Computer Assignment 11 - Tuning Regression Parameters and SVM

Machine Learning, Spring 2020

Rui Li

Greetings everyone! With the final project looming overhead, I have attempted to make this a lighter computer assignment. Since the amount that I need to cover does not really align with my intent here, I am going to provide some examples in this assignment and then simply require you to use the built in R functions on some data. Please don't be intimidated by the number of questions, this assignment is mostly about reading examples and using pre-written functions from R. -Murph

Note: You'll need to install the e1071, HDCI, and stringr packages before this document will compile.

LASSO and Ridge Regression Tuning Parameter

Recall that both LASSO and Ridge have a penalty parameter λ that controls the amount of regularization in our procedure. As you might imagine, a good choice of λ is crucial to finding a good procedure fit. With our goal being to maximize our prediction accuracy, we can actually use what we have learned about cross-validation to choose a good λ. Recall that we use cross-validation to create an estimate for the actual test error of a procedure (the test error we would get for a general procedure, not of a particular classification rule we have created on the training data).

Each distinct value of the penalty parameter λ determines a distinct model we could use to fit our data and our aim is to pick the best procedure. The following algorithm uses cross-validation to choose λ by calculating estimates of prediction accuracy for a set of candidate λs. The λ chosen is the one that has the best estimated accuracy.

K-fold cross validation for choosing λ

1. Divide the set $\{1, \dots, n\}$ in to K subsets (i.e. folds) of roughly equal size, $F_1, \dots, F_K$
2. For $k = 1, \dots, K$:

- Consider training on $(x_i, y_i), i \notin F_k$, and validating on $(x_i, y_i), i \in F_k$
- For each value of the tuning parameter $\lambda \in \{\lambda_1, \dots, \lambda_m\}$, compute the classification rule $\hat{f}_\lambda^{-k}$ using the training set. Here $\hat{f}_\lambda^{-k}$ is the LASSO/Ridge Regression model with tuning parameter λ trained on $(x_i, y_i), i \notin F_k$.

- For each λ, record the total testing error on the validation set:

$$e_k(\lambda) = \frac{1}{|F_k|} \sum_{i \in F_k} I\left(y_i \neq \hat{f}_\lambda^{-k}(x_i)\right).$$

3. For each tuning parameter $\lambda \in \{\lambda_1, \dots, \lambda_m\}$, compute the average error over all folds,

$$CV(\lambda) = \frac{1}{K}\sum_{k=1}^{K} e_k\,(\lambda).$$

4. Choose $\hat{\lambda}$ such that $\hat{\lambda} := \text{argmin}_{\lambda}\{CV(\lambda)\}$.

Further discussion of this process can be found here. Luckily for us, `R` has built-in functionality to perform this entire process for us! We will practice using these built-in functions on the following data.

A. Regression on Tree Leaf Images

We will attempt to identify trees based on image data of their leaves. This is a tough problem, though apps such as iNaturalist now do a pretty good job identifying plants from images taken on your phone.

The data set is from here.

Images have been pre-processed, so the dataset inlcudes vectors for margin, shape and texture attributes for each of almost 1000 images.

We will start by loading the `leaves` dataset and dropping the `id` and `species` variables.

```
leaf = read.csv("leaves.csv")
leaf$id = NULL
leaf$species = NULL
```

1. Build a LASSO model using the `Lasso` function from the last homework. Make your response the `margin1` variable and the rest of the variables your predictors. Set the parameter `fix.lambda` to FALSE.

```
library(MASS);library(HDCI);

## Warning: package 'HDCI' was built under R version 3.6.3

Y = leaf[,1];X = leaf[,-1]
leaf.lasso = Lasso(X,Y,fix.lambda=F)
```

2. When `fix.lambda` is set to FALSE, the `Lasso` function tunes a λ using cross-validation. According to the manual page, what is the default number of folds the `Lasso` function uses?

```
The default number of folds is 10.
```

