Lab5 Answer

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- (I) Validation set approach
- 1) Randomly pick half of the data as the training data. Remember to set a seed to make your result repeatable.

```
library("ISLR")
set.seed(100)
train<-sample(nrow(Auto),nrow(Auto)/2)</pre>
```

2) Build a linear regression model based on the training data.

```
lm.fit.train<-lm(mpg~horsepower,data=Auto,subset=train)</pre>
```

3) Estimate the test MSE based on the other half (as test data)

```
mean((Auto$mpg-predict(lm.fit.train,Auto))[-train]^2)
```

[1] 24.9355

test MSE for linear model is 24.9355

4) Now try to build polynomial regression of degree 2 and 3 using $lm(y\sim poly(x,i))$, where y is the response variable, x is the predictor variable and i is the highest degree of x. Compute the test MSE for the two models.

```
lm.fit2.train<-lm(mpg~poly(horsepower,2),data=Auto,subset=train)
lm.fit3.train<-lm(mpg~poly(horsepower,3),data=Auto,subset=train)
mean((Auto$mpg-predict(lm.fit2.train,Auto))[-train]^2)</pre>
```

[1] 21.61717

```
mean((Auto$mpg-predict(lm.fit3.train,Auto))[-train]^2)
```

[1] 21.70125

MSE for degree 2(quadratic) is 21.61717. (best out of 3) MSE for degree 3(cubic) is 21.70125.

5) What conclusion could we draw from the above comparison of degree 1 (linear) and degree 2 (quadratic) and degree 3 (cubic) regression models?

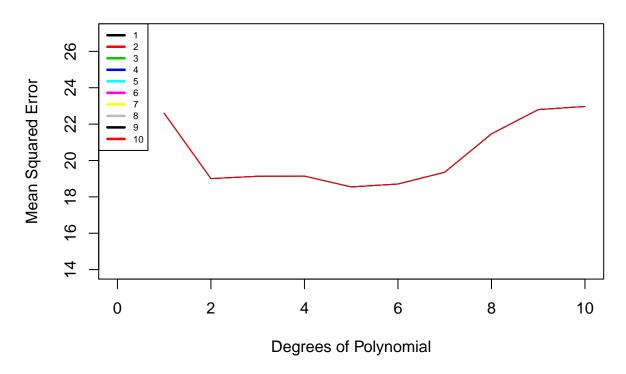
degree 2 has the smallest MSE, and is thus the best out of three.

- 6) Choose 10 different seeds. For each seed, calculate the test MSE for models of degree from 1 to 10. You may use a nested for-loop to do that. Plot the variability on the results. Can you obtain a similar plot as in Figure 1.
- Hint: In order to do that you need to plot one curve first, and repeat the same procedure for another 9 times (using a for-loop) where each time a different seed is chosen.

In order to plot one curve, you need to obtain a vector of size 10, where each element of the vector records the test MSE of the model with degree i (i = 1, 2, .10). This can be implemented by a for-loop to go through degree from 1 to 10.

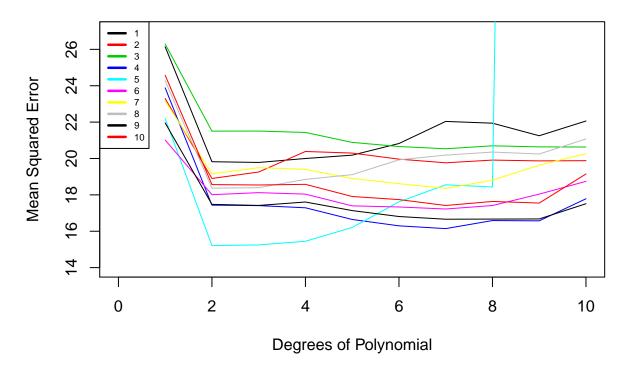
First method - keeping only one vector for errors. It is easier to understand, but all previous data will be lost.

10 times random split



Second method - keeping a two-dimensional matrix. It will store all the errors calculated so far. :

10 times random split



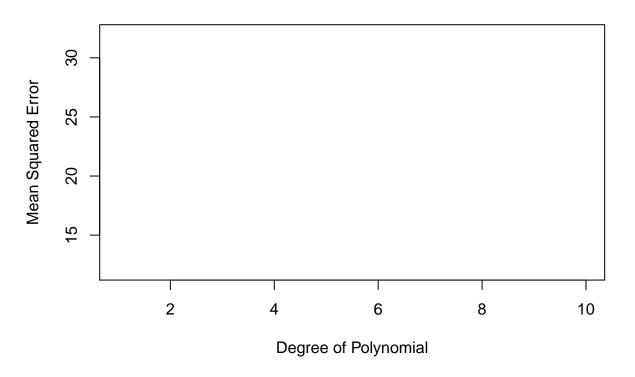
A snippet that returns the square of each number in foo.squared

```
foo=seq(1,100,by=2)
foo.squared=NULL
for(i in 1:50){
        foo.squared[i]=foo[i]^2
print(foo.squared)
                    25
                         49
                              81
                                  121
                                        169
                                             225
                                                  289
                                                       361
                                                            441
         841
              961 1089 1225 1369 1521 1681 1849 2025 2209 2401 2601 2809 3025
   [29] 3249 3481 3721 3969 4225 4489 4761 5041 5329 5625 5929 6241 6561 6889
## [43] 7225 7569 7921 8281 8649 9025 9409 9801
```

