

Package ‘GWASzf’

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Type Package

Title GWASzf

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Description This is R package to implement GWAS for HW04 of of Crops545 Statistical Genomics
This package use GLM model to implement GWAS where user can either use PCs or covariates defined by themselves.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

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AStest	<i>AStest</i>
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Description

AStest is a function to implement GWAS using covariates.

Usage

```
AStest(y, X, C)
```

Arguments

y	phenotype data: n by 1
X	genotype data: n by m
C	covariates defined by user: n by t

Details

This function use GLM modeling snp, covariates and phenotype.

Value

p values list for each SNP

References

Lecture 13_GLM in Crops545 Statistical Genomics

Examples

```
P_values <- AStest(y=myY, X=myGD, C=myC)
```

GWAS	<i>GWAS</i>
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Description

GWAS is a function to implement GWAS using covariates and PCs from PCA.

Usage

```
GWAS(y, X, C, pcas = 3)
```

Arguments

y	phenotype data: n by 1
X	genotype data: n by m
C	covariates defined by user: n by t
pcas	the number of pcas used in GWAS. Default is 3. We can use 'False' to cancel the usage of pcas

Details

This function use GLM modeling snp, covariates, PCs and phenotype.

Value

p values list for each SNP

References

Lecture 13_GLM in Crops545 Statistical Genomics

Examples

```
# to include 3 PCs in calculation
P_values01 <- GWAS(y=myY, X=myGD, C=myC, pcas=3)
# Doesn't include PCs in calculation
P_values02 <- GWAS(y=myY, X=myGD, C=myC, pcas=False)
```

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