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Author Guido Schwarzer <sc@imbi.uni-freiburg.de>
Maintainer Guido Schwarzer <sc@imbi.uni-freiburg.de>
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Description Fixed and random effects meta-analysis. Functions for tests of bias, forest and funnel plot.
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Fleiss93

**Description**

Meta-analysis on Aspirin in Preventing Death after Myocardial Infarction

**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**


**Examples**

data(Fleiss93)
metabin(event.e, n.e, event.c, n.c,
  data=Fleiss93,
  studlab=paste(study, year))

Fleiss93cont

**Description**

Meta-analysis on the Effect of Mental Health Treatment on Medical Utilisation

**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**


**Examples**

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

---

**Olkin95**

*Thrombolytic Therapy after Acute Myocardial Infarction*

**Description**

Meta-analysis on Thrombolytic Therapy after Acute Myocardial Infarction

**Usage**

```r
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


Examples

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

---

**ci**

*Calculation of confidence intervals (normal approximation)*

Description

Calculation of confidence intervals; based on normal approximation.

Usage

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

Arguments

- **TE**: Estimated treatment effect.
- **seTE**: Standard error of treatment estimate.
- **level**: The confidence level required.

Value

List with components

- **TE**: Estimated treatment effect.
- **seTE**: Standard error of treatment estimate.
- **lower**: Lower confidence limits.
- **upper**: Upper confidence limits.
- **zscore**: Test statistic.
- **p**: P-value of test with null hypothesis $TE=0$.
- **level**: The confidence level required.

Note

This function is primarily called from other functions of the library *meta*, e.g. `plot.meta`, `summary.meta`.

Author(s)

Guido Schwarzer (sc@imbi.uni-freiburg.de)
Examples

```r
as.data.frame(ci(170, 10))
as.data.frame(ci(170, 10, 0.99))
```

funnel  
Plot to assess funnel plot asymmetry

Description

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

Usage

```r
funnel(x, y, xlim=NULL, ylim=NULL, xlab=NULL, ylab=NULL, 
comb.f=FALSE, axes=TRUE, 
pch=1, text=NULL, cex=1, col=NULL, 
log="", yaxis="se", sm=NULL, 
level=NULL, ...)
```

```r
radial(x, y, xlim=NULL, ylim=NULL, 
xlab="Inverse of standard error", 
ylab="Standardised treatment effect (z-score)", 
comb.f=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 (mandatory if `x` not of class `meta`).
- `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.f`: A logical indicating whether the pooled fixed 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 color of plotting symbols.
- `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`).
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", "WMD", "SMD" (applies only to function funnel).
- **level**: The confidence level utilised in the plot.
- **...**: Graphical parameters 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.f` is TRUE, the pooled estimate of the fixed effects 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).

**Author(s)**

Guido Schwarzer (sc@imbi.uni-freiburg.de)

**References**


**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), sm="RR", meth="I")

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

funnel(meta1)
##
## Same result as code above:
metabias

##
funnel(metal$TE, metal$seTE, sm="RR")
funnel(metal, comb.f=TRUE, level=0.95)
radial(metal, level=0.95)
par(oldpar)

metabias  

Test for funnel plot asymmetry

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

Usage
metabias(x, seTE, TE.fixed, seTE.fixed,
          method = "rank",
          plotit = FALSE, correct = FALSE)

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).
TE.fixed  Overall treatment estimate (mandatory if x not of class meta and method = "rank").
seTE.fixed  Standard error of overall treatment estimate (mandatory if x not of class meta and method = "rank").
method  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 "rank", "linreg", "mm", or "score".
correct  A logical indicating whether a continuity corrected statistic is used for rank correlation methods "rank" and "count".

Details
If method 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 `method` 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 `method` 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 `method` 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 `method` 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 `method` 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.

Value

A list with class "htest" containing the following components:

- `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.
- `parameter`: 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.

