Package 'meta'

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Title Meta-Analysis with R

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Depends R (>= 2.9.1), grid

Suggests metafor

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R topics documented:

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addvar *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. The function `addvar` can be used to add a single variable to an object of class `meta` which for example is useful to conduct subgroup analysis or meta-regression.

Usage

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

addvar(x, y, varname, by.x="studlab", by.y=by.x)
```

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.
`y`	A data frame with an additional covariate
`varname`	A character specifying name of additional variable
`by.x, by.y`	Specifications of the common columns (see `merge`)
`...`	other arguments

Value

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

A single covariate is returned by the function `addvar` which can be added to an object of class `meta`. Internally, the `merge` function is utilised.

Author(s)

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See Also

`metabin`, `metacont`, `metagen`

Examples

```
data(Fleiss93cont)
meta1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, study,
                  data=Fleiss93cont, sm="SMD")
#
# Generate additional variable
#
Fleiss93cont$group <- c(1,2,1,1,2)
#
# Generate new variable by merging
# object 'meta1' and data frame 'Fleiss93cont'
#
meta1$group <- addvar(meta1, Fleiss93cont, "group", by.y="study")
as.data.frame(meta1)
summary(meta1, byvar=group)
```

---

amlodipine *Amlodipine for Work Capacity*

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).

Usage

```
data(amlodipine)
```

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

Hartung J & Knapp G (2001), On tests of the overall treatment effect in meta-analysis with normally distributed responses. *Statistics in Medicine*, **20**, 1771–82. doi: 10.1002/sim.791 .

See Also

metacont

Examples

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

## Not run:
m.hakn <- metacont(n.amlo, mean.amlo, sqrt(var.amlo),
                   n.plac, mean.plac, sqrt(var.plac),
                   data=amlodipine, studlab=study,
                   hakn=TRUE)

## Results for mean difference - see Table III in Hartung and Knapp (2001)
##
res.md <- rbind(data.frame(summary(m)$fixed)[c("TE", "lower", "upper")],
                data.frame(summary(m)$random)[c("TE", "lower", "upper")],
                data.frame(summary(m.hakn)$random)[c("TE", "lower", "upper")])
##
res.md <- round(res.md, 5)
##
row.names(res.md) <- c("FE", "RE", "RE (HaKn)")
names(res.md) <- c("Absolute difference", "CI lower", "CI upper")
##
res.md

## End(Not run)
```

ci *Calculation of confidence intervals (based on normal approximation or t-distribution)*

Description

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

Usage

```
ci(TE, seTE, level=0.95, df=NULL)
```

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).

Value

List with components

TE	Estimated treatment effect.
seTE	Standard error of treatment estimate.
lower	Lower confidence limits.
upper	Upper confidence limits.
z	Test statistic (either z-score or t-score).
p	P-value of test with null hypothesis TE=0.
level	The confidence level required.
df	Degrees of freedom (t-distribution).

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).

Usage

```
data(cisapride)
```

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

Hartung J & Knapp G (2001), A Refined Method for the Meta-analysis of Controlled Clinical Trials with Binary Outcome. *Statistics in Medicine*, **20**, 3875–89.

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)

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

## Not run:
m.or.hakn <- metabin(event.cisa, n.cisa, event.plac, n.plac,
                     data=cisapride, sm="OR", method="Inverse",
                     studlab=study, addincr=TRUE,
                     hakn=TRUE)
```

```
m.rr.hakn <- metabin(event.cisa, n.cisa, event.plac, n.plac,
                     data=cisapride, sm="RR", method="Inverse",
                     studlab=study, addincr=TRUE,
                     hakn=TRUE)

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


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

## End(Not run)
```

`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.

Usage

```
data(Fleiss93)
```

Format

A data frame with the following columns:

study 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

Source

Fleiss JL (1993), The statistical basis of meta-analysis. *Statistical Methods in Medical Research*, **2**, 121–145.

Examples

```
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.

Usage

```
data(Fleiss93cont)
```

Format

A data frame with the following columns:

study Study label

year Year of publication

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

Source

Fleiss JL (1993), The statistical basis of meta-analysis. *Statistical Methods in Medical Research*, **2**, 121–145.

See Also

Fleiss93

Examples

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

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forest *Generic function to produce a forest plot*

Description

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

Usage

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

Arguments

x	An object of class meta.
...	Additional arguments.

Author(s)

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

See Also

forest.meta, metabin, metacont, metagen

Examples

```
data(Olkin95)
meta1 <- 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))

forest(meta1)
```

forest.meta *Forest plot (new plot function for objects of class meta)*

Description

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

Usage

```
## S3 method for class 'meta'
forest(x, byvar=x$byvar, bylab=x$bylab,
       print.byvar=x$print.byvar, sortvar, studlab=TRUE,
       level=x$level, level.comb=x$level.comb,
       comb.fixed=x$comb.fixed, comb.random=x$comb.random,
       overall=TRUE,
       text.fixed="Fixed effect model", text.random="Random effects model",
       lty.fixed=2, lty.random=3,
       text.fixed.w=text.fixed, text.random.w=text.random,
       pooled.totals=comb.fixed|comb.random, pooled.events=FALSE,
       xlab="", xlab.pos=ref,
       smlab=NULL, smlab.pos=ref, xlim="symmetric",
       allstudies=TRUE,
       weight,
       pscale=1,
       ref=ifelse(x$sm %in% c("RR", "OR", "HR"), 1, 0),
       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,
       lab.NA=".",
       lwd=1,
       at=NULL, label=TRUE,
       col.i="black", col.i.inside.square="white",
       col.square="gray", col.square.lines=col.square,
       col.diamond="gray",
       col.diamond.fixed=col.diamond, col.diamond.random=col.diamond,
       col.diamond.lines="black",
       col.diamond.fixed.lines=col.diamond.lines, col.diamond.random.lines=col.diamond.lines,
       col.by="darkgray",
       print.I2=TRUE, print.tau2=TRUE, print.Q=FALSE, print.pval.Q=TRUE,
       hetstat=print.I2|print.tau2|print.Q|print.pval.Q,
       overall.hetstat=overall&hetstat,
       hetlab="Heterogeneity: ",
       fontsize=12,
       fs.heading=fontsize,
       fs.fixed=fontsize, fs.random=fs.fixed, fs.study=fontsize,
```

```
fs.fixed.labels=fs.fixed, fs.random.labels=fs.random,
fs.study.labels=fs.study, fs.hetstat=fontsize-2,
fs.axis=fontsize,
fs.smlab=fontsize, fs.xlab=fontsize, fs.lr=fontsize,
ff.heading="bold",
ff.fixed="bold", ff.random=ff.fixed, ff.study="plain",
ff.fixed.labels=ff.fixed, ff.random.labels=ff.random,
ff.study.labels=ff.study, ff.hetstat="bold.italic",
ff.axis="plain",
ff.smlab="bold", ff.xlab="plain", ff.lr="plain",
##
squaresize=0.8,
boxsize=squaresize,
##
plotwidth=unit(6, "cm"),
colgap=unit(2, "mm"),
colgap.left=colgap, colgap.right=colgap,
colgap.forest=colgap,
colgap.forest.left=colgap.forest, colgap.forest.right=colgap.forest,
##
just="center",
##
addspace=TRUE,
##
new=TRUE,
##
digits=2, ...)
```

Arguments

x	An object of class meta.
byvar	An optional vector containing grouping information (must be of same length as x$TE). Argument byvar can not be used if x is an object of class metacum or metainf.
bylab	A character string with a label for the grouping variable.
print.byvar	A logical indicating whether the name of the grouping variable should be printed in front of the group labels.
sortvar	An optional vector used to sort the individual studies (must be of same length as x$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).
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 fixed effect estimate should be plotted.
comb.random	A logical indicating whether random effects estimate should be plotted.

overall	A logical indicating whether overall summaries should be plotted. This argument is useful in combination with the argument byvar if summaries should only be plotted on group level.
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).
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 corresponging 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 corresponging labels.
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.
xlab	A label for the x axis.
xlab.pos	A numeric specifying the center of the label on the x axis.
smlab	A label for the summary measurex (printed at top of figure).
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	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.
pscale	A numeric giving scaling factor for probabilities for objects of class metaprop.
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.
leftcols	A character vector specifying (additional) columns to be plotted on the left side of the forest plot or a logical value (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).
leftlabs	A character vector specifying labels for (additional) columns on left side of the forest plot (see Details).
rightlabs	A character vector specifying labels for (additional) columns on right side of the forest plot (see Details).
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.left`
: Graph label on left side of forest plot.

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

`lab.NA`
: A character string to label missing values.

`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`.

`col.i`
: The colour for individual study results and confidence limits.

