

# Package ‘metasens’

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**Title** Statistical Methods for Sensitivity Analysis in Meta-Analysis

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**URL** <https://github.com/guido-s/metasens>

<https://link.springer.com/book/10.1007/978-3-319-21416-0>

**Description** The following methods are implemented to evaluate how sensitive the results of a meta-analysis are to potential bias in meta-analysis and to support Schwarzer et al. (2015) <[DOI:10.1007/978-3-319-21416-0](https://doi.org/10.1007/978-3-319-21416-0)>, Chapter 5 'Small-Study Effects in Meta-Analysis':

- Copas selection model described in Copas & Shi (2001) <[DOI:10.1177/096228020101000402](https://doi.org/10.1177/096228020101000402)>;
- limit meta-analysis by Rücker et al. (2011) <[DOI:10.1093/biostatistics/kxq046](https://doi.org/10.1093/biostatistics/kxq046)>;
- upper bound for outcome reporting bias by Copas & Jackson (2004) <[DOI:10.1111/j.0006-341X.2004.00161.x](https://doi.org/10.1111/j.0006-341X.2004.00161.x)>;
- imputation methods for missing binary data by Gamble & Hollis (2005) <[DOI:10.1016/j.jclinepi.2004.09.013](https://doi.org/10.1016/j.jclinepi.2004.09.013)> and Higgins et al. (2008) <[DOI:10.1177/1740774508091600](https://doi.org/10.1177/1740774508091600)>;
- LFK index test and Doi plot by Furuya-Kanamori et al. (2018) <[DOI:10.1097/XEB.0000000000000141](https://doi.org/10.1097/XEB.0000000000000141)>.

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metasens-package	<i>metasens: Brief overview of methods and general hints</i>
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### Description

R package **metasens** provides advanced statistical methods to model and adjust bias in meta-analysis and supports Schwarzer et al. (2015), Chapter 5 "Small-Study Effects in Meta-Analysis" <https://link.springer.com/book/10.1007/978-3-319-21416-0>.

### Details

R package **metasens** is an add-on package for **meta** providing the following meta-analysis methods:

- Copas selection model (function `copas`) described in Copas & Shi (2001) and evaluated in Schwarzer et al., 2010);
- limit meta-analysis (`limitmeta`) by Rucker et al. (2011);
- upper bound for outcome reporting bias (`orbbound`) described in Copas & Jackson (2004);
- imputation methods for missing binary data (`metamiss`) described in Gamble & Hollis (2005) and Higgins et al. (2008).

Furthermore, functions and datasets from **metasens** are utilised in Schwarzer et al. (2015), Chapter 5 "Small-Study Effects in Meta-Analysis", <https://link.springer.com/book/10.1007/978-3-319-21416-0>.

Type `help(package = "metasens")` for a listing of R functions available in **metasens**.

Type citation("metasens") on how to cite **metasens** in publications.

To report problems and bugs

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

The development version of **metasens** is available on GitHub <https://github.com/guido-s/metasens>.

### Author(s)

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

### References

Copas J, Jackson D (2004): A bound for publication bias based on the fraction of unpublished studies. *Biometrics*, **60**, 146–53

Copas JB, Shi JQ (2001): A sensitivity analysis for publication bias in systematic reviews. *Statistical Methods in Medical Research*, **10**, 251–65

Gamble C, Hollis S (2005): Uncertainty method improved on best–worst case analysis in a binary meta-analysis. *Journal of Clinical Epidemiology*, **58**, 579–88

Higgins JPT, White IR, Wood AM (2008): Imputation methods for missing outcome data in meta-analysis of clinical trials. *Clinical Trials*, **5**, 225–39

Rücker G, Schwarzer G, Carpenter JR, Binder H, Schumacher M (2011): Treatment-effect estimates adjusted for small-study effects via a limit meta-analysis. *Biostatistics*, **12**, 122–42

Schwarzer G, Carpenter J, Rücker G (2010): Empirical evaluation suggests Copas selection model preferable to trim-and-fill method for selection bias in meta-analysis. *Journal of Clinical Epidemiology*, **63**, 282–8

Schwarzer G, Carpenter JR, Rücker G (2015): *Meta-Analysis with R (Use-R!)*. Springer International Publishing, Switzerland

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copas

*Copas selection model analysis*

---

### Description

Perform a Copas selection model analysis for selection bias in meta-analysis.

### Usage

```
copas(
  x,
  level.ma = x$level.ma,
  gamma0.range = NULL,
  gamma1.range = NULL,
```

```

ngrid = 20,
nlevels = 10,
levels = NULL,
slope = NULL,
left = NULL,
rho.bound = 0.9999,
sign.rsb = 0.1,
backtransf = x$backtransf,
title = x$title,
complab = x$complab,
outclab = x$outclab,
silent = TRUE,
warn = options()$warn
)

```

### Arguments

<code>x</code>	An object of class <code>meta</code> , obtained from one of the functions <code>metabin</code> , <code>metacont</code> and <code>metagen</code> in the package <code>meta</code> .
<code>level.ma</code>	The level used to calculate confidence intervals for pooled estimates.
<code>gamma0.range</code>	(Advanced users only) A numerical vector of length two specifying the range of <code>gamma0</code> values the program will explore. The parameter <code>gamma0</code> is the constant in the probit selection model for study publication. Thus, the cumulative normal of <code>gamma0</code> is approximately the probability that a small study is published (in non-technical terms <code>gamma0</code> relates to the probability of publishing a small study, although its values are not restricted to the range $[0,1]$ ; larger values correspond to higher probabilities of publishing a small study). Most users will not need to specify a range for this parameter. When no argument is specified, the program uses an algorithm to determine a suitable range. This is based on the range of treatment effect standard errors in the meta-analysis, and is described in more detail below.
<code>gamma1.range</code>	(Advanced users only) A numerical vector of length two specifying the range of <code>gamma1</code> values the program will explore. The parameter <code>gamma1</code> is the coefficient of study precision ( $1/\text{standard error}$ ) in the probit selection model for study publication (in non-technical terms <code>gamma1</code> relates to the rate at which the probability of publishing a study increases as the standard error of the treatment effect it reports decreases; larger values correspond to higher probabilities of publishing a small study). Most users will not need to specify a range for this parameter. When no argument is specified, the program uses an algorithm to determine a suitable range. This is based on the range of treatment effect standard errors in the meta-analysis, and is described in more detail below.
<code>ngrid</code>	The program fits the Copas selection model over a grid defined by the range of values of <code>gamma0</code> and <code>gamma1</code> specified in the previous two arguments. This parameter fixes the square-root of the number of points in the grid.
<code>nlevels</code>	(Advanced users only). Fitting the Copas model over the grid specified by the previous three arguments results in a treatment estimate at every point in the

grid. These can then be displayed on a contour plot where contours of treatment effect (z-axis) are shown by `gamma0` (x-axis) and `gamma1` (y-axis). This argument specifies the number of contour lines that will be drawn.

**Note**

(i) Calculations for the contour plot are performed by the function `copas`, so this argument has no effect in the `plot` function.

(ii) If a large number of contour lines are desired, then you may wish to consider increasing the grid size (argument `ngrid` above).

Leave this option unspecified if you are using the option `levels` below.

`levels` A numerical vector of treatment values for which contour lines will be drawn. In more detail, fitting the Copas model over the grid specified by the arguments `gamma0.range`, `gamma1.range` and `ngrid` results in a treatment estimate at every point in the grid. These are then displayed on a contour plot where contours of treatment effect (z-axis) are shown by `gamma0` (x-axis) and `gamma1` (y-axis). This argument is a numerical vector which specifies the treatment effects for which contour lines will be drawn.

It is usually not a good idea to set this argument for initial runs, as one does not know the range of treatment values that the contour plot will cover, and treatment values which do not correspond to values in the contour plot (defined by the range of `gamma0` and `gamma1`) will not be plotted.

**Note**

(i) Calculations for the contour plot are performed by the function `copas`, so this argument has no effect in the `plot` function.

(ii) Contours will not be drawn if a large number of contour lines are desired, then you may wish to consider increasing the grid size (argument `ngrid` above).

Leave this option unspecified if you are using the option `nlevels` above.

`slope` A numeric providing the slope of the line approximately orthogonal to contours in the contour plot. If the argument `slope` is `NULL` (default) the program seeks to estimate the slope of the contours in the region of the maximum, which are usually approximately parallel. Most users will leave the argument `slope` unspecified, at least for the first analysis of a data set, but in certain cases setting it manually can improve the results.

