FE590. Assignment #3.

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Instructions

In this assignment, you should use R markdown to answer the questions below. Simply type your R code into embedded chunks as shown above.

When you have completed the assignment, knit the document into a PDF file, and upload *both* the .pdf and .Rmd files to Canvas.

Note that you must have LaTeX installed in order to knit the equations below. If you do not have it installed, simply delete the questions below.

Question 1 (based on JWHT Chapter 5, Problem 8)

In this problem, you will perform cross-validation on a simulated data set.

You will use this personalized simulated data set for this problem:

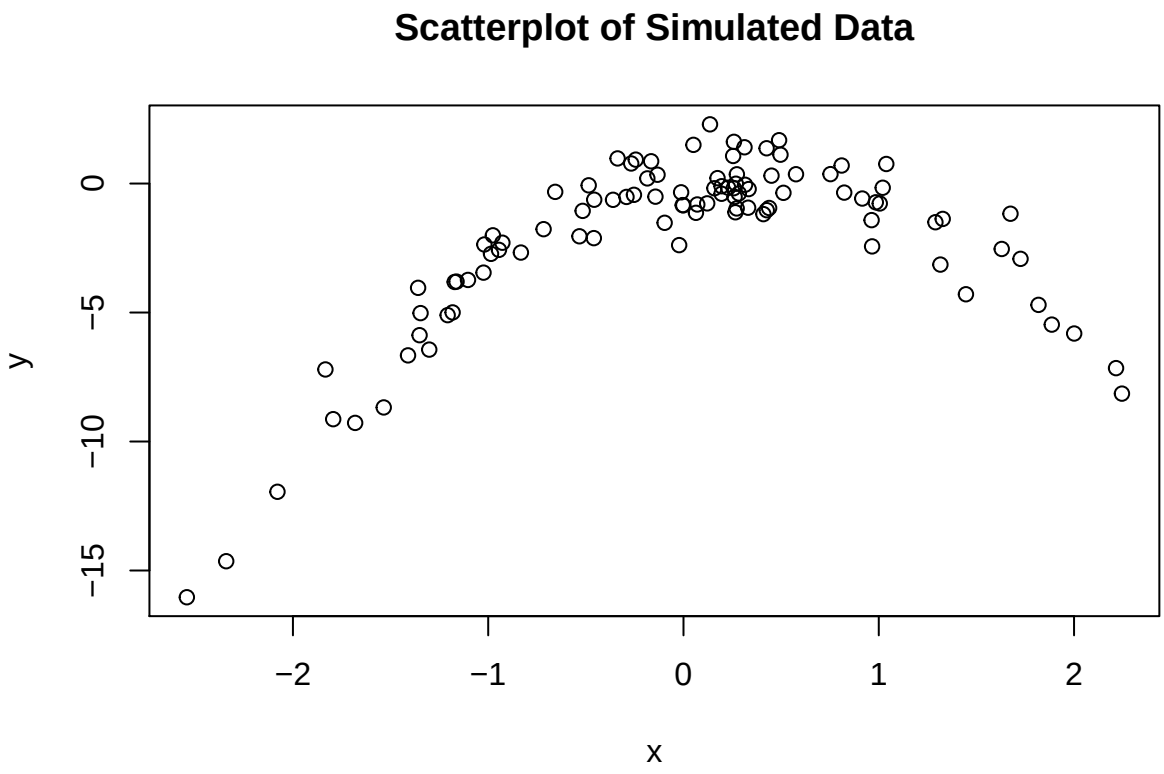
```
CWID = 10402229 #Place here your Campus wide ID number, this will personalize
#your results, but still maintain the reproduceable nature of using seeds.
#If you ever need to reset the seed in this assignment, use this as your seed
#Papers that use -1 as this CWID variable will earn 0's so make sure you change
#this value before you submit your work.
personal = CWID %% 10000
set.seed(personal)



y <- rnorm(100)
x <- rnorm(100)
y <- x - 2*x^2 + rnorm(100)
```

(a) In this data set, what is n and what is p?

n - the number of observations in the data set (100) p - The number of parameters or variables in the data set (1)

(b) Create a scatterplot of x against y. Comment on what you find.

```
plot(x = x, y = y, main = "Scatterplot of Simulated Data")
```



We notice that the data approximately follows a concave (downward) parabola such that $X \in [-2.5, 2.5], Y \in [-16, 5]$, where X is proportional with Y from -2.5 to about 0, and then becomes inversely proportional from 0 to 2.5.

(c) Compute the LOOCV errors that result from fitting the following four models using least squares:

1. $Y = \beta_0 + \beta_1 X + \epsilon$
2. $Y = \beta_0 + \beta_1 X + \beta_2 X^2 + \epsilon$
3. $Y = \beta_0 + \beta_1 X + \beta_2 X^2 + \beta_3 X^3 + \epsilon$
4. $Y = \beta_0 + \beta_1 X + \beta_2 X^2 + \beta_3 X^3 + \beta_4 X^4 + \epsilon$

First, let's do some setup. Define a data.frame to be subset per each model build in LOOCV and a vector `m.cv` to store each model's CV error.

```
library(boot)
```

```
## Warning: package 'boot' was built under R version 3.4.4
```

```
df = data.frame(x=x, y=y)
m.cv = c()
```

Calculate the CV Errors for each model

```
# Model 1
m1 = glm(y ~ poly(x, 1), data = df)
m.cv[1] = cv.glm(data = df, glmfit = m1)$delta[1]

# Model 2
m2 = glm(y ~ poly(x, 2), data = df)
m.cv[2] = cv.glm(data = df, glmfit = m2)$delta[1]
```

```r
# Model 3
m3 = glm(y ~ poly(x, 3), data = df)
m.cv[3] = cv.glm(data = df, glmfit = m3)$delta[1]

# Model 4
m4 = glm(y ~ poly(x, 4), data = df)
m.cv[4] = cv.glm(data = df, glmfit = m4)$delta[1]
```

(d) Which of the models in (c) had the smallest LOOCV error? Is this what you expected? Explain your answer.

```r
m.cv_min = which.min(m.cv)
m.cv
```

```
## [1] 9.6816227 0.9922244 1.0075138 1.0432976
```

```r
m.cv_min
```

```
## [1] 2
```

```r
m.cv[m.cv_min]
```

```
## [1] 0.9922244
```

The second model minimizes the LOOCV error. This is not surprising since we know that the relationship between X and Y is downward parabolic, hence can be modeled by a quadratic fit. Model two fits a quadratic function to the data via OLS, thus it make sense that this best models the data

