

# 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)

**URL** <http://www.korea.ac.kr/~stat2242/>

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/PLPE>

**RemoteRef** HEAD

**RemoteSha** b67b9103be3afb1c0f798fb7b28849de4b78dc94

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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,]
```

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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)
```

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lpe.paired.fdr	<i>FDR for PLPE</i>
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**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,]
```

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plateletSet*LCMS proteomic data for platelet MPs*

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**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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