

Package ‘metap’

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Type Package

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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.

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metap-package	<i>Meta-Analysis of Significance Values</i>
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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.

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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).

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

Author(s)

Michael Dewey

Maintainer: Michael Dewey <lists@dewey.myzen.co.uk>

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 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

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 p -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 $k < 1$ then the corresponding p is not included.

The values of p should be such that $0 < p \leq 1$ and a warning is given if that is not true. An error is given if possibly as a result of deletions fewer than two studies remain.

The plot method for class ‘metap’ calls [schweder](#) on the valid p -values. Inspection of the distribution of p -values is highly recommended as extreme values in opposite directions do not always cancel out especially for small values of k . 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](#)

Examples

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

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

Arguments

p	A vector of p -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 '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 $k < 1$ then the corresponding p is not included.

The values of p should be such that $0 < p \leq 1$ and a warning is given if that is not true. An error is given if possibly as a result of deletions fewer than two studies remain.

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

Value

An object of class 'inv' 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.

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 p values
x	An object of class ‘logitp’
...	Other arguments to be passed through

Details

Defined as

$$t = -\frac{\sum \log \frac{p}{1-p}}{C}$$

where

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

and k is the number of studies.

The values of p should be such that $0 < p < 1$. A warning is issued if this means that studies are omitted and an error results if as a result fewer than two studies remain.

The plot method for class ‘metap’ calls [schweder](#) 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 [schweder](#)

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 p -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 should be such that $0 \leq p \leq 1$. A warning is issued if this means that studies are omitted and an error results if, possibly after deletion of illegal values, fewer than four studies remain.

The plot method for class ‘metap’ calls [schweder](#) 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 [schweder](#)

Examples

```
data(rosenthal)
meanp(rosenthal$p) # 2.17, p = 0.015 one tailed
```

meanz	<i>Combine p values using mean z method</i>
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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 p -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 should be such that $0 \leq p \leq 1$ and a warning is given if this is not true. An error is given if possibly as a result of removing them fewer than two valid p values remain. 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.

The plot method for class 'metap' calls [schweder](#) 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.

Examples

```
data(beckerp)
meanz(beckerp)
```

package-data	<i>Example data</i>
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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, Abrams, Jones, Sheldon, and Song (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.

schweder

Schweder and Spjøtvoll plot

Description

Produces the plot suggested by Schweder and Spjøtvoll 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` specifies 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 p -values
x	An object of class ‘sumlog’
...	Other arguments to be passed through

Details

The method relies on the fact that

$$\sum -2 \log p$$

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

The values of p should be such that $0 < p \leq 1$ and a warning is given if that is not true. An error is given if possibly as a result of deletions fewer than two studies remain.

The plot method for class ‘metap’ calls [schweder](#) 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 [schweder](#)

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 p -values
x	An object of class 'sump'
...	Other arguments to be passed through

Details

Defined as

$$\frac{(\sum p)^k}{k!} - \binom{k-1}{1} \frac{(\sum p-1)^k}{k!} + \binom{k-2}{2} \frac{(\sum p-2)^k}{k!}$$

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

Some authors use a simpler version $\frac{(\sum p)^k}{k!}$ where there are k studies but this can be very conservative when $\sum p > 1$. There seems no particular need to use this method but it is returned as the value of conservative p for use in checking published values.

The values of p should be such that $0 \leq p \leq 1$ and a warning is given if this is not true. An error is given if possibly as a result of removing them fewer than two valid p values remain. 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 [schweder](#) 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 [schweder](#)

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

`p` A vector of p -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
`x` An object of class ‘sumz’
`...` Other arguments to be passed through

Details

Defined as

$$\frac{\sum(wz(p))}{\sqrt{\sum w^2}}$$

is a z where k is the number of studies and w are the weights (Stouffer, Suchman, DeVinney, Star, and Williams 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 should be such that $0 < p < 1$. A warning is issued if this means that studies are omitted and an error results if as a result fewer than two studies remain. If the omitted p values had supplied weights a further warning is issued.

The plot method for class ‘metap’ calls [schweder](#) 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 [schweder](#)

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}
```

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)))
```

votep

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

Combine p -values by the vote counting method

Usage

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

Arguments

<code>p</code>	A vector of p -values
<code>alpha</code>	A vector of length 2 defining the significance values
<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 for a different choice of cut-off and also by specifying two different values for a neutral zone. If either value of alpha is greater than unity it is assumed to be a percentage.

The values of p should be such that $0 \leq p \leq 1$ and a warning is issued if this is not true An error occurs if possibly as a result of deletion fewer than two studies remain.

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

Value

An object of class 'votep' and 'votep', a list with entries

<code>p</code>	p value
<code>pos</code>	Number of positives
<code>neg</code>	Number of negatives
<code>alpha</code>	A vector of length 2 defining the significance values and lying in the range 0 to 1
<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.

See Also

See also [schweder](#)

Examples

```
data(beckerp)
votep(beckerp)
```

wilkinsonp	<i>Combine p-values using Wilkinson’s method</i>
------------	--

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 <i>p</i> -values
r	Use the <i>r</i> th smallest <i>p</i> 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 should be such that $0 \leq p \leq 1$ and a warning is issued if that is not true. An error results if possibly as a result of deletions fewer than two studies remain.

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 [schweder](#) on the valid p -values. Inspection of the p -values is 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 [schweder](#)

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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