Chapter 15 Improving Model Performance

We already explored several alternative machine learning (ML) methods for prediction, classification, clustering, and outcome forecasting. In many situations, we derive models by estimating model coefficients or parameters. The main question now is How can we adopt the advantages of crowdsourcing and biosocial networking to aggregate different predictive analytics strategies? Are there reasons to believe that such ensembles of forecasting methods may actually improve the performance (e.g., increase prediction accuracy) of the resulting consensus metaalgorithm? In this chapter, we are going to introduce ways that we can search for optimal parameters for a single ML method, as well as aggregate different methods into ensembles to enhance their collective performance relative to any of the individual methods part of the meta-aggregate.

After we summarize the core methods, we will present automated and customized parameter tuning, and show strategies for improving model performance based on meta-learning via bagging and boosting.

15.1 Improving Model Performance by Parameter Tuning

One of the methods for improving model performance relies on tuning, which is the process of searching for the best parameters for a specific method. Table [15.1](#page-1-0) summarizes the parameters for each method we covered in previous chapters.

15.2 Using caret for Automated Parameter Tuning

In Chap. [7,](https://doi.org/10.1007/978-3-319-72347-1_7) we used KNN and plugged in random k parameters for the number of clusters. This time, we will test multiple k values simultaneously and pick the one with the highest accuracy. When using the caret package, we need to specify a

Model	Learning task	Method	Parameters	
KNN	Classification	class:: knn	data, k	
K-Means	Classification	stats:: kmeans	data, k	
Naïve Bayes	Classification	e1071: naiveBayes	train, class, laplace	
Decision Trees	Classification	C50::C5.0	train, class, trials, costs	
OneR Rule Learner	Classification	RWeka::OneR	class~predictors, data	
RIPPER Rule Learner	Classification	RWeka:: JRip	formula, data, subset, na.action, control, options	
Linear Regression	Regression	stats:lm	formula, data, subset, weights, na.action, method	
Regression Trees	Regression	rpart:: rpart	dep var ~ indep var, data	
Model Trees	Regression	RWeka:: M5P	formula, data, subset, na.action, control	
Neural Networks	Dual use	n net \ldots nnet	x, y, weights, size, Wts, mask, linout, entropy, softmax, censored, skip, rang, decay, maxit, Hess, trace, MaxNWts, abstol, reltol	
Support Vector Machines (Poly- nomial Kernel)	Dual use	caret:train: svmLinear	\mathcal{C}	
Support Vector Machines (Radial Basis Kernel)	Dual use	caret::train:: svmRadial	C, sigma	
Support Vector Machines (general)	Dual use	kernlab:: ksvm	formula, data, kernel	
Random Forests	Dual use	randomForest:: randomForest	formula, data	

Table 15.1 Synopsis of the basic prediction, classification and clustering methods and their core parameters

