Package ‘mlearning’

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Description A unified interface is provided to various machine learning algorithms like linear or quadratic discriminant analysis, k-nearest neighbors, random forest, support vector machine, ... It allows to train, test, and apply cross-validation using similar functions and function arguments with a minimalist and clean, formula-based interface. Missing data are processed the same way as base and stats R functions for all algorithms, both in training and testing. Confusion matrices are also provided with a rich set of metrics calculated and a few specific plots.
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mllearning-package

Machine Learning Algorithms with Unified Interface and Confusion Matrices

Description

This package provides wrappers around several existing machine learning algorithms in R, under a unified user interface. Confusion matrices can also be calculated and viewed as tables or plots. Key features are:

- Unified, formula-based interface for all algorithms, similar to stats::lm().
- Optimized code when a simplified formula y ~ . is used, meaning all variables in data are used (one of them (y here) is the class to be predicted (classification problem, a factor variable), or the dependent variable of the model (regression problem, a numeric variable).
- Similar way of dealing with missing data, both in the training set and in predictions. Underlying algorithms deal differently with missing data. Some accept them, other not.
- Unified way of dealing with factor levels that have no cases in the training set. The training succeeds, but the classifier is, of course, unable to classify items in the missing class.
- The predict() methods have similar arguments. They return the class, membership to the classes, both, or something else (probabilities, raw predictions, ...) depending on the algorithm or the problem (classification or regression).
- The cvpredict() method is available for all algorithms and it performs very easily a cross-validation, or even a leave_one_out validation (when cv.k = number of cases). It operates transparently for the end-user.
• The `confusion()` method creates a confusion matrix and the object can be printed, summarized, plotted. Various metrics are easily derived from the confusion matrix. Also, it allows to adjust prior probabilities of the classes in a classification problem, in order to obtain more representative estimates of the metrics when priors are adjusted to values closer to real proportions of classes in the data.

See `mlearning()` for further explanations and an example analysis. See `mlLda()` for examples of the different forms of the formula that can be used. See `plot.confusion()` for the different ways to explore the confusion matrix.

Important functions

• `ml_lda()`, `ml_qda()`, `ml_naive_bayes()`, `ml_knn()`, `ml_lvq()`, `ml_nnet()`, `ml_rpart()`, `ml_rforest()` and `ml_svm()` to train classifiers or regressors with the different algorithms that are supported in the package,
• `predict()` and `cvpredict()` for predictions, including using cross-validation,
• `confusion()` to calculate the confusion matrix (with various methods to analyze it and to calculate derived metrics like recall, precision, F-score, ...)
• `prior()` to adjust prior probabilities,
• `response()` and `train()` to extract response and training variables from an `mlearning` object.

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### Description

Confusion matrices compare two classifications (usually one done automatically using a machine learning algorithm versus the true classification done by a specialist... but one can also compare two automatic or two manual classifications against each other).

### Usage

```r
confusion(x, ...)  
```

```r
## Default S3 method: 
confusion(
  x,  
  y = NULL,  
  vars = c("Actual", "Predicted"),  
  labels = vars,  
  merge.by = "Id",  
  useNA = "ifany",  
  prior,  
  ...
)
```
## S3 method for class 'mlearning'
confusion(
  x,
  y = response(x),
  labels = c("Actual", "Predicted"),
  useNA = "ifany",
  prior,
  ...
)

## S3 method for class 'confusion'
print(x, sums = TRUE, error.col = sums, digits = 0, sort = "ward.D2", ...)

## S3 method for class 'confusion'
summary(object, type = "all", sort.by = "Fscore", decreasing = TRUE, ...)

## S3 method for class 'summary.confusion'
print(x, ...)

### Arguments

- **x**: an object with a confusion() method implemented.
- **...**: further arguments passed to the method.
- **y**: another object, from which to extract the second classification, or NULL if not used.
- **vars**: the variables of interest in the first and second classification in the case the objects are lists or data frames. Otherwise, this argument is ignored and x and y must be factors with same length and same levels.
- **labels**: labels to use for the two classifications. By default, they are the same as vars, or the one in the confusion matrix.
- **merge.by**: a character string with the name of variables to use to merge the two data frames, or NULL.
- **useNA**: do we keep NAs as a separate category? The default "ifany" creates this category only if there are missing values. Other possibilities are "no", or "always".
- **prior**: class frequencies to use for first classifier that is tabulated in the rows of the confusion matrix. For its value, see here under, the value= argument.
- **sums**: is the confusion matrix printed with rows and columns sums?
- **error.col**: is a column with class error for first classifier added (equivalent to false negative rate of FNR)?
- **digits**: the number of digits after the decimal point to print in the confusion matrix. The default or zero leads to most compact presentation and is suitable for frequencies, but not for relative frequencies.
- **sort**: are rows and columns of the confusion matrix sorted so that classes with larger confusion are closer together? Sorting is done using a hierarchical clustering with hclust(). The clustering method is "ward.D2" by default, but see the hclust() help for other options). If FALSE or NULL, no sorting is done.
confusion

object  a **confusion** object

type  either "all" (by default), or considering TP is the true positives, FP is the false positives, TN is the true negatives and FN is the false negatives, one can also specify: "Fscore" (F-score = F-measure = F1 score = harmonic mean of Precision and recall), "Recall" (TP / (TP + FN) = 1 - FNR), "Precision" (TP / (TP + FP) = 1 - FDR), "Specificity" (TN / (TN + FP) = 1 - FPR), "NPV" (Negative predicted value = TN / (TN + FN) = 1 - FOR), "FPR" (False positive rate = 1 - Specificity = FP / (FP + TN)), "FNR" (False negative rate = 1 - Recall = FN / (TP + FN)), "FDR" (False Discovery Rate = 1 - Precision = FP / (TP + FP)), "FOR" (False omission rate = 1 - NPV = FN / (FN + TN)), "LRPT" (Likelihood Ratio for Positive Tests = Recall / FPR = Recall / (1 - Specificity)), "LRNT" Likelihood Ratio for Negative Tests = FNR / Specificity = (1 - Recall) / Specificity, "LRPS" (Likelihood Ratio for Positive Subjects = Precision / FOR = Precision / (1 - NPV)), "LRNS" (Likelihood Ratio Negative Subjects = FDR / NPV = (1 - Precision) / (1 - FOR)), "BalAcc" (Balanced accuracy = (Sensitivity + Specificity) / 2), "MCC" (Matthews correlation coefficient), "Chisq" (Chisq metric), or "Bray" (Bray-Curtis metric)

sort.by  the statistics to use to sort the table (by default, Fmeasure, the F1 score for each class = 2 * recall * precision / (recall + precision)).

decreasing  do we sort in increasing or decreasing order?

**Value**

A confusion matrix in a **confusion** object.

**See Also**

`mlearning()`, `plot.confusion()`, `prior()`

**Examples**

```r
# Load the Glass dataset
data("Glass", package = "mlbench")
# Use a little bit more informative labels for Type
Glass$Type <- as.factor(paste("Glass", Glass$Type))
# Use learning vector quantization to classify the glass types
# (using default parameters)
summary(glass_lvq <- ml_lvq(Type ~ ., data = Glass))

# Calculate cross-validated confusion matrix
(glass_conf <- confusion(cvpredict(glass_lvq), Glass$Type))
# Raw confusion matrix: no sort and no margins
print(glass_conf, sums = FALSE, sort = FALSE)

summary(glass_conf)
summary(glass_conf, type = "Fscore")
```
mlearning

Machine learning model for (un)supervised classification or regression

Description

An mlearning object provides an unified (formula-based) interface to several machine learning algorithms. They share the same interface and very similar arguments. They conform to the formula-based approach, of say, stats::lm() in base R, but with a coherent handling of missing data and missing class levels. An optimized version exists for the simplified $y \sim \cdot$ formula. Finally, cross-validation is also built-in.