(e) Comment on the statistical significance of the coefficient estimates that results from fitting each of the models in (c) using least squares. Do these results agree with the conclusions drawnbased on the cross-validation results?

```r
summary(m1)
```

```
##
## Call:
## glm(formula = y ~ poly(x, 1), data = df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -10.2467   -1.0363    0.8618    1.7251    4.1663
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -2.0748     0.3008  -6.898 5.21e-10 ***
## poly(x, 1)   14.7527     3.0077   4.905 3.71e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 9.046258)
##
##     Null deviance: 1104.18  on 99  degrees of freedom
## Residual deviance:  886.53  on 98  degrees of freedom
## AIC: 508
##
## Number of Fisher Scoring iterations: 2
```

Model 1: X is statistically significant at the highest degree (~0), but also has the highest LOOCV error.

```r
summary(m2)
```

```
##
## Call:
## glm(formula = y ~ poly(x, 2), data = df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.37172  -0.65502  -0.00739   0.57782   2.44563
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -2.07482    0.09829  -21.11   <2e-16 ***
## poly(x, 2)1  14.75271    0.98295   15.01   <2e-16 ***
## poly(x, 2)2 -28.15694    0.98295  -28.64   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.9661872)
##
##     Null deviance: 1104.18  on 99  degrees of freedom
## Residual deviance:   93.72  on 97  degrees of freedom
## AIC: 285.3
##
## Number of Fisher Scoring iterations: 2
```

Model 2: X and X^2 are statistically significant at the highest degree with the lowest LOOCV error.

```r
summary(m3)
```

```
##
## Call:
## glm(formula = y ~ poly(x, 3), data = df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.37204  -0.69417  -0.00868   0.58942   2.44098
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -2.07482    0.09874  -21.01   <2e-16 ***
## poly(x, 3)1  14.75271    0.98739   14.94   <2e-16 ***
## poly(x, 3)2 -28.15694    0.98739  -28.52   <2e-16 ***
## poly(x, 3)3   0.35592    0.98739    0.36    0.719
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.9749321)
##
##     Null deviance: 1104.176  on 99  degrees of freedom
## Residual deviance:   93.593  on 96  degrees of freedom
## AIC: 287.17
##
## Number of Fisher Scoring iterations: 2
```

Model 3: X and X^2 are statistically significant at the highest degree, while X^3 is not statistically significant with the 2nd lowest LOOCV error

```
summary(m4)
```

```
##
## Call:
## glm(formula = y ~ poly(x, 4), data = df)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.35467  -0.69598   0.00338   0.60461   2.41284
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -2.07482    0.09923 -20.910   <2e-16 ***
## poly(x, 4)1  14.75271    0.99229  14.867   <2e-16 ***
## poly(x, 4)2 -28.15694    0.99229 -28.376   <2e-16 ***
## poly(x, 4)3   0.35592    0.99229   0.359    0.721
## poly(x, 4)4  -0.23114    0.99229  -0.233    0.816
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.9846322)
##
##     Null deviance: 1104.18  on 99  degrees of freedom
## Residual deviance:   93.54  on 95  degrees of freedom
## AIC: 289.11
##
## Number of Fisher Scoring iterations: 2
```

Model 4: X and X^2 are statistically significant at the highest degree, while X^3 and X^4 are not statistically significant with the 2nd highest LOOCV error

---

Conclusion: The statistical significance of the coefficient estimates are consistent and agree with the LOOCV results. We find that only X and X^2 are ever statistically significant (again indiciative of a quadratic relationship between X and Y). Further, LOOCV shows that the model with the lowest error is Model 2 where all predictors (X, X^2) are statistically significant at the highest degree.

Question 2 (based on JWTH Chapter 7, Problem 10)

The question refers to the 'College' data set

Load ISLR and checkout the data set:

```
library(ISLR)
```

```
## Warning: package 'ISLR' was built under R version 3.4.4
```

```
attach(College)
dim(College)
```

```
## [1] 777  18
```

```
names(College)
```

```
##  [1] "Private"     "Apps"        "Accept"      "Enroll"      "Top10perc"
##  [6] "Top25perc"   "F.Undergrad" "P.Undergrad" "Outstate"    "Room.Board"
## [11] "Books"       "Personal"    "PhD"         "Terminal"    "S.F.Ratio"
## [16] "perc.alumni" "Expend"      "Grad.Rate"
```

(a) Split the data into a training set and a test set. Using out-of-state tuition as the response and the other variables as the predictors, perform subset selection (your choice on how) in order to identify a satisfactory model that uses just a subset of the predictors (if your approach suggests using all of the predictors, then follow your results and use them all).

Split data into non-overlapping test and train subsets:

```
obs <- 1:nrow(College)
train.idx <- sample(x = obs, size = round(nrow(College) / 2))
test.idx <- obs[!(obs %in% train.idx)]

intersect(train.idx, test.idx) # Confirm that training and testing sets do not overlap
```

```
## integer(0)
```

```
# Subset College
train <- College[train.idx,]
test <- College[test.idx,]
```

Perform an exhaustive feature subset selection with the Leaps package:

```
library(leaps)
```

