Package ‘a4Classif’

January 14, 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

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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)
\textbf{rfClass}  \hspace{1cm} 3  

\textbf{Arguments}  

\begin{itemize}  
\item \textbf{object} \hspace{1cm} object containing the expression measurements; currently the only method supported is one for ExpressionSet objects  
\item \textbf{groups} \hspace{1cm} character string indicating the column containing the class membership  
\item \textbf{probe2gene} \hspace{1cm} logical; if \textsf{TRUE} Affymetrix probeset IDs are translated into gene symbols; if \textsf{FALSE} no such translation is conducted  
\end{itemize}  

\textbf{Value}  

Object of class \texttt{pamClass}  

\textbf{Author(s)}  

Willem Talloen  

\textbf{References}  

Available at \url{www.pnas.org}  

\textbf{See Also}  

\texttt{pamr.train}  

\begin{center}  
\begin{tabular}{ll}  
\textbf{rfClass} & \textit{Classify using Random Forests}  
\end{tabular}  
\end{center}  

\textbf{Description}  

Classify using the Random Forest algorithm of Breiman (2001)  

\textbf{Usage}  

\begin{verbatim}  
rfClass(object, groups, probe2gene = TRUE)  
\end{verbatim}  

\textbf{Arguments}  

\begin{itemize}  
\item \textbf{object} \hspace{1cm} object containing the expression measurements; currently the only method supported is one for ExpressionSet objects  
\item \textbf{groups} \hspace{1cm} character string indicating the column containing the class membership  
\item \textbf{probe2gene} \hspace{1cm} logical; if \textsf{TRUE} Affymetrix probeset IDs are translated into gene symbols in the output object; if \textsf{FALSE} no such translation is conducted  
\end{itemize}  

\textbf{Value}  

Object of class \texttt{rfClass}
Note
topTable and plot methods are available for `rfClass` objects.

Author(s)
Tobias Verbeke and Willem Talloen

References

See Also
randomForest

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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**

```r
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
ROC curve

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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