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

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References

Chen,Y.X., Qin,Y.L. (2010) A Two-Sample Test for High-Dimensional Data with Applications to Gene-Set Testing, The Annals of Statistics, 38(2), 808-835.

`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)
```

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"
`threshold`	p-value threshold to be used for determining significant QTL effect; default value is 0.05

Value

`qtl.list`	list containing markers with detected significant QTL effect; has length equal to the number of traits

Author(s)

Jan Michael Yap

See Also

p.adjust

Examples

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

`onesamplemeantest` *Chen-Qin Multidimensional One-Sample Mean Test*

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

Chen,Y.X., Qin,Y.L. (2010) A Two-Sample Test for High-Dimensional Data with Applications to Gene-Set Testing, The Annals of Statistics, 38(2), 808-835.

Examples

```
sample.data <- array(rnorm(100),c(10,10))
onesamplemeantest(sample.data)
```

`sample.markers` *Dummy Marker 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

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

Format

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

Source

Broman,K., et al. (2003) R/qtl: QTL mapping in experimental crosses, Bioinformatics, 19, 889-890.

Examples

```
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

Broman,K., et al. (2003) R/qtl: QTL mapping in experimental crosses, Bioinformatics, 19, 889-890.

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

Chen,Y.X., Qin,Y.L. (2010) A Two-Sample Test for High-Dimensional Data with Applications to Gene-Set Testing, The Annals of Statistics, 38(2), 808-835.

Examples

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

`wcq` *WCQ QTL detection*

Description

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

Usage

```
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

```
data(sample.markers)
data(sample.traits)
alleles <- c(1,2,3)
wcq(sample.markers, sample.traits, alleles)
```

`wcq.fdrc` *WCQ QTL detection with false discovery rate control*

Description

Performs WCQ with optional false discovery rate control.

Usage

```
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

```
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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