

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.

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LazyLoad yes

LazyData yes

License GPL (>= 2)

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lpe.paired

*Local Pooled Error Test for Paired Data***Description**

This investigates 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 second 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	<i>Local Pooled Error Test for Paired Data</i>
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Description

This investigates 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="fixed")
```

Arguments

x	data matrix
design	design matrix; condition index in the first column and pair index in the second 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 parameter between individual variance estimate and pooling variance estimate, $0 \leq w \leq 1$
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 second 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 parameter between individual variance estimate and pooling variance estimate, $0 \leq w \leq 1$
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

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