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, Stouffer, Tippett, and Wilkinson; a number of data-sets to replicate published results; and a routine for graphical display.
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Description

Combine \( p \)-values using a variety of methods

Details

- Package: metap
- Type: Package
- Version: 0.7
- Date: 2016-04-05
- License: GPL-2
- LazyLoad: yes

Provides a number of ways in which significance levels may be combined in a meta-analysis. It includes a number of datasets taken from the literature. It also provides a display and an informal graphical test due to Schweder and Spjotvol and the lowest slope line of Benjamini and Hochberg.

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 <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
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
\[ t = - \sum \log \frac{p}{1-p} \]
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


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 \times 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

\[ z = (0.5 - \bar{p}) \sqrt{\frac{1}{12k}} \]

which is a standard normal

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

- **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 schweder

Examples

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

Description

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

Usage

data(beckerp)
data(cholesterol)
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
cholest $p$-values from studies of cholesterol lowering from Sutton
edgington Hypothetical $p$ values from Edgington
mourning Results from a study of mourning practices of Israeli youth from Benjamini
naep Results on the National Assessment of Educational Progress from Benjamini
rosenthal Hypothetical example from Rosenthal
 teachexpect $p$-values from studies of the effect of manipulating teacher expectancy from Becker
validity $p$-values from studies of validity of student ratings from Becker

References


Description

Produces the plot suggested by Schweder and Spjotvol to display a collection of \( p \)-values and also optionally draws the lowest slope line suggested by Benjamini and Hochberg.

Usage

```r
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 \( \text{frac} \). See Details
- **ls.lwd**: Width of the least squares line
- **ls.lty**: Line type of the least squares line
- **ls.col**: Colour of the least squares line
- **ab.control**: A list containing two elements \( a \) and \( b \). See Details
- **ab.lwd**: Width of the specified line
- **ab.lty**: Line type of the specified line
- **ab.col**: Colour of the specified line
- **...**: Further parameters to be passed through to `plot`
Details

After removing invalid \( p \)-values plots them. Any graphics parameters passed in . . . affect this part of the plot only. Note that the axes are chosen according to the scheme of Banjamini and Hochberg, Schweder and Spjotvol 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 Benjamain and Hochberg is drawn. No further parameters are needed here but the characteristics of the line may be set: width, line type, and colour.

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

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

Value

A list containing

- \( p \): The values of \( p \) plotted
- `bh.params`: A list containing at least items \( a \) and \( b \) the intercept and slope of the line drawn. This is only included if the lowest slope line was drawn
- `ls.params`: A list containing at least items \( a \) and \( b \) the intercept and slope of the line drawn. This is only included if the least squares line was drawn
- `ab.params`: A list containing at least items \( a \) and \( b \) the intercept and slope of the line drawn. This is only included if the user specified line was drawn

Author(s)

Michael Dewey

References


Examples

```
data(teachexpect)
schweder(teachexpect)
```
Combine p-values by the sum of logs 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.

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 `schweber` 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 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(cholesterol)
sumlog(cholesterol) # 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 method also known as Edgington’s method*

Description

Combine p-values using the sum p method

Usage

```r
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

\[
\frac{(\sum p)^k}{k!} - \left(\frac{k-1}{1}\right)\frac{(\sum p - 1)^k}{k!} + \left(\frac{k-2}{2}\right)\frac{(\sum p - 2)^k}{k!}
\]

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

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 \texttt{conservativep} 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 ‘\texttt{metap}’ calls \texttt{schweder} on the valid \(p\)-values

Value

An object of class ‘\texttt{sump}’ and ‘\texttt{metap}’, a list with entries

- \texttt{p} The transformed sum of the \(p\)-values
- \texttt{conservativep} See details
- \texttt{validp} The input vector with illegal values removed

Author(s)

Michael Dewey

References


See Also

See also \texttt{schweder}

Examples

data(edgington)
sump(edgington) # p = 0.097
Combine p-values using the sum of z 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. 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 (see Zaykin reference).

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
- **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 schweder

Examples

data(teachexpect)
sumz(teachexpect) # z = 2.435, p = 0.0074, from Becker
data(beckerp)
sumz(beckerp) # z = 1.53, NS, from Becker
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 \times 10^{-16}

Description

Convert two-sided p-values to one-sided

Usage

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

Arguments

p A vector of p-values

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

invert A logical vector defining which p-values are to be inverted
Details

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

Value

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

Author(s)

Michael Dewey

Examples

data(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 p-values
alpha A vector of length 2 defining the significance values
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 $p$ 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

- $p$ 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 schweder

Examples

data(beckerp)
votep(beckerp)
wilkinsonp  

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 p-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 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.

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


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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