Package 'PLPE'

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

Author HyungJun Cho <hj4cho@korea.ac.kr> and Jae K. Lee <jaeklee@virginia.edu>

Maintainer Soo-heang Eo <hananssh@korea.ac.kr>

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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Contents

`am.trans.paired` *Local Pooled Error Test for Paired Data*

Description

This is internal function in lpe.paired.

Usage

```
am.trans.paired(y, design)
```

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`

`base.error.paired` *Local Pooled Error Test for Paired Data*

Description

This is internal function in lpe.paired.

Usage

```
base.error.paired(x, design,est.A, estimator, q, data.type)
```

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`

generate.null *Local Pooled Error Test for Paired Data*

Description

This is internal function in lpe.paired.

Usage

```
generate.null(x, design, q)
```

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

Value

design	design matrix; condition index in the first column and pair index in the sceond column
q	quantile for intervals of intensities

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

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="f
```

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.

---

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

Description

This print lpe.paired.

Usage

```
## S3 method for class 'lpe.paired'
print(x,...)
```

Arguments

x	an object created from lpe.paired
...	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.

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
```

---

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

Description

This prints lpe.paired.fdr

Usage

```
## S3 method for class 'lpe.paired.fdr'
print(x,...)
```

Arguments

x	an object created from lpe.paired
...	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.

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

Description

This summarize lpe.paired.

Usage

```
## S3 method for class 'lpe.paired'
summary(object,...)
```

Arguments

x	an object created from lpe.paired
...	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.

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")
summary(out)
```

summary.lpe.paired.fdr

Local Pooled Error Test for Paired Data

Description

This summarize lpe.paired.

Usage

```
## S3 method for class 'lpe.paired.fdr'
summary(object,...)
```

Arguments

x	an object created from lpe.paired
...	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.

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