Analytics 512 Homework 4

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Exercsise 5.4 #3

Part A

K fold validation is implimented by first randomly dividing the sets of observations into k groups that should be about equal sizes. The first group (or fold) is treated as the validation set and the method is fit on the remaining k-1 folds. Then the mean-squared error (MSE) is computed for the fold, this method is then repeated on the remaining k-1 folds.

The CV estimate is computed by averaging the various MSEs

$$CV_k = \frac{1}{k}\sum_{i=1}^{k} MSE_i$$

Part B

i

The advantages of k fold over the validation set approach are:

> the validation estimate of the test error rate can be highly variable
>
> There's only one subset used to test and train
>
> the validation set error rate may tend to overestimate the test error rate for the model fit on the entire data set

The disadvantages of k fold over the validation set approach are:

> The validation method is significiantly easier to impliment since we are splitting only two data sets
>
> The validation method has significiantly less bias compared to the k-fold method.

ii

The advantages of k fold over LOOCV approach are:

> The LOOCV is significiantly more comprehensive compared to the k-fold method
>
> has a low bias

The disadvantages of k fold over LOOCV approach are:

> While LOOCV has a low bias, the test error can be highly variable as well
>
> LOOCV requires going trhough every point, so it requires more time to impliment than k-fold

Exercsise 5.4 #5

In [2]:
```
library(ISLR)
attach(Default)
```

Part A

In [3]:
```
glm.default = glm(default~balance, data = Default, family = binomial)
```

Part B

i

In [4]:
```
train = sample(nrow(Default), .5*nrow(Default), replace = F)
training = Default[train,]
validation = Default[-train,]
```

ii

In [5]:
```
glm.default = glm(default~., data = training, family = binomial)
```

iii

In [6]:
```
pred = predict(glm.default, validation, type = "response")
pred.default = rep(x = "No", times = length(pred))
pred.default[pred>0.5] = "Yes"
```

iv

In [7]:
```
mean(pred.default != validation$default)
```

Out[7]: 0.026

I attempted CV by applying K = 10 instead of the validation method as specified by the homework.

In [8]:
```
glm.default = glm(default~income+balance, data = Default, family = binomial)
cost <- function(r, pi = 0){
    mean(abs(r-pi) > 0.5)
    }
library(boot)
cv.default = cv.glm(Default, glm.default, K = 10)
cv.default$delta
```

Out[8]: 0.021473817989738 0.021469868649009

Part C

In [9]:
```
glm.default = glm(default~income+balance, data = Default, family = binomial)
cost <- function(r, pi = 0){
    mean(abs(r-pi) > 0.5)
    }
library(boot)
cv.default = cv.glm(Default, glm.default, cost, K = 10)
cv.default$delta

glm.default = glm(default~income+balance, data = Default, family = binomial)
cost <- function(r, pi = 0){
    mean(abs(r-pi) > 0.5)
    }
library(boot)
cv.default = cv.glm(Default, glm.default, cost, K = 10)
cv.default$delta

glm.default = glm(default~income+balance, data = Default, family = binomial)
cost <- function(r, pi = 0){
    mean(abs(r-pi) > 0.5)
    }
library(boot)
cv.default = cv.glm(Default, glm.default, cost, K = 10)
cv.default$delta
```

Out[9]: 0.0265 0.02648

Out[9]: 0.0263 0.02632

Out[9]: 0.0264 0.02646

Based on the three runs of the, it seems that the CV error holds between 0.026 to 0.0265.

Part D

In [10]:
```
glm.default = glm(default~income+balance+student, data = Default, family = bin
omial)
cost <- function(r, pi = 0){
    mean(abs(r-pi) > 0.5)
    }
library(boot)
cv.default = cv.glm(Default, glm.default, cost, K = 10)
cv.default$delta
```

Out[10]: 0.0268 0.02689

The difference in error seems to by minimal, but lower without the student dummy variable. However, I would argue that the differences between the CV errors are small enough that it wouldn't matter. As to the specific question, adding the student dummy variable does not lead to a reduction in the test errors.

Exercise 6.8 #1

Part A

In the case of Best Subset selection, "This task must be performed with care, because the RSS of these p + 1 models decreases monotonically, and the R^2 increases monotonically, as the number of features included in the models increases." Thus Best Subset selection has the smallest training RSS.

Part B

Best Subset Selection probably has the smallest test RSS, but it's possible for forward stepwise or backwards stepwise to have a smaller test RSS.