`left` A logical indicating whether the cause of any selection bias is due to missing studies on the left or right of the funnel plot: left hand side if `left=TRUE`, right hand side if `left=FALSE`. This information is needed in order to be sure the test for presence of residual selection bias is calculated correctly. If not set, the linear regression test for funnel plot asymmetry (i.e., function `metabias(..., meth="linreg")`) is used to determine whether studies are missing on the left or right hand side. In the majority of cases this will work correctly.

`rho.bound` (Advanced users only) A number giving the upper bound for the correlation parameter `rho` (see details below). This must be  $< 1$ , and usually  $> 0.95$ . The lower bound is calculated as  $-(\text{the upper bound})$ .

`sign.rsb` The significance level for the test of residual selection bias (between 0 and 1).

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

<code>title</code>	Title of meta-analysis / systematic review.
<code>complab</code>	Comparison label.
<code>outclab</code>	Outcome label.
<code>silent</code>	A logical indicating whether information on progress in fitting the Copas selection model should be printed: <code>silent=TRUE</code> , do not print information (the default); <code>silent=FALSE</code> , print information.
<code>warn</code>	A number setting the handling of warning messages. It is not uncommon for numerical problems to be encountered during estimation over the grid of ( <code>gamma0</code> , <code>gamma1</code> ) values. Usually this does not indicate a serious problem. This option specifies what to do with warning messages. <code>warn=-1</code> : ignore all warnings; <code>warn=0</code> (the default): store warnings till function finishes; if there are less than 10, print them, otherwise print a message saying warning messages were generated; <code>warn=1</code> : print warnings as they occur; <code>warn=2</code> : stop the function when the first warning is generated. For further details see <code>help(options)</code> .

## Details

The program takes an object of class `meta`, which is most easily created by an analysis using one of the functions `metabin`, `metacont` and `metagen` in the package `meta`, performs a 'Copas selection model analysis' and presents a graphical and tabular summary of the results. An object of class `copas` is created and this can be used to recreate the results table and graphs subsequently, without re-running the analysis, using the `print`, `summary` and `plot` function.

Conduct a Copas selection model analysis to investigate, and attempt to correct for, selection / publication bias in a meta-analysis.

The Copas selection model consists of two models, which are fitted jointly. The first is the usual random effects meta-analysis model, and the second is a selection model, where study  $i$  is selected for publication if  $Z > 0$ , where

$$Z = \text{gamma0} + \text{gamma1} / (\text{SE}(i)) + \text{delta}(i)$$

The error  $\text{delta}(i)$  is correlated with the error in the random effects meta-analysis, with correlation  $\rho$ . If  $\rho = 0$ , the model corresponds to the usual random effects meta-analysis. As  $\rho$  moves from 0 to 1, studies with larger treatment estimates are more likely to be selected/published.

The software chooses a grid of `gamma0` and `gamma1` values, corresponding to a range of selection / publication probabilities for the study with the largest treatment effect standard error (often the smallest study). For each value in this grid, the treatment effect is estimated using the function `optim`. This information is used to produce the contour plot (top right panel of output from `plot.copas`).

Contours of constant treatment effect are usually locally parallel. The software estimates the slope of these contours, and combines this information with other parameter estimates from the model to explore (i) how the treatment estimate, and its standard error, change with increasing selection (bottom left panel, `plot.copas`) and (ii) how much selection needs to be accounted for before any remaining asymmetry in the funnel plot is likely to have occurred by chance (bottom right panel, `plot.copas`).

A table of results can be produced by the function `summary.copas`. A more detail output is provided by the function `print.copas`.

For a fuller description of the model, our implementation and specifically our approach to estimating the locally parallel contours, see Carpenter et al. (2009) and Schwarzer et al. (2010).

**Value**

An object of class `copas` with corresponding `print`, `summary`, and `plot` function. The object is a list containing the following components:

<code>TE</code>	Vector of treatment effects plotted in treatment effect plot
<code>seTE</code>	Vector of standard error of TE
<code>TE.random</code>	Usual random effects estimate of treatment effect
<code>seTE.random</code>	Standard error of <code>TE.random</code>
<code>lower.random</code>	Lower confidence limit of usual random effects estimate
<code>upper.random</code>	Upper confidence limit of usual random effects estimate
<code>statistic.random</code>	Test statistic of an overall effect (usual random effects model)
<code>pval.random</code>	P-value of test of overall effect (usual random effects model)
<code>TE.adjust</code>	Adjusted random effects estimate from Copas selection model
<code>seTE.adjust</code>	Standard error of <code>TE.adjust</code>
<code>lower.adjust</code>	Lower confidence limit of adjusted treatment estimate
<code>upper.adjust</code>	Upper confidence limit of adjusted treatment estimate
<code>statistic.adjust</code>	Test statistic of an overall effect (Copas selection model)
<code>pval.adjust</code>	P-value of test of overall effect (Copas selection model)
<code>left</code>	Whether selection bias expected on left or right
<code>rho.bound</code>	Bound on rho
<code>gamma0.range</code>	Range of <code>gamma0</code> (see help on <code>copas</code> arguments above)
<code>gamma1.range</code>	Range of <code>gamma1</code> (see help on <code>copas</code> arguments above)
<code>slope</code>	Slope of line approximately orthogonal to contours in contour plot
<code>regr</code>	A list containing information on regression lines fitted to contours in contour plot
<code>ngrid</code>	Square root of grid size
<code>nlevels</code>	Number of contour lines
<code>gamma0</code>	Vector of <code>gamma0</code> values at which model fitted (determined by <code>gamma0.range</code> and <code>grid</code> ). x-axis values for contour plot
<code>gamma1</code>	vector of <code>gamma1</code> values at which model fitted (determined by <code>gamma1.range</code> and <code>grid</code> ). y-axis values for contour plot
<code>TE.contour</code>	Treatment values (ie z-axis values) used to draw contour plot.
<code>x.slope</code>	x coordinates for 'orthogonal line' in contour plot
<code>y.slope</code>	y coordinates for 'orthogonal line' in contour plot
<code>TE.slope</code>	Vector of treatment values plotted in treatment effect plot
<code>seTE.slope</code>	Standard error of <code>TE.slope</code>
<code>rho.slope</code>	Vector of estimated rho values corresponding to treatment estimates in <code>TE.slope</code>

tau.slope	Vector of estimated heterogeneity values corresponding to treatment estimates in TE.slope
loglik1	Vector of log-likelihood values corresponding to treatment estimates in TE.slope
conv1	Numerical vector indicating convergence status for each treatment estimate in TE.slope - see parameter convergence in function optim
message1	Character vector - translation of conv1
loglik2	Vector of log-likelihoods from fitting model to evaluate presence of residual selection bias
conv2	Numerical vector indicating convergence status for models to evaluate presence of residual selection bias - see parameter convergence in function optim
message2	Character vector - translation of conv2
publprob	Vector of probabilities of publishing the smallest study, used in x-axis of bottom two panels in function plot.copas
pval.rsb	P-values for tests on presence of residual selection bias, plotted in bottom right panel in plot.copas
sign.rsb	The significance level for the test of residual selection bias
N.unpubl	Approximate number of studies the model suggests remain unpublished
sm	Effect measure (e.g., for binary data, OR - odds ratio, RR - risk ratio, RD - risk difference, AS - arcsin difference)
title	Title of meta-analysis / systematic review.
complab	Comparison label.
outclab	Outcome label.
call	Call to copas function
version	Version of R package metasens used to create object.
x	Details of meta-analysis object used as input into copas function

### Author(s)

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### References

- Carpenter JR, Schwarzer G, Rücker G, Küntler R (2009): Empirical evaluation showed that the Copas selection model provided a useful summary in 80% of meta-analyses. *Journal of Clinical Epidemiology*, **62**, 624–31
- Copas J (1999): What works?: Selectivity models and meta-analysis. *Journal of the Royal Statistical Society, Series A*, **162**, 95–109
- Copas J, Shi JQ (2000): Meta-analysis, funnel plots and sensitivity analysis. *Biostatistics*, **1**, 247–62
- Copas JB, Shi JQ (2001): A sensitivity analysis for publication bias in systematic reviews. *Statistical Methods in Medical Research*, **10**, 251–65
- Schwarzer G, Carpenter J, Rücker G (2010): Empirical evaluation suggests Copas selection model preferable to trim-and-fill method for selection bias in meta-analysis. *Journal of Clinical Epidemiology*, **63**, 282–8

**See Also**

[plot.copas](#), [summary.copas](#), [metabias](#), [metagen](#), [funnel](#)

