

# *MLInterfaces*: towards uniform behavior of machine learning tools in R

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## 1 Introduction

We define machine learning methods as data based algorithms for prediction. Given data  $D$ , a generic machine learning procedure  $MLP$  produces a function  $ML = MLP(D)$ . For data  $D'$  with structure comparable to  $D$ ,  $ML(D')$  is a set of predictions about elements of  $D'$ .

To be slightly more precise, a dataset  $D$  is a set of records. Each record has the same structure, consisting of a set of features (predictors) and one or more predictands (classes or responses of interest, to be predicted).  $MLP$  uses features, predictands, and tuning parameter settings to construct the function  $ML$ .  $ML$  is to be a function from features only to predictands.

There are many packages and functions in R that provide machine learning procedures. They conform to the abstract setup described above, but with great diversity in the details of implementation and use. The input requirements and the output objects differ from procedure to procedure.

Our objective in *MLInterfaces* is to simplify the use and evaluation of machine learning methods by providing specifications and implementations for a uniform interface. (The `tune` procedures in *e1071* also pursue more uniform interface to machine learning procedures.) At present, we want to simplify use of machine learning with microarray data, assumed to take the form of `ExpressionSets`. The present implementation addresses the following concerns:

- simplify the selection of the predictand from `ExpressionSet` structure;
- simplify (in fact, require) decomposition of input data into training and test set, with output emphasizing test set results;
- provide a uniform output structure.

The output structures currently supported are subclasses of a general class *MLOutput*, described in Section ?? below.

To give a flavor of the current implementation, we perform a few runs with different machine learning tools. We will use 60 genes drawn arbitrarily from Golub's data.

```
> library(MLInterfaces)
> library(golubEsets)

> data(Golub_Merge)
> smallG <- Golub_Merge[200:259, ]
> smallG
```

```
ExpressionSet (storageMode: lockedEnvironment)
assayData: 60 features, 72 samples
  element names: exprs
phenoData
  sampleNames: 39, 40, ..., 33 (72 total)
  varLabels and varMetadata description:
    Samples: Sample index
    ALL.AML: Factor, indicating ALL or AML
    ...: ...
    Source: Source of sample
    (11 total)
featureData
  featureNames: D13627_at, D13628_at, ..., D16469_at (60 total)
  fvarLabels and fvarMetadata description: none
experimentData: use 'experimentData(object)'
  pubMedIds: 10521349
Annotation: hu6800
```

Here is how  $k$ -nearest neighbors is used to get predictions of ALL status, using the first 40 records as the training set:

```
> krun = MLearn(ALL.AML ~ ., smallG, knnI(k = 1), 1:40)
> krun
```

MLInterfaces classification output container

The call was:

```
MLearn(formula = formula, data = data, method = method, trainInd = trainInd)
```

Predicted outcome distribution for test set:

ALL AML

22 10

Summary of scores on test set (use testScores() method for details):

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1	1	1	1	1	1

The `confuMat` method computes the confusion matrix resulting from applying the trained model to the reserved test data:

```
> confuMat(krun)
```

```
      predicted
given ALL AML
  ALL  18   3
  AML   4   7
```

Additional parameters can be supplied as accepted by the target procedure in package *class*. To use a neural net in the same context (with fewer genes to simplify the summary below)

```
> set.seed(1234)
> nns <- MLearn(ALL.AML ~ ., smallG[1:10, ], nnetI, trainInd = 1:40,
+   size = 2, decay = 0.01, maxit = 250)
```

```
# weights:  25
initial  value 27.327352
iter  10 value 25.018790
iter  20 value 21.799662
iter  30 value 19.267441
iter  40 value 15.211472
iter  50 value 12.903478
iter  60 value 10.147235
iter  70 value  8.259017
iter  80 value  7.842199
iter  90 value  7.108711
iter 100 value  6.831116
iter 110 value  6.824352
iter 120 value  6.822548
iter 130 value  6.799872
iter 140 value  6.780290
iter 150 value  6.778714
iter 160 value  6.778414
iter 170 value  6.778372
iter 180 value  6.778349
iter 190 value  6.778342
iter 190 value  6.778342
iter 190 value  6.778342
final  value  6.778342
converged
```

```

> nns

MLInterfaces classification output container
The call was:
MLearn(formula = formula, data = data, method = method, trainInd = trainInd,
       size = 2, decay = 0.01, maxit = 250)
Predicted outcome distribution for test set:

ALL AML
 24   8
Summary of scores on test set (use testScores() method for details):
[1] 0.2689501

> confuMat(nns)

      predicted
given ALL AML
  ALL  18   3
  AML   6   5