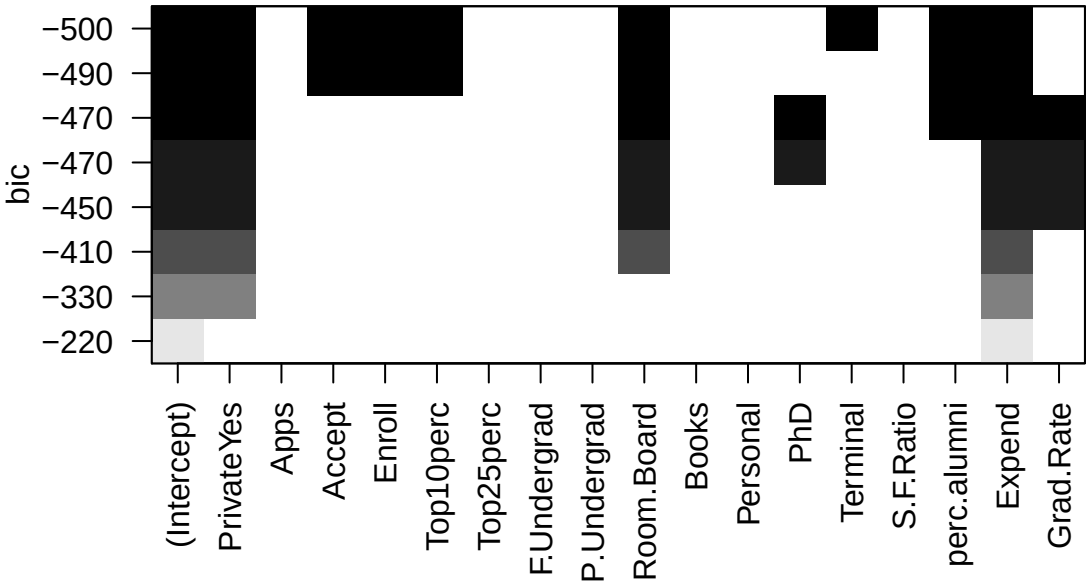
```
## Warning: package 'leaps' was built under R version 3.4.2
```

```
out <- regsubsets(Outstate~., data=train)
summary(out)
```

```
## Subset selection object
## Call: regsubsets.formula(Outstate ~ ., data = train)
## 17 Variables  (and intercept)
##             Forced in Forced out
## PrivateYes      FALSE      FALSE
## Apps            FALSE      FALSE
## Accept          FALSE      FALSE
## Enroll          FALSE      FALSE
## Top10perc       FALSE      FALSE
## Top25perc       FALSE      FALSE
## F.Undergrad     FALSE      FALSE
## P.Undergrad     FALSE      FALSE
## Room.Board      FALSE      FALSE
## Books           FALSE      FALSE
## Personal        FALSE      FALSE
## PhD             FALSE      FALSE
## Terminal        FALSE      FALSE
## S.F.Ratio       FALSE      FALSE
## perc.alumni     FALSE      FALSE
## Expend          FALSE      FALSE
## Grad.Rate       FALSE      FALSE
## 1 subsets of each size up to 8
## Selection Algorithm: exhaustive
##          PrivateYes Apps Accept Enroll Top10perc Top25perc F.Undergrad
## 1  ( 1 ) " "        " "  " "    " "    " "       " "       " "
```

```
## 2  ( 1 ) "*"         " "  " "    " "    " "        " "        " "
## 3  ( 1 ) "*"         " "  " "    " "    " "        " "        " "
## 4  ( 1 ) "*"         " "  " "    " "    " "        " "        " "
## 5  ( 1 ) "*"         " "  " "    " "    " "        " "        " "
## 6  ( 1 ) "*"         " "  " "    " "    " "        " "        " "
## 7  ( 1 ) "*"         " "  "*"    "*"    "*"        " "        " "
## 8  ( 1 ) "*"         " "  "*"    "*"    "*"        " "        " "
##          P.Undergrad Room.Board Books Personal PhD Terminal S.F.Ratio
## 1  ( 1 ) " "          " "        " "   " "      " " " "      " "
## 2  ( 1 ) " "          " "        " "   " "      " " " "      " "
## 3  ( 1 ) " "          "*"        " "   " "      " " " "      " "
## 4  ( 1 ) " "          "*"        " "   " "      " " " "      " "
## 5  ( 1 ) " "          "*"        " "   " "      "*" " "      " "
## 6  ( 1 ) " "          "*"        " "   " "      "*" " "      " "
## 7  ( 1 ) " "          "*"        " "   " "      " " " "      " "
## 8  ( 1 ) " "          "*"        " "   " "      " " "*"      " "
##          perc.alumni Expend Grad.Rate
## 1  ( 1 ) " "         "*"    " "
## 2  ( 1 ) " "         "*"    " "
## 3  ( 1 ) " "         "*"    " "
## 4  ( 1 ) " "         "*"    "*"
## 5  ( 1 ) " "         "*"    "*"
## 6  ( 1 ) "*"         "*"    "*"
## 7  ( 1 ) "*"         "*"    " "
## 8  ( 1 ) "*"         "*"    " "
```

```
plot(out)
```



Given the results of the Linear Regression model subsets, we find that the model that minimizes BIC on the training data set contains the following features: - PrivateYes (Private) - Accept - Enroll - Top10perc
- Room.Board
- Terminal - perc.alumni - Expend