**Examples**

```
data(Fleiss1993bin, package = "meta")

# Perform meta-analysis
# (Note d.asp indicates deaths, n.asp total in aspirin group;
#      d.plac indicates deaths, n.plac total in placebo group)
#
m1 <- metabin(d.asp, n.asp, d.plac, n.plac, data = Fleiss1993bin, sm = "OR")
m1

# Perform a basic Copas selection model analysis
#
cop1 <- copas(m1)
plot(cop1)
cop1
#
# Interpretation:
#
# a. The initial meta-analysis shows the common and random effects
#     pooled ORs differ; consistent with asymmetry in the funnel
#     plot and possible selection bias. Both common effect and random
#     effects model show a significant treatment effect in this
#     dataset.
#
# b. Plotting the copas analysis shows
#
# (i) funnel plot: asymmetry indicates possible selection bias.
#
# (ii) contour plot treatment effect declines steadily as selection
#      increases (no selection, top right, log OR < -0.12;
#      increasing selection as move to left of plot, log OR rises
#      to -0.03.
#
# (iii) Treatment effect plot suggests that even with no selection,
#       p-value for treatment effect is larger than 0.05 which is
#       different from the result of the usual random effects model
#       (see output of summary(cop1). This difference is due to the
#       use of different methods to estimate the between-study
#       variance: maximum-likelihood in Copas analysis compared to
#       method-of-moments in usual random effects model. The
#       p-value for treatment effect is increasing with increasing
#       selection.
#
# (iv) P-value for residual selection bias plot: this shows that
#      even with no selection bias, the p-value for residual
#      selection bias is non-significant at the 10% level. As
#      expected, as selection increases the p-value for residual
```

```

# selection bias increases too.

# Repeat the same example, setting several arguments of the copas
# function:
#
cop2 <- copas(m1,
  gamma0.range = c(-0.5, 2.1), # range of gamma0 parameter
  gamma1.range = c(0, 0.08), # range of gamma1 parameter
  ngrid = 20, # specify a 20x20 grid (finer than default)
  levels = c(-0.13, -0.12, -0.1, -0.09,
    -0.07, -0.05, -0.03), # specify contour lines
  slope = 0.2, # specify slope of 'orthogonal' line in contour plot
  left = FALSE, # as any selection bias due to missing studies on right
  rho.bound = 0.998, # constrain rho between [-0.998, 0.998]
  silent = FALSE, # update user on progress
  warn = -1 # suppress warning messages
)
plot(cop2)
#
# Print table of results used to draw treatment effect plot:
#
cop2

```

---

Crowther2003

*Aspirin after Myocardial Infarction*


---

### Description

Meta-analysis on phenobarbital prior to preterm birth for preventing neonatal periventricular haemorrhage

### Format

A data frame with the following columns:

<i>study</i>	study label
<i>pvh.e</i>	number of periventricular haemorrhages in experimental group
<i>n.e</i>	number of observations in experimental group
<i>pvh.c</i>	number of periventricular haemorrhages in control group
<i>n.c</i>	number of observations in control group

### Source

Crowther CA, Henderson-Smart DJ (2003): Phenobarbital prior to preterm birth for preventing neonatal periventricular haemorrhage. *Cochrane Database of Systematic Reviews*, CD000164

**Examples**

```
data(Crowther2003)
metabin(pvh.e, n.e, pvh.c, n.c, data = Crowther2003, studlab = study)
```

doiplot

*Doi plot for Asymmetry***Description**

Implementation of the Doi plot proposed by Furuya-Kanamori et al. (2018) to evaluate bias in meta-analysis.

**Usage**

```
doiplot(
  TE,
  seTE,
  xlim,
  ylim,
  xlab = "ES",
  ylab = "|Z-score|",
  lfkindex = TRUE,
  pos.lfkindex = "topleft",
  ...
)
```

**Arguments**

TE	An object of class lfkindex or estimated treatment effect in individual studies.
seTE	Standard error of estimated treatment effect (mandatory if TE 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.
lfkindex	A logical indicating whether LFK index should be printed.
pos.lfkindex	A character string with position of text with LFK index (see <a href="#">legend</a> ).
...	Additional arguments (passed on to <a href="#">plot.default</a> ).

**Author(s)**

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**References**

Furuya-Kanamori L, Barendregt JJ, Doi SAR (2018): A new improved graphical and quantitative method for detecting bias in meta-analysis. *International Journal of Evidence-Based Healthcare*, **16**, 195–203

**See Also**

[lfkindex](#), [metabias](#), [funnel.meta](#)

**Examples**

```
# Example from Furuya-Kanamori et al. (2018)
#
pain <- data.frame(SMD = c(-4.270, -1.710, -0.580, -0.190, 0.000),
                  varSMD = c(0.158, 0.076, 0.018, 0.022, 0.040))

lfk.pain <- lfkindex(SMD, sqrt(varSMD), data = pain)
lfk.pain

doiplot(lfk.pain)
```

---

forest.orbbound

*Forest plot for orbbound object (bound for outcome reporting bias)*


---

**Description**

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

**Usage**

```
## S3 method for class 'orbbound'
forest(
  x,
  common = x$x$common,
  random = x$x$random,
  text.common = "CE model",
  text.random = "RE model",
  smlab = NULL,
  leftcols = c("studlab", "maxbias"),
  leftlabs = c("Missing\nstudies", "Maximum\nbias"),
  backtransf = x$backtransf,
  digits = max(3, .Options$digits - 3),
  warn.deprecated = gs("warn.deprecated"),
  ...
)
```

**Arguments**

x	An object of class orbound.
common	A logical indicating whether sensitivity analysis for common effect model should be plotted.
random	A logical indicating whether sensitivity analysis for random effects model should be plotted.
text.common	A character string used in the plot to label subgroup with results for common effect model.
text.random	A character string used in the plot to label subgroup with results for random effects model.
smlab	A label printed at top of figure. If only results for either common effect or random effects model is plotted, text indicates which model was used.
leftcols	A character vector specifying (additional) columns to be plotted on the left side of the forest plot or a logical value (see <a href="#">forest.meta</a> help page for details).
leftlabs	A character vector specifying labels for (additional) columns on left side of the forest plot (see <a href="#">forest.meta</a> help page for details).
backtransf	A logical indicating whether results should be back transformed in printouts and plots. If backtransf=TRUE (default), results for sm="OR" are printed as odds ratios rather than log odds ratio, for example.
digits	Minimal number of significant digits, see print.default.
warn.deprecated	A logical indicating whether warnings should be printed if deprecated arguments are used.
...	Additional arguments for <a href="#">forest.meta</a> function and to catch deprecated arguments.

**Details**

A forest plot, also called confidence interval plot, is drawn in the active graphics window.

For relative effect measures, e.g., 'RR', 'OR', and 'HR', the column labeled "Maximum bias" contains the relative bias, e.g. a value of 1.10 means a maximum overestimation by 10 percent. If backtransf=FALSE for these summary measures, maximum bias is instead printed as absolute bias.

Internally, R function [forest.meta](#) is called to create a forest plot. For more information see help page of the [forest.meta](#) function.

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**See Also**

[orbound](#), [print.orbound](#)

## Examples

```
data(Fleiss1993bin, package = "meta")

m1 <- metabin(d.asp, n.asp, d.plac, n.plac, data = Fleiss1993bin, sm = "OR")

orb1 <- orbbound(m1, k.suspect = 1:5)
print(orb1, digits = 2)
forest(orb1, xlim = c(0.7, 1.5))
## Not run: forest(orb1, backtransf = FALSE)
```

---

funnel.limitmeta

*Funnel plot for limit meta-analysis*

---

## Description

Draws a funnel plot in the active graphics window.

