

# Package ‘PECA’

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**Type** Package

**Title** Probe-level Expression Change Averaging

**Version** 1.2.0

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**Imports** limma, affy, genefilter, preprocessCore

**Suggests** SpikeIn, ROCR, multtest

**Description** Calculates Probe-level Expression Change Averages (PECA) to identify differential expression in Affymetrix gene expression microarray studies or in proteomic studies using peptide-level measurements respectively.

**biocViews** Software, Preprocessing, Microarray, DifferentialExpression, GeneExpression

**License** GPL (>= 2)

**LazyLoad** yes

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PECA *PECA differential gene expression*

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## Description

Calculates the PECA ordinary or modified t-statistic to determine differential expression between two groups of samples in Affymetrix gene expression studies or peptide-based proteomic studies.

**Usage**

```
## Read AffyBatch object
PECA_AffyBatch(affy=NULL, normalize=FALSE, test="t", type="median", paired=FALSE)

## Read CEL-files
PECA_CEL(samplenames1=NULL, samplenames2=NULL, normalize=FALSE, test="t",
type="median", paired=FALSE)

## Read tab separated text file
PECA_tsv(file=NULL, samplenames1=NULL, samplenames2=NULL, normalize=FALSE, test="t",
type="median", paired=FALSE)
```

**Arguments**

|                           |  |
|---------------------------|--|
| <code>affy</code>         | AffyBatch object   |
| <code>normalize</code>    | a logical indicating whether quantile normalization is applied   |
| <code>test</code>         | a character string indicating whether the ordinary ("t") or modified ("modt") t-test is performed.         |
| <code>type</code>         | a character string indicating whether ("median") or ("tukey") is used when calculating gene/protein values |
| <code>paired</code>       | a logical indicating whether a paired test is performed  |
| <code>file</code>         | filename of tab separated data   |
| <code>samplenames1</code> | a character vector containing the names of the .CEL-files/columns in the first group                       |
| <code>samplenames2</code> | a character vector containing the names of the .CEL-files/columns in the second group                      |

**Details**

PECA determines differential gene expression using directly the probe-level measurements from Affymetrix gene expression microarrays or proteomic datasets. An expression change between two groups of samples is first calculated for each probe/peptide on the array. The gene/protein-level expression changes are then defined as medians over the probe-level changes. For more details about the probe-level expression change averaging (PECA) procedure, see Elo et al. (2005), Laajala et al. (2009) and Suomi et al.

PECA calculates the probe-level expression changes using the ordinary or modified t-statistic. The ordinary t-statistic is calculated using the function `rowttests` in the Bioconductor `genefilter` package. The modified t-statistic is calculated using the linear modeling approach in the Bioconductor `limma` package. Both paired and unpaired tests are supported.

The significance of an expression change is determined based on the analytical p-value of the gene-level test statistic. Unadjusted p-values are reported along with the corresponding p-values looked up from beta distribution. The quality control and filtering of the data (e.g. based on low intensity or probe specificity) is left to the user.

## References

T. Suomi, O. Nevalainen and L.L. Elo: Evaluation of probe-level expression change averaging in microarray and proteomics data. 2013

L.L. Elo, L. Lahti, H. Skottman, M. Kylaniemi, R. Lahesmaa and T. Aittokallio: Integrating probe-level expression changes across generations of Affymetrix arrays. *Nucleic Acids Research* 33(22), e193, 2005.

E. Laajala, T. Aittokallio, R. Lahesmaa and L.L. Elo: Probe-level estimation improves the detection of differential splicing in Affymetrix exon array studies. *Genome Biology* 10(7), R77, 2009.

H. Bengtsson, K. Simpson, J. Bullard and K. Hansen: aroma.affymetrix: A generic framework in R for analyzing small to very large Affymetrix data sets in bounded memory. Tech Report \#745, Department of Statistics, University of California, Berkeley, 2008.

## Examples

```
## Load spike-in example
library(SpikeIn)
data(SpikeIn95)

## Subset the data
data <- SpikeIn95[,13:20]

## Run the test
results <- PECA_AffyBatch(affy=data)

## Show portion of the results
head(results)
```

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\*Topic **math**

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