

Package 'nlcv'

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Title Nested Loop Cross Validation

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Description

Nested loop cross validation for classification purposes for misclassification error rate estimation. The package supports several methodologies for feature selection: random forest, Student t-test, limma, and provides an interface to the following classification methods in the 'MLInterfaces' package: linear, quadratic discriminant analyses, random forest, bagging, prediction analysis for microarray, generalized linear model, support vector machine (svm and ksvm). Visualizations to assess the quality of the classifier are included: plot of the ranks of the features, scores plot for a specific classification algorithm and number of features, misclassification rate for the different number of features and classification algorithms tested and ROC plot. For further details about the methodology, please check: Markus Ruschhaupt, Wolfgang Huber, Annemarie Poustka, and Ulrich Mansmann (2004) <doi:10.2202/1544-6115.1078>.

Depends R (>= 2.10), a4Core, MLInterfaces (>= 1.22.0), xtable

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compareOrig	<i>function to compare the original matrix of correct classes to each component of the output object for a certain classifier</i>
-------------	---

Description

function to compare the original matrix of correct classes to each component of the output object for a certain classifier

Usage

```
compareOrig(nlcvObj, techn)
```

Arguments

nlcvObj	return of the <code>nlcv</code> function
techn	technique for which the comparison to correct classes should be made

Value

list with for each number of features selected, a matrix of logical values indicating whether the classifier results correspond (TRUE) or not (FALSE) to the original values to be classified

`confusionMatrix.nlcv` *compute a confusion matrix for the optimal number of features for a given technique used in the nested loop cross validation*

Description

The observed and predicted classes are cross-tabulated for a given classification technique used in the nested loop cross validation. The predicted class that is used to construct the confusion matrix is the class that was predicted most of the time ($\geq 50\%$) across all runs of the nested loop.

Usage

```
## S3 method for class 'nlcv'
confusionMatrix(x, tech, proportions = TRUE, ...)
```

Arguments

x	object for which a confusionMatrix should be produced, e.g. one produced by the <code>nlcv</code> function; for the print method, it is the object to be printed
tech	string indicating the classification technique for which the confusion matrix should be returned
proportions	logical indicating whether the cells of the matrix should contain proportions (TRUE) or raw counts (FALSE)
...	Dots argument to pass additional parameters to the confusionMatrix or print methods

Value

`confusionMatrix` produces an object of class `confusionMatrix` which directly inherits from the `ftable` class (representing the confusion matrix)

Author(s)

Willem Talloen and Tobias Verbeke

inTrainingSample *Function to define a learning sample based on balanced sampling*

Description

This function takes in a factor with class labels of the total dataset, draws a sample (balanced with respect to the different levels of the factor) and returns a logical vector indicating whether the observation is in the learning sample (TRUE) or not (FALSE).

Usage

```
inTrainingSample(y, propTraining = 2/3, classdist = c("balanced",  
  "unbalanced"))
```

Arguments

`y` factor with the class labels for the total data set

`propTraining` proportion of the data that should be in a training set; the default value is 2/3.

`classdist` distribution of classes; allows to indicate whether your distribution 'balanced' or 'unbalanced'. The sampling strategy for each run is adapted accordingly.

Value

logical vector indicating for each observation in `y` whether the observation is in the learning sample (TRUE) or not (FALSE)

Author(s)

Willem Talloen and Tobias Verbeke

Examples

```
### this example demonstrates the logic of sampling in case of unbalanced distribution of classes  
y <- factor(c(rep("A", 21), rep("B", 80)))  
  
nlcv::inTrainingSample(y, 2/3, "unbalanced")  
table(y[nlcv::inTrainingSample(y, 2/3, "unbalanced")]) # should be 14, 14 (for A, B resp.)  
table(y[!nlcv::inTrainingSample(y, 2/3, "unbalanced")]) # should be 7, 66 (for A, B resp.)
```

limmaTwoGroups	<i>Wrapper around limma for the comparison of two groups</i>
----------------	--

Description

Wrapper around limma for the comparison of two groups

Usage

```
limmaTwoGroups(object, group)
```

Arguments

object	object of class ExpressionSet
group	string indicating the variable defining the two groups to be compared

Details

Basically, the wrapper combines the lmFit, eBayes and topTable steps

Value

topTable output for the second (i.e. slope) coefficient of the linear model.

