

# Package ‘gctest’

April 14, 2017

**Title** Genotype Conditional Association TEST

**Version** 1.4.0

**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/gctest/issues>

**URL** <https://github.com/StoreyLab/gctest>

**NeedsCompilation** yes

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`gcat`*Genotype Conditional Association TEST*

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**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**

<code>X</code>	a matrix of SNP genotypes, i.e. an integer matrix of 0's, 1's, and 2's. Sparse matrices of class <code>Matrix</code> are not supported (yet).
<code>LF</code>	matrix of logistic factors outputed from function <code>lfa</code>
<code>trait</code>	vector
<code>adjustment</code>	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_genos, 3)
gcat_p = gcat(sim_genos, LF, sim_trait)
gcat_stat = gcat.stat(sim_genos, LF, sim_trait)
```

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sim_geno	<i>Simulated data from PSD model</i>
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**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

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sim_trait	<i>Simulated data from PSD model</i>
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**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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