

# Package ‘a4Classif’

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**Type** Package

**Title** Automated Affymetrix Array Analysis Classification Package

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**Author** Willem Talloen, Tobias Verbeke

**Maintainer** Tobias Verbeke <tobias.verbeke@openanalytics.eu>, Willem  
Ligtenberg <willem.ligtenberg@openanalytics.eu>

**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

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lassoClass

*Classify using the Lasso*

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**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*

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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](#)

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`rfClass`*Classify using Random Forests*

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**Description**

Classify using the Random Forest algorithm of Breiman (2001)

**Usage**

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

**Arguments**

<code>object</code>	object containing the expression measurements; currently the only method supported is one for ExpressionSet objects
<code>groups</code>	character string indicating the column containing the class membership
<code>probe2gene</code>	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](#)

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ROCcurve	<i>Receiver operating curve</i>
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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>

### 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)

# 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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