Author(s)

Tobias Verbeke

References

Smyth, G. K. (2004). Linear models and empirical Bayes methods for assessing differential expression in microarray experiments. *Statistical Applications in Genetics and Molecular Biology*, Vol. 3, No. 1, Article 3.

<http://www.bepress.com/sagmb/vol3/iss1/art3>

mcrPlot	<i>Misclassification Rate Plot</i>
---------	------------------------------------

Description

plots for each classification technique and a given number of features used the mean misclassification rate (mcr) and its standard error across all runs of the nested loop cross-validation.

Usage

```
mcrPlot(nlcvObj, plot = TRUE, optimalDots = TRUE, rescale = FALSE, layout = TRUE, ...)
```

Arguments

n1cvObj	Object of class 'n1cv' as produced by the n1cv function
plot	logical. If FALSE, nothing is plotted.
optimalDots	Boolean indicating whether dots should be displayed on a panel below the graph to mark the optimal number of features for a given classification technique
rescale	if TRUE, the upper limit of y-axis is dependent on the data (maximum mcr value); defaults to FALSE which implies limits $c(0, 1)$
layout	boolean indicating whether mcrPlot should prespecify a layout for a single plot (default, TRUE) or whether the user takes care of the layout (FALSE)
...	Dots argument to pass additional graphical parameters (such as main) to the plot function

Value

An MCR plot is output to the device of choice. The dots represent the mean MCR across runs. The vertical lines below and above the dots represent the standard deviation of the MCR values across runs.

Below the plot coloured solid dots (one for each classification technique) indicate for which number of features a given technique reached its minimum MCR.

The function invisibly returns an object of class `mcrPlot` which is a list with components:

- `meanMcrMatrix` matrix with for each number of features (rows) and classification technique (columns) the mean of the MCR values across all runs of the n1cv procedure.
- `sdMcrMatrix` matrix with for each number of features (rows) and classification technique (columns) the sd of the MCR values across all runs of the n1cv procedure.

The summary method for the `mcrPlot` object returns a matrix with for each classification technique, the optimal number of features as well as the associated mean MCR and standard deviation of the MCR values.

Author(s)

Willem Talloen and Tobias Verbeke

See Also

[n1cv](#)

 nlcv *Nested Loop Cross-Validation*

Description

This function first proceeds to a feature selection and then applies five different classification algorithms.

Usage

```
nlcv(eset, classVar = "type", nRuns = 2, propTraining = 2/3,
     classdist = c("balanced", "unbalanced"), nFeatures = c(2, 3, 5, 7, 10, 15,
     20, 25, 30, 35), fsMethod = c("randomForest", "t.test", "limma", "none"),
     classifMethods = c("dlda", "randomForest", "bagg", "pam", "svm"),
     fsPar = NULL, initialGenes = seq(length.out = nrow(eset)),
     geneID = "ID", storeTestScores = FALSE, verbose = FALSE)
```

Arguments

eset	ExpressionSet object containing the genes to classify
classVar	String giving the name of the variable containing the observed class labels, should be contained in the phenoData of eset
nRuns	Number of runs for the outer loop of the cross-validation
propTraining	Proportion of the observations to be assigned to the training set. By default propTraining = 2/3.
classdist	distribution of classes; allows to indicate whether your distribution is 'balanced' or 'unbalanced'. The sampling strategy for each run is adapted accordingly.
nFeatures	Numeric vector with the number of features to be selected from the features kept by the feature selection method. For each number n specified in this vector the classification algorithms will be run using only the top n features.
fsMethod	Feature selection method; one of "randomForest" (default), "t.test", "limma" or "none".
classifMethods	character vector with the classification methods to be used in the analysis; elements can be chosen among "dlda", "randomForest", "bagg", "pam", "svm", "glm", "lda", "nlda", "dlda", "ksvm". The first 5 methods are selected by default
fsPar	List of further parameters to pass to the feature selection method; currently the default for "randomForest" is an empty list() whereas for "t.test", one can specify the particular test to be used (the default being list(test = "f").
initialGenes	Initial subset of genes in the ExpressionSet on which to apply the nested loop cross validation procedure. By default all genes are selected.
geneID	string representing the name of the gene ID variable in the fData of the expression set to use; this argument was added for people who use e.g. both Entrez IDs and Ensemble gene IDs

