Package ‘WCQ’

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Type Package
Title Detection of QTL effects in a small mapping population
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Description The package contains the WCQ method for detection of QTL effects in a small mapping population. It also contains implementation of the Chen-Qin two-sample and one-sample test of means.
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WCQ-package

**WCQ: Detection of QTL effects in a small mapping population**

**Description**

Contains implementation of WCQ QTL detection method with optional false discovery rate control as well as the Chen-Qin two-sample and one-sample test of means

**Details**

Package: WCQ  
Type: Package  
Version: 0.2  
Date: 2012-09-15  
License: GPL-3

**Author(s)**

Jan Michael Yap  
Maintainer: Jan Michael Yap <jcyap@dcs.upd.edu.ph>

**References**


detect.qtl

**Detect markers with QTL effects**

**Description**

Performs detection of QTL effects on list of markers on a number of traits. Optional false discovery rate control can also be performed.

**Usage**

detect.qtl(marker_data, trait_data, alleles, fdrc.method = "none", threshold = 0.05)
onesamplemeantest  

Description  
Multidimensional one-sample mean test used by WCQ.

Usage  
onesamplemeantest(X1)

Arguments  
X1  
matrix/array containing population data to be tested
### Value

- **pval**

  P-value of the test

### Author(s)

Jan Michael Yap

### References


### Examples

```r
sample.data <- array(rnorm(100), c(10, 10))
one.sample.mean.test(sample.data)
```

---

### Description

Dummy marker data generated using R/qtl package. 1 and 2 correspond to the marker scores of homozygous alleles, while 3 is for the heterozygous allele.

### Usage

```r
data(sample.markers)
```

### Format

The format is: int [1:200, 1:20] 3 2 2 3 3 2 3 3 3 ... - attr(*, "dimnames")=List of 2 ..$: chr [1:200] "D1M1" "D1M2" "D1M3" "D1M4" ... ..$: NULL

### Source


### Examples

```r
data(sample.markers)
```
sample.traits  Dummy Trait Data

Description

Dummy trait data generated using the R/qtl package.

Usage

data(sample.traits)

Format

The format is: num [1, 1:20] 0.574 1.159 0.253 -0.585 -0.611 ...

Source


Examples

data(sample.traits)

twosamplemeantest  Chen-Qin Multidimensional Two-Sample Mean Test

Description

Multidimensional two-sample test of means used by WCQ

Usage

twosamplemeantest(X1, X2)

Arguments

X1, X2 matrices/arrays containing population values for the test

Value

pval p-value of the test

Author(s)

Jan Michael Yap
References


Examples

```r
sample.data1 <- array(rnorm(100), c(10, 10))
sample.data2 <- array(rnorm(100), c(10, 10))
twosamplemeantest(sample.data1, sample.data2)
```

Description

Performs QTL detection using Chen-Qin two sample mean test.

Usage

```r
wcq(marker_data, trait_data, alleles)
```

Arguments

- `marker_data`: m x n matrix/array containing marker score data; m is the number of markers, n is the number of samples
- `trait_data`: t x n matrix/array containing trait value data; t is the number of traits, n is the number of samples
- `alleles`: vector containing the marker scores representing the alleles; currently supports diploids only; third entry assumed to be score for heterozygous marker

Value

- `pval_matrix`: m x t array/matrix containing p-values of each marker as being a potential QTL for a trait

Author(s)

Jan Michael Yap

Examples

```r
data(sample.markers)
data(sample.traits)
alleles <- c(1, 2, 3)
wcq(sample.markers, sample.traits, alleles)
```
WCQ QTL detection with false discovery rate control

Description

Performs WCQ with optional false discovery rate control.

Usage

```r
wcq.fdrc(marker_data, trait_data, alleles, fdrc.method = "none")
```

Arguments

- `marker_data`: m x n matrix/array containing marker score data; m is the number of markers, n is the number of samples
- `trait_data`: t x n matrix/array containing trait value data; t is the number of traits, n is the number of samples
- `alleles`: vector containing the marker scores representing the alleles; currently supports diploids only; third entry assumed to be score for heterozygous marker
- `fdrc.method`: string value representing method to be used for false discovery rate control; uses the p.adjust method in the R default library; default value is "none"

Value

- `adjusted_pval_matrix`: m x t array/matrix containing adjusted p-values of each marker as being a potential QTL for a trait; if `fdrc.method` is set to "none", returns the `pval_matrix` computed using the `wcq` function

Author(s)

Jan Michael Yap

See Also

- `p.adjust`

Examples

```r
data(sample.markers)
data(sample.traits)
alleles <- c(1,2,3)
wcq.fdrc(sample.markers, sample.traits, alleles, fdrc.method="bonferroni")
```
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