

Package ‘metap’

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Type Package

Title Meta-Analysis of Significance Values

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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 a routine for graphical display.

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

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

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 a routine for graphical display.

Details

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metap-package	Meta-Analysis of Significance Values
plotp	Q-Q plot of p-values
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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
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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 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).

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, Spjøtvoll 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](#)

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(beckerp)
allmetap(beckerp, method = "all")
allmetap(beckerp, method = c("sumz", "sumlog"))
```

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)
## 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
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(beckerp)
invchisq(beckerp, 2) # same as sumlog
invchisq(c(0.999, 0.999, 0.001, 0.001), 4)
```

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

Arguments

<code>p</code>	A vector of significance values
<code>k</code>	A vector of degrees of freedom to use, see details
<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>x</code>	An object of class ‘invt’
<code>...</code>	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(beckerp)
invt(beckerp, 50)
```

logitp

Combine p values using logit method

Description

Combine p values using logit method

Usage

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

Arguments

p A vector of significance values
 x An object of class ‘logitp’
 \dots 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(teachexpect)
logitp(teachexpect) # t = 2.763, df = 99, p = 0.0034, from Becker
data(beckerp)
logitp(beckerp) # t = 1.62, df = 29, NS, from Becker
data(validity)
logitp(validity) # t = 9.521, df = 104, p = 3.89 * 10^{-16}
```

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

Arguments

p A vector of significance values
 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(beckerp)
meanz(beckerp)
meanz(c(0.1, 0.2)) # greater than next example
meanz(c(0.3, 0.31)) # less than above
```

 package-data

Example data

Description

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

Usage

```
data(beckerp)
data(cholest)
data(edgington)
data(mourning)
data(naep)
data(rosenthal)
data(teachexpect)
data(validity)
```

Format

beckerp A vector of length 5

cholest 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 vector of length 20

Details

beckerp Hypothetical p values from Becker (1994)
 cholest p -values from studies of 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 from Benjamini and Hochberg (2000)
 naep Results on 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 from Becker (1994)
 validity p -values from studies of validity of student ratings from Becker (1994)

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.

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 consisting of

`validp` The valid p -values

Author(s)

Michael Dewey

See Also

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

Examples

```
data(cholest)
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, Spjotvoll E (1982). "Plots of P -values to evaluate many tests simultaneously." *Biometrika*, **69**, 493–502.

Examples

```
data(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)
## S3 method for class 'sumlog'
print(x, ...)
```

Arguments

p	A vector of significance values
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 <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(teachexpect)
sumlog(teachexpect) # chisq = 69.473, df = 38, p = 0.0014, from Becker
data(beckerp)
sumlog(beckerp) # chisq = 18.533, df = 10, sig
data(rosenthal)
sumlog(rosenthal$p) # chisq = 22.97, df = 10, p = 0.006 one sided
data(cholest)
sumlog(cholest) # chisq = 58.62, df = 68, p = 0.78
data(validity)
sumlog(validity) # chisq = 159.82, df = 40, p = 2.91 * 10^{-16}
sumlog(c(0.0001, 0.0001, 0.9999, 0.9999)) # is significant
```

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

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

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(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)
## 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>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(teachexpect)
sumz(teachexpect) # z = 2.435, p = 0.0074, from Becker
data(beckerp)
sumz(beckerp) # z = 1.53, NS, from Beckerp
data(rosenthal)
sumz(rosenthal$p) # 2.39, p = 0.009
sumz(p, df, rosenthal) # 3.01, p = 0.0013
data(Validity)
sumz(Validity) # z = 8.191, p = 1.25 * 10^{-16}
```

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

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

<code>p</code>	The resultant overall p -value
<code>stat</code>	The test statistic
<code>validp</code>	The input vector with illegal values removed
<code>ptrunc</code>	The p -value used for truncation
<code>trunc</code>	The rank value used for truncation
<code>n</code>	A vector containing <code>incl</code> , the number of valid values included, <code>excl</code> , the number of valid values not used
<code>method</code>	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(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(rosenthal)
twop <- with(rosenthal, (pt(t, df)))
two2one(twop, two = rep(FALSE, 5), invert = rep(TRUE, 5)) # restore to one-sided
```

votep	<i>Combine p-values by the vote counting method</i>
-------	---

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(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)
maximump(p, alpha = 0.05)
minimump(p, alpha = 0.05)
## 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 r th smallest p value
alpha	The significance level
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 r th smallest p value used
r	The value of r
critp	The critical value at which the r th value would have been significant for the chosen alpha
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.

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(beckerp)
minimump(beckerp) # signif = FALSE, critp = 0.0102, minp = 0.016
data(teachexpect)
minimump(teachexpect) # crit 0.0207, note Becker says minp = 0.0011
wilkinsonp(c(0.223, 0.223), r = 2) # Birnbaum, just signif
data(validity)
minimump(validity) # minp = 0.00001, critp = 1.99 * 10^{-4}
minimump(c(0.0001, 0.0001, 0.9999, 0.9999)) # is significant
```


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