storeTestScores should the test scores be stored in the nlcv object? Defaults to FALSE

verbose Should the output be verbose (TRUE) or not (FALSE).

Value

The result is an object of class 'nlcv'. It is a list with two components, output and features.

The output component is a list of five components, one for each classification algorithm used. Each of these components has as many components as there are elements in the nFeatures vector. These components contain both the error rates for each run (component errorRate) and the predicted labels for each run (character matrix labelsMat).

The features list is a list with as many components as there are runs. For each run, a named vector is given with the variable importance measure for each gene. For t test based feature selection, P-values are used; for random forest based feature selection the variable importance measure is given.

Note

The variable importance measure used is the third column of the output returned by the randomForest function.

Author(s)

Willem Talloen and Tobias Verbeke

nlcvRF_R

nlcv results on random data with random forest feature selection

Description

This data set contains the [nlcv](#) results of selection of features with random forest on a randomly generated dataset.

Usage

nlcvRF_R

Format

nlcv object

nlcvRF_SHS	<i>nlcv results on strong hetero signal data with random forest feature selection</i>
------------	---

Description

This data set contains the [nlcv](#) results of selection of features with random forest on a dataset with strong hetero signal.

Usage

nlcvRF_SHS

Format

nlcv object

nlcvRF_SS	<i>nlcv results on strong signal data a with random forest feature selection</i>
-----------	--

Description

This data set contains the [nlcv](#) results of selection of features with random forest on a dataset with strong signal.

Usage

nlcvRF_SS

Format

nlcv object

nlcvRF_WHS	<i>nlcv results on weak signal data with random forest feature selection</i>
------------	--

Description

This data set contains the [nlcv](#) results of selection of features with random forest on a weak signal dataset.

Usage

nlcvRF_WHS

Format

nlcv object

nlcvRF_WS	<i>nlcv results on weak hetero signal data with random forest feature selection</i>
-----------	---

Description

This data set contains the [nlcv](#) results of selection of features with random forest on a weak hetero signal dataset.

Usage

nlcvRF_WS

Format

nlcv object

n1cvTT_R	<i>n1cv results on random data with t-test feature selection</i>
----------	--

Description

This data set contains the [n1cv](#) results of selection of features with t-test on a randomly generated dataset.

Usage

n1cvTT_R

Format

n1cv object

n1cvTT_SHS	<i>n1cv results on strong hetero signal data with t-test feature selection</i>
------------	--

Description

This data set contains the [n1cv](#) results of selection of features with t-test on a dataset with strong hetero signal.

Usage

n1cvTT_SHS

Format

n1cv object

n1cvTT_SS	<i>n1cv results on strong signal data a with t-test feature selection</i>
-----------	---

Description

This data set contains the [n1cv](#) results of selection of features with t-test on a dataset with strong signal.

Usage

n1cvTT_SS

Format

n1cv object

n1cvTT_WHS	<i>n1cv results on weak signal data with t-test feature selection</i>
------------	---

Description

This data set contains the [n1cv](#) results of selection of features with t-test on a weak signal dataset.

Usage

n1cvTT_WHS

Format

n1cv object

n1cvTT_WS	<i>n1cv results on weak hetero signal data with t-test feature selection</i>
-----------	--

Description

This data set contains the [n1cv](#) results of selection of features with t-test on a weak hetero signal dataset.

