

# Package ‘metap’

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**Type** Package

**Title** Meta-Analysis of Significance Values

**Version** 1.9

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**Description** The canonical way to perform meta-analysis involves using effect sizes. When they are not available this package provides a number of methods for meta-analysis of significance values including the methods of Edgington, Fisher, Lancaster, Stouffer, Tippett, and Wilkinson; a number of data-sets to replicate published results; and routines for graphical display.

**Depends** R (>= 3.5.0)

**Imports** lattice,Rdpack (>= 0.7),TFisher,muttos,mathjaxr (>= 0.8-3),qqconf

**RdMacros** Rdpack,mathjaxr

**License** GPL-2

**LazyLoad** yes

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**Description**

The canonical way to perform meta-analysis involves using effect sizes. When they are not available this package provides a number of methods for meta-analysis of significance values including the methods of Edgington, Fisher, Lancaster, Stouffer, Tippett, and Wilkinson; a number of data-sets to replicate published results; and routines for graphical display.

**Details**

Index of help topics:

albatros	Albatros plot
allmetap	Carry out all or some of the methods in the package
dat.metap	Example data
invchisq	Combine p values using inverse chi squared method
invt	Combine p values using inverse t method
logitp	Combine p values using logit method
meanp	Combine p values by the mean p method
meanz	Combine p values using mean z method
metap-package	Meta-Analysis of Significance Values
plotp	Q-Q plot of p-values
schweder	Schweder and Spjotvoll plot
sumlog	Combine p-values by the sum of logs (Fisher's) method
sump	Combine p-values using the sum of p (Edgington's) method
sumz	Combine p-values using the sum of z (Stouffer's) method
truncated	Truncated product method routine
two2one	Convert two-sided p-values to one-sided
votep	Combine p-values by the vote counting method
wilkinsonp	Combine p-values using Wilkinson's method

Further information is available in the following vignettes:

compare	Comparison of methods in the metap package (source)
metap	Introduction to the metap package (source)
plotmetap	Plotting in the metap package (source)

Provides a number of ways in which significance levels may be combined in a meta-analysis and includes most of the methods in Becker (1994). It includes a number of datasets taken from the literature. It also provides a display and an informal graphical test due to Schweder and Spjotvoll

(Schweder and Spjotvoll 1982) and the lowest slope line of Benjamini and Hochberg (Benjamini and Hochberg 2000). The albatros plot of Harrison et al (Harrison et al. 2017) is also provided.

Some further documentation and, possibly, a development version may be seen at <http://www.dewey.myzen.co.uk/meta/meta.html>

## References

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

Benjamini Y, Hochberg Y (2000). “On the adaptive control of the false discovery rate in multiple testing with independent statistics.” *Journal of Educational and Behavioral Statistics*, **25**, 60–83.

Harrison S, Jones HE, Martin RM, Lewis SJ, Higgins JPT (2017). “The albatros plot: A novel graphical tool for presenting the results of diversely reported studies in a systematic review.” *Research Synthesis Methods*, **8**, 281–289.

Schweder T, Spjotvoll E (1982). “Plots of  $P$ -values to evaluate many tests simultaneously.” *Biometrika*, **69**, 493–502.

## See Also

The issue of meta-analysis of significance levels is not completely unconnected with the topic of adjustment for multiple comparisons as in for example [p.adjust](#)

---

albatros

*Albatros plot*

---

## Description

Produces the albatros plot of Harrison et al

## Usage

```
albatros(p, n, axes = list(xlimit = NULL, ylimit = NULL,
  lefttext = NULL, righttext = NULL),
  contours = list(type = NULL, contvals = NULL, ltys = NULL, contlabs = NULL),
  plotpars = list(yscale = NULL, pchs = NULL, cols = NULL), ...)
docontours(conttype, xvals, contvals, xtrans, ytrans,
  xlims, ylims, ltys, contlabs)
```

## Arguments

- |      |  |
|------|--|
| p    | A vector of $p$ values   |
| n    | A vector of sample sizes   |
| axes | A list containing <ul style="list-style-type: none"> <li>• <code>xlimit</code> a single value, the limit for the x-axis which is used symmetrically</li> <li>• <code>ylimit</code> a vector of length 2, limits for the y-axis</li> <li>• <code>lefttext</code> character, to label below plot</li> <li>• <code>righttext</code> character, to label below plot</li> </ul> |

contours	A list containing <ul style="list-style-type: none"> <li>• type what effect size to use, a character one of "corr", "or", "smd"</li> <li>• contvals a vector, what values to draw the contours at</li> <li>• ltys a vector, what line types to use</li> </ul>
plotpars	A list containing <ul style="list-style-type: none"> <li>• yscale Scaling for y-axis, See details</li> <li>• pchs Symbols to be used</li> <li>• cols Colours for points</li> </ul>
...	Arguments to be passed through to plot
conttype	Character: one of "smd", "or", "corr"
xvals	A vector of values to evaluate the contour
contvals	The values at which contours are drawn
xtrans	A function for transforming the x-axis
ytrans	A function for transforming the y-axis
xlims	The limits for the x-axis in plotting units
ylims	The limits for the y-axis in plotting units
ltys	A vector of line types for the contours
contlabs	Logical, draw the labels of the contours?

### Details

Plots  $n$  against  $p$  and draws contours of constant effect size.