Author(s)

Guido Schwarzer (sc@imbi.uni-freiburg.de)

References


### See Also

funnel, metabin, metacont, metagen

### Examples

```r
data(Olkin95)
meta1 <- metabin(event.e, n.e, event.c, n.c,
data=Olkin95, subset=c(41,47,51,59),
   sm="RR", meth="I")
metabias(meta1)
metabias(meta1, correct=TRUE)
metabias(meta1, method="linreg")
metabias(meta1, method="linreg", plotit=TRUE)
metabias(meta1, method="count")
```

```
##
## Same result:
##
metabias(meta1, method="linreg")$p.value
metabias(meta1$TE, meta1$seTE, method="linreg")$p.value
```

---

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

### Description

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

Usage

```r
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",
      incr = 0.5, allincr = FALSE, addincr = FALSE, allstudies = FALSE,
      MH.exact = FALSE, RR.cochrane = 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 ("RD", "RR", or "OR") is to be used for pooling of studies.
- `incr`: Numerical value 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, `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` = "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 $2*\text{incr}$ instead of $1*\text{incr}$ 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 4, the Cochrane Collaboration’s program for preparing and maintaining Cochrane reviews.
- `warn`: A logical indicating whether the addition of `incr` to studies with zero cell frequencies should result in a warning.

Details

Treatment estimates and standard errors are calculated for each study. For studies with a zero cell count, by default, 0.5 is added to all cell frequencies of these studies. Treatment estimates and
standard errors are only calculated for studies with zero or all events in both groups if \texttt{allstudies} is \texttt{TRUE}.

Both fixed and random effects estimates are calculated. If \texttt{method} is \texttt{"MH"} (default), the Mantel-Haenszel method is used to calculate the fixed effects estimate; if \texttt{method} is \texttt{"Inverse"}, inverse variance weighting is used for pooling; finally, if \texttt{method} is \texttt{"Peto"}, the Peto method is used for pooling. The DerSimonian-Laird estimate is used in the random effects model.

For the Mantel-Haenszel method, by default (if \texttt{MH.exact} is \texttt{FALSE}), 0.5 is added to all cell frequencies of a study with a zero cell count in the calculation of the pooled estimate. This approach is also used in other software, e.g. RevMan 4 and the Stata procedure \texttt{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 (\texttt{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.

\textbf{Value}

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

- \texttt{event.e}, \texttt{n.e}, \texttt{event.c}, \texttt{n.c}, \texttt{studlab},
- \texttt{sm}, \texttt{method}, \texttt{incr}, \texttt{allincr}, \texttt{addincr},
  As defined above.
- \texttt{allstudies}, \texttt{MH.exact}, \texttt{RR.cochrane}, \texttt{warn}

- \texttt{TE}, \texttt{seTE} Estimated treatment effect and standard error of individual studies.
- \texttt{w.fixed}, \texttt{w.random} Weight of individual studies (in fixed and random effects model).
- \texttt{TE.fixed}, \texttt{seTE.fixed} Estimated overall treatment effect and standard error (fixed effect model).
- \texttt{TE.random}, \texttt{seTE.random} Estimated overall treatment effect and standard error (random effects model).
- \texttt{k} Number of studies combined in meta-analysis.
- \texttt{Q} Heterogeneity statistic \texttt{Q}.
- \texttt{tau} Square-root of between-study variance (moment estimator of DerSimonian-Laird).
- \texttt{Q.CMH} Cochrane-Mantel-Haenszel heterogeneity statistic.
- \texttt{sparse} Logical flag indicating if any study included in meta-analysis has any zero cell frequencies.
- \texttt{call} Function call.

\textbf{Author(s)}

Guido Schwarzer (sc@imbi.uni-freiburg.de)
References


DerSimonian R & Laird N (1986), Meta-analysis in clinical trials. *Controlled Clinical Trials, 7*, 177–188.


See Also

funnel, metabias, metacont, metagen, print.meta

Examples

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

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

data(Olkin95)

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

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

**metac**

*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="WMD")
```

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, i.e., `n.e`, `mean.e`, `sd.e`, `n.c`, `mean.c`, and `n.c`.
- `subset`: An optional vector specifying a subset of studies to be used.
- `sm`: A character string indicating which summary measure ("WMD" or "SMD") is to be used for pooling of studies.

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 is used in the random effects model. For the summary measure "SMD", Hedges’ adjusted g is utilised for pooling. The function `metagen` is called internally to calculate individual and overall treatment estimates and standard errors.

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`
- `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.
**metacum**

Q  
Heterogeneity statistic.

tau  
Square-root of between-study variance (moment estimator of DerSimonian-Laird).

method  
Pooling method: "Inverse".

call  
Function call.

Author(s)

Guido Schwarzer (sc@imbi.uni-freiburg.de)

References


See Also

metabim, 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

---

**metacum**  
*Cumulative meta-analysis*

Description

Performs a cumulative meta-analysis.