Usage

n1cvTT_WS

Format

n1cv object

nldaI	<i>new MLInterfaces schema for lda from MASS</i>
-------	--

Description

This interface keeps track of the predictions on the training and test set, contrary to the ldaI interface that is made available in the MLInterfaces package.

Usage

nldaI

Format

An object of class learnerSchema of length 1.

Details

nldaI is an object of class 'learnerSchema' and can be used as such in calls to MLearn (from MLInterfaces).

See Also

See Also [ldaI](#)

pamrI

Instance of a learnerSchema for pamr models

Description

This object is an instance of the learnerSchema object and will be typically used as the method argument of an MLearn call.

Usage

```
pamrI
```

Format

An object of class learnerSchema of length 1.

Author(s)

Tobias Verbeke

See Also

[MLearn](#)

Examples

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
alldf <- cbind.data.frame(t(x), y)

# assure it is a factor (otherwise error message)
alldf$y <- factor(alldf$y)
library(MLInterfaces)
(mlobj <- MLearn(y ~ .,
  data = alldf,
```

```
.method = pamrI,
trainInd = 1:15))
```

pamrIconverter *convert from pamrML to classifierOutput*

Description

convert from pamrML to classifierOutput

Usage

```
pamrIconverter(obj, data, trainInd)
```

Arguments

obj	object as returned by pamrML i.e. of class pamrML
data	original data used as input for MLearn
trainInd	training indices used as input to MLearn

Value

object of class classifierOutput

pamrML *Wrapper function around the pamr.* functions*

Description

The pamrML functions are wrappers around pamr.train and pamr.predict that provide a more classical R modelling interface than the original versions.

Usage

```
pamrML(formula, data, ...)
```

Arguments

formula	model formula
data	data frame
...	argument for the pamrTrain function

Details

The name of the response variable is kept as an attribute in the pamrML object to allow for predict methods that can be easily used for writing converter functions for use in the MLInterfaces framework.

Value

For pamrML an object of class pamrML which adds an attribute to the original object returned by pamr.train (or pamrTrain).

The print method lists the names of the different components of the pamrML object.

The predict method returns a vector of predicted values

Author(s)

Tobias Verbeke

See Also

[pamr.train](#), [pamr.predict](#)

Examples

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
# for original pam
mydata <- list(x=x, y=y)
mytraindata <- list(x=x[,1:15],y=factor(y[1:15]))
mytestdata <- list(x = x[,16:20], y = factor(y[16:20]))

# for formula-based methods including pamrML
alldf <- cbind.data.frame(t(mydata$x), y)
traindf <- cbind.data.frame(t(mytraindata$x), y = mytraindata$y)
testdf <- cbind.data.frame(t(mytestdata$x), y = mytestdata$y)

### create pamrML object
pamrMLObj <- pamrML(y ~ ., traindf)
pamrMLObj

### test predict method
predict(object = pamrMLObj, newdata = testdf,
        threshold = 1) # threshold compulsory
```

pamrTrain	<i>Function providing a formula interface to pamr.train</i>
-----------	---

Description

Function that provides a classical R modelling interface, using a formula and data argument

Usage

```
pamrTrain(formula, data, ...)
```

Arguments

formula	formula
data	data frame
...	further arguments to be passed to pamr.train

Value

Object that is perfectly identical to the object returned by pamr.train

Author(s)

Tobias Verbeke

See Also

[pamr.train](#)

Examples

```
set.seed(120)
x <- matrix(rnorm(1000*20), ncol=20)
y <- sample(c(1:4), size=20, replace=TRUE)
alldf <- cbind.data.frame(t(x), y)
pamrTrain(y ~ ., alldf)
```

predict.pamrML	<i>predict pamrML object</i>
----------------	------------------------------

Description

predict pamrML object

Usage

```
## S3 method for class 'pamrML'  
predict(object, newdata, ...)
```

Arguments

object	pamrML object
newdata	new data
...	additional parameters for the pamr.predict function

