Package ‘rmeta’

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Description Functions for simple fixed and random effects meta-analysis for two-sample comparisons and cumulative meta-analyses. Draws standard summary plots, funnel plots, and computes summaries and tests for association and heterogeneity.

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**Meta-analysis of antibacterial catheter coating**

**Description**

Data on the effectiveness of silver sulfadiazine coating on venous catheters for preventing bacterial colonisation of the catheter and bloodstream infection.

**Usage**

```r
data(catheter)
```

**Format**

A data.frame with 8 variables giving information about 16 controlled trials of antibacterial-coated venous catheters.

- **Name**: Name of principal author
- **n.trt**: number of coated catheters
- **n.ctrl**: number of standard catheters
- **col.trt**: number of coated catheters colonised by bacteria
- **col.ctrl**: number of standard catheters colonised by bacteria
- **inf.trt**: number of coated catheters resulting in bloodstream infection
- **inf.ctrl**: number of standard catheters resulting in bloodstream infection
- **or**: Odds ratio

**Source**


**Examples**

```r
library(rmeta)
data(catheter)
a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter, names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter, names=Name,subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
a
b
summary(a)
summary(b)
```
Data for Cochrane Collaboration logo

Description
Data from randomised trials before 1980 of corticosteroid therapy in premature labour and its effect on neonatal death.

Usage
data(cochrane)

Format
This data frame contains the following columns:

name  Identifier for the study
ev.trt  Number of deaths in the treated group
n.trt  Number in the treated group
ev.ctrl  Number of deaths in the control group
n.ctrl  Number in the control group

Details
This meta-analysis, if done, would likely have resulted in the treatment being widely used a decade earlier than it was, saving many lives. The graph is part of the logo of the Cochrane Collaboration, a group aiming to perform systematic reviews of the entire clinical trial literature.

Source
http://www.cochrane.org

Examples
data(cochrane)
steroid <- meta.MH(n.trt, n.ctrl, ev.trt, ev.ctrl,
                     names=name, data=cochrane)
plot(steroid, col=meta.colors("RoyalBlue"))
cummeta

Cumulative meta-analysis of binary data

Description

A cumulative meta-analysis plot shows how evidence has accumulated over time. The i\textsuperscript{th} line in the cumulative meta-analysis plot is the summary produced by a meta-analysis of the first i trials.

Usage

\begin{verbatim}
cummeta(ntrt, nctrl, ptrt, pctrl, conf.level = 0.95, 
    names = NULL, data = NULL, subset = NULL, 
    na.action = na.fail, 
    method = c("meta.MH", "meta.DSL"), 
    statistic = "OR")
cummeta.summaries(effects, stderrs, conf.level = 0.95, 
    names = NULL, weights=NULL, data = NULL, 
    subset = NULL, na.action = get(option("na.action")), 
    method = c("fixed", "random"), logscale=TRUE) 
\end{verbatim}

\# S3 method for class 'meta.cum'
\begin{verbatim}
plot(x, conf.level = NULL, 
    colors = meta.colors(), xlab = NULL, 
    summary.line = TRUE, summary.conf = FALSE, 
    main="Cumulative meta-analysis", lwd=1, ...)
\end{verbatim}

\# S3 method for class 'meta.cum'
\begin{verbatim}
summary(object, conf.level=NULL, ...)
\end{verbatim}

Arguments

\begin{itemize}
\item \textbf{ntrt} \hspace{1cm} Number of subjects in treated/exposed group \hfill 
\item \textbf{nctrl} \hspace{1cm} Number of subjects in control group \hfill 
\item \textbf{ptrt} \hspace{1cm} Number of events in treated/exposed group \hfill 
\item \textbf{pctrl} \hspace{1cm} Number of events in control group \hfill 
\item \textbf{effects} \hspace{1cm} Difference between control and treatment group \hfill 
\item \textbf{stderrs} \hspace{1cm} Standard errors of effects \hfill 
\item \textbf{weights} \hspace{1cm} Study weights (see \textit{meta.summaries}) \hfill 
\item \textbf{names} \hspace{1cm} names or labels for studies \hfill 
\item \textbf{data} \hspace{1cm} data frame to interpret variables \hfill 
\item \textbf{subset} \hspace{1cm} subset of studies to include \hfill 
\item \textbf{na.action} \hspace{1cm} How to handle missing values \hfill 
\item \textbf{method} \hspace{1cm} Which meta-analysis method to use \hfill 
\item \textbf{statistic} \hspace{1cm} "OR" for odds ratio or "RR" for relative risk. \hfill 
\item \textbf{logscale} \hspace{1cm} The effects values are the logarithms of actual effects (for plotting) \hfill 
\end{itemize}
forestplot

