Package 'medScan'

October 13, 2022

Title Large Scale Single Mediator Hypothesis Testing

Version 1.0.1

URL https://github.com/umich-cphds/medScan

BugReports https://github.com/umich-cphds/medScan/issues

Description A collection of methods for large scale single mediator hypothesis testing. The six included methods for testing the mediation effect are Sobel's test, Max P test, joint significance test under the composite null hypothesis, high dimensional mediation testing, divide-aggregate composite null test, and Sobel's test under the composite null hypothesis. Du, J., Zhou, X., Hao, W., Liu, Y., Smith, J. A., & Mukherjee, B (2022) ``Methods for Large-scale Single Mediator Hypothesis Testing: Possible Choices and Comparisons." arXiv preprint <arXiv:2203.13293>.

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Encoding UTF-8

RoxygenNote 7.2.1

biocViews

Imports HDMT, locfdr, qqman, qvalue, fdrtool

Depends R (>= 3.5),

Suggests knitr, rmarkdown

NeedsCompilation no

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R topics documented:

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Description

A collection of methods for large scale single mediator hypothesis testing. The six included methods for testing the mediation effect are Sobel's test, Max P test, joint significance test under the composite null hypothesis, high dimensional mediation testing, divide-aggregate composite null test, and Sobel's test under the composite null hypothesis. Du, J., Zhou, X., Hao, W., Liu, Y., Smith, J. A., & Mukherjee, B. (2022). "Methods for Large-scale Single Mediator Hypothesis Testing: Possible Choices and Comparisons."

Usage

```
medScan(z.alpha, z.beta, method)
```

Arguments

`z.alpha`	the z-test statistic for alpha (exposure effect on the mediator).
`z.beta`	the z-test statistic for beta (mediator effect on the outcome).
`method`	the method to use for testing the mediation effect. It should belong to one of the six methods: `"Sobel"`, `"MaxP"`, `"JT_comp"`, `"HDMT"`, `"DACT"`, and `"Sobel_comp"`. (1) Sobel's test (`method = "Sobel"`), (2) Max P test (`method = "MaxP"`), (3) joint significance test under the composite null hypothesis (`method = "JT_comp"`), (4) high dimensional mediation testing (`method = "HDMT"`), (5) Divide-Aggregate Composite-null Test (`method = "DACT"`), and (6) Sobel's test under the composite null hypothesis (`method = "Sobel_comp"`).

Details

The available methods are: (1) Sobel's test (`method = "Sobel"`), (2) Max P test (`method = "MaxP"`), (3) joint significance test under the composite null hypothesis (`method = "JT_comp"`), (4) high dimensional mediation testing (`method = "HDMT"`), (5) Divide-Aggregate Composite-null Test (`method = "DACT"`), and (6) Sobel's test under the composite null hypothesis (`method = "Sobel_comp"`).

We incorporated code from the DACT R package formerly on CRAN. Author: Zhonghua Liu Maintainer: Zhonghua Liu, zhhliu@hku.hk.

Value

A list that contains

- pvalues: p-values for all mediators from the chosen method.
- pi: the estimated proportions of the three null cases from the HDMT method. pi00 is the proportion of alpha=beta=0; pi01 is the proportion of alpha=0 and beta!=0; and pi10 is the proportion of alpha!=0 and beta=0.

References

Sobel, M. E. (1982). Asymptotic confidence intervals for indirect effects in structural equation models. Sociological methodology, 13, 290-312. MacKinnon, D. P., Lockwood, C. M., Hoffman, J. M., West, S. G., & Sheets, V. (2002). A comparison of methods to test mediation and other intervening variable effects. Psychological methods, 7(1), 83. Huang, Y. T. (2019). Genome-wide analyses of sparse mediation effects under composite null hypotheses. The Annals of Applied Statistics, 13(1), 60-84. Liu, Z., Shen, J., Barfield, R., Schwartz, J., Baccarelli, A. A., & Lin, X. (2022). Large-scale hypothesis testing for causal mediation effects with applications in genome-wide epigenetic studies. Journal of the American Statistical Association, 117(537), 67-81. Dai, J. Y., Stanford, J. L., & LeBlanc, M. (2022). A multiple-testing procedure for high-dimensional mediation hypotheses. Journal of the American Statistical Association, 117(537), 198-213. Du, J., Zhou, X., Hao, W., Liu, Y., Smith, J. A., & Mukherjee, B. (2022). Methods for Large-scale Single Mediator Hypothesis Testing: Possible Choices and Comparisons. arXiv preprint arXiv:2203.13293.

Examples

```
# simulate data under the mixture null
n=10000
u = runif(n,0,1)
z.alpha = z.beta = rep(NA,0)
pi00 = 0.98
pi10 = 0.01
pi01 = 0.01
for(i in 1:n){
  if(u[i]<=pi00){
    z.alpha[i] = rnorm(1, 0, 1)
    z.beta[i] = rnorm(1, 0, 1)
  } else if (u[i]<= pi00+pi10){
    z.alpha[i] = rnorm(1, 1, 1)
    z.beta[i] = rnorm(1, 0, 1)
  } else {
    z.alpha[i] = rnorm(1, 0, 1)
    z.beta[i] = rnorm(1, 1, 1)
  }
}

# obtain p-values

# method = "Sobel", "MaxP", "HDMT", "Sobel_comp", "JT_comp", "DACT"
obj = medScan(z.alpha = z.alpha, z.beta = z.beta, method = "Sobel")
qqman::qq(obj$pvalues,  xlim = c(0,4), ylim = c(0,4), main = "Sobel")
```

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