

Package ‘GWhEAT’

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Type Package

Title Performed GWAS in a fast and efficient manner

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	2
GWASapply	2
GWASapply_rapid	3
GWAStest	4
manhattan_plot	5
power.fdr	5
qq_plot	6
Index	7

fix_Dep	<i>Detect linear dependencies of one matrix on another</i>
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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 achieve independence and full rank if strict==FALSE). NULL if the two matrices are independent.

GWASapply	<i>GWAS with PCA</i>
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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;0.05/number of SNPs
plots	if TRUE, function plots PCA graphs, Manhattan 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
rapid	this option skips all side options and returns just GWAS results

Value

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

GWASapply_rapid	<i>Rapid GWAS with PCA</i>
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Description

Rapid GWAS with PCA

Usage

```

GWASapply_rapid(
  pheno = NULL,
  geno = NULL,
  Cov = NULL,
  PCA.M = 3,
  cutoff = NULL
)

```

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
PCA.M	number of principal components to use default is 3
cutoff	If cutoff is default, uses Bonferroni; 0.05/number of SNPs

Value

GWAS P-values

GWAS _{test}	<i>GWAS with PCA</i>
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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 $-\log(\text{value})$ of $0.05/\text{number of SNPs}$

Value

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

manhattan_plot	<i>Function to create a manhattan plot</i>
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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; 0.05/number of SNPs
QTN_index	posistion of QTN if applicable
FP	Positions of SNPS that are False positives
TP	Positions of SNPS that are True positives
trait	character value for trait name
messages	if TRUE, returns messages for the GWAS function

Value

Manhattan plot

power.fdr	<i>Function to caculate power, FDR and type-1 error, False Positives, and True Positives</i>
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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
cutoff	If cutoff is default, uses Bonferroni;0.05/number of SNPs
P	list of SNPs order by ascending p-value

Value

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

qq_plot	<i>Function to create a QQ plot</i>
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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

Index

`fix_Dep`, [2](#)

`GWASapply`, [2](#)

`GWASapply_rapid`, [3](#)

`GWAStest`, [4](#)

`manhattan_plot`, [5](#)

`power.fdr`, [5](#)

`qq_plot`, [6](#)