(b) Fit a GAM on the training data, using out-of-state tuition as the response and the features selected in the previous step as the predictors, using splines of each feature with 5 df.

```
library(gam)
```

```
## Warning: package 'gam' was built under R version 3.4.4
```

```
## Loading required package: splines
```

```
## Loading required package: foreach
```

```
## Warning: package 'foreach' was built under R version 3.4.4
```

```
## Loaded gam 1.16
```

```
lm.m1  <- lm(Outstate ~ Private + Accept + Enroll + Top10perc + Room.Board + Terminal + perc.alumni + E
summary(lm.m1)
```

```
##
## Call:
## lm(formula = Outstate ~ Private + Accept + Enroll + Top10perc +
##     Room.Board + Terminal + perc.alumni + Expend, data = train)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -7109.0 -1228.6    25.9  1146.8  9603.7
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.858e+03  6.839e+02  -2.717 0.006888 **
## PrivateYes   2.540e+03  3.331e+02   7.625 1.98e-13 ***
## Accept       7.950e-01  1.201e-01   6.618 1.25e-10 ***
## Enroll      -2.019e+00  3.078e-01  -6.559 1.78e-10 ***
## Top10perc    3.697e+01  8.505e+00   4.347 1.78e-05 ***
## Room.Board   8.379e-01  1.181e-01   7.093 6.46e-12 ***
## Terminal     3.326e+01  8.744e+00   3.803 0.000166 ***
## perc.alumni  5.031e+01  1.014e+01   4.961 1.06e-06 ***
## Expend       2.079e-01  2.772e-02   7.503 4.48e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1941 on 379 degrees of freedom
## Multiple R-squared:  0.7595, Adjusted R-squared:  0.7544
## F-statistic: 149.6 on 8 and 379 DF,  p-value: < 2.2e-16
```

```
gam.m2 <- gam(Outstate ~ Private + s(Accept, 5) + s(Enroll, 5) + s(Top10perc, 5) + s(Room.Board, 5) + s
summary(gam.m2)
```

```
##
## Call: gam(formula = Outstate ~ Private + s(Accept, 5) + s(Enroll, 5) +
##     s(Top10perc, 5) + s(Room.Board, 5) + s(Terminal, 5) + s(perc.alumni,
##     5) + s(Expend, 5), data = train)
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -6642.01  -929.44    76.04  1063.44  7633.87
##
## (Dispersion Parameter for gaussian family taken to be 3060585)
##
##     Null Deviance: 5933703550 on 387 degrees of freedom
## Residual Deviance: 1074265203 on 350.9999 degrees of freedom
## AIC: 6932.649
##
## Number of Local Scoring Iterations: 3
##
## Anova for Parametric Effects
##                    Df     Sum Sq    Mean Sq F value    Pr(>F)
## Private             1 1606802426 1606802426 524.998 < 2.2e-16 ***
## s(Accept, 5)        1  367164734  367164734 119.966 < 2.2e-16 ***
## s(Enroll, 5)        1  266670811  266670811  87.131 < 2.2e-16 ***
## s(Top10perc, 5)     1 1022127223 1022127223 333.965 < 2.2e-16 ***
## s(Room.Board, 5)    1  305284128  305284128  99.747 < 2.2e-16 ***
## s(Terminal, 5)      1   59402742   59402742  19.409 1.403e-05 ***
## s(perc.alumni, 5)   1   90608719   90608719  29.605 9.957e-08 ***
## s(Expend, 5)        1  381354009  381354009 124.602 < 2.2e-16 ***
## Residuals         351 1074265203    3060585
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Anova for Nonparametric Effects
##                    Npar Df  Npar F     Pr(F)
```

```
## (Intercept)
## Private
## s(Accept, 5)            4  8.9574 6.738e-07 ***
## s(Enroll, 5)            4  4.7952 0.0008891 ***
## s(Top10perc, 5)         4  2.0622 0.0853216 .
## s(Room.Board, 5)        4  1.9923 0.0952130 .
## s(Terminal, 5)          4  2.5272 0.0405241 *
## s(perc.alumni, 5)       4  0.5370 0.7086589
## s(Expend, 5)            4 15.4257 1.236e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

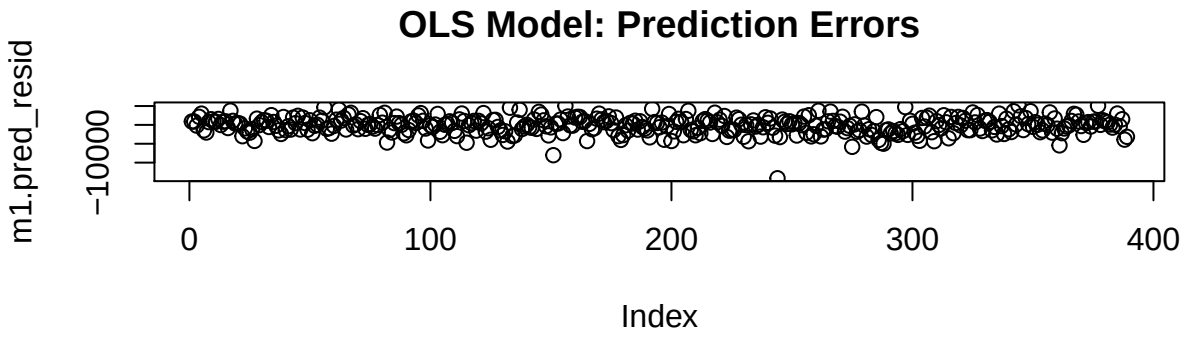
Private is a categorical variable (unordered), splines cannot be applied to such data. Splines, however, are applied to all other selected features with Degrees of Freedom (DF =) 5

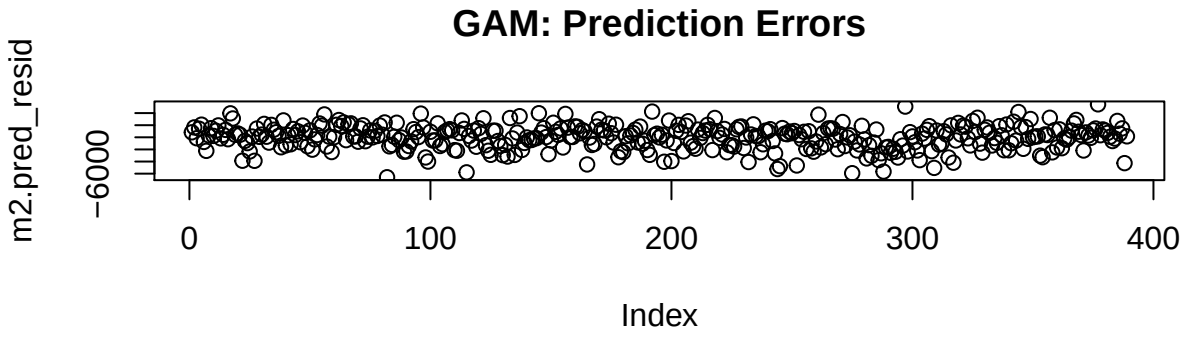
Both an OLS model and a GAM are fit above so as to benchmark the GAM to some other model solely for reference

(c) Evaluate the model obtained on the test set, and explain the results obtained

Evaluating `lm.m1` and `gam.m2` on `test`:

```r
# Predict on test data
m1.pred <- predict(lm.m1, newdata = test)
m2.pred <- predict(gam.m2, newdata = test)

# Get the prediction errors (residuals)
m1.pred_resid <- test$Outstate - m1.pred
m2.pred_resid <- test$Outstate - m2.pred

par(mfrow=c(2,1))
# Plot the residuals
plot(m1.pred_resid, main="OLS Model: Prediction Errors")
plot(m2.pred_resid, main="GAM: Prediction Errors")
```