Usage

metacum(x, pooled="fixed", sortvar)

Arguments

x  
An object of class meta.

pooled  
A character string indicating whether a fixed or random effects model is used for pooling. Either "fixed" or "random", can be abbreviated.

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

A cumulative meta-analysis is performed. Studies are included sequentially as defined by sortvar.

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.
- **studlab**: Study label describing addition of studies.
- **p.value**: P-value for test of overall effect.
- **I2**: Heterogeneity statistic I2.
- **sm**: Summary measure.
- **method**: Method used for pooling.
- **k**: Number of studies combined in meta-analysis.
- **pooled**: As defined above.

Author(s)

Guido Schwarzer ⟨sc@imbi.uni-freiburg.de⟩

References


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", meth="I")

meta1

metacum(meta1)
metacum(meta1, pooled="random")
plot(metacum(meta1, pooled="random"))
Generic inverse variance meta-analysis

Description

Fixed and random effects meta-analysis based on estimates and their standard errors; inverse variance weighting is used for pooling.

Usage

```r
metagen(TE, seTE, studlab, data=NULL, subset=NULL, sm="")
```

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", "WMD", "SMD".

Details

Generic method for meta-analysis, only treatment estimates and their standard error are needed. The method is useful, e.g., for pooling of log hazard ratios. The inverse variance method is used for pooling. Random effects estimate is based on the DerSimonian-Laird method.

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**: As defined above.
- **sm**: 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).
- **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.
- **tau**: Square-root of between-study variance (moment estimator of DerSimonian-Laird).
- **method**: Pooling method: "Inverse".
- **call**: Function call.
**metainf**

*Author(s)*

Guido Schwarzer (sc@imbi.uni-freiburg.de)

**References**


**See Also**

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

**Examples**

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

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

---

**Description**

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

**Usage**

```r
metainf(x, pooled="fixed", sortvar)
```

**Arguments**

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

**Details**

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

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.
- **studlab** Study label describing omission of studies.
- **p.value** P-value for test of overall effect.
- **I2** Heterogeneity statistic I2.
- **sm** Summary measure.
- **method** Method used for pooling.
- **k** Number of studies combined in meta-analysis.
- **pooled** As defined above.

Author(s)

Guido Schwarzer (sc@imbi.uni-freiburg.de)

References


See Also

metabin, metacont, print.meta

Examples

data(Fleiss93)
metal <- metabin(event.e, n.e, event.c, n.c,
data=Fleiss93, studlab=study,
sm="RR", meth="I")
metal
metainf(metal)
metainf(metal, pooled="random")
plot(metainf(metal, pooled="random"))
Plot function for objects of class meta

Description

Draws a forest plot in the active graphics window.

Usage

```r
## S3 method for class 'meta':
plot(x, byvar, bylab, sortvar, studlab = TRUE, level = 0.95,
     level.comb = level, comb.f = FALSE, comb.r = FALSE,
     text.f = "Fixed effect model", text.r = "Random effects model",
     lty.f = 2, lty.r = 3, xlab=NULL, xlim, ylim, lwd = 1, cex = 1,
     cex.comb = 1.2 * cex, cex.axis=cex, cex.lab=cex,
     log = ifelse(x$sm == "RR" | x$sm == "OR" | x$sm == "HR", "x", ""),
     axes = TRUE, allstudies = TRUE, weight = "fixed", scale.diamond = 1,
     scale.square = 1, col.i = "black", ...
)
```

Arguments

- `x` : An object of class `meta`.
- `byvar` : An optional vector containing grouping information (must be of same length as `x$TE`).
- `bylab` : A character string with a label for the grouping variable.
- `sortvar` : An optional vector used to sort the individual studies (must be of same length as `x$TE`).
- `studlab` : A logical indicating whether study labels should be printed in the graph.
- `level` : The level used to calculate confidence intervals for individual studies.
- `level.comb` : The level used to calculate confidence intervals for pooled estimates.
- `comb.f` : A logical indicating whether the pooled fixed effect estimate should be plotted.
- `comb.r` : A logical indicating whether the pooled random effects estimate should be plotted.
- `text.f` : A character string used in the plot to label the pooled fixed effects estimate.
- `text.r` : A character string used in the plot to label the pooled random effects estimate.
- `lty.f` : Line type (pooled fixed effect estimate).
- `lty.r` : 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" and "fixed", i.e., plot symbols have the same size for all studies or represent the weight of the study in the fixed effect 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 parameters as in par may also be passed as arguments.
col.i The color for individual study results and confidence limits.

