Scalable Cauchy Aggregate test using Multiple Phenotypes to test Interactions (SCAMPI)

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R topics documented:

CCT	*Cauchy Combination Test (CCT)*

Description

CCT is used to aggregate multiple p-value developed by Liu and Xie, 202, JASA, 115:529, 393-402, DOI: 10.1080/01621459.2018.1554485 The code used for implementing CCT is adopted from STAAR_v0.9.7 contributed by Xihao Li and Zilin Li at https://github.com/xihaoli/STAAR/blob/master/R/CCT.R

Usage

```
CCT(pvals, weights = NULL)
```

Arguments

pvals   p-values, an array of p-values.

weights   weights associated with each p-value, SCAMPI used the default weight, 1/len(pvals).

Value

a single p-value aggregated from pvals.

Examples

```
set.seed(123)
pval <- runif(20)
CCT(pval)
```

DgLm   *Double Generalized Linear Models (DGLM) for Multiple Outcomes*

Description

Apply Double Generalized Linear Models (DGLM) to standardize each column in matrix y. The mean sub-model will be standardized by one genotype variable g_var and multiple confounders z_var; The variance sub-model will be standardized by confounders z_var. The confounders z_var is optional.

Usage

```
DgLm(y, g_var, z_var = NULL)
```

Arguments

y   outcome, a matrix with multiple columns, representing multiple traits

g_var   genotype, column matrix G with one column, representing one genotype variable

z_var   optional confounder, matrix Z with multiple columns, representing multiple confounders

Value

standardized traits of the original trait matrix y, a matrix with multiple columns

Examples

```
DgLm(
  y = matrix(rnorm(500), ncol = 5),
  z_var = matrix(rnorm(400), ncol = 4),
  g_var = rbinom(100, 2, 0.25)
)
```

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levene_test   *Univariate Levene's Test*

Description

The univariate Levene's test can be applied to a single trait. It is implemented based on the formula in Pare and Cook, 2010, PLoS Genet 6(6): e1000981. doi:10.1371/journal.pgen.1000981

Usage

```
levene_test(y, g_var)
```

Arguments

y   outcome, column matrix, representing one single trait

g_var   genotype, column matrix G with one column, representing one genotype variable

Value

one single p-value

Examples

```
set.seed(123)
N <- 1000
G <- matrix(rbinom(N, 2, 0.25), ncol = 1)
W <- matrix(rnorm(N), ncol = 1)
Y <- 0.2 + 0.1 * G + 0.3 * W + 2 * G * W + rnorm(N)
levene_test(y = Y, g_var = G)
```

```
multivariate_levene_test
```
Multivariate Levene's Test

Description

Multivariate Levene's Test is extended in our paper from the univariate Levene's Test to accomodate multiple traits.

Usage

```
multivariate_levene_test(y, g_var, z_var = NULL)
```

Arguments

y	outcome, a matrix with multiple columns, representing multiple traits
g_var	genotype, column matrix G with one column, representing one genotype variable
z_var	optional confounder, matrix Z with multiple columns, representing multiple confounders

Value

one aggregated p-value for Multivariate Levene's Test

Examples

```
set.seed(123)
multivariate_levene_test(
  y = matrix(rnorm(500), ncol = 5),
  z_var = matrix(rnorm(400), ncol = 4),
  g_var = matrix(rbinom(100, 2, 0.25), ncol = 1)
)
```

`PC_scampi_test`　　　　　*PC SCAMPI*

Description

This is a variation of the SCAMPI method. PC SCAMPI treats the PC of traits as the outcomes.

Usage

```
PC_scampi_test(y, g_var, z_var = NULL)
```

Arguments

y	outcome, a matrix with multiple columns, representing multiple traits
g_var	genotype, column matrix G with one column, representing one genotype variable
z_var	optional confounder, matrix Z with multiple columns, representing multiple confounders

Value

PC SCAMPI p-value

Examples

```
set.seed(123)
PC_scampi_test(
  y = matrix(rnorm(500), ncol = 5),
  z_var = matrix(rnorm(400), ncol = 4),
  g_var = matrix(rbinom(100, 2, 0.25), ncol = 1)
)
```

`SCAMPI`　　　　　*Scalable Cauchy Aggregate test using Multiple Phenotypes to test Interactions (SCAMPI)*

Description

SCAMPI method is applied for detecting the G x E or G x G interaction effects by utilizing both variance and covariance structure of multiple traits.

Usage

```
SCAMPI(y, g_var, z_var = NULL)
```

Arguments

y	outcome, a matrix with multiple columns, representing multiple traits
g_var	genotype, column matrix G with one column, representing one genotype variable
z_var	optional confounder, matrix Z with multiple columns, representing multiple confounders

Value

SCAMPI p-value

Examples

```
SCAMPI(
  y = matrix(rnorm(500), ncol = 5),
  z_var = matrix(rnorm(400), ncol = 4),
  g_var = rbinom(100, 2, 0.25)
)
```