Package ‘a4Classif’

March 22, 2017

Type Package
Title Automated Affymetrix Array Analysis Classification Package
Version 1.22.0
Date 2011-05-21
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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

R topics documented:

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lassoClass

Classify using the Lasso

Description

Classify using the Lasso algorithm as implemented in the glmnet package

Usage

lassoClass(object, groups)
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)
rfClass

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


See Also

pamr.train

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


See Also

randomForest

R function

ROCcurve

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`

Author(s)

Willem Talloen
ROCcurve

References

Some explanation about ROC can be found on http://en.wikipedia.org/wiki/ROC_curve and http://www.anaesthetist.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.

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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