

Package ‘microHIMA’

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Type Package

Title Testing high-dimensional mediation effects in microbiome data

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Description We use the isometric logratio (*ilr*) transformations of the relative abundances as the mediator variables. Moreover, we develop a joint significance test procedure for the mediation effects in microbiome compositional data, which can effectively control the family-wise error rate (FWER).

Depends R (>= 3.3), ncvreg, 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 (ID, M)

Arguments

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 (2019). Testing for mediation effect with application to human microbiome data. *Statistics in Biosciences*. DOI: <https://doi.org/10.1007/s12561-019-09253-3>

Examples

```
library(MASS)
Ind <- 3 # 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(ID =Ind, M) # the ilr-based transformation for M_ID
```

mhima	Microbiome High-Dimensional Mediation Analysis
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Description

mhima is used to test the mediation effects in high-dimensional microbiome compositional data

Usage

```
mhima( X, M, Y)
```

Arguments

X	a vector of exposure
M	a matrix of OTUs. Rows represent samples, columns represent variables
Y	a vector of outcome

Value

ID	the index of significant mediator (with Bonferroni corrected p-value < 0.05)
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<code>alpha_hat</code>	coefficient estimate of exposure (X) \rightarrow significant mediator (M)
<code>alpha_hat_SE</code>	the standard error for <code>alpha_hat</code>
<code>beta_hat</code>	coefficient estimate of the significant mediator (M) \rightarrow outcome (Y) (adjusted for exposure and high-dimensional nuisance mediators)
<code>beta_hat_SE</code>	the standard error for <code>beta_hat</code>
<code>Pval</code>	Bonferroni corrected p-values of the significant mediators (p-value < 0.05)

References

Haixiang Zhang, Jun Chen, Lei Liu (2019). Testing mediation effects in high-dimensional microbiome compositional data. *Submitted*.

Examples

```
library(MASS)
library(ncvreg)
library(microHIMA)
X <- read.csv("exposure.csv") # load the exposure
Y <- read.csv("response.csv") # load the response
M <- read.csv("OTU.csv") # load the matrix of OTUs
mhima.fit <- mhima(X, M, Y) # using the package THIMA
print(mhima.fit)
```