class variable, a dataset containing a class variable, predicting features, and the method we will be using. In Chap. [7,](https://doi.org/10.1007/978-3-319-72347-1_7) we used the Boys Town Study of Youth Development dataset, normalized all the features, stored them in boystown_n, and formulated the outcome class variable first (boystown\$grade).

```
str(boystown_n)
## 'data.frame': 200 obs. of 10 variables:
## $ sex : num 0 0 0 0 1 1 0 0 1 1 ...
## $ gpa : num 1 0 0.6 0.4 0.6 0.6 0.2 1 0.2 0.6 ...
## $ Alcoholuse: num 0.182 0.364 0.182 0.182 0.545 ...
## $ alcatt : num 0.5 0.333 0.5 0.167 0.333 ...
## $ dadjob : num 1 1 1 1 1 1 1 1 1 1 ...
## $ momjob : num 0 0 0 0 1 0 0 0 1 1 ...
## $ dadclose : num 0.143 0.429 0.286 0.143 0.286 ...
## $ momclose : num 0.143 0.571 0.286 0.286 0.143 ...
## $ larceny : num 0.25 0 0 0.75 0.25 0 0 0 0.25 0.25 ...
## $ vandalism : num 0.429 0 0.286 0.286 0.286 ...
boystown_n<-cbind(boystown_n, boystown[, 11])
str(boystown_n)
## 'data.frame': 200 obs. of 11 variables:
## $ sex : num 0 0 0 0 1 1 0 0 1 1 ...
                 ## $ gpa : num 1 0 0.6 0.4 0.6 0.6 0.2 1 0.2 0.6 ...
## $ Alcoholuse : num 0.182 0.364 0.182 0.182 0.545 ...
## $ alcatt : num 0.5 0.333 0.5 0.167 0.333 ...
## $ dadjob : num 1 1 1 1 1 1 1 1 1 1 ...
   ## $ momjob : num 0 0 0 0 1 0 0 0 1 1 ...
## $ dadclose : num 0.143 0.429 0.286 0.143 0.286 ...
## $ momclose : num 0.143 0.571 0.286 0.286 0.143 ...
## $ larceny : num 0.25 0 0 0.75 0.25 0 0 0 0.25 0.25 ...
## $ vandalism : num 0.429 0 0.286 0.286 0.286 ...
## $ boystown[, 11]: Factor w/ 2 levels "above_avg","avg_or_below": 2 1 2 1
2 2 1 2 1 2 ...
```

```
colnames(boystown_n)[11]<-"grade"
```
The dataset including a specific class variable and predictive features is now successfully created. We are using the KNN method as an example with the class variable grade. So, we plug this information into the caret::train() function. Note that caret is using the full dataset because it will automatically do the random sampling for us. To make the results reproducible, we utilize the set. seed () function that we previously used, see Chap. [14.](https://doi.org/10.1007/978-3-319-72347-1_14)

```
library(caret)
set.seed(123)
m<-train(grade~., data=boystown_n, method="knn")
m; summary(m)
## k-Nearest Neighbors
## 
## 200 samples
## 10 predictor
## 2 classes: 'above_avg', 'avg_or_below' 
## 
## No pre-processing
## Resampling: Bootstrapped (25 reps) 
## Summary of sample sizes: 200, 200, 200, 200, 200, 200, ... 
## Resampling results across tuning parameters:
##
```

```
## k Accuracy Kappa 
## 5 0.7952617 0.5193402
## 7 0.8143626 0.5585191
## 9 0.8070520 0.5348281
## 
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was k = 7.
## Length Class Mode 
## learn 2 -none- list 
## k 1 -none- numeric
## theDots 0 -none- list 
## xNames 10 -none- character
## problemType 1 -none- character
## tuneValue 1 data.frame list 
## obsLevels 2 -none- character
```
In this case, using $str(m)$ to summarize the object m may report out too much information. Instead, we can simply type the object name m to get more concise information about it.

- 1. Description about the dataset: number of samples, features, and classes.
- 2. Re-sampling process: here, we use 25 bootstrap samples with 200 observations (same size as the observed dataset) each to train the model.
- 3. Candidate models with different parameters that have been evaluated: by default, caret uses 3 different choices for each parameter, but for binary parameters, it only allows two choices, TRUE and FALSE). As KNN has only one parameter k , we have three candidate models reported in the output above.
- 4. Optimal model: the model with largest accuracy is the one corresponding to $k=5$.

Let's see how accurate this "optimal model" is in terms of the re-substitution error. Again, we will use the predict () function specifying the object m and the dataset boystown_n. Then, we can report the contingency table showing the agreement between the predictions and real class labels.

```
set.seed(1234)
p<-predict(m, boystown_n)
table(p, boystown_n$grade)
## 
             ## p above_avg avg_or_below
## above_avg 132 17
## avg_or_below 2 49
```
This model has $(17 + 2)/200 = 0.09$ re-substitution error (9%). This means that in the 200 observations that we used to train this model, 91% of them were correctly classified. Note that re-substitution error is different from accuracy. The accuracy of this model is 0.8, which is reported by a model summary call. As mentioned in Chap. [14,](https://doi.org/10.1007/978-3-319-72347-1_14) we can obtain prediction probabilities for each observation in the original boystown_n dataset.

