

# Package ‘PLPE’

April 10, 2023

**Version** 1.58.0

**Date** 2009-07-22

**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/>

**git\_url** <https://git.bioconductor.org/packages/PLPE>

**git\_branch** RELEASE\_3\_16

**git\_last\_commit** c009eb8

**git\_last\_commit\_date** 2022-11-01

**Date/Publication** 2023-04-10

## R topics documented:

lpe.paired . . . . .	2
lpe.paired.default . . . . .	3
lpe.paired.fdr . . . . .	4
lpe.paired.fdr.default . . . . .	5
plateletSet . . . . .	7

<b>Index</b>	<b>8</b>
--------------	----------

---

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

---

**Description**

This investigates differential expression for paired high-throughput data.

**Usage**

```
lpe.paired(x, ...)
```

**Arguments**

<code>x</code>	an object for which the extraction of model <code>lpe.paired</code> is meaningful.
<code>...</code>	other arguments

**Value**

<code>x</code>	design matrix; condition index in the first column and pair index in the second column
<code>...</code>	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

*LCMS proteomic data for platelet 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.

# Index

## \* datasets

plateletSet, 7

## \* models

lpe.paired, 2

lpe.paired.default, 3

lpe.paired.fdr, 4

lpe.paired.fdr.default, 5

lpe.paired, 2, 4

lpe.paired.default, 2, 3

lpe.paired.fdr, 4, 6

lpe.paired.fdr.default, 5, 5

plateletSet, 7