## Usage

```
## S3 method for class 'limitmeta'
funnel(
  x,
  pch = 21,
  cex = 1,
  col = "black",
  bg = "darkgray",
  lwd = 1,
  show.ci.adjust = FALSE,
  pch.adjust = 18,
  cex.adjust = 1.5,
  col.adjust = "gray",
  bg.adjust = "gray",
  line = TRUE,
  xmin.line,
  xmax.line,
  lty.line = 1,
  lwd.line = lwd,
  col.line = "gray",
  shrunken = FALSE,
  pch.shrunken = 22,
  cex.shrunken = 1,
  col.shrunken = "black",
  bg.shrunken = "white",
  lty.connect = 1,
  lwd.connect = 0.8,
  col.connect = "black",
```

```

    backtransf = x$backtransf,
    ...
)

```

### Arguments

x	An object of class <code>limitmeta</code> .
pch	The plotting symbol used for individual studies.
cex	The magnification to be used for plotting symbol.
col	A vector with colour of plotting symbols.
bg	A vector with background colour of plotting symbols (only used if pch in 21 : 25).
lwd	The line width for confidence intervals (see <a href="#">funnel</a> ).
show.ci.adjust	A logical indicating whether to show the confidence interval of the adjusted estimate.
pch.adjust	The plotting symbol used for the adjusted effect estimate.
cex.adjust	The magnification to be used for the plotting symbol of the adjusted effect estimate.
col.adjust	Colour of plotting symbol for adjusted effect estimate.
bg.adjust	Background colour of plotting symbol for adjusted effect estimate.
line	A logical indicating whether adjusted regression line should be plotted.
xmin.line	Minimal value for the adjusted regression line (on x-axis).
xmax.line	Maximum value for the adjusted regression line (on x-axis).
lty.line	Line type of the adjusted regression line.
lwd.line	The line width of the adjusted regression line.
col.line	Color of the adjusted regression line.
shrunken	A logical indicating whether shrunken treatment estimates should be plotted.
pch.shrunken	The plotting symbol used for shrunken effect estimates.
cex.shrunken	The magnification to be used for the plotting symbol of the shrunken effect estimates.
col.shrunken	Colour of plotting symbol for shrunken effect estimates.
bg.shrunken	Background colour of plotting symbol for shrunken effect estimates.
lty.connect	Line type for line connecting original and shrunken treatment estimates.
lwd.connect	The line width of the connecting lines.
col.connect	Color of the connecting lines.
backtransf	A logical indicating whether results should be back transformed in printouts and plots. If <code>backtransf=TRUE</code> (default), results for <code>sm="OR"</code> are printed as odds ratios rather than log odds ratio, for example.
...	Additional arguments for <a href="#">funnel</a> function.

**Details**

A funnel plot is drawn in the active graphics window. In addition this function adds the adjusted effect estimate as well as a nonlinear regression line (also called adjusted regression line) if argument `line` is TRUE. The adjusted regression line is representing the dependence of the treatment effect estimate on the standard error across studies. The adjusted regression line is only plotted in addition to the adjusted treatment effect if argument `method.adjust="beta0"` (default) has been used in the `limitmeta` function.

If argument `shrunk` is TRUE the shrunk effect estimates are also plotted. Lines are connecting original and shrunk effect estimates.

Internally, R function `funnel.meta` is called to create a funnel plot. For more information see help page of the `funnel` function.

**Author(s)**

Guido Schwarzer <sc@imbi.uni-freiburg.de>, Gerta Rücker <ruecker@imbi.uni-freiburg.de>

**See Also**

[limitmeta](#), [funnel](#)

**Examples**

```
data(Moore1998)
m1 <- metabin(succ.e, nobs.e, succ.c, nobs.c,
  data = Moore1998, sm = "OR", method = "Inverse")
l1 <- limitmeta(m1)
print(l1, digits = 2)
funnel(l1)

# Print results on log scale
#
print(l1, digits = 2, backtransf = FALSE)
funnel(l1, backtransf = FALSE)
```

---

lfkindex

*LFK Index Test for Asymmetry*


---

**Description**

Implementation of the LFK index test proposed by Furuya-Kanamori et al. (2018) to evaluate bias in meta-analysis.

**Usage**

```
lfkindex(TE, seTE, data = NULL)

## S3 method for class 'lfkindex'
print(x, digits = 2, ...)
```

**Arguments**

TE	An object of class meta or estimated treatment effect in individual studies.
seTE	Standard error of estimated treatment effect (mandatory if TE not of class meta).
data	An optional data frame containing the study information.
x	An object of class lfkindex.
digits	Minimal number of significant digits, see print.default.
...	Additional arguments (ignored).

**Value**

An object of class "lfkindex" with corresponding print function. The object is a list containing the following components:

lfkindex	LFK index.
interpretation	Interpretation of value of LFK index.
abs.zscore	Absolute value of z-score.
N, MidRank, percentile, zscore	Quantities used to calculate LFK index.
TE, seTE	Estimated treatment effect, standard error.
version	Version of R package metasens used to create object.

**Author(s)**

Gerta Rücker <ruecker@imbi.uni-freiburg.de>, Guido Schwarzer <sc@imbi.uni-freiburg.de>

**References**

Furuya-Kanamori L, Barendregt JJ, Doi SAR (2018): A new improved graphical and quantitative method for detecting bias in meta-analysis. *International Journal of Evidence-Based Healthcare*, **16**, 195–203

**See Also**

[doiplot](#), [metabias](#), [funnel.meta](#)

**Examples**

```
# Example from Furuya-Kanamori et al. (2018)
#
pain <- data.frame(SMD = c(-4.270, -1.710, -0.580, -0.190, 0.000),
                  varSMD = c(0.158, 0.076, 0.018, 0.022, 0.040))

lfk.pain <- lfkindex(SMD, sqrt(varSMD), data = pain)
lfk.pain

doiplot(lfk.pain)
```

---

 limitmeta

*Limit meta-analysis*


---

### Description

Implementation of the limit meta-analysis method by Rücker et al. (2011) to adjust for bias in meta-analysis.

### Usage

```
limitmeta(
  x,
  method.adjust = "beta0",
  level = x$level,
  level.ma = x$level.ma,
  backtransf = x$backtransf,
  title = x$title,
  complab = x$complab,
  outclab = x$outclab
)
```

### Arguments

x	An object of class meta.
method.adjust	A character string indicating which adjustment method is to be used. One of "beta0", "betalim", or "mulim", can be abbreviated.
level	The level used to calculate confidence intervals for individual studies.
level.ma	The level used to calculate confidence intervals for pooled estimates.
backtransf	A logical indicating whether results should be back transformed in printouts and plots. If backtransf=FALSE, results for the odds ratio are printed as log odds ratios rather than odds ratio, for example.
title	Title of meta-analysis / systematic review.
complab	Comparison label.
outclab	Outcome label.

### Details

This function provides the method by Rücker et al. (2011) to estimate an effect estimate adjusted for bias in meta-analysis. The underlying model is an extended random effects model that takes account of possible small study effects by allowing the treatment effect to depend on the standard error:

$$\theta(i) = \beta + \sqrt{SE(i)^2 + \tau^2}(\epsilon(i) + \alpha),$$

where  $\epsilon(i)$  follows a standard normal distribution. Here  $\theta(i)$  is the observed effect in study  $i$ ,  $\beta$  the global mean,  $SE(i)$  the within-study standard error, and  $\tau^2$  the between-study variance.

The parameter alpha represents the bias introduced by small-study effects. On the one hand, alpha can be interpreted as the expected shift in the standardized treatment effect if precision is very small. On the other hand,  $\theta(\text{adj}) = \beta + \tau \cdot \alpha$  is interpreted as the limit treatment effect for a study with infinite precision (corresponding to  $\text{SE}(i) = 0$ ).

Note that as alpha is included in the model equation, beta has a different interpretation as in the usual random effects model. The two models agree only if  $\alpha=0$ . If there are genuine small-study effects, the model includes a component making the treatment effect depend on the standard error. The expected treatment effect of a study of infinite precision,  $\beta + \tau \cdot \alpha$ , is used as an adjusted treatment effect estimate.

The maximum likelihood estimates for alpha and beta can be interpreted as intercept and slope in linear regression on a so-called generalised radial plot, where the x-axis represents the inverse of  $\sqrt{\text{SE}(i)^2 + \tau^2}$  and the y-axis represents the treatment effect estimates, divided by  $\sqrt{\text{SE}(i)^2 + \tau^2}$ .

Two further adjustments are available that use a shrinkage procedure. Based on the extended random effects model, a limit meta-analysis is defined by inflating the precision of each study with a common factor. The limit meta-analysis yields shrunken estimates of the study-specific effects, comparable to empirical Bayes estimates. Based on the extended random effects model, we obtain three different treatment effect estimates that are adjusted for small-study effects:

- an estimate based on the expectation of the extended random effects model,  $\beta_0 = \beta + \tau \cdot \alpha$  (`method.adjust="beta0"`)
- the extended random effects model estimate of the limit meta-analysis, including bias parameter (`method.adjust="betalim"`)
- the usual random effects model estimate of the limit meta-analysis, excluding bias parameter (`method.adjust="mulim"`)

See R cker, Schwarzer et al. (2011), Section 7, for the definition of  $G^2$  and the three heterogeneity statistics  $Q$ ,  $Q_{\text{small}}$ , and  $Q_{\text{resid}}$ .

