

Package ‘GWASbyGLM’

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Type Package

Title Perform GWAS using GLM

Version 0.1.0

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Description

This package is used to perform GWAS using the General Linear Model (GLM) with phenotype data, marker data and covariates as an input.

Depends R (>= 3.5)

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

Dependency stats, graphics, utils

BuildVignettes true

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false_positive	<i>False Positives</i>
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Description

Calculates the proportion of False Positives

Usage

```
false_positive(P = P, QTN.position, cutoff)
```

Arguments

P	P values obtained from GWAS
QTN.position	Indexes showing the QTN position in the Genotypic Matrix
cutoff	Threshold/Significance level to assess significance

Value

Proportion of false positives

import_data	<i>Function to import data file</i>
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Description

A function to import data file. The import data contains information about Phenotype (n by 1 form), Markers (Numeric as well as map file with n by m and m by 3 dimension respectively) and Covariates (n by t form) with n the number of individuals in row, m number of markers in column and t number of covariates in column

Usage

```
import_data(filename)
```

Arguments

filename	Input file to import (Requires Phenotype, genotype, map and covariates information)
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Format

matrix

Value

data file

manhattan_plot	<i>Manhattan Plot</i>
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Description

Function to generate Manhattan plot for visual display of significant markers

Usage

```
manhattan_plot(data, cutoff, p, QTN.position = NULL)
```

Arguments

data	the individual and marker information (marker map file with m by 3 dimension where m is number of markers in row)
cutoff	threshold for identifying the significant SNPs
p	p-value of each markers
QTN.position	the position of the significant QTN

Value

plots and graphs

PC	<i>Principle Component Analysis</i>
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Description

Removes PCs that are linearly dependent with the given covariates and also user can specify how many PCs to choose as co-factors

Usage

```
PC(PC_no, X, C)
```

Arguments

PC_no	User specified number of Principle Components (PCs)
X	Markers data in the form n by m with n number of individuals and m number of markers
C	Covariates matrix in the form n by t with n number of individuals and t number of covariates

Value

Principle Component Analysis

p_val_GLM	<i>Function to return p-value for SNP</i>
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Description

This is the function to calculate and return p-values for each SNPs after testing the association between the Phenotypes and SNP along with their Covariates

Usage

```
p_val_GLM(y, X, PC = NULL, C = NULL)
```

Arguments

y	Phenotype matrix in the form n by 1 (n is number of individual in rows)
X	Marker data in matrix form n by m (n is number of individual in row and m is marker data in column)
PC	Principal Components
C	Covariates matrix in the form n by t (n is number of individuals in row and t is number of covariates in column)

Value

p-values

QQPlot_GWAS	<i>QQ plot</i>
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Description

Function to generate QQ-plot

Usage

```
QQPlot_GWAS(p)
```

Arguments

p	p-values of the markers
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Value

qqplot

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