlab`: A label for the x-axis.
- `ylab`: A label for the y-axis.
- `comb.fixed`: A logical indicating whether the pooled fixed effect estimate should be plotted.
- `axes`: A logical indicating whether axes should be drawn on the plot.
- `pch`: The plotting symbol used for individual studies.
- `text`: A character vector specifying the text to be used instead of plotting symbol.
- `cex`: The magnification to be used for plotting symbol.
- `col`: A vector with colour of plotting symbols.
- `level`: The confidence level utilised in the plot.
Details

A radial plot (Galbraith 1988a,b), also called Galbraith plot, is drawn in the active graphics window. If \texttt{comb.fixed} is TRUE, the pooled estimate of the fixed effect model is plotted. If \texttt{level} is not NULL, the corresponding confidence limits are drawn.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

\texttt{metabias}, \texttt{metabin}, \texttt{metagen}, \texttt{funnel}

Examples

data(Olkin95)
m1 <- metabin(event.e, n.e, event.c, n.c,
     data = Olkin95, subset = c(41, 47, 51, 59),
     studlab = paste(author, year),
     sm = "RR", method = "I")
# Radial plot
#
radial(m1, level = 0.95)

---

**read.mtv** Import RevMan 4 data files (.mtv)

Description

Reads a file created with RevMan 4 and creates a data frame from it.

Usage

\texttt{read.mtv(file)}

Arguments

\begin{itemize}
\item {\texttt{file}} The name of a file to read data values from.
\end{itemize}
Details
Reads a file created with RevMan 4 (Menu: “File” - “Export” - “Analysis data file...”) and creates a data frame from it.

Value
A data frame containing the following components:

- **comp.no**: Comparison number.
- **outcome.no**: Outcome number.
- **group.no**: Group number.
- **studlab**: Study label.
- **year**: Year of publication.
- **event.e**: Number of events in experimental group.
- **n.e**: Number of observations in experimental group.
- **event.c**: Number of events in control group.
- **n.c**: Number of observations in control group.
- **mean.e**: Estimated mean in experimental group.
- **sd.e**: Standard deviation in experimental group.
- **mean.c**: Estimated mean in control group.
- **sd.c**: Standard deviation in control group.
- **O.E**: Observed minus expected (IPD analysis).
- **V**: Variance of O.E (IPD analysis).
- **order**: Ordering of studies.
- **conceal**: Concealment of treatment allocation.
- **grplab**: Group label.
- **type**: Type of outcome. D = dichotomous, C = continuous, P = IPD.
- **outclab**: Outcome label.
- **graph.exp**: Graph label for experimental group.
- **graph.cont**: Graph label for control group.
- **label.exp**: Label for experimental group.
- **label.cont**: Label for control group.
- **complab**: Comparison label.

Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

References
See Also

metabin, metacont, metagen

Examples

# Locate MTV-data file "FLEISS93.MTV" in sub-directory of R package
# meta
#
filename <- system.file("extdata/Fleiss93.MTV", package = "meta")
fleiss93.cc <- read.mtv(filename)

# Same result as R Command example(Fleiss93):
#
metabin(event.e, n.e, event.c, n.c,
data = fleiss93.cc, subset = type == "D",
studlab = paste(studlab, year))

# Same result: example(Fleiss93cont)
#
metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c,
data = fleiss93.cc, subset = type == "C",
studlab = paste(studlab, year))

---

read.rm5  
Import RevMan 5 data files (.csv)

Description

Reads data file from Cochrane Intervention review created with RevMan 5 and creates a data frame from it.

Usage

read.rm5(file, sep = ",", quote = "\"", title,
numbers.in.labels = TRUE)

## S3 method for class 'rm5'
print(x, ...)

Arguments

- **file**: The name of a file to read data values from.
- **sep**: The field separator character. Values on each line of the file are separated by this character. The comma is the default field separator character in RevMan 5.
- **quote**: The set of quoting characters. In RevMan 5 a "\"" is the default quoting character.
title
Title of Cochrane review.

numbers.in.labels
A logical indicating whether comparison number and outcome number should be printed at the beginning of the comparison (argument complab) and outcome label (argument outclab); this is the default in RevMan 5.

x
An object of class rm5

... Additional arguments (passed on to print.data.frame).

Details

Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://community.cochrane.org/tools/review-production-tools/revman-5). RevMan 5 includes the ability to write Systematic reviews of interventions, Diagnostic test accuracy reviews, Methodology reviews and Overviews of reviews.

This function provides the ability to read a data file from a Cochrane Intervention review created with RevMan 5; a data frame is created from it. Cochrane Intervention reviews are based on the comparison of two interventions.

In order to generate a data analysis file in RevMan 5 use the following Menu points: "File" - "Export" - "Data and analyses". It is mandatory to include the following fields in the exported data file by selecting them with the mouse cursor in the Export Analysis Data Wizard: (i) Comparison Number, (ii) Outcome Number, (iii) Subgroup Number. When these fields are not selected a corresponding error message will be printed in R. It is recommended to include all fields in the exported data file except for the last field "Risk of bias tables". For example, in order to redo the meta-analysis in R for the RevMan 5 data type "O-E and Variance" the fields "O-E" and "Variance" have to be selected in the Export Analysis Data Wizard. If the last field "Risk of bias tables" is selected the import in R fails with an error message "line X did not have Y elements". By default in RevMan 5, the name of the exported data file is the title of the Cochrane Review. Accordingly, information on the title is extracted from the name of the exported data file (argument: file) if argument title is missing (default).

Each respective meta-analysis for arguments event.e.pooled – df.pooled is defined by values for "comp.no" and "outcome.no", and "grp.no".

