Package 'metamedian'

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Type Package

Title Meta-Analysis of Medians

Version 0.1.5

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Description Implements several methods to meta-analyze studies that report the sample median of the outcome. When the primary studies are one-group studies, the methods of McGrath et al. (2019) <doi:10.1002/sim.8013> can be applied to estimate the pooled median. In the two-group context, the methods of McGrath et al. (2020) <doi:10.1002/bimj.201900036> can be applied to estimate the pooled raw difference of medians across groups.

Imports estmeansd, Hmisc, metafor, stats

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Encoding UTF-8

LazyData true

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URL https://github.com/stmcg/metamedian

BugReports https://github.com/stmcg/metamedian/issues

NeedsCompilation no

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R topics documented:

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metamedian-defunct   *Defunct functions in package 'metamedian'*

Description

These functions are defunct and no longer available.

Details

The following functions are defunct and no longer available:

- qe.fit calls should now be qe.fit (in the 'estmeansd' package) calls. That is, this function has been moved to the 'estmeansd' pacakge.

- Similarly, print.qe.fit calls should now be print.qe.fit (in the 'estmeansd' package) calls.

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pool.med   *Meta-Analysis via median of (the difference of) medians method*

Description

This function meta-analyzes the study-specific effect sizes by applying the (weighted) median of medians method (McGrath et al., 2019) in one-sample contexts and the (weighted) median of the difference of median method (McGrath et al., 2020) in two-sample contexts.

Usage

```
pool.med(yi, wi, norm.approx = TRUE, coverage.prob = 0.95)
```

Arguments

yi	vector of the study-specific effect sizes (e.g., the medians or the difference of medians)
wi	optional vector of positive, study-specific weights (e.g., sample sizes)
norm.approx	optional logical scalar indicating whether normality approximation of the binomial should be used to construct an approximate confidence interval (the default is TRUE).
coverage.prob	optional numeric scalar indicating the desired coverage probability (the default is 0.95).

Details

For one-group studies, authors may report the sample median or mean. If these measures are supplied for `yi` and weights are not provided for `wi`, the function implements the median of medians (MM) method (McGrath et al., 2019).

For two-group studies, authors may report the difference of medians or the difference of means across both groups. If these measures are supplied for `yi` and weights are not provided for `wi`, the function implements the median of the difference of medians (MDM) method (McGrath et al., 2020).

Analogous weighted versions of the MM and MDM methods can be applied when study-specific sample sizes are provided for `wi`.

The confidence interval around the pooled estimate is constructed by inverting the sign test.

Value

A list with components

`pooled.est`	Pooled estimate
`ci.lb`	Lower bound of confidence interval
`ci.ub`	Upper bound of confidence interval
`cov.level`	Theoretical coverage of the confidence interval around the pooled estimate. When `norm.approx` is set to `TRUE`, the theoretical coverage is the same as the value specified by `coverage.prob`. When `norm.approx` is set to `FALSE`, the theoretical coverage is set to the smallest possible value greater than the value specified by `coverage.prob`.

References

McGrath S., Zhao X., Qin Z.Z., Steele R., and Benedetti A. (2019). One-sample aggregate data meta-analysis of medians. *Statistics in Medicine*, **38**, 969-984.

McGrath S., Sohn H., Steele R., and Benedetti A. (2020). Meta-analysis of the difference of medians. *Biometrical Journal*, **62**, 69-98.

Examples

```
## Storing data (study-specific difference of medians)
yi <- c(5.23, 3.10, 0.50, 0.78, 3.48, 0.59, 2.20, 5.06, 4.00)

## Meta-analysis of the difference of medians
pool.med(yi)
```

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qe   *Meta-Analysis via quantile estimation method*

Description

The function applies the quantile estimation (QE) method (McGrath et al., 2020) to meta-analyze one-group or two-group studies where each study reports one of the following summary measures:

- S1: median, minimum and maximum values, and sample size
- S2: median, first and third quartiles, and sample size
- S3: median, minimum and maximum values, first and third quartiles, and sample size
- S4: mean, standard deivation, and sample size.

For one-group studies, the function estimates the pooled median. For two-group studies, the function estimates the pooled raw difference of medians across groups. The convention used for calculating differences in two-group studies is: value in group 1 minus value in group 2.

