

Package: HIMA (via r-universe)

October 23, 2024

Type Package

Title High-Dimensional Mediation Analysis

Version 2.3.0

Date 2024-10-21

Description Allows to estimate and test high-dimensional mediation effects based on advanced mediator screening and penalized regression techniques. Methods used in the package refer to Zhang H, Zheng Y, Zhang Z, Gao T, Joyce B, Yoon G, Zhang W, Schwartz J, Just A, Colicino E, Vokonas P, Zhao L, Lv J, Baccarelli A, Hou L, Liu L. Estimating and Testing High-dimensional Mediation Effects in Epigenetic Studies. *Bioinformatics*. (2016) <[doi:10.1093/bioinformatics/btw351](https://doi.org/10.1093/bioinformatics/btw351)>. PMID: 27357171.

License GPL-3

Depends R (>= 3.4.0), ncvreg, glmnet

Imports utils, stats, MASS, survival, HDMT, hdi, conquer, quantreg, hommel, iterators, parallel, foreach, doParallel

Collate utils.R classicHIMA.R dlassoHIMA.R survHIMA.R microHIMA.R qHIMA.R eHIMA.R himaFit.R himaDat.R onAttach.R HIMA-package.R

Encoding UTF-8

LazyData true

URL <https://github.com/YinanZheng/HIMA/>

BugReports <https://github.com/YinanZheng/HIMA/issues/>

RoxygenNote 7.3.2

Repository <https://epiverse-connect.r-universe.dev>

RemoteUrl <https://github.com/YinanZheng/HIMA>

RemoteRef HEAD

RemoteSha 3448f1324ec2afc01278bf76f0afdfa0fddebb0d

Contents

HIMA-package	2
classicHIMA	3
dblassoHIMA	6
eHIMA	8
himaDat	9
himaFit	11
microHIMA	14
qHIMA	16
survHIMA	18
Index	21

HIMA-package	<i>High-Dimensional Mediation Analysis for 'Omic' Data</i>
--------------	--

Description

HIMA is an R package for estimating and testing high-dimensional mediation effects in omic studies. HIMA can perform high-dimensional mediation analysis on a wide range of omic data types as potential mediators, including epigenetics, transcriptomics, proteomics, metabolomics, and microbiomics. HIMA can also handle survival data mediation analysis and perform quantile mediation analysis.

Package: HIMA
 Type: Package
 Version: 2.3.0
 Date: 2024-10-21
 License: GPL-3

Details

If package "qvalue" is not found during installation, please first install "qvalue" package # through Bioconductor: <https://www.bioconductor.org/packages/release/bioc/html/qvalue.html>

Author(s)

Yinan Zheng <y-zheng@northwestern.edu>, Haixiang Zhang <haixiang.zhang@tju.edu.cn>, Lei liu (Contact) <lei.liu@wustl.edu>

Maintainer: Yinan Zheng <y-zheng@northwestern.edu>

References

1. Zhang H, Zheng Y, Zhang Z, Gao T, Joyce B, Yoon G, Zhang W, Schwartz J, Just A, Colicino E, Vokonas P, Zhao L, Lv J, Baccarelli A, Hou L, Liu L. Estimating and Testing High-dimensional Mediation Effects in Epigenetic Studies. *Bioinformatics*. 2016. DOI: 10.1093/bioinformatics/btw351. PMID: 27357171; PMCID: PMC5048064
2. Zhang H, Zheng Y, Hou L, Zheng C, Liu L. Mediation Analysis for Survival Data with High-Dimensional Mediators. *Bioinformatics*. 2021. DOI: 10.1093/bioinformatics/btab564. PMID: 34343267; PMCID: PMC8570823
3. Zhang H, Chen J, Feng Y, Wang C, Li H, Liu L. Mediation Effect Selection in High-dimensional and Compositional Microbiome data. *Stat Med*. 2021. DOI: 10.1002/sim.8808. PMID: 33205470; PMCID: PMC7855955
4. Zhang H, Chen J, Li Z, Liu L. Testing for Mediation Effect with Application to Human Microbiome Data. *Stat Biosci*. 2021. DOI: 10.1007/s12561-019-09253-3. PMID: 34093887; PMCID: PMC8177450
5. Perera C, Zhang H, Zheng Y, Hou L, Qu A, Zheng C, Xie K, Liu L. HIMA2: High-dimensional Mediation Analysis and Its Application in Epigenome-wide DNA Methylation Data. *BMC Bioinformatics*. 2022. DOI: 10.1186/s12859-022-04748-1. PMID: 35879655; PMCID: PMC9310002
6. Zhang H, Hong X, Zheng Y, Hou L, Zheng C, Wang X, Liu L. High-Dimensional Quantile Mediation Analysis with Application to a Birth Cohort Study of Mother–Newborn Pairs. *Bioinformatics*. 2024. DOI: 10.1093/bioinformatics/btae055. PMID: 38290773; PMCID: PMC10873903
7. Bai X, Zheng Y, Hou L, Zheng C, Liu L, Zhang H. An Efficient Testing Procedure for High-dimensional Mediators with FDR Control. *Statistics in Biosciences*. 2024. DOI: 10.1007/s12561-024-09447-4.

