Package 'rmeta'

October 14, 2022

Version 3.0

Author Thomas Lumley

Maintainer Thomas Lumley <t.lumley@auckland.ac.nz>

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.

Title Meta-Analysis

License GPL-2

Imports grid, stats, graphics

NeedsCompilation no

Repository CRAN

Date/Publication 2018-03-20 12:01:32 UTC

R topics documented:

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catheter   *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

```
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

Veenstra D et al (1998) "Efficacy of Antiseptic Impregnated Central Venous Catheters in Preventing Nosocomial Infections: A Meta-analysis" JAMA 281:261-267

Examples

```
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)
```

```
plot(a)
plot(b)
```

---

cochrane   *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 `ith` line in
the cumulative meta-analysis plot is the summary produced by a meta-analysis of the first `i` trials.

Usage

```
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(getOption("na.action")),
   method = c("fixed", "random"), logscale=TRUE)
## S3 method for class 'meta.cum'
plot(x, conf.level = NULL,
    colors = meta.colors(), xlab = NULL,
    summary.line = TRUE, summary.conf = FALSE,
     main="Cumulative meta-analysis", lwd=1, ...)
## S3 method for class 'meta.cum'
summary(object ,conf.level=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
effects	Difference between control and treatment group
stderrs	Standard errors of `effects`
weights	Study weights (see [`meta.summaries`](#))
names	names or labels for studies
data	data frame to interpret variables
subset	subset of studies to include
na.action	How to handle missing values
method	Which meta-analysis method to use
statistic	"OR" for odds ratio or "RR" for relative risk.
logscale	The `effects` values are the logarithms of actual effects (for plotting)

`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<-cummeta(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 <- cummeta.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))
         )
```

```
m<- c(NA,NA,steroid$logOR,NA,steroid$logMH)
l<- m-c(NA,NA,steroid$selogOR,NA,steroid$selogMH)*2
u<- m+c(NA,NA,steroid$selogOR,NA,steroid$selogMH)*2
forestplot(tabletext,m,l,u,zero=0,
   is.summary=c(TRUE,TRUE,rep(FALSE,8),TRUE),
   clip=c(log(0.1),log(2.5)), xlog=TRUE,
   col=meta.colors(box="royalblue",
       line="darkblue", summary="royalblue"))

forestplot(tabletext,m,l,u,zero=0,
    is.summary=c(TRUE,TRUE,rep(FALSE,8),TRUE),
   clip=c(log(0.1),log(2.5)), xlog=TRUE, boxsize=0.75,
   col=meta.colors(box="royalblue",line="darkblue",
    summary="royalblue"))
```

---

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 a 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)
```

---

meta.colors   *Control colours in meta-analysis plot*

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)
```

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="#FFFF50",zero="grey90",text="white",background="darkblue",
        axes="grey90"))
```

---

meta.DSL   *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

```
meta.DSL(ntrt, nctrl, ptrt, pctrl, conf.level=0.95,
         names=NULL, data=NULL, subset=NULL, na.action=na.fail,statistic="OR")
## S3 method for class 'meta.DSL'
summary(object, conf.level=NULL, ...)
## S3 method for class 'meta.DSL'
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

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

---

meta.MH   *Fixed effects (Mantel-Haenszel) meta-analysis*

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

```
meta.MH(ntrt, nctrl, ptrt, pctrl, conf.level=0.95,
        names=NULL, data=NULL, subset=NULL, na.action = na.fail,statistic="OR")
## S3 method for class 'meta.MH'
summary(object, conf.level=NULL, ...)
## 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

```
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)
## S3 method for class 'meta.summaries'
summary(object,conf.level=NULL,...)
## S3 method for class 'meta.summaries'
plot(x,summary=TRUE,summlabel="Summary",
                  conf.level=NULL,colors=meta.colors(),
                  xlab=NULL,logscale=NULL,...)
```

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.
...	further arguments to be passed to or from methods.

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

```
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 ares 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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