head(predict(m, boystown_n, type = "prob")) ## above_avg avg_or_below ## 1 0.0000000 1.0000000 ## 2 1.0000000 0.0000000 ## 3 0.7142857 0.2857143 ## 4 0.8571429 *## 5 0.2857143 0.7142857 ## 6 0.5714286 0.4285714*

15.2.1 Customizing the Tuning Process

The default setting of $train()$ might not meet the specific needs for every study. In our case, the optimal k might be smaller than 5. The caret package allows us to customize the settings for train().

caret::trianControl() can help us to customize re-sampling methods. There are 6 popular re-sampling methods that we might want to use in the following table (Table 15.2).

These methods are helping us find representative samples to train the model. Let's use 0.632 bootstrap for example. Just specify method="boot632" in the trainControl() function. The number of different samples to include can be customized by number = option. Another option in trainControl() is about the model performance evaluation. We can change our preferred method of evaluation to select the optimal model. The oneSE method chooses the simplest model within one standard error of the best performance to be the optimal model. Other methods are also available in caret package. For detailed information, type best in R console.

We can also specify a list of k values we want to test by creating a matrix or a grid.

```
ctrl<-trainControl(method="boot632", number=25, selectionFunction="oneSE")
grid<-expand.grid(.k=c(1, 3, 5, 7, 9)) 
# Creates a data frame from all combinations of the supplied factors
```

Resampling method	Method name	Additional options and default values
Holdout sampling	LGOCV	$p = 0.75$ (training data proportion)
k-fold cross-validation	CV	$number = 10$ (number of folds)
Repeated k-fold cross validation	repeatedcv	number $= 10$ (number of folds), repeats $= 10$ (number of iterations)
Bootstrap sampling	boot.	$number = 25$ (resampling iterations)
0.632 bootstrap	boot632	$number = 25$ (resampling iterations)
Leave-one-out cross-validation	LOOCV	None

Table 15.2 Six complementary methods for customizing the caret::trainControl() re-sampling

Usually, to avoid ties, we prefer to choose an odd number of clusters k . Now the constraints are all set. We can start to select models again using $train()$.

```
set.seed(123)
m<-train(grade~., data=boystown_n, method="knn", 
        metric="Kappa", 
        trControl=ctrl, 
        tuneGrid=grid)
m
## k-Nearest Neighbors
## 
## 200 samples
## 10 predictor
## 2 classes: 'above_avg', 'avg_or_below' 
## 
## No pre-processing
## Resampling: Bootstrapped (25 reps) 
## Summary of sample sizes: 200, 200, 200, 200, 200, 200, ... 
## Resampling results across tuning parameters:
## 
## k Accuracy Kappa 
## 1 0.8726660 0.7081751
## 3 0.8457584 0.6460742
## 5 0.8418226 0.6288675
## 7 0.8460327 0.6336463
## 9 0.8381961 0.6094088
## 
## Kappa was used to select the optimal model using the one SE rule.
## The final value used for the model was k = 1.
```
Here we added metric="Kappa" to include the Kappa statistics as one of the criteria to select the optimal model. We can see the output accuracy for all the candidate models are better than the default bootstrap sampling. The optimal model has $k=3$, a high accuracy 0.846, and a high Kappa statistic, which is much better than the model we had in Chap. [7.](https://doi.org/10.1007/978-3-319-72347-1_7) As you can see from the output, the SE rule no longer choses the model with the highest accuracy or Kappa statistic to be the "optimal model". It is a more comprehensive method than only looks at one statistic or a single quality measure.

15.2.2 Improving Model Performance with Meta-learning

Meta-learning involves building multiple learners (can be single or multiple learning algorithms) at the same time. It combines the output from these learners and generates more effective meta-classifiers.

To decrease the variance (bagging) or bias (boosting), random forests attempt in two steps to correct the general decision trees' trend to overfit the model to the training set:

- 1. Producing a distribution of simple ML models on subsets of the original data.
- 2. Combining the distribution into one "aggregated" model.