`col.i.inside.square`
: The colour for individual study results and confidence limits if confidence limits are completely within squares.

`col.square`
: The colour for squares reflecting study's weight in the meta-analysis.

`col.square.lines`
: The colour for the outer lines of squares reflecting study's weight in the meta-analysis.

`col.diamond`
: The colour of diamonds representing the results for fixed effect and random effects models.

`col.diamond.fixed`
: The colour of diamonds for fixed effect estimates.

`col.diamond.random`
: The colour of diamonds for random effects estimates.

`col.diamond.lines`
: The colour of the outer lines of diamonds representing the results for fixed effect and random effects models.

`col.diamond.fixed.lines`
: The colour of the outer lines of diamond for fixed effect estimate.

`col.diamond.random.lines`
: The colour of the outer lines of diamond for random effects estimate.

`col.by`
: The colour to print information on subgroups.

`print.I2`
: A logical value indicating whether to print the value of the I-squared statistic.

`print.tau2`
: A logical value indicating whether to print the value of the between-study variance tau-squared.

`print.Q`
: A logical value indicating whether to print the value of the heterogeneity statistic Q.

`print.pval.Q`
: A logical value indicating whether to print the p-value of the heterogeneity statistic Q.

`hetstat`
: A logical value indicating whether to print results for heterogeneity measures at all.

`overall.hetstat`
: A logical value indicating whether to print results for heterogeneity measures for overall treatment comparisons. This argument is useful in combination with the argument `byvar` if heterogeneity statistics should only be printed on group level.

`hetlab`
: Label printed in front of results for heterogeneity measures.

`fontsize`
: The size of text (in points), see gpar.

`fs.heading`
: The size of text for column headings, see gpar.

`fs.fixed`
: The size of text for results of fixed effect model, see gpar.

`fs.random`
: The size of text for results of random effects model, see gpar.

`fs.study`
: The size of text for results of individual studies, see gpar.

`fs.fixed.labels`
: The size of text for label of fixed effect model, see gpar.

`fs.random.labels`
: The size of text for label of random effects model, see gpar.

`fs.study.labels`
: The size of text for labels of individual studies, see gpar.

`fs.hetstat`
: The size of text for heterogeneity measures, see gpar.

`fs.axis`
: The size of text on x-axis, see gpar.

`fs.smlab`
: The size of text of label for summary measure, see gpar.

`fs.xlab`
: The size of text of label on x-axis, see gpar.

`fs.lr`
: The size of text of label on left and right side of forest plot, see gpar.

`ff.heading`
: The fontface for column headings, see gpar.

`ff.fixed`
: The fontface of text for results of fixed effect model, see gpar.

`ff.random`
: The fontface of text for results of random effects model, see gpar.

`ff.study`
: The fontface of text for results of individual studies, see gpar.

`ff.fixed.labels`
: The fontface of text for label of fixed effect model, see gpar.

`ff.random.labels`
: The fontface of text for label of random effects model, 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.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.

`boxsize`
: Use of this argument is deprecated.

`plotwidth`
: A unit object specifying width of the forest plot.

colgap	A unit object specifying gap between columns printed on left and right side of forest plot.
colgap.left	A unit object specifying gap between columns printed on left side of forest plot.
colgap.right	A unit object specifying gap between columns printed on right side of forest plot.
colgap.forest	A unit object specifying gap between column adjacent to forest plot and the forest plot.
colgap.forest.left	A unit object specifying gap between column on the left side of forest plot and the forest plot.
colgap.forest.right	A unit object specifying gap between column on the right side of forest plot and the forest plot.
just	Justification of text for additional columns (possible values: "left", "right", "center").
addspace	A logical value indicating whether additional space (i.e. a blank row) is printed above and below study results.
new	A logical value indicating whether a new figure should be printed in an existing graphics window.
digits	Minimal number of significant digits, see print.default.
...	Additional graphical arguments (ignored at the moment).

Details

A forest plot, also called confidence interval plot, is drawn in the active graphics window. Subgroup analyses are conducted and displayed in the plot if byvar is not missing.

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.

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.

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, the following default columns will be plotted.

Argument rightcols: rightcols=c("effect", "ci"), i.e., estimated treatment effect and its level-confidence interval. In addition, weights of the fixed ("w.fixed") and/or random effects model ("w.random") will be given, if comb.fixed=TRUE and/or comb.random=TRUE. For an object of class metacum or metainf only the estimated treatment effect with level-confidence interval are plotted.

Argument leftcols: (i) leftcols=c("studlab", "event.e", "n.e", "event.c", "n.c") for an object of class metabin, (ii) leftcols=c("studlab", "n.e", "mean.e", "sd.e", "n.c", "mean.c", "sd.c") for an object of class metacont, (iii) leftcols=c("studlab", "TE", "seTE") for an object of

class metagen, (iv) leftcols=c("studlab", "event", "n") for an object of class metaprop, (v) leftcols=c("studlab", "n") for an object of class metacor, (vi) leftcols=c("studlab") for an object of class metacum or metainf.

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: for columns c("studlab", "TE", "seTE", "n.e", "n.c", "event.e", "event.c", "mean.e", "mean.c", "sd.e", the labels c("Study", "TE", "seTE", "Total", "Total", "Events", "Events", "Mean", "Mean", "SD", "SD", For additional columns the column name will be used as 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. The value NA can be used to specify columns using the default labels (see Example).

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

The arguments pscale can be used to rescale proportions for objects of class metaprop, e.g. pscale=100 means that proportions are expressed per 100 observations. This is useful in situations with (very) low proportions. For pscale=100, column heading and x-axis label are changed to "Prop (in %)" and "Proportion (in %)", respectively.

Author(s)

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

See Also

plot.meta, metabin, metacont, metagen

Examples

```
data(Olkin95)
meta1 <- 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))


##
## Do (symmetric) forest plot
##
forest(meta1)


##
## Forest plot specifying argument xlim
##
forest(meta1, xlim=c(0.01, 10))


##
## Forest plot with 'classic' layout used in
```

```
## R package meta, version < 1.6-0
##
forest(meta1, col.square="black", hetstat=FALSE)


##
## Change set of columns printed on left side
## of forest plot
##
forest(meta1, comb.random=FALSE,
       leftcols="studlab")


##
## Do not print columns on right side of forest plot
##
forest(meta1, rightcols=FALSE)


##
## Change study label to "Author"
##
forest(meta1, comb.random=FALSE,
       leftlabs=c("Author", NA, NA, NA, NA))


##
## Just give effect estimate and 95% confidence interval
## on right side of forest plot
##
forest(meta1, 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(meta1,
       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")


Olkin95$studlab <- paste(Olkin95$author, Olkin95$year)
##
## Add variables 'year' and 'author' to meta-analysis object
##
meta1$year <- addvar(meta1, Olkin95, "year")
meta1$author <- addvar(meta1, Olkin95, "author")

##
## Specify column labels only for newly created variables
```

```
## 'year' and 'author'
##
forest(meta1,
       leftcols=c("studlab", "event.e", "n.e", "event.c", "n.c",
                  "author", "year"),
       leftlabs=c("Author", "Year of Publ"))


##
## Change some fontsizes and fontfaces
##
forest(meta1,
       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(meta1,
       col.diamond="green", col.diamond.lines="red",
       col.i=c("green", "blue", "red", "orange"),
       col.square="pink", col.square.lines="black")
```

`funnel` *Generic function to produce a funnel or radial plot.*

Description

Draw a funnel or radial plot to assess funnel plot asymmetry in the active graphics window.

A contour-enhanced funnel plot can be produced for assessing causes of funnel plot asymmetry.

Usage

```
funnel(x, ...)
radial(x, ...)
```

Arguments

`x`	An object of class `meta`, or estimated treatment effect in individual studies.
`...`	Additional arguments as in `par`.

Details

For simple funnel plots, `funnel.default` will be used. For an object of class `meta` the function `funnel.meta` will be used instead.

A funnel plot or radial plot, also called Galbraith plot, 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

Galbraith RF (1988a), Graphical display of estimates having differing standard errors. *Technometrics*, **30**, 271–281.

Galbraith RF (1988b), A note on graphical presentation of estimated odds ratios from several clinical trials. *Statistics in Medicine*, **7**, 889–894.

Light RJ & Pillemer DB (1984), *Summing Up. The Science of Reviewing Research*. Cambridge: Harvard University Press.

Peters JL, Sutton AJ, Jones DR, Abrams KR, Rushton L (2008), Contour-enhanced meta-analysis funnel plots help distinguish publication bias from other causes of asymmetry. *Journal of Clinical Epidemiology*, **61**, 991–996.