x, object  a meta.cum object
...  other graphical arguments for metaplot
conf.level  Coverage for confidence intervals
colors  see meta.colors
xlab  X-axis label
summary.line  Plot a vertical line at the final summary value?
summary.conf  Plot vertical lines at the final confidence interval limits?
main,lwd  graphical parameters

Value

Object of class meta.cum.

See Also

meta.MH, meta.DSL

Examples

data(cochrane)
steroid<-cumm ETA(n.trt, n.ctrl, ev.trt, ev.ctrl, names=name, data=cochrane,
  statistic="RR", method="meta.MH")
plot(steroid)
summary(steroid)
data(catheter)
b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
  names=Name, subset=c(13, 6, 5, 3, 12, 4, 11, 1, 8, 10, 2))
d <- cumm.meta.summaries(b$logs, b$selogs, names=b$names,
  method="random", logscale=TRUE)
plot(d, summary.conf=TRUE)
summary(d)

---

forestplot  Forest plots

Description

Draw a forest plot together with a table of text.

Usage

forestplot(labeltext, mean, lower, upper, align = NULL,
is.summary = FALSE, clip = c(-Inf, Inf), xlab = "",
zero = 0, graphwidth = unit(2, "inches"), col = meta.colors(),
xlog = FALSE, xticks=NULL, boxsize=NULL,...)
Arguments

- **labeltext**: Matrix of strings or NAs for blank spaces
- **mean**: Vector of centers of confidence intervals (or NAs for blank space)
- **lower**: Vector of lower ends of confidence intervals
- **upper**: Vector of upper ends of confidence intervals
- **align**: Vector giving alignment (l,r,c) for columns of table
- **is.summary**: Vector of logicals. Summary lines have bold text and diamond confidence intervals.
- **clip**: Lower and upper limits for clipping confidence intervals to arrows
- **xlab**: x-axis label
- **zero**: x-axis coordinate for zero line
- **graphwidth**: Width of confidence interval graph
- **col**: See `meta.colors`
- **xlog**: If TRUE, x-axis tick marks are exponentiated
- **xticks**: Optional user-specified x-axis tick marks. Specify NULL to use the defaults, numeric(0) to omit the x-axis.
- **boxsize**: Override the default box size based on precision
- ... Not used.

Details

This function is more flexible than `metaplot` and the plot methods for meta-analysis objects, but requires more work by the user.

In particular, it allows for a table of text, and clips confidence intervals to arrows when they exceed specified limits.

Value

None

See Also

`metaplot`

Examples

data(cochrane)
steroid <- meta.MH(n.trt, n.ctrl, ev.trt, ev.ctrl,
                        names=name, data=cochrane)

tabletext<-cbind(c("","Study",steroid$names,NA,"Summary"),
                        c("Deaths","(steroid)",cochrane$ev.trt,NA,NA),
                        c("Deaths","(placebo)", cochrane$ev.ctrl, NA,NA),
                        c("","OR",format(exp(steroid$logOR),digits=2),NA,format(exp(steroid$logMH),digits=2))
)
funnelplot

Funnel plot for publication bias

Description

Plots the treatment difference for trials against the size of the trial (or other specified variable). Asymmetry in the plot often indicates publication bias. Generic, with methods for meta-analysis objects.

Usage

funnelplot(x,...)

## Default S3 method:
funnelplot(x, se, size=1/se, summ=NULL,
  xlab="Effect", ylab="Size", colors=meta.colors(),
  conf.level=0.95, plot.conf=FALSE,
  zero=NULL, mirror=FALSE, ...)