classicHIMA

Classic high-dimensional mediation analysis

Description

classicHIMA is used to estimate and test classic high-dimensional mediation effects (linear & logistic regression).

Usage

```
classicHIMA(  
  X,  
  M,  
  Y,  
  COV.XM = NULL,  
  COV.MY = COV.XM,  
  Y.type = c("continuous", "binary"),  
  M.type = c("gaussian", "negbin"),  
  penalty = c("MCP", "SCAD", "lasso"),  
  topN = NULL,
```

```

parallel = FALSE,
ncore = 1,
scale = TRUE,
Bonfcut = 0.05,
verbose = FALSE,
...
)

```

Arguments

X	a vector of exposure. Do not use data.frame or matrix.
M	a data.frame or matrix of high-dimensional mediators. Rows represent samples, columns represent variables.
Y	a vector of outcome. Can be either continuous or binary (0-1). Do not use data.frame or matrix.
COV.XM	a data.frame or matrix of covariates dataset for testing the association $M \sim X$. Covariates specified here will not participate penalization. Default = NULL. If the covariates contain mixed data types, please make sure all categorical variables are properly formatted as factor type.
COV.MY	a data.frame or matrix of covariates dataset for testing the association $Y \sim M$. Covariates specified here will not participate penalization. If not specified, the same set of covariates for $M \sim X$ will be applied. Using different sets of covariates is allowed but this needs to be handled carefully.
Y.type	data type of outcome (Y). Either 'continuous' (default) or 'binary'.
M.type	data type of mediator (M). Either 'gaussian' (default) or 'negbin' (i.e., negative binomial).
penalty	the penalty to be applied to the model. Either 'MCP' (the default), 'SCAD', or 'lasso'.
topN	an integer specifying the number of top markers from sure independent screening. Default = NULL. If NULL, topN will be either $\text{ceiling}(n/\log(n))$ for continuous outcome, or $\text{ceiling}(n/(2*\log(n)))$ for binary outcome, where n is the sample size. If the sample size is greater than topN (pre-specified or calculated), all mediators will be included in the test (i.e. low-dimensional scenario).
parallel	logical. Enable parallel computing feature? Default = FALSE.
ncore	number of cores to run parallel computing Valid when parallel == TRUE. By default max number of cores available in the machine will be utilized.
scale	logical. Should the function scale the data? Default = TRUE.
Bonfcut	Bonferroni-corrected p value cutoff applied to select significant mediators. Default = 0.05.
verbose	logical. Should the function be verbose? Default = FALSE.
...	other arguments passed to ncvreg.

Value

A data.frame containing mediation testing results of selected mediators.

Index: mediation name of selected significant mediator.

alpha_hat: coefficient estimates of exposure (X) → mediators (M) (adjusted for covariates).

beta_hat: coefficient estimates of mediators (M) → outcome (Y) (adjusted for covariates and exposure).

IDE: mediation (indirect) effect, i.e., $\alpha \cdot \beta$.

rimp: relative importance of the mediator.

pmax: joint raw p-value of selected significant mediator (based on Bonferroni method).

