

Package ‘SMUT’

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Type Package

Title Multi-SNP Mediation Intersection-Union Test

Version 1.0

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Description Testing the mediation effect of multiple SNPs on an outcome through a gene.

LazyData true

License GPL (>= 2)

Depends R (>= 2.10)

Imports Rcpp (>= 0.12.14), SKAT, MASS

LinkingTo Rcpp, RcppEigen

NeedsCompilation yes

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eigenMapMatMult *Matrix multiplication using RcppEigen*

Description

Matrix multiplication using RcppEigen.

Usage

```
eigenMapMatMult(A,B)
```

Arguments

A, B numeric (double) complex matrices or vectors.

Value

The matrix product. The value is the same as A %*% B

Examples

```
library(SMUT)
A=matrix(1:9,3,3)
A=A+0
B=as.matrix(c(5.0, 2.0, 0.0))
eigenMapMatMult(A,B)
# the result is the same as A %*% B

# Thanks for using our R package SMUT ~~
```

Genotype_data *Example genotype data for SMUT*

Description

Example genotype data for SMUT. It is a matrix with 100 rows and 200 columns. Each row is an individual; each column is a SNP.

Format

It is a matrix with 100 rows and 200 columns. Each row is an individual; each column is a SNP.

Description

Testing the mediation effect of multiple SNPs on an outcome through a gene.

Usage

```
SMUT(G, mediator, outcome,
      outcome_type="continuous", method="score", approxi=TRUE, debug=FALSE)
```

Arguments

G	n by p matrix (n rows and p columns). Each row is one individual; each column is one SNP.
mediator	a vector length of n. It is the mediator variable.
outcome	a vector length of n. It is the outcome variable.
outcome_type	Type of the outcome variable. For now, this package only deals with continuous outcome. Default is "continuous".
method	The method of testing coefficient of mediator in the outcome model. The score test is used. Default is "score".
approx	a boolean value. This is an indicator whether the approximation of the score statistic is applied to save computing time. Default is TRUE.
debug	a boolean value. If TRUE a lot of computing details is printed; otherwise the function is completely silent. Default is FALSE.

Value

p_value_IUT	The p value for testing the mediation effect ($\theta \cdot \beta$) based on intersection-union test.
p_value_theta	The p value for testing θ in the outcome model. The outcome model is the following. $\text{outcome} \sim \text{intercept} + G \cdot \gamma + \text{mediator} \cdot \theta + \text{error}.$
p_value_beta	The p value for testing β in the mediator model. The mediator model is the following. $\text{mediator} \sim \text{intercept} + G \cdot \beta + \text{error}$

Author(s)

Wujuan Zhong

Examples

```

library(SMUT)
# load the Genotype data included in this R package
data("Genotype_data")

# generate one mediator and one outcome

# first example, the mediation effect is significant
set.seed(1)
beta=rnorm(ncol(Genotype_data),1,2)
e1 = rnorm(nrow(Genotype_data), 0, 1)
mediator = 1 + eigenMapMatMult(Genotype_data,beta) + e1

theta=0.8
gamma=rnorm(ncol(Genotype_data),0.5,2)
e2 = rnorm(nrow(Genotype_data), 0, 1)
outcome = 2 + eigenMapMatMult(Genotype_data,gamma) + theta*mediator + e2

p_value=SMUT(G=Genotype_data,mediator=mediator,outcome=outcome)
print(p_value)

# p_value_IUT is the p value for the mediation effect.
# we have significant(at alpha level 0.05) mediation effects (p_value_IUT = 0.001655787).

# second example, the mediation effect is non-significant
set.seed(1)
beta=rnorm(ncol(Genotype_data),1,2)
e1 = rnorm(nrow(Genotype_data), 0, 1)
mediator = 1 + eigenMapMatMult(Genotype_data,beta) + e1

theta=0
gamma=rnorm(ncol(Genotype_data),0.5,2)
e2 = rnorm(nrow(Genotype_data), 0, 1)
outcome = 2 + eigenMapMatMult(Genotype_data,gamma) + theta*mediator + e2

p_value=SMUT(G=Genotype_data,mediator=mediator,outcome=outcome)
print(p_value)

# p_value_IUT is the p value for the mediation effect.
# we have non-significant(at alpha level 0.05) mediation effects (p_value_IUT = 0.3281677).

# third example, the mediation effect is non-significant
set.seed(1)
beta=rep(0,ncol(Genotype_data))
e1 = rnorm(nrow(Genotype_data), 0, 1)
mediator = 1 + eigenMapMatMult(Genotype_data,beta) + e1

theta=0.8
gamma=rnorm(ncol(Genotype_data),0.5,2)
e2 = rnorm(nrow(Genotype_data), 0, 1)
outcome = 2 + eigenMapMatMult(Genotype_data,gamma) + theta*mediator + e2

```

```

p_value=SMUT(G=Genotype_data,mediator=mediator,outcome=outcome)
print(p_value)

# p_value_IUT is the p value for the mediation effect.
# we have non-significant(at alpha level 0.05) mediation effects (p_value_IUT = 0.5596977).

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```

Testing_coefficient_of_mediator

Testing coefficient of mediator in the outcome model

Description

Testing coefficient of mediator, namely theta, in the outcome model. The outcome model is the following.

$$\text{outcome} \sim \text{intercept} + G * \gamma + \text{mediator} * \theta + \text{error}$$

Usage

```

Testing_coefficient_of_mediator(G, mediator, outcome,
outcome_type="continuous", method="score", approxi=TRUE, debug=FALSE)

```

Arguments

G	n by p matrix (n rows and p columns). Each row is one individual; each column is one SNP.
mediator	a vector length of n. It is the mediator variable.
outcome	a vector length of n. It is the outcome variable.
outcome_type	Type of the outcome variable. For now, this package only deals with continuous outcome. Default is "continuous".
method	The method of testing coefficient of mediator in the outcome model. The score test is used. Default is "score".
appoxi	a boolean value. This is an indicator whether the approximation of the score statistic is applied to save computing time. Default is TRUE.
debug	a boolean value. If TRUE a lot of computing details is printed; otherwise the function is completely silent. Default is FALSE.

Value

P value for testing the coefficient of mediator in the outcome model.

Author(s)

Wujuan Zhong

Examples

```
library(SMUT)
# load the Genotype data included in this R package
data("Genotype_data")

# generate one mediator and one outcome

set.seed(1)
beta=rnorm(ncol(Genotype_data),1,2)
e1 = rnorm(nrow(Genotype_data), 0, 1)
mediator = 1 + eigenMapMatMult(Genotype_data,beta) + e1

theta=0.8
gamma=rnorm(ncol(Genotype_data),0.5,2)
e2 = rnorm(nrow(Genotype_data), 0, 1)
outcome = 2 + eigenMapMatMult(Genotype_data,gamma) + theta*mediator + e2

p_value=Testing_coefficient_of_mediator(G=Genotype_data,mediator=mediator,outcome=outcome)
print(p_value)

# Thanks for using our R package SMUT ~~
```

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