For comparison, the original random effects meta-analysis is always printed in the sensitivity analysis.

## Value

An object of class "limitmeta" with corresponding `print`, `summary` and `funnel` function. The object is a list containing the following components:

<code>x</code> , <code>level</code> , <code>level.ma</code> , <code>method.adjust</code> , <code>title</code> , <code>complab</code> , <code>outclab</code>	As defined above.
<code>TE</code> , <code>seTE</code>	Estimated treatment effect and standard error of individual studies.
<code>TE.limit</code> , <code>seTE.limit</code>	Shrunken estimates and standard error of individual studies.
<code>studlab</code>	Study labels.
<code>TE.random</code> , <code>seTE.random</code>	Unadjusted overall treatment effect and standard error (random effects model).
<code>lower.random</code> , <code>upper.random</code>	Lower and upper confidence interval limits (random effects model).

statistic.random, pval.random	Statistic and corresponding p-value for test of overall treatment effect (random effects model).
w.random	Weight of individual studies (in random effects model).
tau	Square-root of between-study variance.
TE.adjust, seTE.adjust	Adjusted overall effect and standard error (random effects model).
lower.adjust, upper.adjust	Lower and upper confidence interval limits for adjusted effect estimate (random effects model).
statistic.adjust, pval.adjust	Statistic and corresponding p-value for test of overall treatment effect for adjusted estimate (random effects model).
alpha.r	Intercept of the linear regression line on the generalised radial plot, here interpreted as bias parameter in an extended random effects model. Represents the expected shift in the standardized treatment effect if precision is very small.
beta.r	Slope of the linear regression line on the generalised radial plot.
Q	Heterogeneity statistic.
Q.small	Heterogeneity statistic for small study effects.
Q.resid	Heterogeneity statistic for residual heterogeneity beyond small study effects.
G.squared	Heterogeneity statistic $G^2$ (ranges from 0 to 100%).
k	Number of studies combined in meta-analysis.
call	Function call.
version	Version of R package metasens used to create object.

**Author(s)**

Gerta Rücker <ruecker@imbi.uni-freiburg.de>, Guido Schwarzer <sc@imbi.uni-freiburg.de>

**References**

- Rücker G, Carpenter JR, Schwarzer G (2011): Detecting and adjusting for small-study effects in meta-analysis. *Biometrical Journal*, **53**, 351–68
- Rücker G, Schwarzer G, Carpenter JR, Binder H, Schumacher M (2011): Treatment-effect estimates adjusted for small-study effects via a limit meta-analysis. *Biostatistics*, **12**, 122–42

**See Also**

[funnel.limitmeta](#), [print.limitmeta](#)

**Examples**

```
data(Moore1998)
m1 <- metabin(succ.e, nobs.e, succ.c, nobs.c,
  data = Moore1998, sm = "OR", method = "Inverse")

print(limitmeta(m1), digits = 2)
```

metamiss

*Imputation methods for missing binary data***Description**

Imputation methods for the meta-analysis of binary outcomes with missing data.

**Usage**

```
metamiss(
  x,
  miss.e,
  miss.c,
  IMOR.e,
  IMOR.c = IMOR.e,
  method.miss = if (missing(IMOR.e)) "0" else "IMOR",
  small.values = "good",
  common = x$common,
  random = x$random,
  prediction = x$prediction,
  warn.deprecated = gs("warn.deprecated"),
  fixed
)
```

**Arguments**

x	An object of class metabin.
miss.e	Number of missing observations in experimental group.
miss.c	Number of missing observations in control group.
IMOR.e	IMOR in experimental group (see Details).
IMOR.c	IMOR in control group (see Details).
method.miss	A character string indicating which method is used to impute missing values. Either "GH", "IMOR", "0", "1", "pc", "pe", "p", "b", or "w", can be abbreviated (see Details).
small.values	A character string specifying whether small treatment effects indicate a beneficial ("good") or harmful ("bad") effect, can be abbreviated (see Details).
common	A logical indicating whether a common effect meta-analysis should be conducted.
random	A logical indicating whether a random effects meta-analysis should be conducted.
prediction	A logical indicating whether a prediction interval should be printed.
warn.deprecated	A logical indicating whether warnings should be printed if deprecated arguments are used.
fixed	Deprecated argument (replaced by 'common').

## Details

This function provides several imputation methods to deal with missing data in the meta-analysis of binary outcomes (Gamble & Hollis, 2005; Higgins et al., 2008). In order to utilise these methods, the number of observations with missing outcomes must be provided for the experimental and control group (arguments `miss.e` and `miss.c`).

The following imputation methods for missing binary data are available.

Argument	Method
<code>method.miss = "GH"</code>	Method by Gamble & Hollis (2005)
<code>method.miss = "IMOR"</code>	Based on group-specific IMORs
<code>method.miss = "0"</code>	Imputed as no events, (i.e., 0)
<code>method.miss = "1"</code>	Imputed as events (i.e., 1)
<code>method.miss = "pc"</code>	Based on observed risk in control group
<code>method.miss = "pe"</code>	Based on observed risk in experimental group
<code>method.miss = "p"</code>	Based on group-specific risks
<code>method.miss = "b"</code>	Best case scenario for experimental group
<code>method.miss = "w"</code>	Worst case scenario for experimental group

The method by Gamble & Hollis (2005) is based on uncertainty intervals for individual studies resulting from best and worst case scenarios taking the missing data into account. The uncertainty intervals are used to calculate (inflated) standard errors which are considered in a generic inverse variance meta-analysis instead of the standard errors from the complete case meta-analysis.

All other methods are based on the Informative Missingness Odds Ratio (IMOR) which is defined as the odds of an event in the missing group over the odds of an event in the observed group (Higgins et al., 2008). For example, an IMOR of 2 means that the odds for an event is assumed to be twice as likely for missing observations. For `method.miss = "IMOR"`, the IMORs in the experimental (argument `IMOR.e`) and control group (argument `IMOR.c`) must be specified by the user. For all other methods, the input for arguments `IMOR.e` and `IMOR.c` is ignored as these values are determined by the respective imputation method (see Table 2 in Higgins et al., 2008).

For the best and worst case scenarios (i.e., argument `method.miss` equal to "b" or "w"), the user has to specify whether the outcome is beneficial (argument `small.values = "good"`) or harmful (`small.values = "bad"`).

## Value

An object of class `c("metamiss", "metagen", "meta")` with corresponding `print`, `summary`, and `forest` functions. See [metagen](#) for more information.

## Author(s)

Guido Schwarzer <[sc@imbi.uni-freiburg.de](mailto:sc@imbi.uni-freiburg.de)>

## References

- Gamble C, Hollis S (2005): Uncertainty method improved on best–worst case analysis in a binary meta-analysis. *Journal of Clinical Epidemiology*, **58**, 579–88
- Higgins JPT, White IR, Wood AM (2008): Imputation methods for missing outcome data in meta-analysis of clinical trials. *Clinical Trials*, **5**, 225–39

**See Also**

[metabin](#), [metagen](#)

**Examples**

```
d1 <- data.frame(author = c("Beasley", "Selman"),
  resp.h = c(29, 17), fail.h = c(18, 1), drop.h = c(22, 11),
  resp.p = c(20, 7), fail.p = c(14, 4), drop.p = c(34, 18))
m1 <- metabin(resp.h, resp.h + fail.h, resp.p, resp.p + fail.p,
  data = d1, studlab = author, sm = "RR", method = "I")
m1

# Treat missings as no events
metamiss(m1, drop.h, drop.p)

# Assume IMORs of 2 for both experimental and control group
metamiss(m1, drop.h, drop.p, IMOR.e = 2)

# Gamble & Hollis (2005)
d2 <- data.frame(author = c("Lefevre", "van Vugt", "van Vugt"),
  year = c(2001, 2000, 1998),
  para.al = c(7, 4, 49), n.al = c(155, 134, 273),
  miss.al = c(9, 16, 36),
  para.ma = c(0, 0, 7), n.ma = c(53, 47, 264),
  miss.ma = c(2, 3, 44))

m2 <- metabin(para.al, n.al, para.ma, n.ma,
  data = d2, studlab = paste0(author, " (", year, ")"),
  method = "Inverse", method.tau = "DL",
  sm = "OR")

metamiss(m2, miss.al, miss.ma, method = "GH")
```

---

 Moore1998

*NSAIDs in acute pain*


---

**Description**

Meta-analysis on the effectiveness of topical non-steroidal anti-inflammatory drugs (NSAIDs) in acute pain.

