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
NeedsCompilation yes

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**Genotype Conditional Association TEST**

**Description**

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

**Usage**

```r
gcat(X, LF, trait, adjustment = NULL)
gcat.test(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**

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

**References**


**Examples**

```r
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_genos**

*Simulated data from PSD model*

**Description**

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

**Usage**

`sim_genos`

**Format**

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

**Value**

simulated genotype matrix

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**sim_traits**

*Simulated data from PSD model*

**Description**

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

**Usage**

`sim_traits`

**Format**

a vector of traits

**Value**

simulated traits
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