Package 'PLPE'

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Title Local Pooled Error Test for Differential Expression with Paired High-throughput Data

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Depends R (>= 2.6.2), Biobase (>= 2.5.5), LPE, MASS, methods

Description This package performs tests for paired high-throughput data.

biocViews Proteomics, Microarray, DifferentialExpression

LazyLoad yes

LazyData yes

License GPL (>= 2)

URL http://www.korea.ac.kr/~stat2242/

R topics documented:

lpe.paired *Local Pooled Error Test for Paired Data*

Description

This invetigates differential expression for paired high-throughput data.

Usage

```
lpe.paired(x,...)
```

Arguments

x	an object for which the extraction of model lpe.paired is meaningful.
...	other arguments

Value

x	design matrix; condition index in the first column and pair index in the sceond column
...	data type: 'ms' for mass spectrometry data, 'cdna' for cDNA microarray data

Author(s)

HyungJun Cho and Jae K. Lee

References

Cho H, Smalley DM, Ross MM, Theodorescu D, Ley K and Lee JK (2007). Statistical Identification of Differentially Labelled Peptides from Liquid Chromatography Tandem Mass Spectrometry, Proteomics, 7:3681-3692.

See Also

lpe.paired.default

Examples

```
#LC-MS/MS proteomic data for platelets MPs
library(PLPE)
data(plateletSet)
x <- exprs(plateletSet)
x <- log2(x)

cond <- c(1, 2, 1, 2, 1, 2)
pair <- c(1, 1, 2, 2, 3, 3)
design <- cbind(cond, pair)
```

```
out <- lpe.paired(x, design, q=0.1, data.type="ms")
out$test.out[1:10,]
```

`lpe.paired.default` *Local Pooled Error Test for Paired Data*

Description

This invetigates differential expression for paired high-throughput data.

Usage

```
## Default S3 method:
lpe.paired(x, design, data.type, q=0.01, probe.ID = NULL, estimator="median", w=0.5, w.estimator="fixe
```

Arguments

`x`	data matrix
`design`	design matrix; condition index in the first column and pair index in the sceond column
`q`	quantile for intervals of intensities
`probe.ID`	probe set IDs; if NULL, row numbers are assigned.
`data.type`	data type: 'ms' for mass spectrometry data, 'cdna' for cDNA microarray data
`estimator`	specification for the estimator: 'median', 'mean' and 'huber'
`w`	weight paramter between individual variance estimate and pooling variance estimate, 0<= w <=1
`w.estimator`	two approaches to estimate the weight: 'random' or 'fixed'
`iseed`	seed number
`...`	other arguments

Value

`design`	design matrix; condition index in the first column and pair index in the sceond column
`data.type`	data type: 'ms' for mass spectrometry data, 'cdna' for cDNA microarray data
`q`	quantile for intervals of intensities
`estimator`	specification for the estimator: 'median', 'mean' and 'huber'
`w.estimator`	two approaches to estimate the weight: 'random' or 'fixed'
`w`	weight paramter between individual variance estimate and pooling variance estimate, 0<= w <=1
`test.out`	matrix for test results

Author(s)

HyungJun Cho and Jae K. Lee

References

Cho H, Smalley DM, Ross MM, Theodorescu D, Ley K and Lee JK (2007). Statistical Identification of Differentially Labelled Peptides from Liquid Chromatography Tandem Mass Spectrometry, Proteomics, 7:3681-3692.

See Also

lpe.paired

Examples

```
#LC-MS/MS proteomic data for platelets MPs
library(PLPE)
data(plateletSet)
x <- exprs(plateletSet)
x <- log2(x)

cond <- c(1, 2, 1, 2, 1, 2)
pair <- c(1, 1, 2, 2, 3, 3)
design <- cbind(cond, pair)

out <- lpe.paired(x, design, q=0.1, data.type="ms")
out$test.out[1:10,]
summary(out)
```

---

lpe.paired.fdr *FDR for PLPE*

Description

This computes FDR for PLPE.

Usage

```
lpe.paired.fdr(x,...)
```

Arguments

x	data matrix
...	other arguments

Author(s)

HyungJun Cho and Jae K. Lee

References

Cho H, Smalley DM, Ross MM, Theodorescu D, Ley K and Lee JK (2007). Statistical Identification of Differentially Labelled Peptides from Liquid Chromatography Tandem Mass Spectrometry, Proteomics, 7:3681-3692.

See Also

lpe.paired.fdr.default

Examples

```
#LC-MS/MS proteomic data for platelets MPs
library(PLPE)
data(plateletSet)
x <- exprs(plateletSet)
x <- log2(x)

cond <- c(1, 2, 1, 2, 1, 2)
pair <- c(1, 1, 2, 2, 3, 3)
design <- cbind(cond, pair)

out <- lpe.paired(x, design, q=0.1, data.type="ms")
out.fdr <- lpe.paired.fdr(x,obj=out)
out.fdr$FDR[1:10,]
```

---

lpe.paired.fdr.default

FDR for PLPE

Description

This computes FDR for PLPE.

Usage

```
## Default S3 method:
lpe.paired.fdr(x, obj, n.iter=5, lambda=0.9, ...)
```

Arguments

x	data matrix
obj	object created from lpe.paired
n.iter	number of iterations
lambda	numeric vector of probabilities with values in [0,1]
...	other argument

Value

design	design matrix; condition index in the first column and pair index in the sceond column
data.type	data type: 'ms' for mass spectrometry data, 'cdna' for cDNA microarray data
estimator	specification for the estimator: 'median', 'mean' and 'huber'
w.estimator	two approaches to estimate the weight: 'random' or 'fixed'
w	weight paramter between individual variance estimate and pooling variance estimate, 0<= w <=1
pi0	estimated proportion of non-null peptides
FDR	matrix for test results including FDRs
...	other arguments

Author(s)

HyungJun Cho and Jae K. Lee

References

Cho H, Smalley DM, Ross MM, Theodorescu D, Ley K and Lee JK (2007). Statistical Identification of Differentially Labelled Peptides from Liquid Chromatography Tandem Mass Spectrometry, Proteomics, 7:3681-3692.

See Also

lpe.paired.fdr

Examples

```
#LC-MS/MS proteomic data for platelets MPs
library(PLPE)
data(plateletSet)
x <- exprs(plateletSet)
x <- log2(x)

cond <- c(1, 2, 1, 2, 1, 2)
pair <- c(1, 1, 2, 2, 3, 3)
design <- cbind(cond, pair)

out <- lpe.paired(x, design, q=0.1, data.type="ms")
out.fdr <- lpe.paired.fdr(x,obj=out)
out.fdr$FDR[1:10,]
```

plateletSet *LCMS proteomic data for platelte MPs*

Description

This data set consists of LC-MS/MS data with three replicates of paired samples.

Source

Garcia BA, Smalley DM, Cho H, Shabanowitz J, Ley K and Hunt DF (2005). The Platelet Microparticle Proteome, Journal of Proteome Research, 4:1516-1521.

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