Before stepping into the details, let's briefly summarize:

- Bagging (stands for Bootstrap Aggregating) is a way to decrease the variance of your prediction by generating additional data for training from your original dataset. It generates multiple sets of the same cardinality/size as your original data, as combinations with repetitions. By increasing the size of your training set you can't improve the model predictive force, but just decrease the variance, narrowly tuning the prediction to the expected outcome.
- Boosting is a two-step approach, where one first uses subsets of the original data to produce a series of moderately performing models and then "boosts" their performance by combining them together using a particular cost function (e.g., Accuracy). Unlike bagging, in classical boosting, the subset creation is not random and depends upon the performance of the previous models: every new subset contains the elements that were (likely to be) misclassified by previous models. Usually, we prefer weaker classifiers in boosting. For example, a prevalent choice is to use stump (level-one decision tree) in AdaBoost (Adaptive Boosting).

15.2.3 Bagging

One of the most well-known meta-learning method is bootstrap aggregating or bagging. It builds multiple models with bootstrap samples using a single algorithm. The models' predictions are combined with voting (for classification) or averaging (for numeric prediction). Voting means that bagging model's prediction is based on the majority of learners' predictions for a class. Bagging is especially good with unstable learners like decision trees or SVM models.

To illustrate the Bagging method, we will again use the Quality of Life and chronic disease dataset in Chap. [9.](https://doi.org/10.1007/978-3-319-72347-1_9) Just like we did in the second practice problem in Chap. [11](https://doi.org/10.1007/978-3-319-72347-1_11), we will use CHARLSONSCORE as the classes labels, which has 11 different class labels.

```
qol<-read.csv("https://umich.instructure.com/files/481332/download?download_
frd=1")
qol<-qol[!qol$CHARLSONSCORE==-9 , -c(1, 2)]
qol$CHARLSONSCORE<-as.factor(qol$CHARLSONSCORE)
```
To apply bagging(), we need to download the ipred package first. After loading the package, we build a bagging model with CHARLSONSCORE as class label and all other variables in the dataset as predictors. We can specify the number of voters (decision tree models we want to have), the default number is 25.

```
# install.packages("ipred")
library(ipred)
set.seed(123)
mybag<-bagging(CHARLSONSCORE~., data=qol, nbagg=25)
```
Next, we shall use the predict () function to apply this model for prediction. For evaluation purposes, we create a table reporting the re-substitution error.

```
bt_pred<-predict(mybag, qol)
agreement<-bt_pred==qol$CHARLSONSCORE
prop.table(table(agreement))
## agreement
## FALSE TRUE 
## 0.001718213 0.998281787
```
This model works very well with its training data. It labeled 99.8% of the cases correctly. To see its performances on feature data, we apply the caret train() function again with 10 repeated CV as re-sampling method. In caret, bagged trees method is called treebag.

```
library(caret)
set.seed(123)
ctrl<-trainControl(method="repeatedcv", number = 10, repeats = 10)
train(CHARLSONSCORE~., data=as.data.frame(qol), method="treebag", trControl=
ctrl)
## Bagged CART 
## 
## 2328 samples
## 38 predictor
## 11 classes: '0', '1', '2', '3', '4', '5', '6', '7', '8', '9', '10' 
## 
## No pre-processing
## Resampling: Cross-Validated (10 fold, repeated 10 times) 
## Summary of sample sizes: 2095, 2096, 2093, 2094, 2098, 2097, ... 
## Resampling results:
## 
## Accuracy Kappa 
## 0.5234615 0.2173193
```
We got an accuracy of 52% and a fair Kappa statistics. This result is better than our previous prediction attempt in Chap. [11](https://doi.org/10.1007/978-3-319-72347-1_11) using the ksvm() function alone (-50%) . Here, we combined the prediction results of 38 decision trees to get this level of prediction accuracy.

