

# Package ‘a4Classif’

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**Type** Package

**Title** Automated Affymetrix Array Analysis Classification Package

**Version** 1.54.0

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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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**Author** Willem Talloen [aut],  
Tobias Verbeke [aut],  
Laure Cougnaud [cre]

**Maintainer** Laure Cougnaud <[laure.cougnaud@openanalytics.eu](mailto:laure.cougnaud@openanalytics.eu)>

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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**

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*

---

### 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)
}
```

ROCurve

*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**

```
ROCurve(
  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
```

---

**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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