Usage

mlearning(
  formula,
  data,
  method,
  model.args,
  call = match.call(),
  ..., 
  subset,
  na.action = na.fail
)

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

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

## S3 method for class 'summary.mlearning'
print(x, ...)

## S3 method for class 'mlearning'
plot(x, y, ...)

## S3 method for class 'mlearning'
predict(
  object,
  newdata,
  type = c("class", "membership", "both"),
  method = c("direct", "cv"),
  na.action = na.exclude,
  ... 
)
cvpredict(object, ...)

## S3 method for class 'mlearning'
cvpredict(
  object,
  type = c("class", "membership", "both"),
  cv.k = 10,
  cv.strat = TRUE,
  ...
)

Arguments

formula a formula with left term being the factor variable to predict (for supervised classification), a vector of numbers (for regression) or nothing (for unsupervised classification) and the right term with the list of independent, predictive variables, separated with a plus sign. If the data frame provided contains only the dependent and independent variables, one can use the class ~ . short version (that one is strongly encouraged). Variables with minus sign are eliminated. Calculations on variables are possible according to usual formula convention (possibly protected by using I()). Supervised classification, regression or unsupervised classification are not available for all algorithms. Check respective help pages.

data a data.frame to use as a training set.

method "direct" (default) or "cv". "direct" predicts new cases in newdata= if this argument is provided, or the cases in the training set if not. Take care that not providing newdata= means that you just calculate the self-consistency of the classifier but cannot use the metrics derived from these results for the assessment of its performances. Either use a different dataset in newdata= or use the alternate cross-validation ("cv") technique. If you specify method = "cv" then cvpredict() is used and you cannot provide newdata= in that case. Other methods may be provided by the various algorithms (check their help pages)

model.args arguments for formula modeling with substituted data and subset... Not to be used by the end-user.

call the function call. Not to be used by the end-user.

... further arguments (depends on the method).

subset index vector with the cases to define the training set in use (this argument must be named, if provided).

na.action function to specify the action to be taken if NAs are found. For ml_qda() na.fail is used by default. The calculation is stopped if there is any NA in the data. Another option is na.omit, where cases with missing values on any required variable are dropped (this argument must be named, if provided). For the predict() method, the default, and most suitable option, is na.exclude. In that case, rows with NAs in newdata= are excluded from prediction, but reinserted in the final results so that the number of items is still the same (and in the same order as newdata=).
x, object  
an **mlearning** object

y  
a second **mlearning** object or nothing (not used in several plots)

newdata  
a new dataset with same conformation as the training set (same variables, except may by the class for classification or dependent variable for regression). Usually a test set, or a new dataset to be predicted.

type  
the type of prediction to return. "class" by default, the predicted classes. Other options are "membership" the membership (a number between 0 and 1) to the different classes, or "both" to return classes and memberships. Other types may be provided for some algorithms (read respective help pages).

cv.k  
k for k-fold cross-validation, cf `ipred::errorest()`. By default, 10.

cv.strat  
is the subsampling stratified or not in cross-validation, cf `ipred::errorest()`. TRUE by default.

Value  
an **mlearning** object for **mlearning()**. Methods return their own results that can be a **mlearning**, data.frame, vector, etc.

See Also  
`ml_lda()`, `ml_qda()`, `ml_naive_bayes()`, `ml_nnet()`, `ml_rpart()`, `ml_rforest()`, `ml_svm()`, `confusion()` and `prior()`. Also `ipred::errorest()` that internally computes the cross-validation in `cvpredict()`.

Examples  

```r
# mlearning() should not be called directly. Use the mlXXX() functions instead
# for instance, for Random Forest, use ml_rforest()/mlRforest()
# A typical classification involves several steps:
#
# 1) Prepare data: split into training set (2/3) and test set (1/3)
#    Data cleaning (elimination of unwanted variables), transformation of
#    others (scaling, log, ratios, numeric to factor, ...) may be necessary
#    here. Apply the same treatments on the training and test sets
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133) # Also random or stratified sampling
iris_train <- iris[train,]
iris_test <- iris[-train,]

# 2) Train the classifier, use of the simplified formula class ~ . encouraged
#    so, you may have to prepare the train/test sets to keep only relevant
#    variables and to possibly transform them before use
iris_rf <- ml_rforest(data = iris_train, Species ~ .)
iris_rf
summary(iris_rf)
train(iris_rf)
response(iris_rf)

# 3) Find optimal values for the parameters of the model
#    This is usually done iteratively. Just an example with ntree where a plot
```
# exists to help finding optimal value
plot(iris_rf)
# For such a relatively simple case, 50 trees are enough, retrain with it
iris_rf <- ml_rforest(data = iris_train, Species ~ ., ntree = 50)
summary(iris_rf)

# 4) Study the classifier performances. Several metrics and tools exists
# like ROC curves, AUC, etc. Tools provided here are the confusion matrix
# and the metrics that are calculated on it.
predict(iris_rf) # Default type is class
predict(iris_rf, type = "membership")
predict(iris_rf, type = "both")
# Confusion matrice and metrics using 10-folds cross-validation
iris_rf_conf <- confusion(iris_rf, method = "cv")
iris_rf_conf
summary(iris_rf_conf)
# Note you may want to manipulate priors too, see ?prior

# 5) Go back to step #1 and refine the process until you are happy with the
# results. Then, you can use the classifier to predict unknown items.

---

**mlKnn**  
*Supervised classification using k-nearest neighbor*

**Description**

Unified (formula-based) interface version of the k-nearest neighbor algorithm provided by `class::knn()`.

**Usage**

mlKnn(train, ...)

ml_knn(train, ...)

## S3 method for class 'formula'
mlKnn(formula, data, k.nn = 5, ..., subset, na.action)

## Default S3 method:
mlKnn(train, response, k.nn = 5, ...)

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

## S3 method for class 'summary.mlKnn'
print(x, ...)

## S3 method for class 'mlKnn'
predict(
  object,
newdata,
  type = c("class", "prob", "both"),
  method = c("direct", "cv"),
  na.action = na.exclude,
...)

Arguments

train a matrix or data frame with predictors.

... further arguments passed to the classification method or its predict() method
(not used here for now).

formula a formula with left term being the factor variable to predict and the right term
with the list of independent, predictive variables, separated with a plus sign. If
the data frame provided contains only the dependent and independent variables,
one can use the class ~ . short version (that one is strongly encouraged). Vari-
nables with minus sign are eliminated. Calculations on variables are possible
according to usual formula convention (possibly protected by using I()).

data a data.frame to use as a training set.

k.nn k used for k-NN number of neighbor considered. Default is 5.

subset index vector with the cases to define the training set in use (this argument must
be named, if provided).

na.action function to specify the action to be taken if NAs are found. For ml_knn()
na.fail is used by default. The calculation is stopped if there is any NA in
the data. Another option is na.omit, where cases with missing values on any
required variable are dropped (this argument must be named, if provided). For
the predict() method, the default, and most suitable option, is na.exclude.
In that case, rows with NAs in newdata= are excluded from prediction, but rein-
jected in the final results so that the number of items is still the same (and in the
same order as newdata=).

response a vector of factor for the classification.

x, object an mlKnn object

newdata a new dataset with same conformation as the training set (same variables, except
may by the class for classification or dependent variable for regression). Usually
a test set, or a new dataset to be predicted.

type the type of prediction to return. "class" by default, the predicted classes. Other
options are "prob" the "probability" for the different classes as assessed by the
number of neighbors of these classes, or "both" to return classes and "probabil-
ities".

method "direct" (default) or "cv". "direct" predicts new cases in newdata= if this
argument is provided, or the cases in the training set if not. Take care that not
providing newdata= means that you just calculate the self-consistency of the
classifier but cannot use the metrics derived from these results for the assess-
ment of its performances. Either use a different data set in newdata= or use the
alternate cross-validation ("cv") technique. If you specify method = "cv" then
cvpredict() is used and you cannot provide newdata= in that case.
Value

`ml_knn()` creates an `mlKnn`, `mlearning` object containing the classifier and a lot of additional metadata used by the functions and methods you can apply to it like `predict()` or `cvpredict()`. In case you want to program new functions or extract specific components, inspect the "unclassed" object using `unclass()`.

