Package 'metap'

October 31, 2021

Type Package

Title Meta-Analysis of Significance Values

Version 1.6

Date 2021-10-31

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 a routine for graphical display.

URL http://www.dewey.myzen.co.uk/meta/meta.html

Depends R (>= 3.5.0)

Imports lattice,Rdpack (>= 0.7),TFisher,mutoss,mathjaxr (>= 0.8-3)

RdMacros Rdpack,mathjaxr

License GPL-2

LazyLoad yes

R topics documented:

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metap-package   *Meta-Analysis of Significance Values*

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 a routine for graphical display.

Details

Index of help topics:

```
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)

Provides a number of ways in which significance levels may be combined in a meta-analysis and includes most ot 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).

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.

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 signficance levels is not completely unconnected with the topic of adjustment for multiple comparisons as in for example p.adjust

---

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

Arguments

p	A vector of p-values
method	A vector of character containing names of methods or 'all'
x	An object of class 'allmetap'
digits	How many digits to print?
...	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

p	The value of p returned
valid	The number of valid p values used for that method
eponym	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, and validity.

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

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 Itzakh Rabin from Benjamini and Hochberg (2000)

naep Results of mathematical achievment 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

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.

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

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

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

The values of p_i should be such that $0 < p_i \le 1$ 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)
```

---

invt   *Combine p values using inverse t method*

Description

Combine p values using the inverse t method

Usage

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

z	Value of z
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.

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   *Combine p values by the mean p method*

Description

Combine p values by the mean p method

Usage

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

Arguments

p	A vector of significance values
x	An object of class 'meanp'
...	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

z	Value of z
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.

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 $0 \le p_i \le 1$ 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, ...)
```

Arguments

pvals   A vector of p–values

...   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 and the line through the quantiles (by default the 0.25 and 0.75).

Value

Invisibly returns a list conisting of

validp   The valid p–values

Author(s)

Michael Dewey

See Also

[qqplot](#) and [qqline](#)

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

p	A vector of p-values
xlab	Label for plot x-axis
ylab	Label for plot y-axis
drawline	Which line, if any, to draw. See Details
bh.lwd	Width of the lowest slope line
bh.lty	Line type of the lowest slope line
bh.col	Colour of the lowest slope line
ls.control	A list containing a named element frac. See Details
ls.lwd	Width of the least squares line
ls.lty	Line type of the least squares line
ls.col	Colour of the least squares line
ab.control	A list containing two elements a and b. See Details
ab.lwd	Width of the specified line
ab.lty	Line type of the specified line
ab.col	Colour of the specified line
...	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 Banjamini and Hochberg, Schweder and Spjotvoll 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 Benjaimin 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

p	The values of p plotted
bh.params	A list containing at least items a and b the intercept and slope of the line drawn. This is only included if the lowest slope line was drawn
ls.params	A list containing at least items a and b the intercept and slope of the line drawn. This is only included if the least squares line was drawn
ab.params	A list containing at least items a and b 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, Spjotvoll 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

p	A vector of significance values
log.p	Logical, if TRUE result is returned as log(p)
x	An object of class 'sumlog'
...	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 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.

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'
...	Other arguments to be passed through

Details

Defined as

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

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 $0 \le p_i \le 1$ 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

p	A vector of significance values
weights	A vector of weights
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)
log.input	Logical, if TRUE the input p values are assumed to be logged
x	An object of class 'sumz'
...	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

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

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   *Truncated product method routine*

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

p   A vector of p-values

two   A logical vector defining which p-values are two-sided and to be converted

invert   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

p	A vector of significance values
alpha	A value defining the significance value limits, see Details
x	An object of class 'votep'
...	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	p 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

p	A vector of significance values
r	Use the rth smallest p value
alpha	The significance level
log.p	Logical, if TRUE result is returned as log(p)
x	An object of class 'wilkinsonp' or of class 'maximump' or of class 'minimump'
...	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

p	The p-value resulting from the meta–analysis
pr	The rth smallest p value used
r	The value of r
critp	The critical value at which the rth value would have been significant for the chosen alpha
validp	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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