Package ‘MiST’

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Type Package

Title Mixed effects Score Test for continuous outcomes

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Author Jianping Sun, Yingye Zheng, and Li Hsu

Maintainer Jianping Sun <jsun@fhcrc.org>

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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.

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R topics documented:

MiST-package .................................................. 2
linear.test ..................................................... 2
linear.weight.test ............................................. 4
logit.test ...................................................... 6
logit.weight.test ............................................. 7
MiST.data ...................................................... 9

Index 10
**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

<table>
<thead>
<tr>
<th>Package:</th>
<th>MiST</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type:</td>
<td>Package</td>
</tr>
<tr>
<td>Version:</td>
<td>1.0</td>
</tr>
<tr>
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<td>LazyLoad:</td>
<td>yes</td>
</tr>
</tbody>
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```r
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


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


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.test(y, X, G, Z)

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

out <- linear.test(y, 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

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.
linear.weight.test

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 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


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**

```r
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 chi^2. 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(mistNdata)
attach(mistNdata)

######################################################################
# test the association between a set of SNPs and binary outcomes
# without information about SNP characteristics. Z is a vector of 1's.
out <- logitNtest(yNbinN, X, g, Z)

######################################################################
# test the association between a set of SNPs and binary outcomes
# including SNP characteristics
out <- logitNtest(yNbinN, X, g, ZNfunc)

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, weightNbeta = 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 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


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)

---

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 represents a continuous covariate, and the third column represents 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)
Index

*Topic datasets
  MiST.data, 9
*Topic package
  MiST-package, 2

linear.test, 2
linear.weight.test, 4
logit.test, 6
logit.weight.test, 7

MiST (MiST-package), 2
MiST-package, 2
MiST.data, 9