Package 'SLIDE'

April 10, 2018

Type Package

Title Retrospective Score Test for Case-Control Association Study

Version 0.1.0

Author Chan Wang and Yue-Qing Hu

Maintainer Chan Wang <cwang0789@gmail.com> and Yue-Qing Hu <yuehu@fudan.edu.cn>

Depends MASS

Description R package with Score statistic tests incorporating linkage disequilibrium information for genetic association studies with multiple genetic variants and binary trait

License GPL

LazyData TRUE

URL http://github.com/chanw0/SLIDE

BugReports http://github.com/chanw0/SLIDE/issues

R topics documented:

`LD-EM` *Estimating LD using EM algorithm*

Description

This function is to estimate pairwise linkage disequilibrium with EM algorithm.

Usage

```
ld.em(genotype)
```

Arguments

`genotype`	numeric matrix or data frame with genotype data coded as 0, 1, 2. No missing data is allowed.

Details

There is no missing data.

Value

The list contains the LD matrix, D' matrix and r^2 matrix.

Author(s)

Chan Wang and Yue-Qing Hu

References

Chan Wang, Leiming Sun, Liming Li and Yue-Qing Hu, Linkage Disequilibrium on Improving Power in Case-Control Association Study

Examples

```
genotype<-matrix(sample(c(0,1,2),5000,replace=TRUE),500,10) ### 500 individuals and 10 SNPs

LD<-ld.em(genotype)

LD_orignal<-LD[[1]]

LD_D<-LD[[2]]

LD_r<-LD[[3]]
```

---

permutation *permutation for case-control data*

Description

This function is to permute cases and controls randomly.

Usage

```
permuC(phenotype,genotype)
```

Arguments

phenotype	numeric vector with phenotype status: 0=controls, 1=cases. No missing data allowed
genotype	numeric matrix or data frame with genotype data coded as 0, 1, 2. No missing data is allowed.

Value

The matrix in which the first column is the phenotype and others are the corresponding genotype after permutation.

Author(s)

Chan Wang and Yue-Qing Hu

References

Chan Wang, Leiming Sun, Liming Li and Yue-Qing Hu, Retrospective Score Test for Case-Control Association Study

---

SLIDE *Retrospective Score Test for Case-Control Association Study*

Description

To explain more heritability in GWAS, the score test statistics incorporating linkage disequilibrium information in the retrospective perspective for case-control studies are proposed. To be specific, the score is defined as the difference of the average multi-locus genotypes between cases and controls and then its variance-covariance matrix involves linkage disequilibrium information. The essential difference of the variance-covariance matrix of the proposed test with Score test exists, despite that the forms are similar. A noticeable merit/feature of SLDE is that it could borrow the strength from a database with several thousands to hundreds of thousands size to improve the power for detecting association.

Usage

```
SILDE(pheno_geno,method,LD=NULL,num_per=200)
```

Arguments

pheno_geno	Matrix in which the first column is the phenotype (0=control, 1=case) and others are the corresponding genotype (0, 1, or 2). Each row represents an individual.
LD	The known LD of the underling population of the cases and controls. By default, argument LD=NULL meaning that the LD of the underling population is unknown.
method	The method is to calculate the LD using sample data. Argument method="Cov" meaning that the variance-covariance matrix is calculated by function cov(); meanwhile, method="EM" meaning that the variance-covariance matrix is calculated by EM algorithm.
num_per	Positive integer indicating the number of permutations (200 by default).

Details

The results with argument method="Cov" are similar to the results with method="EM", whereas the calculation with method="Cov" is simple and fast.

The asymptotical p-value of SILDE may be little inflated when the sample size is not enough big, especially for rare variants.

Value

A vector with the following elements:

SILDE	Statistic SILDE with the estimated LD using controls, the corresponding asymptotical p-value and permuted p-value.
SILDE.pop	Statistic SILDE with the known LD of underling population, the corresponding asymptotical p-value and permuted p-value. If LD=NULL, then this is NULL.

Author(s)

Chan Wang and Yue-Qing Hu

References

Chan Wang, Leiming Sun, Liming Li and Yue-Qing Hu, Retrospective Score Test for Case-Control Association Study

Examples

```
library(MASS)

set.seed(1234)

genotype<-matrix(sample(c(0,1,2),5000,replace=TRUE),500,10) ### 500 individuals and 10 SNPs

phenotype<-c(rep(1,200),rep(0,300)) ### 200 cases and 300 controls

Statistics<-SILDE(cbind(phenotype,genotype),method=c("Cov"),LD=NULL,num_per=200)

SLIDE<-Statistics[[1]]

## 21.2053, 0.0200, 0.0197
```

Index