Package 'RVMMAT'

October 20, 2022

Title Retrospective Varying Coefficient Mixed Model Association Test

Version 0.0.1.0

Author Gang Xu [aut, cre], Amei Amei [aut], Zuoheng Wang [aut]

Maintainer Gang Xu <xug3@unlv.nevada.edu>

Description We propose a GLMM-based retrospective varying coefficient mixed model association test, RVMMAT, to detect genetic variant that affects the developmental patterns of a trait.

License GPL (>= 3)

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

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:

---

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),
  Hd = 2,
  VCcorrection = FALSE
)
```

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
Hd	Numeric, degree of derivative of smooth function which lead to smooth spline of order 2Hd
VCcorrection	Logical variable, indicating whether apply correction for variance components and natural parameters

Value

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

---

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(),
  genetic.effect = 0.6,
  time_cov = TRUE,
  snp.count = 100,
  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 covariates and individual specific time dependent random effects
genetic.effect	Numeric, genetic effect size (gamma) in genetic effect function
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 RVMMAT test

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 pvalue and the second colum is the restrospective pvalue.

Index