References

Zhang H, Zheng Y, Zhang Z, Gao T, Joyce B, Yoon G, Zhang W, Schwartz J, Just A, Colicino E, Vokonas P, Zhao L, Lv J, Baccarelli A, Hou L, Liu L. Estimating and Testing High-dimensional Mediation Effects in Epigenetic Studies. *Bioinformatics*. 2016. DOI: 10.1093/bioinformatics/btw351. PMID: 27357171; PMCID: PMC5048064

Examples

```
## Not run:
# Note: In the following examples, M1, M2, and M3 are true mediators.
data(himaDat)
```

```
# When Y is continuous and normally distributed
# Example 1 (continuous outcome):
head(himaDat$Example1$PhenoData)
```

```
hima.fit <- classicHIMA(
  X = himaDat$Example1$PhenoData$Treatment,
  Y = himaDat$Example1$PhenoData$Outcome,
  M = himaDat$Example1$Mediator,
  COV.XM = himaDat$Example1$PhenoData[, c("Sex", "Age")],
  Y.type = "continuous",
  scale = FALSE, # Disabled only for simulation data
  verbose = TRUE
)
hima.fit
```

```
# When Y is binary
# Example 2 (binary outcome):
head(himaDat$Example2$PhenoData)
```

```
hima.logistic.fit <- classicHIMA(
  X = himaDat$Example2$PhenoData$Treatment,
  Y = himaDat$Example2$PhenoData$Disease,
  M = himaDat$Example2$Mediator,
  COV.XM = himaDat$Example2$PhenoData[, c("Sex", "Age")],
  Y.type = "binary",
  scale = FALSE, # Disabled only for simulation data
```

```

    verbose = TRUE
  )
  hima.logistic.fit

## End(Not run)

```

dblassoHIMA

High-dimensional mediation analysis with de-biased lasso penalty

Description

dblassoHIMA is used to estimate and test high-dimensional mediation effects using de-biased lasso penalty.

Usage

```

dblassoHIMA(
  X,
  M,
  Y,
  COV = NULL,
  topN = NULL,
  scale = TRUE,
  FDRcut = 0.05,
  verbose = FALSE
)

```

Arguments

X	a vector of exposure.
M	a data.frame or matrix of high-dimensional mediators. Rows represent samples, columns represent variables.
Y	a vector of outcome. Can be either continuous or binary (0-1).
COV	a data.frame or matrix of covariates dataset for testing the association $M \sim X$ and $Y \sim M$.
topN	an integer specifying the number of top markers from sure independent screening. Default = NULL. If NULL, topN will be $\text{ceiling}(n/\log(n))$, where n is the sample size. If the sample size is greater than topN (pre-specified or calculated), all mediators will be included in the test (i.e. low-dimensional scenario).
scale	logical. Should the function scale the data? Default = TRUE.
FDRcut	HDMT pointwise FDR cutoff applied to select significant mediators. Default = 0.05.
verbose	logical. Should the function be verbose? Default = FALSE.

Value

A data.frame containing mediation testing results of significant mediators (FDR < FDRcut).

Index: mediation name of selected significant mediator.

alpha_hat: coefficient estimates of exposure (X) → mediators (M) (adjusted for covariates).

alpha_se: standard error for alpha.

beta_hat: coefficient estimates of mediators (M) → outcome (Y) (adjusted for covariates and exposure).

beta_se: standard error for beta.

IDE: mediation (indirect) effect, i.e., $\alpha \cdot \beta$.

rimp: relative importance of the mediator.

pmax: joint raw p-value of selected significant mediator (based on HDMT pointwise FDR method).

References

Perera C, Zhang H, Zheng Y, Hou L, Qu A, Zheng C, Xie K, Liu L. HIMA2: high-dimensional mediation analysis and its application in epigenome-wide DNA methylation data. BMC Bioinformatics. 2022. DOI: 10.1186/s12859-022-04748-1. PMID: 35879655; PMCID: PMC9310002

Examples

```
## Not run:
# Note: In the following examples, M1, M2, and M3 are true mediators.
data(himaDat)

# Y is continuous and normally distributed
# Example:
head(himaDat$Example1$PhenoData)

dbleSSohima.fit <- dbleSSoHIMA(
  X = himaDat$Example1$PhenoData$Treatment,
  Y = himaDat$Example1$PhenoData$Outcome,
  M = himaDat$Example1$Mediator,
  COV = himaDat$Example1$PhenoData[, c("Sex", "Age")],
  scale = FALSE, # Disabled only for simulation data
  FDRcut = 0.05,
  verbose = TRUE
)
dbleSSohima.fit

## End(Not run)
```

eHIMA

*Efficient high-dimensional mediation analysis***Description**

eHIMA is used to estimate and test high-dimensional mediation effects using an efficient algorithm. It provides higher statistical power than the standard hima. Note: efficient HIMA is only applicable to mediators and outcomes that are both continuous and normally distributed.