Sterne JAC & Egger M (2001), Funnel plots for detecting bias in meta-analysis: Guidelines on choice of axis. *Journal of Clinical Epidemiology*, **54**, 1046–1055.

See Also

`metabias`, `funnel.default`, `funnel.meta`

Examples

```
data(Olkin95)
meta1 <- 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))
```

```
##
## Funnel plots
##
funnel(meta1)
##
## Same result as code above:
##
funnel(meta1$TE, meta1$seTE, sm="RR")

##
## Funnel plot with confidence intervals,
## fixed effect estimate and contours
##
cc <- funnel(meta1, 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(meta1, comb.fixed=TRUE,
       level=0.95, contour=c(0.9, 0.95, 0.99),
       col.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)
```

`funnel.meta` *Plot to assess funnel plot asymmetry*

Description

Draw a funnel or radial plot to assess funnel plot asymmetry in the active graphics window.

A contour-enhanced funnel plot can be produced for assessing causes of funnel plot asymmetry.

Usage

```
## 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=NULL,
        contour.levels=NULL, col.contour,
        ref=ifelse(sm %in% c("RR", "OR", "HR"), 1, 0),
        level=NULL,
        studlab=FALSE, cex.studlab=0.8, ...)

## 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$trimfill, 1, 21),
       text=NULL, cex=1,
       lty.fixed=2, lty.random=9,
       lwd=1, lwd.fixed=lwd, lwd.random=lwd,
       col="black", bg="darkgray",
       col.fixed="black", col.random="black",
       log="", yaxis="se",
       contour.levels=NULL, col.contour,
       ref=ifelse(x$sm %in% c("RR", "OR", "HR"), 1, 0),
       level=x$level,
       studlab=FALSE, cex.studlab=0.8, ...)

## 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.
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.
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).
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 representign fixed effect estimate.
col.random	Color of line representign 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).
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", "AS", "MD", "SMD" (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.
...	Graphical arguments as in par may also be passed as arguments.

Details

A funnel plot or radial plot, also called Galbraith plot, 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

Galbraith RF (1988a), Graphical display of estimates having differing standard errors. *Technometrics*, **30**, 271–281.

Galbraith RF (1988b), A note on graphical presentation of estimated odds ratios from several clinical trials. *Statistics in Medicine*, **7**, 889–894.

Light RJ & Pillemer DB (1984), *Summing Up. The Science of Reviewing Research*. Cambridge: Harvard University Press.

Peters JL, Sutton AJ, Jones DR, Abrams KR, Rushton L (2008), Contour-enhanced meta-analysis funnel plots help distinguish publication bias from other causes of asymmetry. *Journal of Clinical Epidemiology*, **61**, 991–996.

Sterne JAC & Egger M (2001), Funnel plots for detecting bias in meta-analysis: Guidelines on choice of axis. *Journal of Clinical Epidemiology*, **54**, 1046–1055.

See Also

`metabias`, `metabin`, `metagen`

Examples

```
data(Olkin95)
meta1 <- 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(meta1, level=0.95)
```

```
oldpar <- par(mfrow=c(2, 2))

##
## Funnel plots
##
funnel(meta1)
##
## Same result as code above:
##
funnel(meta1$TE, meta1$seTE, sm="RR")

##
## Funnel plot with confidence intervals,
## fixed effect estimate and contours
##
cc <- funnel(meta1, 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(meta1, comb.fixed=TRUE,
       level=0.95, contour=c(0.9, 0.95, 0.99),
       col.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)
```

---

labbe *L'Abbe plot*

Description

Generic function for drawing a L'Abbe plot.

Usage

```
labbe(x, ...)
```

Arguments

x	The x coordinates of points of the L'Abbe plot. Alternatively, an object of class `metabin`.
...	Arguments used in other L'Abbe plot functions.

Details

Generic function for drawing a L'Abbe plot.

Author(s)

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

References

L'Abbe KA, Detsky AS, O'Rourke K (1987), Meta-analysis in clinical research. *Annals of Internal Medicine*, **107**, 224–233.

See Also

labbe.metabin, metabin

Examples

```
data(Olkin95)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95,
                 studlab=paste(author, year),
                 sm="RR")


##
## L'Abbe plot
##
labbe(meta1)
```

---

labbe.metabin *L'Abbe plot*

Description

Draw a L'Abbe plot.

Usage

```
## Default S3 method:
labbe(x, y,
      xlim, ylim,
      xlab=NULL, ylab=NULL,
      TE.fixed, TE.random,
      comb.fixed=FALSE, comb.random=FALSE,
      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,
      sm=NULL, weight,
      studlab=FALSE, cex.studlab=0.8,
      ...)

## 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,
      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,
      sm=x$sm, weight,
      studlab=FALSE, cex.studlab=0.8, ...)
```

Arguments

x	The x coordinates of points of the L'Abbe plot. Alternatively, an object of class metabin.
y	The y coordinates of the L'Abbe plot, optional if x is an appropriate structure.
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.
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.
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 for fixed effect estimate (if comb.fixed is not NULL or FALSE).

lwd.random	The line width for random effects estimate (if comb.random is not NULL or FALSE).
lty.fixed	Line type (pooled fixed effect estimate).
lty.random	Line type (pooled random effects estimate).
sm	A character string indicating underlying summary measure, i.e., "RD", "RR", "OR".
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.
...	Graphical arguments as in par may also be passed as arguments.

Details

A L'Abbe plot is drawn in the active graphics window.

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

L'Abbe KA, Detsky AS, O'Rourke K (1987), Meta-analysis in clinical research. *Annals of Internal Medicine*, **107**, 224–233.

See Also

metabin

Examples

```
data(Olkin95)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95,
                 studlab=paste(author, year),
                 sm="RR", method="I")
```

```
##
## L'Abbe plot
##
labbe(meta1)
```

`metabias` *Generic function to test for funnel plot asymmetry*

Description

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

Usage

```
metabias(x, ...)
```

Arguments

`x`	An object of class `meta` or estimated treatment effect in individual studies.
`...`	Additional arguments.

Details

For more details, see commands `metabias.meta` and `metabias.default`.

Author(s)

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

See Also

`metabias.meta`, `funnel`, `funnel.meta`, `metabin`

Examples

```
data(Olkin95)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95, subset=1:10,
                 sm="RR", method="I")

##
## Using function metabias.meta:
##
metabias(meta1)

##
## Same result using function metabias.default:
```

```
##
metabias(meta1$TE, meta1$seTE)
```

`metabias.meta` *Test for funnel plot asymmetry*

Description

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

Usage

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

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

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 correlation methods `"rank"` and `"count"`.
`k.min`	Minimum number of studies to perform test for funnel plot asymmetry.
`...`	Additional arguments (ignored at the moment).

Details

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 "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). 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.

In order to calculate an arcsine test for funnel plot asymmetry (Ruecker et al., 2008), one has to use the metabin function with argument sm="AS" as input to the metabias command. The three arcsine tests described in Ruecker 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.
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

Begg CB & Mazumdar M (1994), Operating characteristics of a rank correlation test for publication bias. *Biometrics*, **50**, 1088–1101.

Egger M, Smith GD, Schneider M & Minder C (1997), Bias in meta-analysis detected by a simple, graphical test. *British Medical Journal*, **315**, 629–634.

Harbord RM, Egger M & Sterne J (2006), A modified test for small-study effects in meta-analyses of controlled trials with binary endpoints. *Statistics in Medicine*, **25**, 3443–3457.

Kendall M & Gibbons JD (1990), *Rank Correlation Methods*. London: Edward Arnold.

Peters JL, Sutton AJ, Jones DR, Abrams KR & Rushton L (2006), Comparison of two methods to detect publication bias in meta-analysis. *Journal of the American Medical Association*, **295**, 676–680.

Ruecker G, Schwarzer G, Carpenter JR (2008) Arcsine test for publication bias in meta-analyses with binary outcomes. *Statistics in Medicine*, **27**,746–763.

Schwarzer G, Antes G & Schumacher M (2007), A test for publication bias in meta-analysis with sparse binary data. *Statistics in Medicine*, **26**, 721–733.

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, doi: 10.1136/bmj.d4002 .

Thompson SG & Sharp, SJ (1999), Explaining heterogeneity in meta-analysis: A comparison of methods, *Statistics in Medicine*, **18**, 2693–2708.

See Also

`funnel`, `funnel.meta`, `metabin`, `metacont`, `metagen`

Examples