See Also

`mlearning()`, `cvpredict()`, `confusion()`, also `class::knn()` and `ipred::predict.ipredknn()` that actually do the classification.

Examples

```r
# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
iris_train <- iris[train, ]
iris_test <- iris[-train, ]
# One case with missing data in train set, and another case in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA

iris_knn <- ml_knn(data = iris_train, Species ~ .)
summary(iris_knn)
predict(iris_knn) # This object only returns classes
# Self-consistency, do not use for assessing classifier performances!
confusion(iris_knn)
# Use an independent test set instead
confusion(predict(iris_knn, newdata = iris_test), iris_test$Species)
```
mlLda(train, response, ...)  

# S3 method for class 'mlLda'
predict(
  object,
  newdata,
  type = c("class", "membership", "both", "projection"),
  prior = object$prior,
  dimension = NULL,
  method = c("plug-in", "predictive", "debiased", "cv"),
  ...
)

Arguments

train a matrix or data frame with predictors.

... further arguments passed to MASS::lda() or its predict() method (see the corresponding help page).

formula a formula with left term being the factor variable to predict and the right term with the list of independent, predictive variables, separated with a plus sign. If the data frame provided contains only the dependent and independent variables, one can use the class ~ . short version (that one is strongly encouraged). Variables with minus sign are eliminated. Calculations on variables are possible according to usual formula convention (possibly protected by using I()).

data a data.frame to use as a training set.

subset index vector with the cases to define the training set in use (this argument must be named, if provided).

na.action function to specify the action to be taken if NAs are found. For ml_1da() na.fail is used by default. The calculation is stopped if there is any NA in the data. Another option is na.omit, where cases with missing values on any required variable are dropped (this argument must be named, if provided). For the predict() method, the default, and most suitable option, is na.exclude. In that case, rows with NAs in newdata= are excluded from prediction, but reinserted in the final results so that the number of items is still the same (and in the same order as newdata=).

response a vector of factor for the classification.

object an ml.Lda object

newdata a new dataset with same conformation as the training set (same variables, except may by the class for classification or dependent variable for regression). Usually a test set, or a new dataset to be predicted.

type the type of prediction to return. "class" by default, the predicted classes. Other options are "membership" the membership (a number between 0 and 1) to the different classes, or "both" to return classes and memberships. The type = "projection" returns a projection of the individuals in the plane represented by the dimension= discriminant components.
prior the prior probabilities of class membership. By default, the prior are obtained from the object and, if they where not changed, correspond to the proportions observed in the training set.
dimension the number of the predictive space to use. If NULL (the default) a reasonable value is used. If this is less than min(p, ng-1), only the first dimension discriminant components are used (except for method = "predictive"), and only those dimensions are returned in x.
method "plug-in", "predictive", "debiased", or "cv". "plug-in" (default) the usual unbiased parameter estimates are used. With "predictive", the parameters are integrated out using a vague prior. With "debiased" an unbiased estimator of the log posterior probabilities is used. With "cv", cross-validation is used instead. If you specify method = "cv" then cvpredict() is used and you cannot provide newdata in that case.

Value

ml_lda() creates an mllda, mlearning object containing the classifier and a lot of additional metadata used by the functions and methods you can apply to it like predict() or cvpredict(). In case you want to program new functions or extract specific components, inspect the "unclassed" object using unclass().

See Also

mlearning(), cvpredict(), confusion(), also MASS::lda() that actually does the classification.

Examples

# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
iris_train <- iris[train, ]
iris_test <- iris[-train, ]
# One case with missing data in train set, and another case in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA
iris_lda <- ml_lda(data = iris_train, Species ~ .)
iris_lda
summary(iris_lda)
plot(iris_lda, col = as.numeric(response(iris_lda)) + 1)
# Prediction using a test set
predict(iris_lda, newdata = iris_test) # class (default type)
predict(iris_lda, type = "membership") # posterior probability
predict(iris_lda, type = "both") # both class and membership in a list
# Type projection
predict(iris_lda, type = "projection") # Projection on the LD axes
# Add test set items to the previous plot
points(predict(iris_lda, newdata = iris_test, type = "projection"),
       col = as.numeric(predict(iris_lda, newdata = iris_test)) + 1, pch = 19)
# predict() and confusion() should be used on a separate test set
# for unbiased estimation (or using cross-validation, bootstrap, ...)
# Wrong, cf. biased estimation (so-called, self-consistency)
confusion(iris_lda)

# Estimation using a separate test set
confusion(predict(iris_lda, newdata = iris_test), iris_test$Species)

# Another dataset (binary predictor... not optimal for lda, just for test)
data("HouseVotes84", package = "mlbench")
house_lda <- ml_lda(data = HouseVotes84, na.action = na.omit, Class ~ .)
summary(house_lda)
confusion(house_lda) # Self-consistency (biased metrics)
print(confusion(house_lda), error.col = FALSE) # Without error column

# More complex formulas
# Exclude one or more variables
iris_lda2 <- ml_lda(data = iris, Species ~ . - Sepal.Width)
summary(iris_lda2)

# With calculation
iris_lda3 <- ml_lda(data = iris, Species ~ log(Petal.Length) +
log(Petal.Width) + I(Petal.Length/Sepal.Length))
summary(iris_lda3)

# Factor levels with missing items are allowed
ir2 <- iris[-(51:100), ] # No Iris versicolor in the training set
iris_lda4 <- ml_lda(data = ir2, Species ~ .)
summary(iris_lda4) # missing class

# Missing levels are reinjected in class or membership by predict()
predict(iris_lda4, type = "both")
# ... but, of course, the classifier is wrong for Iris versicolor
confusion(predict(iris_lda4, newdata = iris), iris$Species)

# Simpler interface, but more memory-effective
iris_lda5 <- ml_lda(train = iris[, -5], response = iris$Species)
summary(iris_lda5)

---

mlLvq

**Supervised classification using learning vector quantization**

**Description**

Unified (formula-based) interface version of the learning vector quantization algorithms provided by `class::olvq1()`, `class::lvq1()`, `class::lvq2()`, and `class::lvq3()`.

**Usage**

```r
mlLvq(train, ...)

ml_lvq(train, ...)
```

## S3 method for class 'formula'

```r
mlLvq(
```
mlLvq

formula,
data,
k.nn = 5,
size,
prior,
algorithm = "olvq1",
...,subset,
na.action
}

## Default S3 method:
mlLvq(train, response, k.nn = 5, size, prior, algorithm = "olvq1", ...)

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

## S3 method for class 'summary.mlLvq'
print(x, ...)

## S3 method for class 'mlLvq'
predict(
  object,
  newdata,
  type = "class",
  method = c("direct", "cv"),
  na.action = na.exclude,
  ...
)

Arguments

train a matrix or data frame with predictors.
...
further arguments passed to the classification method or its predict() method
(not used here for now).

formula a formula with left term being the factor variable to predict and the right term
with the list of independent, predictive variables, separated with a plus sign. If
the data frame provided contains only the dependent and independent variables,
one can use the class ~ . short version (that one is strongly encouraged). Vari-
ables with minus sign are eliminated. Calculations on variables are possible
according to usual formula convention (possibly protected by using I()).

data a data.frame to use as a training set.

k.nn k used for k-NN number of neighbor considered. Default is 5.

size the size of the codebook. Defaults to min(\text{round}(0.4 \times nc \times (nc - 1 + p/2), 0), n)
where nc is the number of classes.

prior probabilities to represent classes in the codebook (default values are the propor-
tions in the training set).
algorithm
subset
na.action
response
tax,
object
newdata
type
method

Value

mlLvq() creates an mlLvq, mlearning object containing the classifier and a lot of additional metadata used by the functions and methods you can apply to it like predict() or cvpredict(). In case you want to program new functions or extract specific components, inspect the "unclassed" object using unclass().