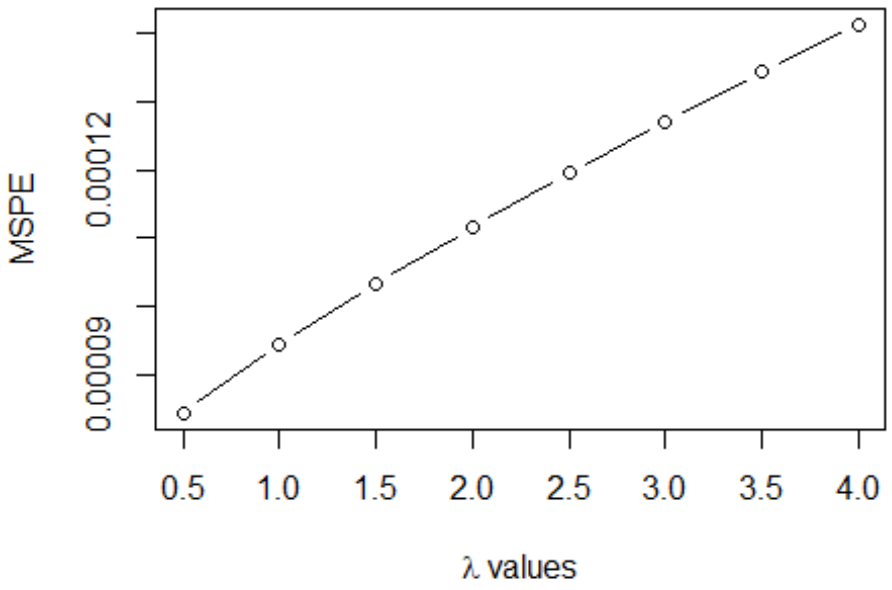
3. Print out the λ value that your LASSO model selects. Report how many non-zero parameter values there are in your LASSO model.

```
print(leaf.lasso$lambda)

## [1] 2.533211e-06

sum(leaf.lasso$beta!=0)
```

```
## [1] 127

There are 127 non-zero parameter values.
```

4. With the same predictors and response, let us do the same thing with a Ridge Regression model. Cross validation with Ridge Regression in R is done with the `ridgereg.cv` function in the `MXM` package. `ridgereg.cv` cross validates on every value of λ you provide and plots the Mean Square Prediction Error (MSPE) for each λ. Use `ridgereg.cv` for $\lambda \in \{0.5,1.0,1.5, \ldots,3.5,4.0\}$.

```
library(MXM)

## Warning: package 'MXM' was built under R version 3.6.3

## Registered S3 method overwritten by 'sets':
##   method        from
##   print.element ggplot2

ridge.reg = ridgereg.cv(Y,data = X, lambda = seq(0.5,4, by=0.5))
```