```
print(paste("OLS Residual Mean: ", mean(m1.pred_resid)))
```

```
## [1] "OLS Residual Mean:  -104.034603931161"
```

```
print(paste("GAM Residual Mean: ", mean(m2.pred_resid)))
```

```
## [1] "GAM Residual Mean:  -3.28994397011662"
```

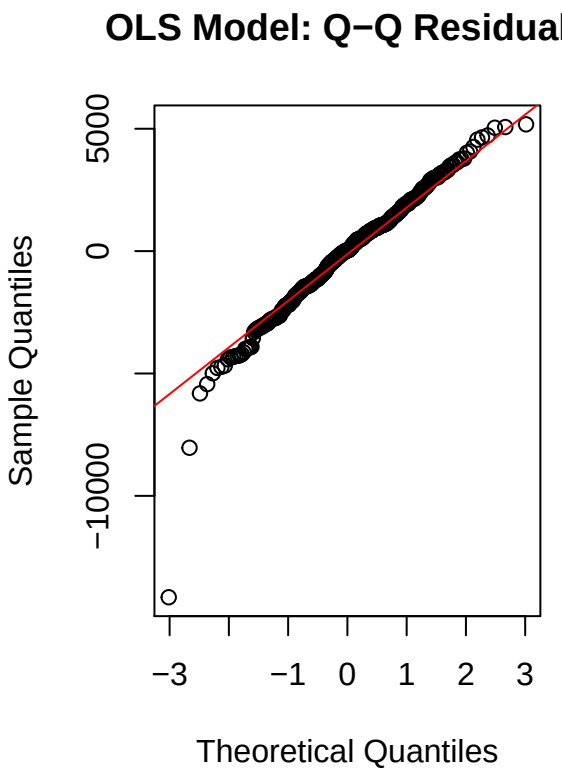
```
print(paste("OLS Residual Variance: ", var(m1.pred_resid)))
```

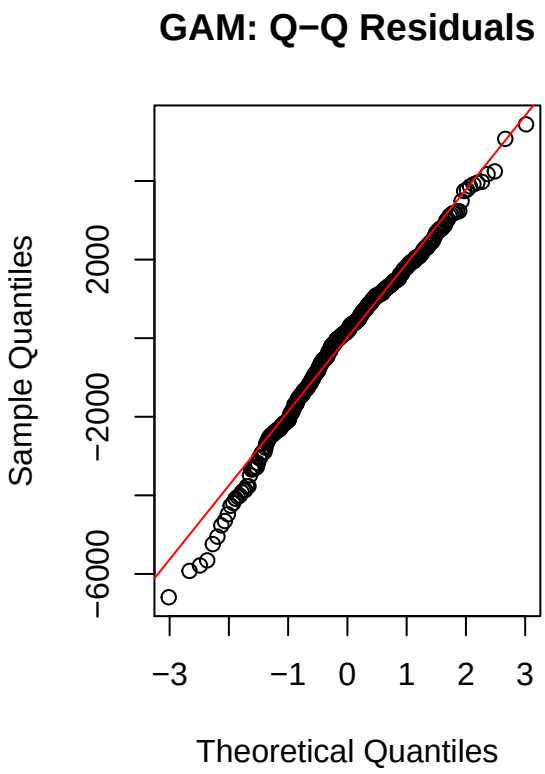
```
## [1] "OLS Residual Variance:  4809283.08361994"
```

```
print(paste("GAM Residual Variance: ", var(m2.pred_resid)))
```

```
## [1] "GAM Residual Variance:  3820180.07761222"
```

```
par(mfrow=c(1,2))

{
  qqnorm(m1.pred_resid, main = "OLS Model: Q-Q Residuals")
  qqline(m1.pred_resid, col = "red")
}

{
  qqnorm(m2.pred_resid, main = "GAM: Q-Q Residuals")
  qqline(m2.pred_resid, col = "red")
}
```






```
# check the MSE
print(paste("OLS MSE: ", sum(m1.pred_resid^2)/length(m1.pred_resid)))
```