See Also

mlearning(), cvpredict(), confusion(), also class::olvq1(), class::lvq1(), class::lvq2(), and class::lvq3() that actually do the classification.

Examples

# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
iris_train <- iris[train, ]
iris_test <- iris[-train, ]
# One case with missing data in train set, and another case in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA

iris_lvq <- ml_lvq(data = iris_train, Species ~ .)
summary(iris_lvq)
predict(iris_lvq) # This object only returns classes
#' # Self-consistency, do not use for assessing classifier performances!
confusion(iris_lvq)
# Use an independent test set instead
confusion(predict(iris_lvq, newdata = iris_test), iris_test$Species)

---

**mlNaiveBayes**

*Supervised classification using naive Bayes*

**Description**

Unified (formula-based) interface version of the naive Bayes algorithm provided by `e1071::naiveBayes()`.

**Usage**

```r
mlNaiveBayes(train, ...)
ml_naive_bayes(train, ...)
```

```
## S3 method for class 'formula'
mlNaiveBayes(formula, data, laplace = 0, ..., subset, na.action)

## Default S3 method:
mlNaiveBayes(train, response, laplace = 0, ...)

## S3 method for class 'mlNaiveBayes'
predict(
  object,
  newdata,
  type = c("class", "membership", "both"),
  method = c("direct", "cv"),
  na.action = na.exclude,
  threshold = 0.001,
  eps = 0,
  ...
)
```

**Arguments**

- `train` a matrix or data frame with predictors.
- `...` further arguments passed to the classification method or its `predict()` method (not used here for now).
formula  a formula with left term being the factor variable to predict and the right term
with the list of independent, predictive variables, separated with a plus sign. If
the data frame provided contains only the dependent and independent variables,
one can use the class ~ . short version (that one is strongly encouraged). Vari-
ables with minus sign are eliminated. Calculations on variables are possible
according to usual formula convention (possibly protected by using I()).
data   a data.frame to use as a training set.
laplace  positive number controlling Laplace smoothing for the naive Bayes classifier.
The default (0) disables Laplace smoothing.
subset  index vector with the cases to define the training set in use (this argument must
be named, if provided).
na.action  function to specify the action to be taken if NAs are found. For ml_naive_bayes()
na.fail is used by default. The calculation is stopped if there is any NA in the
data. Another option is na.omit, where cases with missing values on any re-
quired variable are dropped (this argument must be named, if provided). For
the predict() method, the default, and most suitable option, is na.exclude.
In that case, rows with NAs in newdata= are excluded from prediction, but rein-
jected in the final results so that the number of items is still the same (and in the
same order as newdata=).
response  a vector of factor with the classes.
object  an mlNaiveBayes object
newdata  a new dataset with same conformation as the training set (same variables, except
may by the class for classification or dependent variable for regression). Usually
a test set, or a new dataset to be predicted.
type  the type of prediction to return. "class" by default, the predicted classes. Other
options are "membership", the posterior probability or "both" to return classes
and memberships,
method  "direct" (default) or "cv". "direct" predicts new cases in newdata= if this
argument is provided, or the cases in the training set if not. Take care that not
providing newdata= means that you just calculate the self-consistency of the
classifier but cannot use the metrics derived from these results for the assess-
ment of its performances. Either use a different dataset in newdata= or use the
alternate cross-validation ("cv") technique. If you specify method = "cv" then
cvpredict() is used and you cannot provide newdata= in that case.
threshold  value replacing cells with probabilities within 'eps' range.
eps  number for specifying an epsilon-range to apply Laplace smoothing (to replace
zero or close-zero probabilities by 'threshold').

Value

ml_naive_bayes()/mlNaiveBayes() creates an mlNaiveBayes, mlearning object containing the
classifier and a lot of additional metadata used by the functions and methods you can apply to it
like predict() or cvpredict(). In case you want to program new functions or extract specific
components, inspect the "unclassed" object using unclass().
mlNnet

Supervised classification and regression using neural network

Description

Unified (formula-based) interface version of the single-hidden-layer neural network algorithm, possibly with skip-layer connections provided by nnet::nnet().

Usage

mlNnet(train, ...)

ml_nnet(train, ...)

## S3 method for class 'formula'
mlNnet(

See Also

mlearning(), cvpredict(), confusion(), also e1071::naiveBayes() that actually does the classification.

Examples

# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
iris_train <- iris[train, ]
iris_test <- iris[-train, ]
# One case with missing data in train set, and another case in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA

iris_nb <- ml_naive_bayes(data = iris_train, Species ~ .)
summary(iris_nb)
predict(iris_nb) # Default type is class
predict(iris_nb, type = "membership")
predict(iris_nb, type = "both")
# Self-consistency, do not use for assessing classifier performances!
confusion(iris_nb)
# Use an independent test set instead
confusion(predict(iris_nb, newdata = iris_test), iris_test$Species)

# Another dataset
data("HouseVotes84", package = "mlbench")
house_nb <- ml_naive_bayes(data = HouseVotes84, Class ~ .,
na.action = na.omit)
summary(house_nb)
confusion(house_nb) # Self-consistency
confusion(cvpredict(house_nb), na.omit(HouseVotes84)$Class)
formula,  
data,  
size = NULL,  
rang = NULL,  
decay = 0,  
maxit = 1000,  
...,  
subset,  
na.action  
)  

## Default S3 method:  
mlNnet(train, response, size = NULL, rang = NULL, decay = 0, maxit = 1000, ...)  

## S3 method for class 'mlNnet'  
predict(  
  object,  
  newdata,  
  type = c("class", "membership", "both", "raw"),  
  method = c("direct", "cv"),  
  na.action = na.exclude,  
  ...  
)  

Arguments  

train  
a matrix or data frame with predictors.  

...  
further arguments passed to nnet::nnet() that has many more parameters (see its help page).  

formula  
a formula with left term being the factor variable to predict (for supervised classification), a vector of numbers (for regression) and the right term with the list of independent, predictive variables, separated with a plus sign. If the data frame provided contains only the dependent and independent variables, one can use the class ~ . short version (that one is strongly encouraged). Variables with minus sign are eliminated. Calculations on variables are possible according to usual formula convention (possibly protected by using I()).  

data  
a data.frame to use as a training set.  

size  
number of units in the hidden layer. Can be zero if there are skip-layer units. If NULL (the default), a reasonable value is computed.  

rang  
initial random weights on [-rang, rang]. Value about 0.5 unless the inputs are large, in which case it should be chosen so that rang * max(|x|) is about 1. If NULL, a reasonable default is computed.  

decay  
parameter for weight decay. Default to 0.  

maxit  
maximum number of iterations. Default 1000 (it is 100 in nnet::nnet()).  

subset  
index vector with the cases to define the training set in use (this argument must be named, if provided).
**na.action** function to specify the action to be taken if NAs are found. For `ml_nnet()` `na.fail` is used by default. The calculation is stopped if there is any NA in the data. Another option is `na.omit`, where cases with missing values on any required variable are dropped (this argument must be named, if provided). For the `predict()` method, the default, and most suitable option, is `na.exclude`. In that case, rows with NAs in `newdata=` are excluded from prediction, but reinserted in the final results so that the number of items is still the same (and in the same order as `newdata=`).