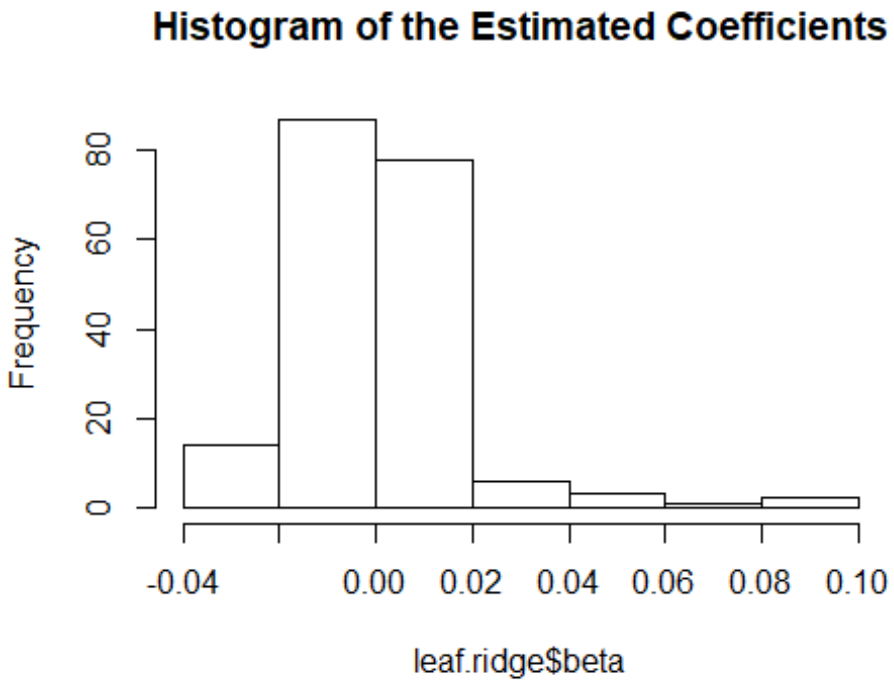


5. According to the output for `ridgereg.cv`, which value of λ should we choose?

```
From the plot above, we should choose lambda=0.5, which has the lowest `Mean
Square Prediction Error`.
```

6. Build a Ridge Regression model using this λ. Print a histogram of the estimated coefficients for the fitted model

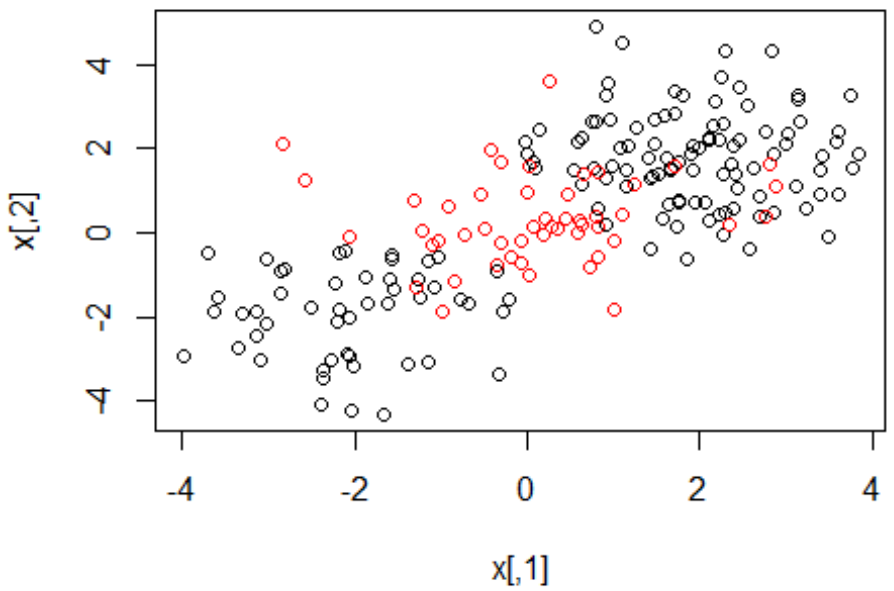
```
leaf.ridge=ridge.reg(Y, X, lambda = 0.5)
hist(leaf.ridge$beta, main = "Histogram of the Estimated Coefficients")
```



