Package 'QQperm'

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Type Package

Title Permutation Based QQ Plot and Inflation Factor Estimation

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Description This package provides utility functions for permutation based inflation factor estimation and QQ plot.While the utility can be used in general cases, it is particular helpful in situation where there is significant lambda inflation arising from imbalanced case/control sample sizes.

License GPL (>= 2)

Depends R (>= 3.1.0)

LazyData TRUE

RoxygenNote 5.0.1

R topics documented:

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estlambda2   *Estimate the inflation factor for a distribution of P-values or 1df chi-square test.*

Description

Estimate the inflation factor for a distribution of P-values or 1df chi-square test using a NULL distribution of P-values provided by user. The implementation is similar to the default implementation in GenABEL but does not assume the NULL distribution of P-values to be uniform.

Usage

```
estlambda2(p.o, p.e, plot = FALSE, filter = TRUE, adjust.xy = FALSE, ...)
```

Arguments

p.o	Observed P-values from the data.
p.e	Expected P-values from the NULL distribution, usually obtained through label permutations of the data.
plot	Indicate if a plot should be produced.
filter	Indicate if the filter should be applied. This parameter behaves the same as in estlambda in GenABEL.
adjust.xy	Indicate if the x-axis and y-axis should be adjusted to their own range.
...	arguments passed the plot function.

Value

Returns a list containing the estimated lambda value (estimate) and its standard deviation (se).

Author(s)

Slave Petrovski and Quanli Wang

Examples

```
#load pre-computed p-values for igm dataset
library(QQperm)
data("example.Ps")

#print output to pdf file only if not running in interactive mode
if (!interactive()) {
 pdf("lambda.pdf")
}

#estimate inflation factor and generate plot.
lambda <-estlambda2(example.Ps$observed,example.Ps$perm, plot = TRUE, adjust.xy = TRUE)

if (!interactive()) {
 dev.off()
}
```

---

   example.data   *An example collapsing data matrx and associated case/control status*

Description

An example collapsing data matrx and associated case/control status

Usage

```
example.data
```

Format

A list contains both genotype data matrix and case/control status:

data a named data matrix, with rows for genes and columns for samples. Each cell in the matrix represent the counts of variants for given (gene,sample) pair.

is.case case/control indicator. The order of indicators must matches that of the samples defined in data matrix.

Source

http://ask.slave.for.it/

---

example.Ps	*Distributions of expected and observed P-values from igm.data data set.*

Description

Distributions of expected and observed P-values from igm.data data set.

Usage

```
example.Ps
```

Format

A list contains both expected and observed P-values.

perm A vector for expected P-values.

observed A vector for observed P-values.

Source

http://ask.slave.for.it/

---

igm.get.pvalues	*Generate NULL distribution of P-values through label switching and permutation and compute distribution of observed P-values.*

Description

Generate NULL distribution of P-values through label switching and permutation and compute distribution of observed P-values.

Usage

```
igm.get.pvalues(matrix, is.case, n.permutations = 1000)
```

Arguments

matrix	The input genotype matrix, with rows for genes and columns for samples.
is.case	The case/control indicator.
n.permutations	Number of label permutaitons.

Value

Returns A list contains observed P-values (observed) and permuted P-Values for NULL distribution (perm).

Author(s)

Slave Petrovski and Quanli Wang

Examples

```
#Ps  <- igm.get.pvalues(matrix, is.case)
```

---

igm.read.data	*Read sample file and genotype collipsing matrix in IGM format.*

Description

Read sample file and genotype collipsing matrix in IGM format.

Usage

```
igm.read.data(sample.file, matrix.file, filter.list = NULL)
```

Arguments

sample.file	The input sample file.
matrix.file	The input matrix file.
filter.list	A list of genes that will be excluded from the analysis.

Value

Returns A list contains data matrix (matrix) and phenotype indicators (is.case).

Author(s)

Slave Petrovski and Quanli Wang

Examples

```
#igm.data <- igm.read.data(sample.file, matrix.file)
```

QQperm   *QQperm: A package for inflation factor estimation and QQ plot.*

Description

QQperm: A package for inflation factor estimation and QQ plot.

Author(s)

Slave Petrovski and Quanli Wang

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qqplot   *QQ plot of observed P-values vs expected P-values.*

Description

QQ plot of observed P-values vs expected P-values.

Usage

```
qqplot(P.perm, P.observed, adjust.xy = TRUE, ...)
```

Arguments

`P.perm`	Expected P-values from NULL distribution, which is generated through permutation in our example.
`P.observed`	Observed P-values from data.
`adjust.xy`	Indicates if the x-axis and y-axis should be adjusted based on their own range in the plot.
`...`	arguments passed the plot function.

Value

None.

Author(s)

Slave Petrovski and Quanli Wang

Examples

```
library(QQperm)
data("example.Ps")

#print output to pdf file only if not running in interactive mode
if (!interactive()) {
 pdf("qqplot.pdf")
}

qqplot(example.Ps$perm, example.Ps$observed)
```

```
if (!interactive()) {
 dev.off()
}
```

---

toy.data   *An example collapsing data matrx and associated case/control status*

Description

An example collapsing data matrx and associated case/control status

Usage

```
toy.data
```

Format

A list contains both genotype data matrix and case/control status:

data a named data matrix, with rows for genes and columns for samples. Each cell in the matrix represent the counts of variants for given (gene,sample) pair.

is.case case/control indicator. The order of indicators must matches that of the samples defined in data matrix.

Source

<http://ask.slave.for.it/>

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