```
data(Olkin95)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95, subset=1:10,
                 sm="RR", method="I")

metabias(meta1)
```

```
metabias(meta1, plotit=TRUE)

metabias(meta1, method.bias="rank")
metabias(meta1, method.bias="rank", correct=TRUE)


metabias(meta1, method.bias="count")

metabias(meta1, method.bias="linreg")$p.value


##
## Arcsine test (based on linear regression):
##
meta1.as <- metabin(event.e, n.e, event.c, n.c,
                    data=Olkin95, subset=1:10,
                    sm="AS", method="I")
metabias(meta1.as)
##
## Same result (using function metabias.default):
##
metabias(meta1.as$TE, meta1.as$seTE)


##
## No test for funnel plot asymmetry calculated:
##
meta2 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95, subset=1:5,
                 sm="RR", method="I")
metabias(meta2)

meta3 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95, subset=1:2,
                 sm="RR", method="I")
metabias(meta3)

## Test for funnel plot asymmetry calculated
## (use of argument k.min):
##
metabias(meta2, k.min=5)
```

`metabin` *Meta-analysis of binary outcome data*

Description

Calculation of fixed and random effects estimates (risk ratio, odds ratio, risk difference or arcsine difference) for meta-analyses with binary outcome data. Mantel-Haenszel, inverse variance and Peto method are available for pooling.

Usage

```
metabin(event.e, n.e, event.c, n.c, studlab,
        data=NULL, subset=NULL, method="MH",
        sm=ifelse(!is.na(charmatch(method, c("Peto", "peto"),
                                   nomatch=NA)), "OR", "RR"),
        incr=0.5, allincr=FALSE, addincr=FALSE, allstudies=FALSE,
        MH.exact=FALSE, RR.cochrane=FALSE,
        level=0.95, level.comb=level,
        comb.fixed=TRUE, comb.random=TRUE,
        hakn=FALSE,
        method.tau="DL", tau.preset=NULL, TE.tau=NULL,
        method.bias=NULL,
        title="", complab="", outclab="",
        label.e="Experimental", label.c="Control",
        label.left="", label.right="",
        byvar, bylab, print.byvar=TRUE,
        print.CMH=FALSE, warn=TRUE)
```

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.
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", or "AS") 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 "TA" 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 if 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*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, the Cochrane Collaboration's program for preparing and maintaining Cochrane reviews.
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 τ^2. Either "DL", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.
tau.preset	Prespecified value for between-study variance τ^2.
TE.tau	Overall treatment effect used to estimate the between-study variance τ^2.
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.
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.
print.CMH	A logical indicating whether result of the Cochran-Mantel-Haenszel test for overall effect should be printed.
warn	A logical indicating whether warnings should be printed (e.g., if incr is added to studies with zero cell frequencies).

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="AS")

For studies with a zero cell count, by default, 0.5 is added to all cell frequencies of these studies; if incr is "TA" a treatment arm continuity correction is used instead (Sweeting et al., 2004; Diamond et al., 2007). Treatment estimates and standard errors are only calculated for studies with zero or all events in both groups if allstudies is TRUE.

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 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 (arguments comb.fixed=TRUE and comb.random=TRUE). 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; finally, if method is "Peto", the Peto method is used for pooling. By default, the DerSimonian-Laird estimate is used in the random effects model (see paragraph on argument method.tau). 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".

For the Mantel-Haenszel method, by default (if MH.exact is FALSE), 0.5 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, the estimate based on the exact method is not defined if the number of events is zero in all studies either in the experimental or control group.

If R package metafor (Viechtbauer 2010) is installed, the following statistical methods are also available.

For the random effects model (argument comb.random=TRUE), the method by Hartung and Knapp (Hartung, Knapp 2001; Knapp, Hartung 2003) is used to adjust test statistics and confidence intervals if argument hakn=TRUE (internally R function rma.uni of R package metafor is called).

Several methods are available to estimate the between-study variance τ^2 (argument method.tau):

- DerSimonian-Laird estimator (method.tau="DL") (default)
- 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 all but the DerSimonian-Laird method the R function `rma.uni` of R package metafor is called internally. See help page of R function `rma.uni` for more details on the various methods to estimate between-study variance τ^2.

Value

An object of class `c("metabin", "meta")` with corresponding `print`, `summary`, `plot` function. The object is a list containing the following components:

`event.e, n.e, event.c, n.c, studlab,`

`sm, method, incr, allincr, addincr,`

`allstudies, MH.exact, RR.cochrane, warn,`

`level, level.comb, comb.fixed, comb.random,`

`hakn, method.tau, tau.preset, TE.tau, method.bias,`

`label.e, label.c, label.left, label.right,`

`byvar, bylab, print.byvar`
: As defined above.

`TE, seTE`
: Estimated treatment effect and standard error of 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).

`k`
: Number of studies combined in meta-analysis.

`Q`
: Heterogeneity statistic Q.

`tau`
: Square-root of between-study variance.

`Q.CMH`
: Cochran-Mantel-Haenszel test statistic for overall effect.

`incr.e, incr.c`
: Increment added to cells in the experimental and control group, respectively

`sparse`
: Logical flag indicating if any study included in meta-analysis has any zero cell frequencies.

df.hakn	Degrees of freedom for test of treatment effect for Hartung-Knapp method (only if hakn=TRUE).
call	Function call.
version	Version of R package meta used to create object.

Author(s)

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

References

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Knapp G & Hartung J (2003), Improved Tests for a Random Effects Meta-regression with a Single Covariate. *Statistics in Medicine*, **22**, 2693-710, doi: 10.1002/sim.1482 .

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Viechtbauer W (2010), Conducting Meta-Analyses in R with the Metafor Package. *Journal of Statistical Software*, **36**, 1–48.

See Also

funnel, metabias, metacont, metagen, print.meta

Examples

```
metabin(10, 20, 15, 20, sm="OR", warn=FALSE)

##
## Different results:
##
metabin(0, 10, 0, 10, sm="OR", warn=FALSE)
metabin(0, 10, 0, 10, sm="OR", allstudies=TRUE, warn=FALSE)


data(Olkin95)

meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95, subset=c(41,47,51,59),
                 sm="RR", method="I")
summary(meta1)
funnel(meta1)

meta2 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95, subset=Olkin95$year<1970,
                 sm="RR", method="I")
summary(meta2)
```

---

metacont *Meta-analysis of continuous outcome data*

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, sm="MD",
         level = 0.95, level.comb = level,
         comb.fixed=TRUE, comb.random=TRUE,
         hakn=FALSE,
         method.tau="DL", tau.preset=NULL, TE.tau=NULL,
         method.bias="linreg",
         title="", complab="", outclab="",
         label.e="Experimental", label.c="Control",
         label.left="", label.right="",
         byvar, bylab, print.byvar=TRUE, warn=TRUE)
```

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.
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-squared. Either "DL", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.
tau.preset	Prespecified value for between-study variance tau-squared.
TE.tau	Overall treatment effect used to estimate the between-study variance tau-squared.
method.bias	A character string indicating which test is to be used. Either "rank", "linreg", or "mm", can be abbreviated.
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.
sm	A character string indicating which summary measure ("MD" or "SMD") is to be used for pooling of studies.
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.
warn	A logical indicating whether warnings should be printed (e.g., if studies are excluded from meta-analysis due to zero standard deviations).

Details

Calculation of fixed and random effects estimates for meta-analyses with continuous outcome data; inverse variance weighting is used for pooling. The DerSimonian-Laird estimate for the between-study variance is used in the random effects model by default (see paragraph on argument `method.tau`). The mean difference is used as measure of treatment effect if `sm="MD"` – which correspond to `sm="WMD"` in older versions (<0.9) of the meta package. For the summary measure `"SMD"`, Hedges' adjusted g is utilised for pooling.

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 `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.

If R package metafor (Viechtbauer 2010) is installed, the following statistical methods are also available.

For the random effects model (argument `comb.random=TRUE`), the method by Hartung and Knapp (Hartung, Knapp 2001; Knapp, Hartung 2003) is used to adjust test statistics and confidence intervals if argument `hakn=TRUE` (internally R function `rma.uni` of R package metafor is called).

Several methods are available to estimate the between-study variance τ^2 (argument `method.tau`):

- DerSimonian-Laird estimator (`method.tau="DL"`) (default)
- 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 all but the DerSimonian-Laird method the R function `rma.uni` of R package metafor is called internally. See help page of R function `rma.uni` for more details on the various methods to estimate between-study variance τ^2.

Value

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

`n.e, mean.e, sd.e,`

`n.c, mean.c, sd.c,`

`studlab, sm, level, level.comb,`

`comb.fixed, comb.random,`

`hakn, method.tau, tau.preset, TE.tau, method.bias,`

`label.e, label.c, label.left, label.right,`

`byvar, bylab, print.byvar, warn`
: As defined above.

`TE, seTE`
: Estimated treatment effect and standard error of 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).

`k`
: Number of studies combined in meta-analysis.

`Q`
: Heterogeneity statistic.