Value

A data frame containing the following components:

- comp.no: Comparison number.
- outcome.no: Outcome number.
- group.no: Group number.
- studlab: Study label.
- year: Year of publication.
- event.e: Number of events in experimental group.
- n.e: Number of observations in experimental group.
- event.c: Number of events in control group.
- n.c: Number of observations in control group.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mean.e</td>
<td>Estimated mean in experimental group.</td>
</tr>
<tr>
<td>sd.e</td>
<td>Standard deviation in experimental group.</td>
</tr>
<tr>
<td>mean.c</td>
<td>Estimated mean in control group.</td>
</tr>
<tr>
<td>sd.c</td>
<td>Standard deviation in control group.</td>
</tr>
<tr>
<td>O.E</td>
<td>Observed minus expected (IPD analysis).</td>
</tr>
<tr>
<td>V</td>
<td>Variance of O.E (IPD analysis).</td>
</tr>
<tr>
<td>TE, seTE</td>
<td>Estimated treatment effect and standard error of individual studies.</td>
</tr>
<tr>
<td>lower, upper</td>
<td>Lower and upper limit of 95% confidence interval for treatment effect in individual studies.</td>
</tr>
<tr>
<td>weight</td>
<td>Weight of individual studies (according to meta-analytical method used in respective meta-analysis - see below for details).</td>
</tr>
<tr>
<td>order</td>
<td>Ordering of studies.</td>
</tr>
<tr>
<td>grplab</td>
<td>Group label.</td>
</tr>
<tr>
<td>type</td>
<td>Type of outcome. D = dichotomous, C = continuous, P = IPD.</td>
</tr>
<tr>
<td>method</td>
<td>A character string indicating which method has been used for pooling of studies. One of “Inverse”, “MH”, or “Peto”.</td>
</tr>
<tr>
<td>sm</td>
<td>A character string indicating which summary measure has been used for pooling of studies.</td>
</tr>
<tr>
<td>model</td>
<td>A character string indicating which meta-analytical model has been used (either &quot;Fixed&quot; or &quot;Random&quot;).</td>
</tr>
<tr>
<td>comb.fixed</td>
<td>A logical indicating whether fixed effect meta-analysis has been used in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>comb.random</td>
<td>A logical indicating whether random effects meta-analysis has been used in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>outclab</td>
<td>Outcome label.</td>
</tr>
<tr>
<td>k</td>
<td>Total number of studies combined in respective meta-analysis).</td>
</tr>
<tr>
<td>event.e.pooled</td>
<td>Number of events in experimental group in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>n.e.pooled</td>
<td>Number of observations in experimental group in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>event.c.pooled</td>
<td>Number of events in control group in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>n.c.pooled</td>
<td>Number of observations in control group in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>TE.pooled</td>
<td>Estimated treatment effect in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>lower, upper</td>
<td>Lower and upper limit of 95% confidence interval for treatment effect in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>weight.pooled</td>
<td>Total weight in respective meta-analysis (see below for details).</td>
</tr>
<tr>
<td>Z.pooled</td>
<td>Z-score for test of overall treatment effect in respective meta-analysis (see below for details).</td>
</tr>
</tbody>
</table>
pval.pooled  P-value for test of overall treatment effect in respective meta-analysis (see below for details).

Q  Heterogeneity statistic Q in respective meta-analysis (see below for details).
pval.Q  P-value of heterogeneity statistic Q in respective meta-analysis (see below for details).

I2  Heterogeneity statistic I2 in respective meta-analysis (see below for details).
tau2  Between-study variance (moment estimator of DerSimonian-Laird) in respective meta-analysis.

Q.w  Heterogeneity statistic Q within groups in respective meta-analysis (see below for details).
pval.Q.w  P-value of heterogeneity statistic Q within groups in respective meta-analysis (see below for details).

I2.w  Heterogeneity statistic I2 within groups in respective meta-analysis (see below for details).

label.e  Label for experimental group.

label.c  Label for control group.

label.left  Graph label on left side of forest plot.

label.right  Graph label on right side of forest plot.

RR.cochrane  A logical indicating if 2*incr instead of 1*incr is to be added to n.e and n.c in the calculation of the risk ratio (i.e., sm = "RR") for studies with a zero cell. This is used in RevMan 5.

complab  Comparison label.

Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

summary.rm5, metabias.rm5, metabin, metacont, metagen, metacr

Examples

# Locate export data file "Fleiss93_CR.csv"
# in sub-directory of package "meta"
#
filename <- system.file("extdata", "Fleiss93_CR.csv", package = "meta")
Fleiss93_CR <- read.rm5(filename)

# Same result as R command example(Fleiss93):
#
settings.meta

metacr(Fleiss93_CR)

# Same result as R command example(Fleiss93cont):
#
metacr(Fleiss93_CR, 1, 2)

**settings.meta**

*Print and change default settings to conduct and print or plot meta-analyses in R package *meta*.*

**Description**

Print and change default settings to conduct and print or plot meta-analyses in R package *meta*. The following general settings are available: *Review Manager 5, Journal of the American Medical Association*.

**Usage**

settings.meta(...)

**Arguments**

... Arguments to change default settings.

**Details**

This function can be used to define defaults for several arguments (i.e., assignments using gs) of the following R functions: *metabin, metacont, metacor, metacr, metagen, metainc, metaprop, metarate*.

Furthermore, some of these settings are considered to print meta-analysis results using *print.meta* and *print.summary.meta*, and to produce forest plots using *forest.meta*.

The function can be used to either change individual settings (see Examples) or use one of the following general settings:

- settings.meta("revman5")
- settings.meta("jama")

The first command can be used to reproduce meta-analyses from Cochrane reviews conducted with *Review Manager 5* (RevMan 5, [http://community.cochrane.org/tools/review-production-tools/revman-5](http://community.cochrane.org/tools/review-production-tools/revman-5)) and specifies to use a RevMan 5 layout in forest plots. The second command can be used to generate forest plots following instructions for authors of the *Journal of the American Medical Association* ([http://jamanetwork.com/journals/jama/pages/instructions-for-authors](http://jamanetwork.com/journals/jama/pages/instructions-for-authors)).

RevMan 5 settings, in detail:

<table>
<thead>
<tr>
<th>Argument</th>
<th>Value</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
<tr>
<td>hakn</td>
<td>FALSE</td>
<td>method not available in RevMan 5</td>
</tr>
</tbody>
</table>
settings.meta

method.tau  "DL"  only available method in RevMan 5
tau.common  FALSE  common between-study variance in subgroups
MH.exact   FALSE  exact Mantel-Haenszel method
RR.cochrane TRUE  calculation of risk ratios
layout     "RevMan5" layout for forest plots
test.overall TRUE  print information on test of overall effect
digits.I2   0      number of digits for I-squared measure
digits.tau2 0      number of digits for tau-squared
CIbracket   "["  print confidence intervals as "[. .]
CIsseparator ",,"  print confidence intervals as ",. ."

JAMA settings:

<table>
<thead>
<tr>
<th>Argument</th>
<th>Value</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
<tr>
<td>layout</td>
<td>&quot;JAMA&quot;</td>
<td>layout for forest plots</td>
</tr>
<tr>
<td>test.overall</td>
<td>TRUE</td>
<td>print information on test of overall effect</td>
</tr>
<tr>
<td>digits.I2</td>
<td>0</td>
<td>number of digits for I-squared measure</td>
</tr>
<tr>
<td>CIbracket</td>
<td>&quot;(&quot;</td>
<td></td>
</tr>
</tbody>
</table>
| CIsseparator | ",."  | print confidence intervals as "(. .)"

