# Package ‘a4Classif’

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**Type**  Package

**Title**  Automated Affymetrix Array Analysis Classification Package

**Version**  1.52.0

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**Description**  Functionalities for classification of Affymetrix microarray data, integrating within the Automated Affymetrix Array Analysis set of packages.

**Depends**  a4Core, a4Preproc

**Imports**  methods, Biobase, ROCR, pamr, glmnet, varSelRF, utils, graphics, stats

**Suggests**  ALL, hgu95av2.db, knitr, rmarkdown

**License**  GPL-3

**biocViews**  Microarray, GeneExpression, Classification

**VignetteBuilder**  knitr

**RoxygenNote**  7.1.1

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lassoClass

Classify using the Lasso

Description

Classify using the Lasso

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."
       )
  topTable(resultLasso, n = 15)
}
```

---

**pamClass**

*Classify using Prediction Analysis for MicroArrays*

**Description**

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

**Usage**

```r
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**


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
ROC curve

References


See Also

randomForest

Examples

if(require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))
  # select only a subset of the data for computation time reason
  ALLSubset <- ALL[sample.int(n = nrow(ALL), size = 100, replace = TRUE), ]
  resultRf <- rfClass(object = ALLSubset, groups = "BTtype")
  plot(resultRf)
  topTable(resultRf, n = 15)
}

ROC curve

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.
The gene symbol. These should be stored in the column `Gene Symbol` in the featureData of the expressionSet object.

Main title on top of the graph

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`

a plot is drawn in the current device. prediction object is returned invisibly.

Willem Talloen

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.anesthetist.com/mmm/stats/roc/Findex.htm](http://www.anesthetist.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.

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

**Description**

Top table for pamClass object

**Usage**

```r
## S4 method for signature 'pamClass'
topTable(fit, n)
```

**Arguments**

- `fit`: object for which to obtain a top table, generally a fit object for a given model class
- `n`: number of features (variables) to list in the top table, ranked by importance
Value
topTableRfClass object

Description
Top table for rfClass object

Usage
## S4 method for signature 'rfClass'
topTable(fit, n)

Arguments
fit object for which to obtain a top table, generally a fit object for a given model class
n number of features (variables) to list in the top table, ranked by importance

Value
topTableRfClass object
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