**response** a vector of factor (classification) or numeric (regression).

**object** an `mlNnet` object

**newdata** a new dataset with same conformation as the training set (same variables, except may by the class for classification or dependent variable for regression). Usually a test set, or a new dataset to be predicted.

**type** the type of prediction to return. "class" by default, the predicted classes. Other options are "membership" the membership (number between 0 and 1) to the different classes, or "both" to return classes and memberships. Also type "raw" as non normalized result as returned by `nnet::nnet()` (useful for regression, see examples).

**method** "direct" (default) or "cv". "direct" predicts new cases in `newdata=` if this argument is provided, or the cases in the training set if not. Take care that not providing `newdata=` means that you just calculate the self-consistency of the classifier but cannot use the metrics derived from these results for the assessment of its performances. Either use a different data set in `newdata=` or use the alternate cross-validation ("cv") technique. If you specify method = "cv" then `cvpredict()` is used and you cannot provide `newdata=` in that case.

**Value**

`ml_nnet()`/`mlNnet()` creates an `mlNnet`, `mlearning` object containing the classifier and a lot of additional metadata used by the functions and methods you can apply to it like `predict()` or `cvpredict()`. In case you want to program new functions or extract specific components, inspect the "unclassed" object using `unclass()`.

**See Also**

`mlearning()`, `cvpredict()`, `confusion()`, also `nnet::nnet()` that actually does the classification.

**Examples**

```r
# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
iris_train <- iris[train, ]
iris_test <- iris[-train, ]
# One case with missing data in training set, and another case in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA
```
set.seed(689) # Useful for reproducibility, use a different value each time!
iris_nnet <- ml_nnet(data = iris_train, Species ~ .)
summary(iris_nnet)
predict(iris_nnet) # Default type is class
predict(iris_nnet, type = "membership")
predict(iris_nnet, type = "both")
# Self-consistency, do not use for assessing classifier performances!
confusion(iris_nnet)
# Use an independent test set instead
confusion(predict(iris_nnet, newdata = iris_test), iris_test$Species)

# Idem, but two classes prediction
data("HouseVotes84", package = "mlbench")
set.seed(325)
house_nnet <- ml_nnet(data = HouseVotes84, Class ~ ., na.action = na.omit)
summary(house_nnet)
# Cross-validated confusion matrix
confusion(cvpredict(house_nnet), na.omit(HouseVotes84)$Class)

# Regression
data(airquality, package = "datasets")
set.seed(74)
ozone_nnet <- ml_nnet(data = airquality, Ozone ~ ., na.action = na.omit,
  skip = TRUE, decay = 1e-3, size = 20, linout = TRUE)
summary(ozone_nnet)
plot(na.omit(airquality)$Ozone, predict(ozone_nnet, type = "raw"))
abline(a = 0, b = 1)

---

**mlQda**  
**Supervised classification using quadratic discriminant analysis**

**Description**

Unified (formula-based) interface version of the quadratic discriminant analysis algorithm provided by MASS::qda().

**Usage**

mlQda(train, ...)

ml_qda(train, ...)

# S3 method for class 'formula'
mlQda(formula, data, ..., subset, na.action)

# Default S3 method:
mlQda(train, response, ...)
## S3 method for class 'mlQda'
predict(
  object,
  newdata,
  type = c("class", "membership", "both"),
  prior = object$prior,
  method = c("plug-in", "predictive", "debiased", "looCV", "cv"),
  ...)

### Arguments

- **train**: a matrix or data frame with predictors.
- **...**: further arguments passed to `MASS::lda()` or its `predict()` method (see the corresponding help page).
- **formula**: a formula with left term being the factor variable to predict and the right term with the list of independent, predictive variables, separated with a plus sign. If the data frame provided contains only the dependent and independent variables, one can use the class ~ . short version (that one is strongly encouraged). Variables with minus sign are eliminated. Calculations on variables are possible according to usual formula convention (possibly protected by using `I()`).
- **data**: a data.frame to use as a training set.
- **subset**: index vector with the cases to define the training set in use (this argument must be named, if provided).
- **na.action**: function to specify the action to be taken if NAs are found. For `ml_qda()` `na.fail` is used by default. The calculation is stopped if there is any NA in the data. Another option is `na.omit`, where cases with missing values on any required variable are dropped (this argument must be named, if provided). For the `predict()` method, the default, and most suitable option, is `na.exclude`. In that case, rows with NAs in `newdata=` are excluded from prediction, but reinserted in the final results so that the number of items is still the same (and in the same order as `newdata=`).
- **response**: a vector of factor for the classification.
- **object**: an `mlQda` object
- **newdata**: a new dataset with same conformation as the training set (same variables, except may by the class for classification or dependent variable for regression). Usually a test set, or a new dataset to be predicted.
- **type**: the type of prediction to return. "class" by default, the predicted classes. Other options are "membership" the membership (a number between 0 and 1) to the different classes, or "both" to return classes and memberships.
- **prior**: the prior probabilities of class membership. By default, the prior are obtained from the object and, if they where not changed, correspond to the proportions observed in the training set.
- **method**: "plug-in", "predictive", "debiased", "looCV", or "cv". "plug-in" (default) the usual unbiased parameter estimates are used. With "predictive",
the parameters are integrated out using a vague prior. With "debiased", an unbiased estimator of the log posterior probabilities is used. With "looCV", the leave-one-out cross-validation fits to the original data set are computed and returned. With "cv", cross-validation is used instead. If you specify method = "cv" then cvpredict() is used and you cannot provide newdata= in that case.

Value

ml_qda() / mlQda() creates an mlQda, mlearning object containing the classifier and a lot of additional metadata used by the functions and methods you can apply to it like predict() or cvpredict(). In case you want to program new functions or extract specific components, inspect the "unclassed" object using unclass().

See Also

mlearning(), cvpredict(), confusion(), also MASS::qda() that actually does the classification.

Examples

# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
iris_train <- iris[train, ]
iris_test <- iris[-train, ]

# One case with missing data in train set, and another case in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA

iris_qda <- ml_qda(data = iris_train, Species ~ .)
summary(iris_qda)
confusion(iris_qda)
confusion(predict(iris_qda, newdata = iris_test), iris_test$Species)

# Another dataset (binary predictor... not optimal for qda, just for test)
data("HouseVotes84", package = "mlbench")
house_qda <- ml_qda(data = HouseVotes84, Class ~ ., na.action = na.omit)
summary(house_qda)
Usage

mlRforest(train, ...)
ml_rforest(train, ...)

## S3 method for class 'formula'
mlRforest(
  formula,
  data,
  ntree = 500,
  mtry,
  replace = TRUE,
  classwt = NULL,
  ..., 
  subset,
  na.action
)

## Default S3 method:
mlRforest(
  train,
  response,
  ntree = 500,
  mtry,
  replace = TRUE,
  classwt = NULL,
  ...
)

## S3 method for class 'mlRforest'
predict(
  object,
  newdata,
  type = c("class", "membership", "both", "vote"),
  method = c("direct", "oob", "cv"),
  ...
)

Arguments

train

... further arguments passed to randomForest::randomForest() or its predict() method. There are many more arguments, see the corresponding help page.

formula

a matrix or data frame with predictors.

a formula with left term being the factor variable to predict (for supervised classification), a vector of numbers (for regression) or nothing (for unsupervised classification) and the right term with the list of independent, predictive variables, separated with a plus sign. If the data frame provided contains only the dependent and independent variables, one can use the class ~. short version
Variables with minus sign are eliminated. Calculations on variables are possible according to usual formula convention (possibly protected by using I()).