Part C

i

True, forward selection adds predictors to a model until it goes through each predictor, adding them if they meet the specified criteria.

ii

True, Backward selection starts by looking at all $k+1$ predictors, removing ones that don't fit a criteria.

iii

False, the methods could lead to different models thus one cannot be a subset of the other.

iv

False,the methods could lead to different models thus one cannot be a subset of the other.

v

False, since best subset selection looks at all possible comination, there are multiple models with k+1 predictors, so it doesn't the same values as the lower subsets.

Exercise 6.8 #8

Part A

In [11]:
```
X = rnorm(100)
e = rnorm(100)
```

Part B

In [12]:
```
Y = 1 +2*X+3*X^2+4*X^3+e
```

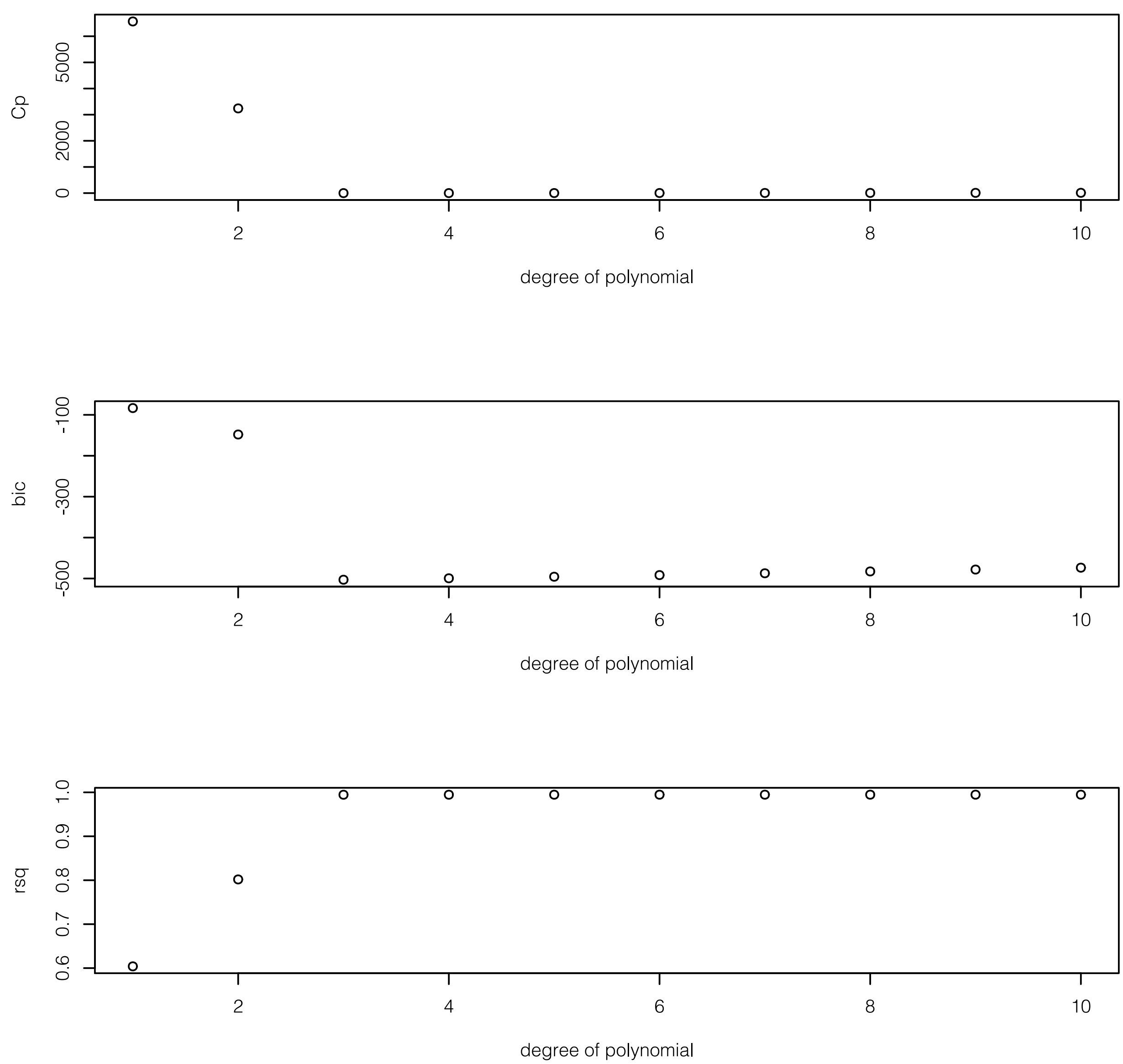
Part C

In [13]:
```
XY = data.frame(Y,X)
names(XY)
library(leaps)
best_selection = regsubsets(Y~poly(X, 10), data = XY,nvmax=10)
```

