
EigenCorr	<i>Compute EigenCorr score and P-values of EigenCorr1 and EigenCorr2</i>
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Description

EigenCorr computes the p-values based on EigenCorr1, EigenCorr2 and Tracy-Widom, which can be used for selecting principal components for adjusting population stratification in genome-wide association studies.

Usage

```
EigenCorr( Y,PC,EVAL,N.Pval=200,N.Simu=10000)
```

Arguments

Y	an output phenotype vector.
PC	a matrix of principal components. Kth column is the kth principal components with respect to eigenvalues. The order of rows and columns should be corresponded with Y and EVAL vector. This matrix does not need to have all principal components
EVAL	an vector of all eigenvalues. It should have all eigenvalues !!
N.Pval	an integer, the number of first principal components whose p-values will be computed. If the number of principal components is smaller than N.Pval, p-values of all principal components (except last 2) will be computed.
N.Simu	an integer, the number of simulation for simulated NULL distribution.

Value

EigenCorr returns an dataframe object which has 5 columns. Kth row is the result of kth principal components.

Gamma	Correlations between Y and PCs
EigenCorr_Score	EigenCorr Scores. EigenCorr score is defined as multiplication of square correlation and eigenvalue
EigenCorr1	P-values of EigenCorr1. These are computed based on the simulated null distribution, thus 0 doesn't means p-value is actually 0.
EigenCorr2	P-values of EigenCorr2.
TW	P-values from Tracy-Widom distribution.

Author(s)

Seunggeun Lee (slee@bios.unc.edu)

Examples

```
library(EigenCorr)
data(EigenCorr_Data) # EigenCorr example dataset

Y<-EigenCorr_Data$Y
PC<-EigenCorr_Data$PC
EVAL<-EigenCorr_Data$EVAL

re<-EigenCorr( Y,PC,EVAL)
```

EigenCorr_Data	<i>Example data for EigenCorr</i>
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Description

This is an example dataset for EigenCorr. It contains disease phenotype, principal components and eigenvalues.

Usage

```
EigenCorr_Data
```

Format

List object.

Y a vector of the disease phenotype

PC a matrix of the principal components

EVAL a vector of the eigenvalues

Read_PCA	<i>Read EigenStrat and ShrukenPCA output file</i>
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Description

Read_PCA reads EigenStrat and ShrukenPCA main output file. This file is formatted as 1) First line indicates number of principal components (k) 2) Next k lines have top k eigenvalues 3) N additional lines for k principal components where N is the number of samples.

Usage

```
ReadPCA(FileName)
```

Arguments

FileName an EigenStrat or ShrukenPCA output file.

Value

ReadPCA returns a list object.

K an integer, the number of principal components.

EVAL a eigen value vector.

PC a matrix of K principal components. The kth column is the kth principal component with respect to EVAL

Author(s)

Seunggeun Lee (slee@bios.unc.edu)