Package 'PECA'

November 12, 2026

Type Package

Title Probe-level Expression Change Averaging

Version 1.48.0

Author Tomi Suomi, Jukka Hiissa, Laura L. Elo

Maintainer Tomi Suomi <tomi.suomi@utu.fi>

Imports ROTS, limma, affy, genefilter, preprocessCore, aroma.affymetrix, aroma.core

Depends R (>= 3.3)

Suggests SpikeIn

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 mesurements respectively.

biocViews Software, Proteomics, Microarray, DifferentialExpression, GeneExpression, ExonArray, DifferentialSplicing

License GPL (>= 2)

LazyLoad yes

git_url https://git.bioconductor.org/packages/PECA

git_branch RELEASE_3_23

git_last_commit 31763c7

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

Contents

PECA 2
PECASI 4

Index **6**

PECA *PECA differential gene expression*

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, log=TRUE, test="t", type="median",
   paired=FALSE, progress=FALSE)

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

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

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

Arguments

affy	AffyBatch object.
normalize	A character string indicating if ("quantile") or ("median") normalization is performed.
log	A logical indicating whether log2 scaling is performed.
test	A character string indicating whether the ordinary t-test ("t"), modified t-test ("modt"), or reproducibility-optimized test statistic ("rots") is performed.
type	A character string indicating whether ("median") or ("tukey") is used when calculating gene/protein values.
paired	A logical indicating whether a paired test is performed.
file	Filename of tab separated data.
samplenames1	A character vector containing the names of the .CEL-files/columns in the first group.
samplenames2	A character vector containing the names of the .CEL-files/columns in the second group.
df	Dataframe to be used as an input.
id	Column name of dataframe used for aggregating results.
progress	A logical indicating whether a progress bar is shown.

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 ditribution. The quality control and filtering of the data (e.g. based on low intensity or probe specificity) is left to the user.

Value

PECADE returns a matrix which rows correspond to the genes under analysis and columns indicate the corresponding signal log-ratio (slr), t-statistic, p-value and FDR adjusted p-value.

References

T. Suomi, G.L. Corthals, O. Nevalainen and L.L. Elo: Using peptide-level proteomics data for detecting differentially expressed proteins. 2015

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

```
## Generate example data frame
df <- data.frame(id=c(rep("a",10),rep("b",10),rep("c",10)))
df$A1 <- rnorm(30, mean=50, sd=5)
df$A2 <- rnorm(30, mean=48, sd=5)
df$A3 <- rnorm(30, mean=50, sd=5)
df$B1 <- rnorm(30, mean=52, sd=5)
df$B2 <- rnorm(30, mean=53, sd=5)
df$B3 <- rnorm(30, mean=51, sd=5)

## Run the test
group1 <- c("A1","A2","A3")
group2 <- c("B1","B2","B3")
```

```
results <- PECA_df(df, group1, group2, id=id)
```

PECASI *PECA splicing index*

Description

Calculates the PECA splicing index to determine differentially spliced exons between two groups of samples in Affymetrix exon array studies.

Usage

```
PECASI(path, dataFolder, chipType, cdfTag=NULL, samplenames1, samplenames2, test="t")
```

Arguments

path	A character string specifying the path of the working directory containing the expression and annotation data.
dataFolder	A character string specifying the name of the directory containing the raw expression data (.CEL-files).
chipType	A character string specifying the microarray (chip) type.
cdfTag	A character string indicating an optional suffix added to the name of the particular chip definition file (CDF).
samplenames1	A character vector containing the names of the .CEL-files in the first group without the extension .CEL.
samplenames2	A character vector containing the names of the .CEL-files in the second group without the extension .CEL. The paired samples are assumed to be in the same order in both of the vectors samplenames1 and samplenames2.
test	A character string indicating whether the ordinary ("t") or modified ("modt") t-test is performed.

Details

PECASI determines differential alternative splicing using directly the probe-level measurements from Affymetrix exon microarrays. Differential splicing between two groups of samples is first calculated for each probe on the array. The exon-level differential splicing is then defined as the median over the probe-level differences. For more details about the probe-level expression change averaging (PECA) procedure, see Elo et al. (2005), Elo et al. (2006) and Laajala et al.

The current implementation of PECASI calculates the probe-level differential splicing using the ordinary or modified t-statistic over splicing index values. 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. The samples are assumed to be paired. For more details about the PECA splicing index procedure, see Laajala et al.

PECASI uses the aroma.affymetrix package to normalize and extract the probe-level data from the .CEL-files (Bengtsson et al. 2008). Therefore, it is important that the naming and structure of the data files follow exactly the rules specified in the aroma.affymetrix package.

The raw expression data (.CEL-files) need to be in the directory rawData/<dataFolder>/<chipType>, where rawData is a directory under the current working directory specified by the path, dataFolder is the name of the dataset given by the user, and chipType indicates the type of the microarray used in the experiment.

In addition to the expression data, a chip definition file (CDF) is required. The CDF-file(s) for a particular microarray type chipType need to be in the directory annotationData/chipTypes/<chipType>, where annotationData is a directory under the current working directory specified by the path. Besides the CDF-files provided by Affymetrix, various custom CDF-files are available for a particular microarray type. The different versions can be separated by adding a suffix cdfTag to the name of the CDF-file: <chipType>,<cdfTag>.cdf

The quality control and filtering of the data (e.g. based on low intensity or probe specificity) is left to the user.

Value

PECASI returns a matrix which rows correspond to the exons under analysis and columns indicate the corresponding splicing index (si), t-statistic, p-value and FDR adjusted p-value.

References

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.

L.L. Elo, M. Katajamaa, R. Lund, M. Oresic, R. Lahesmaa and T. Aittokallio: Improving identification of differentially expressed genes by integrative analysis of Affymetrix and Illumina arrays. OMICS A Journal of Integrative Biology 10(3), 369–380, 2006.

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.

See Also

PECA

Index

∗ **math**
PECA, 2
PECASI, 4

PECA, 2, *5*
PECA_AffyBatch *(*PECA*)*, 2
PECA_CEL *(*PECA*)*, 2
PECA_df *(*PECA*)*, 2
PECA_tsv *(*PECA*)*, 2
PECASI, 4