Usage

```
eHIMA(
  X,
  M,
  Y,
  COV = NULL,
  topN = NULL,
  scale = TRUE,
  FDRcut = 0.05,
  verbose = FALSE
)
```

Arguments

X	a vector of exposure.
M	a data.frame or matrix of high-dimensional mediators. Rows represent samples, columns represent mediator variables. M has to be continuous and normally distributed.
Y	a vector of continuous outcome. Do not use data.frame or matrix.
COV	a matrix of adjusting covariates. Rows represent samples, columns represent variables. Can be NULL.
topN	an integer specifying the number of top markers from sure independent screening. Default = NULL. If NULL, topN will be $2 * \text{ceiling}(n / \log(n))$, where n is the sample size. If the sample size is greater than topN (pre-specified or calculated), all mediators will be included in the test (i.e. low-dimensional scenario).
scale	logical. Should the function scale the data? Default = TRUE.
FDRcut	Benjamini-Hochberg FDR cutoff applied to select significant mediators. Default = 0.05.
verbose	logical. Should the function be verbose? Default = FALSE.

Value

A data.frame containing mediation testing results of significant mediators ($\text{FDR} < \text{FDRcut}$).

Index: mediation name of selected significant mediator.

alpha_hat: coefficient estimates of exposure (X) → mediators (M) (adjusted for covariates).
alpha_se: standard error for alpha.
beta_hat: coefficient estimates of mediators (M) → outcome (Y) (adjusted for covariates and exposure).
beta_se: standard error for beta.
IDE: mediation (indirect) effect, i.e., $\alpha \cdot \beta$.
rimp: relative importance of the mediator.
pmax: joint raw p-value of selected significant mediator (based on divide-aggregate composite-null test [DACT] method).

References

Bai X, Zheng Y, Hou L, Zheng C, Liu L, Zhang H. An Efficient Testing Procedure for High-dimensional Mediators with FDR Control. *Statistics in Biosciences*. 2024. DOI: 10.1007/s12561-024-09447-4.

Examples

```
## Not run:
# Note: In the following example, M1, M2, and M3 are true mediators.
data(himaDat)

# Y is continuous and normally distributed
# Example (continuous outcome):
head(himaDat$Example1$PhenoData)

eHIMA.fit <- eHIMA(
  X = himaDat$Example1$PhenoData$Treatment,
  Y = himaDat$Example1$PhenoData$Outcome,
  M = himaDat$Example1$Mediator,
  COV = himaDat$Example1$PhenoData[, c("Sex", "Age")],
  scale = FALSE, # Disabled only for simulation data
  FDRcut = 0.05,
  verbose = TRUE
)
eHIMA.fit

## End(Not run)
```

himaDat

Example datasets for HIMA demo

Description

A list containing datasets for various scenarios of HIMA. Each dataset contains a phenotype data frame and a high-dimension mediator data matrix. The datasets are simulated using parameters generated from real datasets. The code used to generate the data can be found in `"/inst/script"` folder of the source package.

Usage

himaDat

Format

An object of class `list` of length 5.

Value

A list of example datasets for HIMA demo and testing.

→ **Example dataset 1 for HIMA: Continuous outcome** ←

Treatment: treated (value = 1) or not treated (value = 0)

Outcome: outcome of the treatment- a normally distributed continuous variable

Sex: female (value = 1) or male (value = 0)

Age: Age of the participant

→ **Example dataset 2 for HIMA: Binary outcome** ←

Treatment: treated (value = 1) or not treated (value = 0)

Disease: diseased (value = 1) or healthy (value = 0)

Sex: female (value = 1) or male (value = 0)

Age: Age of the participant

→ **Example dataset 3 for HIMA: Survival data outcome** ←

Treatment: treated (value = 1) or not treated (value = 0)

Status: Status indicator: dead (value = 1) or alive (value = 0)

Time: time to event

Sex: female (value = 1) or male (value = 0)

Age: Age of the participant

→ **Example dataset 4 for HIMA: Compositional mediator (e.g., microbiome)** ←

Treatment: treated (value = 1) or not treated (value = 0)

Outcome: outcome of the treatment- a normally distributed continuous variable

Sex: female (value = 1) or male (value = 0)

Age: Age of the participant

→ **Example dataset 5 for HIMA: High-dimensional quantile mediation analysis** ←

Treatment: treated (value = 1) or not treated (value = 0)

Outcome: outcome of the treatment- abnormally distributed continuous variable

Sex: female (value = 1) or male (value = 0)

Age: Age of the participant

Description

himaFit is a wrapper function designed to perform various HIMA methods for estimating and testing high-dimensional mediation effects. himaFit can automatically select the appropriate HIMA method based on the outcome and mediator data type.

