

# Package ‘RSIT’

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**Title** Retrospective Set-Based Gene-Environment Interaction Tests

**Version** 0.0.1.0

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**Description** We propose retrospective set-based gene-environment interaction tests for binary 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,  
MASS,  
utils

**VignetteBuilder** knitr

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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

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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 iputation method when there is missing genotype. Optional options are: 'random', 'fixed' or 'bestguess'.

**Value**

This function returns a vector of the pvalue of RSIT-B,RSIT-S,RSIT-V,RSIT-A,RSIT-O, and RSIT-E.

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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 RSVMMAT 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  
)
```

**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 RSVMMAT test

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