A list of all arguments with current settings is printed using the command `settings.meta("print")`. In order to reset all settings of R package `meta` the command `settings.meta("reset")` can be used.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

See Also

`gs`, `forest.meta`

Examples

```r
# Get listing of current settings
#
settings.meta("print")

# Meta-analyses using default settings
#
metabin(10, 20, 15, 20)
metaprop(4, 20)
metabin(10, 20, 15, 20, sm = "RD")
metaprop(4, 20, sm = "PLN")

# Change summary measure for R functions metabin and metaprop
# and store old settings
#
oldset <- settings.meta(smbin = "RD", smprop = "PLN")
```
settings.meta

# metabin(10, 20, 15, 20)
metaprop(4, 20)

# Use old settings
#
settings.meta(oldset)

# Change level used to calculate confidence intervals
# (99%-CI for studies, 99.9%-CI for pooled effects)
#
metagen(1:3, 2:4 / 10, sm = "MD")
settings.meta(level = 0.99, level.comb = 0.999)
metagen(1:3, 2:4 / 10, sm = "MD")

# Always print a prediction interval
#
settings.meta(prediction = TRUE)
metagen(1:3, 2:4 / 10, sm = "MD")
metagen(4:6, 4:2 / 10, sm = "MD")

# Try to set unknown argument results in a warning
#
try(settings.meta(unknownarg = TRUE))

# Reset to default settings of R package meta
#
settings.meta("reset")
metabin(10, 20, 15, 20)
metaprop(4, 20)
metagen(1:3, 2:4 / 10, sm = "MD")

# Do not back transform results (e.g. print log odds ratios instead
# of odds ratios, print transformed correlations / proportions
# instead of correlations / proportions)
#
settings.meta(backtransf = FALSE)
metabin(10, 20, 15, 20)
metaprop(4, 20)
metacor(c(0.85, 0.7, 0.95), c(20, 40, 10))

# Forest plot using RevMan 5 style
#
settings.meta("revman5")
forest(metagen(1:3, 2:4 / 10, sm = "MD", comb.fixed = FALSE),
  label.left = "Favours A", label.right = "Favours B",
  colgap.studlab = "2cm",
  colgap.forest.left = "0.2cm")

# Forest plot using JAMA style
#
settings.meta("jama")
forest(metagen(1:3, 2:4 / 10, sm = "MD", comb.fixed = FALSE),
Conversion from standardised mean difference to log odds ratio

Description

Conversion from standardised mean difference to log odds ratio using method by Hasselblad & Hedges (1995) or Cox (1970).

Usage

smd2or(smd, se.smd, studlab, data = NULL, subset = NULL, exclude = NULL, method = "HH", backtransf = gs("backtransf"), ...)

Arguments

smd Standardised mean difference(s) (SMD) or meta-analysis object.
se.smd Standard error(s) of SMD (ignored if argument smd is a meta-analysis object).
studlab An optional vector with study labels (ignored if argument smd is a meta-analysis object).
data An optional data frame containing the study information (ignored if argument smd is a meta-analysis object).
subset An optional vector specifying a subset of studies to be used (ignored if argument smd is a meta-analysis object).
exclude An optional vector specifying studies to exclude from meta-analysis, however, to include in printouts and forest plots (ignored if argument smd is a meta-analysis object).
method A character string indicating which method is used to convert SMDs to log odds ratios. Either "HH" or "CS", can be abbreviated.
backtransf A logical indicating whether odds ratios (if TRUE) or log odds ratios (if FALSE) should be shown in printouts and plots.

Additional arguments passed on to `metagen` (ignored if argument `smd` is a meta-analysis object).

Details

This function implements the following methods for the conversion from standardised mean difference to log odds ratio:

- Hasselblad & Hedges (1995) assuming logistic distributions (`method == "HH"`)
- Cox (1970) and Cox & Snell (1989) assuming normal distributions (`method == "CS"`)

Internally, `metagen` is used to conduct a meta-analysis with the odds ratio as summary measure.

Argument `smd` can be either a vector of standardised mean differences or a meta-analysis object created with `metacont` or `metagen` and the standardised mean difference as summary measure.

Argument `se.smd` is mandatory if argument `smd` is a vector and ignored otherwise. Additional arguments in ... are only passed on to `metagen` if argument `smd` is a vector.

Value

An object of class "meta" and "metagen"; see `metagen`.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

`or2smd, metacont, metagen, metabin`

Examples

```r
# Example from Borenstein et al. (2009), Chapter 7
#
# mb <- smd2or(0.5, sqrt(0.0205), backtransf = FALSE)
# TE = log odds ratio; seTE = standard error of log odds ratio
data.frame(lnOR = round(mb$TE, 4), varlnOR = round(mb$seTE^2, 4))
```

---

`smd2or`
# Use dataset from Fleiss (1993)
#
data(Fleiss93cont)
m1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, study,
    data = Fleiss93cont, sm = "SMD")
smd2or(m1)

smoking

Smoking example

Description

Meta-analyses on the effect of smoking on mortality risk.

Format

A data frame with the following columns:

- **study**: study label
- **participants**: total number of participants
- **d.smokers**: number of deaths in smokers’ group
- **py.smokers**: person years at risk in smokers’ group
- **d.nonsmokers**: number of deaths in non-smokers’ group
- **py.nonsmokers**: person years at risk in non-smokers’ group

Details

Data have been reconstructed based on the famous Smoking and Health Report to the Surgeon General (Bayne-Jones S et al., 1964). Data sets can be used to evaluate the risk of smoking on overall mortality (dataset smoking) and lung-cancer deaths (dataset lungcancer), respectively.

The person time is attributed such that the rate ratios are equal to the reported mortality ratios implicitly assuming that the data have arisen from a homogeneous age group; more detailed information by age is not available from the report. Note, the group of "non-smokers" actually consists of all participants except those who are smokers of cigarettes only. Information on real non-smokers is not available from the published Smoking and Health Report.

Source


See Also

metainc
Examples

data(smoking)

m1 <- metainc(d.smokers, py.smokers, 
  d.nonsmokers, py.nonsmokers, 
  data = smoking, studlab = study)
print(m1, digits = 2)

data(lungcancer)

m2 <- metainc(d.smokers, py.smokers, 
  d.nonsmokers, py.nonsmokers, 
  data = lungcancer, studlab = study)
print(m2, digits = 2)

---

summary.meta

Summary of meta-analysis results

Description

Summary method for objects of class meta.

