

Package ‘THIMA’

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Type Package

Title Testing targeted mediation effect in microbiome data

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Description We propose an estimating and testing procedure for a targeted mediator of interest in the presence of a large number of mediators. Specially, we present a de-biased Lasso estimate for the targeted mediator and derive its standard error estimator, which can be used to develop a joint significance test procedure for the mediation effect in microbiome compositional data.

Depends R (>= 3.3), hdi, MASS

ilr Isometric Logratio Transformation

Description

ilr is used to transform the compositional data from the simplex S^p to Euclidean space R^{p-1} .

Usage

ilr (target.ID, M)

Arguments

target.ID the index of targeted mediator

M a matrix of high-dimensional compositional mediators. Rows represent samples, columns represent variables

Value

MT a matrix after *ilr*-based transformation

References

- [1] Egozcue, J., Pawlowsky-Glahn, V., Mateu-Figueras, G. and BarcelÓ-Vidal, C. (2003). Isometric logratio transformations for compositional data analysis. *Mathematical Geology*, 35, 279-300.
- [2] Haixiang Zhang, Jun Chen, Zhigang Li, Lei Liu (2018). Testing for targeted mediation effect with application to human microbiome data. *Submitted*.

Examples

```
library(MASS)
tid <- 3 # The index of targeted mediator, i.e., the third mediator is the targeted mediator
n <- 100 # sample size
p <- 200 # the number of mediators
E <- matrix(rexp(n*p,1),n,p)
M <- matrix(0,n,p)
for (i in 1:n){
  M[i,] <- E[i,]/sum(E[i,]) # generate compositional mediators
}

MT <- ilr(target.id = tid, M) # the ilr-based transformation for the targeted mediator
```

thima	Targeted High-dimensional Mediation Analysis
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Description

thima is used to test the mediation effect in high-dimensional microbiome compositional data

Usage

```
thima(target.ID, X, MT, Y,...)
```

Arguments

target.ID	the index of targeted mediator
X	a vector of exposure
MT	a matrix of high-dimensional mediators after <i>ilr</i> -based transformation. Rows represent samples, columns represent variables
Y	a vector of outcome
...	other arguments passed to hdi

Value

target.ID	ID of the targeted mediator
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alpha_hat	coefficient estimate of exposure (X) \rightarrow targeted mediator (M)
alpha_hat_SE	the standard error for alpha_hat
beta_hat	coefficient estimate of the targeted mediator (M) \rightarrow outcome (Y) (adjusted for exposure and high-dimensional nuisance mediators)
beta_hat_SE	the standard error for beta_hat
Pval	P-value of the joint significance test

References

Haixiang Zhang, Jun Chen, Zhigang Li, Lei Liu (2018). Testing for targeted mediation effect with application to human microbiome data. *Submitted*.

Examples

```
library(MASS)
library(hdi)
tid <- 5 # The index of targeted mediator
n <- 100 # sample size
p <- 200 # the number of mediators
E <- matrix(rexp(n*p,1),n,p)
M <- matrix(0,n,p)
for (i in 1:n){
  M[i,] <- E[i,]/sum(E[i,]) # generate compositional mediators
}

MT <- ilr(target.ID =tid, M) # the ilr-based transformation for M_ID
##### The following codes generate X and Y
c <- 1 # the intercept term in Y
gamma <- 0.5
beta <- matrix(0,1,p-1)
b0 <- c(1,0.25,0.30,0.35,0.55)
L <- length(b0)
beta[1:L] <- b0
X <- matrix(rnorm(n, mean=0, sd=1.5),n,1)
X <- matrix(as.numeric(scale(X)),nrow(scale(X)),ncol(scale(X)))
XM <- cbind(X,MT)
B <- t(t(c(gamma, beta))) # (p) times 1
e <- rnorm(n,0,1)
Y <- c + XM%*%B + t(t(e))

###
thima.fit <- thima(target.ID = tid, X, MT, Y) # using the package THIMA

print(thima.fit)
```