The  $p$  value scale on the  $x$ -axis is a logarithmic one but folded at the null value so that the extreme values represent small probabilities in each direction. The scale for the  $y$ -axis is user selectable. The original scale in the Stata version is  $(\log_{10} n)^2$  which is obtained by setting `yscale` to "classic" but it is also possible to use  $\sqrt{n}$  which is the default or  $n$  by setting `yscale` to "n". If the dataset contains extreme values the plot may be uninformative and the `xlimit` and `ylimit` parameters may be helpful to clip the plot. If they are not specified the function tries to choose suitable values.

For the contours if the `type` parameter in `contours` is NULL (the default) no contours will be plotted. The options available are "smr" (Standardised mean difference) "corr" (Correlation) "or" (Odds ratio).

The contours are labelled unless `contlabs` is set to FALSE. The function tries to position these so they are not obscured by the contour lines but if that is unsatisfactory then it is best to suppress them and position them manually or use a legend to identify line types.

The `pch` parameter may either be a single value or a vector of the same length as  $p$ . It may contain anything which is legal as input to the parameter of the same name in the graphics library and will be used for the plotted points. The `cols` parameter works similarly.

The values of `lefttext` and `righttext` are used to produce labels under the  $x$ -axis and are placed level with the label. By default they are not produced.

The return values from the function may be useful if further annotations are required as they give the axis limits in plotting units.

### Value

Returns A list containing

<code>xlims</code>	The limits for the $x$ -axis in plotting units
<code>ylims</code>	The limits for the $y$ -axis in plotting units

**Note**

The docontours function is for internal use only

**Author(s)**

Michael Dewey

**References**

Harrison S, Jones HE, Martin RM, Lewis SJ, Higgins JPT (2017). “The albatros plot: A novel graphical tool for presenting the results of diversely reported studies in a systematic review.” *Research Synthesis Methods*, **8**, 281–289.

**See Also**

For plotting parameters see [par](#)

**Examples**

```
data(dat.metap)
validity <- dat.metap$validity
fit.v <- albatros(validity$p, validity$n,
  contours = list(type = "corr", contvals = c(0.25, 0.5, 0.8), ltys = 1:3),
  axes = list(ylimin = c(1,200), lefttext = "Negative correlation",
    righttext = "Positive correlation"),
  main = "Validity")
#
fit.z <- albatros(dat.metap$zhang$p, dat.metap$zhang$n,
  contours = list(type = "smd", contvals = c(0.25, 0.5, 1), ltys = 1:3),
  plotpars = list(pchs = letters[unclass(dat.metap$zhang$phase)]),
  axes = list(lefttext = "Favours control", righttext = "Favours exercise"),
  main = "Zhang"
)
```

---

allmetap

*Carry out all or some of the methods in the package*

---

**Description**

Enables all or a selected number of the package methods to be executed on the same dataset

**Usage**

```
allmetap(p, method = NULL, log.p = FALSE)
## S3 method for class 'allmetap'
print(x, digits = 5, ...)
```

**Arguments**

<code>p</code>	A vector of $p$ -values
<code>method</code>	A vector of character containing names of methods or 'all'
<code>log.p</code>	Logical, are the $p$ -values passed as logs?
<code>x</code>	An object of class 'allmetap'
<code>digits</code>	How many digits to print?
<code>...</code>	Other arguments to be passed through

**Details**

The function uses each of the methods specified on the data-set in `p`. If method contains 'all' then this over-rides any specific method(s) named.

**Value**

Returns an object of class 'allmetap' and 'data.frame' containing columns

<code>p</code>	The value of <code>p</code> returned
<code>valid</code>	The number of valid <code>p</code> values used for that method
<code>eponym</code>	The eponym, if any, for the method

The row names are the names of the methods used. If any of the methods cannot be applied to that data-set NA are returned for `p` and `valid`.

**Author(s)**

Michael Dewey

**Examples**

```
data(dat.metap)
beckerp <- dat.metap$beckerp
allmetap(beckerp, method = "all")
allmetap(beckerp, method = c("sumz", "sumlog"))
```

---

dat.metap

*Example data*

---

**Description**

The package contains the following datasets: beckerp, cholest, edgington, mourning, naep, rosenthal, teachexpect, validity, and zhang.

**Usage**

```
data(dat.metap)
```

**Format**

A list with the following elements:

beckerp A vector of length 5

cholest A data frame with 34 observations on the following 5 variables.

ntreat A numeric vector of number treated

ncontrol A numeric vector of number in the control group

dtreat A numeric vector of number of deaths in the treated group

dcontrol A numeric vector of number of deaths in the control group

p a numeric vector of one sided  $p$  values

A vector of length 34

edgington A vector of length 7

naep A data frame with 34 observations on the following 2 variables.

state a factor with levels AL, AR, AZ, CA, CO, CT, DE, FL, GA, HI, IA, ID, IN, KY, LA, MD, MI, MN, NC, ND, NE, NH, NJ, NM, NY, OH, OK, PA, RI, TX, VA, WI, WV, WY,

p a numeric vector

mourning A data frame with 9 observations on the following 3 variables.

stance a factor with levels No stand, Opponent, Supporter

grade a factor with levels G11-12, G7-8, G9-10

p a numeric vector

rosenthal A data frame with 5 observations on the following 3 variables.