Usage

## S3 method for class 'meta'
summary(object, comb.fixed = object$comb.fixed, 
  comb.random = object$comb.random, prediction = object$prediction, 
  backtransf = object$backtransf, pscale = object$pscale, 
  irscale = object$irscale, irunit = object$irunit, 
  bylab = object$bylab, print.byvar = object$print.byvar, 
  byseparator = object$byseparator, bystud = FALSE, 
  print.CMH = object$print.CMH, warn = object$warn, ...)

## S3 method for class 'summary.meta'
print(x, comb.fixed = x$comb.fixed, 
  comb.random = x$comb.random, prediction = x$prediction, 
  print.byvar = x$print.byvar, byseparator = x$byseparator, 
  print.CMH = x$print.CMH, header = TRUE, backtransf = x$backtransf, 
  pscale = x$pscale, irscale = x$irscale, irunit = x$irunit, 
  bylab.nchar = 35, digits = gs("digits"), 
  digits.zval = gs("digits.zval"), digits.pval = max(gs("digits.pval"), 2), 
  digits.pval.Q = max(gs("digits.pval.Q"), 2), 
  digits.Q = gs("digits.Q"), digits.tau2 = gs("digits.tau2"), 
  scientific.pval = gs("scientific.pval"), big.mark = gs("big.mark"), 
  print.Rb = gs("print.Rb"), text.tau2 = gs("text.tau2"), 
  text.I2 = gs("text.I2"), text.Rb = gs("text.Rb"), 
  warn.backtransf = FALSE, ...)
Arguments

- **object**: An object of class `meta`.
- **comb.fixed**: A logical indicating whether a fixed effect meta-analysis should be conducted.
- **comb.random**: A logical indicating whether a random effects meta-analysis should be conducted.
- **prediction**: A logical indicating whether a prediction interval should be printed.
- **backtransf**: A logical indicating whether printed results should be back transformed. If `backtransf=TRUE`, results for `sm="OR"` are printed as odds ratios rather than log odds ratios and results for `sm="ZCOR"` are printed as correlations rather than Fisher's z transformed correlations, for example.
- **pscale**: A numeric giving scaling factor for printing of single event probabilities or risk differences, i.e. if argument `sm` is equal to "PLOGIT", "PLN", "PRAW", "PAS", "PFT", or "RD".
- **irscale**: A numeric defining a scaling factor for printing of single incidence rates or incidence rate differences, i.e. if argument `sm` is equal to "IR", "IRLN", "IRS", "IRFT", or "IRD".
- **irunit**: A character specifying the time unit used to calculate rates, e.g. person-years.
- **bylab**: A character string with a label for the grouping variable.
- **print.byvar**: A logical indicating whether the name of the grouping variable should be printed in front of the group labels.
- **byseparator**: A character string defining the separator between label and levels of grouping variable.
- **bystud**: A logical indicating whether results of individual studies should be printed by grouping variable.
- **print.CMH**: A logical indicating whether result of the Cochran-Mantel-Haenszel test for overall effect should be printed.
- **warn**: A logical indicating whether the use of `summary.meta` in connection with `metacum` or `metainf` should result in a warning.
- **...**: Additional arguments (ignored).
- **x**: An object of class `summary.meta`.
- **header**: A logical indicating whether information on title of meta-analysis, comparison and outcome should be printed at the beginning of the printout.
- **bylab.nchar**: A numeric specifying the number of characters to print from label for the grouping variable.
- **digits**: Minimal number of significant digits, see `print.default`.
- **digits.zval**: Minimal number of significant digits for z- or t-value, see `print.default`.
- **digits.pval**: Minimal number of significant digits for p-value of overall treatment effect, see `print.default`.
- **digits.pval.Q**: Minimal number of significant digits for p-value of heterogeneity test, see `print.default`.
- **digits.Q**: Minimal number of significant digits for heterogeneity statistic Q, see `print.default`.
- **digits.tau2**: Minimal number of significant digits for between-study variance, see `print.default`.
digits.H  Minimal number of significant digits for H statistic, see print.default.
digits.I2  Minimal number of significant digits for I-squared and Rb statistic, see print.default.
scientific.pval  A logical specifying whether p-values should be printed in scientific notation, e.g., 1.2345e-01 instead of 0.12345.
big.mark  A character used as thousands separator.
print.I2  A logical specifying whether heterogeneity statistic I^2 should be printed.
print.H  A logical specifying whether heterogeneity statistic H should be printed.
print.Rb  A logical specifying whether heterogeneity statistic Rb should be printed.
text.tau2  Text printed to identify between-study variance tau^2.
text.I2  Text printed to identify heterogeneity statistic I^2.
text.Rb  Text printed to identify heterogeneity statistic Rb.
warn.backtransf  A logical indicating whether a warning should be printed if backtransformed proportions and rates are below 0 and backtransformed proportions are above 1.

Details

Note, in R package meta, version 3.0-0 some arguments have been removed from R functions summary.meta (arguments: byvar, level, level.comb, level.prediction) and print.summary.meta (arguments: level, level.comb, level.prediction). This functionality is now provided by R function update.meta (or directly in meta-analysis functions, e.g., metabin, metacont, metagen, metacor, and metaprop).

Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://community.cochrane.org/tools/review-production-tools/revman-5). In RevMan 5, subgroup analyses can be defined and data from a Cochrane review can be imported to R using the function read.rm5. If a meta-analysis is then conducted using function metacr, information on subgroups is available in R (components byvar, bylab, and print.byvar, byvar in an object of class "meta"). Accordingly, by using function metacr there is no need to define subgroups in order to redo the statistical analysis conducted in the Cochrane review.

Note, for an object of type metaprop, starting with version 3.7-0 of meta, list elements TE, lower and upper in element study correspond to transformed proportions and confidence limits (regardless whether exact confidence limits are calculated; argument ciexact=TRUE in metaprop function). Accordingly, the following results are based on the same transformation defined by argument sm: list elements TE, lower and upper in elements study, fixed, random, within.fixed and within.random.

R function cilayout can be utilised to change the layout to print confidence intervals (both in printout from print.meta and print.summary.meta function as well as in forest plots). The default layout is "[lower; upper]". Another popular layout is "(lower - upper)" which is used throughout an R session by using R command cilayout("(", "-").