B. SVM

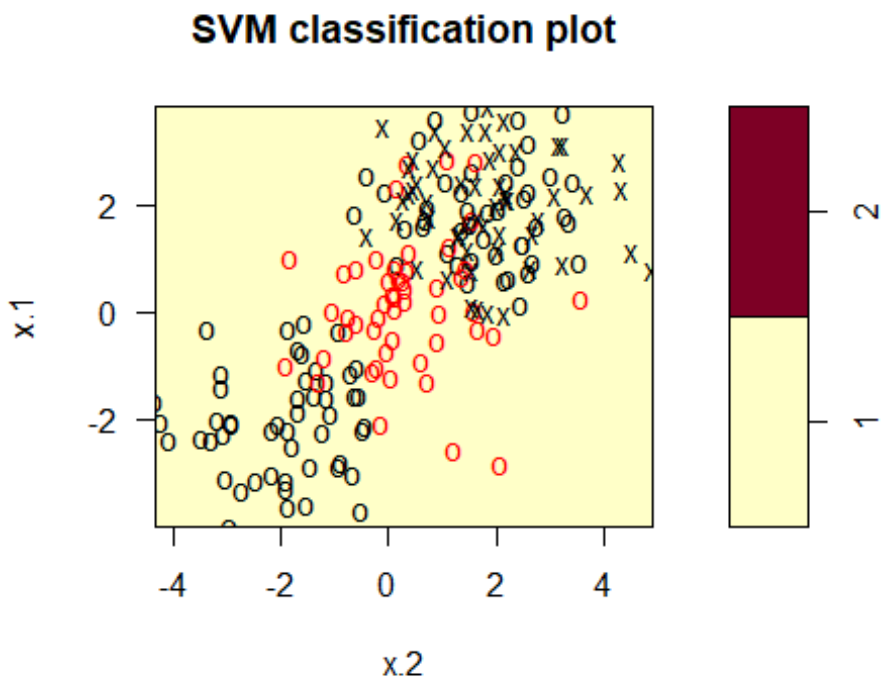
For this section we will use the `svm` function in package `e1071`. Let us walk through a simple example (originally found here) to see how the `svm` function works:

```
set.seed(13)
x=matrix(rnorm(200*2) , ncol =2)
x[1:100 ,] = x[1:100 ,] + 2
x[101:150 ,]= x[101:150,] - 2
y=c(rep(1 ,150) ,rep(2 ,50) )
dat=data.frame(x=x,y=as.factor(y))

plot(x, col =y)
```



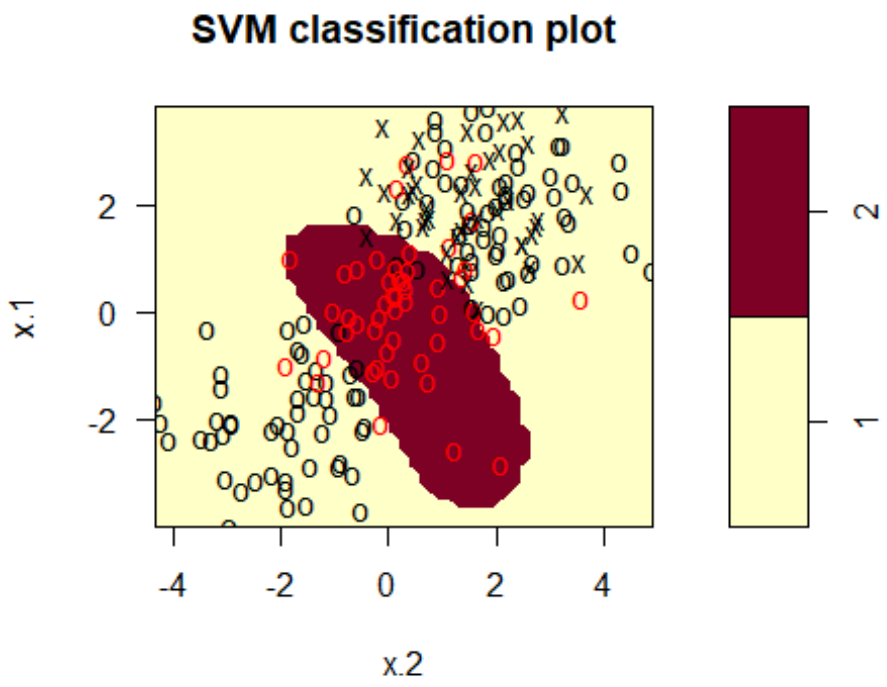
Note here that our data are NOT linearly seperable! In fact, it does not appear that a linear seperation rule will work here. Let us verify this using a linear kernel with our SVM:

```
library(e1071)

## Warning: package 'e1071' was built under R version 3.6.3

train=sample(200 ,100)
svmfit = svm(y~., data=dat[train ,], kernel ="linear", gamma = 1, cost = 1)
plot(svmfit , dat)
```



It would appear that all observations are classified as 1s, confirming our suspicions. Luckily, SVMs are not limited to linear kernels:

```
library(e1071)
train=sample(200 ,100)
svmfit = svm(y~., data=dat[train ,], kernel ="radial", gamma = 1, cost = 1)
plot(svmfit , dat)
```



The above is a special form of SVM where we used a radial kernel. While the use of non-linear kernels is an interesting topic to explore, we merely introduce it here. For the following example and exercise, we will use a linear kernel.

