Package 'RSVMMAT'

February 12, 2022

Title Retrospective Set-Based Varying Coefficient Mixed Model Association Tests

Version 0.0.1.0

Description We propose a set-based retrospective varying coefficient mixed model association test, RSVMMAT, to detect genes that affects the developmental patterns of a trait.

License GPL (>= 3)

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Depends R (>= 2.12.1)

Suggests rmarkdown,
knitr

Imports expm,
stats,
mvtnorm,
MASS,
utils

VignetteBuilder knitr

R topics documented:

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rsvmmat_est *NULL model estimation*

Description

This function estimate the parameters and residuals for the NULL model in RSVMMAT

Usage

```
rsvmmat_est(
  y.long,
  time,
  y.cov,
  phe.model = phe.model,
  maxiter = 50,
  tol = 10^(-6)
)
```

Arguments

y.long	Long-formatted phenotype vector
time	Time covarites matched with phenotype vector
y.cov	Covariate matrix denoting the covariate variables measured at each time
phe.model	String, the phenotype model, two optional values: 'logistic', 'liability'
maxiter	Numeric, the maximum count for the iterative estimation in when using mixture correlation structure
tol	Numeric, tolerance for the iterative estimation in when using mixture correlation structure

Value

This function returns a list object with model parameters and residuals of the NULL model

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rsvmmat_simu *Simulation for RSVMMAT test*

Description

This function use pre-defined parameters to make the simulation data for the RSVMMAT test (including type I and power test)

Usage

```
rsvmmat_simu(
  n.sample = 1000,
  n.time = 5,
  par = list(),
  time_cov = TRUE,
  gene.count = 10,
  intercept = TRUE,
  causalpara = list(),
  power = FALSE,
  phe.model = "logistic",
  oversampling = "random"
)
```

Arguments

n.sample	Numeric, sample size, number of individuals
n.time	Numeric, number of measurements for each individual
par	List, the parameters for the phenotype traits, including covaraites and individual specific time dependent random effects
time_cov	Logical variable, indicating whether time effect is included in phenotypic traits
gene.count	Numeric, number of genes
intercept	Logical variable, indicating whether intercept is used in phenotypic traits
causalpara	List, the parameters for causal genes
power	Logical variable, indicating whether include disease genes in the generated genes
phe.model	String, the phenotype model, two optional values: 'logistic', 'liability'
oversampling	String, the ascertainment scheme, three optional value: 'random', 'baseline', 'sum'

Value

A list object is returned to be used as object for RSVMMAT test

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rsvmmat_test	*Calculate prospective and retrospective P-values*

Description

This function tests a SNPs for a given SNP set for a given rsvmmat estimated null model.

Usage

```
rsvmmat_test(rsvmmat.est, G, impute.method = "fixed", GRM = NULL)
```

Arguments

rsvmmat.est	The output of function "rsvmmat_est()"
G	The genotype matrix, an m*q matrix where m is the number of subjects and q is the total number genetic variants.
impute.method	choose the iputation method when there is missing genotype. Optional options are: 'random', 'fixed' or 'bestguess'.
GRM	takes m-by-m genetic correlation matrix or kinship matrix.

Value

This function returns a vector of the pvalue of SVMMAT-B, SVMMAT-S,SVMMAT-A, RSVMMAT-B, RSVMMAT-S, and RSVMMAT-A.

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