Package ‘geNetClassifier’

March 21, 2017

Type Package
Title Classify diseases and build associated gene networks using gene expression profiles
Version 1.14.0
Date 2015-05-05
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Depends R (>= 2.10.1), Biobase (>= 2.5.5), EBarrays, minet, methods
Imports e1071, graphics
Suggests leukemiasEset, RUnit, BiocGenerics
Enhances RColorBrewer, igraph, infotheo
Description Comprehensive package to automatically train and validate a multi-class SVM classifier based on gene expression data. Provides transparent selection of gene markers, their co-expression networks, and an interface to query the classifier.
License GPL (>= 2)
ZipData no
URL http://www.cicancer.org
LazyLoad yes
bioViews Classification, DifferentialExpression, Microarray
NeedsCompilation no

R topics documented:

geNetClassifier-package ........................................... 2
calculateGenesRanking ............................................. 4
externalValidation.probMatrix .................................... 6
externalValidation.stats ............................................ 8
gClasses-methods ................................................. 9
GeneralizationError-class ..................................... 10
classify diseases and build associated gene networks using gene expression profiles

Description

Comprehensive package to automatically train a multi-class SVM classifier based on gene expression data. Provides transparent selection of gene markers, their coexpression networks, and an interface to query the classifier.

Details

Package: geNetClassifier
Type: Package
Version: 1.0
Date: 2013-02-28
License: GPL (>=2)
LazyLoad: yes
Depends: R (>= 2.10.1), Biobase (>= 2.5.5), EBarrays, minet, methods
Imports: e1071, ipred, graphics
Suggests: leukemiasEset
Enhances: RColorBrewer, igraph
Author(s)
Sara Aibar, Celia Fontanillo and Javier De Las Rivas
Maintainer: Sara Aibar <saibar@usal.es>

See Also
Main functions included in this package:

- geNetClassifier
- queryGeNetClassifier

Query stats functions:

- querySummary
- externalValidation.probMatrix
- externalValidation.stats
- plotAssignments

Plots and genes info:

- calculateGenesRanking
- plotNetwork
- plotDiscriminantPower
- plotExpressionProfiles

Classes:

- GenesRanking
- GenesNetwork
- GeNetClassifierReturn
- GeneralizationError

Related data sets:

- leukemiasEset
**calculateGenesRanking**  
*Calculate GenesRanking*

**Description**  
Calculates the genes ranking and/or plots the posterior probability of the genes ordered by class ranking.

**Usage**

```r
calculateGenesRanking(eset=NULL, sampleLabels=NULL, numGenesPlot=1000, plotTitle="Significant genes", plotLp=TRUE, lpThreshold = 0.95, numSignificantGenesType="ranked", returnRanking="full", nullHypothesisFilter=0.95, nGenesExprDiff=1000, geneLabels=NULL, precalcGenesRanking=NULL, IQRfilterPercentage= 0, verbose=TRUE)
```

**Arguments**

- `eset`: ExpressionSet or Matrix. Gene expression of the train samples (positive & non-logarithmic normalized values).
- `sampleLabels`: Character. PhenoData variable (column name) containing the train samples class labels. Matrix or Factor. Class labels of the train samples.
- `numGenesPlot`: Integer. Number of genes to plot.
- `plotTitle`: Character. Plot title.
- `plotLp`: Logical. If FALSE no plot is drawn.
- `lpThreshold`: Numeric between 0 and 1. Required posterior probability value to consider a gene 'significant'.
- `numSignificantGenesType`: Character. Type of count for number of genes over lpThreshold.  
  - "global". Counts all genes of a class with posterior probability over lpThreshold, even if in the final ranking they were assigned to another class.  
  - "ranked". Counts only genes assigned to each class.
- `returnRanking`: Character. Type of ranking to return:  
  - "full". Ranking of all available genes.  
  - "lp"/"significant"/"lpThreshold"/TRUE. Ranking of the significant genes (genes with posterior probability over lpThreshold).  
  - FALSE/NULL. No ranking is returned.
- `nullHypothesisFilter`: Numeric between 0 and 1. Genes with a Null Hypothesis with a posterior probability over this threshold will be removed from the ranking. Null Hypothesis: They don’t represent any class.
- `nGenesExprDiff`: Numeric. Number of top genes to calculate the differencial expression for.
- `geneLabels`: Vector or Matrix. Gene name, ID or label which should be shown in the returned results and plots.
calculateGenesRanking

IQRfilterPercentage
Integer. InterQuartile Range (IQR) filter applied to the initial data. Not recommended for more than two classes.

precalcGenesRanking
Allows providing a genesRanking provided by geNetClassifier or by a previous execution for the same data and parameters.

verbose
Logical. If TRUE, messages indicating the execution progress will be printed on screen.

Details

Significant genes: Genes with posterior probability over 'lpThreshold'.
More significant genes may mean:

• Very different class
• More systemic disease

Plot lines represent the posterior probability of genes, sorted by rank from left to right.

In order to find genes that differentiate the classes from each other, the function ranks the genes based on their posterior probability for each class. The posterior probability represents how well a gene differentiates samples from a class, from samples from other classes. Therefore, Genes with high posterior probability are good to differentiate a class from all the others. This posterior probability is calculated by emfit (pkg: EBarrays), an expectation-maximization (EM) algorithm for gene expression mixture model.

Value

• GenesRanking Optional. Requested genes ranking.
• Plot Optional. Plot of the posterior probability of the top genes.

See Also

plot.GenesRanking is a shortcut to plotting a previously calculated genes ranking. i.e. plot(genesRanking)

Examples

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Not run:

####

# Calculate/plot the significant genes (+ info) of a dataset
# without training classifier/calculating network
### return only significant genes ranking (default)

```r
signGenesRanking <- calculateGenesRanking(leukemiasEset[,trainSamples],
                                          sampleLabels="LeukemiaType")
numGenes(signGenesRanking)
```

### Return the full genes ranking:

```r
fullRanking <- calculateGenesRanking(leukemiasEset[,trainSamples],
                                       sampleLabels="LeukemiaType", returnRankings="full")
numGenes(fullRanking)
numSignificantGenes(fullRanking)
```

### The significant genes can then be extracted from it:

```r
signGenesRanking2 <- getTopRanking(fullRanking,
                                     numGenesClass=numSignificantGenes(fullRanking))
numGenes(signGenesRanking2)
```

### Changing the posterior probability required to consider genes significant:

```r
signGenesRanking90 <- calculateGenesRanking(leukemiasEset[,trainSamples],
                                              sampleLabels="LeukemiaType", lpThreshold=0.9)
numGenes(signGenesRanking90)
```

## End (Not run)

### Plotting previously calculated rankings:

#### Load or calculate a ranking (or a classifier with geNetClassifier)

```r
data(leukemiasClassifier) # Sample trained classifier, @genesRanking
```

#### Default plot:

```r
# - equivalent to plot(leukemiasClassifier@genesRanking)
# - in this case, the previously calculated 'fullRanking'
# is equivalent to 'leukemiasClassifier@genesRanking'
calculateGenesRanking(precalcGenesRanking=leukemiasClassifier@genesRanking)
```

#### Changing arguments:

```r
calculateGenesRanking(precalcGenesRanking=leukemiasClassifier@genesRanking,
                       numGenesPlot=5000, plotTitle="Leukemias", lpThreshold=0.9)
```

### Description

 Generates the probability matrix.

### Usage

```r
externalValidation.probMatrix(queryResult, realLabels, numDecimals=2)
```
Arguments

queryResult  Object returned by \texttt{query\textbf{G}eNet\textbf{C}lassifier}
realLabels  Factor. Actual/real class of the samples.
numDecimals  Integer. Number of decimals to return.