```

## 2 Usage

The basic call sequence for supervised learning for `ExpressionSets` is

```
MLearn(formula, data, learnerSchema, trainInd, ...)
```

The parameter `formula` is a standard R formula, with `y~xz+` indicating that `x` and `\verbz+` are predictors of response `y`. If `data` is a `data.frame` instance, then the formula has the usual interpretation for R. If `data` is an `ExpressionSet` instance, then it is assumed that the dependent variable is present in the `pData` component of `phenoData`, and the variables on the RHS are found in the `exprs` component of `assayData`. If `.` is used on the RHS, then all features in the `exprs` component are used as predictors. The `learnerSchema` parameter is bound by instances of the `learnerSchema` class. Many examples are provided with `MLInterfaces`, see the page from `help(MLearn)` for a complete list. Parameter `trainInd` is a numeric sequence isolating the samples to be used for training; it may also be bound by an instance of `xvalSpec` to define a cross-validation of a learning process (see section ??).

For unsupervised learning, there are a number of methods of the form

```
methB(eset, k, height, ...)
```

The idea here is that one may specify a number `k` of clusters, or a height of a clustering tree that will be cut to form clusters from the `eset` samples. Note that there is no training/test dichotomy for clustering at this stage.

The `RObject` method will access the fit object from the basic procedure. Thus, returning to the `nnetB` invocation above, we have

```
> summary(RObject(nns))
```

```
a 10-2-1 network with 25 weights
```

```
options were - entropy fitting decay=0.01
```

```

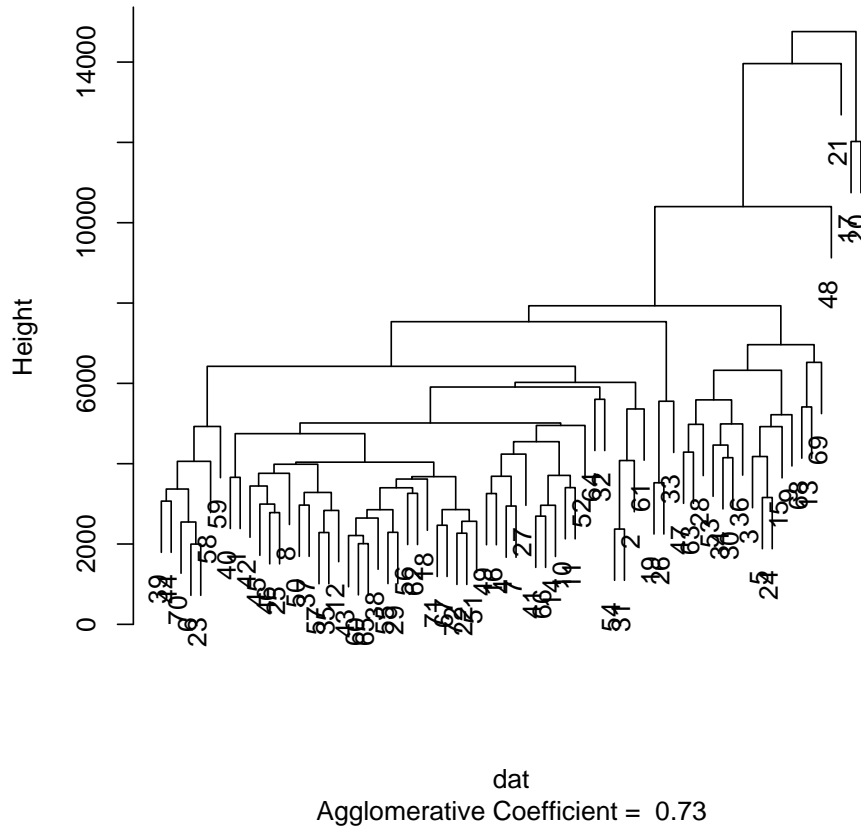
  b->h1  i1->h1  i2->h1  i3->h1  i4->h1  i5->h1  i6->h1  i7->h1  i8->h1  i9->h1
    0.00    0.02   -0.17    0.07    0.03   -0.02   -0.05   -0.06   -0.07    0.01
i10->h1
    0.00
  b->h2  i1->h2  i2->h2  i3->h2  i4->h2  i5->h2  i6->h2  i7->h2  i8->h2  i9->h2
    0.00   -0.10    0.12   -0.10    0.16    0.08    0.21    0.00   -0.10    0.00
i10->h2
    0.02
  b->o h1->o h2->o
0.59 -3.64  5.94
```