t A numeric vector of values of  $t$

df a numeric vector of degrees of freedom

p a numeric vector of one sided  $p$  values

teachexpect A vector of length 19

validity A data frame with 20 observations on the following 3 variables

n A numeric vector of sample sizes

r a numeric vector of correlation coefficients

p a numeric vector of one sided  $p$  values

zhang A data frame with 22 observations on the following 11 variables

study Character, the study names

smd numeric, the standardised mean difference

lo numeric, the lower confidence limit

hi numeric, the upper confidence limit

ntreat numeric, the treated sample size

ncont numeric, the control sample size

n numeric, the total sample size

phase factor, what phase the patients were in: acute, healing, healed

sd numeric, the calculated standard deviation

z numeric, the calculated  $z$

p numeric, the probability associated with  $z$

**Details**

- beckerp Hypothetical  $p$  values from Becker (1994)
- cholest  $p$  values from trials of interventions for lowering cholesterol lowering from Sutton et al. (2000)
- edgington Hypothetical  $p$  values from Edgington (1972)
- mourning Results from a study of mourning practices of Israeli youth following the assassination of Itzhak Rabin from Benjamini and Hochberg (2000)
- naep Results of mathematical achievement scores from the National Assessment of Educational Progress from Benjamini and Hochberg (2000)
- rosenthal Hypothetical example from Rosenthal (1978)
- teachexpect  $p$ -values from studies of the effect of manipulating teacher expectancy on student IQ from Becker (1994)
- validity Data from studies of validity of student ratings of their instructors from Becker (1994) including correlations and sample sizes as well as  $p$ -values
- zhang Data from trials of exercise training for patients with cardiovascular disease from Zhang et al. (2016)

**Note**

The  $p$ -values in `cholest` have been re-calculated and are of higher accuracy than the ones given in the book.

**Author(s)**

Michael Dewey

**References**

- Becker BJ (1994). "Combining significance levels." In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.
- Benjamini Y, Hochberg Y (2000). "On the adaptive control of the false discovery rate in multiple testing with independent statistics." *Journal of Educational and Behavioral Statistics*, **25**, 60–83.
- Edgington ES (1972). "An additive method for combining probability values from independent experiments." *Journal of Psychology*, **80**, 351–363.
- Rosenthal R (1978). "Combining results of independent studies." *Psychological Bulletin*, **85**, 185–193.
- Sutton AJ, Abrams KR, Jones DR, Sheldon TA, Song F (2000). *Methods for meta-analysis in medical research*. Wiley, Chichester.
- Zhang YM, Lu Y, Yang D, Wu HF, Bian ZP, Xu JD, Gu CR, Wang LS, Chen XJ (2016). "The effects of different initiation time of exercise training on left ventricular remodeling and cardiopulmonary rehabilitation in patients with left ventricular dysfunction after myocardial infarction." *Disability and Rehabilitation*, **38**, 268–276.

**Examples**

`data(dat.metap)`



---

invchisq *Combine p values using inverse chi squared method*

---

### Description

Combine  $p$ -values by the inverse chi-squared method, also known as Lancaster's method

### Usage

```
invchisq(p, k, data = NULL, subset = NULL, na.action = na.fail, log.p = FALSE)
## S3 method for class 'invchisq'
print(x, ...)
```

### Arguments

p	A vector of significance values
k	A vector of degrees of freedom to use, see details
data	Optional data frame containing variables
subset	Optional vector of logicals to specify a subset of the $p$ -values
na.action	A function indicating what should happen when data contains NAs
log.p	Logical, if TRUE result is returned as log(p)
x	An object of class 'invchisq'
...	Other arguments to be passed through

### Details

Defined as

$$\sum_{i=1}^n \chi_{k_i}^2(p_i) > \chi_{\sum k_i}^2(\alpha)$$

If  $k$  is a single value it is used for all the  $p$  of which there are  $n$ . If any value of  $k_i \leq 0$  then the corresponding  $p_i$  is not included.

The values of  $p_i$  should be such that  $0 < p_i \leq 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to NA.

The plot method for class 'metap' calls `plotp` on the valid  $p$ -values. Inspection of the distribution of  $p$ -values is highly recommended as extreme values in opposite directions do not cancel out. See last example. This may not be what you want.

### Value

An object of class 'invchisq' and 'metap', a list with entries

chisq	Value of chi-squared statistic
df	Associated degrees of freedom
p	Associated p-value
validp	The input vector with the illegal values removed

**Author(s)**

Michael Dewey

**References**

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

Lancaster HO (1949). “Combination of probabilities arising from data in discrete distributions.” *Biometrika*, **36**, 370–382.

**See Also**

See also [sumlog](#) and [plotp](#)

**Examples**

```
data(dat.metap)
beckerp <- dat.metap$beckerp
invchisq(beckerp, 2) # same as sumlog
invchisq(c(0.999, 0.999, 0.001, 0.001), 4)
all.equal(exp(invchisq(beckerp, 2, log.p = TRUE)$p), invchisq(beckerp, 2)$p)
```

---

inv

*Combine p values using inverse t method*

---

**Description**

Combine p values using the inverse t method

**Usage**

```
inv(p, k, data = NULL, subset = NULL, na.action = na.fail,
    log.p = FALSE)
## S3 method for class 'inv'
print(x, ...)
```

**Arguments**

p	A vector of significance values
k	A vector of degrees of freedom to use, see details
data	Optional data frame containing variables
subset	Optional vector of logicals to specify a subset of the <i>p</i> -values
na.action	A function indicating what should happen when data contains NAs
log.p	Logical, if TRUE result is returned as log(p)
x	An object of class ‘inv’
...	Other arguments to be passed through

**Details**

Defined as

$$\frac{\sum_{i=1}^n t_{k_i}(p_i)}{\sqrt{\sum_{i=1}^n \frac{k_i}{k_i-2}}} > z(\alpha)$$

If  $k$  is a single value it is used for all the  $p$  of which there are  $n$ . If any value of  $k_i \leq 2$  then the corresponding  $p_i$  is not included.