Arguments

x            Treatment difference
se           Standard error of x
size         Variable for the vertical axis
summ         summary treatment difference
xlab         x-axis label
ylab         y-axis label
colors        list of colors for components of the plot
conf.level    For confidence interval plotting
plot.conf     Plot confidence intervals instead of just points
zero  location of a null hypothesis line
mirror  Add points reflected around summ?
...  further arguments to be passed from or to methods.

Details

With the default value of size the plot should appear as an upwards-pointing funnel shape. Publication bias often causes one side of the funnel to be trimmed near the base. The mirror plot creates a symmetric funnel by reflecting the plot around the summ value. In the presence of publication bias the added points will separate from the real studies.

Value

Used for its side-effect.

Author(s)

Thomas Lumley

See Also

meta.DSL, meta.MH, meta.summaries, metaplot

Examples

data(catheter)
a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
           names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
funnelplot(a$logOR, a$selogOR)
funnelplot(a$logOR, a$selogOR,
           plot.conf=TRUE, summ=a$logMH, mirror=TRUE)
funnelplot(a, plot.conf=TRUE)

Description

Wrapper function for specifying colours to meta-analysis plots

Usage

meta.colors(all.elements, box="black", lines="gray", summary="black",
zero="lightgray", mirror="lightblue", text="black",
axes="black", background=NA)
meta.colors

Arguments

- **all.elements**: if present, overrides other arguments
- **box**: Colour of sample size box
- **lines**: Colour of confidence intervals
- **summary**: Colour of summary estimate
- **zero**: Colour of null hypothesis line
- **mirror**: Colour of reflected points (in funnelplot)
- **text**: Colour of labels
- **axes**: Colour of x-axis and axis labels
- **background**: Background colour.

Value

A list of colors

See Also

plot.meta.MH, plot.meta.DSL, plot.meta.summaries, funnelplot, metaplot

Examples

data(cochrane)
steroid <- meta.MH(n.trt, n.ctrl, ev.trt, ev.ctrl,
  names=name, data=cochrane)

## All black, for better photocopying
plot(steroid, col=meta.colors("black"))

## Distinguish the summary
plot(steroid, colors=meta.colors(summary="forestgreen"))

data(catheter)
e <- meta.DSL(n.trt, n.ctrl, inf.trt, inf.ctrl, data=catheter,
  names=Name, subset=c(13,6,3,12,4,11,1,14,8,10,2))

## Truly awful colour scheme to illustrate flexibility
plot(e, colors=meta.colors(summary="green", lines=c("purple","skyblue"),
  box="red", zero="yellow", text=palette(), background="tomato",
  axes="lightgreen"))

## Dark blue background popular for presentations.
plot(e, colors=meta.colors(summary="white", lines="#FFFFF0",
  box="#FFFFF0", zero="grey90", text="white", background="darkblue",
  axes="grey90"))
Random effects (DerSimonian-Laird) meta-analysis

Description

Computes the individual odds ratios or relative risks, the summary, the random effects variance, and Woolf’s test for heterogeneity. The print method gives the summary and test for heterogeneity; the summary method also gives all the individual odds ratios and confidence intervals. Studies with zero or infinite odds ratio are omitted, as their variance cannot be calculated sensibly.

The plot method draws a standard meta-analysis plot. The confidence interval for each study is given by a horizontal line, and the point estimate is given by a square whose height is inversely proportional to the standard error of the estimate. The summary odds ratio, if requested, is drawn as a diamond with horizontal limits at the confidence limits and width inversely proportional to its standard error.

Usage

```r
meta.DSL(ntrt, nctrl, ptrt, pctrl, conf.level=0.95,
        names=NULL, data=NULL, subset=NULL, na.action=na.fail, statistic="OR")
```

```r
summary(object, conf.level=NULL, ...)
```

```r
plot(x, summary=TRUE, summlabel="Summary",
     conf.level=NULL, colors=meta.colors(), xlab=NULL,...)
```