Recall from class that SVM requires a tuning parameter C (which, if you check the manual page, the `svm` function calls `cost`). Like the `ridgereg.cv` function, the `e1071` library has a built-in cross-validation function for choosing a good value of C. Observe the following:

```
set.seed(13)
tune.out=tune(svm ,y~.,data=dat ,kernel ="linear",
              ranges =list(cost=c(0.001,0.01,0.1, 1,5,10,100)))
summary(tune.out)

##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##   cost
##  0.001
##
## - best performance: 0.25
##
## - Detailed performance results:
##    cost error dispersion
## 1 1e-03  0.25  0.0745356
```

```
## 2 1e-02  0.25  0.0745356
## 3 1e-01  0.25  0.0745356
## 4 1e+00  0.25  0.0745356
## 5 5e+00  0.25  0.0745356
## 6 1e+01  0.25  0.0745356
## 7 1e+02  0.25  0.0745356
```

According to the output, our best choice of the `cost` parameter would be 0.001. The tune() function stores the best model obtained, which can be accessed as follows:

```
bestmod =tune.out$best.model
```

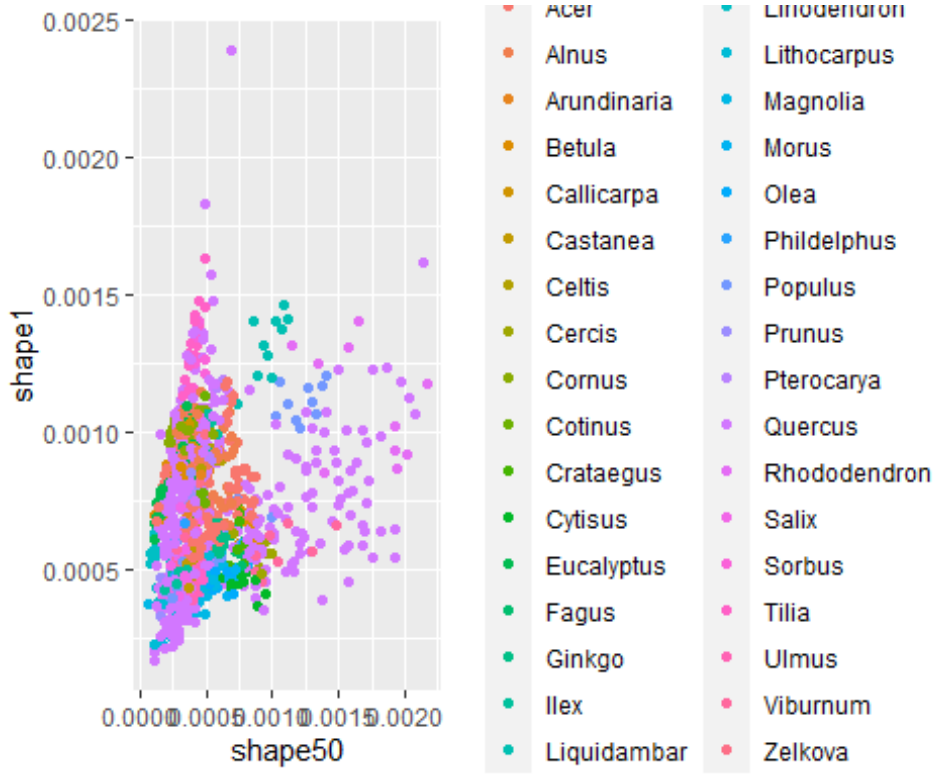
C. Applying SVM to Tree Leaf Images

We begin by loading the `leaves` dataset again and this time only dropping the `id` variable. We will further extract the `genus` of each observation using the `stringr` package in `R`.

```
library(stringr)

## Warning: package 'stringr' was built under R version 3.6.3

leaf = read.csv("leaves.csv", stringsAsFactors = FALSE)
leaf$id = NULL
leaf$genus <- str_split(leaf$species, "_", simplify = TRUE)[, 1]
leaf$genus = as.factor(leaf$genus)
leaf$species = NULL
```

1. Make a scatter plot of `shape1` by `shape50`, coloring by `genus` label. Does this data look linearly seperable?

```
library(ggplot2)

## Warning: package 'ggplot2' was built under R version 3.6.3

ggplot(leaf, aes(x = shape50, y = shape1, color = genus)) + geom_point()
```




```
This data does not look linearly seperable.
```

2. Randomly split your data into test and training sets. About 35 percent of the data should be in the test set. Display a summary of genus labels in the training set. **Note: In the rare event that one class in the training data is not represented, you may reduce the test set percentage to 30 percent and resample.**

```
training_size <- round(.65 * nrow(leaf))
indices = sample(1:nrow(leaf), training_size)
training_set <- leaf[indices,]
testing_set <- leaf[-(indices),]
summary(training_set$genus)
```

```
