Package 'a4Classif'

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Type Package

Title Automated Affymetrix Array Analysis Classification Package

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Description Automated Affymetrix Array Analysis Classification Package

Depends methods, a4Core, a4Preproc, MLInterfaces, ROCR, pamr, glmnet,
    varSelRF

Imports a4Core

Suggests ALL

License GPL-3

biocViews Microarray

NeedsCompilation no

R topics documented:

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lassoClass	*Classify using the Lasso*

Description

Classify using the Lasso algorithm as implemented in the glmnet package

Usage

```
lassoClass(object, groups)
```

Arguments

object	object containing the expression measurements; currently the only method supported is one for ExpressionSet objects
groups	character string indicating the column containing the class membership

Value

object of class `glmnet`

Author(s)

Willem Talloen

References

Goehlmann, H. and W. Talloen (2009). Gene Expression Studies Using Affymetrix Microarrays, Chapman \& Hall/CRC, pp. 183, 205 and 212.

See Also

glmnet

Examples

```
if (require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))

  resultLasso <- lassoClass(object = ALL, groups = "BTtype")
  plot(resultLasso, label = TRUE,
    main = "Lasso coefficients in relation to degree of
  penalization.")
  featResultLasso <- topTable(resultLasso, n = 15)
}
```

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pamClass | *Classify using Prediction Analysis for MicroArrays*

Description

Classify using the Prediction Analysis for MicroArrays (PAM) algorithm as implemented in the pamr package

Usage

```
pamClass(object, groups, probe2gene = TRUE)
```

Arguments

object
: object containing the expression measurements; currently the only method supported is one for ExpressionSet objects

groups
: character string indicating the column containing the class membership

probe2gene
: logical; if TRUE Affymetrix probeset IDs are translated into gene symbols; if FALSE no such translation is conducted

Value

object of class pamClass

Author(s)

Willem Talloen

References

Robert Tibshirani, Trevor Hastie, Balasubramanian Narasimhan, and Gilbert Chu (1999). Diagnosis of multiple cancer types by shrunken centroids of gene expression. PNAS 99: 6567-6572.

Available at www.pnas.org

Goehlmann, H. and W. Talloen (2009). Gene Expression Studies Using Affymetrix Microarrays, Chapman \& Hall/CRC, p. 221.

See Also

pamr.train

rfClass   *Classify using Random Forests*

Description

Classify using the Random Forest algorithm of Breiman (2001)

Usage

```
rfClass(object, groups, probe2gene = TRUE)
```

Arguments

object	object containing the expression measurements; currently the only method supported is one for ExpressionSet objects
groups	character string indicating the column containing the class membership
probe2gene	logical; if TRUE Affymetrix probeset IDs are translated into gene symbols in the output object; if FALSE no such translation is conducted

Value

Object of class 'rfClass'

Note

topTable and plot methods are available for 'rfClass' objects.

Author(s)

Tobias Verbeke and Willem Talloen

References

Breiman, L. (2001), *Random Forests*, Machine Learning 45(1), 5-32.

See Also

randomForest

ROCcurve   *Receiver operating curve*

Description

A ROC curve plots the fraction of true positives (TPR = true positive rate) versus the fraction of false positives (FPR = false positive rate) for a binary classifier when the discrimination threshold is varied. Equivalently, one can also plot sensitivity versus (1 - specificity).

Usage

```
ROCcurve(object, groups, probesetId = NULL, geneSymbol = NULL, main = NULL, probe2gene = TRUE, ...)
```

Arguments

object	ExpressionSet object for the experiment
groups	String containing the name of the grouping variable. This should be a the name of a column in the pData of the expressionSet object.
probesetId	The probeset ID. These should be stored in the featureNames of the expressionSet object.
geneSymbol	The gene symbol. These should be stored in the column `Gene Symbol` in the featureData of the expressionSet object.
main	Main title on top of the graph
probe2gene	Boolean indicating whether the probeset should be translated to a gene symbol (used for the default title of the plot)
...	Possibility to add extra plot options. See par

Author(s)

Willem Talloen

References

Some explanation about ROC can be found on http://en.wikipedia.org/wiki/ROC_curve and http://www.anaesthetist.com/mnm/stats/roc/Findex.htm. The latter has at the bottom a nice interactive tool to scroll the cut-off and to see how it affects the FP/TP table and the ROC curve.

Examples

```
# simulated data set
esSim <- simulateData()
ROCcurve(probesetId = 'Gene.1', object = esSim, groups = 'type', addLegend = FALSE)

# ALL data set
if (require(ALL)){
```

```
    data(ALL, package = "ALL")
    ALL <- addGeneInfo(ALL)
    ALL$BTtype <- as.factor(substr(ALL$BT,0,1))
    ROCres <- ROCcurve(gene = "ABL1", object = ALL, groups = "BTtype")
}
```

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