Details

A probability matrix contains the probabilities of assigning each assigned sample to each class.
They help identifying where errors are likely to occur even though there were not actual errors in
the external/cross validation.

Value

The probability matrix.

Author(s)

Bioinformatics and Functional Genomics Group. Centro de Investigacion del Cancer (CIC-IBMCC,
USAL-CSIC). Salamanca. Spain

See Also

Main package function and classifier training: \texttt{geNetClassifier}
Query the classifier: \texttt{queryGeNetClassifier}
Query summary: \texttt{querySummary}
External validation stats: \texttt{externalValidation.stats}

Examples

```
# Classifier training

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Train a classifier or load a trained one:
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
#    sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier)  # Sample trained classifier

# External Validation

# Select the samples to query the classifier
# - External validation: samples not used for training
testSamples <- c(1:60)[-trainSamples]

# Make a query to the classifier:
queryResult <- queryGeNetClassifier(leukemiasClassifier, leukemiasEset[,testSamples])
```
# Obtain the probability matrix for the assigned samples:
externalValidation.probMatrix(queryResult, leukemiasEset[,testSamples]$LeukemiaType)

### externalValidation.stats

*Statistics of the external validation.*

#### Description

Taking as input the confusion matrix resulting from external validation calculates the global Accuracy, Call Rate, Sensitivity, Specificity and Matthews Correlation Coefficient.

#### Usage

```r
externalValidation.stats(confussionMatrix, numDecimals = 2)
```

#### Arguments

- **confussionMatrix**
  - Confussion matrix containing the real class as rows and the assigned class as columns.

- **numDecimals**
  - Integer. Number of decimals to show on the statistics.

#### Value

List:

- **global General classifier stats.**
  - Accuracy: Percentage of correctly assigned samples within all assigned samples.
  - CallRate: Percentage of samples which were assigned to a class.

- **byClass Stats by class.**
  - Sensitivity: Percentage of samples of each class which were correctly identified (Rate of true positives)
  - Specificity: Percentage of samples assigned to a given class that really belonged to the class (Rate of true negatives)
  - MCC (Matthews Correlation Coefficient): Measure which takes into account both, true and false positives and negatives. (100%: Perfect assignments) confMatrix Confussion matrix.

#### Author(s)


#### See Also

Main package function and classifier training: `geNetClassifier`
Querying the classifier: `queryGeNetClassifier`
Generating the probability matrix: `externalValidation.probMatrix`
## Classifier training

```r
# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Train a classifier or load a trained one:
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
# sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier) # Sample trained classifier
```

## External Validation:

```r
# Select the samples to query the classifier
# - External validation: samples not used for training
# testSamples <- c(1:60)[-trainSamples]

# Make a query to the classifier:
queryResult <- queryGeNetClassifier(leukemiasClassifier, leukemiasEset[,testSamples])

# Create the confusion matrix
confMatrix <- table(leukemiasEset[,testSamples]$LeukemiaType,queryResult$class)

# Calculate its accuracy, call rate, sensitivity and specificity:
externalValidation.stats(confMatrix)
```

---

### gClasses-methods

**Classes in the ranking.**

#### Description

Returns the names of the classes in a GenesRanking

#### Methods

- `signature(object = "GenesRanking")`

#### See Also

Main package function and classifier training: `geNetClassifier`
This method’s class (`GenesRanking`) help page.

#### Examples

```r
data(leukemiasClassifier)
gClasses(leukemiasClassifier@genesRanking)
```
Description

Contains the estimation of the Generalization Error and the gene stats for `geNetClassifier` executed with the given data and parameters. Calculated by 5-fold cross-validation.

Slots

- **accuracy**: "Matrix". Accuracy and call rate.
- **sensitivitySpecificity**: "Matrix". Sensitivity, Specificity, Matthews Correlation Coefficient and Call Rate for each of the classes.
- **confMatrix**: "Matrix". Confussion matrix.
- **probMatrix**: "Matrix". Probabilities of belonging to each class for the assigned samples. Helps identifying where errors are likely to occur even though there were not actual errors in the cross-validation.
- **querySummary**: "List". Stats regarding the probability and number of assigned test samples to each class.
- **classificationGenes.stats**: "List". Some basic statistics regarding the chosen genes.
- **classificationGenes.num**: "Matrix". Number of genes used for each of the 5 cross-validation classifiers.

Methods

- **overview** signature(object = "GeneralizationError"): Shows an overview of all the slots in the object.

Author(s)


See Also

Main package function and classifier training: `geNetClassifier`

Examples

```r
# Load data and train a classifier

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
```
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Train a classifier or load a trained one:
# Note: Required 'estimateGError=TRUE'
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
# sampleLabels="LeukemiaType", plotsName="leukemiasClassifier",
# estimateGError=TRUE)
data(leukemiasClassifier) # Sample trained classifier

# Global view of the returned object and its structure:
leukemiasClassifier
names(leukemiasClassifier)

#########
# Exploring the cross validation stats
# Note: Required 'estimateGError=TRUE' in geNetClassifier()
#########
# Generalization Error estimated by cross-validation:
leukemiasClassifier@generalizationError
overview(leukemiasClassifier@generalizationError)
# i.e. probabilityMatrix:
leukemiasClassifier@generalizationError@probMatrix
# i.e. statistics of the genes chosen in any of the CV loops for for AML:
leukemiasClassifier@generalizationError@classificationGenes.stats$AML

---

**genesDetails-methods**  
Details of the genes in the network.

**Description**

Information of the genes in the ranking (table format).

**Arguments**

- object: a GenesRanking
- nGenes: integer. Number of genes to show per class
- numDecimals: integer. Number of decimals to show in the numeric values
- classes: character. Classes of the genes to show
- genes: character. Genes to show

**Value**

A list containing a dataframe with the details of the genes of each class. For each gene, the following information is provided:

- ranking: Ranking of the gene.
- gERankMean: Mean rank the gene obtained in the cross-validation loops. Only available if geNetClassifier() was called with option estimateGError=TRUE (False by default).
- class: Class the gene was chosen for (the class the gene differentiates from the other classes).
postProb  Posterior probability which the gene was assigned by the expectation-maximization algorithm (emfit). Tied values are ranked based on the higher absolute value of exprsMeanDiff. Values are rounded. Several genes may look tied at posterior probability '1' but may actually be i.e. 0.999998 and 0.999997.
exprsMeanDiff  Difference between the mean expression of the gene within its class and its mean expression in the other classes.
exprsUpDw  Gene repressed (DOWN) or over-expressed (UP) for the current class (compared to the other classes).
discriminantPower  Measure calculated based on the coordinates of the support vectors. Represents the weight that the classifier gives to each gene to separate the classes.
discrPwClass  Class for which the Discriminant Power was calculated for.
isRedundant  Does the gene have a high correlation or mutual information with other genes in the list? The threshold to consider a gene redundant can be set through the arguments (by default: correlationsThreshold=0.8 and interactionsThreshold=0.5).

Methods

genesDetails(object, nGenes=NULL, numDecimals=4, classes=NULL, genes=NULL)

See Also

Main package function and classifier training: geNetClassifier
This method’s class (GenesRanking) help page.