`tau`
: Square-root of between-study variance.

`method`
: Pooling method: `"Inverse"`.

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

`call`
: Function call.

`version`
: Version of R package meta used to create object.

Author(s)

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

References

Cooper H & Hedges LV (1994), *The Handbook of Research Synthesis*. Newbury Park, CA: Russell Sage Foundation.

Hartung J & Knapp G (2001), On tests of the overall treatment effect in meta-analysis with normally distributed responses. *Statistics in Medicine*, **20**, 1771–82. doi: 10.1002/sim.791 .

Knapp G & Hartung J (2003), Improved Tests for a Random Effects Meta-regression with a Single Covariate. *Statistics in Medicine*, **22**, 2693-710, doi: 10.1002/sim.1482 .

Viechtbauer W (2010), Conducting Meta-Analyses in R with the Metafor Package. *Journal of Statistical Software*, **36**, 1–48.

See Also

metabin, metagen

Examples

```
data(Fleiss93cont)
meta1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, data=Fleiss93cont, sm="SMD")
meta1

meta2 <- metacont(Fleiss93cont$n.e, Fleiss93cont$mean.e,
                  Fleiss93cont$sd.e,
                  Fleiss93cont$n.c, Fleiss93cont$mean.c,
                  Fleiss93cont$sd.c,
                  sm="SMD")
meta2
```

---

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

```
metacor(cor, n, studlab,
        data=NULL, subset=NULL,
        sm="ZCOR",
        level=0.95, level.comb=level,
        comb.fixed=TRUE, comb.random=TRUE,
        hakn=FALSE,
        method.tau="DL", tau.preset=NULL, TE.tau=NULL,
        method.bias="linreg",
        title="", complab="", outclab="",
        byvar, bylab, print.byvar=TRUE
        )
```

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.

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 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-squared. Either "DL", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.
tau.preset	Prespecified value for between-study variance tau-squared.
TE.tau	Overall treatment effect used to estimate the between-study variance tau-squared.
method.bias	A character string indicating which test is to be used. Either "rank", "linreg", or "mm", can be abbreviated.
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.

Details

Fixed effect and random effects meta-analysis of correlations based either on Fisher's z transformation of proportions (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.

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 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 R package metafor (Viechtbauer 2010) is installed, the following statistical methods are also available.

For the random effects model (argument comb.random=TRUE), the method by Hartung and Knapp (Knapp, Hartung 2003) is used to adjust test statistics and confidence intervals if argument hakn=TRUE (internally R function rma.uni of R package metafor is called).

Several methods are available to estimate the between-study variance τ^2 (argument method.tau):

- DerSimonian-Laird estimator (method.tau="DL") (default)
- 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 all but the DerSimonian-Laird method the R function rma.uni of R package metafor is called internally. See help page of R function rma.uni for more details on the various methods to estimate between-study variance τ^2.

Value

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

cor, n, studlab,

sm, level, level.comb,

comb.fixed, comb.random,

hakn, method.tau, tau.preset, TE.tau, method.bias,

byvar, bylab, print.byvar
: As defined above.

TE, seTE
: Either Fisher's z transformation of correlations (sm="ZCOR") or correlations (sm="COR") for 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 its 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 its 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).

`k`
: Number of studies combined in meta-analysis.

`Q`
: Heterogeneity statistic Q.

`tau`
: Square-root of between-study variance.

`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`).

`call`
: Function call.

`version`
: Version of R package meta used to create object.

Author(s)

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References

Cooper H, Hedges LV, Valentine JC (2009), *The Handbook of Research Synthesis and Meta-Analysis*, 2nd Edition. New York: Russell Sage Foundation.

Knapp G & Hartung J (2003), Improved Tests for a Random Effects Meta-regression with a Single Covariate. *Statistics in Medicine*, **22**, 2693-710, doi: 10.1002/sim.1482 .

Viechtbauer W (2010), Conducting Meta-Analyses in R with the Metafor Package. *Journal of Statistical Software*, **36**, 1–48.

See Also

`metacont`, `metagen`, `print.meta`

Examples

```
metacor(c(0.85, 0.7, 0.95), c(20, 40, 10))
metacor(c(0.85, 0.7, 0.95), c(20, 40, 10), sm="cor")
```

`metacr` *Meta-analysis of outcome data from Cochrane review*

Description

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

Usage

```
metacr(x, comp.no=1, outcome.no=1,
       sm, method, comb.fixed, comb.random, swap.events, logscale,
       method.tau="DL", hakn=FALSE,
       title, complab, outclab, warn=FALSE)
```

Arguments

x	An object of class rm5 created by R function read.rm5.
comp.no	Comparison number.
outcome.no	Outcome number.
sm	A character string indicating which summary measure ("RR", "OR", "RD", "AS", "HR", "MD", or "SMD") is to be used for pooling of studies.
method	A character string indicating which method is to be used for pooling of studies. One of "Inverse", "MH", or "Peto", can be abbreviated.
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.
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.
method.tau	A character string indicating which method is used to estimate the between-study variance τ^2. Either "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.
title	Title of meta-analysis / systematic review.
complab	Comparison label.
outclab	Outcome label.
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 seperate meta-analysis is conducted. Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://www.cc-ims.net/revman/).

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.

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

Review Manager (RevMan) [Computer program]. Version 5.1. Copenhagen: The Nordic Cochrane Centre, The Cochrane Collaboration, 2011.

See Also

metabin, metacont, metagen, read.rm5

Examples

```
## Locate export data file "Fleiss93_CR.csv"
## in sub-directory of package "meta"
##
filename <- system.file("data/Fleiss93_CR.csv.gz", package = "meta")
##
Fleiss93_CR <- read.rm5(filename)

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

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

---

metacum *Cumulative meta-analysis*

Description

Performs a cumulative meta-analysis.

Usage

```
metacum(x, pooled, sortvar, level.comb=x$level.comb)
```

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

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, plot function. The object is a list containing the following components:

TE, seTE	Estimated treatment effect and standard error of pooled estimate in cumulative meta-analyses.
lower, upper	Lower and upper confidence interval limits.
studlab	Study label describing addition 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.
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.
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 τ^2.

`tau.preset` Prespecified value for between-study variance τ^2.

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

`n.harmonic.mean` Harmonic mean of number of observations (for backtransformation 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

Cooper H & Hedges LV (1994), *The Handbook of Research Synthesis*. Newbury Park, CA: Russell Sage Foundation.

See Also

`metabin`, `metacont`, `print.meta`

Examples

```
data(Fleiss93)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Fleiss93, studlab=study,
                 sm="RR", method="I")
meta1

metacum(meta1)
metacum(meta1, pooled="random")

forest(metacum(meta1, pooled="random"))
```

---

metagen *Generic inverse variance meta-analysis*

Description

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

Usage

```
metagen(TE, seTE, studlab, data=NULL, subset=NULL, sm="",
        level = 0.95, level.comb = level,
        comb.fixed=TRUE, comb.random=TRUE,
        hakn=FALSE,
        method.tau="DL", tau.preset=NULL, TE.tau=NULL,
        method.bias="linreg",
        n.e=NULL, n.c=NULL,
        title="", complab="", outclab="",
        label.e="Experimental", label.c="Control",
        label.left="", label.right="",
        byvar, bylab, print.byvar=TRUE, warn=TRUE)
```

Arguments

TE	Estimate of treatment effect.
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.
sm	A character string indicating underlying summary measure, e.g., "RD", "RR", "OR", "AS", "MD", "SMD".
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.
n.e	Number of observations in experimental group.
n.c	Number of observations in control group.
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-squared. Either "DL", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.
tau.preset	Prespecified value for between-study variance tau-squared.
TE.tau	Overall treatment effect used to estimate the between-study variance tau-squared.
method.bias	A character string indicating which test is to be used. Either "rank", "linreg", or "mm", can be abbreviated.
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 TE).
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.
warn	A logical indicating whether warnings should be printed (e.g., if studies are excluded from meta-analysis due to zero standard errors).

Details

Generic method for meta-analysis, only treatment estimates and their standard error are needed. The method is useful, e.g., for pooling of survival data (using log hazard ratio and standard errors as input). The inverse variance method is used for pooling. Random effects estimate is based on the DerSimonian-Laird method.

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 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 R package metafor (Viechtbauer 2010) is installed, the following statistical methods are also available.

For the random effects model (argument comb.random=TRUE), the method by Hartung and Knapp (Knapp, Hartung 2003) is used to adjust test statistics and confidence intervals if argument hakn=TRUE (internally R function rma.uni of R package metafor is called).

Several methods are available to estimate the between-study variance τ^2 (argument method.tau):

- DerSimonian-Laird estimator (method.tau="DL") (default)
- 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 all but the DerSimonian-Laird method the R function rma.uni of R package metafor is called internally. See help page of R function rma.uni for more details on the various methods to estimate between-study variance τ^2.

Value

An object of class `c("metagen", "meta")` with corresponding `print`, `summary`, `plot` function. The object is a list containing the following components:

`TE, seTE, studlab, n.e, n.c`

`sm, level, level.comb,`

`comb.fixed, comb.random,`

`hakn, method.tau, tau.preset, TE.tau, method.bias,`

`label.e, label.c, label.left, label.right,`

`byvar, bylab, print.byvar, warn`
: As defined above.

`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).

`k`
: Number of studies combined in meta-analysis.

`Q`
: Heterogeneity statistic.

`tau`
: Square-root of between-study variance.

`method`
: Pooling method: `"Inverse"`.

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

`call`
: Function call.

`version`
: Version of R package meta used to create object.

Author(s)

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

References

Cooper H & Hedges LV (1994), *The Handbook of Research Synthesis*. Newbury Park, CA: Russell Sage Foundation.

Knapp G & Hartung J (2003), Improved Tests for a Random Effects Meta-regression with a Single Covariate. *Statistics in Medicine*, **22**, 2693-710, doi: 10.1002/sim.1482 .

Viechtbauer W (2010), Conducting Meta-Analyses in R with the Metafor Package. *Journal of Statistical Software*, **36**, 1–48.

See Also

metabin, metacont, print.meta

Examples

