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
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biocViews Microarray
NeedsCompilation no

R topics documented:

lassoClass ................................................................. 1
pamClass ................................................................. 2
rfClass ................................................................. 3
ROCCurve ............................................................... 4

Index 6

lassoClass  Classify using the Lasso

Description

Classify using the Lasso algorithm as implemented in the glmmnet 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


See Also

glmnet

Examples

```r
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)
}
```

Description

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

Usage

pamClass(object, groups, probe2gene = TRUE)
**rfClass**

**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**

**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

See Also
randomForest

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](http://en.wikipedia.org/wiki/ROC_curve) and [http://www.anaesthetist.com/mmm/stats/roc/Findex.htm](http://www.anaesthetist.com/mmm/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

```r
# 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")
}
```
Index

*Topic models
  lassoClass, 1
  pamClass, 2
  rfClass, 3

glmnet, 2

lassoClass, 1

pamClass, 2
pamr.train, 3
par, 4
plot.rfClass (rfClass), 3

randomForest, 4
rfClass, 3
ROCcurve, 4