

# 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)

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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](#)

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

---

**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](#)

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

---

**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 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> |
|--------------------|------------------------------------------------|

---

**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="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, $0 \leq w \leq 1$ |
| 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 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, $0 \leq w \leq 1$ |
| 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 platelets 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

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

---

## 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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