Usage

```
himaFit(
  formula,
  data.pheno,
  data.M,
  mediator.type = c("gaussian", "negbin", "compositional"),
  penalty = c("DBlasso", "MCP", "SCAD", "lasso"),
  quantile = FALSE,
  efficient = FALSE,
  scale = TRUE,
  Sigcut = 0.05,
  verbose = FALSE,
  ...
)
```

Arguments

formula	an object of class formula: a symbolic description of the overall effect model, i.e., $\text{outcome} \sim \text{exposure} + \text{covariates}$, to be fitted. Make sure the "exposure" is the variable of interest, which must be listed as the first variable in the right hand side of the formula.
data.pheno	a data frame containing exposure and covariates that are listed in the right hand side of the formula. The variable names must match those listed in formula. By default himaFit will scale data.pheno.
data.M	a data.frame or matrix of high-dimensional mediators. Rows represent samples, columns represent variables. By default himaFit will scale data.M.
mediator.type	data type of high-dimensional mediators (data.M). Either 'gaussian' (default, for continuous mediators), 'negbin' (i.e., negative binomial, for RNA-seq data as mediators), or 'compositional' (for microbiome data as mediators).
penalty	the penalty to be applied to the model. Either 'DBlasso' (De-biased LASSO, default), 'MCP', 'SCAD', or 'lasso'. Please note, survival HIMA and microbiome HIMA can be only performed with 'DBlasso'; Quantile HIMA cannot be performed with 'DBlasso'. Not applicable for efficient HIMA (when efficient = TRUE), as it will always apply 'MCP'.

quantile	use quantile HIMA (qHIMA). Only applicable for classic HIMA with continues outcome. Please add parameter tau to specify the desired quantile (can be a vector), otherwise the default tau = 0.5 will be used.
efficient	use efficient HIMA (eHIMA). Only applicable for classic HIMA with continuous outcome. and mediator.type = "gaussian"). Default = FALSE.
scale	logical. Should the function scale the data (exposure, mediators, and covariates)? Default = TRUE. Note: for simulation study, scale can be turned off to avoid estimate compression.
Sigcut	cutoff applied to select significant mediators. Default = 0.05.
verbose	logical. Should the function be verbose and show the progression? Default = FALSE.
...	reserved passing parameter.

Value

A data.frame containing mediation testing results of selected mediators.

ID: Mediator ID/name.

alpha: Coefficient estimates of exposure (X) → mediators (M) (adjusted for covariates).

beta: Coefficient estimates of mediators (M) → outcome (Y) (adjusted for covariates and exposure).

alpha*beta: Mediation (indirect) effect.

Relative Importance: Relative importance of the mediator. It is the proportion of the mediation effect for each mediator out of the sum of the mediation effect (absolute value) across all significant mediators selected.

p-value: Joint raw p-value of significant mediators selected based on corresponding approach.

tau: Quantile level of the outcome (applicable only to the quantile mediation model).

References

1. Zhang H, Zheng Y, Zhang Z, Gao T, Joyce B, Yoon G, Zhang W, Schwartz J, Just A, Colicino E, Vokonas P, Zhao L, Lv J, Baccarelli A, Hou L, Liu L. Estimating and Testing High-dimensional Mediation Effects in Epigenetic Studies. *Bioinformatics*. 2016. DOI: 10.1093/bioinformatics/btw351. PMID: 27357171; PMCID: PMC5048064
2. Zhang H, Zheng Y, Hou L, Zheng C, Liu L. Mediation Analysis for Survival Data with High-Dimensional Mediators. *Bioinformatics*. 2021. DOI: 10.1093/bioinformatics/btab564. PMID: 34343267; PMCID: PMC8570823
3. Zhang H, Chen J, Feng Y, Wang C, Li H, Liu L. Mediation Effect Selection in High-dimensional and Compositional Microbiome data. *Stat Med*. 2021. DOI: 10.1002/sim.8808. PMID: 33205470; PMCID: PMC7855955
4. Zhang H, Chen J, Li Z, Liu L. Testing for Mediation Effect with Application to Human Microbiome Data. *Stat Biosci*. 2021. DOI: 10.1007/s12561-019-09253-3. PMID: 34093887; PMCID: PMC8177450

