Package ‘MTAR’

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Description

An example of calculating U and V for MTAR given the genetic effect estimates and their standard errors.

Usage

data(beta.example)

Format

A list with 3 sublists:

**Beta** a list of genetic effect estimates, each sublist is $m \times K$ matrix for each study

**Beta.se** a list of standard errors of genetic effect estimates, each sublist is $m \times K$ matrix for each study

**R** a SNP correlation matrix for the union of SNPs appearing in all the studies

Get_UV_from_beta

*Compute the summary statistics given the genetic effect estimates and their standard errors*

Description

This function allows you to calculate the score summary statistics $U$ and their covariance matrix $V$ for MTAR, given the genetic effect estimates and their standard errors.

Usage

Get_UV_from_beta(Beta, Beta.se, R)
Get_UV_from_data

Arguments

Beta

A numeric list, each sublist containing estimation information of genetic effect estimates $\beta$ for each study. In each study, a numeric $m \times K$ matrix with each row as a SNP and each column as a separate trait. The number of traits and the number of SNPs in each study can be different but their names are required.

Beta.se

A numeric list, each sublist containing the standard error of estimators information for each study. In each study, a numeric $m \times K$ matrix with each row as a SNP and each column as a separate trait.

R

A SNP correlation matrix, which should contain the correlation of all the SNPs in these studies.

Value

A list containing summary statistics for each traits, including the score summary statistics $U$ and their covariance matrix $V$.

Author(s)

Lan Luo

Examples

data("beta.example")
attach(beta.example)
obs.stat <- Get_UV_from_beta(Beta = Beta, Beta.se = Beta.se, R = R)
detach(beta.example)

Get_UV_from_data

Compute the summary statistics given the individual-level data

Description

This function allows you to calculate the score summary statistics $U$ and their covariance matrix $V$ for MTAR, given the traits, covariates and genotype data sets. If one trait only takes no more than two values, this function will treat this trait as a binary trait.

Usage

Get_UV_from_data(traits, covariates, genotype, covariance = TRUE)

Arguments

traits

A numeric list, each sublist containing trait information for each study. In each study, a numeric $n \times K$ matrix with each row as an independent individual and each column as a separate trait. If subject $i$ is without trait $k$, the corresponding value is set as NA. The number of traits in each study can be different but the names of traits are required.
Get_UV_from_data

covariates  a numeric list, each sublist containing covariates information for each study. In each study, a numeric \( n \times D \) matrix with each row as an independent individual and each column as a covariate.

genotype  a numeric list, each sublist containing genotype information for each study. In each study, a numeric \( n \times m \) matrix with each row as an independent individual and each column as a SNP. Each genotype should be coded as 0, 1, 2, and NA for AA, Aa, aa, and missing, where A and a represents a major and minor allele, respectively. The number of SNPs in each study can be different but the names of SNPs are required. Also, the number of studies must be the same in genotype, covariates and traits lists. The order of subject ID must be the same among traits, covariates, and genotype within each study.

covariance  a logical value indicating whether to calculate the covariance matrix of score summary statistics \( U \). The default value is TRUE. If covariance is set as FALSE, then only the diagonal values of the covariance matrix are calculated, which is faster. In estimating the zeta matrix correcting for overlap samples, we recommend set covariance as FALSE in calculating the summary statistics for common variants. Since the number of common variants may be large and time-consuming.

Value

A list containing summary statistics for each trait. If covariance is TRUE, the score summary statistics \( U \) and its covariance matrix \( V \) are returned. Otherwise, only \( U \) and the diagonal elements of covariance matrix are returned.

Author(s)

Lan Luo

References


Examples

data(rawdata)
attach(rawdata)
obs.stat <- Get_UV_from_data(traits = traits.dat,
covariates = cov.dat,
genotype = geno.dat,
covariance = TRUE)

obs.stat
detach(rawdata)
Get_UV_from_varU

Compute the summary statistics given the score statistics and their variance.

Description

This function allows you to calculate the score summary statistics $U$ and their covariance matrix $V$ for MTAR, given the score summary statistics and their variance.