The values of  $p_i$  should be such that  $0 < p_i \leq 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to NA.

The plot method for class ‘metap’ calls `plotp` on the valid  $p$ -values.

**Value**

An object of class ‘invt’ and ‘metap’, a list with entries

<code>z</code>	Value of $z$
<code>p</code>	Associated $p$ -value
<code>validp</code>	The input vector with the illegal values removed

**Author(s)**

Michael Dewey

**References**

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

**See Also**

See also `plotp`

**Examples**

```
data(dat.metap)
beckerp <- dat.metap$beckerp
invt(beckerp, 50)
all.equal(exp(invt(beckerp, 50, log.p = TRUE)$p), invt(beckerp, 50)$p)
```

---

logitp

*Combine p values using logit method*

---

**Description**

Combine  $p$  values using logit method

**Usage**

```
logitp(p, log.p = FALSE)
## S3 method for class 'logitp'
print(x, ...)
```

**Arguments**

p	A vector of significance values
log.p	Logical, if TRUE result is returned as log(p)
x	An object of class ‘logitp’
...	Other arguments to be passed through

**Details**

Defined as

$$t = - \frac{\sum_{i=1}^k \log \frac{p_i}{1-p_i}}{C}$$

where

$$C = \sqrt{\frac{k\pi^2(5k+2)}{3(5k+4)}}$$

and  $k$  is the number of studies.

The values of  $p_i$  should be such that  $0 < p_i < 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to NA.

The plot method for class ‘metap’ calls [plotp](#) on the valid  $p$ -values.

**Value**

An object of class ‘logitp’ and ‘metap’, a list with entries

t	Value of Student’s $t$
df	Associated degrees of freedom
p	Associated $p$ -value
validp	The input vector with illegal values removed

**Author(s)**

Michael Dewey

**References**

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

**See Also**

See also [plotp](#)

**Examples**

```
data(dat.metap)
teachexpect <- dat.metap$teachexpect
logitp(teachexpect) # t = 2.763, df = 99, p = 0.0034, from Becker
beckerp <- dat.metap$beckerp
logitp(beckerp) # t = 1.62, df = 29, NS, from Becker
validity <- dat.metap$validity$p
logitp(validity) # t = 9.521, df = 104, p = 3.89 * 10^{-16}
all.equal(exp(logitp(validity, log.p = TRUE)$p), logitp(validity)$p)
```

---

meanp	<i>Combine p values by the mean p method</i>
-------	--

---

**Description**

Combine  $p$  values by the mean  $p$  method

**Usage**

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

**Arguments**

<code>p</code>	A vector of significance values
<code>x</code>	An object of class 'meanp'
<code>...</code>	Other arguments to be passed through

**Details**

Defined as

$$z = (0.5 - \bar{p})\sqrt{12k}$$

which is a standard normal and due to Edgington (1972)

The values of  $p_i$  should be such that  $0 \leq p_i \leq 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than four values remain and the return values are set to NA.

The plot method for class 'metap' calls `plotp` on the valid  $p$ -values.

**Value**

An object of class 'meanp' and 'metap', a list with entries

<code>z</code>	Value of $z$
<code>p</code>	Associated $p$ -value
<code>validp</code>	The input vector with illegal values removed

**Author(s)**

Michael Dewey

**References**

Becker BJ (1994). "Combining significance levels." In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

Edgington ES (1972). "A normal curve method for combining probability values from independent experiments." *Journal of Psychology*, **82**, 85–89.

Rosenthal R (1978). "Combining results of independent studies." *Psychological Bulletin*, **85**, 185–193.

**See Also**

See also [plotp](#)

**Examples**

```
data(dat.metap)
rosenthal <- dat.metap$rosenthal
meanp(rosenthal$p) # 2.17, p = 0.015 one tailed
```

---

meanz

*Combine p values using mean z method*

---

**Description**

Combines p values using the mean of z method

**Usage**

```
meanz(p, log.p = FALSE)
## S3 method for class 'meanz'
print(x, ...)
```

**Arguments**

p	A vector of significance values
log.p	Logical, if TRUE result is returned as log(p)
x	An object of class 'meanz'
...	Other arguments to be passed through

**Details**

Let

$$\bar{z} = \sum_{i=1}^k \frac{z(p_i)}{k}$$

and

$$s_{\bar{z}} = \frac{s_z}{\sqrt{k}}$$

Defined as

$$\frac{\bar{z}}{s_{\bar{z}}} > t_{k-1}(\alpha)$$

The values of  $p_i$  should be such that  $0 \leq p_i \leq 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to NA. As can be seen if all the  $p_i$  are equal or close to equal this gives a  $t = \pm\infty$  leading to a returned value of 0 or 1. A set of  $p$  values with small variance will necessarily give a small  $p$  value which may be smaller than that for another set all of whose primary values are less than any in the first set. See examples for a demonstration.

The plot method for class 'metap' calls [plotp](#) on the valid  $p$ -values.

