

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.

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

Imports lattice

License GPL-2

LazyLoad yes

NeedsCompilation no

Repository CRAN

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metap-package	<i>Meta-analysis of p-values</i>
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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 Spjøtvoll 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

Becker, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.

Benjamini, Y and Hochberg, Y. On the adaptive control of the false discovery rate in multiple testing with independent statistics. *Journal of Educational and Behavioral Statistics*, 25: 60–83, 2000.

Rosenthal, R. Combining the results of independent studies. *Psychological Bulletin*, 85:185–193, 1978.

Schweder, T and Spjøtvoll, E. Plots of P -values to evaluate many tests simultaneously. *Biometrika*, 69:493–502, 1982.

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	<i>Carry out all or some of the methods</i>
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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

<code>p</code>	A vector of p -values
<code>method</code>	A vector of character containing names of methods or 'all'
<code>x</code>	An object of class 'allmetap'
<code>digits</code>	How many digits to print?
<code>...</code>	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

<code>p</code>	The value of <code>p</code> returned
<code>valid</code>	The number of valid <code>p</code> values used for that method
<code>eponym</code>	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"))
```

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, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.

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

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

Becker, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.

Rosenthal, R. Combining the results of independent studies. *Psychological Bulletin*, 85:185–193, 1978.

See Also

See also [schweder](#)

Examples

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

package-data

Example data

Description

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

Usage

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

Format

beckerp A vector of length 5
 cholest A vector of length 34
 edgington A vector of length 7
 naep A data frame with 34 observations on the following 2 variables.
 state a factor with levels AL AR AZ CA CO CT DE FL GA HI IA ID IN KY LA MD MI MN NC ND NE
 NH NJ NM NY OH OK PA RI TX VA WI WV WY
 p a numeric vector
 mourning A data frame with 9 observations on the following 3 variables.
 stance a factor with levels No stand Opponent Supporter
 grade a factor with levels G11-12 G7-8 G9-10
 p a numeric vector
 rosenthal A data frame with 5 observations on the following 3 variables.
 t A numeric vector of values of t
 df a numeric vector of degrees of freedom
 p a numeric vector of one sided p values
 teachexpect A vector of length 19
 validity A vector of length 20

Details

beckerp Hypothetical p values from Becker
 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

Becker, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.
 Benjamini, Y and Hochberg, Y. On the adaptive control of the false discovery rate in multiple testing with independent statistics. *Journal of Educational and Behavioral Statistics*, 25: 60–83, 2000.
 Edgington, E S. An additive method for combining probability values from independent experiments. *Journal of Psychology*, 80:351-363, 1972.
 Rosenthal, R. Combining the results of independent studies. *Psychological Bulletin*, 85:185–193, 1978.
 Sutton A J, Abrams, K R, Jones D R, Sheldon T A and Song, F. *Methods for meta-analysis in medical research*. Wiley, Chichester, 2000.

schweder

*Schweder and Spjotvoll plot***Description**

Produces the plot suggested by Schweder and Spjotvoll to display a collection of p -values and also optionally draws the lowest slope line suggested by Benjamini and Hochberg

Usage

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

Arguments

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

Details

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

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

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

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

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

Value

A list containing

<code>p</code>	The values of p plotted
<code>bh.params</code>	A list containing at least items <code>a</code> and <code>b</code> the intercept and slope of the line drawn. This is only included if the lowest slope line was drawn
<code>ls.params</code>	A list containing at least items <code>a</code> and <code>b</code> the intercept and slope of the line drawn. This is only included if the least squares line was drawn
<code>ab.params</code>	A list containing at least items <code>a</code> and <code>b</code> the intercept and slope of the line drawn. This is only included if the user specified line was drawn

Author(s)

Michael Dewey

References

Benjamini, Y and Hochberg, Y. On the adaptive control of the false discovery rate in multiple testing with independent statistics. *Journal of Educational and Behavioral Statistics*, 25: 60–83, 2000.

Schweder, T and Spjøtvoll, E. Plots of P -values to evaluate many tests simultaneously. *Biometrika*, 69:493–502, 1982.

Examples

```
data(teachexpect)
schweder(teachexpect)
```

sumlog *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

<code>p</code>	A vector of p -values
<code>x</code>	An object of class 'sumlog'
<code>...</code>	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 [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

<code>chisq</code>	Value of chi-squared statistic
<code>df</code>	Associated degrees of freedom
<code>p</code>	Associated p-value
<code>validp</code>	The input vector with the illegal values removed

Author(s)

Michael Dewey

References

- Becker, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.
- Rosenthal, R. Combining the results of independent studies. *Psychological Bulletin*, 85:185–193, 1978.
- Sutton A J, Abrams, K R, Jones D R, Sheldon T A and Song, F. *Methods for meta-analysis in medical research*. Wiley, Chichester, 2000.

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 method also known as 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 <i>p</i> -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.

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 `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

<code>p</code>	The transformed sum of the p -values
<code>conservativep</code>	See details
<code>validp</code>	The input vector with illegal values removed

Author(s)

Michael Dewey

References

Becker, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.

Edgington, E S. An additive method for combining probability values from independent experiments. *Journal of Psychology*, 80:351-363, 1972.

See Also

See also [schweder](#)

Examples

```
data(edgington)
sump(edgington) # p = 0.097
```

sumz *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

<code>p</code>	A vector of p -values
<code>weights</code>	A vector of weights
<code>data</code>	Optional data frame containing variables
<code>subset</code>	Optional vector of logicals to specify a subset of the p -values
<code>na.action</code>	A function indicating what should happen when data contains NAs
<code>x</code>	An object of class 'sumz'
<code>...</code>	Other arguments to be passed through

Details

Defined as

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

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

<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, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.

Rosenthal, R. Combining the results of independent studies. *Psychological Bulletin*, 85:185–193, 1978.

Zaykin, D V. Optimally weighted Z-test is a powerful method for combining probabilities in meta-analysis. *Journal of Evolutionary Biology* 24:1836-1841, 2011

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

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

Becker, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.

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

<code>p</code>	A vector of p -values
<code>r</code>	Use the r th smallest p value
<code>alpha</code>	The significance level
<code>x</code>	An object of class 'wilkinsonp' or of class 'maximump' or of class 'minimump'
<code>...</code>	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

Becker, B J. Combining significance levels. In Cooper, H and Hedges, L V, editors *A handbook of research synthesis*, chapter 15, pages 215–230. Russell Sage, New York, 1994.

Birnbaum, A. Combining independent tests of significance. *Journal of the American Statistical Association*, 49:559–574, 1954.

Wilkinson, B. A statistical consideration in psychological research. *Psychological Bulletin*, 48:156–158, 1951.

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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