Examples

data(leukemiasClassifier) # Sample geNetClassifier() return
options(width=200) # Optional, use in case the table rows are wrapped
genesDetails(leukemiasClassifier@classificationGenes)$CML
genesDetails(leukemiasClassifier@genesRanking, nGenes=5, numDecimals=2, classes="AML")
genesDetails(leukemiasClassifier@genesRanking, genes=c("ENSG00000096006", "ENSG00000168081","ENSG00000105699"))$CLL

Description

Contains the network returned by geNetClassifier. (Slot: @genesNetwork)

Methods

getNodes signature(object = "GenesNetwork"): Returns the network nodes (genes).
getEdges signature(object = "GenesNetwork"): Returns the network edges (relationships).
getNumNodes signature(object = "GenesNetwork"): Returns the number of nodes (genes) in the network.
getNumEdges signature(object = "GenesNetwork"): Returns the number of edges (relationships) in the network,
GenesNetwork-class

**getSubNetwork** signature(network = "GenesNetwork"): Returns a new network containing only the given genes.

**network2txt** signature(network = "GenesNetwork"): Exports the network as text file.

Author(s)


See Also

Main package function and classifier training: `geNetClassifier` Plot network or export as iGraph: `plotNetwork`

Examples

```
#####
# Load data and train a classifier
#####

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Train a classifier or load a trained one:
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
# sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier) # Sample trained classifier

#####
# Explore the returned object
#####
# Global view of the object and its structure:
names(leukemiasClassifier)

# List of Networks by classes:
leukemiasClassifier@genesNetwork

# Access to the nodes or edges of each network:
getEdges(leukemiasClassifier@genesNetwork$AML)[1:5,]
getNodes(leukemiasClassifier@genesNetwork$AML)[1:50]

#####
# Plotting
#####
# Example: Plotting the sub-network of a class classificationGenes
# Get the sub-network containing only the classification genes:
subNet <- getSubNetwork(leukemiasClassifier@genesNetwork,
                        leukemiasClassifier@classificationGenes)

# Get the classification genes' info/details:
clGenesInfo <- genesDetails(leukemiasClassifier@classificationGenes)
```
# Plot the network of the class "ALL"
plotNetwork(subNet$ALL, genesInfo=clGenesInfo,
            plotOnlyConnectedNodesNetwork=FALSE)

## GenesRanking-class

**Class "GenesRanking"**

### Description

Contains a genes ranking and the genes info calculated by `geNetClassifier`. (Slots `@classificationGenes` and `@genesRanking` from `geNetClassifier` output)

### Methods

- `genesDetails` signature(object = "GenesRanking"); Returns dataframes with information about the genes.
- `getRanking` signature(object = "GenesRanking"); Returns a matrix containing the ranked genes.
- `getTopRanking` signature(object = "GenesRanking", numGenesClass); Returns a new GenesRanking object containing only the top genes of each class.
- `gClasses` signature(object = "GenesRanking"); Returns the classes for which the genes are ranked.
- `numGenes` signature(object = "GenesRanking"); Returns the number of available ranked genes per class.
- `numSignificantGenes` signature(object = "GenesRanking"); Returns the number of significant genes per class (genes over the given posterior probability threshold).
- `plot` signature(x = "GenesRanking", y = "missing"); Plots the genes' posterior probability. Wrapper of `calculateGenesRanking`.

### Author(s)


### See Also

For more information on how the ranking is calculated and how to interpret the given information, see the package vignette.

Main package function and classifier training: `geNetClassifier`

Plot the ranking genes’s posterior probability: `plot.GenesRanking`

### Examples

```r
# Calculate a genesRanking

# Load an expressionSet:
library(leukemiasEset)
```
# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Calculate the genesRanking with calculateGenesRanking()
## Not run:
gegenesRanking <- calculateGenesRanking(leukemiasEset[, trainSamples],
  sampleLabels = "LeukemiaType", returnRanking = "full")
## End(Not run)

# geNetClassifier() also calculates a genes ranking
# Sample output:
data(leukemiasClassifier)
genesRanking <- leukemiasClassifier@genesRanking

### 1. Calculate gene scores
# Two classes:
geneScore <- matrix(sample(seq(0, 1, by = 0.01), size = 100, replace = TRUE))
colnames(geneScore) <- "BothClasses"
rownames(geneScore) <- paste("Gene", 1:100, sep = "")
More than two classes:
```
geneScore <- matrix(sample(seq(0,1,by=0.01), size=300, replace=TRUE), ncol=3)
colnames(geneScore) <- paste("Class", 1:3, sep="")
rownames(geneScore) <- paste("Gene", 1:100, sep="")

### 2. Create object
postProb <- geneScore
ord <- apply(postProb, 2, function(x) order(x, decreasing=TRUE))
numGenesClass <- apply(postProb, 2, function(x) sum(!is.na(x)))
customRanking <- new("GenesRanking", postProb=postProb, ord=ord, numGenesClass=numGenesClass)

```

# GenesRanking object ready:
customRanking
genDetails(customRanking)
customRanking$numGenesClass
numSignificantGenes(customRanking)

# geNetClassifier(..., precalcGenesRanking = customRanking)

---

geneSymbols  

*Gene symbols associated to human Ensemble IDs.*

**Description**

Gene symbols to use as gene labels in the package examples.

Source: simplified version of genes.human.annotation from GATExplorer ([http://bioinfow.dep.usal.es/xgate/mapping/mapping.php?content=annotationfiles](http://bioinfow.dep.usal.es/xgate/mapping/mapping.php?content=annotationfiles)).

**Usage**

```
data(geneSymbols)
```

**Format**

Named character vector containing the gene symbol as content, and the associated Ensemble ID as name.

**Examples**

```
data(geneSymbols)
head(geneSymbols)
```
geNetClassifier

Main function of the geNetClassifier package. Trains the multi-class SVM classifier based on the given gene expression data through transparent detection of gene markers and their associated networks.

Description

Allows to train the classifier, calculate the genes network...

Usage

geneClassifier(eset, sampleLabels, plotsName = NULL, buildClassifier = TRUE, estimateGError = FALSE, calculateNetwork = TRUE, labelsOrder = NULL, geneLabels = NULL, numGenesNetworkPlot = 100, minGenesTrain = 1, maxGenesTrain = 100, continueZeroError = FALSE, numIters = 6, lpThreshold = 0.95, numDecimals = 3, removeCorrelations = FALSE, correlationsThreshold = 0.8, correlationMethod = "pearson", removeInteractions = FALSE, interactionsThreshold = 0.5, minProbAssignCoeff = 1, minDiffAssignCoeff = 0.8, IQRfilterPercentage = 0, skipInteractions = TRUE, precalcGenesNetwork = NULL, precalcGenesRanking = NULL, returnAllGenesRanking = TRUE, verbose = TRUE)

Arguments

eset ExpressionSet or matrix. Gene expression of the train samples (positive & non-logarithmic normalized values).
sampleLabels Character. PhenoData variable (column name) containing the train samples class labels.
labelsOrder Vector or Factor. Order in which the labels should be shown in the returned results and plots.
plotsName Character. File name with which the plots should be saved. If not provided, no plots will be drawn.
buildClassifier Logical. If TRUE trains a classifier with the given samples.
estimateGError Logical. If TRUE uses cross-validation to estimate the Generalization Error of a classifier trained with the given samples.
calculateNetwork Logical. If TRUE calculates the coexpression network between the best genes.
geneLabels Vector or Matrix. Gene name, ID or label which should be shown in the returned results and plots.
numGenesNetworkPlot Integer. Number of genes to show in the coexpression network for each class.
minGenesTrain Integer. Maximum number of genes per class to train the classifier with.
maxGenesTrain Integer. Maximum number of genes per class to train the classifier with.

continueZeroError Logical. If TRUE, the program will continue testing combinations with more genes even if error 0 has been reached.

numIters Integer. Number of iterations to determine the optimum number of genes (between minGenesTrain and maxGenesTrain).

lpThreshold Numeric between 0 and 1. Required posterior probability value to consider a gene 'significant'.

removeCorrelations Logical. If TRUE, no correlated genes will be chosen to train the classifier.

correlationsThreshold Numeric between 0 and 1. Minimum Pearson’s correlation coefficient to consider genes correlated.

correlationMethod "pearson", "kendall" or "spearman". Type of correlation to calculate between genes.

removeInteractions Logical. If TRUE, genes with Mutual Information coefficient over the threshold will not be chosen to train the classifier.

