Package 'GWAStest'

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Type Package

Title this package test our ability in making packages (Title Case)

Version 0.1.0

Author Lance Merrick, Samuel Prather

Maintainer Samuel Prather <stp4freedom@gmail.com>

Description This package is a test for hw4 in crop_sci_545 class More about what it does (maybe more than one line) Use four spaces when indenting paragraphs within the Description.

License What license is it under?

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

R topics documented:

GWAStest *GWAS with PCA*

Description

GWAS with PCA

Usage

```
GWAStest(
  phenotypes = NULL,
  genotypes = NULL,
  Cov = NULL,
  GM = NULL,
  PCA.M = 3,
  QTN.position = NULL,
  cutoff = NULL
)
```

Arguments

phenotypes	file with numeric phenotypic values
genotypes	data.frame with genotype calls coded as 0,1,2.
Cov	numeric data.frame with covariates values
GM	genetic map of data with chr and position of each SNP
PCA.M	number of principal components to use default is 3
QTN.position	posistion of QTN if applicable
cutoff	If cutoff is default, uses Bonferroni; else uses -log(value) of 0.05/number of SNPs

Value

Manhatten plot, QQ plot plus p-values, type-1 error and power for every SNP

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power.fdr *Function to caculate power, FDR and type-1 error*

Description

Function to caculate power, FDR and type-1 error

Usage

```
power.fdr(order.SNP, QTN.position = NULL)
```

Arguments

order.SNP	list of SNPs order by ascending p-value
QTN.position	position of QTN if known

Value

list of power, FDR and type-1 error

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