Package 'GWhEAT'

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Type Package

Title Performed GWAS in a fast and efficient manor

Version 0.1.0

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Description This package can run GWAS with PCA and user imputed covariates.
It's design is to reduce false positives and increases the power of a GWAS by taking into account population structure.

License What license is it under?

Encoding UTF-8

LazyData true

Imports ggplot2,
knitr,
gridExtra,
data.table

RoxygenNote 7.0.2

R topics documented:

fix_Dep *Detect linear dependencies of one matrix on another*

Description

Detect linear dependencies of one matrix on another

Usage

```
fix_Dep(X1, X2, tol = .Machine$double.eps^0.5, rank.def = 0, strict = FALSE)
```

Arguments

X1	A matrix.
X2	A matrix, the columns of which may be partially linearly dependent on the columns of X1.
tol	The tolerance to use when assessing linear dependence.
rank.def	If the degree of rank deficiency in X2, given X1, is known, then it can be supplied here, and tol is then ignored. Unused unless positive and not greater than the number of columns in X2.
strict	if TRUE then only columns individually dependent on X1 are detected, if FALSE then enough columns to make the reduced X2 full rank and independent of X1 are detected.

Value

A vector of the columns of X2 which are linearly dependent on columns of X1 (or which need to be deleted to acheive independence and full rank if strict==FALSE). NULL if the two matrices are independent.

GWASapply *GWAS with PCA*

Description

GWAS with PCA

Usage

```
GWASapply(
  pheno = NULL,
  geno = NULL,
  Cov = NULL,
  GM = NULL,
  PCA.M = 3,
  QTN.position = NULL,
  cutoff = NULL,
  plots = FALSE,
```

```
  messages = FALSE,
  print = FALSE,
  trait = "unknown",
  rapid = FALSE
)
```

Arguments

pheno	file with numeric phenotypic values
geno	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
plots	if TRUE, function plots PCA graphs, Manhatten Plot and QQ plot
messages	if TRUE, returns messages for the GWAS function
print	if TRUE, results are saved in a CSV
trait	character value for trait name

Value

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

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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hello *Hello, World!*

Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

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manhattan_plot *Function to create a manhattan plot*

Description

Function to create a manhattan plot

Usage

```
manhattan_plot(
  GM,
  pvals,
  cutoff = NULL,
  QTN_index = c(),
  FP = NULL,
  TP = NULL,
  trait = "unknown",
  messages = FALSE
)
```

Arguments

GM	genetic map of data with chr and position of each SNP
pvals	pvals from gwas results for each SNP
cutoff	If cutoff is default, uses Bonferroni; else uses -log(value) of 0.05/number of SNPs
QTN_index	posistion of QTN if applicable
FP	Positions of SNPS that are False positive
TP	Positions of SNPS that are True positive
trait	character value for trait name

Value

Manhatten plot

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

Description

Function to caculate power, FDR and type-1 error, False Positives, and True Positives

Usage

```
power.fdr(P.value, QTN.position = NULL, cutoff = NULL)
```

Arguments

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

Value

list of power, FDR, type-1 error, False Positives, and True Positives

qq_plot *Function to create a QQ plot*

Description

Function to create a QQ plot

Usage

```
qq_plot(GM, pvals, QTN_index = c(), trait = "unknown")
```

Arguments

GM	genetic map of data with chr and position of each SNP
pvals	pvals from gwas results for each SNP
QTN_index	posistion of QTN if applicable
trait	character value for trait name

Value

QQ plot

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