Value

output of the pamr.predict function

print.nlcvConfusionMatrix	<i>print object nlcvConfusionMatrix</i>
---------------------------	---

Description

print object nlcvConfusionMatrix

Usage

```
## S3 method for class 'nlcvConfusionMatrix'  
print(x, ...)
```

Arguments

x	object of class nlcvConfusionMatrix
...	additional parameters for the print function

Value

no returned value, the object is printed in the output

`print.pamrML` *print pamrML object*

Description

print pamrML object

Usage

```
## S3 method for class 'pamrML'
print(x, ...)
```

Arguments

`x` object of class `pamrML`
`...` additional parameters for the `print` function

`print.summary.mcrPlot` *print function for summary.mcrPlot object*

Description

print function for `summary.mcrPlot` object

Usage

```
## S3 method for class 'summary.mcrPlot'
print(x, digits = 2, ...)
```

Arguments

`x` Object of class 'summary.mcrPlot' as produced by the function of the same name
`digits` number of digits to be passed to the default print method
`...` additional parameters for the `print.default` function

rankDistributionPlot *Plot the Distribution of Ranks of Features Across nlcV Runs*

Description

This plot offers an overview of the distribution of the ranks of the n best-ranked features. The order of the features is determined by the median rank of the feature across all nlcV runs.

Usage

```
rankDistributionPlot(nlcVObj, n = 5, ...)
```

Arguments

nlcVObj	object of class nlcV as produced by the nlcV function
n	number of features for which the distribution should be displayed
...	additional arguments to the boxplot functions (such as main, sub, etc.)

Value

For each of the n features, a boxplot is displayed.

Author(s)

Willem Talloen and Tobias Verbeke

Examples

```
{  
  data(nlcVRF_SS)  
  rankDistributionPlot(nlcVRF_SS, n = 9)  
}
```

rocPlot *Produce a ROC plot for a classification model belonging to a given technique and with a given number of features.*

Description

Produce a ROC plot for a classification model belonging to a given technique and with a given number of features.

Usage

```
rocPlot(nlcVObj, tech, nfeat, main = NULL, globalAUCcol = "#FF9900", ...)
```

Arguments

n1cvObj	object of class 'n1cv' as produced by the n1cv function
tech	technique; character of length one; one of 'dlda', 'lda', 'nlda', 'qda', 'glm', 'randomForest', 'bagg', 'pam', 'svm' or 'ksvm'
nfeat	number of features used in the classification model; numeric of length one
main	main title to be used for the ROC plot
globalAUCcol	color for the global AUC (defaults to '#FF9900')
...	further arguments for the plot call (such as sub e.g.)

Value

A ROC plot is drawn to the current device

Author(s)

Tobias Verbeke

scoresPlot

Function to Plot a Scores Plot

Description

Function to plot, for a given nested loop cross-validation object, a given classification technique and a given number of features used for the classification, the scores plot. This plot displays the proportion of correctly-classified per sample across all runs of the nested loop cross-validation. The class membership of the samples is displayed using a colored strip (with legend below the plot).

Usage

```
scoresPlot(n1cvObj, tech, nfeat, plot = TRUE, barPlot = FALSE,
  layout = TRUE, main = NULL, sub = NULL, ...)
```

Arguments

n1cvObj	Object of class 'n1cv' as produced by the n1cv function
tech	string denoting the classification technique used; one of 'dlda', 'bagg', 'pam', 'rf', or 'svm'.
nfeat	integer giving the number of features; this number should be part of the initial set of number of features that was specified during the nested loop cross-validation (nFeatures argument of the n1cv function)
plot	logical. If FALSE, nothing is plotted.
barPlot	Should a barplot be drawn (TRUE) or the alternative MCREstimate-type scores plot (the default, FALSE).

layout	boolean indicating whether mcrPlot should prespecify a layout for a single plot (default, TRUE) or whether the user takes care of the layout (FALSE)
main	Main title for the scores plot; if not supplied, 'Scores Plot' is used as a default
sub	Subtitle for the scores plot; if not supplied, the classification technique and the chosen number of features are displayed
...	Additional graphical parameters to pass to the plot function

Value

A scores plot is displayed (for the device specified).

