

Package ‘a4Classif’

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Type Package

Title Automated Affymetrix Array Analysis Classification Package

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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

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biocViews Microarray, GeneExpression, Classification

VignetteBuilder knitr

RoxygenNote 7.1.1

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| | |
|------------|---------------------------------|
| lassoClass | <i>Classify using the Lasso</i> |
|------------|---------------------------------|

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

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)
}
```

 ROCcurve

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. |

| | |
|------------|------------------------------------------------------------------------------------------------------------------------|
| 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 |

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 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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