In addition to decision tree classification, caret allows us to explore alternative bag() functions. For instance, instead of bagging based on decision trees, we can bag using an SVM model. caret provides a nice setting for SVM training, making predictions and counting votes in a list object svmBag. We can examine these objects by using the $str()$ function.

```
str(svmBag)
## List of 3
## $ fit :function (x, y, ...) 
             ## $ pred :function (object, x) 
## $ aggregate:function (x, type = "class")
```
Clearly, fit provides the training functionality, pred the prediction and forecasting on new data, and aggregate is a way to combine many models and achieve voting-based consensus. Using the member operator, the \$ sign, we can explore these three types of elements of the svmBag object. For instance, the fit element may be extracted from the SVM object by:

```
svmBag$fit
## function (x, y, ...) 
## {
## loadNamespace("kernlab")
## out <- kernlab::ksvm(as.matrix(x), y, prob.model = is.factor(y), 
## ...)
      \alpha \mu \tau## }
## <environment: namespace:caret>
```
fit relies on the ksvm() function in the kernlab package, which means this package needs to be loaded. The other two methods, pred and aggregate, may be explored in a similar way. They just follow the SVM model building and testing process we discussed in Chap. [11](https://doi.org/10.1007/978-3-319-72347-1_11).

This svmBag object could be used as an optional setting in the train() function. However, this option requires that all features are linearly independent with trivial covariances, which may be rare in real world data.

15.2.4 Boosting

Bagging uses equal weights for all learners we included in the model. Boosting is quite different in terms of weights. Suppose we have the first learner correctly classifying 60% of the observations. This 60% of data may be less likely to be included in the training dataset for the next learner. So, we have more learners working on "hard-to-classify" observations.

Mathematically, we are using a weighted sum of functions to predict the outcome class labels. We can try to fit the true model using weighted additive modeling. We start with a random learner that can classify some of the observations correctly, possibly with some errors.

$$
\hat{y}_1 = l_1.
$$

This l_1 is our first learner and \hat{y}_1 denotes its predictions (this equation is in matrix form). Then, we can calculate the residuals of our first learner.

$$
\epsilon_1 = y - v_1 \times \hat{y}_1,
$$

where v_1 is a shrinkage parameter to avoid overfitting. Next, we fit the residual with another learner. This learner minimizes the following function $\sum_{i=1}^{N} ||y_i - L_{k-1} - l_k||$, here k=2. Then we obtain a second model l_2 with:

$$
\hat{y}_2 = l_2.
$$

After that, we can update the residuals:

$$
\epsilon_2=\epsilon_1-\nu_2\times\hat{y}_2.
$$

We repeat this residual fitting until adding another learner l_k results in an updated residual ϵ_k that is smaller than a small predefined threshold. At the end, we will have an additive model like:

$$
L = v_1 \times l_1 + v_2 \times l_2 + \ldots + v_k \times l_K,
$$

where we have k weak learners, but a very strong ensemble model.

Schapire and Freund found that although individual learners trained on the pilot observations might be very weak in predicting in isolation, boosting the collective power of all of them is expected to generate a model no worse than the best of all individual constituent models included in the boosting ensemble. Usually, the boosting results are quite a bit better than the best single model.

Boosting can be used for almost all models. Most commonly, it is applied to decision trees.

15.2.5 Random Forests

Random forests, or decision tree forests, represent a boosting method focusing on decision tree learners.

Training Random Forests

One approach to train and build random forests relies on using randomForest() under the randomForest package. It has the following components:

```
m<-randomForest(expression, data, ntree=500, mtry=sqrt(p))
```
- *expression*: the class variable and features we want to include in the model.
- *data*: training data containing class and features.
- *ntree*: number of voting decision trees.
- *mtry*: optional integer specifying the number of features to randomly select at each split. The p stands for number of features in the data.