**Value**

An object of class ‘meanz’ and ‘metap’, a list with entries

z	The value of the mean $z$ statistic
p	The associated $p$ value
validp	The input vector with illegal values removed

**Author(s)**

Michael Dewey

**References**

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

**See Also**

See also [plotp](#)

**Examples**

```
data(dat.metap)
beckerp <- dat.metap$beckerp
meanz(beckerp)
meanz(c(0.1, 0.2)) # greater than next example
meanz(c(0.3, 0.31)) # less than above
all.equal(exp(meanz(beckerp, log.p = TRUE)$p), meanz(beckerp)$p)
```

---

plotp

*Q-Q plot of p-values*

---

**Description**

Produces a Q–Q plot of the  $p$ -values supplied

**Usage**

```
plotp(pvals, plotversion = "qqconf", ...)
```

**Arguments**

pvals	A vector of $p$ -values
plotversion	Whether to use the qqconf version or the original
...	Other parameters to pass through to qqplot and qqline

**Details**

After eliminating out of range  $p$ -values and missing values produces a Q-Q plot. If the package `qqconf` is unavailable or `plotversion` is set other than "qqconf" then the plot uses the function from base graphics. The line shown is through the quantiles (by default the 0.25 and 0.75).

If the package `qqconf` is available then the plot uses that package's function and as well as the Q-Q plot produces a confidence region. Parameters can be passed to `qq_conf_plot` to exert further control over the plot.

If `plotversion` is set to "qqconf" but package `qqconf` is not available then a warning is given and no plot is produced.

**Value**

Invisibly returns a list consisting of

`validp`            The valid  $p$ -values

**Author(s)**

Michael Dewey

**See Also**

[qqplot](#) and [qqline](#) for the original plot and [qq\\_conf\\_plot](#) for the new version.

**Examples**

```
data(dat.metap)
cholest <- dat.metap$cholest$p
plotp(cholest)
```

---

schweder

*Schweder and Spjotvoll plot*

---

**Description**

Produces the plot suggested by Schweder and Spjotvoll to display a collection of  $p$ -values and also optionally draws the lowest slope line suggested by Benjamini and Hochberg

**Usage**

```
schweder(p, xlab = "Rank of p", ylab = "p", drawline = NULL,
  bh.lwd = 1, bh.lty = "solid", bh.col = "black",
  ls.control = list(frac = NULL),
  ls.lwd = 1, ls.lty = "dotted", ls.col = "black",
  ab.control = list(a = NULL, b = NULL),
  ab.lwd = 1, ab.lty = "dashed", ab.col = "black", ...)
```



**Arguments**

<code>p</code>	A vector of $p$ -values
<code>xlab</code>	Label for plot $x$ -axis
<code>ylab</code>	Label for plot $y$ -axis
<code>drawline</code>	Which line, if any, to draw. See Details
<code>bh.lwd</code>	Width of the lowest slope line
<code>bh.lty</code>	Line type of the lowest slope line
<code>bh.col</code>	Colour of the lowest slope line
<code>ls.control</code>	A list containing a named element <code>frac</code> . See Details
<code>ls.lwd</code>	Width of the least squares line
<code>ls.lty</code>	Line type of the least squares line
<code>ls.col</code>	Colour of the least squares line
<code>ab.control</code>	A list containing two elements <code>a</code> and <code>b</code> . See Details
<code>ab.lwd</code>	Width of the specified line
<code>ab.lty</code>	Line type of the specified line
<code>ab.col</code>	Colour of the specified line
<code>...</code>	Further parameters to be passed through to plot

**Details**

After removing invalid  $p$ -values plots them. Any graphics parameters passed in `...` affect this part of the plot only. Note that the axes are chosen according to the scheme of Benjamini and Hochberg, Schweder and Spjøtvoll used a different system.

By setting `drawline` appropriately up to three lines may be drawn.

If `drawline` includes the string "bh" the lowest slope line of Benjamini and Hochberg is drawn. No further parameters are needed here but the characteristics of the line may be set: width, line type, and colour.

If `drawline` includes the string "ls" a least squares line is drawn passing through the point  $k + 1, 1$ . The parameter `frac` specified what fraction of the values be used for this and may need experimentation to obtain a suitable line. The characteristics of the line may be set: width, line type, and colour.

If `drawline` includes the string "ab" a user specified line is drawn. The parameters `a` and `b` specify the intercept and slope. The characteristics of the line may be set: width, line type, and colour.

**Value**

A list containing

<code>p</code>	The values of $p$ plotted
<code>bh.params</code>	A list containing at least items <code>a</code> and <code>b</code> the intercept and slope of the line drawn. This is only included if the lowest slope line was drawn
<code>ls.params</code>	A list containing at least items <code>a</code> and <code>b</code> the intercept and slope of the line drawn. This is only included if the least squares line was drawn
<code>ab.params</code>	A list containing at least items <code>a</code> and <code>b</code> the intercept and slope of the line drawn. This is only included if the user specified line was drawn

**Author(s)**

Michael Dewey

**References**

Becker BJ (1994). "Combining significance levels." In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

Benjamini Y, Hochberg Y (2000). "On the adaptive control of the false discovery rate in multiple testing with independent statistics." *Journal of Educational and Behavioral Statistics*, **25**, 60–83.

Schweder T, Spjøtvoll E (1982). "Plots of  $P$ -values to evaluate many tests simultaneously." *Biometrika*, **69**, 493–502.

**Examples**

```
data(dat.metap)
teachexpect <- dat.metap$teachexpect
schweder(teachexpect)
```

sumlog

*Combine p-values by the sum of logs (Fisher's method)***Description**

Combine  $p$ -values by the sum of logs method, also known as Fisher's method, and sometimes as the chi-square (2) method

**Usage**

```
sumlog(p, log.p = FALSE)
## S3 method for class 'sumlog'
print(x, ...)
```

**Arguments**

<code>p</code>	A vector of significance values
<code>log.p</code>	Logical, if TRUE result is returned as $\log(p)$
<code>x</code>	An object of class 'sumlog'
<code>...</code>	Other arguments to be passed through

**Details**

The method relies on the fact that

$$\sum_{i=1}^k -2 \log p_i$$

is a chi-squared with  $2k$  df where  $k$  is the number of studies (Fisher 1925).

