Package ‘metap’

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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.

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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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- sumlog: Combine p-values by the sum of logs (Fisher's) method
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- votep: Combine p-values by the vote counting method
- wilkinsonp: Combine p-values using Wilkinson's method

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
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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*

**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, ...)
```

**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

```r
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

```r
invchisq(p, k, data = NULL, subset = NULL, na.action = na.fail)
```

---

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
**invchisq**

**Details**

Defined as

\[ \sum_{i=1}^{n} \chi^2_{i}(p_i) > \chi^2_{k}(\alpha) \]

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**


**See Also**

See Also *sumlog*

**Examples**

```r
data(beckerp)
invchisq(beckerp, 2) # same as sumlog
invchisq(c(0.999, 0.999, 0.001, 0.001), 4)
```
Combine p values using inverse t method

**Description**

Combine p values using the inverse t method

**Usage**

```r
invt(p, k, data = NULL, subset = NULL, na.action = na.fail)
```

## S3 method for class 'invt'

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 ‘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 \( k < 1 \) 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 ‘invt’ and ‘metap’, a list with entries

- `z`: Value of z
- `p`: Associated p-value
- `validp`: The input vector with the illegal values removed
**logitp**

**Author(s)**

Michael Dewey

**References**


**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
Combine p values by the mean p method

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

Author(s)
Michael Dewey

References

See Also
See also schweder

Examples
```r
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}
```

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 \( p \)-values
- \( x \) An object of class ‘meanp’
- \( ... \) Other arguments to be passed through
Details

Defined as

\[ z = (0.5 - \bar{p}) \sqrt{\frac{1}{2} k} \]

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

- \( z \) Value of \( z \)
- \( p \) Associated \( p \)-value
- \( \text{validp} \) The input vector with illegal values removed

Author(s)

Michael Dewey

References


See Also

See also schweder

Examples

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

Combines p values using the mean of z method

**Usage**

```r
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

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

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 ≤ p ≤ 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 = ±∞ 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


Examples

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

Description

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

Usage

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

Format

```r
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
```


\texttt{schweder} \hspace{7cm} \textit{Schweder and Spjotvoll plot}

\subsection*{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

\begin{verbatim}

p  a numeric vector of one sided \(p\) values
teachexpect  A vector of length 19
validity  A vector of length 20

Details

becker  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


\end{verbatim}
Usage

schweder(p, xlab = "Rank of p", ylab = "p", drawline = NULL, 
bh.lwd = 1, bh.lty = "solid", bh.col = "black", 
ls.control = list(frac = NULL), 
ls.lwd = 1, ls.lty = "dotted", ls.col = "black", 
ab.control = list(a = NULL, b = NULL), 
ab.lwd = 1, ab.lty = "dashed", ab.col = "black", ...)

Arguments

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

Details

After removing invalid p-values plots them. Any graphics parameters passed in ... affect this part of the plot only. Note that the axes are chosen according to the scheme of Banjamini and Hochberg. Schweder and Spjotvoll used a different system.

By setting drawline appropriately up to three lines may be drawn.

If drawline includes the string "bh" the lowest slope line of Benjaimin and Hochberg is drawn. No further parameters are needed here but the characteristics of the line may be set: width, line type, and colour.

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

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

A list containing

- The values of \( p \) plotted
- 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
- 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
- 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

```r
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


See Also

See also `schweder`
Examples

data(teachexpect)
sumlog(teachexpect) # chisq = 69.473, df = 38, p = 0.0014, from Becker
data(becker)
sumlog(becker) # chisq = 18.533, df = 10, sig
data(rosenthal)
sumlog(rosenthal) # 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

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

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

Some authors use a simpler version \((\sum p)^k\) 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 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 '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


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

\[
\text{sumz}(p, \text{weights} = \text{NULL}, \text{data} = \text{NULL}, \text{subset} = \text{NULL}, \text{na.action} = \text{na.fail})
\]

## S3 method for class 'sumz'

print(x, ...)

Arguments

- \( p \): A vector of \( p \)-values
- \( \text{weights} \): A vector of weights
- \( \text{data} \): Optional data frame containing variables
- \( \text{subset} \): Optional vector of logicals to specify a subset of the \( p \)-values
- \( \text{na.action} \): 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

- $z$: 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 * 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

- **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

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 ≤ p ≤ 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 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  

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 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 (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 \texttt{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.

\texttt{maximump} and \texttt{minimump} each provide a wrapper for \texttt{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 \texttt{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 \texttt{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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