##         Acer        Alnus  Arundinaria       Betula   Callicarpa     Casta
nea
##           58           26            7           14            8
  6
##       Celtis       Cercis       Cornus      Cotinus    Crataegus      Cyti
sus
##            7            7           20            5            7
  6
##   Eucalyptus        Fagus       Ginkgo         Ilex  Liquidambar Liriodend
ron
##           20            6            7           13            7
  7
##  Lithocarpus     Magnolia        Morus         Olea  Phildelphus      Popu
lus
```

```
##           12           13            8            7            3
 24
##       Prunus   Pterocarya      Quercus Rhododendron       Salix       Sor
bus
##            8            8          249            6           16
  6
##        Tilia        Ulmus     Viburnum      Zelkova
##           22            9           14            8
```

3. Tune a SVM model with a linear kernel on the training set. Use $cost \in \{0.001,0.01,0.1,1,5,10,100\}$ (this may take a while for your computer to run). Report the `cost` value of the best model. Use the `predict` function to classify the data from the test set and the training set. Report both the testing and training errors

```
tune.out=tune(svm ,genus~.,data=training_set ,kernel ="linear", ranges =list
(cost=c(0.001,0.01,0.1,1,5,10,100)))
summary(tune.out)
```

```
##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  cost
##   0.1
##
## - best performance: 0.02175481
##
## - Detailed performance results:
##    cost      error dispersion
## 1 1e-03 0.54653846 0.04186424
## 2 1e-02 0.06980769 0.02935388
## 3 1e-01 0.02175481 0.01498601
## 4 1e+00 0.02175481 0.01498601
## 5 5e+00 0.02175481 0.01498601
## 6 1e+01 0.02175481 0.01498601
## 7 1e+02 0.02175481 0.01498601
```

```
bestmod =tune.out$best.model
best_cost = bestmod$cost
print(paste0("The cost of the best model is ",best_cost,"."))
```

```
## [1] "The cost of the best model is 0.1."
```

```
train_pre = predict(bestmod, training_set[,1:192])
test_pre = predict(bestmod, testing_set[,1:192])
```

```
train_error = sum(train_pre!=training_set$genus)/length(training_set$genus)
test_error = sum(test_pre!=testing_set$genus)/length(testing_set$genus)

print(paste0("The training error is ",train_error,"."))
```

```
## [1] "The training error is 0."
```

```
print(paste0("The testing error is ",test_error,"."))
```

```
## [1] "The testing error is 0.0260115606936416."
```