The values of  $p_i$  should be such that  $0 < p_i \leq 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to NA.

The plot method for class 'metap' calls `plotp` on the valid  $p$ -values. Inspection of the distribution of  $p$ -values is highly recommended as extreme values in opposite directions do not cancel out. See last example. This may not be what you want.

**Value**

An object of class ‘sumlog’ and ‘metap’, a list with entries

chisq	Value of chi-squared statistic
df	Associated degrees of freedom
p	Associated <i>p</i> -value
validp	The input vector with the illegal values removed

**Author(s)**

Michael Dewey

**References**

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

Fisher RA (1925). *Statistical methods for research workers*. Oliver and Boyd, Edinburgh.

Rosenthal R (1978). “Combining results of independent studies.” *Psychological Bulletin*, **85**, 185–193.

Sutton AJ, Abrams KR, Jones DR, Sheldon TA, Song F (2000). *Methods for meta-analysis in medical research*. Wiley, Chichester.

**See Also**

See also [plotp](#)

**Examples**

```
data(dat.metap)
teachexpect <- dat.metap$teachexpect
sumlog(teachexpect) # chisq = 69.473, df = 38, p = 0.0014, from Becker
beckerp <- dat.metap$beckerp
sumlog(beckerp) # chisq = 18.533, df = 10, sig
rosenthal <- dat.metap$rosenthal
sumlog(rosenthal$p) # chisq = 22.97, df = 10, p = 0.006 one sided
cholest <- dat.metap$cholest$p
sumlog(cholest) # chisq = 58.62, df = 68, p = 0.78
validity <- dat.metap$validity$p
sumlog(validity) # chisq = 159.82, df = 40, p = 2.91 * 10^{-16}
sumlog(c(0.0001, 0.0001, 0.9999, 0.9999)) # is significant
all.equal(exp(sumlog(validity, log.p = TRUE)$p), sumlog(validity)$p)
```

sump

*Combine p-values using the sum of p (Edgington's) method***Description**

Combine  $p$ -values using the sum  $p$  method

**Usage**

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

**Arguments**

$p$                     A vector of significance values  
 $x$                      An object of class 'sump'  
 $\dots$                    Other arguments to be passed through

**Details**

Defined as

$$\frac{(\sum_{i=1}^k p_i)^k}{k!} - \binom{k}{1} \frac{(\sum_{i=1}^k p_i - 1)^k}{k!} + \binom{k}{2} \frac{(\sum_{i=1}^k p_i - 2)^k}{k!} \dots$$

where there are  $k$  studies and the series continues until the numerator becomes negative (Edgington 1972).

Some authors use a simpler version

$$\frac{(\sum_{i=1}^k p_i)^k}{k!}$$

but this can be very conservative when  $\sum_{i=1}^k p_i > 1$ . There seems no particular need to use this method but it is returned as the value of `conservativep` for use in checking published values.

The values of  $p_i$  should be such that  $0 \leq p_i \leq 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to NA. A warning is given when the internal calculations are likely to have been subject to numerical error and an alternative method should be used to check the result.

The plot method for class 'metap' calls `plotp` on the valid  $p$ -values.

**Value**

An object of class 'sump' and 'metap', a list with entries

$p$                         The transformed sum of the  $p$ -values  
`conservativep`        See details  
`validp`                The input vector with illegal values removed

**Author(s)**

Michael Dewey

## References

Edgington ES (1972). “An additive method for combining probability values from independent experiments.” *Journal of Psychology*, **80**, 351–363.

## See Also

See also [plotp](#)

## Examples

```
data(dat.metap)
edgington <- dat.metap$edgington
sump(edgington) # p = 0.097
```

---

sumz

*Combine p-values using the sum of z (Stouffer's) method*

---

## Description

Combine  $p$ -values using the sum  $z$  method

## Usage

```
sumz(p, weights = NULL, data = NULL, subset = NULL, na.action = na.fail,
     log.p = FALSE, log.input = FALSE)
## S3 method for class 'sumz'
print(x, ...)
```

## Arguments

<code>p</code>	A vector of significance values
<code>weights</code>	A vector of weights
<code>data</code>	Optional data frame containing variables
<code>subset</code>	Optional vector of logicals to specify a subset of the $p$ -values
<code>na.action</code>	A function indicating what should happen when data contains NAs
<code>log.p</code>	Logical, if TRUE result is returned as $\log(p)$
<code>log.input</code>	Logical, if TRUE the input $p$ values are assumed to be logged
<code>x</code>	An object of class ‘sumz’
<code>...</code>	Other arguments to be passed through

## Details

Defined as

$$\frac{\sum_{i=1}^k w_i z(p_i)}{\sqrt{\sum_{i=1}^k w_i^2}}$$

is a  $z$  where  $k$  is the number of studies and  $w$  are the weights (Stouffer et al. 1949). By default the weights are equal. In the absence of effect sizes (in which case a method for combining effect

sizes would be more appropriate anyway) best results are believed to be obtained with weights proportional to the square root of the sample sizes (Zaykin 2011)

The values of  $p_i$  should be such that  $0 < p_i < 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to NA. If the omitted  $p$  values had supplied weights a further warning is issued.

The plot method for class ‘metap’ calls `plotp` on the valid  $p$ -values.

