

# 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	<i>Classify using the Lasso</i>
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### 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

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

---

pamClass

*Classify using Prediction Analysis for MicroArrays*

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**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](http://www.pnas.org)

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

**See Also**

[pamr.train](#)

**Examples**

```
if(require(ALL)){
  data(ALL, package = "ALL")
  ALL <- addGeneInfo(ALL)
  ALL$BTtype <- as.factor(substr(ALL$BT,0,1))
  resultPam <- pamClass(object = ALL, groups = "BTtype")
  plot(resultPam)
  topTable(resultPam, n = 5)
  confusionMatrix(resultPam)
}
```

---

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](#)

**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)
}
```

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 ROCcurve

*Receiver operating curve*


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**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 <a href="#">par</a>

**Value**

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

**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/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)
```

---

topTable,pamClass-method

*Top table for pamClass object*

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**Description**

Top table for pamClass object

**Usage**

```
## 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**

topTablePam object

---

topTable,rfClass-method

*Top table for rfClass 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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