Usage

```
qe(min.g1, q1.g1, med.g1, q3.g1, max.g1, n.g1, mean.g1, sd.g1, min.g2,
  q1.g2, med.g2, q3.g2, max.g2, n.g2, mean.g2, sd.g2,
  single.family = FALSE, loc.shift = FALSE, ...)
```

Arguments

min.g1	vector of study-specific sample minimum values (first group for two-group studies). See 'Details'.
q1.g1	vector of study-specific sample first quartile values (first group for two-group studies). See 'Details'.
med.g1	vector of study-specific sample median values (first group for two-group studies). See 'Details'.
q3.g1	vector of study-specific sample third quartile values (first group for two-group studies). See 'Details'.
max.g1	vector of study-specific sample maximum values (first group for two-group studies). See 'Details'.
n.g1	vector of study-specific sample sizes (first group for two-group studies). See 'Details'.
mean.g1	vector of study-specific sample mean values (first group for two-group studies). See 'Details'.
sd.g1	vector of study-specific sample standard deviation values (first group for two-group studies). See 'Details'.
min.g2	vector of study-specific sample minimum values of the second group for two-group studies. See 'Details'.

q1.g2	vector of study-specific sample first quartile values of the second group for two-group studies. See 'Details'.
med.g2	vector of study-specific sample median values of the second group for two-group studies. See 'Details'.
q3.g2	vector of study-specific sample third quartile values of the second group for two-group studies. See 'Details'.
max.g2	vector of study-specific sample maximum values of the second group for two-group studies. See 'Details'.
n.g2	vector of study-specific sample sizes of the second group for two-group studies. See 'Details'.
mean.g2	vector of study-specific sample mean values of the second group for two-group studies. See 'Details'.
sd.g2	vector of study-specific sample standard deviation values of the second group for two-group studies. See 'Details'.
single.family	logical scalar indicating that for two-group studies, the parametric family of distributions is assumed to be the same across both groups (the default is FALSE). See 'Details' of qe.study.level.
loc.shift	logical scalar indicating that for two-group studies, distributions are assumed to only differ by a location shift (the default is FALSE). See 'Details' of qe.study.level.
...	optional arguments for pooling. See documentation of rma.uni.

Details

Letting k denote the number of studies, provide study-specific summary data as vectors of length k. If a study does not report a given summary measure (e.g., the minimum value), give a value of NA for the position in the relevant vector. If no studies report a given summary measure, a vector of only NA values need not be provided. See 'Examples' for appropriate use.

The sampling variance of the effect size for each study is estimated via the QE method. The default starting values and box constraints of the parameters in the minimization algorithm (qe.fit) are used. After estimating the sampling variances for all studies, studies are meta-analyzed using the rma.uni function.

Value

An object of class "rma.uni". See documentation of rma.uni.

References

McGrath S., Sohn H., Steele R., and Benedetti A. (2020). Meta-analysis of the difference of medians. *Biometrical Journal*, **62**, 69-98.

Examples

```
## Example 1: Meta-analysis of one-group studies

## Storing data
## Note: All 6 studies report S2
```

```
med.vals <- c(6.1, 5.2, 3.1, 2.8, 4.5)
q1.vals <- c(2.0, 1.6, 2.6, 0.9, 3.2)
q3.vals <- c(10.2, 13.0, 8.3, 8.2, 9.9)
n.vals <- c(100, 92, 221, 81, 42)

## Meta-analyze studies via QE method
qe(q1.g1 = q1.vals, med.g1 = med.vals, q3.g1 = q3.vals, n.g1 = n.vals)


## Example 2: Meta-analysis of one-group studies

## Storing data
## Note: Studies 1, 2, 3, and 4 report S1, S2, S3, and S4, respectively
min.vals <- c(0.7, NA, 1.1, NA)
q1.vals <- c(NA, 5.2, 5.3, NA)
med.vals <- c(8.7, 10.7, 11.0, NA)
q3.vals <- c(NA, 5.2, 5.3, NA)
max.vals <- c(22.2, NA, 24.7, NA)
n.vals <- c(52, 34, 57, 90)
sd.vals <- c(NA, NA, NA, 4.2)
mean.vals <- c(NA, NA, NA, 12.2)

## Meta-analyze studies via QE method
qe(min.g1 = min.vals, q1.g1 = q1.vals, med.g1 = med.vals, q3.g1 = q3.vals,
   max.g1 = max.vals, n.g1 = n.vals, mean.g1 = mean.vals, sd.g1 = sd.vals)


## Example 3: Meta-analysis of two-group studies

## Storing data
## Note: All 4 studies report S3
min.g1 <- c(2.3, 3.2, 1.9, 1.7)
q1.g1 <- c(6.0, 7.1, 3.5, 3.8)
med.g1 <- c(8.7, 9.5, 5.9, 6.0)
q3.g1 <- c(11.3, 13.1, 10.8, 11.0)
max.g1 <- c(20.6, 25.3, 17.0, 18.6)
n.g1 <- c(53, 49, 66, 75)
min.g2 <- c(0.4, 0.9, 0.5, 0.3)
q1.g2 <- c(2.5, 3.1, 2.7, 2.3)
med.g2 <- c(5.1, 6.2, 4.9, 4.7)
q3.g2 <- c(9.6, 10.1, 8.8, 9.2)
max.g2 <- c(20.2, 21.4, 18.8, 19.2)
n.g2 <- c(50, 45, 60, 73)

## Meta-analyze studies via QE method
qe(min.g1 = min.g1, q1.g1 = q1.g1, med.g1 = med.g1, q3.g1 = q3.g1,
   max.g1 = max.g1, n.g1 = n.g1, min.g2 = min.g2, q1.g2 = q1.g2,
   med.g2 = med.g2, q3.g2 = q3.g2, max.g2 = max.g2, n.g2 = n.g2)
```

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qe.study.level   *Study-Level application of quantile estimation method*

Description

This function estimates the asymptotic sampling variance of either the (estimated) median or the (estimated) difference of medians for a primary study that reports one of the following summary measures:

- S1: median, minimum and maximum values, and sample size
- S2: median, first and third quartiles, and sample size
- S3: median, minimum and maximum values, first and third quartiles, and sample size
- S4: mean, standard deivation, and sample size.