### Value

An object of class ‘sumz’ and ‘metap’, a list with entries

<code>z</code>	Transformed sum of $z$ values
<code>p</code>	Associated $p$ -value
<code>validp</code>	The input vector with illegal values removed
<code>weights</code>	The weight vector corresponding to <code>validp</code>

### Author(s)

Michael Dewey

### References

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

Rosenthal R (1978). “Combining results of independent studies.” *Psychological Bulletin*, **85**, 185–193.

Stouffer SA, Suchman EA, DeVinney LC, Star SA, Williams RMJ (1949). *The American soldier, vol 1: Adjustment during army life*. Princeton University Press, Princeton.

Zaykin DV (2011). “Optimally weighted  $Z$ -test is a powerful method for combining probabilities in meta-analysis.” *Journal of Evolutionary Biology*, **24**, 1836–1841.

### See Also

See also `plotp`

### Examples

```
data(dat.metap)
teachexpect <- dat.metap$teachexpect
sumz(teachexpect) # z = 2.435, p = 0.0074, from Becker
beckerp <- dat.metap$beckerp
sumz(beckerp) # z = 1.53, NS, from Beckerp
rosenthal <- dat.metap$rosenthal
sumz(rosenthal$p) # 2.39, p = 0.009
sumz(p, df, rosenthal) # 3.01, p = 0.0013
validity <- dat.metap$validity$p
sumz(validity) # z = 8.191, p = 1.25 * 10^{-16}
all.equal(exp(sumz(validity, log.p = TRUE)$p), sumz(validity)$p)
all.equal(sumz(log(validity), log.input = TRUE)$p, sumz(validity)$p)
```

---

truncated	<i>Truncated product method routine</i>
-----------	---

---

## Description

Implements two procedures for truncated versions of Fisher's method

## Usage

```
truncated(p, ptrunc = NULL, rtrunc = NULL, ...)
## S3 method for class 'truncated'
print(x, ...)
## S3 method for class 'truncated'
summary(object, ...)
## S3 method for class 'truncated'
plot(x, pparams = list(pchs = c(16, 1),
  pcols = c("black", "black")), ...)
```

## Arguments

p	A vector of significance values
ptrunc	Value of $p$ to truncate at. See Details
rtrunc	Which rank $p$ to truncate at. See Details
x	An object of class 'truncated'
object	An object of class 'truncated'
...	Other arguments to be passed through
pparams	A list containing a vector pchs of plotting symbols and a vector pcols of colours

## Details

Uses routines from TFisher to implement truncated Fisher (Zaykin et al. 2007; Zhang et al. 2018) and from mutoss to implement rank-truncated Fisher (Dudbridge and Koeleman 2003)

The print method prints the statistic and its associated  $p$ -value. The summary method also prints how many of the input values were actually used. The plot method provides an index plot of the  $p$ -values. By default used  $p$ -values are plotted with a black filled circle and those not used with a black unfilled circle. The colours and plotting symbols can be changed in pparams. The first element of each vector is for the used  $p$ -values and the second for the unused ones.

## Value

An object of class 'truncated' a list with entries

p	The resultant overall $p$ -value
stat	The test statistic
validp	The input vector with illegal values removed
ptrunc	The $p$ -value used for truncation
trunc	The rank value used for truncation
n	A vector containing incl, the number of valid values included, excl, the number of valid values not used
method	The method used

**Note**

Only one of `ptrunc` or `rtrunc` is returned as appropriate. If the function encounters an error it returns NA for the value of `p` and gives a warning message. The effect of specifying both `ptrunc` and `rtrunc` is undefined.

**Author(s)**

Michael Dewey

**References**

Dudbridge F, Koeleman BPC (2003). “Rank truncated product of  $P$ -values, with application to genomewide association scans.” *Genetic Epidemiology*, **25**, 360–366.

Zaykin DV, Zhivotovsky LA, Czika W, Shao S, Wolfinger RD (2007). “Combining  $p$ -values in large-scale genomics experiments.” *Pharmaceutical Statistics*, **6**, 217–236.

Zhang H, Tong T, Landers J, Wu Z (2018). “TFisher tests: optimal and adaptive thresholding for combining  $p$ -values.” *arXiv*. <https://arxiv.org/abs/1801.04309>.

**See Also**

[ranktruncated](#), [stat.tpm](#), and [p.tpm](#)

**Examples**

```
data(dat.metap)
validity <- dat.metap$validity
truncated(validity, ptrunc = 0.5)
truncated(validity, rtrunc = 5)
```

---

two2one

*Convert two-sided  $p$ -values to one-sided*

---

**Description**

Convert two-sided  $p$ -values to one-sided

**Usage**

```
two2one(p, two = NULL, invert = NULL)
```

**Arguments**

<code>p</code>	A vector of $p$ -values
<code>two</code>	A logical vector defining which $p$ -values are two-sided and to be converted
<code>invert</code>	A logical vector defining which $p$ -values are to be inverted



**Details**

The  $p$ -values supplied to the other functions should be one-sided and all in the same direction. This convenience function will convert two-sided to one-sided and invert as necessary. By default it is assumed that all  $p$ -values are two-sided and the function converts them all to one-sided. Use `invert` to specify if some of the tests resulted in outcomes in the other direction. So for example a value of 0.05 will be converted to 0.025 unless `invert` is `TRUE` in which case it is converted to 0.975.

