Package 'LBRAT'

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Type Package

Title Retrospective Association Testing for Longitudinal Binary
Outcomes

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Description Retrospective Association Testing for Longitudinal Binary Outcomes.

License GPL (>= 2)

Depends R (>= 2.12.1), nleqslv, lme4, geepack, mvtnorm, data.table,
plyr

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R topics documented:

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lbrat.SSD.All   *LBRAT test or RGMMAT test using SSD format files*

Description

LBRAT test or RGMMAT test using SSD format files

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Usage

```
lbrat.SSD.All(SSD.INFO, lbrat_est.obj, ...)
```

Arguments

SSD.INFO	SSD format information file, output of function "Open_SSD". The genome wide scan are run set by set.
lbrat_est.obj	ouput from lbrat_est.R
...	Other options of the LBRAT or RGMMAT test. Defined same as in function "lbrat_test()".

Value

reults of the LBRAT or RGMMAT test. First column contains batchID, second column contains SNP ID, third column concains prospective P-value and forth column contains retrospective P-value

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lbrat_est.gee	*GEE NULL model estimation*

Description

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

Usage

```
lbrat_est.gee(y.long, time, y.cov, timecov = TRUE, corstr = "ar1",
  tol = 10^-6, max.iter = 50)
```

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
timecov	Logical variable, indicating whether the time fixed effect is estimated
corstr	String, correlation structure for GEE model, optional values are: 'ar1', 'ind', 'mixture'
tol	Numeric, tolerance for the iterative estimation in when using mixture correlation structure
max.iter	Numeric, the maximum count 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 GEE model

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lbrat_est.glmm   *GLMM NULL model estimation*

Description

This function estimate the parameters and residuals for the NULL model in RGMMAT test

Usage

```
lbrat_est.glmm(y.long, time, y.cov, timecov = TRUE)
```

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
`timecov`	Logical variable, indicating whether the time fixed effect is estimated

Value

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

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lbrat_read_phe   *Read in Phenotype and Genotype Files*

Description

This function loads a phenotype file, a covariates file and a plink fam file it's able to match the phenotype ID with genotype ID and generate input dataframe for L-BRAT/RGMMAT test.

Usage

```
lbrat_read_phe(y.file, cov.file, plink.file)
```

Arguments

`y.file`	Path to the input file
`cov.file`	Path to the covariates file
`plink.file`	Path to the plink file frefix

Value

A formatted dataframe used as L-BRAT/RGMMAT test input

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lbrat_simu *Simulation for LBRAT test*

Description

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

Usage

```
lbrat_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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lbrat_test *Calculate prospective and retrospective P-values for GEE or GLMM model*

Description

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

Usage

```
lbrat_test(lbrat.est, G, impute.method = "fixed", GRM = NULL)
```

Arguments

`lbrat.est`	The output of function "lbrat_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

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