Package 'RVMMAT'

August 22, 2021

Title Retrospective Varying Coefficient Mixed Model Association Test

Version 0.0.1.0

Description

We propose a GLMM-based retrospective varying coefficient mixed model association test, RVM-MAT, to detect genetic variant, one at a time, that affects the developmental patterns of a trait.

License GPL (>= 3)

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Depends R (>= 2.12.1)

Suggests knitr,
rmarkdown,
testthat (>= 3.0.0)

Config/testthat/edition 3

Imports expm,
stats,
mvtnorm,
MASS,
utils

VignetteBuilder knitr

R topics documented:

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rvmmat_est   *NULL model estimation*

Description

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

Usage

```
rvmmat_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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rvmmat_simu   *Simulation for RVMMAT test*

Description

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

Usage

```
rvmmat_simu(
  n.sample = 1000,
  n.time = 5,
  par = list(),
  time_cov = TRUE,
  snp.count = 1000,
  intercept = TRUE,
  disease.para = list(),
  onlypower = 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
`snp.count`	Numeric, number of SNPs
`intercept`	Logical variable, indicating whether intercept is used in phenotypic traits
`disease.para`	List, the parameters for disease allele and its effect size for power simulation
`onlypower`	Logical variable, indicating whether include disease SNPs in the generated SNPs
`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 LBRAT test

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rvmmat_test	*Calculate prospective and retrospective P-values for RVMMAT test*

Description

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

Usage

```
rvmmat_test(rvmmat.est, G, impute.method = "fixed", GRM = NULL)
```

Arguments

`rvmmat.est`	The output of function "rvmmat_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 dataframe. The row name is the SNP ID, the first column is the prospective score statistics, the second colum is the retrospective score statistics, the third column is the prospective pvalue and the forth column is the restrospective pvalue

Index