Package ‘MultiMed’

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Title Testing multiple biological mediators simultaneously
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Suggests RUnit, BiocGenerics
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Description Implements permutation method with joint correction for
testing multiple mediators
License GPL (>= 2) + file LICENSE
biocViews MultipleComparison, StatisticalMethod, Software
NeedsCompilation no

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medTest  Permutation test for multiple mediators which uses a joint correction

Description

Implements Boca et al. 2014 method of testing multiple biological mediators simultaneously, which
uses a permutation test with a joint correction based on the maximal test statistics.

Usage

medTest(E, M, Y, Z = NULL, useWeightsZ = TRUE, nperm = 100, w = 1)
Arguments

E  Exposure: numerical vector of length n or numerical n x 1 matrix, where n is the number of samples or subjects.
M  Mediators: numerical matrix of dimension n x p, where p is the number of mediators.
Y  Outcome: numerical vector of length n or numerical n x 1 matrix
Z  Additional covariates: NULL or numerical matrix having n rows. If it is not NULL, then the exposure, mediators, and outcome will all be initially regressed on Z, with the residuals being used in the mediation analysis.
nperm  Number of permutations performed. One of the permutations always consists of the observed data.
w  Weight assigned to each subject or sample for the E-M associations. Useful for case-control sampling.
useWeightsZ  If TRUE, use the weights in w for the initial regression of E and M on Z, in the case where Z is not null. If FALSE, use equal weights.

Details

See Boca et al. 2014 paper for a more in-depth description of this method.

Value

Matrix with p rows and 2 columns, where the first column (labeled "S") gives the S-statistics and the second column (labeled "p") gives the p-values for each mediator, where the mediators correspond to the rows. For each mediator, the S-statistic is the absolute value of the product of the correlation between the exposure and the mediator and the conditional (or partial) correlation between the mediator and the outcome conditional on the exposure. Thus, the larger the S-statistic is, the smaller the p-value is, and the more likely it is that the mediator is statistically significant.

Author(s)

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References


See Also

NavyAdenoma

Examples

```r
data(NavyAdenoma)
```
## get weights needed due to retrospective sampling, to use for all regressions
## that do not have adenoma status as the outcome
prev <- 0.228
p <- sum(NavyAdenoma$Adenoma==1)/nrow(NavyAdenoma)
w <- rep(NA, nrow(NavyAdenoma))
w[NavyAdenoma$Adenoma == 1] <- prev/p
w[NavyAdenoma$Adenoma == 0] <- (1-prev)/(1-p)

## perform the test of mediation, adjusting for the covariates
## BMI, gender, age, and current smoking status
## (only running 10 permutations in this example – would need to
## perform more to get an accurate p-value)
set.seed(840218)
medsFish <- medTest(E=NavyAdenoma$Fish, M=NavyAdenoma[, 6:154], Y=NavyAdenoma$Adenoma, Z=NavyAdenoma[, 2:5], nperm=10, w=w)

## get metabolite with lowest p-value
medsFish[which.min(medsFish[,"p"]),]
colnames(NavyAdenoma,-(1:5))[which.min(medsFish[,"p"])]
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