```
## [1] "OLS MSE:  4807743.08684734"
```

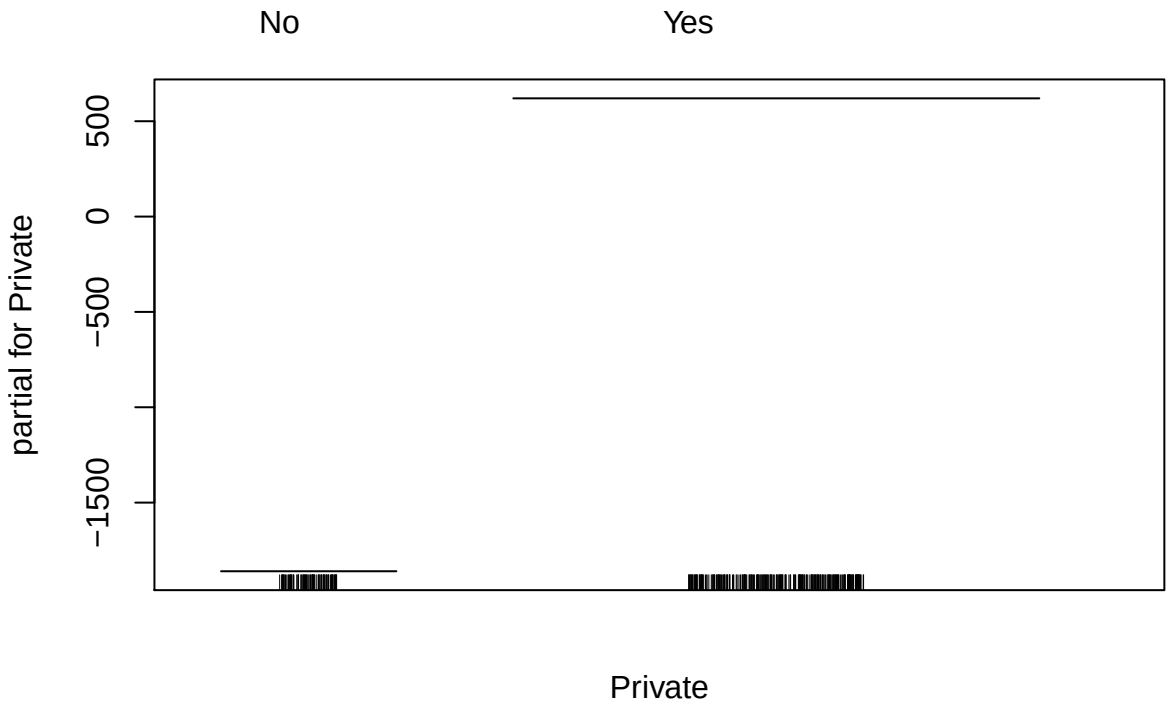
```
print(paste("GAM MSE: ", sum(m2.pred_resid^2)/length(m2.pred_resid)))
```

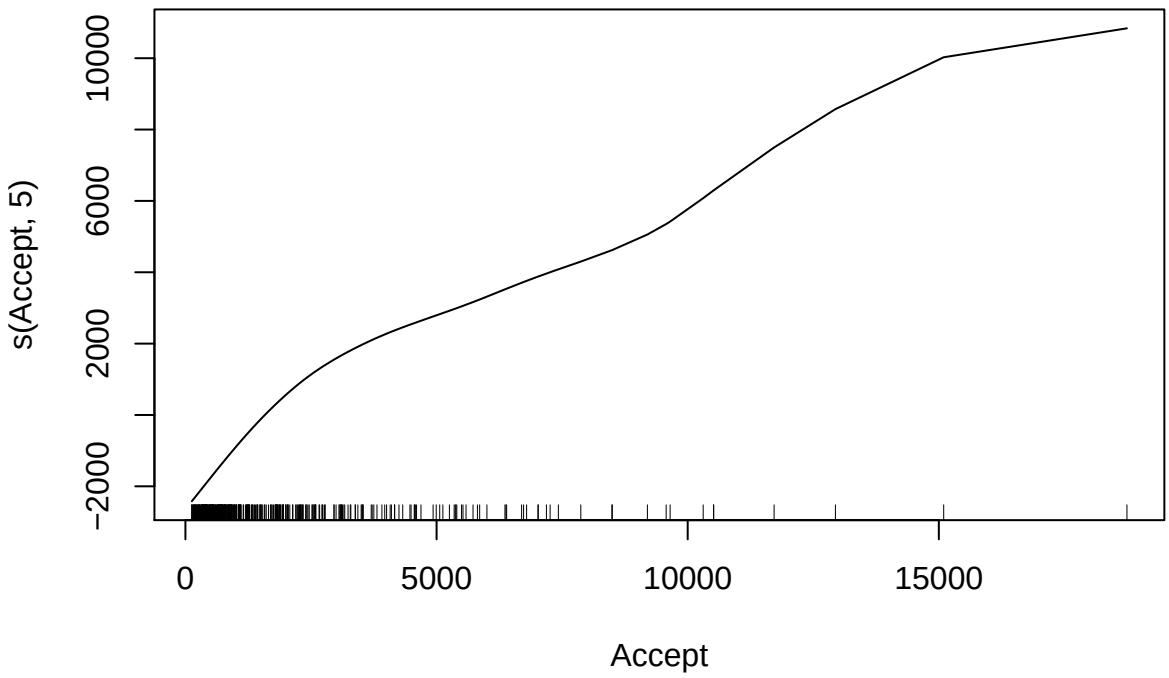
```
## [1] "GAM MSE:  3810370.38700521"
```

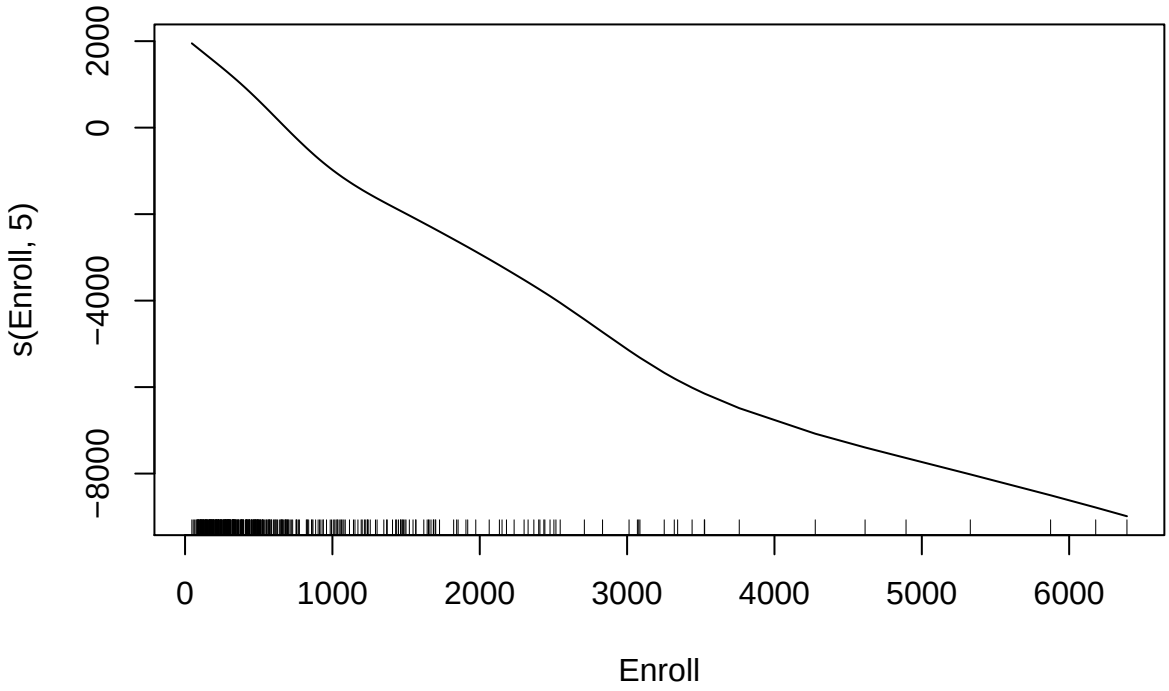
We find that the model that minimizes the MSE on the testing data is the `gam.m2` model. Comparatively, the results show that the residuals of the GAM model most closely resemble a white noise error term with mean 0, smaller variance term. Further, the GAM's MSE is less than that of the OLS model. Therefore, the GAM shows better out of sample performance than the benchmark OLS

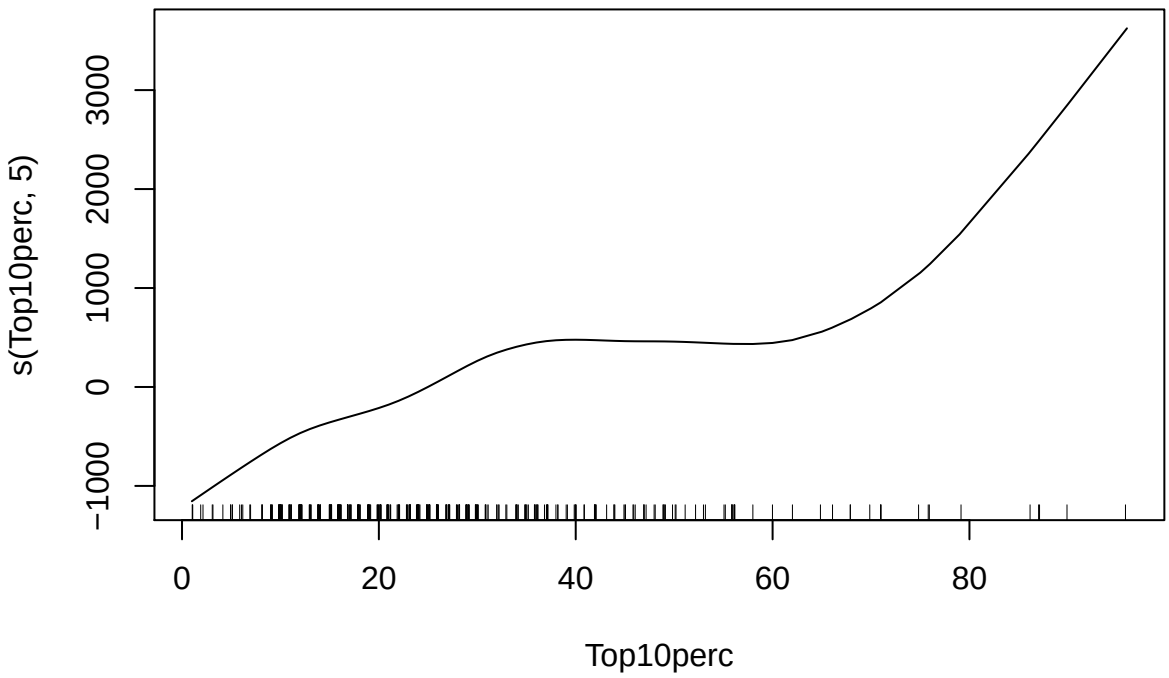
(d) For which variables, if any, is there evidence of a non-linear relationship with the response? Which are probably linear? Justify your answers.

