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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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

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

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_genome

**Simulated data from PSD model**

**Description**

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

**Usage**

`sim_genome`

**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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