Treatment success is defined as a reduction in pain of at least 50%.

**Format**

A data frame with the following columns:

<i>study</i>	study number
<i>succ.e</i>	number of treatment successes in NSAIDs group

**nobs.e** number of patients in NSAIDS group  
**succ.c** number of treatment successes in control group  
**nobs.c** number of patients in control group

### Source

Moore RA, Tramer MR, Carroll D, Wiffen PJ, McQuay HJ (1998): Quantitive systematic review of topically applied non-steroidal anti-inflammatory drugs. *British Medical Journal*, **316**, 333–8

### Examples

```
data(Moore1998)
m1 <- metabin(succ.e, nobs.e, succ.c, nobs.c,
             data = Moore1998, sm = "OR", method = "Inverse")

print(limitmeta(m1), digits = 2)
```

---

 orbbound

*Sensitivity Analysis for Outcome Reporting Bias (ORB)*


---

### Description

Implementation of the method by Copas & Jackson (2004) to evaluate outcome reporting bias in meta-analysis. An upper bound for outcome reporting bias is estimated for a given number of studies suspected with outcome reporting bias.

### Usage

```
orbbound(x, k.suspect = 1, tau = x$tau, left = NULL, backtransf = x$backtransf)
```

### Arguments

x	An object of class meta.
k.suspect	Number of studies with suspected outcome reporting bias.
tau	Square-root of between-study variance tau-squared.
left	A logical indicating whether the cause of any selection bias is due to missing studies on the left or right of the funnel plot: left hand side if left=TRUE, right hand side if left=FALSE. If not set, the linear regression test for funnel plot asymmetry (i.e., function metabias(...,meth="linreg")) is used to determine whether studies are missing on the left or right hand side.
backtransf	A logical indicating whether results should be back transformed in printouts and plots. If backtransf=TRUE (default), results for sm="OR" are printed as odds ratios rather than log odds ratio, for example.

## Details

This function provides the method by Copas and Jackson (2004) to estimate an upper bound for bias for a given number of studies with suspected outcome reporting bias.

Based on the upper bound of outcome reporting bias, treatment estimates and confidence limits adjusted for bias are calculated.

For comparison, the original meta-analysis is always considered in the sensitivity analysis (i.e. value 0 is always added to `k.suspect`).

## Value

An object of class `c("orbbound")` with corresponding `print` and `forest` function. The object is a list containing the following components:

<code>k.suspect, tau</code>	As defined above.
<code>maxbias</code>	Maximum bias for given values of <code>k.suspect</code> .
<code>common</code>	Adjusted treatment estimates and corresponding quantities for common effect model (a list with elements <code>TE</code> , <code>seTE</code> , <code>lower</code> , <code>upper</code> , <code>z</code> , <code>p</code> , <code>level</code> , <code>df</code> ).
<code>random</code>	Adjusted treatment estimates and corresponding quantities for random effects model (a list with elements <code>TE</code> , <code>seTE</code> , <code>lower</code> , <code>upper</code> , <code>z</code> , <code>p</code> , <code>level</code> , <code>df</code> ).
<code>left</code>	Whether selection bias expected on left or right
<code>x</code>	Meta-analysis object (i.e. argument <code>x</code> from function call).
<code>call</code>	Function call.
<code>version</code>	Version of R package <code>metasens</code> used to create object.

## Author(s)

Guido Schwarzer <[sc@imbi.uni-freiburg.de](mailto:sc@imbi.uni-freiburg.de)>

## References

Copas J, Jackson D (2004): A bound for publication bias based on the fraction of unpublished studies. *Biometrics*, **60**, 146–53

## See Also

[forest.orbbound](#), [print.orbbound](#)

## Examples

```
data(Fleiss1993bin, package = "meta")

m1 <- metabin(d.asp, n.asp, d.plac, n.plac, data = Fleiss1993bin, sm = "OR")

orb1 <- orbbound(m1, k.suspect = 1:5)
print(orb1, digits = 2)
forest(orb1, xlim = c(0.75, 1.5))
```

```
# Same result
#
orb2 <- orbbound(m1, k.suspect = 1:5, left = FALSE)
print(orb2, digits = 2)

# Assuming bias in other direction
#
orb3 <- orbbound(m1, k.suspect = 1:5, left = TRUE)
print(orb3, digits = 2)
```

---

plot.copas

*Display results of Copas selection modelling*


---

## Description

Four plots (selectable by 'which') are currently available: (1) funnel plot, (2) contour plot, (3) treatment effect plot, (4) p-value for residual publication bias plot. By default, all plots are provided.

## Usage

```
## S3 method for class 'copas'
plot(
  x,
  which = 1:4,
  main = c("Funnel plot", "Contour plot", "Treatment effect plot",
    "P-value for residual selection bias"),
  xlim.pp,
  orthogonal.line = TRUE,
  lines = FALSE,
  warn = -1,
  ...
)
```

## Arguments

x	An object of class copas, generated by the copas function
which	Specify plots required: 1:4 produces all plots (default); 3 produces plot 3 etc; c(1,3) produces plots 1 and 3, and so on.
main	Specify plot captions. Must be of same length as argument which.
xlim.pp	A vector of x-axis limits for plots 3 and 4, i.e. for the probability of publishing the study with largest standard deviation. E.g. to specify limits between 0.3 and 0.1 set xlim.pp=c(0.3, 0.1).
orthogonal.line	A logical indicating whether the orthogonal line should be displayed in plot 2 (contour plot).

lines	(Diagnostic use only) A logical indicating whether regression lines should be plotted in contour plot. These regression lines attempt to summarise each contour of constant treatment effect by a straight line, prior to calculating the orthogonal line. Regression lines with a positive adjusted $R^2$ will be printed in green color, others will be printed in red color.
warn	A number setting the handling of warning messages. It is not uncommon for numerical problems to be encountered during estimation over the grid of ( $\gamma_0$ , $\gamma_1$ ) values. Usually this does not indicate a serious problem. This option specifies what to do with warning messages. warn=-1: ignore all warnings; warn=0 (the default): store warnings till function finishes; if there are less than 10, print them, otherwise print a message saying warning messages were generated; warn=1: print warnings as they occur; warn=2: stop the function when the first warning is generated. For further details see <code>help(options)</code> .
...	Other arguments (to check for deprecated argument 'caption').

## Details

Takes an object created by the copas function and draws up to four plots to display the results of the Copas selection modelling.

The argument which specifies the plots to be drawn; plot numbers below will be produced by setting which=1, etc.

Plot 1: Funnel plot of studies in meta-analysis. Vertical grey line is usual random effects estimate (DerSimonian-Laird method); vertical broken line is common effects estimate.

Plot 2: Plot of contours of treatment effect (estimated by the Copas model) as the selection probability varies (the selection probability is a function of  $\gamma_0$  and  $\gamma_1$  - see `help(copas)` or the reference below).

Plot 3: Assuming the contours of treatment effect in Plot 2 are locally parallel, the results can be summarised in terms of the probability of publishing the study with the largest standard error. This plot displays the results of doing this, showing how the estimated treatment effect (and  $100 \times \text{level}\%$  confidence interval) vary as the probability of publishing the study with the largest standard error decreases.

The three horizontal grey lines are the usual random effects treatment estimate (center) +/- the  $100 \times \text{level}\%$  confidence interval (upper/lower grey lines).

Plot 4: For any degree of selection (i.e. probability of the study with largest SE being published), we can calculate a p-value for the hypothesis that no further selection remains unexplained in the data. These plot displays these p-values against the probability that the study with the largest SE is published.

Under the copas selection model, probabilities of the smallest study being published which correspond to p-values for residual selection bias that are larger than 0.1 are more plausible. The corresponding treatment effect in plot 3 is thus the most plausible under the copas selection model.

## Note

In the current version, fine control of the graphics parameters for the individual panels is not possible. However, all the data used to create the plots can be extracted manually from the object created by the copas function (see attributes list for copas) and used to create tailor-made plots.

