Package ‘MiST’

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Type Package

Title Mixed effects Score Test for continuous outcomes

Version 1.0

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Author Jianping Sun, Yingye Zheng, and Li Hsu

Maintainer Jianping Sun <jsun@fhcrc.org>

Depends CompQuadForm

Description Test for association between a set of SNPS/genes and continuous or binary outcomes by including variant characteristic information and using (weighted) score statistics.

License LGPL (>= 2.0)

LazyLoad yes

NeedsCompilation no

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**MiST-package**  
**Mixed effects Score Test**

**Description**
Test for association between a set of SNPS/genes and continuous or binary outcomes by including variant characteristic information and using score statistics.

**Details**

Package: MiST  
Type: Package  
Version: 1.0  
Date: 2013-03-18  
License: LGPL (>= 2.0)  
LazyLoad: yes

```
linear.test(y, X, G, Z, method = "liu")
linear.weight.test(y, X, G, Z, maf, weight.beta = c(1, 25), method = "liu")
logit.test(y, X, G, Z, method = "liu")
logit.weight.test(y, X, G, Z, maf, weight.beta = c(1, 25), method = "liu")
```

**Author(s)**
Jianping Sun, Yingye Zheng, and Li Hsu.

**References**


**Description**
Test for association between a set of SNPS/genes and continuous outcomes by including variant characteristic information and using score statistics.
Usage

linear.test(y, X, G, Z, method = "liu")

Arguments

y  
a numeric vector of the continuous outcome variables. Missing values are not allowed.

X  
a numeric matrix of covariates with rows for individuals and columns for covariates.

G  
a numeric genotype matrix with rows for individuals and columns for SNPs. Each SNP should be coded as 0, 1, and 2 for AA, Aa, aa, where A is a major allele and a is a minor allele. Missing genotypes are not allowed.

Z  
a numeric matrix of second level covariates for variant characteristics. Each row corresponds to a variant and each column corresponds to a variant characteristic. If there is no second level covariates, a vector of 1 should be used.

method  
a method to compute the p-value and the default value is "liu". Method "davies" represents an exact method that computes the p-value by inverting the characteristic function of the mixture chisq. Method "liu" represents an approximation method that matches the first 3 moments.

Value

S.tau  
score statistic for the variant heterogeneous effect.

S.pi  
score statistic for the variant mean effect.

p.value.S.tau  
p-value for testing the variant heterogeneous effect.

p.value.S.pi  
p-value for testing the variant mean effect.

p.value.overall  
overall p-value for testing the association between the set of SNPS/genes and outcomes. It combines p.value.S.pi and p.value.S.tau by using Fisher’s procedure.

Author(s)

Jianping Sun, Yingye Zheng, and Li Hsu.

References


linear.weight.test

### Examples

```r
data(MiST.data)
attach(MiST.data)

#########################################################################
# test the association between a set of SNPs and continuous outcomes
# M without information about SNP characteristics. Z is a vector of 1's.
out <- linear.test(y,con, X, g, Z)

#########################################################################
# test the association between a set of SNPs and continuous outcomes
# M including SNP characteristics
out <- linear.test(y,con, X, g, Z.func)
```

---

#### linear.weight.test

**Weighted Mixed effects Score Test for continuous outcomes**

#### Description

Test for association between a set of SNPS/genes and continuous outcomes by including variant characteristic information and using weighted score statistics.

#### Usage

```r
linear.weight.test(y, X, G, Z, maf, weight.beta = c(1, 25), method = "liu")
```

#### Arguments

- **y**: a numeric vector of the continuous outcome variables. Missing values are not allowed.
- **X**: a numeric matrix of covariates with rows for individuals and columns for covariates.
- **G**: a numeric genotype matrix with rows for individuals and columns for SNPs. Each SNP should be coded as 0, 1, and 2 for AA, Aa, aa, where A is a major allele and a is a minor allele. Missing genotypes are not allowed.
- **Z**: a numeric matrix of second level covariates for variant characteristics. Each row corresponds to a variant and each column corresponds to a variant characteristic. If there is no second level covariates, a vector of 1 should be used.
- **maf**: a numeric vector of MAF (minor allele frequency) for each SNP.
weight.beta: a numeric vector of parameters of beta function which is the weight for score statistics. The default value is "c(1,25)".

method: a method to compute the p-value and the default value is "liu". Method "davies" represents an exact method that computes the p-value by inverting the characteristic function of the mixture chisq. Method "liu" represents an approximation method that matches the first 3 moments.

Value

- S.tau: score statistic for the variant heterogenous effect.
- S.pi: score statistic for the variant mean effect.
- p.value.S.tau: p-value for testing the variant heterogenous effect.
- p.value.S.pi: p-value for testing the variant mean effect.
- p.value.overall: overall p-value for testing the association between the set of SNPS/genes and outcomes. It combines p.value.S.pi and p.value.S.tau by using Fisher’s procedure.

Author(s)

Jianping Sun, Yingye Zheng, and Li Hsu.

References


Examples

data(MiST.data)
attach(MiST.data)

# Test the association between a set of SNPs and continuous outcomes
# - without information about SNP characteristics. Z is a vector of 1's.

out <- linear.weight.test(y.con, X, G, Z, maf)

# Test the association between a set of SNPs and continuous outcomes
# - including SNP characteristics

out <- linear.weight.test(y.con, X, G, Z.func, maf)
**logit.test**

Mixed effects Score Test for binary outcomes

**Description**

Test for association between a set of SNPS/genes and binary outcomes by including variant characteristic information and using score statistics.

