Package ‘gcatest’

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Title Genotype Conditional Association TEST

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LazyData true

Description GCAT is an association test for genome wide association studies
that controls for population structure under a general class of trait.
models.

Imports lfa

Depends R (>= 3.2)

Suggests knitr, ggplot2

VignetteBuilder knitr

License GPL-3

biocViews SNP, DimensionReduction, PrincipalComponent,
GenomeWideAssociation

BugReports `https://github.com/StoreyLab/gcatest/issues`

URL `https://github.com/StoreyLab/gcatest`

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R topics documented:

`gcat` *Genotype Conditional Association TEST*

Description

Performs the GCAT test for association between SNPs and trait, and returns the p-values.

Usage

```
gcat(X, LF, trait, adjustment = NULL)

gcatest(X, LF, trait, adjustment = NULL)

gcat.stat(X, LF, trait, adjustment = NULL)
```

Arguments

`X`	a matrix of SNP genotypes, i.e. an integer matrix of 0's, 1's, and 2's. Sparse matrices of class Matrix are not supported (yet).
`LF`	matrix of logistic factors outputed from function `lfa`
`trait`	vector
`adjustment`	matrix of adjustment variables

Value

vector of p-values

Functions

- `gcatest`:
- `gcat.stat`: returns the association statistics instead of the p-value.

References

Song, M, Hao, W, Storey, JD (2015). Testing for genetic associations in arbitrarily structured populations. Nat. Genet., 47, 5:550-4.

Examples

```
library(lfa)
LF = lfa(sim_geno, 3)
gcat_p = gcat(sim_geno, LF, sim_trait)
gcat_stat = gcat.stat(sim_geno, LF, sim_trait)
```

`sim_geno` *Simulated data from PSD model*

Description

10,000 SNPs, 1,000 individuals, first five SNPs are associated.

Usage

```
sim_geno
```

Format

a matrix of 0's, 1's and 2's for the genotypes

Value

simulated genotype matrix

`sim_trait` *Simulated data from PSD model*

Description

10,000 SNPs, 1,000 individuals, first five SNPs are associated.

Usage

```
sim_trait
```

Format

a vector of traits

Value

simulated traits

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