5. Perera C, Zhang H, Zheng Y, Hou L, Qu A, Zheng C, Xie K, Liu L. HIMA2: High-dimensional Mediation Analysis and Its Application in Epigenome-wide DNA Methylation Data. *BMC Bioinformatics*. 2022. DOI: 10.1186/s12859-022-04748-1. PMID: 35879655; PMCID: PMC9310002
6. Zhang H, Hong X, Zheng Y, Hou L, Zheng C, Wang X, Liu L. High-Dimensional Quantile Mediation Analysis with Application to a Birth Cohort Study of Mother–Newborn Pairs. *Bioinformatics*. 2024. DOI: 10.1093/bioinformatics/btae055. PMID: 38290773; PMCID: PMC10873903
7. Bai X, Zheng Y, Hou L, Zheng C, Liu L, Zhang H. An Efficient Testing Procedure for High-dimensional Mediators with FDR Control. *Statistics in Biosciences*. 2024. DOI: 10.1007/s12561-024-09447-4.

Examples

```
## Not run:
# Note: In the following examples, M1, M2, and M3 are true mediators.
data(himaDat)

# Example 1 (continuous outcome - linear HIMA):
head(himaDat$Example1$PhenoData)

e1 <- himaFit(Outcome ~ Treatment + Sex + Age,
  data.pheno = himaDat$Example1$PhenoData,
  data.M = himaDat$Example1$Mediator,
  mediator.type = "gaussian",
  penalty = "MCP", # Can be "DBlasso" for dbllassoHIMA
  scale = FALSE
) # Disabled only for simulation data
e1
attributes(e1)$variable.labels

# Efficient HIMA (only applicable to mediators and outcomes that are
# both continuous and normally distributed.)
e1e <- himaFit(Outcome ~ Treatment + Sex + Age,
  data.pheno = himaDat$Example1$PhenoData,
  data.M = himaDat$Example1$Mediator,
  mediator.type = "gaussian",
  efficient = TRUE,
  scale = FALSE
) # Disabled only for simulation data
e1e
attributes(e1e)$variable.labels

# Example 2 (binary outcome - logistic HIMA):
head(himaDat$Example2$PhenoData)

e2 <- himaFit(Disease ~ Treatment + Sex + Age,
  data.pheno = himaDat$Example2$PhenoData,
  data.M = himaDat$Example2$Mediator,
  mediator.type = "gaussian",
  penalty = "MCP",
  scale = FALSE
) # Disabled only for simulation data
```

```

e2
attributes(e2)$variable.labels

# Example 3 (time-to-event outcome - survival HIMA):
head(himaDat$Example3$PhenoData)

e3 <- himaFit(Surv(Status, Time) ~ Treatment + Sex + Age,
  data.pheno = himaDat$Example3$PhenoData,
  data.M = himaDat$Example3$Mediator,
  mediator.type = "gaussian",
  penalty = "DBlasso",
  scale = FALSE
) # Disabled only for simulation data
e3
attributes(e3)$variable.labels

# Example 4 (compositional data as mediator, e.g., microbiome):
head(himaDat$Example4$PhenoData)

e4 <- himaFit(Outcome ~ Treatment + Sex + Age,
  data.pheno = himaDat$Example4$PhenoData,
  data.M = himaDat$Example4$Mediator,
  mediator.type = "compositional",
  penalty = "DBlasso"
) # Scaling is always enabled internally for microHIMA
e4
attributes(e4)$variable.labels

#' # Example 5 (quantile mediation analysis - quantile HIMA):
head(himaDat$Example5$PhenoData)

# Note that the function will prompt input for quantile level.
e5 <- himaFit(Outcome ~ Treatment + Sex + Age,
  data.pheno = himaDat$Example5$PhenoData,
  data.M = himaDat$Example5$Mediator,
  mediator.type = "gaussian",
  quantile = TRUE,
  penalty = "MCP", # Quantile HIMA does not support DBlasso
  scale = FALSE, # Disabled only for simulation data
  tau = c(0.3, 0.5, 0.7)
) # Specify multiple quantile level
e5
attributes(e5)$variable.labels

## End(Not run)

```

Description

microHIMA is used to estimate and test high-dimensional mediation effects for compositional microbiome data.