Let's build a random forest using the Quality of Life dataset.

```
# install.packages("randomForest")
library(randomForest)
set.seed(123)
rf<-randomForest(CHARLSONSCORE~., data=qol)
rf
## 
## Call:
## randomForest(formula = CHARLSONSCORE ~ ., data = qol) 
## Type of random forest: classification
## Number of trees: 500
## No. of variables tried at each split: 6
## 
## OOB estimate of error rate: 46.13%
## Confusion matrix:
## 0 1 2 3 4 5 6 7 8 9 10 class.error
## 0 574 301 2 0 0 0 0 0 0 0 0 0.3454960
## 1 305 678 1 0 0 0 0 0 0 0 0 0.3109756
## 2 90 185 2 0 0 0 0 0 0 0 0 0.9927798
## 3 25 101 1 0 0 0 0 0 0 0 0 1.0000000
## 4 5 19 0 0 0 0 0 0 0 0 0 1.0000000
## 5 3 4 0 0 0 0 0 0 0 0 0 1.0000000
## 6 1 4 0 0 0 0 0 0 0 0 0 1.0000000
## 7 1 1 0 0 0 0 0 0 0 0 0 1.0000000
## 8 7 8 0 0 0 0 0 0 0 0 0 1.0000000
## 9 3 5 0 0 0 0 0 0 0 0 0 1.0000000
## 10 1 1 0 0 0 0 0 0 0 0 0 1.0000000
```
By default the model contains 500 decision trees and tried 6 variables at each split. Its OOB, or out-of-bag, error rate is about 46%, which corresponds to a poor accuracy rate (54%). Note that the OOB error rate is not re-substitution error. The confusion matrix next to it is reflecting OOB error rate for specific classes. All of these error rates are reasonable estimates of future performances with unseen data. We can see that this model is so far the best of all models, although it is still not good at predicting high CHARLSONSCORE.

Evaluating Random Forest Performance

The caret package also supports random forest model building and evaluation. It reports more detailed model performance evaluations. As usual, we need to specify a re-sampling method and a parameter grid. As an example, we use the 10-fold CV

re-sampling method. The grid for this model contains information about the m try parameter (the only tuning parameter for random forest). Previously we tried the default value $\sqrt{38} = 6$ (38 is the number of features). This time we could compare multiple mtry parameters.

```
library(caret)
ctrl<-trainControl(method="cv", number=10)
grid_rf<-expand.grid(.mtry=c(2, 4, 8, 16))
```
Next, we apply the train() function with our $ctrl$ and grid rf settings.

```
set.seed(123)
m_rf <- train(CHARLSONSCORE ~ ., data = qol, method = "rf", 
metric = "Kappa", trControl = ctrl, 
tuneGrid = grid_rf)
m_rf
## Random Forest 
## 
## 2328 samples
## 38 predictor
## 11 classes: '0', '1', '2', '3', '4', '5', '6', '7', '8', '9', '10' 
## 
## No pre-processing
## Resampling: Cross-Validated (10 fold) 
## Summary of sample sizes: 2095, 2096, 2093, 2094, 2098, 2097, ... 
## Resampling results across tuning parameters:
## 
## mtry Accuracy Kappa 
## 2 0.5223871 0.1979731
## 4 0.5403799 0.2309963
## 8 0.5382674 0.2287595
## 16 0.5421562 0.2367477
## 
## Kappa was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 16.
```
This call may take a while to complete. The result appears to be a good model, when $mtry=16$ we reached a relatively high accuracy and good kappa statistic. This is a very good result for a learner with 11 classes.

15.2.6 Adaptive Boosting

We may achieve even higher accuracy using **AdaBoost**. Adaptive boosting (AdaBoost) can be used in conjunction with many other types of learning algorithms to improve their performance. The output of the other learning algorithms ('weak learners') is combined into a weighted sum that represents the final output of the boosted classifier. AdaBoost is adaptive in the sense that subsequent weak learners are tweaked in favor of those instances misclassified by the previous classifiers.