Argument pscale can be used to rescale single proportions or risk differences, e.g. pscale=1000 means that proportions are expressed as events per 1000 observations. This is useful in situations with (very) low event probabilities.

Argument irscale can be used to rescale single rates or rate differences, e.g. irscale=1000 means that rates are expressed as events per 1000 time units, e.g. person-years. This is useful in...
situations with (very) low rates. Argument `irunit` can be used to specify the time unit used in individual studies (default: "person-years"). This information is printed in summaries and forest plots if argument `irscale` is not equal to 1.

**Value**

A list is returned by the function `summary.meta` with the following elements:

- **study**
  Results for individual studies (a list with elements `TE`, `seTE`, lower, upper, `z`, `p`, `level`, `df`).

- **fixed**
  Results for fixed effect model (a list with elements `TE`, `seTE`, lower, upper, `z`, `p`, `level`, `df`).

#

- **random**
  Results for random effects model (a list with elements `TE`, `seTE`, lower, upper, `z`, `p`, `level`, `df`).

- **k**
  Number of studies combined in meta-analysis.

- **Q**
  Heterogeneity statistic Q.

- **tau**
  Square-root of between-study variance.

- **se.tau**
  Standard error of square-root of between-study variance.

- **C**
  Scaling factor utilised internally to calculate common tau-squared across subgroups.

- **H**
  Heterogeneity statistic H (a list with elements `TE`, lower, upper).

- **I2**
  Heterogeneity statistic I2 (a list with elements `TE`, lower, upper), see Higgins & Thompson (2002).

- **Rb**
  Heterogeneity statistic Rb (a list with elements `TE`, lower, upper), see Crippa et al. (2016).

#

- **k.all**
  Total number of studies.

- **Q.CMH**
  Cochran-Mantel-Haenszel test statistic for overall effect.

- **sm**
  A character string indicating underlying summary measure.

- **method**
  A character string with the pooling method.

- **call**
  Function call.

- **ci.lab**
  Label for confidence interval.

- **hakn**
  A logical indicating whether method by Hartung and Knapp was used.

- **method.tau**
  A character string indicating which method is used to estimate the between-study variance tau-squared.

- **tau.common**
  A logical indicating whether tau-squared is assumed to be the same across subgroups.

- **within.fixed**
  Result for fixed effect model within groups (a list with elements `TE`, `seTE`, lower, upper, `z`, `p`, `level`, `df`, `harmonic.mean`) - if `byvar` is not missing.
Result for random effects model within groups (a list with elements TE, seTE, lower, upper, z, p, level, df, harmonic.mean) - if byvar is not missing.

Number of studies combined within groups - if byvar is not missing.

Heterogeneity statistic Q within groups - if byvar is not missing.

Heterogeneity statistic Q between groups (based on fixed effect model) - if byvar is not missing.

Heterogeneity statistic Q between groups (based on random effects model) - if byvar is not missing.

Square-root of between-study variance within subgroups - if byvar is not missing.

Scaling factor utilised internally to calculate common tau-squared across subgroups.

Heterogeneity statistic H within subgroups (a list with elements TE, lower, upper) - if byvar is not missing.

Heterogeneity statistic I2 within subgroups (a list with elements TE, lower, upper) - if byvar is not missing.

Heterogeneity statistic Rb within subgroups (a list with elements TE, lower, upper) - if byvar is not missing.

Statistic H for residual heterogeneity (a list with elements TE, lower, upper) - if byvar is not missing.

Statistic I2 for residual heterogeneity (a list with elements TE, lower, upper) - if byvar is not missing.

Levels of grouping variable - if byvar is not missing.

Title of meta-analysis / systematic review.

Comparison label.

Outcome label.

Original data (set) used to create meta object.

Information on subset of original data used in meta-analysis.

As defined above.

As defined above.

Version of R package meta used to create object.

Guido Schwarzer <sc@imbi.uni-freiburg.de>


**See Also**

`update.meta`, `metabin`, `metacont`, `metagen`

**Examples**

```r
data(fleiss93cont)
m1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c,
data = Fleiss93cont, sm = "SMD",
studlab = paste(study, year))
summary(m1)

summary(update(m1, byvar = c(1, 2, 1, 1, 2), bylab = "group"))
forest(update(m1, byvar = c(1, 2, 1, 1, 2), bylab = "group"))

## Not run:
# Use unicode characters to print tau^2 and I^2
print(summary(m1), text.tau2 = "\u03c4\u00b2", text.I2 = "I\u00b2")
## End(Not run)
```

**summary.rm5**

*Cochrane review: Summary of meta-analyses*

**Description**

Calculate and print a summary of all meta-analyses in a Cochrane review.

**Usage**

```r
## S3 method for class 'rm5'
summary(object, comp.no, outcome.no, ...)

## S3 method for class 'summary.rm5'
print(x, ...)
```

**Arguments**

- `object` An object of class *rm5*.
- `comp.no` Comparison number.
- `outcome.no` Outcome number.
- `...` Additional arguments (passed on to `metacr`).
- `x` An object of class `summary.rm5`.
Details

This function can be used to redo all or selected meta-analyses of a Cochrane Review.

Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://community.cochrane.org/tools/review-production-tools/revman-5). In RevMan 5, subgroup analyses can be defined and data from a Cochrane review can be imported to R using the function read.rm5.

The R function metacr is called internally.

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

References


See Also

summary.meta, metacr, read.rm5, metabias.rm5

Examples

# Locate export data file "Fleiss93_CR.csv"
# in sub-directory of package "meta"
#
filename <- system.file("extdata", "Fleiss93_CR.csv", package = "meta")
Fleiss93_CR <- read.rm5(filename)

# Print summary results for all meta-analysis
#
summary(Fleiss93_CR)

# Print summary results only for second outcome of first comparison
#
summary(Fleiss93_CR, comp.no = 1, outcome.no = 2)

trimfill

Trim-and-fill method to adjust for bias in meta-analysis

Description

Trim-and-fill method for estimating and adjusting for the number and outcomes of missing studies in a meta-analysis.
Usage

trimfill(x, ...)

## Default S3 method:
trimfill(x, seTE, left = NULL, ma.fixed = TRUE,
  type = "L", n.iter.max = 50, sm = ",", studlab = NULL,
  level = 0.95, level.comb = level, comb.fixed = FALSE,
  comb.random = TRUE, hakn = FALSE, method.tau = "DL",
  prediction = FALSE, level.predict = level, backtransf = TRUE,
  pscale = 1, irscale = 1, irunit = "person-years", silent = TRUE,
  ...)