data  
a data.frame to use as a training set.
nmtree  
the number of trees to generate (use a value large enough to get at least a few predictions for each input row). Default is 500 trees.
mtry  
number of variables randomly sampled as candidates at each split. Note that the default values are different for classification (sqrt(p) where p is number of variables in x) and regression (p/3)?
replace  
sample cases with or without replacement (TRUE by default)?
classwt  
priors of the classes. Need not add up to one. Ignored for regression.
subset  
index vector with the cases to define the training set in use (this argument must be named, if provided).
na.action  
function to specify the action to be taken if NAs are found. For ml_rforest() na.fail is used by default. The calculation is stopped if there is any NA in the data. Another option is na.omit, where cases with missing values on any required variable are dropped (this argument must be named, if provided). For the predict() method, the default, and most suitable option, is na.exclude. In that case, rows with NAs in newdata= are excluded from prediction, but rejected in the final results so that the number of items is still the same (and in the same order as newdata=).
response  
a vector of factor (classification) or numeric (regression), or NULL (unsupervised classification).
object  
an mlRforest object
newdata  
a new dataset with same conformation as the training set (same variables, except may by the class for classification or dependent variable for regression). Usually a test set, or a new dataset to be predicted.
type  
the type of prediction to return. "class" by default, the predicted classes. Other options are "membership" the membership (number between 0 and 1) to the different classes as assessed by the number of neighbors of these classes, or "both" to return classes and memberships. One can also use "vote", which returns the number of trees that voted for each class.
methode  
"direct" (default), "oob" or "cv". "direct" predicts new cases in newdata= if this argument is provided, or the cases in the training set if not. Take care that not providing newdata= means that you just calculate the self-consistency of the classifier but cannot use the metrics derived from these results for the assessment of its performances (in the case of Random Forest, these metrics would most certainly falsely indicate a perfect classifier). Either use a different data set in newdata= or use the alternate approaches: out-of-bag ("oob") or cross-validation ("cv"). The out-of-bag approach uses individuals that are not used to build the trees to assess performances. It is an unbiased estimates. If you specify method = "cv" then cvpredict() is used and you cannot provide newdata= in that case.
Value

`ml_rforest()` creates an **mlRforest, mlearning** object containing the classifier and a lot of additional metadata used by the functions and methods you can apply to it like `predict()` or `cvpredict()`. In case you want to program new functions or extract specific components, inspect the "unclassed" object using `unclass()`.

See Also

`mlearning()`, `cvpredict()`, `confusion()`, also `randomForest::randomForest()` that actually does the classification.

Examples

```r
# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
iris_train <- iris[train, ]
iris_test <- iris[-train, ]
# One case with missing data in train set, and another case in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA
iris_rf <- ml_rforest(data = iris_train, Species ~ .)
summary(iris_rf)
plot(iris_rf) # Useful to look at the effect of ntree=
# For such a relatively simple case, 50 trees are enough
iris_rf <- ml_rforest(data = iris_train, Species ~ ., ntree = 50)
summary(iris_rf)
predict(iris_rf) # Default type is class
predict(iris_rf, type = "membership")
predict(iris_rf, type = "both")
predict(iris_rf, type = "vote")
# Out-of-bag prediction (unbiased)
predict(iris_rf, method = "oob")
# Self-consistency (always very high for random forest, biased, do not use!)
confusion(iris_rf)
# This one is better
confusion(iris_rf, method = "oob") # Out-of-bag performances
# Cross-validation prediction is also a good choice when there is no test set
predict(iris_rf, method = "cv") # Idem: cvpredict(res)
# Cross-validation for performances estimation
confusion(iris_rf, method = "cv")
# Evaluation of performances using a separate test set
confusion(predict(iris_rf, newdata = iris_test), iris_test$Species)

# Regression using random forest (from ?randomForest)
set.seed(131) # Useful for reproducibility (use a different number each time)
ozone_rf <- ml_rforest(data = airquality, Ozone ~ ., mtry = 3,
  importance = TRUE, na.action = na.omit)
summary(ozone_rf)
# Show "importance" of variables: higher value mean more important variables
round(randomForest::importance(ozone_rf), 2)
```
mlRpart

Supervised classification and regression using recursive partitioning

Description

Unified (formula-based) interface version of the recursive partitioning algorithm as implemented in \texttt{rpart::rpart()}.  

Usage

\begin{verbatim}
mlRpart(train, ...)  
ml_rpart(train, ...)  
## S3 method for class 'formula'
mlRpart(formula, data, ..., subset, na.action)

## Default S3 method:
mlRpart(train, response, ..., .args. = NULL)

## S3 method for class 'mlRpart'
predict(
  object,
  newdata,
  type = c("class", "membership", "both"),
  method = c("direct", "cv"),
  ...
)
\end{verbatim}

Arguments

- \texttt{train} a matrix or data frame with predictors.
- \texttt{...} further arguments passed to \texttt{rpart::rpart()} or its \texttt{predict()} method (see the corresponding help page.)
formula

A formula with left term being the factor variable to predict (for supervised classification), a vector of numbers (for regression) and the right term with the list of independent, predictive variables, separated with a plus sign. If the data frame provided contains only the dependent and independent variables, one can use the class formula with a short version (that one is strongly encouraged). Variables with minus sign are eliminated. Calculations on variables are possible according to usual formula convention (possibly protected by using I()).

data

A data.frame to use as a training set.

subset

Index vector with the cases to define the training set in use (this argument must be named, if provided).

na.action

Function to specify the action to be taken if NAs are found. For ml_rpart() na.fail is used by default. The calculation is stopped if there is any NA in the data. Another option is na.omit, where cases with missing values on any required variable are dropped (this argument must be named, if provided). For the predict() method, the default, and most suitable option, is na.exclude. In that case, rows with NAs in newdata= are excluded from prediction, but reinserted in the final results so that the number of items is still the same (and in the same order as newdata=).

response

A vector of factor (classification) or numeric (regression).

.args.

Used internally, do not provide anything here.

object

An mlRpart object.

newdata

A new dataset with same conformation as the training set (same variables, except may by the class for classification or dependent variable for regression). Usually a test set, or a new dataset to be predicted.

type

The type of prediction to return. "class" by default, the predicted classes. Other options are "membership" the membership (number between 0 and 1) to the different classes, or "both" to return classes and memberships.

method

"direct" (default) or "cv". "direct" predicts new cases in newdata= if this argument is provided, or the cases in the training set if not. Take care that not providing newdata= means that you just calculate the self-consistency of the classifier but cannot use the metrics derived from these results for the assessment of its performances. Either use a different data set in newdata= or use the alternate cross-validation ("cv") technique. If you specify method = "cv" then cvpredict() is used and you cannot provide newdata= in that case.

Value

ml_rpart()mlRpart() creates an mlRpart, mlearning object containing the classifier and a lot of additional metadata used by the functions and methods you can apply to it like predict() or cvpredict(). In case you want to program new functions or extract specific components, inspect the "unclassed" object using unclass().

See Also

mlearning(), cvpredict(), confusion(), also rpart::rpart() that actually does the classification.
Examples

# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
iris_train <- iris[train, ]
iris_test <- iris[-train, ]
# One case with missing data in train set, and another case in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA

iris_rpart <- ml_rpart(data = iris_train, Species ~ .)
summary(iris_rpart)
# Plot the decision tree for this classifier
plot(iris_rpart, margin = 0.03, uniform = TRUE)
text(iris_rpart, use.n = FALSE)
# Predictions
predict(iris_rpart) # Default type is class
predict(iris_rpart, type = "membership")
predict(iris_rpart, type = "both")
# Self-consistency, do not use for assessing classifier performances!
confusion(iris_rpart)
# Cross-validation prediction is a good choice when there is no test set
predict(iris_rpart, method = "cv") # Idem: cvpredict(res)
confusion(iris_rpart, method = "cv")
# Evaluation of performances using a separate test set
confusion(predict(iris_rpart, newdata = iris_test), iris_test$Species)

mlSvm

Supervised classification and regression using support vector machine

Description

Unified (formula-based) interface version of the support vector machine algorithm provided by e1071::svm().