**Usage**

logit.test(y, X, g, Z, method = "liu")

**Arguments**

- **y**
  a numeric (0 or 1) vector of the binary outcome variables. Missing values are not allowed.
- **X**
  a numeric matrix of covariates with rows for individuals and columns for covariates.
- **g**
  a numeric genotype matrix with rows for individuals and columns for SNPs. Each SNP should be coded as 0, 1, and 2 for AA, Aa, aa, where A is a major allele and a is a minor allele. Missing genotypes are not allowed.
- **Z**
  a numeric matrix of second level covariates for variant characteristics. Each row corresponds to a variant and each column corresponds to a variant characteristic. If there is no second level covariates, a vector of 1 should be used.
- **method**
  a method to compute the p-value and the default value is "liu". Method "davies" represents an exact method that computes the p-value by inverting the characteristic function of the mixture chisq. Method "liu" represents an approximation method that matches the first 3 moments.

**Value**

- **S.tau**
  score statistic for the variant heterogenous effect.
- **S.pi**
  score statistic for the variant mean effect.
- **p.value.S.tau**
  p-value for testing the variant heterogenous effect.
- **p.value.S.pi**
  p-value for testing the variant mean effect.
- **p.value.overall**
  overall p-value for testing the association between the set of SNPS/genes and outcomes. It combines p.value.S.pi and p.value.S.tau by using Fisher’s procedure.

**Author(s)**

Jianping Sun, Yingye Zheng, and Li Hsu.
logit.weight.test

References


Examples

data(MiST.data)
attach(MiST.data)

# Test the association between a set of SNPs and binary outcomes
# - without information about SNP characteristics. Z is a vector of 1's.

out <- logit.test(y.bin, X, G, Z)

# Test the association between a set of SNPs and binary outcomes
# - including SNP characteristics

out <- logit.test(y.bin, X, G, Z.func)

logit.weight.test  Weighted Mixed effects Score Test for binary outcomes

Description

Test for association between a set of SNPs/genes and binary outcomes by including variant characteristic information and using weighted score statistics.

Usage

logit.weight.test(y, X, G, Z, maf, weight.beta = c(1, 25), method = "liu")

Arguments

y  a numeric vector (0 or 1) of the binary outcome variables. Missing values are not allowed.

X  a numeric matrix of covariates with rows for individuals and columns for covariates.

G  a numeric genotype matrix with rows for individuals and columns for SNPs. Each SNP should be coded as 0, 1, and 2 for AA, Aa, aa, where A is a major allele and a is a minor allele. Missing genotypes are not allowed.
logit.weight.test

Z a numeric matrix of second level covariates for variant characteristics. Each row corresponds to a variant and each column corresponds to a variant characteristic. If there is no second level covariates, a vector of 1 should be used.

maf a numeric vector of MAF (minor allele frequency) for each SNP.

weight.beta a numeric vector of parameters of beta function which is the weight for score statistics. The default value is "c(1,25)".

method a method to compute the p-value and the default value is "liu". Method "davies" represents an exact method that computes the p-value by inverting the characteristic function of the mixture chisq. Method "liu" represents an approximation method that matches the first 3 moments.

Value

S.tau score statistic for the variant heterogenous effect.
S.pi score statistic for the variant mean effect.
p.value.S.tau p-value for testing the variant heterogenous effect.
p.value.S.pi p-value for testing the variant mean effect.
p.value.overall overall p-value for testing the association between the set of SNPS/genes and outcomes. It combines p.value.S.pi and p.value.S.tau by using Fisher's procedure.

Author(s)

Jianping Sun, Yingye Zheng, and Li Hsu.

References


Examples

data(MiST.data)
attach(MiST.data)

######################################################################
# Test the association between a set of SNPs and binary outcomes
# - without information about SNP characteristics. Z is a vector of 1's.
out <- logit.weight.test(y.bin, X, G, Z, maf)

######################################################################
# Test the association between a set of SNPs and binary outcomes
MiST.data

# - including SNP characteristics

out <- logit.weight.test(y.bin, X, G, Z.func, maf)

<table>
<thead>
<tr>
<th>MiST.data</th>
<th>Data Example for MiST</th>
</tr>
</thead>
</table>

### Description

A numerical data example for MiST

### Usage

data(MiST.data)

### Format

MiST.data contains the following objects:

- **G**: a numeric genotype matrix of 3400 individuals and 93 SNPs. Each row represents an individual, and each column represents a SNP marker.
- **X**: a numeric matrix of covariates with the first column representing intercept, the second column representing a continuous covariate, and the third column representing a binary covariate.
- **Z**: a numeric vector of 1s for the second level covariate.
- **Z.func**: a numeric matrix for the second level covariate. The first column contains all 1s, representing the intercept, and the second column is 0 or 1, representing whether a SNP marker is functional or non-functional.
- **maf**: a numeric vector for the Minor Allele Frequency of 93 SNPs.
- **y.con**: a numeric vector of continuous outcomes.
- **y.bin**: a numeric vector of binary outcomes.

### Examples

data(MiST.data)
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