Package 'MRmediation'

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Type Package

Title A Causal Mediation Method with Methylated Region (MR) as the Mediator

Version 1.0.1

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Description A causal mediation approach under the counterfactual framework to test the significance of total, direct and indirect effects. In this approach, a group of methylated sites from a predefined region are utilized as the mediator, and the functional transformation is used to reduce the possible high dimension in the region-based methylated sites and account for their location information.

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Encoding UTF-8

LazyData true

Depends R (>= 3.5.0), fda

Imports MASS, stats

RoxygenNote 7.1.0

Collate 'MRmediation.R' 'mediation_single.R' 'example_data.R'

NeedsCompilation no

Repository CRAN

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Contents

`example_data` *This is the data for examples*

Description

- data. phenotype file. 1st column is ID, 2nd column is continuous outcome, 3rd column is binary outcome, 4th column is exposure, 5th column is age, 6th column is gender, 7th-last columns are CpGs
- pos. CpG locations from the defined region and they are from the same chromosome.

Usage

```
data(example_data)
```

`mediation` *A causal mediation method with methylated region as the mediator*

Description

A causal mediation method with methylated region as the mediator

Usage

```
mediation(
  pheno,
  predictor,
  region,
  pos,
  order,
  gbasis,
  covariate,
  base = "bspline",
  family = "gaussian"
)
```

Arguments

`pheno`	A vector of continuous or binary phenotypes (class: numeric).
`predictor`	A vector of values for the exposure variable (class: numeric).
`region`	A matrix of CpGs in a region. Each column is a CpG (class: data.frame).
`pos`	A vector of CpG locations from the defined region and they are from the same chromosome (class: integer).
`order`	A value for the order of bspline basis. 1: constant, 2: linear, 3: quadratic and 4: cubic.

`gbasis`	A value for the number of basis being used for functional transformation on CpGs.
`covariate`	A matrix of covariates. Each column is a covariate (class: data.frame).
`base`	"bspline" for B-spline basis or "fspline" for Fourier basis.
`family`	"gaussian" for continuous outcome or "binomial" for binary outcome.

Value

1. pval$TE: total effect (TE) p-value
2. pval$DE: direct effect (DE) p-value
3. pval$IE: indirect effect (IE) p-value
4. pval_MX: p-value for the association between methylation and exposure

Examples

```
#################
### Examples ###
#################
data("example_data")
predictor = data$exposure
region = data[,7:dim(data)[2]]
covariates = subset(data, select=c("age","gender"))
# binary outcome
pheno_bin = data$pheno_bin
mediation(pheno_bin, predictor, region, pos, covariate=covariates, order=4,
gbasis=4, base="bspline", family="binomial")
# continuous outcome
pheno_con = data$pheno_con
mediation(pheno_con, predictor, region, pos, covariate=covariates, order=4,
gbasis=4, base="bspline", family="gaussian")
```

`mediation_single` *A causal mediation method with a single CpG site as the mediator*

Description

A causal mediation method with a single CpG site as the mediator

Usage

```
mediation_single(pheno, predictor, cpg, covariate, family = "gaussian")
```

Arguments

`pheno`	A vector of continuous or binary phenotypes (class: numeric).
`predictor`	A vector of values for the exposure variable (class: numeric).
`cpg`	A vector of a CpG (class: numeric).
`covariate`	A matrix of covariates. Each column is a covariate (class: data.frame).
`family`	"gaussian" for continuous outcome or "binomial" for binary outcome.

Value

1. pval$TE: total effect (TE) p-value
2. pval$DE: direct effect (DE) p-value
3. pval$IE: indirect effect (IE) p-value
4. pval_MX: p-value for the association between methylation and exposure

Examples

```
################
### Examples ###
################
data("example_data")
predictor = data$exposure
cpg = data[,9] #any number in c(7:dim(data)[2])
covariates = subset(data, select=c("age","gender"))
# binary outcome
pheno_bin = data$pheno_bin
mediation_single(pheno_bin, predictor, cpg, covariate=covariates, family="binomial")
# continuous outcome
pheno_con = data$pheno_con
mediation_single(pheno_con, predictor, cpg, covariate=covariates, family="gaussian")
```

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