which is the customary `nnet` summary. This also gives access to visualization.

```
> ags <- agnesB(smallG, k = 4, height = 0, stand = FALSE)
```

```
> plot(RObject(ags), which.plot = 2)
```

```
am of cluster::agnes(x = dat, metric = metric, stand = stand, meth
Dendrogram of keep.diss = keep.diss, keep.data = keep.dat:
```



### 3 Classes

For input to MLearn, to define the procedure to be used, two major classes are defined: learnerSchema, and xvalSpec.

```
> getClass("learnerSchema")
```

Slots:

```
Name:  packageName  mlFunName  converter
Class:  character    character   function
```

Known Subclasses: "nonstandardLearnerSchema"

```
> getClass("xvalSpec")
```

Slots:

Name:	type	niter	partitionFunc	fsFun
Class:	character	numeric	function	function

For output, we have only the classifierOutput class:

```
> getClass("classifierOutput")
```

Slots:

Name:	testOutcomes	testPredictions	testScores	trainOutcomes
Class:	factor	factor	ANY	factor

Name:	trainPredictions	trainScores	fsHistory	RObject
Class:	factor	ANY	list	ANY

Name:	call
Class:	call

Some legacy classes for output structures exist but are too complex and will be abandoned after a deprecation cycle. The clustOutput class will be replaced by a clusteringOutput class:

```
> getClass("clustOutput")
```

Slots:

Name:	clustIndices	clustScores	method	RObject	call
Class:	MLLabel	MLScore	character	ANY	call

Name:	distMat
Class:	dist

Extends: "MLOutput"

## 4 Cross-validation

Instances of the xvalSpec class are bound to the trainInd parameter of MLearn to perform cross-validation. The constructor `xvalSpec` can be used in line. It has parameters `type` (only relevant to select "LOO", for leave-one out), `niter` (number of partitions to use), `partitionFunc` (function that returns indices of members of partitions), `fsFunc` (function that performs feature selection and returns a formula with selected features on right-hand side).

The `partitionFunc` must take parameters `data`, `clab`, `iternum`. `data` is the usual data frame to be supplied to the learner function. `clab` must be the name of a column in `data`. Values of the variable in that column are balanced across cross-validation partitions. `iternum` is used to select the partition elements as we iterate through cross validation.

- straight leave-one-out (LOO) – note the group parameter must be integer; it is irrelevant for the LOO method.

```
> library(golubEsets)
> data(Golub_Merge)
> smallG <- Golub_Merge[200:250, ]
> lk1 <- MLearn(ALL.AML ~ ., smallG, knnI(k = 1, l = 0), xvalSpec("LOO"))
> confuMat(lk1)
```

```
      predicted
given AML ALL
  ALL   10   37
  AML   15   10
```

- Now do a random 8-fold cross-validation.

```
> ranpart = function(K, data) {
+   N = nrow(data)
+   cu = as.numeric(cut(1:N, K))
+   sample(cu, size = N, replace = FALSE)
+ }
> ranPartition = function(K) function(data, clab, iternum) {
+   p = ranpart(K, data)
+   which(p == iternum)
+ }
> lkran <- MLearn(ALL.AML ~ ., smallG, knnI(k = 1, l = 0), xvalSpec("LOG",
+   8, partitionFunc = ranPartition(8)))
> confuMat(lkran)
```

```
      predicted
given ALL AML
  ALL   25   22
  AML    7   18
```

- Now do an 8-fold cross-validation with approximate balance among groups with respect to frequency of ALL and AML. The utility function `balKfold.xvspec` helps for this.

```
> lk3 <- MLearn(ALL.AML ~ ., smallG, knnI(k = 1, l = 0), xvalSpec("LOG",
+      8, partitionFunc = balkfold.xvspec(8)))
> confuMat(lk3)
```

```
      predicted
given ALL AML
  ALL   39    8
  AML    8   17
```