Usage

Get_UV_from_varU(U, varU, R)

Arguments

- **U** a numeric list, each sublist containing score summary statistics $U$ for each study. In each study, a numeric $m \times K$ matrix with each row as a SNP and each column as a separate trait. The number of traits and the number of SNPs in each study can be different but their names are required.

- **varU** a numeric list, each sublist containing the variance of score summary statistics information for each study. In each study, a numeric $m \times K$ matrix with each row as a SNP and each column as a separate trait.

- **R** a SNP correlation matrix, which should contain the correlation of all the SNPs in these studies.

Value

A list containing summary statistics for each traits, the score summary statistics $U$ and their covariance matrix $V$.

Author(s)

Lan Luo

Examples

data("varU.example")
attach(varU.example)
obs.stat <- Get_UV_from_varU(U = U, varU = varU, R = R)
obs.stat
detach(varU.example)
Get_zeta  

Calculate Covariances of Z-scores between Traits from Overlapping Samples

Description

This function allows you to estimate the matrix $\zeta$ to adjust for the potential sample overlap in the data set. Here we applied LD pruning ($r^2 < 0.1$ in 500kb region) on 1000 Genome genotype dataset (hg19) as a list of reference independent SNPs. The SNP ID is chr:pos.

Usage

Get_zeta(Zscore, pval_cutoff = 0.05, Indp_common_snp)

Arguments

- **Zscore**: a numeric list, each sublist containing a vector of Z scores of SNPs with minor allele frequency (MAF) larger than 0.05. The chr:pos for each SNP is required.
- **pval_cutoff**: a numeric value indicating the cutoff threshold of p-values. The default value is 0.05. Variants with p-value less than or equal to this threshold will be automatically removed.
- **Indp_common_snp**: a numeric list of independent common SNPs

Value

A $K \times K$ matrix $\zeta$, where $K$ is the number of traits.

Author(s)

Lan Luo

Examples

```r
data(zeta.example)
attach(zeta.example)
# Downloading independent common SNPs from 1000Genome data set.
githubURL <- "https://github.com/lan/MTAR/blob/master/indp_snps.1KG.rda?raw=true"
utils::download.file(githubURL,"1kgfile")
load("1kgfile")
zeta1 <- Get_zeta(Zscore = Zscore, Indp_common_snp = indp_snps.1KG)
zeta1
detach(zeta.example)
```
**MTAR**

*Multiple-Traits Analysis of Rare-Variant Association Test*

**Description**

Test for association between a set of rare SNPs and multiple traits with input of summary statistics, possibly from overlap samples. The input number of SNPs in each trait can be different, MTAR function will analyze the union of SNPs that show up in at least one trait, and automatically handle the non-polymorphic SNPs.

**Usage**

```r
MTAR(
  U,
  V,
  MAF,
  MAF_UB = 0.05,
  zeta = NULL,
  genetic_cor.trait = NULL,
  rho.SNP = c(0, 0.5, 1),
  rho.trait = c(0, 0.5, 1),
  weight.SNP = c(1, 25)
)
```

**Arguments**

- **U**
  
a numeric list, each sublist containing summary statistics U for each traits. The SNP IDs must be provided.

- **V**
  
a numeric list, each sublist containing the corresponding covariance matrix of summary statistics. If your original summary statistics are other format, please use Get_UV_from_data, Get_UV_from_varU or Get_UV_from_beta to generate the summary statistics U and V for MTAR.

- **MAF**
  
a numeric vector containing minor allele frequency for the SNPs show up in at least one trait. The SNP IDs must be provided.

- **MAF_UB**
  
a numeric value indicating the cutoff threshold of minor allele frequency for SNPs The default value is 0.05.

- **zeta**
  
a numeric matrix containing the sample correlation of Z-scores over a large number of independent null common SNPs across genome. The default value is NULL, where MTAR assumes there are no overlap samples. However, if there is overlapping in subjects, zeta must be provided. zeta can be estimated using MTAR::Get_zeta.