Arguments

- `ntrt`: Number of subjects in treated/exposed group
- `nctrl`: Number of subjects in control group
- `ptrt`: Number of events in treated/exposed group
- `pctrl`: Number of events in control group
- `conf.level`: Coverage for confidence intervals
- `names`: names or labels for studies
- `data`: data frame to interpret variables
- `subset`: subset of studies to include
- `na.action`: a function which indicates what should happen when the data contain NAs. Defaults to `na.fail`.
- `statistic`: "OR" for odds ratio, "RR" for relative risk
- `x,object`: a meta.DSL object
- `summary`: Plot the summary odds ratio?
- `summlabel`: Label for the summary odds ratio
- `colors`: see `meta.colors`
- `xlab`: x-axis label, default is based on statistic
- `...`: further arguments to be passed from or to methods.
**Value**

An object of class `meta.DSL` with `print`, `plot`, `funnelplot` and `summary` methods.

**Author(s)**

Thomas Lumley

**See Also**

`plot`, `par`, `meta.MH`, `funnelplot`

**Examples**

```r
data(catheter)
b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
          names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
b
summary(b)
plot(b)
e <- meta.DSL(n.trt, n.ctrl, inf.trt, inf.ctrl, data=catheter,
          names=Name, subset=c(13,6,3,12,4,11,1,14,8,10,2))
e
summary(e)
```

```r
## tasteless
plot(e, colors=meta.colors(summary="green", lines="purple", box="orange"))
```

**Description**

Computes the individual odds ratio or relative risk, the Mantel-Haenszel summary, and Woolf’s test for heterogeneity. The `print` method gives the summary and test for heterogeneity; the `summary` method also gives all the individual odds ratios and confidence intervals.

The `plot` method draws a standard meta-analysis plot. The confidence interval for each study is given by a horizontal line, and the point estimate is given by a square whose height is inversely proportional to the standard error of the estimate. The summary odds ratio, if requested, is drawn as a diamond with horizontal limits at the confidence limits and width inversely proportional to its standard error.

**Usage**

```r
meta.MH(ntrt, nctrl, ptrt, pctrl, conf.level=0.95,
         names=NULL, data=NULL, subset=NULL, na.action = na.fail, statistic="OR")
```

```r
## S3 method for class 'meta.MH'
summary(object, conf.level=NULL, ...)
```

```r
## S3 method for class 'meta.MH'
plot(x, summary=TRUE, summlabel="Summary",
     conf.level=NULL, colors=meta.colors(), xlab=NULL, ...)```
**Arguments**

- `ntrt` Number of subjects in treated/exposed group
- `nctrl` Number of subjects in control group
- `ptrt` Number of events in treated/exposed group
- `pctrl` Number of events in control group
- `names` names or labels for studies
- `data` data frame to interpret variables
- `subset` subset of studies to include
- `na.action` a function which indicates what should happen when the data contain NAs. Defaults to `na.fail`.
- `statistic` "OR" for odds ratio, "RR" for relative risk
- `x,object` a `meta.MH` object
- `summary` Plot the summary odds ratio?
- `summlabel` Label for the summary odds ratio
- `conf.level` Coverage for confidence intervals
- `colors` see `meta.colors`
- `xlab` x-axis label, default is based on `statistic`
- `...` further arguments to be passed to or from methods.

**Value**

An object of class `meta.MH` with `print`, `plot`, `funnelplot` and `summary` methods.

**Note**

There are at least two other ways to do a fixed effects meta-analysis of binary data. Peto’s method is a computationally simpler approximation to the Mantel-Haenszel approach. It is also possible to weight the individual odds ratios according to their estimated variances. The Mantel-Haenszel method is superior if there are trials with small numbers of events (less than 5 or so in either group)

**Author(s)**

Thomas Lumley

**See Also**

`plot.par.meta.DSL,funnelplot`
Examples
data(catheter)
a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
   names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
a
summary(a)
plot(a)
d <- meta.MH(n.trt, n.ctrl, inf.trt, inf.ctrl, data=catheter,
   names=Name, subset=c(13,6,3,12,4,11,1,14,8,10,2))
d
summary(d)
## plot with par("fg")
plot(d, colors=meta.colors(NULL))

---

meta.summaries  

Meta-analysis based on effect estimates

Description
Computes a summary estimate and confidence interval from a collection of treatment effect estimates and standard errors. Allows fixed or random effects, optional quality weights.

Usage