- (II) LOOCV
 - 7) Experiment on the LOOCV for increasingly complex polynomial fits. More specifically, write a for-loop to increase the degree i, as in $lm(y\sim poly(x,i))$, from 1 to 10 and record the LOOCV estimate for the test error for each degree.
 - 8) Plot the result from 7) where x-axis is the degree i and y-axis is the LOOCV estimate for the test error. Can you plot a similar one as in Figure 2?

```
library(boot)
plot(0,xlab="Degree of Polynomial",ylab="Mean Squared Error", main = "LOOCV",xlim=c(1,10),ylim=c(12,32)
```

LOOCV



```
errorMatrix<-matrix(nrow = 10,ncol = 2)
errors <-rep(0,10)
for(i in 1:10){
    set.seed(i)
        glm.fit<-glm(mpg~poly(horsepower,i),data=Auto)
        cv.err<-cv.glm(Auto,glm.fit)
        errors[i]<-cv.err$delta
}

## Warning in errors[i] <- cv.err$delta: le nombre d'objets à remplacer n'est
## pas multiple de la taille du remplacement</pre>
```

warning in errors[i] <- cv.err\$delta: le nombre d'objets à remplacer n'est
pas multiple de la taille du remplacement
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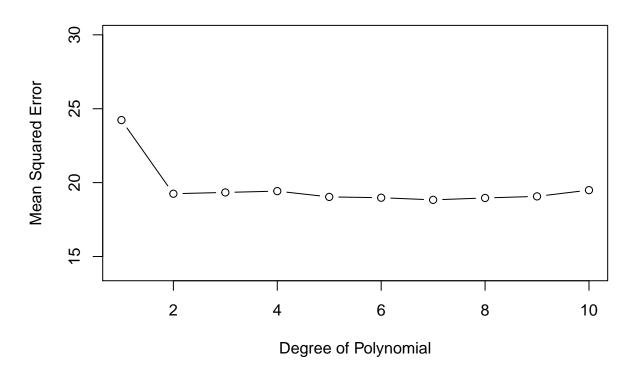
## Warning in errors[i] <- cv.err$delta: le nombre d'objets à remplacer n'est
## pas multiple de la taille du remplacement

## Warning in errors[i] <- cv.err$delta: le nombre d'objets à remplacer n'est
## pas multiple de la taille du remplacement

## Warning in errors[i] <- cv.err$delta: le nombre d'objets à remplacer n'est
## pas multiple de la taille du remplacement</pre>
```

```
errorMatrix[,2]<-errors
errorMatrix[,1]<-seq(1,10)
plot(errorMatrix,ylim=c(14,30),type="b",xlab="Degree of Polynomial",ylab="Mean Squared Error",main="L00")</pre>
```

LOOCV



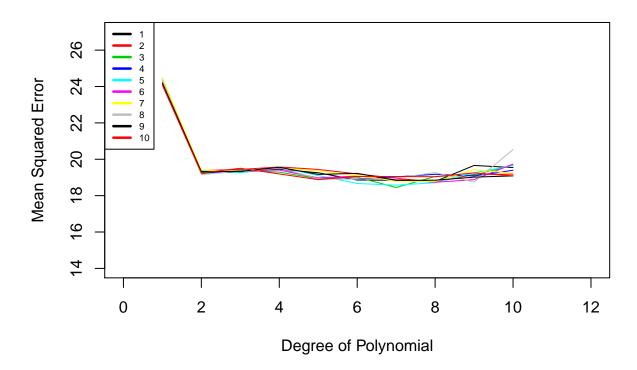
(III) K-fold CV

Implement k-fold CV by passing the argument K in cv.glm(data, glmfit, cost, K). The errors are recorded in delta. There are two numbers associated with delta: \bullet The first number is the raw/standard CV estimate of prediction error. \bullet The second number is the adjusted CV estimate. The adjustment is designed to compensate for the bias introduced by not using leave-one-out cross-validation.

It is sufficient to report the raw CV error to estimate the test errors. The following three questions can be answered by one chunk of code.

9) Set a seed. Write a for-loop to increase the degree i, as in $lm(y\sim poly(x,i))$, from 1 to 10 and record the 10-fold CV estimate for the test error for each degree.

10-fold CV



- 10) Plot the result from 9) where x-axis is the degree i and y-axis is the 10-fold CV estimate for the test error.
- 11) Set 9 different seeds and repeat 9) and 10). Plot all the results into one plot like the one in Figure 3.