- **genetic_cor.trait**
  
a numeric matrix containing the genetic correlation among traits. The default value of genetic_cor.trait is NULL, where an exchangeable correlation structure with the correlation coefficient denoted by rho.trait ($\rho_2$) is assumed. In this case, there is no difference between cMTAR and iMTAR.
rho.SNP  a numeric vector containing all the possible values of $\rho_1$. The default value is c(0, 0.5, 1).

rho.trait  a numeric vector containing all the possible values of $\rho_2$. The default value is c(0, 0.5, 1).

weight.SNP  a numeric vector containing the parameters in Beta density function to calculate the weight among SNPs. The default value is c(1, 25).

Details

MTAR assumes that the genetic effect estimates $\beta$ has covariance matrix $B$, which is a Kronecker product of two pre-specified matrices: among-variant effect covariance $B_1$ and among-trait effect covariance $B_2$. An exchangeable correlation structure with the correlation coefficient denoted by rho.SNPs ($\rho_1$) for $B_1$ is assumed. The default MTAR requires the input of genetic correlation matrix genetoc_cor.trait, if missing, then an exchangeable correlation structure for rho.trait ($\rho_2$) is assumed. The default weight of $B_1$ is $dBeta(MAF, 1, 25)$, which can be changed freely by users.

Value

a list of p-values of MTAR-O, cMTAR, iMTAR and cctP as well as ancillary information. Here cctP is the Cauchy-combined p-value of SKAT and burden tests with default weight $dBeta(MAF, 1, 25)$.

Author(s)

Lan Luo

References


Examples

data(MTAR.example)
attach(MTAR.example)
pval <- MTAR(U = U, V = V, MAF = MAF, genetic_cor.trait = genetic_cor.trait, zeta = zeta)
pval
detach(MTAR.example)
**MTAR.example**

**PNPLA2 Gene**

**Description**

PNPLA2 Gene Information required by MTAR function.

**Usage**

data(MTAR.example)

**Format**

A list with 6 sublists:

- **annotation** some annotation information of gene PNPLA2
- **U** a list containing the summary statistics for each trait
- **V** a list containing the covariance matrix of summary statistics for each trait
- **MAF** the minor allele frequency of all the rare variants in this gene
- **genetic_cor.trait** the genetic correlation among traits
- **zeta** the overlapping estimation matrix, which is approximated by the sample correlation matrix of the scaled summary statistics over a large number of independent null common SNPs

**rawdata**

**Example1: individual-level data**

**Description**

An example of calculating U and V for MTAR given the individual-level data set.

**Usage**

data(rawdata)

**Format**

A list with 3 sublists:

- **geno.dat** a list of genotype data, each sublist is $n \times m$ matrix for each study
- **traits.dat** a list of trait data, each sublist is $n \times K$ matrix for each study
- **cov.dat** a list of covariates data, each sublist is $n \times D$ matrix for each study

There are 3 studies, 3 continuous traits and 10 rare variants. Specifically, there are 1500 subjects in study1, but each subject only has one trait measurement. In study2 and study3, the sample size is 500 and each subject has two or three traits measurements.
### varU.example  
#### Example 2: The Summary Statistics and Their Variance

**Description**

An example of calculating U and V for MTAR given the summary statistics and its variance.

**Usage**

```r
data(varU.example)
```

**Format**

A list with 3 sublists:

- U  
  a list of summary statistics, each sublist is $m \times K$ matrix for each study
- varU  
  a list of variance of summary statistics, each sublist is $m \times K$ matrix for each study
- R  
  a SNP correlation matrix for the union of SNPs appearing in all the studies

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### zeta.example  
#### Example 4: The Summary Statistics of 737 Common and Null SNPs

**Description**

An example of estimating matrix $\zeta$ given the summary statistics information of null and common SNPs.

**Usage**

```r
data(zeta.example)
```

**Format**

A list with 1 sublist:

- Zscore  
  a list, each sublist contains the Z-scores of 737 null and common SNPs for each trait
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