Package ‘gcatest’

March 22, 2017

Title Genotype Conditional Association TEST
Version 1.4.0
Date 2015-10-09
Author Wei Hao, Minsun Song, John D. Storey
Maintainer Wei Hao <whao@princeton.edu>, John D. Storey <jstorey@princeton.edu>
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**

```r

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**


**Examples**

```r
library(lfa)
LF = lfa(sim_geno, 3)
gcat_p = gcatre(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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