Usage

mlSvm(train, ...)
ml_svm(train, ...)

## S3 method for class 'formula'
mlSvm(
  formula,
  data,
  scale = TRUE,
  type = NULL,
  kernel = "radial",
)
classwt = NULL,
..., 
subset, 
n.a.action 
)

## Default S3 method:
mlSvm(
  train, 
  response, 
  scale = TRUE, 
  type = NULL, 
  kernel = "radial", 
  classwt = NULL, 
  ...
)

## S3 method for class 'mlSvm'
predict(
  object, 
  newdata, 
  type = c("class", "membership", "both"), 
  method = c("direct", "cv"), 
  na.action = na.exclude, 
  ...
)

Arguments

train a matrix or data frame with predictors.
...

further arguments passed to the classification or regression method. See e1071::svm().

formula a formula with left term being the factor variable to predict (for supervised classification), a vector of numbers (for regression) or nothing (for unsupervised classification) and the right term with the list of independent, predictive variables, separated with a plus sign. If the data frame provided contains only the dependent and independent variables, one can use the \texttt{class ~ .} short version (that one is strongly encouraged). Variables with minus sign are eliminated. Calculations on variables are possible according to usual formula convention (possibly protected by using \texttt{I()}).

data a data.frame to use as a training set.

scale are the variables scaled (so that mean = 0 and standard deviation = 1)? \texttt{TRUE} by default. If a vector is provided, it is applied to variables with recycling.

type For \texttt{ml_svm()}/\texttt{mlSvm()}, the type of classification or regression machine to use. The default value of \texttt{NULL} uses \texttt{"C-classification"} if response variable is factor and \texttt{eps-regression} if it is numeric. It can also be \texttt{"nu-classification"} or \texttt{"nu-regression"}. The \texttt{"C"} and \texttt{"nu"} versions are basically the same but with a different parameterisation. The range of \texttt{C} is from zero to infinity, while the
range for nu is from zero to one. A fifth option is "one-classification" that is specific to novelty detection (find the items that are different from the rest). For predict(), the type of prediction to return. "class" by default, the predicted classes. Other options are "membership" the membership (number between 0 and 1) to the different classes, or "both" to return classes and memberships.

**kernel**
the kernel used by svm, see `e1071::svm()` for further explanations. Can be "radial", "linear", "polynomial" or "sigmoid".

**classwt**
priors of the classes. Need not add up to one.

**subset**
index vector with the cases to define the training set in use (this argument must be named, if provided).

**na.action**
function to specify the action to be taken if NAs are found. For `ml_svm()` `na.fail` is used by default. The calculation is stopped if there is any NA in the data. Another option is `na.omit`, where cases with missing values on any required variable are dropped (this argument must be named, if provided). For the `predict()` method, the default, and most suitable option, is `na.exclude`. In that case, rows with NAs in `newdata=` are excluded from prediction, but reinserted in the final results so that the number of items is still the same (and in the same order as `newdata=`).

**response**
a vector of factor (classification) or numeric (regression).

**object**
an `mlSvm` object

**newdata**
a new dataset with same conformation as the training set (same variables, except may by the class for classification or dependent variable for regression). Usually a test set, or a new dataset to be predicted.

**method**
"direct" (default) or "cv". "direct" predicts new cases in `newdata=` if this argument is provided, or the cases in the training set if not. Take care that not providing `newdata=` means that you just calculate the self-consistency of the classifier but cannot use the metrics derived from these results for the assessment of its performances. Either use a different data set in `newdata=` or use the alternate cross-validation ("cv") technique. If you specify `method = "cv"` then `cvpredict()` is used and you cannot provide `newdata=` in that case.

### Value

`ml_svm()`/`mlSvm()` creates an `mlSvm`, `mlearning` object containing the classifier and a lot of additional metadata used by the functions and methods you can apply to it like `predict()` or `cvpredict()`. In case you want to program new functions or extract specific components, inspect the "unclassed" object using `unclass()`.

### See Also

`mlearning()`, `cvpredict()`, `confusion()`, also `e1071::svm()` that actually does the calculation.

### Examples

```r
# Prepare data: split into training set (2/3) and test set (1/3)
data("iris", package = "datasets")
train <- c(1:34, 51:83, 101:133)
```
iris_train <- iris[train,]
iris_test <- iris[-train,]
# One case with missing data in train set, and another in test set
iris_train[1, 1] <- NA
iris_test[25, 2] <- NA

iris_svm <- ml_svm(data = iris_train, Species ~ .)
summary(iris_svm)
predict(iris_svm) # Default type is class
predict(iris_svm, type = "membership")
predict(iris_svm, type = "both")
# Self-consistency, do not use for assessing classifier performances!
confusion(iris_svm)
# Use an independent test set instead
confusion(predict(iris_svm, newdata = iris_test), iris_test$Species)

# Another dataset
data("HouseVotes84", package = "mlbench")
house_svm <- ml_svm(data = HouseVotes84, Class ~ ., na.action = na.omit)
summary(house_svm)
# Cross-validated confusion matrix
confusion(cvpredict(house_svm), na.omit(HouseVotes84)$Class)

# Regression using support vector machine
data(airquality, package = "datasets")
ozone_svm <- ml_svm(data = airquality, Ozone ~ ., na.action = na.omit)
summary(ozone_svm)
plot(na.omit(airquality)$Ozone, predict(ozone_svm))
abline(a = 0, b = 1)

---

**plot.confusion**  
*Plot a confusion matrix*

**Description**

Several graphical representations of `confusion` objects are possible: an image of the matrix with colored squares, a barplot comparing recall and precision, a stars plot also comparing two metrics, possibly also comparing two different classifiers of the same dataset, or a dendrogram grouping the classes relative to the errors observed in the confusion matrix (classes with more errors are pooled together more rapidly).

**Usage**

```r
## S3 method for class 'confusion'
plot(  
  x,  
  y = NULL,
  type = c("image", "barplot", "stars", "dendrogram"),
  stat1 = "Recall",
```
stat2 = "Precision",
names,
...
)

confusion_image(
  x,
  y = NULL,
  labels = names(dimnames(x)),
  sort = "ward.D2",
  numbers = TRUE,
  digits = 0,
  mar = c(3.1, 10.1, 3.1, 3.1),
  cex = 1,
  asp = 1,
  colfun,
  ncols = 41,
  col0 = FALSE,
  grid.col = "gray",
  ...
)

confusionImage(
  x,
  y = NULL,
  labels = names(dimnames(x)),
  sort = "ward.D2",
  numbers = TRUE,
  digits = 0,
  mar = c(3.1, 10.1, 3.1, 3.1),
  cex = 1,
  asp = 1,
  colfun,
  ncols = 41,
  col0 = FALSE,
  grid.col = "gray",
  ...
)

confusion_barplot(
  x,
  y = NULL,
  col = c("PeachPuff2", "green3", "lemonChiffon2"),
  mar = c(1.1, 8.1, 4.1, 2.1),
  cex = 1,
  cex.axis = cex,
  cex.legend = cex,
  main = "F-score (precision versus recall)",

numbers = TRUE,
min.width = 17,
...
)

confusion_barplot(
  x,
  y = NULL,
  col = c("PeachPuff2", "green3", "lemonChiffon2"),
  mar = c(1.1, 8.1, 4.1, 2.1),
  cex = 1,
  cex.axis = cex,
  cex.legend = cex,
  main = "F-score (precision versus recall)",
  numbers = TRUE,
  min.width = 17,
  ...
)

confusion_stars(
  x,
  y = NULL,
  stat1 = "Recall",
  stat2 = "Precision",
  names,
  main,
  col = c("green2", "blue2", "green4", "blue4"),
  ...
)

confusion_stars(
  x,
  y = NULL,
  stat1 = "Recall",
  stat2 = "Precision",
  names,
  main,
  col = c("green2", "blue2", "green4", "blue4"),
  ...
)

confusion_dendrogram(
  x,
  y = NULL,
  labels = rownames(x),
  sort = "ward.D2",
  main = "Groups clustering",
  ...
confusionDendrogram(
  x,
  y = NULL,
  labels = rownames(x),
  sort = "ward.D2",
  main = "Groups clustering",
  ...
)