```
data(Fleiss93)
meta1 <- metabin(event.e, n.e, event.c, n.c, data=Fleiss93, sm="RR", method="I")
meta1

##
## Identical results by using the following commands:
##
meta1
metagen(meta1$TE, meta1$seTE, sm="RR")


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

metagen(logHR, selogHR, sm="HR")
```

---

metainf *Influence analysis in meta-analysis*

Description

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

Usage

```
metainf(x, pooled, sortvar, level.comb=x$level.comb)
```

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

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, plot function. 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.
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.
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 τ^2.
tau.preset	Prespecified value for between-study variance τ^2.
TE.tau	Overall treatment effect used to estimate the between-study variance τ^2.
n.harmonic.mean	Harmonic mean of number of observations (for backtransformation 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

Cooper H & Hedges LV (1994), *The Handbook of Research Synthesis*. Newbury Park, CA: Russell Sage Foundation.

See Also

metabin, metacont, print.meta

Examples

```
data(Fleiss93)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Fleiss93, studlab=study,
                 sm="RR", method="I")
meta1

metainf(meta1)
metainf(meta1, pooled="random")

forest(metainf(meta1, pooled="random"), comb.random=TRUE)
```

---

metaprop *Meta-analysis of single proportions*

Description

Calculation of an overall proportion from studies reporting a single proportion.

Usage

```
metaprop(event, n, studlab,
         data = NULL, subset = NULL,
         sm="PFT", freeman.tukey,
         incr=0.5, allincr=FALSE, addincr=FALSE,
         level = 0.95, level.comb = level,
         comb.fixed=TRUE, comb.random=TRUE,
         hakn=FALSE,
         method.tau="DL", tau.preset=NULL, TE.tau=NULL,
         method.bias="linreg",
         title="", complab="", outclab="",
         byvar, bylab, print.byvar=TRUE,
         warn=TRUE)
```

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.
sm	A character string indicating which summary measure ("PFT", "PAS", "PRAW", "PLN", or "PLOGIT") is to be used for pooling of studies, see Details.
freeman.tukey	Use of this argument is deprecated, please instead use argument sm, see Details.
incr	A numeric which is added to each cell frequency for studies with a zero cell count.
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.
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-squared. Either "DL", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.
tau.preset	Prespecified value for between-study variance tau-squared.
TE.tau	Overall treatment effect used to estimate the between-study variance tau-squared.

method.bias	A character string indicating which test is to be used. Either "rank", "linreg", or "mm", can be abbreviated.
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.
warn	A logical indicating whether the addition of incr to studies with zero cell frequencies should result in a warning.

Details

Fixed effect and random effects meta-analysis of single proportions to calculate an overall proportion.

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

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

In older versions of the R package meta (< 1.5.0), only the Freeman-Tukey Double arcsine transformation and the arcsine transformation were implemented and an argument freeman.tukey could be used to distinguish between these two methods. The use of the argument freeman.tukey is deprecated and the argument will probably removed from the function metaprop in the future. At the moment, a correponding warning message is printed if the argument freeman.tukey is used.

If the summary measure is equal to "PRAW", "PLN", or "PLOGIT", a continuity correction is applied if any studies has a zero cell count. By default, 0.5 is added to all cell frequencies of studies with a zero cell count (argument incr).

Note, exact binomial confidence intervals will be calculated for individual study results, e.g. in R function summary.meta.

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 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 R package metafor (Viechtbauer 2010) is installed, the following statistical methods are also available.

For the random effects model (argument comb.random=TRUE), the method by Hartung and Knapp (Knapp, Hartung 2003) is used to adjust test statistics and confidence intervals if argument hakn=TRUE (internally R function rma.uni of R package metafor is called).

Several methods are available to estimate the between-study variance τ^2 (argument method.tau):

- DerSimonian-Laird estimator (method.tau="DL") (default)
- 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 all but the DerSimonian-Laird method the R function rma.uni of R package metafor is called internally. See help page of R function rma.uni for more details on the various methods to estimate between-study variance τ^2.

Value

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

event, n, studlab,

sm, incr, allincr, addincr,

level, level.comb,
: As defined above.

comb.fixed, comb.random,

hakn, method.tau, tau.preset, TE.tau, method.bias,

byvar, bylab, print.byvar, warn

TE, seTE
: Estimated (un)transformed proportion and its standard error 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).

`k`
: Number of studies combined in meta-analysis.

`Q`
: Heterogeneity statistic Q.

`tau`
: Square-root of between-study variance.

`sm`
: A character string: `"proportion"`

`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`).

`call`
: Function call.

`version`
: Version of R package meta used to create object.

Author(s)

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

References

Edward JM et al. (2006), Adherence to antiretroviral therapy in sub-saharan Africa and North America - a meta-analysis. *Journal of the American Medical Association*, **296**, 679–690.

Freeman MF & Tukey JW (1950), Transformations related to the angular and the square root. *Annals of Mathematical Statistics*, **21**, 607–611.

Knapp G & Hartung J (2003), Improved Tests for a Random Effects Meta-regression with a Single Covariate. *Statistics in Medicine*, **22**, 2693-710, doi: 10.1002/sim.1482 .

Miller JJ (1978), The inverse of the Freeman-Tukey double arcsine transformation. *The American Statistician*, **32**, 138.

Pettigrew HM, Gart JJ, Thomas DG (1986), The bias and higher cumulants of the logarithm of a binomial variate. *Biometrika*, **73**, 425–435.

Viechtbauer W (2010), Conducting Meta-Analyses in R with the Metafor Package. *Journal of Statistical Software*, **36**, 1–48.

See Also

`metacont`, `metagen`, `print.meta`

Examples

```
metaprop(4:1, c(10, 20, 30, 40))
metaprop(4:1, c(10, 20, 30, 40), sm="PAS")
metaprop(4:1, c(10, 20, 30, 40), sm="PRAW")
metaprop(4:1, c(10, 20, 30, 40), sm="PLN")
metaprop(4:1, c(10, 20, 30, 40), sm="PLOGIT")
```

---

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

```
metareg(formula, data, method.tau=data$method.tau)
```

Arguments

`formula`	A formula object.
`data`	An object of class `meta`.
`method.tau`	A character string indicating which method is used to estimate the between-study variance tau-squared. Either `"DL"`, `"REML"`, `"ML"`, `"HS"`, `"SJ"`, `"HE"`, or `"EB"`, can be abbreviated.

Details

This R function is a wrapper function for R function `rma.uni` in the R package metafor (Viechtbauer 2010), i.e. the function `metareg` can only be used if the R package metafor is installed.

Value

An object of class `c("rma.uni","rma")`. Please look at the help page of R function `rma.uni` for more details.

Author(s)

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

References

Viechtbauer W (2010), Conducting Meta-Analyses in R with the Metafor Package. *Journal of Statistical Software*, **36**, 1–48.

See Also

summary.meta, metagen

Examples

```
data(Fleiss93cont)
meta1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, data=Fleiss93cont, sm="MD")
meta1$grp <- c(1,2,1,1,2)
metareg(~grp, data=meta1)
```

Olkin95 *Thrombolytic Therapy after Acute Myocardial Infarction*

Description

Meta-analysis on Thrombolytic Therapy after Acute Myocardial Infarction

Usage