Usage

```
microHIMA(X, OTU, Y, COV = NULL, FDRcut = 0.05, verbose = FALSE)
```

Arguments

X	a vector of exposure.
OTU	a data.frame or matrix of high-dimensional Operational Taxonomic Unit (OTU) data (mediators). Rows represent samples, columns represent variables.
Y	a vector of continuous outcome. Binary outcome is not allowed.
COV	a data.frame or matrix of adjusting covariates. Rows represent samples, columns represent microbiome variables. Can be NULL.
FDRcut	Hommel FDR cutoff applied to select significant mediators. Default = 0.05.
verbose	logical. Should the function be verbose? Default = FALSE.

Value

A data.frame containing mediation testing results of significant mediators ($FDR < FDRcut$).

Index: mediation name of selected significant mediator.

alpha_hat: coefficient estimates of exposure (X) \rightarrow mediators (M) (adjusted for covariates).

alpha_se: standard error for alpha.

beta_hat: coefficient estimates of mediators (M) \rightarrow outcome (Y) (adjusted for covariates and exposure).

beta_se: standard error for beta.

IDE: mediation (indirect) effect, i.e., $\alpha * \beta$.

rimp: relative importance of the mediator.

pmax: joint raw p-value of selected significant mediator (based on Hommel FDR method).

References

1. Zhang H, Chen J, Feng Y, Wang C, Li H, Liu L. Mediation effect selection in high-dimensional and compositional microbiome data. *Stat Med.* 2021. DOI: 10.1002/sim.8808. PMID: 33205470; PMCID: PMC7855955
2. Zhang H, Chen J, Li Z, Liu L. Testing for mediation effect with application to human microbiome data. *Stat Biosci.* 2021. DOI: 10.1007/s12561-019-09253-3. PMID: 34093887; PMCID: PMC8177450

Examples

```
## Not run:
# Note: In the following example, M1, M2, and M3 are true mediators.
data(himaDat)

head(himaDat$Example4$PhenoData)

microHIMA.fit <- microHIMA(
  X = himaDat$Example4$PhenoData$Treatment,
  Y = himaDat$Example4$PhenoData$Outcome,
  OTU = himaDat$Example4$Mediator,
  COV = himaDat$Example4$PhenoData[, c("Sex", "Age")],
  FDRcut = 0.05,
  verbose = TRUE
)
microHIMA.fit

## End(Not run)
```

qHIMA

High-dimensional quantile mediation analysis

Description

qHIMA is used to estimate and test high-dimensional quantile mediation effects.

Usage

```
qHIMA(
  X,
  M,
  Y,
  COV = NULL,
  penalty = c("MCP", "SCAD", "lasso"),
  topN = NULL,
  tau = 0.5,
  scale = TRUE,
  Bonfcut = 0.05,
  verbose = FALSE,
  ...
)
```

Arguments

X a vector of exposure.

M a data.frame or matrix of high-dimensional mediators. Rows represent samples, columns represent mediator variables.

Y	a vector of continuous outcome. Do not use data.frame or matrix.
COV	a matrix of adjusting covariates. Rows represent samples, columns represent variables. Can be NULL.
penalty	the penalty to be applied to the model (a parameter passed to function <code>conquer.cv.reg</code> in package <code>conquer</code> . Either 'MCP' (the default), 'SCAD', or 'lasso'.
topN	an integer specifying the number of top markers from sure independent screening. Default = NULL. If NULL, topN will be $2 \times \text{ceiling}(n/\log(n))$, where n is the sample size. If the sample size is greater than topN (pre-specified or calculated), all mediators will be included in the test (i.e. low-dimensional scenario).
tau	quantile level of outcome. Default = 0.5. A vector of tau is accepted.
scale	logical. Should the function scale the data? Default = TRUE.
Bonfcut	Bonferroni-corrected p value cutoff applied to select significant mediators. Default = 0.05.
verbose	logical. Should the function be verbose? Default = FALSE.
...	reserved passing parameter.

Value

A data.frame containing mediation testing results of selected mediators (Bonferroni-adjusted p value < Bonfcut).

Index: mediation name of selected significant mediator.

alpha_hat: coefficient estimates of exposure (X) → mediators (M) (adjusted for covariates).

alpha_se: standard error for alpha.

beta_hat: coefficient estimates of mediators (M) → outcome (Y) (adjusted for covariates and exposure).

beta_se: standard error for beta.

IDE: mediation (indirect) effect, i.e., $\alpha \times \beta$.

rimp: relative importance of the mediator.

pmax: joint raw p-value of selected significant mediator (based on Bonferroni method).