## 5 Cross validation with feature selection

Stephen Henderson of UC London supplied infrastructure to allow embedding of feature selection in the cross-validation process. See the manual page on `xval` for more details.

```
> t.fun <- function(data, fac) {
+   require(genefilter)
+   xd <- matrix(as.double(exprs(data)), nrow = nrow(exprs(data)))
+   return(abs(rowttests(xd, pData(data)[[fac]], tstatOnly = FALSE)$statistic))
+ }
> lk3f <- xval(smallG, "ALL.AML", knnB, xvalMethod = "LOO", 0:0,
+   fsFun = t.fun)
> table(lk3f$out, smallG$ALL.AML)
```

```
      ALL AML
ALL   41   12
AML    6   13
```

## 6 A sketch of a ‘doubt’ computation

The `nnet` function returns a structure encoding predicted probabilities of class occupancy. We will use this to enrich the `MLearn/nnetI` output to include a “doubt” outcome. As written this code will handle a two-class outcome; additional structure emerges with more than two classes and some changes will be needed for such cases.

First we obtain the predicted probabilities (for the test set) and round these for display purposes.

```
> predProb <- round(testScores(nns), 3)
```

We save the true labels and the predicted labels.

```
> truth <- as.character(smallG$ALL.AML[-c(1:40)])
> simpPred <- as.character(testPredictions(nns))
```

We create a closure that allows boundaries of class probabilities to be specified for assertion of “doubt”:

```
> douClo <- function(pprob) function(lo, hi) pprob > lo & pprob <
+      hi
```

Evaluate the closure on the predicted probabilities, yielding a function of two arguments (lo, hi).

```
> smallDou <- douClo(predProb)
```

Now replace the labels for those predictions that are very close to .5.

```
> douPred <- simpPred
> douPred[smallDou(0.48, 0.52)] <- "doubt"
```

The resulting modified predictions are in the fourth column:

```
> mm <- cbind(predProb, truth, simpPred, douPred)
> mm
```

		truth	simpPred	douPred
7	"0.643"	"ALL"	"AML"	"AML"
8	"0.045"	"ALL"	"ALL"	"ALL"
9	"0.045"	"ALL"	"ALL"	"ALL"
10	"0.045"	"ALL"	"ALL"	"ALL"
11	"0.045"	"ALL"	"ALL"	"ALL"
12	"0.936"	"ALL"	"AML"	"AML"
13	"0.045"	"ALL"	"ALL"	"ALL"
14	"0.045"	"ALL"	"ALL"	"ALL"
15	"0.045"	"ALL"	"ALL"	"ALL"
16	"0.045"	"ALL"	"ALL"	"ALL"
17	"0.999"	"ALL"	"AML"	"AML"
18	"0.045"	"ALL"	"ALL"	"ALL"
19	"0.045"	"ALL"	"ALL"	"ALL"
20	"0.045"	"ALL"	"ALL"	"ALL"
21	"0.045"	"ALL"	"ALL"	"ALL"
22	"0.045"	"ALL"	"ALL"	"ALL"
23	"0.045"	"ALL"	"ALL"	"ALL"
24	"0.045"	"ALL"	"ALL"	"ALL"
25	"0.045"	"ALL"	"ALL"	"ALL"
26	"0.045"	"ALL"	"ALL"	"ALL"
27	"0.045"	"ALL"	"ALL"	"ALL"
34	"0.999"	"AML"	"AML"	"AML"
35	"0.999"	"AML"	"AML"	"AML"

```

36 "0.045" "AML" "ALL" "ALL"
37 "0.045" "AML" "ALL" "ALL"
38 "0.045" "AML" "ALL" "ALL"
28 "0.045" "AML" "ALL" "ALL"
29 "0.045" "AML" "ALL" "ALL"
30 "0.045" "AML" "ALL" "ALL"
31 "0.999" "AML" "AML" "AML"
32 "0.999" "AML" "AML" "AML"
33 "0.947" "AML" "AML" "AML"

```

```
> table(mm[, "truth"], mm[, "simpPred"])
```

	ALL	AML
ALL	18	3
AML	6	5

```
> table(mm[, "truth"], mm[, "douPred"])
```

	ALL	AML
ALL	18	3
AML	6	5