.

Usage

```
qe.study.level(min.g1, q1.g1, med.g1, q3.g1, max.g1, n.g1, mean.g1, sd.g1,
  min.g2, q1.g2, med.g2, q3.g2, max.g2, n.g2, mean.g2, sd.g2,
  single.family = FALSE, loc.shift = FALSE,
  qe.fit.control.g1 = list(), qe.fit.control.g2 = list())
```

Arguments

`min.g1`	numeric value giving the sample minimum (first group for two-group studies).
`q1.g1`	numeric value giving the first quartile (first group for two-group studies).
`med.g1`	numeric value giving the sample median (first group for two-group studies).
`q3.g1`	numeric value giving the sample third quartile (first group for two-group studies).
`max.g1`	numeric value giving the sample maximum (first group for two-group studies).
`n.g1`	numeric value giving the sample size (first group for two-group studies).
`mean.g1`	numeric value giving the sample mean (first group for two-group studies).
`sd.g1`	numeric value giving the sample standard deviation (first group for two-group studies).
`min.g2`	numeric value giving the sample minimum of the second group for two-group studies.
`q1.g2`	numeric value giving the sample first quartile of the second group for two-group studies.
`med.g2`	numeric value giving the sample median of the second group for two-group studies.
`q3.g2`	numeric value giving the sample third quartile of the second group for two-group studies.
`max.g2`	numeric value giving the sample maximum of the second group for two-group studies.
`n.g2`	numeric value giving the sample size of the second group for two-group studies.
`mean.g2`	numeric value giving the sample mean of the second group for two-group studies.

sd.g2	numeric value giving the sample standard deviation of the second group for two-group studies.
single.family	logical scalar indicating that for two-group studies, the parametric family of distributions is assumed to be the same across both groups (the default is FALSE). See 'Details'.
loc.shift	logical scalar indicating that for two-group studies, distributions are assumed to only differ by a location shift (the default is FALSE). See 'Details'.
qe.fit.control.g1	
	optional list of control parameters for qe.fit (first group for two-group studies).
qe.fit.control.g2	
	optional list of control parameters for qe.fit of the second group for two-group studies.

Details

In order to estimate the asymptotic sampling variance of the median (in S1, S2, or S3), one must have an estimate of the probability density function of the outcome evaluated at the population median. The qe.fit function is applied to estimate the outcome distribution.

For two-group studies studies, one may assume that the outcome in both groups follows the same parametric family of distributions. In this case, distribution selection for the QE method is applied as follows. The qe.fit function is applied to fit the candidate distributions of each group separately. However, for each candidate distribution, the objective function evaluated at the fitting parameters are summed over the two groups. The parametric family of distributions with the smallest sum is used as the underlying distribution of the both groups. If single.family is TRUE, then selected.dist is a character string indicating the selected parametric family. If single.family is FALSE, then selected.dist is a vector of length 2 where elements 1 and 2 are character strings of the selected parametric families in groups 1 and 2, respectively.

One may also assume for two-group studies that the outcome distributions in the two groups only differ by a location shfit. In this case, a weighted mean (weighted by sample size) of the estimated probability density functions evaluated at the population medians is used to estimate the asymptotic sampling variance of the difference of medians. See McGrath et al. (2020) for further details.

When a study provides S4 summary measures, the outcome distribution is assumed to be normal. The sample median is estimated by the sample mean, and its variance is estimated by the sample variance divided by the sample size. In this case, the single.family and loc.shift arguments are not used.

Value

A list with the following components:

var	Estimated sampling variance of the effect size.
effect.size	Effect size of study.
selected.dist	Selected outcome distribution(s). See 'Details'.
study.type	Character string specifying whether one-group or two-group summary data was provided.

References

McGrath S., Sohn H., Steele R., and Benedetti A. (2020). Meta-analysis of the difference of medians. *Biometrical Journal*, **62**, 69-98.

Examples

```
## Generate S2 summary data
set.seed(1)
n <- 100
x <- stats::rlnorm(n, 2.5, 1)
quants <- stats::quantile(x, probs = c(0.25, 0.5, 0.75))

## Estimate sampling variance of the median
qe.study.level(q1.g1 = quants[1], med.g1 = quants[2], q3.g1 = quants[3],
               n.g1 = n)
```

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