For binary classification, we could use ada() in package ada and for multiple classes (multinomial/polytomous outcomes) we can use the package adabag. The boosting() function allows us to select a type method by setting coeflearn. Two prevalent types of adaptive boosting methods can be used. One is AdaBoost. M1 algorithm including Breiman and Freund, and the other is Zhu's SAMME algorithm. Let's see some examples:

```
set.seed(123)
qol<-read.csv("https://umich.instructure.com/files/481332/download?download_
frd=1")
qol<-qol[!qol$CHARLSONSCORE==-9 , -c(1, 2)]
qol$CHARLSONSCORE<-as.factor(qol$CHARLSONSCORE)
```
The key parameter in the adabag:: boosting() method is *coeflearn*:

- *Breiman* (default), corresponding to $\alpha = \frac{1}{2} \times \ln\left(\frac{1-err}{err}\right)$, using the AdaBoost.M1 algorithm, where α is the weight updating coefficient
- *Freund*, corresponding to $\alpha = \ln\left(\frac{1-err}{err}\right)$, or
- *Zhu*, corresponding to $\alpha = \ln\left(\frac{1-err}{err}\right) + \ln\left(nclasses 1\right)$.

The generalizations of AdaBoost for multiple classes $(≥2)$ include AdaBoost. M1 (where individual trees are required to have an error $\langle \frac{1}{2} \rangle$ and SAMME (where individual trees are required to have an error $\lt 1 - \frac{1}{n \cdot classes}$).

```
# install.packages("ada"); install.packages("adabag")
library("ada"); library("adabag")
qol_boost <- boosting(CHARLSONSCORE~.,data=qol,mfinal = 100,coeflearn = 
'Breiman')
mean(qol_boost$class==qol$CHARLSONSCORE)
## [1] 0.5425258
qol_boost <- boosting(CHARLSONSCORE~.,data=qol,mfinal = 100,coeflearn = 
'Freund')
mean(qol_boost$class==qol$CHARLSONSCORE)
## [1] 0.5524055
qol_boost <- boosting(CHARLSONSCORE~.,data=qol, mfinal = 100, coeflearn =
'Zhu')
mean(qol_boost$class==qol$CHARLSONSCORE)
## [1] 0.6542096
```
We observe that in this case, the Zhu approach achieves the best results. Notice that the default method is M1 Breiman and mfinal is the number of iterations for which boosting is run or the number of trees to use.

Try applying model improvement techniques using other data from the list of our Case-Studies (Fig. 15.1).

15.3 Assignment: 15. Improving Model Performance

Use some of the methods below to do classification, prediction, and model performance evaluation (Table 15.3).

Fig. 15.1 Live demo: Iris flowers classification using adabag

Model	Learning task	Method	Parameters
KNN	Classification	knn	k
Naïve Bayes	Classification	nb	fL, usekernel
Decision Trees	Classification	C5.0	model, trials, winnow
OneR Rule Learner	Classification	OneR	None
RIPPER Rule Learner	Classification	JRip	NumOpt
Linear Regression	Regression	lm	None
Regression Trees	Regression	rpart	cp
Model Trees	Regression	M5	pruned, smoothed, rules
Neural Networks	Dual use	nnet	size, decay
Support Vector Machines (Linear Kernel)	Dual use	symLinear	C
Support Vector Machines (Radial Basis Kernel)	Dual use	svmRadial	C, sigma
Random Forests	Dual use	rf	mtry

Table 15.3 Performance evaluation for several classification, prediction, and clustering methods

15.3.1 Model Improvement Case Study

From the course datasets, use the 05 PPMI top UPDRS Integrated LongFormat1. csv case-study data to perform a multi-class prediction.

Use ResearchGroup as response, which have "PD", "Control" and "SWEDD" three classes.

- Delete ID column, impute missing value with mean or median and justify your choice.
- Normalize the covariates.
- Implement automated parameter tuning process and report the optimal accuracy and κ .
- Set arguments and rerun the tuning, trying different method and number settings.
- Train a random forest, tune the parameters, report the result and output cross table.
- Use bagging algorithm and report the accuracy and κ .
- Perform randomForest and report the accuracy and κ .
- Report the accuracy by AdaBoost and make sure to try all three methods.
- Finally, give a brief summary about all the model improvement approaches.
- Try the procedure on other data in the list of Case-Studies, e.g., Traumatic Brain Injury Study and the corresponding dataset.

References

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