

Package ‘PECA’

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Type Package

Title Probe-level Expression Change Averaging

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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, Proteomics, Microarray, DifferentialExpression, GeneExpression

License GPL (>= 2)

LazyLoad yes

NeedsCompilation no

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PECA	<i>PECA differential gene expression</i>
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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)

## Read dataframe
PECA_df(df=NULL, id=NULL, samplenames1=NULL, samplenames2=NULL, normalize=FALSE, test="t", type="median", paired=FALSE)

```

Arguments

<code>affy</code>	AffyBatch object
<code>normalize</code>	a character string indicating if ("quantile") or ("median") normalization is performed
<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
<code>df</code>	dataframe to be used as an input
<code>id</code>	column name of dataframe used for aggregating results

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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