References

Zhang H, Hong X, Zheng Y, Hou L, Zheng C, Wang X, Liu L. High-Dimensional Quantile Mediation Analysis with Application to a Birth Cohort Study of Mother–Newborn Pairs. *Bioinformatics*. 2024. DOI: 10.1093/bioinformatics/btae055. PMID: 38290773; PMCID: PMC10873903

Examples

```
## Not run:
# Note: In the following example, M1, M2, and M3 are true mediators.
data(himaDat)

head(himaDat$Example5$PhenoData)
```

```

qHIMA.fit <- qHIMA(
  X = himaDat$Example5$PhenoData$Treatment,
  M = himaDat$Example5$Mediator,
  Y = himaDat$Example5$PhenoData$Outcome,
  COV = himaDat$Example5$PhenoData[, c("Sex", "Age")],
  tau = c(0.3, 0.5, 0.7),
  scale = FALSE, # Disabled only for simulation data
  Bonfcut = 0.05,
  verbose = TRUE
)
qHIMA.fit

## End(Not run)

```

survHIMA

High-dimensional mediation analysis for survival data

Description

survHIMA is used to estimate and test high-dimensional mediation effects for survival data.

Usage

```

survHIMA(
  X,
  M,
  OT,
  status,
  COV = NULL,
  topN = NULL,
  scale = TRUE,
  FDRcut = 0.05,
  verbose = FALSE
)

```

Arguments

X	a vector of exposure.
M	a data.frame or matrix of high-dimensional mediators. Rows represent samples, columns represent mediator variables.
OT	a vector of observed failure times.
status	a vector of censoring indicator (status = 1: uncensored; status = 0: censored)
COV	a matrix of adjusting covariates. Rows represent samples, columns represent variables. Can be NULL.

topN	an integer specifying the number of top markers from sure independent screening. Default = NULL. If NULL, topN will be $\text{ceiling}(n/\log(n))$, where n is the sample size. If the sample size is greater than topN (pre-specified or calculated), all mediators will be included in the test (i.e. low-dimensional scenario).
scale	logical. Should the function scale the data? Default = TRUE.
FDRcut	HDMT pointwise FDR cutoff applied to select significant mediators. Default = 0.05.
verbose	logical. Should the function be verbose? Default = FALSE.

Value

A data.frame containing mediation testing results of significant mediators ($\text{FDR} < \text{FDRcut}$).

Index: mediation name of selected significant mediator.

alpha_hat: coefficient estimates of exposure (X) \rightarrow mediators (M) (adjusted for covariates).

alpha_se: standard error for alpha.

beta_hat: coefficient estimates of mediators (M) \rightarrow outcome (Y) (adjusted for covariates and exposure).

beta_se: standard error for beta.

IDE: mediation (indirect) effect, i.e., $\alpha \cdot \beta$.

rimp: relative importance of the mediator.

pmax: joint raw p-value of selected significant mediator (based on HDMT pointwise FDR method).

References

Zhang H, Zheng Y, Hou L, Zheng C, Liu L. Mediation Analysis for Survival Data with High-Dimensional Mediators. *Bioinformatics*. 2021. DOI: 10.1093/bioinformatics/btab564. PMID: 34343267; PMCID: PMC8570823

Examples

```
## Not run:
# Note: In the following example, M1, M2, and M3 are true mediators.
data(himaDat)

head(himaDat$Example3$PhenoData)

survHIMA.fit <- survHIMA(
  X = himaDat$Example3$PhenoData$Treatment,
  M = himaDat$Example3$Mediator,
  OT = himaDat$Example3$PhenoData$Time,
  status = himaDat$Example3$PhenoData$Status,
  COV = himaDat$Example3$PhenoData[, c("Sex", "Age")],
  scale = FALSE, # Disabled only for simulation data
  FDRcut = 0.05,
  verbose = TRUE
)
survHIMA.fit
```

End(Not run)

Index

* **datasets**

himaDat, [9](#)

* **package**

HIMA-package, [2](#)

classicHIMA, [3](#)

dblassoHIMA, [6](#)

eHIMA, [8](#)

HIMA (HIMA-package), [2](#)

hima (HIMA-package), [2](#)

HIMA-package, [2](#)

himaDat, [9](#)

himaFit, [11](#)

microHIMA, [14](#)

qHIMA, [16](#)

survHIMA, [18](#)