Package: PLPE (via r-universe)

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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 `<hanansh@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.

biocViews Proteomics, Microarray, DifferentialExpression

LazyLoad yes

LazyData yes

License GPL (>= 2)

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Contents

`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)
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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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