# Package ‘gcatest’

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**Title**  Genotype Conditional Association TEST  
**Version**  1.6.0  
**Date**  2015-10-09  
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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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Description
Performs the GCAT test for association between SNPs and trait, and returns the p-values.

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

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

Value
vector of p-values

Functions
- \text{gcatest}: \\
- \text{gcat.stat}: returns the association statistics instead of the p-value.

References

Examples
\[
\text{library(lfa)} \\
LF = \text{lfa(sim\_geno, 3)} \\
\text{gcat\_p} = \text{gcat(sim\_geno, LF, sim\_trait)} \\
\text{gcat\_stat} = \text{gcat.stat(sim\_geno, LF, sim\_trait)}
\]
**sim_genotype**

*Simulated data from PSD model*

### 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

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**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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