

Package ‘RSIT’

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Title Retrospective Set-Based Gene-Environment Interaction Tests

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Description We propose retrospective set-based gene-environment interaction tests for binary trait.

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

Depends R (>= 2.12.1)

Suggests rmarkdown,
knitr

Imports expm,
stats,
MASS,
utils

VignetteBuilder knitr

R topics documented:

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RSIT_est	<i>NULL model estimation</i>
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Description

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

Usage

```
RSIT_est(Y, X, E, family = "Guassian", GRM = NULL)
```

Arguments

Y	phenotype vector
X	Covariate matrix denoting the covariate variables
E	environment vector
family	String, the phenotype model, two optional values: 'Guassian', 'binomial'
GRM	takes m-by-m genetic correlation matrix or kinship matrix.

Value

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

RSIT_pvalue	<i>Calculate P-values</i>
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Description

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

Usage

```
RSIT_pvalue(TYall, G, impute.method = "fixed")
```

Arguments

TYall	The output of function "RSIT_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 imputation method when there is missing genotype. Optional options are: 'random', 'fixed' or 'bestguess'.

Value

This function returns a vector of the P-value of RSIT-B, RSIT-S, and RSIT-E.

simu.binary.phe	<i>Simulation for RSIT test</i>
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Description

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

Usage

```
simu.binary.phe(  
  n.sample,  
  geno,  
  n_casual = c(2, 8),  
  main_effect = c(0.1, 0.2),  
  GE_effect = c(0.3, 0.88),  
  direction = c("same", "same"),  
  GEindependent = T,  
  power = T,  
  maineffect = T,  
  SNPtype = "rare_common",  
  main_GE = T  
)
```

Arguments

n.sample	Numeric, sample size, number of individuals
geno	matrix, genotype matrix
n_casual	Vector, number of causal SNPs for common SNPs and rare SNPs
main_effect	Vector, gene-environment interaction effect for common SNPs and rare SNPs
direction	Vector, main effect and gene-environment interaction effect direction
GEindependent	Logical variable, indicating whether gene and environment variable are independent
power	Logical variable, indicating whether include disease genes in the generated genes
maineffect	Logical variable, indicating whether include main effect

Value

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

simu_snp_mat	<i>Simulate the genotype data</i>
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Description

This function use pre-defined parameters to simulate the genotype data

Usage

```
simu_snp_mat(n.sample, mat.count, common_snp = F, independent = F)
```

Arguments

n.sample	Numeric, sample size, number of individuals
mat.count	Numeric, number of SNP regions
common_snp	Logical variable, indicating whether the region include common SNPs
independent	Logical variable, indicating whether SNPs in the same region are independent

Value

A list object is returned to be used as genotype for RSIT test

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