

Package ‘DJ.GLM.GWAS’

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Type Package

Title GLM GWAS

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Description Performs GLM GWAS. DJ is the first initials of the authors

License What license is it under?

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detectTop10

detectTop10

Description

Finds how many simulated genes made it into top ten

Usage

```
detectTop10(P, QTN.position)
```

Arguments

P	vector of p-values of all genes
QTN.position	position of the simulated QTNs

Value

number of QTN detected in top 10

G2P

G2P

Description

Genotype 2 Phenotype function. Taken from Lecture, using for simulation.

Usage

```
G2P(X, h2, alpha, NQTN, distribution)
```

Arguments

X	A Genotype Matrix (n x m)
h2	Heritability
alpha	affect of the qtns
NQTN	Number of QTNS to be simulated
distrubution	which distribution to use, only "norm" is available

Value

simulated phenotype list

graphPCA	<i>PCA plots</i>
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Description

graphPCA Plots the necessary graphs to determine the required number of PC's for the dataset.

Usage

graphPCA(allPC)

Arguments

allPC matrix:the PC matrix provided by "prcomp".

Details

Plots the Scree/Elbow plot,the Proportion of the variance explained by the PC's and the Cumulative Proportion of the variance explained by the PC's.

Value

plots:Scree plot,Proportion of variance explained plot,Cumulative proportion. of variance explained plot and 2D plots.

GWASbyCor	<i>GWAS by Cor</i>
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Description

Performs GWAS by Correlation

Usage

GWASbyCor(X, Y)

Arguments

X A Genotype Matrix (n x m)
Y A Phenotype Matrix (n x 1)

Value

P A P-value vector (n) representing importance of each gene

GWASbyGLM

GWASbyGLM

Description

Performs GLM on a Genotype, Phenotype and Covariate Matrix.

Usage

```
GWASbyGLM(X, y, C)
```

Arguments

X	A Genotype Matrix (n x m)
C	A Covariate Matrix (n x c)
Y	A Phenotype Matrix (n x 1)

Value

P A P-value vector (n) representing importance of each gene

pca3D

PCA 3D plots

Description

pca3D Plots the 3D graphs for PC's of a dataset.

Usage

```
pca3D(pca_comp_plot_data)
```

Arguments

pca_comp_plot_data	
data_frame:	contains all the principal components provided by "prcomp"

Value

PCA3D.html:A html file containg the 3D plots.

pcCoVariance	<i>Choosing and removing dependent PC's</i>
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Description

pcCoVariance() Determines principle components (PC) that are in linear dependence to the covariates (C).Also,removes PC's that are in linear dependence with the covariates

Usage

```
pcCoVariance(PC, C, threshold)
```

Arguments

PC	matrix(n x p): p Principle components for n samples
C	matrix(n x c):c Covariates for n samples
threshold	numeric: the value above which one determines the variables to have high correlation

Details

Determines the principle components (PC) that are not in linear dependence to the covariates (C).

Value

PC_C matrix(n x (p + c - linear dependent)):Principle Components and Covariates which are not dependent

pcThreshold	<i>Choosing PC's</i>
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Description

To determine/choose the Principal component Threshold pcThreshold() Determines principle components to use in model based on set threshold

Usage

```
pcThreshold(PC, threshold = 0.014)
```

Arguments

PC	numeric : principal components generated by "prcomp".
threshold	numeric: the chosen amount or proportion of variance explained by the number of principle components to remain in the model.

Value

PC_T matrix: The chosen number of principal components agreeing with the threshold.

plotManhattan	<i>Plot Manhattan</i>
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Description

Plots manhattan plot of P values

Usage

```
plotManhattan(P, main)
```

Arguments

P	A P-value vector (n) representing importance of each gene
main	Name of plot

plotQQ	<i>Plot QQ</i>
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Description

Plots Q plot of P-value vector

Usage

```
plotQQ(P, main)
```

Arguments

P	A P-value vector (n) representing importance of each gene
main	Name of plot

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