**Value**

A vector of one-sided  $p$ -values all in the correct direction

**Author(s)**

Michael Dewey

**Examples**

```
data(dat.metap)
rosenthal <- dat.metap$rosenthal
twop <- with(rosenthal, (pt(t, df)))
two2one(twop, two = rep(FALSE, 5), invert = rep(TRUE, 5)) # restore to one-sided
```

---

votep

---

*Combine  $p$ -values by the vote counting method*


---

**Description**

Combine  $p$ -values by the vote counting method

**Usage**

```
votep(p, alpha = 0.5)
## S3 method for class 'votep'
print(x, ...)
```

**Arguments**

<code>p</code>	A vector of significance values
<code>alpha</code>	A value defining the significance value limits, see Details
<code>x</code>	An object of class 'votep'
<code>...</code>	Other arguments to be passed through

**Details**

By default splits the  $p$ -values at 0.5 with those below counting as positive and those above counting as negative. However setting `alpha` allows specifying a neutral zone. In that case values between `alpha` and `1 - alpha` will be assumed to be neutral and only those outside the zone counted as positive or negative. If the value of `alpha` is greater than unity it is assumed to be a percentage.

The values of  $p_i$  should be such that  $0 < p_i < 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to `NA`.

The plot method for class 'metap' calls `plotp` on the valid  $p$ -values.

**Value**

An object of class ‘votep’ and ‘votep’, a list with entries

p	<i>p</i> value
pos	Number of positives
neg	Number of negatives
alpha	The cut-off significance value lying in the range 0 to 1
validp	The input vector with illegal values removed

**Author(s)**

Michael Dewey

**References**

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

**See Also**

See also [plotp](#)

**Examples**

```
data(dat.metap)
beckerp <- dat.metap$beckerp
votep(beckerp)
```

---

wilkinsonp

*Combine p-values using Wilkinson’s method*

---

**Description**

Combine *p*-values using Wilkinson’s method

**Usage**

```
wilkinsonp(p, r = 1, alpha = 0.05, log.p = FALSE)
maximump(p, alpha = 0.05, log.p = FALSE)
minimump(p, alpha = 0.05, log.p = FALSE)
## S3 method for class 'wilkinsonp'
print(x, ...)
## S3 method for class 'maximump'
print(x, ...)
## S3 method for class 'minimump'
print(x, ...)
```

**Arguments**

<code>p</code>	A vector of significance values
<code>r</code>	Use the $r$ th smallest $p$ value
<code>alpha</code>	The significance level
<code>log.p</code>	Logical, if TRUE result is returned as $\log(p)$
<code>x</code>	An object of class 'wilkinsonp' or of class 'maximump' or of class 'minimump'
<code>...</code>	Other arguments to be passed through

**Details**

Wilkinson (Wilkinson 1951) originally proposed his method in the context of simultaneous statistical inference: the probability of obtaining  $r$  or more significant statistics by chance in a group of  $k$ . The values are obtained from the Beta distribution, see [pbeta](#).

If `alpha` is greater than unity it is assumed to be a percentage. Either values greater than 0.5 (assumed to be confidence coefficient) or less than 0.5 are accepted.

The values of  $p_i$  should be such that  $0 \leq p_i \leq 1$  and a warning is given if that is not true. A warning is given if, possibly as a result of removing illegal values, fewer than two values remain and the return values are set to NA.

`maximump` and `minimump` each provide a wrapper for `wilkinsonp` for the special case when  $r = \text{length}(p)$  or  $r = 1$  respectively and each has its own print method. The method of minimum  $p$  is also known as Tippett's method (Tippett 1931).

The plot method for class 'metap' calls `plotp` on the valid  $p$ -values. Inspection of the distribution of  $p$ -values is highly recommended as extreme values in opposite directions do not cancel out. See last example. This may not be what you want.

**Value**

An object of class 'wilkinsonp' and 'metap' or of class 'maximump' and 'metap' or of class 'minimump' and 'metap', a list with entries

<code>p</code>	The $p$ -value resulting from the meta-analysis
<code>pr</code>	The $r$ th smallest $p$ value used
<code>r</code>	The value of $r$
<code>critp</code>	The critical value at which the $r$ th value would have been significant for the chosen <code>alpha</code>
<code>validp</code>	The input vector with illegal values removed

**Note**

The value of `critp` is always on the raw scale even if `log.p` has been set to TRUE

**Author(s)**

Michael Dewey

## References

Becker BJ (1994). “Combining significance levels.” In Cooper H, Hedges LV (eds.), *A handbook of research synthesis*, 215–230. Russell Sage, New York.

Birnbaum A (1954). “Combining independent tests of significance.” *Journal of the American Statistical Association*, **49**, 559–574.

Tippett LHC (1931). *The methods of statistics*. Williams and Norgate, London.

Wilkinson B (1951). “A statistical consideration in psychological research.” *Psychological Bulletin*, **48**, 156–158.

## See Also

See also [plotp](#)

## Examples

```
data(dat.metap)
beckerp <- dat.metap$beckerp
minimump(beckerp) # signif = FALSE, critp = 0.0102, minp = 0.016
teachexpect <- dat.metap$teachexpect
minimump(teachexpect) # crit 0.0207, note Becker says minp = 0.0011
wilkinsonp(c(0.223, 0.223), r = 2) # Birnbaum, just signif
validity <- dat.metap$validity$p
minimump(validity) # minp = 0.00001, critp = 1.99 * 10^{-4}
minimump(c(0.0001, 0.0001, 0.9999, 0.9999)) # is significant
all.equal(exp(minimump(validity, log.p = TRUE)$p), minimump(validity)$p)
all.equal(exp(maximump(validity, log.p = TRUE)$p), maximump(validity)$p)
```

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