interactionsThreshold Numeric between 0 and 1. Minimum Mutual Information coefficient to consider two genes equivalent.

numDecimals Integer. Number of decimals to show in the statistics.

minProbAssignCoeff Numeric. Allows modifying the required probability to assign a sample to a class in the internal crossvalidation. For details see: queryGeNetClassifier

minDiffAssignCoeff Numeric. Allows modifying the difference of probabilities required between the most likely class and second most likely class to assign a sample. For details see: queryGeNetClassifier

IQRfilterPercentage Integer. InterQuartile Range (IQR) filter applied to the initial data. Not recommended for more than two classes.

skipInteractions Logical. If TRUE, the interactions between genes are not calculated (they will not appear on the genes network). Saves some execution time. Only available if removeInteractions=FALSE.

precalcGenesNetwork GenesNetwork from a previous execution with the same expression data and parameters.

precalcGenesRanking GenesRanking from a previous execution with the same expression data and parameters.

returnAllGenesRanking Logical. If TRUE, returns the whole genes ranking. If FALSE the returned ranking contains only the significant genes (genes over lpThreshold).

verbose Logical. If TRUE, messages indicating the execution progress will be shown.
Value

A `GeNetClassifierReturn` object containing the classifier and the genes chosen to train it (`classificationGenes`), Cross-Validation statistics, the whole `GenesRanking` and each class' `GenesNetwork` (if requested). Several plots saved as `plotsName_....pdf` in the working directory.

Author(s)


References

Packages used by this function:

- **EBarrays:** `emfit` (Implements EM algorithm for gene expression mixture model) and `ebPatterns`, for calculating the gene ranking.
- **e1071:** `svm`.
- **ipred:** `kfoldcv` (computes feasible sample sizes for the k groups in k-fold cv) for the cross-validations.
- **minet** for the Mutual Information network.
- **RColorBrewer** for palettes in some of the plots.
- **igraph** for the graphical representation of the networks.

See Also

To query the classifier: `queryGeNetClassifier`

All functions in the package: `geNetClassifier-package`

Examples

```
# Load libraries and training data
```
# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

########
# Training
########

# NOTE: Training the classifier takes a while...
# Choose ONE of the followings, or modify to suit your needs:
## Not run:
# "Basic" execution: All default parameters
leukemiasClassifier <- geNetClassifier(eset=leukemiasEset[,trainSamples],
sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")

# All default parameters also estimating the classifier's Generalization Error:
# ( by default: buildClassifier=TRUE, calculateNetwork=TRUE)
# Takes longer time than the basic execution
leukemiasClassifier <- geNetClassifier(eset=leukemiasEset[,trainSamples],
sampleLabels="LeukemiaType", plotsName="leukemiasClassifier",
estimateGError=TRUE)

# Faster execution (few minutes - depending on the computer):
# By skipping the calculation of the interactions (MI) between the genes,
# and reducing the number of genes to explore when training the classifier
# (100 by default), the execution time can be slightly reduced
leukemiasClassifier <- geNetClassifier(eset=leukemiasEset[,trainSamples],
sampleLabels="LeukemiaType", plotsName="leukemiasClassifier",
skipInteractions= TRUE, maxGenesTrain=20)

# To any of these examples, you can add/remove the argument geneLabels,
# in order to show/remove the gene name in the rankings and plots:
# The argument labelsOrder allows showing the classes in a specific order
# i.e.: labelsOrder=c("ALL","CLL","AML","MCL","NoL")

save(leukemiasClassifier, file="leukemiasClassifier.RData")  # Save execution result
# For loading the saved object in the future...
# (If it doesn't find it, use getwd() to make sure you are in the right directory)
#load("leukemiasClassifier.RData")

# To avoid having to train a classifier to continue learning to use the package,
# you can load the package's pre-executed example:
data(leukemiasClassifier)
#This example classifier was trained with the following code:
data(leukemiasClassifier)
#LeukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
#    "LeukemiaType", plotsName="leukemiasClassifier", buildClassifier=TRUE,
#    estimateGError=TRUE, calculateNetwork=TRUE, geneLabels=geneSymbols)

########
GeNetClassifierReturn-class

Class "GeNetClassifierReturn"

Description

Object wich wraps all the items returned by `geNetClassifier`. It usually contains the classifier, the genes ranking and information, the network and any other requested statistics.

Methods

`names` signature(x = "GeNetClassifierReturn"): Shows the available slots in the object.

`overview` signature(object = "GeNetClassifierReturn"): Shows an overview of all the slots in the object.

Slots

Available slots deppends on the arguments used to call `geNetClassifier()`:

`call`: call. Always available.

`classifier`: list. SVM classifier. Only available if `geNetClassifier()` was called with option `buildClassifier=TRUE` (default settings).

`classificationGenes`: `GenesRanking`. Genes used to train the classifier. Only available if `geNetClassifier()` was called with option `buildClassifier=TRUE` (default settings).

`generalizationError`: `GeneralizationError`. Statistics calculated for the current training set and options. Only available if `geNetClassifier()` was called with option `estimateGError=TRUE` (False by default).

`genesRanking`: `GenesRanking`. Whole genes ranking (if `returnAllGenesRanking=TRUE`) or significant genes ranking (if `returnAllGenesRanking=FALSE`, includes only the genes with posterior probability over `lpThreshold`)
genesRankingType: character. "all", "significant" or "significantNonRedundant"

genesNetwork: List of GenesNetwork. Only available if geNetClassifier() was called with option calculateNetwork=TRUE (default settings).

genesNetworkType: character. At the moment, only "topGenes" available.

Author(s)

See Also
Main package function and classifier training: geNetClassifier plot.GeNetClassifierReturn

Examples

# Load data and train a classifier

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Train a classifier or load a trained one:
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
# sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier) # Sample trained classifier

# Explore the returned object

# Global view of the object and its structure:
leukemiasClassifier
names(leukemiasClassifier)

# Depending on the available slots:
# Call and access to the classifier:
leukemiasClassifier@call
leukemiasClassifier@classifier

# Genes used for training the classifier:
numGenes(leukemiasClassifier@classificationGenes)
leukemiasClassifier@classificationGenes
# Show de tdetails of the genes of a class
genesDetails(leukemiasClassifier@classificationGenes)$AML
# If your R console wraps the table rows, try widening your display width:
# options(width=200)
getEdges-methods

# Generalization Error estimated by cross-validation:
leukemiasClassifier@generalizationError
overview(leukemiasClassifier@generalizationError)
# i.e. probability Matrix:
leukemiasClassifier@generalizationError@probMatrix
# i.e. statistics of the genes chosen in any of the CV loops for AML:
leukemiasClassifier@generalizationError@classificationGenes.stats$AML

# List of Networks by classes:
leukemiasClassifier@genesNetwork
# Access to the nodes or edges of each network:
getEdges(leukemiasClassifier@genesNetwork$AML)
getNodes(leukemiasClassifier@genesNetwork$AML)

# Genes ranking:
leukemiasClassifier@genesRanking
# Number of available genes in the ranking:
umGenes(leukemiasClassifier@genesRanking)
# Number of significant genes
numSignificantGenes(leukemiasClassifier@genesRanking)
# Top 10 genes of CML:
genesDetails(leukemiasClassifier@genesRanking)$CML[1:10,]
# To get a sub ranking with the top 10 genes:
getTopRanking(leukemiasClassifier@genesRanking, 10)
# Genes details of the top 10 genes:
genesDetails(getTopRanking(leukemiasClassifier@genesRanking, 10))

---

getEdges-methods  Edges in the network.

Description

Returns the network’s edges (relations between genes).

Methods

signature(object = “GenesNetwork”)  

See Also

Main package function and classifier training: geNetClassifier
This method’s class (GenesNetwork) help page.