**Author(s)**

James Carpenter <James.Carpenter@lshtm.ac.uk>, Guido Schwarzer <sc@imbi.uni-freiburg.de>

**References**

Carpenter JR, Schwarzer G, Rücker G, Küntler R (2009): Empirical evaluation showed that the Copas selection model provided a useful summary in 80% of meta-analyses. *Journal of Clinical Epidemiology*, **62**, 624–31

Schwarzer G, Carpenter J, Rücker G (2010): Empirical evaluation suggests Copas selection model preferable to trim-and-fill method for selection bias in meta-analysis. *Journal of Clinical Epidemiology*, **63**, 282–8

**See Also**

[copas](#), [summary.copas](#), [metabias](#), [metagen](#)

**Examples**

```
data(Fleiss1993bin, package = "meta")

# Perform meta-analysis (outcome measure is OR = odds ratio)
#
m1 <- metabin(d.asp, n.asp, d.plac, n.plac, data = Fleiss1993bin, sm = "OR")

# Perform Copas analysis
#
cop1 <- copas(m1)

# Plot results
#
plot(cop1)

# Only show plots 1 and 2 (without orthogonal line)
#
plot(cop1, which = 1:2, orth = FALSE)

# Another example showing use of more arguments
# Note the use of "\n" to create a new line in the caption
#
plot(cop1, which = 3, xlim.pp = c(1, 0.5),
     main = "Variation in estimated treatment\n effect with selection")
```

## Description

Print method for objects of class copas.

This function prints the main results of a Copas analysis, performed using the function copas. It complements the graphical summary of the results, generated using `plot.copas`.

Specifically it prints a table where the:

first column corresponds to the x-axis in plots 3 & 4 from `plot.copas`;

second column corresponds to the treatment effect displayed in plot 3 from `plot.copas`;

third and fourth columns give the confidence intervals for this treatment effect,

fifth column gives the p-value for an overall treatment effect,

sixth column gives the p-value for residual publication bias (the y-axis of plot 4 from `plot.copas` (see `plot.copas` under plot 4 for a further explanation of this p-value))

seventh column gives an approximate estimate of the number of studies the model suggests remain unpublished if the probability of publishing the study with the largest SE is as in column 1.

Below this is displayed the results of the Copas analysis (Adjusted estimate) for the smallest degree of selection for which the p-value for evidence of residual selection bias exceeds `sign.rsb` (default: 0.1). This is simply extracted from the corresponding row in the table above.

Lastly, the unadjusted random effects estimate and 95% confidence interval is printed.

## Usage

```
## S3 method for class 'copas'
print(
  x,
  backtransf = x$backtransf,
  digits = gs("digits"),
  digits.pval = max(gs("digits.pval"), 2),
  digits.prop = gs("digits.prop"),
  scientific.pval = gs("scientific.pval"),
  big.mark = gs("big.mark"),
  header = TRUE,
  legend = TRUE,
  ...
)
```

## Arguments

<code>x</code>	An object of class <code>copas</code> .
<code>backtransf</code>	A logical indicating whether results should be back transformed in printouts and plots. If <code>backtransf = TRUE</code> (default), results are printed as odds ratios rather than log odds ratio, for example.
<code>digits</code>	Minimal number of significant digits, see <code>print.default</code> .
<code>digits.pval</code>	Minimal number of significant digits for p-value of overall treatment effect, see <code>print.default</code> .
<code>digits.prop</code>	Minimal number of significant digits for proportions, see <code>print.default</code> .

<code>scientific.pval</code>	A logical specifying whether p-values should be printed in scientific notation, e.g., 1.2345e-01 instead of 0.12345.
<code>big.mark</code>	A character used as thousands separator.
<code>header</code>	A logical indicating whether information on title of meta-analysis, comparison and outcome should be printed at the beginning of the printout.
<code>legend</code>	A logical indicating whether a legend should be printed.
<code>...</code>	Additional arguments (ignored).

**Author(s)**

James Carpenter <James.Carpenter@lshtm.ac.uk>, Guido Schwarzer <sc@imbi.uni-freiburg.de>

**See Also**

[copas](#), [plot.copas](#), [summary.copas](#)

**Examples**

```
data(Fleiss1993bin, package = "meta")

# Perform meta analysis, effect measure is odds ratio (OR)
#
m1 <- metabin(d.asp, n.asp, d.plac, n.plac, data = Fleiss1993bin, sm = "OR")

# Perform Copas analysis
#
cop1 <- copas(m1)
cop1
```

---

`print.limitmeta`

*Print results for limit meta-analysis*

---

**Description**

Print method for objects of class `limitmeta`.

**Usage**

```
## S3 method for class 'limitmeta'
print(
  x,
  backtransf = x$backtransf,
  digits = gs("digits"),
  header = TRUE,
  pscale = x$x$pscale,
```

```

    irscale = x$x$irscale,
    irunit = x$x$irunit,
    digits.stat = gs("digits.stat"),
    digits.pval = gs("digits.pval"),
    digits.Q = gs("digits.Q"),
    digits.tau2 = gs("digits.tau2"),
    digits.I2 = gs("digits.I2"),
    scientific.pval = gs("scientific.pval"),
    big.mark = gs("big.mark"),
    print.Rb = gs("print.Rb"),
    warn.backtransf = FALSE,
    ...
)

```

## Arguments

x	An object of class <code>limitmeta</code> .
backtransf	A logical indicating whether results should be back transformed in printouts and plots. If <code>backtransf=TRUE</code> (default), results for <code>sm="OR"</code> are printed as odds ratios rather than log odds ratio, for example.
digits	Minimal number of significant digits, see <code>print.default</code> .
header	A logical indicating whether information on title of meta-analysis, comparison and outcome should be printed at the beginning of the printout.
pscale	A numeric giving scaling factor for printing of single event probabilities, i.e. if argument <code>sm</code> is equal to "PLOGIT", "PLN", "PRAW", "PAS", or "PFT".
irscale	A numeric defining a scaling factor for printing of rates, i.e. if argument <code>sm</code> is equal to "IR", "IRLN", "IRS", or "IRFT".
irunit	A character specifying the time unit used to calculate rates, e.g. person-years.
digits.stat	Minimal number of significant digits for z- or t-value, see <code>print.default</code> .
digits.pval	Minimal number of significant digits for p-value of overall treatment effect, see <code>print.default</code> .
digits.Q	Minimal number of significant digits for heterogeneity statistic Q, see <code>print.default</code> .
digits.tau2	Minimal number of significant digits for between-study variance, see <code>print.default</code> .
digits.I2	Minimal number of significant digits for I-squared and Rb statistic, see <code>print.default</code> .
scientific.pval	A logical specifying whether p-values should be printed in scientific notation, e.g., 1.2345e-01 instead of 0.12345.
big.mark	A character used as thousands separator.
print.Rb	A logical specifying whether heterogeneity statistic Rb should be printed.
warn.backtransf	A logical indicating whether a warning should be printed if backtransformed proportions and rates are below 0 and backtransformed proportions are above 1.
...	Additional arguments (ignored).

**Details**

This function prints the main results of a limit meta-analysis (Rücker et al., 2011).

**Author(s)**

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

**See Also**

[limitmeta](#), [summary.limitmeta](#), [print.summary.limitmeta](#)

**Examples**

```
data(Moore1998)
m1 <- metabin(succ.e, nobs.e, succ.c, nobs.c,
  data = Moore1998, sm = "OR", method = "Inverse")

print(limitmeta(m1), digits = 2)
```

---

print.orbound

*Print method for objects of class orbound*

---

**Description**

Print method for objects of class orbound.

**Usage**

```
## S3 method for class 'orbound'
print(
  x,
  common = x$x$common,
  random = x$x$random,
  header = TRUE,
  backtransf = x$backtransf,
  digits = gs("digits"),
  digits.stat = gs("digits.stat"),
  digits.pval = max(gs("digits.pval"), 2),
  digits.tau2 = gs("digits.tau2"),
  scientific.pval = gs("scientific.pval"),
  big.mark = gs("big.mark"),
  warn.deprecated = gs("warn.deprecated"),
  ...
)
```

**Arguments**

x	An object of class orbbound.
common	A logical indicating whether sensitivity analysis for common effect model should be printed.
random	A logical indicating whether sensitivity analysis for random effects model should be printed.
header	A logical indicating whether information on meta-analysis should be printed at top of printout.
backtransf	A logical indicating whether printed results should be back transformed. If backtransf=TRUE, results for sm="OR" are printed as odds ratios rather than log odds ratios and results for sm="ZCOR" are printed as correlations rather than Fisher's z transformed correlations, for example.
digits	Minimal number of significant digits, see print.default.
digits.stat	Minimal number of significant digits for z- or t-value, see print.default.
digits.pval	Minimal number of significant digits for p-value of overall treatment effect, see print.default.
digits.tau2	Minimal number of significant digits for between-study variance, see print.default.
scientific.pval	A logical specifying whether p-values should be printed in scientific notation, e.g., 1.2345e-01 instead of 0.12345.
big.mark	A character used as thousands separator.
warn.deprecated	A logical indicating whether warnings should be printed if deprecated arguments are used.
...	Additional arguments to catch deprecated arguments.