```
data(Olkin95)
```

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

Olkin I (1995), Statistical and theoretical considerations in meta-analysis. *Journal of Clinical Epidemiology*, **48**, 133–146.

Examples

```
data(Olkin95)
summary(metabin(event.e, n.e, event.c, n.c, data=Olkin95))
```

plot.meta *Plot function for objects of class meta (deprecated)*

Description

Draws a forest plot in the active graphics window.

Usage

```
## S3 method for class 'meta'
plot(x, byvar=x$byvar, bylab=x$bylab,
     print.byvar=x$print.byvar,
     sortvar, studlab=TRUE, level=x$level, level.comb=x$level.comb,
     comb.fixed=x$comb.fixed, comb.random=x$comb.random, overall=TRUE,
     text.fixed="Fixed effect model", text.random="Random effects model",
     lty.fixed=2, lty.random=3, xlab=NULL, xlim, ylim, lwd=1, cex=1,
     cex.comb=1.2 * cex, cex.axis=cex, cex.lab=cex,
     log=ifelse(x$sm %in% c("RR", "OR", "HR"), "x", ""),
     axes=TRUE, allstudies=TRUE,
     weight=ifelse(comb.random, "random", "fixed"), scale.diamond=1,
     scale.square= 1, col.i="black",
     clim=xlim, arrow.length=0.1,
     ref=ifelse(x$sm %in% c("RR", "OR", "HR"), 1, 0),
     ...)
```

Arguments

x	An object of class meta.
byvar	An optional vector containing grouping information (must be of same length as x$TE).
bylab	A character string with a label for the grouping variable.
print.byvar	A logical indicating whether the name of the grouping variable should be printed in front of the group labels.
sortvar	An optional vector used to sort the individual studies (must be of same length as x$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).
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 fixed effect estimate should be plotted.
comb.random	A logical indicating whether random effects estimate should be plotted.
overall	A logical indicating whether overall summaries should be plotted. This argument is useful in combination with the argument byvar if summaries should only be plotted on group level.

text.fixed	A character string used in the plot to label the pooled fixed effects 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).
xlab	A label for the x axis.
xlim	The x limits (min,max) of the plot.
ylim	The y limits (min,max) of the plot.
lwd	The line width.
cex	A numerical value giving the amount by which plotting text and symbols should be scaled relative to the default.
cex.comb	A numerical value giving the amount by which plotting text and symbols for pooled fixed and random effects estimates should be scaled.
cex.axis	The magnification to be used for axis annotation relative to the current setting of cex.
cex.lab	The magnification to be used for x and y labels relative to the current setting of cex.
log	A character string which contains "x" if the x axis is to be logarithmic (other values for log are not reasonable).
axes	A logical indicating whether the x axis should be drawn on the plot.
allstudies	A logical indicating whether studies with inestimable treatment effects should be plotted.
weight	A character string indicating which type of plotting symbols is to be used for individual treatment estimates. One of "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.
scale.diamond	A numerical value giving the amount by which the diamond representing pooled treatment effects should be scaled relative to the default.
scale.square	A numerical value giving the amount by which the square representing treatment effects in individual studies should be scaled relative to the default.
...	Graphical arguments as in par may also be passed as arguments.
col.i	The colour for individual study results and confidence limits.
clim	Limits (min,max) where to cut confidence limits; arrows are plotted if confidence limits are outside the range of clim.
arrow.length	Length of the edges of the arrow head (in inches) which is plotted if confidence limits are outside the range of clim. See also function arrows.
ref	A numerical value defining a reference value which is plotted as a vertical line.

Details

Please note, the R code of the function plot.meta is no longer maintained. Use of the function might result in (unexpected) error messages or even in wrong results. Please use the function forest.meta instead.

A forest plot, also called confidence interval plot, is drawn in the active graphics window. Subgroup analyses are conducted and displayed in the plot if byvar is not missing.

Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://www.cc-ims.net/revman/). 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.

Author(s)

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

See Also

forest.meta, metabin, metacont, metagen

Examples

```
data(Olkin95)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Olkin95, subset=c(41,47,51,59),
                 sm="RR", method="I")

oldpar <- par(mfrow=c(2, 2))

plot(meta1)
plot(meta1, byvar=c(1,2,1,2), bylab="label")
plot(meta1, byvar=1:4, xlim=c(0.02, 10))

par(oldpar)
```

---

print.meta *Print and summary method for objects of class meta*

Description

Print and summary method for objects of class meta.

Usage

```
## S3 method for class 'meta'
print(x, sortvar, level=x$level, level.comb=x$level.comb,
        comb.fixed=x$comb.fixed, comb.random=x$comb.random,
        details=FALSE, ma=TRUE, digits=max(4, .Options$digits - 3), ...)

## S3 method for class 'metabias'
```

```
print(x, ...)

## S3 method for class 'meta'
summary(object, byvar=object$byvar,
        bylab=object$bylab, print.byvar=object$print.byvar,
        bystud=FALSE,
        level=object$level, level.comb=object$level.comb,
        comb.fixed=object$comb.fixed, comb.random=object$comb.random,
        print.CMH=object$print.CMH, warn=object$warn, ...)

## S3 method for class 'summary.meta'
print(x, digits = max(3, .Options$digits - 3),
        print.byvar=x$print.byvar,
        comb.fixed=x$comb.fixed, comb.random=x$comb.random,
        header=TRUE, print.CMH=x$print.CMH, bylab.nchar=35, ...)
```

Arguments

x	An object of class meta, metabias, or summary.meta.
object	An object of class meta.
sortvar	An optional vector used to sort the individual studies (must be of same length as x$TE).
level	The level used to calculate confidence intervals for individual studies.
level.comb	The level used to calculate confidence intervals for pooled estimates.
comb.fixed	A logical indicating whether a fixed effect meta-analysis should be conducted.
comb.random	A logical indicating whether a random effects meta-analysis should be conducted.
header	A logical indicating whether information on title of meta-analysis, comparison and outcome should be printed at the beginning of the printout.
details	A logical indicating whether further details of individual studies should be printed.
ma	A logical indicating whether the summary results of the meta-analysis should be printed.
byvar	An optional vector containing grouping information (must be of same length as x$TE).
bylab	A character string with a label for the grouping variable.
bylab.nchar	A numeric specifying the number of characters to print from label for the grouping variable.
bystud	A logical indicating whether results of individual studies should be printed by grouping variable.
digits	Minimal number of significant digits, see print.default.
print.byvar	A logical indicating whether the name of the grouping variable should be printed in front of the group labels. By default, the value of print.byvar is set to TRUE.
warn	A logical indicating whether the use of summary.meta in connection with metacum or metainf should result in a warning.

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

Details

Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://www.cc-ims.net/revman/). 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.

For subgroups (argument byvar not NULL), results for the fixed effect model will be printed if both arguments comb.fixed and comb.random are TRUE. In order to get results for the random effects model within subgroups, use comb.fixed==FALSE and comb.random==TRUE.

Note, for an object of type metaprop, exact binomial confidence intervals are calculated for individual study results using the R function binom.test internally. Accordingly, list elements TE, lower and upper in element study correspond to proportions and exact confidence limits on the natural scale (irrespective of the transformation used in meta-analysis). Contrary, meta-analysis results are transformed as defined by argument sm, i.e. list elements TE, lower and upper in elements fixed, random, within.fixed and within.random.

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).
fixed	Results for fixed effect model (a list with elements TE, seTE, lower, upper, z, p, level).
random	Results for random effects model (a list with elements TE, seTE, lower, upper, z, p, level).
k	Number of studies combined in meta-analysis.
Q	Heterogeneity statistic Q.
tau	Square-root of between-study variance.
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).
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.
within.fixed	Result for fixed effect model within groups (a list with elements TE, seTE, lower, upper, z, p, level) - if byvar is not missing.
within.random	Result for random effects model within groups (a list with elements TE, seTE, lower, upper, z, p, level) - if byvar is not missing.
k.w	Number of studies combined within groups - if byvar is not missing.
Q.b.fixed	Heterogeneity statistic Q between groups (based on fixed effect model) - if byvar is not missing.
Q.b.random	Heterogeneity statistic Q between groups (based on random effects model) - if byvar is not missing.
Q.w	Heterogeneity statistic Q within groups - if byvar is not missing.
bylab	Label for grouping variable - if byvar is not missing.
by.levs	Levels of grouping variable - if byvar is not missing.
comb.fixed, comb.random, print.CMH	As defined above.
version	Version of R package meta used to create object.

Author(s)

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

References

Cooper H & Hedges LV (1994), *The Handbook of Research Synthesis*. Newbury Park, CA: Russell Sage Foundation.

Higgins JPT & Thompson SG (2002), Quantifying heterogeneity in a meta-analysis. *Statistics in Medicine*, **21**, 1539–1558.

See Also

metabin, metacont, metagen

Examples

```
data(Fleiss93cont)
meta1 <- metacont(n.e, mean.e, sd.e, n.c, mean.c, sd.c, data=Fleiss93cont, sm="SMD")
summary(meta1)
summary(meta1, byvar=c(1,2,1,1,2), bylab="group")
```

print.rm5 *Print and summary methods for objects of class rm5*

Description

Print and summary methods for objects of class rm5.

Usage

```
## S3 method for class 'rm5'
print(x, ...)