Examples

data(leukemiasClassifier)
getEdges(leukemiasClassifier@genesNetwork$AML)[1:5,]
**getNodes-methods**

*Nodes in the network.*

**Description**

Returns the network’s nodes (genes).

**Methods**

```r
signature(object = "GenesNetwork")
```

**See Also**

Main package function and classifier training: `geNetClassifier`
This method’s class (`GenesNetwork`) help page.

**Examples**

```r
data(leukemiasClassifier)
getNodes(leukemiasClassifier@genesNetwork$AML)[1:5]
```

---

**getNumEdges-methods**

*Number of edges in the network.*

**Description**

Returns the number of edges (relationships) in the network.

**Methods**

```r
signature(object = "GenesNetwork")
```

**See Also**

Main package function and classifier training: `geNetClassifier`
This method’s class (`GenesNetwork`) help page.

**Examples**

```r
data(leukemiasClassifier)
getNumEdges(leukemiasClassifier@genesNetwork$AML)
```
getNumNodes-methods

Number of nodes in the network.

Description

Returns the number of nodes (genes) in the network.

Methods

signature(object = "GenesNetwork")

See Also

Main package function and classifier training: geNetClassifier
This method's class (GenesNetwork) help page.

Examples

data(leukemiasClassifier)
getNumNodes(leukemiasClassifier@genesNetwork$AML)

getRanking-methods

Shows the genes ranking.

Description

Shows the ranking as matrix: Ranked genes by classes.

Arguments

object a GenesRanking
showGeneID boolean. If TRUE, the genes will be shown with the gene IDs used in the expressionSet. This matrix will be ...$geneID in the returned list.
showGeneLabels boolean. If TRUE, and if the ranking contains gene labels, the ranking matrix will use them. This matrix will be ...$geneLabels in the returned list.

Value

The method returns a list with one or two matrices: ...$geneLabels and ...$geneID.

See Also

Main package function and classifier training: geNetClassifier
This method’s class (GenesRanking) help page.
getSubNetwork-methods

Get a sub-network.

Description

Returns the sub-network formed by the given genes.

Usage

getSubNetwork(network, genes, showWarnings=TRUE)

Arguments

network GenesNetwork or GenesNetwork list containing the whole network.
genes GenesRanking or character vector. Genes in the new network.
showWarnings Logical. If true, shows warnings if the given genes are not in the network.

Value

A GenesNetwork or list of networks between the given genes.

See Also

Main package function and classifier training: geNetClassifier
This method’s class (GenesNetwork) help page.

Examples

data(leukemiasClassifier)
clGenesSubNet <- getSubNetwork(leukemiasClassifier@genesNetwork,
leukemiasClassifier@classificationGenes)
getSubNetwork(leukemiasClassifier@genesNetwork, getTopRanking(leukemiasClassifier@genesRanking, numGenesClass=30))
getTopRanking-methods

Gets a new ranking with the given top genes.

Description
Returns a new ranking containing only the top genes of each class.

Arguments

- object: a GenesRanking
- numGenesClass: integer. Number of genes per class.

Methods

getTopRanking(object, numGenesClass)

See Also

Main package function and classifier training: geNetClassifier
This method’s class (GenesRanking) help page.

Examples

data(leukemiasClassifier) # Sample classifier

# Sub-ranking with the top 10 genes:
getTopRanking(leukemiasClassifier@genesRanking, 10)

leukemiasClassifier Sample leukemias classifier

Description
A sample of the object returned by geNetClassifier. Contains the classifier, the network, and the gene statistics.

Usage
data(leukemiasClassifier)

Format

GeNetClassifierReturn object
Examples

data(leukemiasClassifier)
# Global view of the object and its structure:
leukemiasClassifier
names(leukemiasClassifier)

# Call and access to the classifier:
leukemiasClassifier@call
leukemiasClassifier@classifier

# Genes used for training the classifier:
numGenes(leukemiasClassifier@classificationGenes)
leukemiasClassifier@classificationGenes
genesDetails(leukemiasClassifier@classificationGenes)

# Generalization Error estimated by cross-validation:
# leukemiasClassifier@generalizationError
# overview(leukemiasClassifier@generalizationError)

# List of Networks by classes:
leukemiasClassifier@genesNetwork

# Access to the nodes or edges of each network:
getEdges(leukemiasClassifier@genesNetwork$AML)[1:5,]
getNodes(leukemiasClassifier@genesNetwork$AML)[1:50]

# Global genes ranking:
leukemiasClassifier@genesRanking
numGenes(leukemiasClassifier@genesRanking)
numSignificantGenes(leukemiasClassifier@genesRanking)
# getTopRanking(leukemiasClassifier@genesRanking, 10)

network2txt

Description
Saves the GenesNetwork as text file.

Usage

network2txt(network, filePrefix = NULL, nwClass = NULL)

Arguments

network GenesNetwork or list of GenesNetworks.
filePrefix Character. File name prefix.
wClass Character. Network class.

Value
Saves the networks as text (.txt) files. The files will be saved in the current working directory as filePrefix_className.txt.
See Also

Main package function and classifier training: geNetClassifier
This method’s class (GenesNetwork) help page.

Examples

```r
## Load or calculate a network:
data(leukemiasClassifier)

## Export as text:
network2txt(leukemiasClassifier@genesNetwork, filePrefix="leukemiasNetwork")
```

---

### numGenes-methods

**Number of genes in the genesRanking.**

**Description**

Provides the number of genes in the genesRanking.

**Methods**

```r
signature(object = "GenesRanking")
```

See Also

Main package function and classifier training: geNetClassifier
This method’s class (GenesRanking) help page.

Examples

```r
data(leukemiasClassifier)
numGenes(leukemiasClassifier@genesRanking)
```

---

### numSignificantGenes-methods

**Number of ranked genes over the posterior probability threshold.**

**Description**

Provides the number of ranked genes over the posterior probability threshold.
Arguments

object a GenesRanking
lpThreshold Posterior probability threshold
numSignificantGenesType "ranked" or "global".
Ranked will show the count of genes on the ranking of each class. Each gene will be counted only once, since it is only kept in the class for which it had better ranking.
Global counts the genes over the threshold before assigning them to a class. i.e. a gene might have 0.3 for one class, and 0.25 for another, if we are taking a threshold of 0.20, it will be counted on both classes.

Methods

numSignificantGenes(object, lpThreshold=0.95, numSignificantGenesType="ranked")

See Also

Main package function and classifier training: geNetClassifier
This method’s class (GenesRanking) help page.

Examples

data(leukemiasClassifier)
# Total number of genes in the ranking:
numGenes(leukemiasClassifier@genesRanking)
# Number of genes over the posterior probability threshold
# Default: lpThreshold=0.95, numSignificantGenesType="ranked"
numSignificantGenes(leukemiasClassifier@genesRanking)
numSignificantGenes(leukemiasClassifier@genesRanking, numSignificantGenesType="global")
numSignificantGenes(leukemiasClassifier@genesRanking, lpThreshold=0.90)
plot.GenesRanking

**See Also**

Main package function and classifier training: geNetClassifier
This method's classes help pages:
GenesRanking
GenesNetwork
GeNetClassifierReturn
GeneralizationError

**Examples**

data(leukemiasClassifier)
# geNetClassifier return:
overview(leukemiasClassifier)
# Generalization Error and stats estimated by cross-validation:
overview(leukemiasClassifier@generalizationError)
# A GenesNetwork:
# (a class has to be selected, otherwise it is a list)
overview(leukemiasClassifier@genesNetwork$ALL)

# For a GenesRanking, we recommend to use genesDetails() instead:
genesDetails(leukemiasClassifier@classificationGenes)$AML

---

**plot.GenesRanking**  

**Plot GenesRanking**

**Description**

Plots the posterior probability of the genes ordered by class ranking.