Arguments

x a confusion object
y NULL (not used), or a second confusion object when two different classifications
are compared in the plot ("stars" type).
type the kind of plot to produce ("image", the default, or "barplot", "stars", 
dendrogram").
stat1 the first metric to plot for the "stars" type (Recall by default).
stat2 the second metric to plot for the "stars" type (Precision by default).
names names of the two classifiers to compare
... further arguments passed to the function. It can be all arguments or the corre-
sponding plot.
labels labels to use for the two classifications. By default, they are the same as vars, 
or the one in the confusion matrix.
sort are rows and columns of the confusion matrix sorted so that classes with larger 
confusion are closer together? Sorting is done using a hierarchical clustering 
with hclust(). The clustering method is "ward.D2" by default, but see the 
hclust() help for other options). If FALSE or NULL, no sorting is done.
numbers are actual numbers indicated in the confusion matrix image?
digits the number of digits after the decimal point to print in the confusion matrix. The
default or zero leads to most compact presentation and is suitable for frequen-
cies, but not for relative frequencies.
mar graph margins.
cex text magnification factor.
asp graph aspect ratio. There is little reasons to change the default value of 1.
colfun a function that calculates a series of colors, like e.g., cm.colors() that accepts 
one argument being the number of colors to be generated.
ncols the number of colors to generate. It should preferably be 2 * number of levels 
+ 1, where levels is the number of frequencies you want to evidence in the plot. 
Default to 41.
cole should null values be colored or not (no, by default)?
grid.col color to use for grid lines, or NULL for not drawing grid lines.
prior

col  color(s) to use for the plot.
cex.axis  idem for axes. If NULL, the axis is not drawn.
cex.legend  idem for legend text. If NULL, no legend is added.
main  main title of the plot.
min.width  minimum bar width required to add numbers.

Value

Data calculate to create the plots are returned invisibly. These functions are mostly used for their side-effect of producing a plot.

Examples

data("Glass", package = "mlbench")
# Use a little bit more informative labels for Type
Glass$Type <- as.factor(paste("Glass", Glass$Type))

# Use learning vector quantization to classify the glass types
# (using default parameters)
summary(glass_lvq <- ml_lvq(Type ~ ., data = Glass))

# Calculate cross-validated confusion matrix and plot it in different ways
(glass_conf <- confusion(cvpredict(glass_lvq), Glass$Type))
# Raw confusion matrix: no sort and no margins
print(glass_conf, sums = FALSE, sort = FALSE)
# Plots
plot(glass_conf) # Image by default
plot(glass_conf, sort = FALSE) # No sorting
plot(glass_conf, type = "barplot")
plot(glass_conf, type = "stars")
plot(glass_conf, type = "dendrogram")

# Build another classifier and make a comparison
summary(glass_naive_bayes <- ml_naive_bayes(Type ~ ., data = Glass))
(glass_conf2 <- confusion(cvpredict(glass_naive_bayes), Glass$Type))

# Comparison plot for two classifiers
plot(glass_conf, glass_conf2)

prior  Get or set priors on a confusion matrix

Description

Most metrics in supervised classifications are sensitive to the relative proportion of the items in the different classes. When a confusion matrix is calculated on a test set, it uses the proportions observed on that test set. If they are representative of the proportions in the population, metrics are not biased. When it is not the case, priors of a confusion object can be adjusted to better reflect proportions that are supposed to be observed in the different classes in order to get more accurate metrics.
Usage

prior(object, ...)

## S3 method for class 'confusion'
prior(object, ...)

prior(object, ...) <- value

## S3 replacement method for class 'confusion'
prior(object, ...) <- value

Arguments

- object: a confusion object (or another class if a method is implemented)
- ...: further arguments passed to methods
- value: a (named) vector of positive numbers of zeros of the same length as the number of classes in the confusion object. It can also be a single >= 0 number and in this case, equal probabilities are applied to all the classes (use 1 for relative frequencies and 100 for relative frequencies in percent). If the value has zero length or is NULL, original prior probabilities (from the test set) are used. If the vector is named, names must correspond to existing class names in the confusion object.

Value

prior() returns the current class frequencies associated with the first classification tabulated in the confusion object, i.e., for rows in the confusion matrix.

See Also

confusion()

Examples

data("Glass", package = "mlbench")
# Use a little bit more informative labels for Type
Glass$Type <- as.factor(paste("Glass", Glass$Type))
# Use learning vector quantization to classify the glass types
# (using default parameters)
summary(glass_lvq <- ml_lvq(Type ~ ., data = Glass))

# Calculate cross-validated confusion matrix
(glass_conf <- confusion(cvpredict(glass_lvq), Glass$Type))

# When the probabilities in each class do not match the proportions in the training set, all these calculations are useless. Having an idea of the real proportions (so-called, priors), one should first reweight the confusion matrix before calculating statistics, for instance:
prior1 <- c(10, 10, 10, 100, 100, 100) # Glass types 1-3 are rare
prior(glass_conf) <- prior1

glass_conf
response

summary(glass_conf, type = c("Fscore", "Recall", "Precision"))

# This is very different than if glass types 1-3 are abundants!
prior2 <- c(100, 100, 100, 10, 10, 10) # Glass types 1-3 are abundants
prior(glass_conf) <- prior2
glass_conf
summary(glass_conf, type = c("Fscore", "Recall", "Precision"))

# Weight can also be used to construct a matrix of relative frequencies
# In this case, all rows sum to one
prior(glass_conf) <- 1
print(glass_conf, digits = 2)
# However, it is easier to work with relative frequencies in percent
# and one gets a more compact presentation
prior(glass_conf) <- 100
glass_conf

# To reset row class frequencies to original proportions, just assign NULL
prior(glass_conf) <- NULL
glass_conf
prior(glass_conf)

response  

Get the response variable for a mlearning object

Description

The response is either the class to be predicted for a classification problem (and it is a factor), or
the dependent variable in a regression model (and it is numeric in that case). For unsupervised
classification, response is not provided and should return NULL.

Usage

response(object, ...)

## Default S3 method:
response(object, ...)

Arguments

object an object having a response variable.

... further parameter (depends on the method).

Value

The response variable of the training set, or NULL for unsupervised classification.

See Also

mlearning(), train(), confusion()
Examples

```r
data("HouseVotes84", package = "mlbench")
house_rf <- ml_rforest(data = HouseVotes84, Class ~ .)
house_rf
response(house_rf)
```

---

**train**  
*Get the training variable for a mlearning object*

**Description**

The training variables (train) are the variables used to train a classifier, excepted the prediction (class or dependent variable).

**Usage**

```r
train(object, ...)
```

```r
## Default S3 method:
train(object, ...)
```

**Arguments**

- `object`  
a object having a train attribute.
- `...`  
further parameter (depends on the method).

**Value**

A data frame containing the training variables of the model.

**See Also**

- `mlearning()`, `response()`, `confusion()`

**Examples**

```r
data("HouseVotes84", package = "mlbench")
house_rf <- ml_rforest(data = HouseVotes84, Class ~ .)
house_rf
response(house_rf)
```
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