## S3 method for class 'summary.rm5'
print(x, ...)

## S3 method for class 'rm5'
summary(object, comp.no, outcome.no, ...)

## 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.
object	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.
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.
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.
k.min	Minimum number of studies to perform test for small-study effects.
...	Additional arguments (ignored at the moment)

Details

Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://www.cc-ims.net/revman/). 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 `summary.rm5` can be used to redo all meta-analyses of the imported Cochrane Review.

The R function `metabias.rm5` can be used to conduct a test for funnel plot asymmetry for all meta-analyses of the imported Cochrane Review.

The R function `metacr` is called internally.

Author(s)

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

References

Higgins, J.P.T and S. Green (2011), *Cochrane Handbook for Systematic Reviews of Interventions Version 5.1.0 [Updated March 2011]*. The Cochrane Library: http://www.cochrane-handbook.org

See Also

`metabias.meta`, `summary.meta`, `read.rm5`

Examples

```
## Locate export data file "Fleiss93_CR.csv"
## in sub-directory of package "meta"
##
filename <- system.file("data/Fleiss93_CR.csv.gz", package = "meta")
##
Fleiss93_CR <- read.rm5(filename)

##
## Print summary results for all meta-analysis:
##
summary(Fleiss93_CR)

##
## Print results for tests of small-study effects:
##
metabias(Fleiss93_CR, k.min=5)
```

`read.mtv` *Import RevMan 4 data files (.mtv)*

Description

Reads a file created with RevMan 4 and creates a data frame from it.

Usage

```
read.mtv(file)
```

Arguments

`file`	The name of a file to read data values from.

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

Review Manager (RevMan) [Computer program]. Version 4.2 for Windows. Copenhagen: The Nordic Cochrane Centre, The Cochrane Collaboration, 2003.

See Also

metabin, metacont, metagen

Examples

```
## Locate MTV-data file "FLEISS93.MTV" in sub-directory of 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)
```

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 comparision 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.

Details

Review Manager 5 (RevMan 5) is the current software used for preparing and maintaining Cochrane Reviews (http://www.cc-ims.net/revman/). 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.
`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).
`TE, seTE`	Estimated treatment effect and standard error of individual studies.
`lower.TE, upper.TE`	Lower and upper limit of 95% confidence interval for treatment effect in individual studies.
`weight`	Weight of individual studies (according to meta-analytical method used in respective meta-analysis - see below for details).
`order`	Ordering of studies.
`grplab`	Group label.
`type`	Type of outcome. D = dichotomous, C = continuous, P = IPD.
`method`	A character string indicating which method has been used for pooling of studies. One of `"Inverse"`, `"MH"`, or `"Peto"`.
`sm`	A character string indicating which summary measure has been used for pooling of studies.
`model`	A character string indicating which meta-analytical model has been used (either `"Fixed"` or `"Random"`).
`comb.fixed`	A logical indicating whether fixed effect meta-analysis has been used in respective meta-analysis (see below for details).

comb.random	A logical indicating whether random effects meta-analysis has been used in respective meta-analysis (see below for details).
outclab	Outcome label.
k	Total number of studies combined in respective meta-analysis).
event.e.pooled	Number of events in experimental group in respective meta-analysis (see below for details).
n.e.pooled	Number of observations in experimental group in respective meta-analysis (see below for details).
event.c.pooled	Number of events in control group in respective meta-analysis (see below for details).
n.c.pooled	Number of observations in control group in respective meta-analysis (see below for details).
TE.pooled	Estimated treatment effect in respective meta-analysis (see below for details).
lower.TE, upper.TE	Lower and upper limit of 95% confidence interval for treatment effect in respective meta-analysis (see below for details).
weight.pooled	Total weight in respective meta-analysis (see below for details).
Z.pooled	Z-score for test of overall treatment effect in respective meta-analysis (see below for details).
pval.TE.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 (see below for details).
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 relative risk (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

Review Manager (RevMan) [Computer program]. Version 5.1. Copenhagen: The Nordic Cochrane Centre, The Cochrane Collaboration, 2011.

See Also

metabin, metacont, metagen, metacr

Examples

```
## Locate export data file "Fleiss93_CR.csv"
## in sub-directory of package "meta"
##
filename <- system.file("data/Fleiss93_CR.csv.gz", package = "meta")
##
Fleiss93_CR <- read.rm5(filename)

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

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

---

trimfill *Generic function for trim-and-fill method*

Description

Trim and fill method for estimating and adjusting for the number and outcomes of missing studies in a meta-analysis.

Usage

```
trimfill(x, ...)
```

Arguments

x	An object of class meta, or estimated treatment effect in individual studies.
...	Additional arguments as in par.

Details

The trim and fill method 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.

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, level, level.comb,`
As defined above.

`comb.fixed, comb.random`

`TE, seTE` Estimated treatment effect and standard error of 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).

`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.

`k0` Number of studies added by trim and fill.

Author(s)

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

References

Duval S & Tweedie R (2000), A nonparametric "Trim and Fill" method of accounting for publication bias in meta-analysis. *Journal of the American Statistical Association*, **95**, 89–98.

Duval S & Tweedie R (2000), Trim and Fill: A simple funnel-plot-based method of testing and adjusting for publication bias in meta-analysis. *Biometrics*, **56**, 455–463.

See Also

metagen, metabias, trimfill.meta, funnel

Examples

```
data(Fleiss93)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Fleiss93, sm="OR")
tf1 <- trimfill(meta1)
summary(tf1)
funnel(tf1, pch=ifelse(tf1$trimfill, 1, 16),
       level=0.95, comb.fixed=TRUE)

trimfill(meta1$TE, meta1$seTE, sm=meta1$sm)
```

---

trimfill.meta *Trim and fill method for meta-analysis*

Description

Trim and fill method for estimating and adjusting for the number and outcomes of missing studies in a meta-analysis.

Usage

```
## Default S3 method:
trimfill(x, seTE, left=NULL, ma.fixed=TRUE, type="L", n.iter.max=50,
         sm=NULL, studlab=NULL, level=0.95, level.comb=0.95,
         comb.fixed=TRUE, comb.random=TRUE,
         hakn=FALSE, method.tau="DL", silent=TRUE, ...)

## S3 method for class 'meta'
trimfill(x, left=NULL, ma.fixed=TRUE, type="L", n.iter.max=50,
         sm=NULL, studlab=NULL, level=x$level, level.comb=x$level.comb,
         comb.fixed=x$comb.fixed, comb.random=x$comb.random,
         hakn=x$hakn, method.tau=x$method.tau, silent=TRUE, ...)
```

Arguments

x	An object of class meta, or estimated treatment effect in individual studies.
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", "AS", "MD", "SMD"; 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-squared. Either "DL", "REML", "ML", "HS", "SJ", "HE", or "EB", can be abbreviated.
silent	A logical indicating whether basic information on iterations shown.
...	other arguments

Details

The trim and fill method 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.

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 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.

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, level, level.comb,
: As defined above.

comb.fixed, comb.random, hakn, method.tau

TE, seTE
: Estimated treatment effect and standard error of 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).

`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`).

`k0`
: Number of studies added by trim and fill.

`version`
: Version of R package meta used to create object.

Author(s)

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

References

Duval S & Tweedie R (2000), A nonparametric "Trim and Fill" method of accounting for publication bias in meta-analysis. *Journal of the American Statistical Association*, **95**, 89–98.

Duval S & Tweedie R (2000), Trim and Fill: A simple funnel-plot-based method of testing and adjusting for publication bias in meta-analysis. *Biometrics*, **56**, 455–463.

See Also

`metagen`, `metabias`, `funnel`

Examples

```
data(Fleiss93)
meta1 <- metabin(event.e, n.e, event.c, n.c,
                 data=Fleiss93, sm="OR")
tf1 <- trimfill(meta1)
summary(tf1)
funnel(tf1)
funnel(tf1, pch=ifelse(tf1$trimfill, 1, 16),
       level=0.9, comb.random=FALSE)

trimfill(meta1$TE, meta1$seTE, sm=meta1$sm)
```

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