

Package ‘PLPE’

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

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

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LazyData yes

License GPL (>= 2)

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| | |
|-----------------|--|
| am.trans.paired | <i>Local Pooled Error Test for Paired Data</i> |
|-----------------|--|

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 | <i>Local Pooled Error Test for Paired Data</i> |
|-------------------|--|

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 second column |
| q | quantile for intervals of intensities |

Value

| | |
|--------|--|
| design | design matrix; condition index in the first column and pair index in the second 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 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 *Local Pooled Error Test for Paired Data*

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

| | |
|-------------|--|
| 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 |
| 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, $0 \leq w \leq 1$ |
| 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 | <i>LCMS proteomic data for platelet MPs</i> |
|-------------|---|

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 | <i>Local Pooled Error Test for Paired Data</i> |
|------------------|--|

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

| | |
|------------------|--|
| <code>x</code> | an object created from <code>lpe.paired</code> |
| <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.

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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