Out[13]: 'Y' 'X'

In [14]:
```
best_selection_summary = summary(best_selection)
```

In [15]:
```
par(mfrow = c(3,1))
plot(best_selection_summary$cp, xlab = "degree of polynomial" , ylab = "Cp")
plot(best_selection_summary$bic, xlab = "degree of polynomial" , ylab = "bic")
plot(best_selection_summary$rsq, xlab = "degree of polynomial" , ylab = "rsq")
```



In [16]:
```
print("Based on Cp, the best model is:")
coef(best_selection,which.min(best_selection_summary$cp))
print("Based on BIC, the best model is:")
coef(best_selection,which.min(best_selection_summary$bic))
print("Based on R squared, the best model is:")
coef(best_selection,which.max(best_selection_summary$rsq))
```

```
[1] "Based on Cp, the best model is:"
```

Out[16]:

(Intercept)	3.6998393567294
poly(X, 10)1	105.629130559038
poly(X, 10)2	59.6661724142847
poly(X, 10)3	60.4528273101325

```
[1] "Based on BIC, the best model is:"
```

Out[16]:

(Intercept)	3.6998393567294
poly(X, 10)1	105.629130559038
poly(X, 10)2	59.6661724142847
poly(X, 10)3	60.4528273101325

```
[1] "Based on R squared, the best model is:"
```

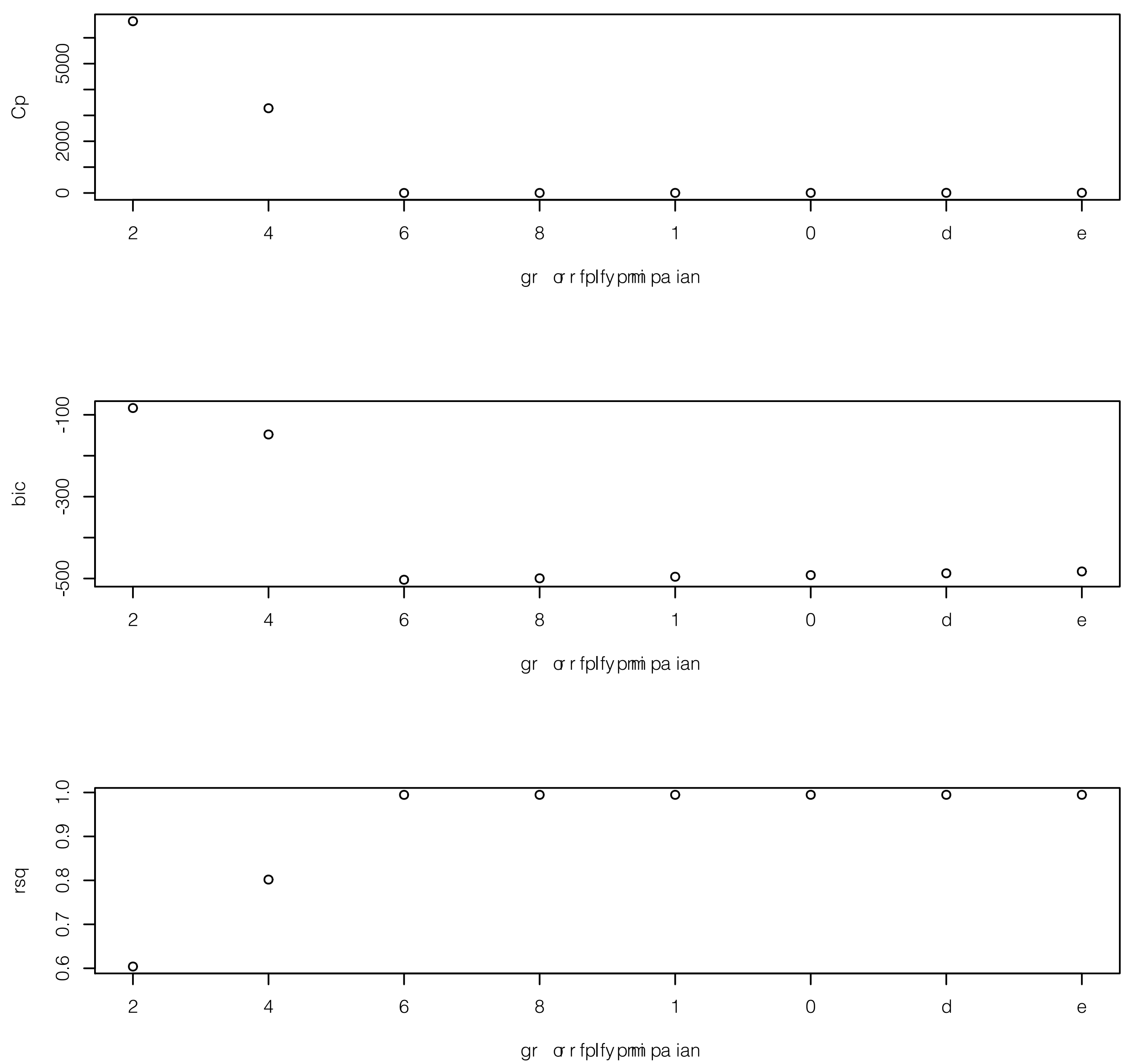
Out[16]:

(Intercept)	3.6998393567294
poly(X, 10)1	105.629130559038
poly(X, 10)2	59.6661724142847
poly(X, 10)3	60.4528273101325
poly(X, 10)4	-0.428862843315038
poly(X, 10)5	-0.123771722284301
poly(X, 10)6	-0.31462546850288
poly(X, 10)7	-0.879019730689118
poly(X, 10)8	1.03857084094882
poly(X, 10)9	0.76599542646805
poly(X, 10)10	0.0988153889934791

Part D

In [17]:

```
forward_selection = regsubsets(Y~poly(X, 9), data = XY, method ="forward")
forward_selection_summary = summary(forward_selection)
par(mfrow = c(3,1))
plot(forward_selection_summary$cp, xlab = "degree of polynomial" , ylab = "C
p")
plot(forward_selection_summary$bic, xlab = "degree of polynomial" , ylab = "bi
c")
plot(forward_selection_summary$rsq, xlab = "degree of polynomial" , ylab = "rs
q")
```



In [18]:
```
print("Based on Cp, the best model is:")
coef(forward_selection,which.min(forward_selection_summary$cp))
print("Based on BIC, the best model is:")
coef(forward_selection,which.min(forward_selection_summary$bic))
print("Based on R squared, the best model is:")
coef(forward_selection,which.max(forward_selection_summary$rsq))
```

```
[1] "Based on Cp, the best model is:"
```

Out[18]:

(Intercept)	3.6998393567294
poly(X, 9)1	105.629130559038
poly(X, 9)2	59.6661724142847
poly(X, 9)3	60.4528273101325

```
[1] "Based on BIC, the best model is:"
```

Out[18]:

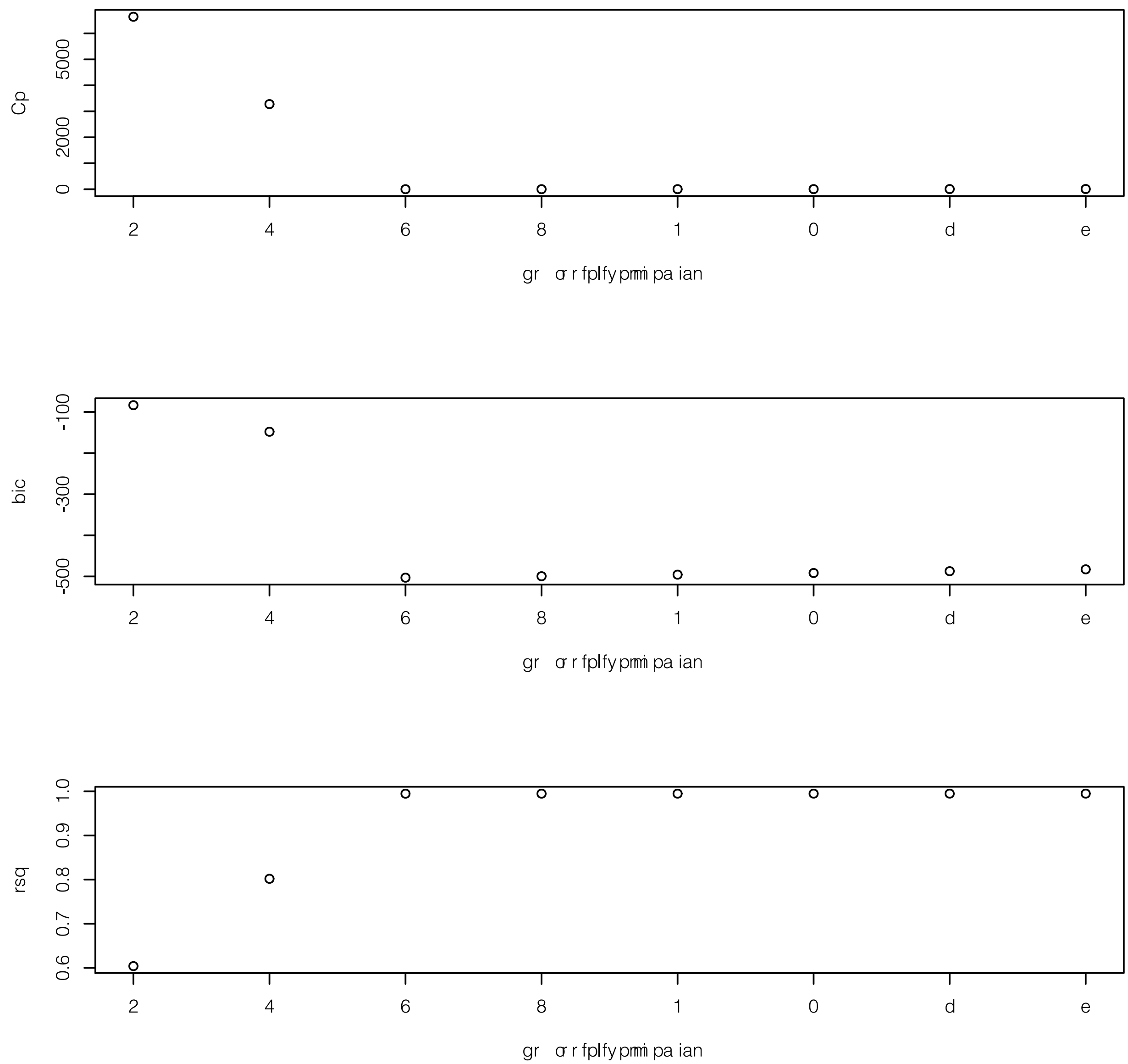
(Intercept)	3.6998393567294
poly(X, 9)1	105.629130559038
poly(X, 9)2	59.6661724142847
poly(X, 9)3	60.4528273101325

```
[1] "Based on R squared, the best model is:"
```

Out[18]:

(Intercept)	3.6998393567294
poly(X, 9)1	105.629130559038
poly(X, 9)2	59.6661724142847
poly(X, 9)3	60.4528273101325
poly(X, 9)4	-0.428862843315038
poly(X, 9)6	-0.31462546850288
poly(X, 9)7	-0.879019730689118
poly(X, 9)8	1.03857084094882
poly(X, 9)9	0.76599542646805

In [19]:
```
backward_selection = regsubsets(Y~poly(X, 9), data = XY, method ="backward")
backward_selection_summary = summary(backward_selection)
par(mfrow = c(3,1))
plot(backward_selection_summary$cp, xlab = "degree of polynomial" , ylab = "C
p")
plot(backward_selection_summary$bic, xlab = "degree of polynomial" , ylab = "b
ic")
plot(backward_selection_summary$rsq, xlab = "degree of polynomial" , ylab = "r
sq")
```



In [20]:
```
print("Based on Cp, the best model is:")
coef(backward_selection,which.min(backward_selection_summary$cp))
print("Based on BIC, the best model is:")

coef(backward_selection,which.min(backward_selection_summary$bic))
print("Based on R squared, the best model is:")

coef(backward_selection,which.max(backward_selection_summary$rsq))
```

```
[1] "Based on Cp, the best model is:"
```

Out[20]:

(Intercept)	3.6998393567294
poly(X, 9)1	105.629130559038
poly(X, 9)2	59.6661724142847
poly(X, 9)3	60.4528273101325

```
[1] "Based on BIC, the best model is:"
```

Out[20]:

(Intercept)	3.6998393567294
poly(X, 9)1	105.629130559038
poly(X, 9)2	59.6661724142847
poly(X, 9)3	60.4528273101325

```
[1] "Based on R squared, the best model is:"
```

Out[20]:

(Intercept)	3.6998393567294
poly(X, 9)1	105.629130559038
poly(X, 9)2	59.6661724142847
poly(X, 9)3	60.4528273101325
poly(X, 9)4	-0.428862843315038
poly(X, 9)6	-0.31462546850288
poly(X, 9)7	-0.879019730689118
poly(X, 9)8	1.03857084094882
poly(X, 9)9	0.76599542646805

Whereas, Best Subset selection identified a model with all ten polynomials as the best model based on R^2, both Forward and Backwards selection dropped the 10th degree polynomial. However, for both BIC and Cp, the Forward and Backward selection was similiar to best subset selection.