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

Author(s)
Guido Schwarzer ⟨sc@imbi.uni-freiburg.de⟩

See Also
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", meth="I")
oldpar <- par(mfrow=c(2, 2))
print.meta

plot(metal)
plot(metal, byvar=c(1,2,1,2), bylab="label")
plot(metal, 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=0.95, level.comb=level,
  details=FALSE, ma=TRUE, digits=max(0, .Options$digits - 3), ...)

## S3 method for class 'meta':
summary(object, byvar, bylab, bystud=FALSE, level.comb=0.95, ...)

## S3 method for class 'summary.meta':
print(x, digits = max(0, .Options$digits - 3),
  print.byvar = TRUE, ...)

Arguments

x
  An object of class meta 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$TE).
level
  The level used to calculate confidence intervals for individual studies.
level.comb
  The level used to calculate confidence intervals for pooled estimates.
details
  A logical indicating whether further details of individual studies should be printed.
ma
  A logical indicating whether the summary results of the meta-analysis should be printed.
byvar
  An optional vector containing grouping information (must be of same length as x$TE).
bylab
  A character string with a label for the grouping variable.
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.
...
  other arguments
Value

A list is returned by the function `summary.meta` with the following elements:

- **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).
- **random**: A list with elements TE, lower, upper, seTE, z, p, level, scale.
- **k**: Number of studies combined in meta-analysis.
- **Q**: Heterogeneity statistic Q.
- **tau**: Square-root of between-study variance (moment estimator of DerSimonian-Laird).
- **H**: Heterogeneity statistic H (a list with elements TE, lower, upper).
- **I2**: Heterogeneity statistic I2 (a list with elements TE, lower, upper).
- **k.all**: Total number of trials.
- **Q.CMH**: Cochrane-Mantel-Haenszel heterogeneity statistic.
- **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**: Results 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.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.

Author(s)

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

References


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="label")
Import RevMan 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.
<table>
<thead>
<tr>
<th>function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>Type of outcome. D = dichotomous, C = continuous, P = IPD.</td>
</tr>
<tr>
<td>outclab</td>
<td>Outcome label.</td>
</tr>
<tr>
<td>graph.exp</td>
<td>Graph label for experimental group.</td>
</tr>
<tr>
<td>graph.cont</td>
<td>Graph label for control group.</td>
</tr>
<tr>
<td>label.exp</td>
<td>Label for experimental group.</td>
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<tr>
<td>label.cont</td>
<td>Label for control group.</td>
</tr>
<tr>
<td>complab</td>
<td>Comparison label.</td>
</tr>
</tbody>
</table>

**Author(s)**

Guido Schwarzer (sc@imbi.uni-freiburg.de)

**References**


**See Also**

`metabin`, `metacont`, `metagen`

**Examples**

```r
## Locate MTV-data file "FLEISS93.MTV" in sub-directory of package "meta"
##
filename <- paste(searchpaths()[seq(along=search())][search()==
"package:meta"], "/data/FLEISS93.MTV", sep="")
##
fleiss93.cc <- read.mtv(filename)
##
## Same result: 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))
```
**trimfill**

*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**

```r
trimfill(x, seTE, left=NULL, ma.fixed=TRUE,
    type="L", n.iter.max=50,
    sm=NULL, studlab=NULL,
    silent=TRUE)
```

**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`).
- `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(..., meth="linreg")) is used to determine whether trials are missing on the left or right side.
- `ma.fixed` A logical indicating whether a fixed 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", "WMD", "SMD"; ignored if `x` is of class `meta`.
- `studlab` An optional vector with study labels; ignored if `x` is of class `meta`.
- `silent` A logical indicating whether basic information on iterations shown.

**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.

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

As defined above.
type, n.iter.max

TE, seTE
w.fixed, w.random

Estimated treatment effect and standard error of individual studies.

Weight of individual studies (in fixed and random effects model).

TE.fixed, seTE.fixed
w.fixed, w.random

Estimated overall treatment effect and standard error (fixed effect model).

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 (moment estimator of DerSimonian-Laird).

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


See Also

metagen, metabias, funnel

Examples

data(Fleiss93)
metal <- metabin(event.e, n.e, event.c, n.c, data=Fleiss93, sm="OR")

trimfill <- trimfill(metal)

summary(trimfill)

funnel(trimfill, pch=ifelse(trimfill, 1, 16))
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