The function invisibly returns a named vector containing (for each sample) the proportion of times the sample was correctly classified (for a given technique and a given number of features used).

Author(s)

Willem Talloen and Tobias Verbeke

summary.mcrPlot	summary <i>function for mcrPlot object</i>
-----------------	--

Description

summary function for mcrPlot object

Usage

```
## S3 method for class 'mcrPlot'
summary(object, ...)
```

Arguments

object	Object of class 'mcrPlot' as produced by the function of the same name
...	additional arguments, not used here

topTable-methods *Methods for topTable*

Description

Methods for topTable. topTable extracts the top n most important features for a given classification or regression procedure.

Usage

```
## S4 method for signature 'nlcv'  
topTable(fit, n = 5, method = "percentage")
```

Arguments

fit	object resulting from a classification or regression procedure
n	number of features that one wants to extract from a table that ranks all features according to their importance in the classification or regression model
method	method used to rank the features; one of percentage (percentage of runs the feature is selected in the top n), meanrank (mean rank of the feature across runs) or medianrank (median rank of the feature across runs); percentage is the default method

Details

The top n features are extracted across all runs of the nested loop cross-validation. After ranking on their frequency of selection, the top n are retained and returned.

Value

a data frame of one column (percentage) with percentages reflecting the frequency of selection of a feature in the top n across all runs; the features are sorted on decreasing frequency.

Methods

nlcv
nlcv objects are produced by nlcv

Author(s)

fit = "nlcv" Willem Talloen and Tobias Verbeke

Examples

```
data(nlcvRF_SS)  
topTable(nlcvRF_SS, n = 7, method = "medianrank")
```

xtable.confusionMatrix
xtable method for confusionMatrix objects

Description

xtable method for confusionMatrix objects

Usage

```
## S3 method for class 'confusionMatrix'  
xtable(x, caption = NULL, label = NULL,  
       align = NULL, digits = NULL, display = NULL, ...)
```

Arguments

x	object of class 'confusionMatrix' as produced by the confusionMatrix
caption	LaTeX caption, see the xtable help page
label	LaTeX label, see the xtable help page
align	alignment specification, see the xtable help page
digits	number of digits to display, see the xtable help page
display	format of the columns, see the xtable help page
...	additional arguments to be passed to xtable

Value

LaTeX table representing the confusion matrix

Author(s)

Willem Talloen and Tobias Verbeke

See Also

[confusionMatrix](#), [xtable](#)

`xtable.summary.mcrPlot`*xtable method for summary.mcrPlot objects*

Description

xtable method for summary.mcrPlot objects

Usage

```
## S3 method for class 'summary.mcrPlot'  
xtable(x, caption = NULL, label = NULL,  
       align = NULL, digits = NULL, display = NULL, ...)
```

Arguments

<code>x</code>	object of class 'summary.mcrPlot' as produced by the <code>summary.mcrPlot</code>
<code>caption</code>	LaTeX caption, see the <code>xtable</code> help page
<code>label</code>	LaTeX label, see the <code>xtable</code> help page
<code>align</code>	alignment specification, see the <code>xtable</code> help page
<code>digits</code>	number of digits to display, see the <code>xtable</code> help page
<code>display</code>	format of the columns, see the <code>xtable</code> help page
<code>...</code>	additional arguments to be passed to <code>xtable</code>

Value

LaTeX table representing the summary of the `mcrPlot` output, i.e. the optimal number of features, the mean MCR and the standard deviation on the MCR for each of the classification methods used.

Author(s)

Willem Talloen and Tobias Verbeke

See Also

[summary.mcrPlot](#), [mcrPlot](#), [xtable](#)

Examples

```
data(n1cvRF_SS)  
mp <- mcrPlot(n1cvRF_SS, plot = FALSE)  
smp <- summary(mp)  
xtable(smp)
```


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