**Usage**

```r
## S3 method for class 'GenesRanking'
plot(x, y="missing", numGenesPlot=1000,
    plotTitle="Significant genes", lpThreshold = 0.95, ...)
```

**Arguments**

- `x`  
  GenesRanking.
- `numGenesPlot`  
  Numeric. Number of genes to plot.
- `plotTitle`  
  Character. Plot main title.
- `lpThreshold`  
  Numeric between 0 and 1. Required posterior probability value to consider a gene 'significant'.
- `y`  
  Not required.
- `...`  
  Not required
Details

Significant genes: Genes with posterior probability over 'lpThreshold'.
More significant genes may mean:

- Very different class
- More systemic disease

Plot lines represent the posterior probability of genes, sorted by rank from left to right.

In order to find genes that differentiate the classes from each other, the function ranks the genes based on their posterior probability for each class. The posterior probability represents how well a gene differentiates samples from a class, from samples from other classes. Therefore, Genes with high posterior probability are good to differentiate a class from all the others. This posterior probability is calculated by `emfit (pkg:EBarrays)`, an expectation-maximization (EM) algorithm for gene expression mixture model.

Value

Posterior probability plot of the top genes.

Examples

```r
# Load or calculate a ranking (or a classifier with geNetClassifier)
data(leukemiasClassifier) # Sample trained classifier, @genesRanking

# Default plot:
plot(leukemiasClassifier@genesRanking)

# Changing options:
plot(leukemiasClassifier@genesRanking,
    numGenesPlot=5000, plotTitle="Leukemias", lpThreshold=0.9)
```

Description

Allows generating the plots from the object created by `geNetClassifier`.

Usage

```r
## S3 method for class 'GeNetClassifierReturn'
plot(x, y="missing", fileName = NULL, lpThreshold = 0.95,
numGenesLpPlot = 1000, numGenesNetworkPlot = 100,
geneLabels = NULL, verbose = TRUE, ...)
```
Arguments

- **x**: GeNetClassifierReturn. Object returned by the main function "geNetClassifier".
- **fileName**: Character. File name to save the plots.
- **lpThreshold**: Numeric between 0 and 1. Required posterior probability value to consider a gene 'significant'.
- **numGenesLpPlot**: Integer. Number of genes to show in the significant genes plot.
- **numGenesNetworkPlot**: Integer. Number of genes (nodes) to plot in the network.
- **geneLabels**: Vector or Matrix. Gene name, ID or label which should be shown in the returned results and plots.
- **verbose**: Logical. If TRUE, messages indicating the execution progress will be printed on screen.
- **y**: Not required.
- **...**: Not required

Details

The plots are generated by default by **geNetClassifier**. This function allows re-plotting them with different parameters.

Value

Plots (depending on the available info):
- Significant genes
- Classification genes’ Discriminant Power
- Top ranked genes network (for each class)

See Also

Main package function and classifier training: **geNetClassifier**
Class **GeNetClassifierReturn**
Other plotting functions:
- **plotDiscriminantPower**
- **plot.GenesRanking**
- **plotNetwork**

Examples

```r
# Train or load an already trained classifier
data(leukemiasClassifier)

# Plot default plots on-screen
plot(leukemiasClassifier)

# Save plots on file
# (includes Discriminant Power of all genes, but the networks will not be interactive)
plot(leukemiasClassifier, fileName="newPlots")
```
plotAssignments  Plot assignment probabilities

Description
Plots the assignment probabilities of a previous query.

Usage
plotAssignments(queryResult, realLabels, 
minProbAssignCoeff = 1, minDiffAssignCoeff = 0.8, 
totalNumberOfClasses = NULL, pointSize=0.8, identify = FALSE)

Arguments
queryResult  Object returned by queryGeNetClassifier
realLabels  Factor. Actual/real class of the samples.
minProbAssignCoeff  Numeric. See queryGeNetClassifier for details.
minDiffAssignCoeff  Numeric. See queryGeNetClassifier for details.
totalNumberOfClasses  Numeric. Total number of classes the classifier was trained with. The assignment probability is determined based on it. It is not needed if there are samples of all the training classes.
pointSize  Numeric. Point size modifier.
identify  Logical. If TRUE and supported (X11 or quartz devices), the plot will be interactive and clicking on a point will identify the sample the point represents. Press ESC or right-click on the plot screen to exit.

Value
Plot.

See Also
Main package function and classifier training: geNetClassifier
Querying the classifier: queryGeNetClassifier

Examples
##########################
## Classifier training
##########################

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Train a classifier or load a trained one:
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
# sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier) # Sample trained classifier

######################
## External Validation:
######################
# Select the samples to query the classifier
# - External validation: samples not used for training
testSamples <- c(1:60)[-trainSamples]

# Make a query to the classifier:
queryResult <- queryGeNetClassifier(leukemiasClassifier, leukemiasEset[,testSamples])

######################
## Plot:
######################
plotAssignments(queryResult, realLabels=leukemiasEset[,testSamples]$LeukemiaType)

---

plotDiscriminantPower

Plots the genes' Discriminant Power.

Description
Calculates and plots the Discriminant Power of the genes in the given classifier.

Usage
plotDiscriminantPower(classifier, classificationGenes = NULL, geneLabels = NULL, classNames = NULL, plotDP = TRUE, fileName = NULL, returnTable = FALSE, verbose = TRUE)

Arguments

classifier  Classifier returned by geNetClassifier. (@classifier)
classificationGenes  Vector or Matrix. IDs of the genes to plot. If matrix: genes should be ordered by classes. Columns should be named after the classes.
geneLabels  Vector or Matrix. Gene name, ID or label which should be shown in the returned results and plots.
classNames  Named vector. Short version of the class names if different from the ones used to train the classifier.
plotDP  Logical. If TRUE, plots the discriminant power of the given genes.
fileName  Character. File name to save the plot with. If not provided, the plots will be shown through the standard output device.
returnTable Logical. If TRUE, returns a table with the genes discriminant power.
verbose Logical. If TRUE, messages indicating the execution progress will be printed on screen.

Details
The Discriminant Power represents the weight the (SVM) classifier gives each gene to separate the classes. It is calculated based on the coordinates of the support vectors. Genes with a high Discriminant Power are better for identifying samples from the class.

Value
- Data frame Optional. Data.frame containing the genes and their Discriminant Power.
- Discriminant Power plot Optional. Shown through the standard output device or saved in the working directory as 'fileName.pdf' if fileName was provided.

Author(s)

See Also
Main package function and classifier training: geNetClassifier

Examples
```
# Load data and train a classifier

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Train a classifier or load a trained one:
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
# sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier) # Sample trained classifier

# Discriminant Power

# Default (plots up to 20 genes)
plotDiscriminantPower(leukemiasClassifier)

# Plot a specific gene:
plotDiscriminantPower(leukemiasClassifier, classificationGenes="ENSG00000169575")
# Plot top5 genes of a class, and return their discriminant power:
# Note: The discriminant Power can only be calculated for 'classificationGenes'
# (genes chosen for training the classifier)
genes <- getRanking(leukemiasClassifier@classificationGenes,
```
plotExpressionProfiles

Expression profiles plot.

Description
Plots the expression profiles of the given genes.