## S3 method for class 'meta'
trimfill(x, left = NULL, ma.fixed = TRUE, type = "L",
  n.iter.max = 50, level = x$level, level.comb = x$level.comb,
  comb.fixed = FALSE, comb.random = TRUE, hakn = x$hakn,
  method.tau = x$method.tau, prediction = x$prediction,
  level.predict = x$level.predict, backtransf = x$backtransf,
  pscale = x$pscale, irscale = x$irscale, irunit = x$irunit,
  silent = TRUE, ...)

Arguments

x An object of class meta, or estimated treatment effect in individual studies.

... other arguments

seTE Standard error of estimated treatment effect.

left A logical indicating whether studies are supposed to be missing on the left or right side of the funnel plot. If NULL, the linear regression test for funnel plot symmetry (i.e., function metabias(..., method="linreg")) is used to determine whether studies are missing on the left or right side.

ma.fixed A logical indicating whether a fixed effect or random effects model is used to estimate the number of missing studies.

type A character indicating which method is used to estimate the number of missing studies. Either "L" or "R".

n.iter.max Maximum number of iterations to estimate number of missing studies.

sm An optional character string indicating underlying summary measure, e.g., "RD", "RR", "OR", "ASD", "HR", "MD", "SMD", or "ROM"; ignored if x is of class meta.

studlab An optional vector with study labels; ignored if x is of class meta.

level The level used to calculate confidence intervals for individual studies. If existing, x$level is used as value for level; otherwise 0.95 is used.

level.comb The level used to calculate confidence interval for the pooled estimate. If existing, x$level.comb is used as value for level.comb; otherwise 0.95 is used.

comb.fixed A logical indicating whether a fixed effect meta-analysis should be conducted.

comb.random A logical indicating whether a random effects meta-analysis should be conducted.
hakn A logical indicating whether the method by Hartung and Knapp should be used to adjust test statistics and confidence intervals.

method.tau A character string indicating which method is used to estimate the between-study variance $\tau^2$. Either "DL", "PM", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.

prediction A logical indicating whether a prediction interval should be printed.

level.predict The level used to calculate prediction interval for a new study.

backtransf A logical indicating whether results should be back transformed in printouts and plots. If backtransf=TRUE, results for sm="OR" are printed as odds ratios rather than log odds ratios and results for sm="ZCOR" are printed as correlations rather than Fisher's z transformed correlations, for example.

pscale A numeric giving scaling factor for printing of single event probabilities or risk differences, i.e. if argument sm is equal to "PLOGIT", "PLN", "PRAW", "PAS", "PFT", or "RD".

irscale A numeric defining a scaling factor for printing of single incidence rates or incidence rate differences, i.e. if argument sm is equal to "IR", "IRLN", "IRS", "IRFT", or "IRD".

irunit A character specifying the time unit used to calculate rates, e.g. person-years.

silent A logical indicating whether basic information on iterations shown.

Details

The trim-and-fill method (Duval, Tweedie 2000a, 2000b) can be used for estimating and adjusting for the number and outcomes of missing studies in a meta-analysis. The method relies on scrutiny of one side of a funnel plot for asymmetry assumed due to publication bias.

Three different methods have been proposed originally to estimate the number of missing studies. Two of these methods (L- and R-estimator) have been shown to perform better in simulations, and are available in this R function (argument type).

A fixed effect or random effects model can be used to estimate the number of missing studies (argument ma.fixed). Furthermore, a fixed effect and/or random effects model can be used to summaries study results (arguments comb.fixed and comb.random). Simulation results (Peters et al. 2007) indicate that the fixed-random model, i.e. using a fixed effect model to estimate the number of missing studies and a random effects model to summaries results, (i) performs better than the fixed-fixed model, and (ii) performs no worse than and marginally better in certain situations than the random-random model. Accordingly, the fixed-random model is the default.

An empirical comparison of the trim-and-fill method and the Copas selection model (Schwarzer et al. 2010) indicates that the trim-and-fill method leads to excessively conservative inference in practice. The Copas selection model is available in R package metasens.

The function metagen is called internally.

Value

An object of class c("metagen","meta","trimfill"). The object is a list containing the following components:
studlab, sm, left, ma.fixed, type, n.iter.max
  As defined above.
level, level.comb, level.predict
  As defined above.
comb.fixed, comb.random, prediction, hakn, method.tau
  As defined above.
TE, seTE
  Estimated treatment effect and standard error of individual studies.
lower, upper
  Lower and upper confidence interval limits for individual studies.
zval, pval
  z-value and p-value for test of treatment effect for individual studies.
w.fixed, w.random
  Weight of individual studies (in fixed and random effects model).
TE.fixed, seTE.fixed
  Estimated overall treatment effect and standard error (fixed effect model).
TE.random, seTE.random
  Estimated overall treatment effect and standard error (random effects model).
seTE.predict
  Standard error utilised for prediction interval.
lower.predict, upper.predict
  Lower and upper limits of prediction interval.
k
  Number of studies combined in meta-analysis.
Q
  Heterogeneity statistic Q.
tau
  Square-root of between-study variance.
method
  Pooling method: "Inverse".
call
  Function call.
n.iter
  Actual number of iterations to estimate number of missing studies.
trimfill
  A logical vector indicating studies that have been added by trim-and-fill method.
df.hakn
  Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn=TRUE).
title
  Title of meta-analysis / systematic review.
complab
  Comparison label.
outclab
  Outcome label.
label.e
  Label for experimental group.
label.c
  Label for control group.
label.left
  Graph label on left side of forest plot.
label.right
  Graph label on right side of forest plot.
k0
  Number of studies added by trim-and-fill.
n.e
  Number of observations in experimental group (only for object x of class metabin or metacont).
n.c
  Number of observations in control group (only for object x of class metabin or metacont).
event.e
  Number of events in experimental group (only for object x of class metabin).
trimfill

event.c Number of events in control group (only for object x of class metabin).
mean.e Estimated mean in experimental group (only for object x of class metacont).
sd.e Standard deviation in experimental group (only for object x of class metacont).
mean.c Estimated mean in control group (only for object x of class metacont).
sd.c Standard deviation in control group (only for object x of class metacont).
n Number of observations (only for object x of class metaprop).
event Number of events (only for object x of class metaprop).
cor Corelation (only for object x of class metacor).
class.x Main class of object x (e.g. 'metabin' or 'metacont').
version Version of R package meta used to create object.

Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

References

See Also
metagen, metabias, funnel

Examples
data(Fleiss93)
m1 <- metabin(event.e, n.e, event.c, n.c, data = Fleiss93, sm = "OR")
tf1 <- trimfill(m1)
summary(tf1)
funnel(tf1)
funnel(tf1, pch = ifelse(tf1$trimfill, 1, 16),
      level = 0.9, comb.random = FALSE)
#
# Use log odds ratios on x-axis
#
funnel(tf1, backtransf = FALSE)
funnel(tf1, pch = ifelse(tf1$trimfill, 1, 16),
      level = 0.9, comb.random = FALSE, backtransf = FALSE)
trimfill(m1$TE, m1$seTE, sm = m1$sm)

update.meta

Update a meta-analysis object

Description

Update an existing meta-analysis object.

Usage

```r
## S3 method for class 'meta'
update(object, data = object$data,
        subset = object$subset, studlab = object$data$.studlab,
        exclude = object$data$.exclude, method = object$method,
        sm = object$sm, incr, allincr = object$allincr,
        addincr = object$addincr, allstudies = object$allstudies,
        MH.exact = object$MH.exact, RR.cochrane = object$RR.cochrane,
        model.glmm = object$model.glmm, level = object$level,
        level.comb = object$level.comb, comb.fixed = object$comb.fixed,
        comb.random = object$comb.random, hakn = object$hakn,
        method.tau = object$method.tau, tau.preset = object$tau.preset,
        TE.tau = object$TE.tau, tau.common = object$tau.common,
        prediction = object$prediction, level.predict = object$level.predict,
        null.effect = object$null.effect, method.bias = object$method.bias,
        backtransf = object$backtransf, pscale = object$pscale,
        irscale = object$irscale, irunit = object$irunit,
        title = object$title, complab = object$complab,
        outclab = object$outclab, label.e = object$label.e,
        label.c = object$label.c, label.left = object$label.left,
        label.right = object$label.right, n.e = object$n.e,
        n.c = object$n.c, pooledvar = object$pooledvar,
        method.smd = object$method.smd, sd.glass = object$sd.glass,
        exact.smd = object$exact.smd, method.ci = object$method.ci,
        byvar = object$byvar, bylab = object$bylab,
        print.byvar = object$print.byvar, byseparator = object$byseparator,
        print.CMH = object$print.CMH, keepdata = TRUE, left = object$left,
        ma.fixed = object$ma.fixed, type = object$type,
        n.iter.max = object$n.iter.max, warn = object$warn,
        control = object$control, ...)
```

Arguments

- `object` An object of class `meta`.
- `data` Dataset.
subset            Subset.
studlab           Study label.
exclude           An optional vector specifying studies to exclude from meta-analysis, however, 
to include in printouts and forest plots.
method            A character string indicating which method is to be used for pooling of studies; 
                  see \texttt{metabin} and \texttt{metainc} function for admissible values.
sm                 A character string indicating which summary measure is used for pooling.
incr               Either a numerical value or vector which can be added to each cell frequency 
                  for studies with a zero cell count or the character string "TA" which stands for 
treatment arm continuity correction.
allincr            A logical indicating if \texttt{incr} is added to each cell frequency of all studies if at 
                  least one study has a zero cell count. If FALSE (default), \texttt{incr} is added only to 
                  each cell frequency of studies with a zero cell count.
addincr            A logical indicating if \texttt{incr} is added to each cell frequency of all studies irre-
                  spective of zero cell counts.
allstudies         A logical indicating if studies with zero or all events in both groups are to be 
                  included in the meta-analysis (applies only if \texttt{sm} is equal to "RR" or "OR").
MH.exact           A logical indicating if \texttt{incr} is not to be added to all cell frequencies for studies 
                  with a zero cell count to calculate the pooled estimate based on the Mantel-
                  Haenszel method.
RR.cochrane       A logical indicating if 2*\texttt{incr} instead of 1*\texttt{incr} is to be added to \texttt{n.e} and \texttt{n.c} 
in the calculation of the risk ratio (i.e., \texttt{sm} = "RR") for studies with a zero cell. 
                  This is used in RevMan 5, the Cochrane Collaboration's program for preparing 
                  and maintaining Cochrane reviews.
model.glmm         A character string indicating which GLMM model should be used.
level              The level used to calculate confidence intervals for individual studies.
level.comb         The level used to calculate confidence intervals for pooled estimates.
comb.fixed         A logical indicating whether a fixed effect meta-analysis should be conducted.
comb.random        A logical indicating whether a random effects meta-analysis should be con-
                  ducted.
hakn               A logical indicating whether the method by Hartung and Knapp should be used 
                  to adjust test statistics and confidence intervals.
method.tau         A character string indicating which method is used to estimate the between-
                  study variance $\tau^2$. Either "DL", "PM", "REML", "ML", "HS", "SJ", "HE", or "EB", 
                  can be abbreviated. See function \texttt{metagen}.
tau.preset          Prespecified value for the square-root of the between-study variance $\tau^2$.
TE.tau             Overall treatment effect used to estimate the between-study variance $\tau^2$.
tau.common          A logical indicating whether tau-squared should be the same across subgroups.
prediction          A logical indicating whether a prediction interval should be printed.
level.predict      The level used to calculate prediction interval for a new study.
null.effect         A numeric value specifying the effect under the null hypothesis.
method.bias A character string indicating which test for funnel plot asymmetry is to be used. Either "rank", "linreg", "mm", "count", "score", or "peters", can be abbreviated. See function metabias.

backtransf A logical indicating whether results should be back transformed in printouts and plots. If backtransf = TRUE, results for sm = "OR" are printed as odds ratios rather than log odds ratios and results for sm = "ZCOR" are printed as correlations rather than Fisher's z transformed correlations, for example.

pscale A numeric giving scaling factor for printing of single event probabilities or risk differences, i.e. if argument sm is equal to "PLOGIT", "PLN", "PRAW", "PAS", "PFT", or "RD".

irscale A numeric defining a scaling factor for printing of single incidence rates or incidence rate differences, i.e. if argument sm is equal to "IR", "IRLN", "IRS", "IRFT", or "IRD".

irunit A character specifying the time unit used to calculate rates, e.g. person-years.

title A character specifying the time unit used to calculate rates, e.g. person-years.

complab Comparison label.

outclab Outcome label.

label.e Label for experimental group.

label.c Label for control group.

label.left Graph label on left side of forest plot.

label.right Graph label on right side of forest plot.

n.e Number of observations in experimental group. (only for metagen object)

n.c Number of observations in control group. (only for metagen object)

pooledvar A logical indicating if a pooled variance should be used for the mean difference (only for metacont object with sm = "MD").