```r
d <- meta.summaries(d, se, method=c("fixed", "random"), weights=NULL,
   logscale=FALSE, names=NULL, data=NULL, conf.level=0.95, subset=NULL, na.action=na.fail)
```

Arguments

d  Effect estimates

se  standard errors for d

method  Standard errors and default weights from fixed or random-effects?

weights  Optional weights (eg quality weights)

logscale  Effect is on a log scale? (for plotting)

names  labels for the separate studies

data  optional data frame to find variables in

conf.level  level for confidence intervals

subset  Which studies to use
na.action a function which indicates what should happen when the data contain NAs. Defaults to na.fail.

x,object a meta.summaries object

summary Plot the summary odds ratio?

summlabel Label for the summary odds ratio

colors see meta.colors

xlab label for the effect estimate axis.

Details

The summary estimate is a weighted average. If weights are specified they are used, otherwise the reciprocal of the estimated variance is used.

The estimated variance is the square of se for a fixed analysis. For a random analysis a heterogeneity variance is estimated and added.

The variance of a weighted average is a weighted average of the estimated variances using the squares of the weights. This is the square of the summary standard error.

With the default weights these are the standard fixed and random effects calculations.

Value

An object of class meta.summaries, which has print, plot, summary and funnelplot methods.

Author(s)

Thomas Lumley

See Also

meta.DSL, meta.MH, funnelplot, metaplot

Examples

data(catheter)
b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
  names=Name, subset=c(13,6,5,3,12,4,11,1,8,10,2))
d <- meta.summaries(b$logs, b$selogs, names=b$names,
  method="random", logscale=TRUE)
**metaplot**

*Meta-analysis plot (forest plot)*

**Description**

Plot confidence intervals with boxes indicating the sample size/precision and optionally a diamond indicating a summary confidence interval. This function is usually called by plot methods for meta-analysis objects.

**Usage**

```r
metaplot(mn, se, nn=NULL, labels=NULL, conf.level=0.95,
          xlab="Odds ratio", ylab="Study Reference", xlim=NULL,
          summn=NULL, sumse=NULL, sumnn=NULL, summlabel="Summary",
          logeffect=FALSE, lwd=2, boxsize=1,
          zero=as.numeric(logeffect), colors=meta.colors(),
          xaxt="s", logticks=TRUE, ...)
```

**Arguments**

- `mn` point estimates from studies
- `se` standard errors of `mn`
- `nn` precision: box area is proportional to this. `1/se^2` is the default
- `labels` labels for each interval
- `conf.level` Confidence level for confidence intervals
- `xlab` label for the point estimate axis
- `ylab` label for the axis indexing the different studies
- `xlim` the range for the x axis.
- `summn` summary estimate
- `sumse` standard error of summary estimate
- `sumnn` precision of summary estimate
- `summlabel` label for summary estimate
- `logeffect` TRUE to display on a log scale
- `lwd` line width
- `boxsize` Scale factor for box size
- `zero` "Null" effect value
- `xaxt` use "n" for no x-axis (to add a customised one)
- `logticks` if TRUE and logscale, have tick values approximately equally spaced on a log scale.
- `colors` see `meta.colors`
- `...` Other graphical parameters
Value

This function is used for its side-effect.

See Also

*forestplot* for more flexible plots

*plot.meta.DSL, plot.meta.MH, plot.meta.summaries*

Examples

data(catheter)
a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter, names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
metaplot(a$logOR, a$selogOR, nn=a$selogOR^-2, a$names, summn=a$logMH, sumse=a$selogMH, sumnn=a$selogMH^-2, logeffect=TRUE)
metaplot(a$logOR, a$selogOR, nn=a$selogOR^-2, a$names, summn=a$logMH, sumse=a$selogMH, sumnn=a$selogMH^-2, logeffect=TRUE, logticks=FALSE)
## angry fruit salad
metaplot(a$logOR, a$selogOR, nn=a$selogOR^-2, a$names, summn=a$logMH, sumse=a$selogMH, sumnn=a$selogMH^-2, logeffect=TRUE, colors=meta.colors(box="magenta", lines="blue", zero="red", summary="orange", text="forestgreen"))
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