Usage

plotExpressionProfiles(eset, genes=NULL, fileName=NULL, geneLabels=NULL, type="lines", sampleLabels=NULL, sampleColors=NULL, labelsOrder=NULL, classColors=NULL, sameScale=TRUE, showSampleNames=FALSE, showMean=FALSE, identify=TRUE, verbose=TRUE)

Arguments

eset         ExpressionSet or Matrix. Gene expression of the samples.
genesis      Vector or Matrix. IDs of the genes to plot.
If matrix: genes should be ordered by classes. Columns should be named after the classes. If not provided, all available genes will be plot. Warning: If a list of genes is not provided, it will plot all available genes.
fileName      Character. File name to save the plots. If not provided, up to 20 genes will be shown on screen.
geneLabels    Vector or Matrix. Gene name, ID or label which should be shown in the returned results and plots.
type          Character. Plot type: "lines" or "boxplot".
sampleLabels  Character. PhenoData variable (column name) containing the train samples class labels.
Matrix or Factor. Class labels of the train samples.
sampleColors  Character. Colors for the lines of the samples.
labelsOrder   Vector or Factor. Order in which the labels should be shown in the returned results and plots.
classColors   Character. Colors for each of the classes or samples of the class. Provide either sampleColors or classColors, not both.
sameScale     Logical. If TRUE, plots all the genes in the same expression scale.
showSampleNames Logical. If TRUE, the sample names are shown in the plot. Not recommended for big datasets.
showMean      Logical. If TRUE, plots the class expression mean.
plotExpressionProfiles

identify Logical. If TRUE and supported (X11 or quartz devices), the plot will be interactive and clicking on a point will identify the sample the point represents. Press ESC or right-click on the plot screen to exit.

verbose Logical. If TRUE, a message indicating where the pdf is saved will be printed on screen.

Value

The expression profiles plot, saved in the working directory as ‘fileName.pdf’.

Author(s)


Examples

#####
# Load libraries and expression data
#####

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

#####
# Generic expression profile plot
#####

# Plot expression of specific genes:
selectedGenes <- c("ENSG00000169575","ENSG00000078399","ENSG00000005381","ENSG00000154511")
plotExpressionProfiles(leukemiasEset, genes=selectedGenes, sampleLabels="LeukemiaType", type="boxplot")

# Color samples:
plotExpressionProfiles(leukemiasEset, genes="ENSG00000078399", sampleLabels="LeukemiaType", showMean=TRUE, identify=FALSE, sampleColors=c("grey","red"))

# Color classes:
plotExpressionProfiles(leukemiasEset, genes="ENSG00000078399", sampleLabels="LeukemiaType", showMean=TRUE, identify=TRUE, classColors=c("red","blue","red","red","red"))

#####
# Expression profiles related to a classifier
#####

# Train a classifier or load a trained one:
# summary(leukemiasEset$LeukemiaType[trainSamples])
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples], sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier) # Sample trained classifier

# Plot expression of the selected genes in the train samples:
plotNetwork

plotExpressionProfiles(leukemiasEset[,trainSamples, leukemiasClassifier, sampleLabels="LeukemiaType", fileName="leukExprs.pdf")

# Plot expression of all the genes of specific classes:
classGenes <- getRanking(leukemiasClassifier@classificationGenes, showGeneID=TRUE)$geneID[,c("CLL"), drop=FALSE] # Feel free to modify
pplotExpressionProfiles(leukemiasEset, genes=classGenes, sampleLabels="LeukemiaType", type="boxplot")

# Plot (on screen) the expression of the top ranked genes of each class
plotExpressionProfiles(leukemiasEset, leukemiasClassifier, sampleLabels="LeukemiaType")

---

plotNetwork

**Plot GenesNetwork**

**Description**

Plots the coexpression and/or mutual information network for the given genes.

**Usage**

```r
plotNetwork(genesNetwork, classificationGenes=NULL, genesRanking=NULL, genesInfo=NULL, geneLabels=NULL, returniGraphs=FALSE, plotType="dynamic", fileName=NULL, plotAllNodesNetwork=TRUE, plotOnlyConnectedNodesNetwork=FALSE, plotClassificationGenesNetwork=FALSE, labelSize=0.5, vertexSize=NULL, width=NULL, height=NULL, verbose=TRUE)
```

**Arguments**

- `genesNetwork`: List of GenesNetwork returned by `geNetClassifier`. (`@genesNetwork`)
- `classificationGenes`: Matrix or classificationGenes returned by `geNetClassifier`. (`@classificationGenes`)
- `genesRanking`: Matrix or genesRanking returned by `geNetClassifier`. (`@genesRanking`)
- `genesInfo`: List or data.frame with the properties of the genes to plot: genesDetails(_@genesRanking)
- `geneLabels`: Vector or Matrix. Gene name, ID or label which should be shown in the returned results and plots.
- `returniGraphs`: deprecated. A list with the plotted networks as igraph objects is always returned (see `invisible`), assign it to a variable if needed.
- `plotType`: Character. "dynamic": Interactive plot. "static": One canvas split for the different networks. "pdf": All the networks are saved into a pdf file.
- `fileName`: Character. File name to save the plot with. If not provided, the plots will be shown through the standard output device.
- `plotAllNodesNetwork`: Logical. If TRUE, plots a network only with all the available genes
- `plotOnlyConnectedNodesNetwork`: Logical. If TRUE, plots a network only with the connected nodes/genes
- `plotClassificationGenesNetwork`: Logical. If TRUE, plots a network only with the classification genes
plotNetwork

labelSize  Integer. Gene/node label size for static and pdf plots.
vertexSize Integer. Vertex minimum size.
width Numeric. Dynamic or pdf plot width.
height Numeric. Dynamic or pdf plot height.
verbose Logical. If TRUE, messages indicating the execution progress will be shown.

Value

Graph list List with the plotted igraph objects.
Network plots Shown through the standard output device or saved in the working directory as 'fileName.pdf' if fileName was provided.

Author(s)


References

Main package function and classifier training: geNetClassifier

Package igraph

See Also

plot.GenesNetwork() is an alias to this function. It can also be called as i.e. plotNetwork(clGenesSubNet$ALL)

Note: The slot @genesNetwork returned by geNetClassifier is a List of GenesNetworks!

Examples

data(leukemiasClassifier)

# Step 1: Select a network or sub network
# Sub-network containing only the classification genes:
clGenesSubNet <- getSubNetwork(leukemiasClassifier@genesNetwork,
    leukemiasClassifier@classificationGenes)

# Step 2: Select the details/info about the genes to plot
# Classification genes' info:
clGenesInfo <- genesDetails(leukemiasClassifier@classificationGenes)

# Step 3: Plot the network
# Network plots can be interactive or plotted as PDF file.
# - - Use plotType="pdf" to save the network as a static pdf file.
#    This option is recommended for getting an overview of several networks.
# - - To get an interactive network, just skip this argument.

# Plot ALL network:
plotNetwork(clGenesSubNet$ALL, genesInfo=clGenesInfo)

# Plot AML network containing only the connected nodes:
plotNetwork(clGenesSubNet$ALL, genesInfo=clGenesInfo,
    plotAllNodesNetwork=FALSE, plotOnlyConnectedNodesNetwork=TRUE)
queryGeNetClassifier

Queries the classifier trained with geNetClassifier.

Description

Queries the classifier trained by geNetClassifier in order to find out the class of new samples.