method.smd A character string indicating which method is used to estimate the standardised mean difference (only for metacont object with sm = "SMD"). Either "Hedges" for Hedges' g (default), "Cohen" for Cohen's d, or "Glass" for Glass' delta, can be abbreviated.

sd.glass A character string indicating which standard deviation is used in the denominator for Glass' method to estimate the standardised mean difference (only for metacont object with sm = "SMD"). Either "control" using the standard deviation in the control group (sd.c) or "experimental" using the standard deviation in the experimental group (sd.e), can be abbreviated.

exact.smd A logical indicating whether exact formulae should be used in estimation of the standardised mean difference and its standard error.

method.ci A character string indicating which method is used to calculate confidence intervals for individual studies. Either "CP", "WS", "WSCC", "AC", "SA", "SACC", or "NAsm", can be abbreviated. See function metaprop.

byvar An optional vector containing grouping information (must be of same length as event.e).

bylab A character string with a label for the grouping variable.
print.byvar A logical indicating whether the name of the grouping variable should be printed in front of the group labels.

byseparator A character string defining the separator between label and levels of grouping variable.

print.CMH A logical indicating whether result of the Cochran-Mantel-Haenszel test for overall effect should be printed.

keepdata A logical indicating whether original data (set) should be kept in meta object.

left A logical indicating whether studies are supposed to be missing on the left or right side of the funnel plot. If NULL, the linear regression test for funnel plot symmetry (i.e., function metabias(..., method = "linreg")) is used to determine whether studies are missing on the left or right side.

ma.fixed A logical indicating whether a fixed effect or random effects model is used to estimate the number of missing studies.

type A character indicating which method is used to estimate the number of missing studies. Either "L" or "R".

n.iter.max Maximum number of iterations to estimate number of missing studies.

warn A logical indicating whether warnings should be printed (e.g., if incr is added to studies with zero cell frequencies).

control An optional list to control the iterative process to estimate the between-study variance tau^2. This argument is passed on to rma.uni or rma.glmm, respectively.

... Additional arguments (ignored at the moment).

Details

Wrapper function to update an existing meta-analysis object which was created with R function metabin, metacont, metacor, metagen, metainc, metamean, metaprop, or metarate. More details on function arguments are available in help files of respective R functions.

This function can also be used for objects of class 'trimfill', 'metacum', and 'metainf'.

Value

An object of class "meta" and "metabin", "metacont", "metacor", "metagen", "metainc", "metamean", "metaprop", or "metarate".

Author(s)

Guido Schwarzer <sc@imbi.uni-freiburg.de>

See Also

metabin, metacont, metacor, metagen, metainc, metamean, metaprop, metarate
Examples

```r
data(Fleiss93cont)
m1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c,
    data = Fleiss93cont, sm = "SMD", studlab = study)
m1

# Change summary measure (from 'SMD' to 'MD')
#
update(m1, sm = "MD")

# Restrict analysis to subset of studies
#
update(m1, subset = 1:2)

# Use different levels for confidence intervals
#
m2 <- update(m1, level = 0.66, level.comb = 0.99)
print(m2, digits = 2)
forest(m2)
```

weights.meta

*Calculate absolute and percentage weights for meta-analysis*

Description

This function returns a data frame containing information on absolute and percentage weights of individual studies contributing to fixed effect and random effects meta-analysis.

Usage

```r
## S3 method for class 'meta'
weights(object, comb.fixed = object$comb.fixed,
    comb.random = object$comb.random, ...)
```

Arguments

- **object**: An object of class `meta`.
- **comb.fixed**: A logical indicating whether absolute and percentage weights from the fixed effect model should be calculated.
- **comb.random**: A logical indicating whether absolute and percentage weights from the random effects model should be calculated.
- **...**: Additional arguments (ignored at the moment).

Value

A data frame with the following variables is returned:
Variable | Definition | Condition
---|---|---
w.fixed | absolute weights in fixed effect model | (if comb.fixed = TRUE)
p.fixed | percentage weights in fixed effect model | (if comb.fixed = TRUE)
w.random | absolute weights in random effects model | (if comb.random = TRUE)
p.random | percentage weights in random effects model | (if comb.random = TRUE)

Author(s)
Guido Schwarzer <sc@imbi.uni-freiburg.de>

See Also
`metabin`, `metacont`, `metagen`

Examples
```r
data(Fleiss93cont)
# Do meta-analysis (fixed effect and random effects model)
#
meta1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, study,
data = Fleiss93cont, sm = "SMD")

# Print weights for fixed effect and random effects meta-analysis
#
weights(meta1)

# Do meta-analysis (only random effects model)
#
meta2 <- update(meta1, comb.fixed = FALSE)

# Print weights for random effects meta-analysis
#
weights(meta2)

# Print weights for fixed effect and random effects meta-analysis
#
weights(meta2, comb.fixed = TRUE)
```

woodyplants | *Elevated CO_2 and total biomass of woody plants*

Description

Meta-analysis on effects of elevated CO_2 on total biomass of woody plants.

This dataset has been used as an example in Hedges et al. (1999) to describe methods for the meta-analysis of response ratios. The complete dataset with 102 observations and 26 variables is available online as a supplement. Here only a subset of 10 variables is provided and used in the examples.
Format

A data frame with the following columns:

- obsno: observation number
- papno: database paper number
- treat: treatment code
- level: treatment level
- n.elev: number of observations in experimental group (elevated CO_2-level)
- mean.elev: estimated mean in experimental group
- sd.elev: standard deviation in experimental group
- n.amb: number of observations in control group (ambient CO_2-level)
- mean.amb: estimated mean in control group
- sd.amb: standard deviation in control group

Source

Website [http://www.esapubs.org/archive/ecol/E080/008/](http://www.esapubs.org/archive/ecol/E080/008/)

References


Examples

data(woodyplants)

# Meta-analysis of response ratios (Hedges et al., 1999)
#
m1 <- metacont(n.elev, mean.elev, sd.elev,
               n.amb, mean.amb, sd.amb,
               data = woodyplants, sm = "ROM",
               studlab = paste(obsno, papno, sep = " / "))
summary(m1, prediction = TRUE)

# Meta-analysis for plants grown with low soil fertility treatment
#
m2 <- update(m1, subset = (treat == "fert" & level == "low"))
summary(m2, prediction = TRUE)

# Meta-analysis for plants grown under low light conditions
#
m3 <- update(m1, subset = (treat == "light" & level == "low"))
summary(m3, prediction = TRUE)
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