**Details**

For summary measures 'RR', 'OR', and 'HR' column labeled maxbias contains the relative bias, e.g. a value of 1.10 means a maximum overestimation by 10 percent. If logscale=TRUE for these summary measures, maximum bias is instead printed as absolute bias.

**Author(s)**

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

**See Also**

[orbbound](#), [forest.orbbound](#)

**Examples**

```
data(Fleiss1993bin, package = "meta")

m1 <- metabin(d.asp, n.asp, d.plac, n.plac,
  data = Fleiss1993bin, sm = "OR")
```

```

orb1 <- orbbound(m1, k.suspect = 1:5)
print(orb1, digits = 2)

# Print log odds ratios instead of odds ratios
#
print(orb1, digits = 2, backtransf = FALSE)

# Assuming that studies are missing on the left side
#
orb1.missleft <- orbbound(m1, k.suspect = 1:5, left = TRUE)
orb1.missleft

m2 <- metabin(d.asp, n.asp, d.plac, n.plac,
  data = Fleiss1993bin, sm = "OR", method = "Inverse")

orb2 <- orbbound(m2, k.suspect = 1:5)
print(orb2, digits = 2)

```

---

`print.summary.copas`     *Print detailed results of Copas selection model*

---

### Description

Print method for objects of class `summary.copas`.

This function prints the following information:

Range of `gamma0` values used (see `help(copas)`);

Range of `gamma1` values used (see `help(copas)`);

Largest SE of all studies in meta-analysis;

Range of probability publishing trial with largest SE;

The next table gives details relating to the summary of the contour plot. Specifically, it gives details from fitting a straight line to each treatment-contour in the contour plot. Column 1 (headed level) shows the treatment-contours; column 2 (`nobs`) shows the number of observations used by the contour plot command within the `copas` function to plot this contour line; column 3 (`adj.r.square`) shows the adjusted r-square from fitting a straight line to this contour; columns 4 & 5 show the slope and its standard error from fitting a straight line to this contour.

Next, the printout of `summary.copas` is shown.

### Usage

```

## S3 method for class 'summary.copas'
print(
  x,
  backtransf = x$backtransf,
  legend = TRUE,

```

```

    digits = gs("digits"),
    digits.se = gs("digits.se"),
    ...
  )

```

### Arguments

x	An object of class <code>summary.copas</code> .
backtransf	A logical indicating whether results should be back transformed in printouts and plots. If <code>backtransf = TRUE</code> (default), results are printed as odds ratios rather than log odds ratio, for example.
legend	A logical indicating whether a legend should be printed.
digits	Minimal number of significant digits, see <code>print.default</code> .
digits.se	Minimal number of significant digits for standard deviations and standard errors, see <code>print.default</code> .
...	Additional arguments (ignored).

### Author(s)

James Carpenter <James.Carpenter@lshtm.ac.uk>, Guido Schwarzer <sc@imbi.uni-freiburg.de>

### See Also

[copas](#), [plot.copas](#), [summary.copas](#)

### Examples

```

data(Fleiss1993bin, package = "meta")

# Perform meta analysis, effect measure is odds ratio (OR)
#
m1 <- metabin(d.asp, n.asp, d.plac, n.plac, data=Fleiss1993bin, sm="OR")

# Print summary of Copas analysis
#
summary(copas(m1), level = 0.95)

```

---

print.summary.limitmeta

*Print detailed results for limit meta-analysis*

---

**Description**

Print method for objects of class `summary.limitmeta`.

This function prints the main results of a limit meta-analysis (Rücker et al., 2011) as well as the following study information:

- Effect estimate with confidence interval
- Shrunk effect estimates with confidence interval

**Usage**

```
## S3 method for class 'summary.limitmeta'
print(
  x,
  sortvar,
  backtransf = x$backtransf,
  digits = gs("digits"),
  big.mark = gs("big.mark"),
  truncate,
  text.truncate = "*** Output truncated ***",
  ...
)
```

**Arguments**

<code>x</code>	An object of class <code>summary.limitmeta</code>
<code>sortvar</code>	An optional vector used to sort the individual studies (must be of same length as <code>x\$TE</code> ).
<code>backtransf</code>	A logical indicating whether results should be back transformed in printouts and plots. If <code>backtransf=TRUE</code> (default), results for <code>sm="OR"</code> are printed as odds ratios rather than log odds ratio, for example.
<code>digits</code>	Minimal number of significant digits, see <code>print.default</code> .
<code>big.mark</code>	A character used as thousands separator.
<code>truncate</code>	An optional vector used to truncate the printout of results for individual studies (must be a logical vector of same length as <code>x\$TE</code> or contain numerical values).
<code>text.truncate</code>	A character string printed if study results were truncated from the printout.
<code>...</code>	Additional arguments which are passed on to <code>print.limitmeta</code> called internally.

**Author(s)**

Guido Schwarzer <[sc@imbi.uni-freiburg.de](mailto:sc@imbi.uni-freiburg.de)>

**See Also**

[limitmeta](#), [summary.limitmeta](#)

**Examples**

```
data(Moore1998)
m1 <- metabin(succ.e, nobs.e, succ.c, nobs.c,
  data = Moore1998, sm = "OR", method = "Inverse")

print(summary(limitmeta(m1)), digits = 2)
```

summary.copas

*Summary method for Copas selection model***Description**

Summary method for objects of class copas.

**Usage**

```
## S3 method for class 'copas'
summary(object, ...)
```

**Arguments**

object	An object of class copas.
...	other arguments to the function will be ignored (this option included only to conform with R standards)

**Details**

This function complements the graphical summary of the results of a Copas selection model, generated using plot.copas.

**Value**

An object of class "summary.copas" with corresponding print function. The object is a list containing the following components:

slope	Results for points on orthogonal line (a list with elements TE, seTE, lower, upper, statistic, p, level).
publprob	Vector of probabilities of publishing the smallest study.
pval.rsb	P-values for tests on presence of residual selection bias
N.unpubl	Approximate number of studies the model suggests remain unpublished
adjust	Result of Copas selection model adjusted for selection bias (a list with elements TE, seTE, lower, upper, statistic, p, level).
sign.rsb	The significance level for the test of residual selection bias.
pval.rsb.adj	P-value for test on presence of residual selection bias for adjusted effect given in adjust.

N.unpubl.adj	Approximate number of studies the model suggests remain unpublished for adjusted effect given in adjust
random	Results for usual random effects model (a list with elements TE, seTE, lower, upper, statistic, p, level).
sm	A character string indicating underlying summary measure.
ci.lab	Label for confidence interval.
title	Title of meta-analysis / systematic review.
complab	Comparison label.
outclab	Outcome label.
version	Version of R package metasens used to create object.

**Author(s)**

James Carpenter <James.Carpenter@lshtm.ac.uk>, Guido Schwarzer <sc@imbi.uni-freiburg.de>

**See Also**

[copas](#), [plot.copas](#), [metabias](#), [metagen](#)

**Examples**

```
data(Fleiss1993bin, package = "meta")

# Perform meta analysis, effect measure is odds ratio (OR)
#
m1 <- metabin(d.asp, n.asp, d.plac, n.plac, data = Fleiss1993bin, sm = "OR")

# Print summary of Copas analysis
#
summary(copas(m1, level.ma = 0.95))
```

---

summary.limitmeta      *Summary method for limit meta-analysis*

---

**Description**

Summary method for objects of class limitmeta.

**Usage**

```
## S3 method for class 'limitmeta'
summary(object, ...)
```

### **Arguments**

object	An object of class <code>limitmeta</code> .
...	Additional arguments (ignored).

### **Value**

This function returns the same list as the function `limitmeta`, however class `"summary.limitmeta"` is added to the object in order to print a detailed summary of the limit meta-analysis object.

### **Author(s)**

Guido Schwarzer <[sc@imbi.uni-freiburg.de](mailto:sc@imbi.uni-freiburg.de)>

### **See Also**

[limitmeta](#), [funnel.limitmeta](#), [print.summary.limitmeta](#)

### **Examples**

```
data(Moore1998)
m1 <- metabin(succ.e, nobs.e, succ.c, nobs.c,
  data = Moore1998, sm = "OR", method = "Inverse")

summary(limitmeta(m1))
```

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