Usage

queryGeNetClassifier(classifier, eset, minProbAssignCoeff = 1, 
                         minDiffAssignCoeff = 0.8, verbose = TRUE)

Arguments

classifier: Classifier returned by geNetClassifier. (@classifier)
eset: ExpressionSet or Matrix. Gene expression matrix of the new samples.
minProbAssignCoeff: Numeric. Coefficient to modify the minimum probability required to assign a sample to a class. Reduce to improve call rate. Increase to reduce error. 0: Removes this restriction. The sample will always be assigned to the class with the highest probability. between 0 and 1: Reduces the required probability to assign a sample to a class. >1: Increases the required probability. Warning: if minProbCoeff is equal to 2*number of classes, all the samples will be left as 'NotAssigned'.
minDiffAssignCoeff: Numeric. Coefficient to modify the required difference between the two most likely classes. Reduce to improve call rate. Increase to reduce error. 0: Removes this restriction. The probability of the second most-likely class will not be taken into account. between 1 and 1: Reduces the required difference to assign the sample. >1: Increases the required difference. Warning: if minDiffAssignCoeff is equal to the number of classes, all the samples will be left as 'NotAssigned'.
verbose: Logical. If TRUE, messages indicating the execution progress will be printed on screen.
queryGeNetClassifier

Details

By default, in order to assign a sample two conditions must be met:

- if minProbAssignCoeff = 1 The probability of belonging to the class should be at least double of the random probability.
- if minDiffAssignCoeff = 0.8 The difference of probabilities between the most likely class and the second most likely class should be more than 80%

This means, that in a 4-class classifier, in order to assign a sample, the highest probability should be at least 0.5 (2x0.25), and the next most-likely-class should have a probability at least 0.2 (80% of 0.5). If these conditions are not met, the sample will be left as notAssigned.

Modify the arguments values in order to modify these assignment conditions. Setting minProbAssignCoeff = 0 and minDiffAssignCoeff = 0 all samples will be assigned to the most likely class without any further restrictions.

Value

List:

- call Command used to execute the function.
- classes Classes to which each of the samples were assigned to.
- probabilities Probabilities to the 2 classes each sample is most likely to belong to.

Author(s)


See Also

Main package function and classifier training: geNetClassifier
Query summary: querySummary
External validation stats: externalValidation.stats and externalValidation.probMatrix

Examples

# Classifier training

# Load an expressionSet:
library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:
# There should be the same number of samples from each class.
# summary(leukemiasEset$LeukemiaType[trainSamples])

# Train a classifier or load a trained one:
# leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
# sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier) # Sample trained classifier
querySummary

## Classifier Query

### Make a query to the classifier ("ask" about what class the new samples are):

```r
queryResult <- queryGeNetClassifier(leukemiasClassifier, leukemiasEset[,querySamples])
```

### See the class it assigned to each sample:

```r
queryResult$class[1:5]
```

### Or the samples which it wasn’t sure about:

```r
t(queryResult$probabilities[,queryResult$class=="NotAssigned"])
```

### Obtain an overview of the results

```r
querySummary(queryResult)
```

### Optional: Modify assignment conditions

```r
queryResult_AssignAll <- queryGeNetClassifier(leukemiasClassifier, leukemiasEset[,querySamples], minDiffAssignCoeff=0, minProbAssignCoeff=0)
```

### No samples are left as "NotAssigned":

```r
queryResult$probabilities[,queryResult_AssignAll$class=="NotAssigned"]
```

### External validation:

#### Confusion matrix:

```r
confMatrix <- table(leukemiasEset[,querySamples]$LeukemiaType, queryResult_AssignAll$class)
```

#### New accuracy, call rate, sensitivity and specificity:

```r
externalValidation.stats(confMatrix)
```

#### Probability matrix for the assigned samples

```r
externalValidation.probMatrix(queryResult, leukemiasEset[,querySamples]$LeukemiaType)
```

---

**querySummary**

**Summary of the query.**

**Description**

Counts the number of samples assigned to each class and calculates basic statistics regarding the assignment probabilities.

**Usage**

```r
querySummary(queryResult, showNotAssignedSamples = TRUE, numDecimals = 2, verbose = TRUE)
```

**Arguments**

- `queryResult` Object returned by `queryGeNetClassifier`
querySummary

- `showNotAssignedSamples` Logical. Shows the two most likely classes for the NotAssigned samples and the probabilities of belonging to each of them.

- `numDecimals` Integer. Number of decimals to show on the statistics.

- `verbose` Logical. If TRUE, messages indicating the execution progress will be printed on screen.

**Value**

Returns a list with the following fields:

- `callRate` Count and percentage of assigned samples.
- `assigned` Number of samples assigned to each class and mean and SD of the assignment probabilities.
- `notAssignedSamples` Optional. Most likely classes for the Not Assigned samples.

**Author(s)**


**See Also**

Main package function and classifier training: `geNetClassifier`  
Query the classifier: `queryGeNetClassifier`

**Examples**

```
# Classifier training

library(leukemiasEset)
data(leukemiasEset)

# Select the train samples:

# Train a classifier or load a trained one:
leukemiasClassifier <- geNetClassifier(leukemiasEset[,trainSamples],
sampleLabels="LeukemiaType", plotsName="leukemiasClassifier")
data(leukemiasClassifier) # Sample trained classifier

# Classifier query

# Select the samples to query the classifier
# - Real use: samples whose class we want to known
querySamples <- "GSM330154.CEL"
# - External validation: samples not used for training
querySamples <- c(1:60)[-trainSamples]

# Make a query to the classifier:
queryResult <- queryGeNetClassifier(leukemiasClassifier, leukemiasEset[,querySamples])
```
# Query Summary

# Obtain an overview of the results
querySummary(queryResult)

---

**setProperties-methods  Set properties**

---

### Description

Allows setting or modifying the GenesRanking properties.

### Methods

```r
setProperties(object, geneLabels=NULL, discriminantPower=NULL, meanDif=NULL, isRedundant=NULL, gERankMean=NULL)
```

### See Also

Main package function and classifier training: `geNetClassifier`
This method’s class (`GenesRanking`) help page.
Index

*Topic classes
  GeneralizationError-class, 10
  GenesNetwork-class, 12
  GenesRanking-class, 14
  GeNetClassifierReturn-class, 21

*Topic classif
  calculateGenesRanking, 4
  externalValidation.probMatrix, 6
  externalValidation.stats, 8
  geNetClassifier, 17
  geNetClassifier-package, 2
  leukemiasClassifier, 27
  plot.GenesRanking, 31
  plot.GeNetClassifierReturn, 32
  plotAssignments, 34
  plotDiscriminantPower, 35
  plotExpressionProfiles, 37
  plotNetwork, 39
  queryGeNetClassifier, 41
  querySummary, 43

*Topic leukemia
  leukemiasClassifier, 27

*Topic methods
  gClasses-methods, 9
  genesDetails-methods, 11
  getEdges-methods, 23
  getNumEdges-methods, 24
  getNumNodes-methods, 25
  getRanking-methods, 25
  getSubNetwork-methods, 26
  getTopRanking-methods, 27
  network2txt, 28
  numGenes-methods, 29
  numSignificantGenes-methods, 29
  overview-methods, 30
  setProperties-methods, 45

*Topic package
  geNetClassifier-package, 2

  calculateGenesRanking, 3, 4, 14

  Classification genes’ Discriminant Power, 33
plotAssignments, 3, 34
plotDiscriminantPower, 3, 33, 35
plotExpressionProfiles, 3, 37
plotGenesRanking(plot.GenesRanking), 31
plotGeNetClassifierReturn
  (plot.GeNetClassifierReturn), 32
plotGeNetClassifierReturn, GeNetClassifierReturn-method
  (plot.GeNetClassifierReturn), 32
plotNetwork, 3, 13, 33, 39
plotNetwork, GenesNetwork-method
  (plotNetwork), 39
queryGeNetClassifier, 3, 7, 8, 18, 19, 34, 41, 43, 44
querySummary, 3, 7, 42, 43
RColorBrewer, 19
setProperties(setProperties-methods), 45
setProperties, GenesRanking-method
  (setProperties-methods), 45
setProperties-methods, 45
setProperties, GenesRanking
  (setProperties-methods), 45
show, GeneralizationError-method
  (GeneralizationError-class), 10
show, GenesNetwork-method
  (GenesNetwork-class), 12
show, GenesRanking-method
  (GenesRanking-class), 14
show, GeNetClassifierReturn-method
  (GeNetClassifierReturn-class), 21
Significant genes, 33

Top ranked genes network (for each class), 33