Package ‘metap’

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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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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


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

```r
allmetap(p, method = NULL)
```

## S3 method for class 'allmetap'

print(x, digits = 5, ...)

invchisq

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"))

---

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, ...)

Combine *p* values using inverse chi squared method
invchisq

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

\[ \sum_{i=1}^{n} \frac{\chi^2_k(p_i)}{\sum k_i(\alpha)} \]

If \( k \) is a single value it is used for all the \( p \) of which there are \( n \). If any value of \( k_i \leq 0 \) 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. An 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


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

- `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 `invt`
- `...`: Other arguments to be passed through

Details

Defined as

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

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. An 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


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’
- **...**: Other arguments to be passed through
Details

Defined as

\[ t = -\sum_{i=1}^{k} \log \frac{p_i}{1-p_i} \]

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. An 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 \texttt{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


See Also

See also \texttt{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 \times 10^{-16}
**meanp**  

*Combine p values by the mean p method*

**Description**

Combine p values by the mean p method

**Usage**

```r
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. An 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


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

\[ z = \frac{\sum_{i=1}^{k} z(p_i)}{k} \]

and

\[ s_z = \frac{s_z}{\sqrt{k}} \]
Defined as
\[ \bar{z} > t_{k-1}(\alpha) \]

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. An 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.

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
- \( \text{validp} \) The input vector with illegal values removed

**Author(s)**

Michael Dewey

**References**


**See Also**

See also `plotp`

**Examples**

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

---

**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, 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
 validation  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)
validation  \( p \)-values from studies of validity of student ratings from Becker (1994)
References


---

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

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 \ldots 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 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

\[ p \] The values of \( p \) plotted

\[ \text{bh.params} \] 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

\[ \text{ls.params} \] 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

\[ \text{ab.params} \] 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


Examples

```r
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. An 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


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

summary

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

\[ \frac{\left(\sum_{i=1}^{k} p_i\right)^k}{k!} - \binom{k}{1} \frac{\left(\sum_{i=1}^{k} p_i - 1\right)^k}{k!} + \binom{k}{2} \frac{\left(\sum_{i=1}^{k} p_i - 2\right)^k}{k!} \ldots \]

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

Some authors use a simpler version

\[ \frac{\left(\sum_{i=1}^{k} p_i\right)^k}{k!} \]

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 \( \text{conservativep} \) 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. An error 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 \( \text{plotp} \) 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
- \( \text{conservativep} \) See details
- \( \text{validp} \) The input vector with illegal values removed

Author(s)

Michael Dewey

References


See Also

See also \( \text{plotp} \)

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

- `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
- `x`: An object of class 'sumz'
- `...`: Other arguments to be passed through

Details

Defined as

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

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. An 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


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}

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

See Also
ranktruncated, stat.tpm, and p.tpm

Examples
```r
data(validity)
truncated(validity, ptrunc = 0.5)
truncated(validity, rtrunc = 5)
```

<table>
<thead>
<tr>
<th>two2one</th>
<th>Convert two-sided $p$-values to one-sided</th>
</tr>
</thead>
</table>

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

Usage
```r
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(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

p A vector of significance values
alpha A vector of length 2 defining the significance value limits
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 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 \( p_i \) should be such that \( 0 < p_i < 1 \) and a warning is given if that is not true. An 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**: A vector of length 2 defining the significance values and lying in the range 0 to 1
- **validp**: The input vector with illegal values removed

Author(s)

Michael Dewey

References


See Also

See also `plotp`

Examples

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

---

**wilkinsonp** Combine p-values using Wilkinson’s method

Description

Combine p-values using Wilkinson’s method

Usage

```r
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 rth 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. An 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


See Also

See also `plotp`

Examples

```r
data(beckerp)
minimump(beckerp) # signif = FALSE, critp = 0.0102, minp = 0.016
```

```r
data(teachexpect)
minimump(teachexpect) # crit 0.0207, note Becker says minp = 0.0011
```

```r
wilkinsonp(c(0.223, 0.223), r = 2) # Birnbaum, just signif
```

```r
data(validity)
minimump(validity) # minp = 0.00001, critp = 1.99 * 10^{-4}
```

```r
minimump(c(0.0001, 0.0001, 0.9999, 0.9999)) # is significant
```
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