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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**gcat**

*Genotype Conditional Association TEST*

**Description**

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

**Usage**

\[
gcat(X, LF, \text{trait}, \text{adjustment} = \text{NULL})
\]

\[
gcatest(X, LF, \text{trait}, \text{adjustment} = \text{NULL})
\]

\[
gcat.stat(X, LF, \text{trait}, \text{adjustment} = \text{NULL})
\]

**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**


**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_genotype

**Description**

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

**Usage**

sim_genotype

**Format**

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

**Value**

simulated genotype matrix

---

sim_trait

**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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