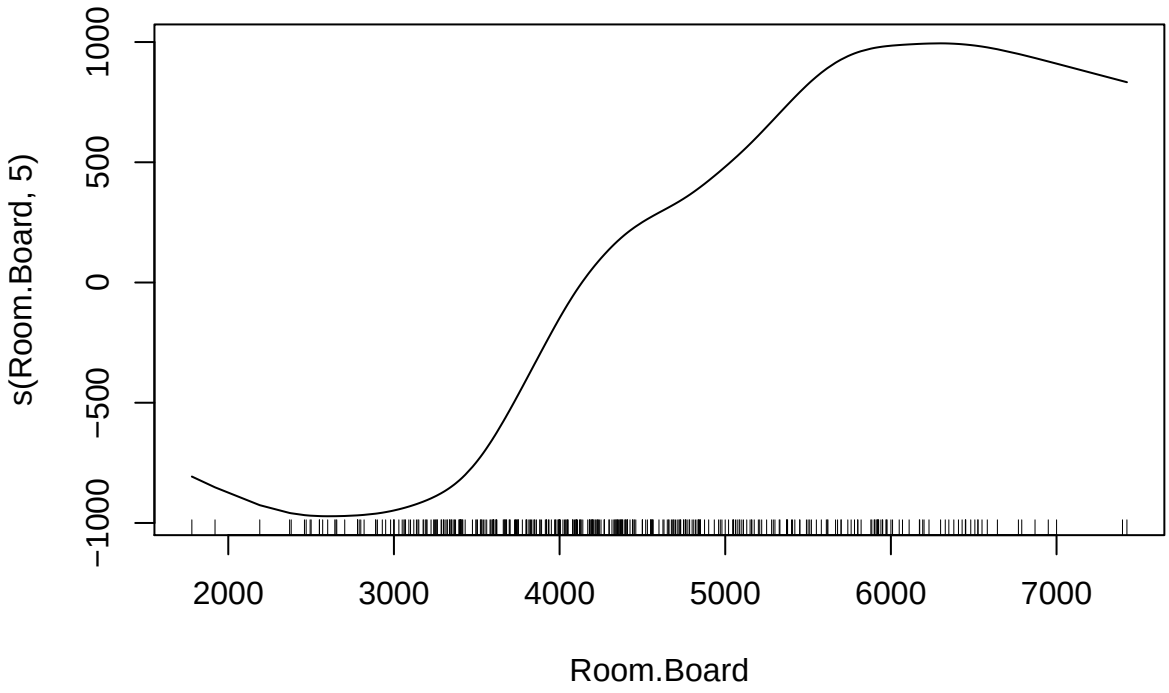
```
par(mfrow=c(1,1))
plot(gam.m2)
```

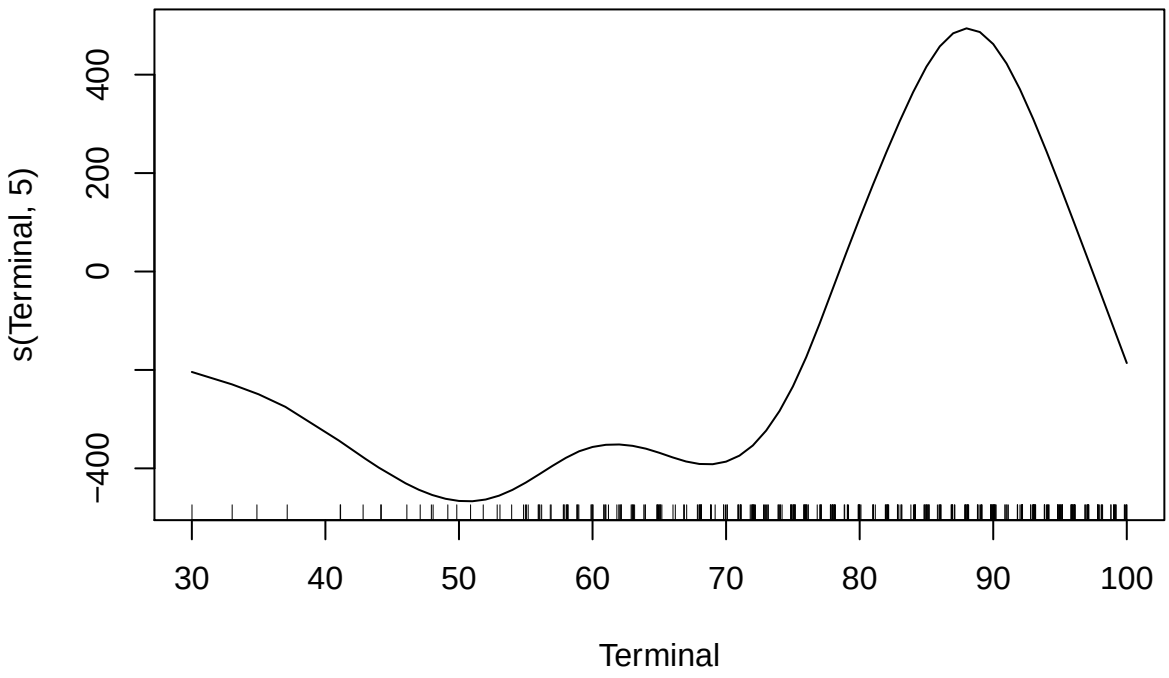

No
Yes
partial for Private
500
0
−500
−1500
Private

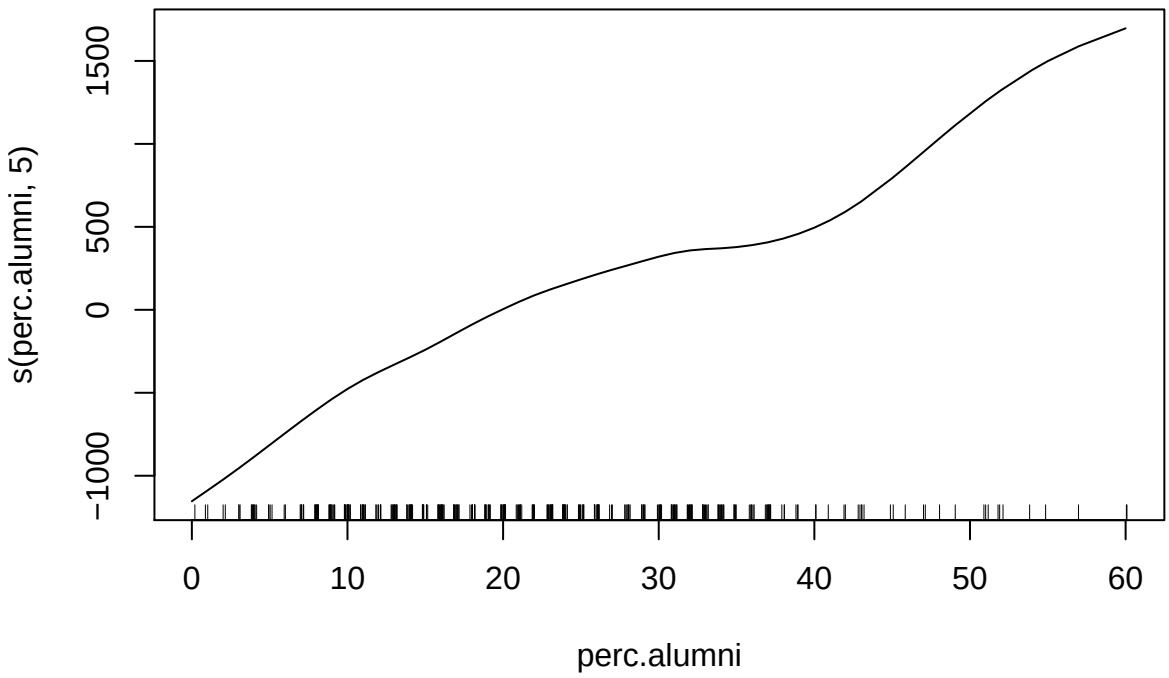

s(Accept, 5)
−2000
2000
6000
10000
0
5000
10000
15000
Accept

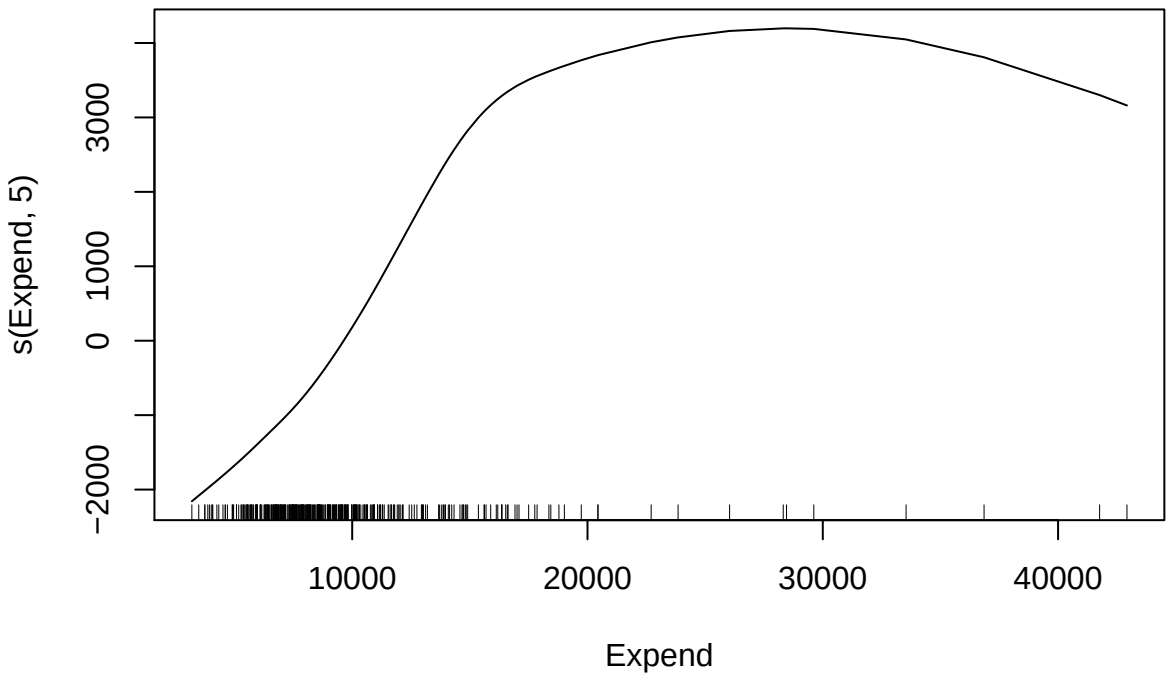

s(Enroll, 5)
2000
0
−4000
−8000
0
1000
2000
3000
4000
5000
6000
Enroll


s(Top10perc, 5)
−1000
0
1000
2000
3000
0
20
40
60
80
Top10perc


s(Room.Board, 5)
1000
500
0
−500
−1000
2000
3000
4000
5000
6000
7000
Room.Board


s(Terminal, 5)
−400
0
200
400
30
40
50
60
70
80
90
100
Terminal


s(perc.alumni, 5)
−1000
0
500
1500
0
10
20
30
40
50
60
perc.alumni



`plot.gam()` plots the partial terms (primary effects) of each compnent on the outcome variable. Terms like `Accept`, `Enroll`, and `perc.alumni` show approximately linear relationship with the response as their plots above show roughly constant proportional relationships throughout the domain of the input feature. `Expend` most closely resembelse a concave parabola. `Top10perc` is roughly similar to a nonlinear polynomial of the 3rd degree as it increases proportionally from [0, 40], flattens from [40, 60] and then increases again from [60, 100]. `Room.Board` also appears to be a nonlinear polynomial of the 3rd degree. For [2000, 4500], the relationship is a convex parabola while from [4500, 7000] is a concave parabola. Lastly, `Terminal` is a higher order polynomial (>= 5) since the relationship varies throughout the domain of the feature.

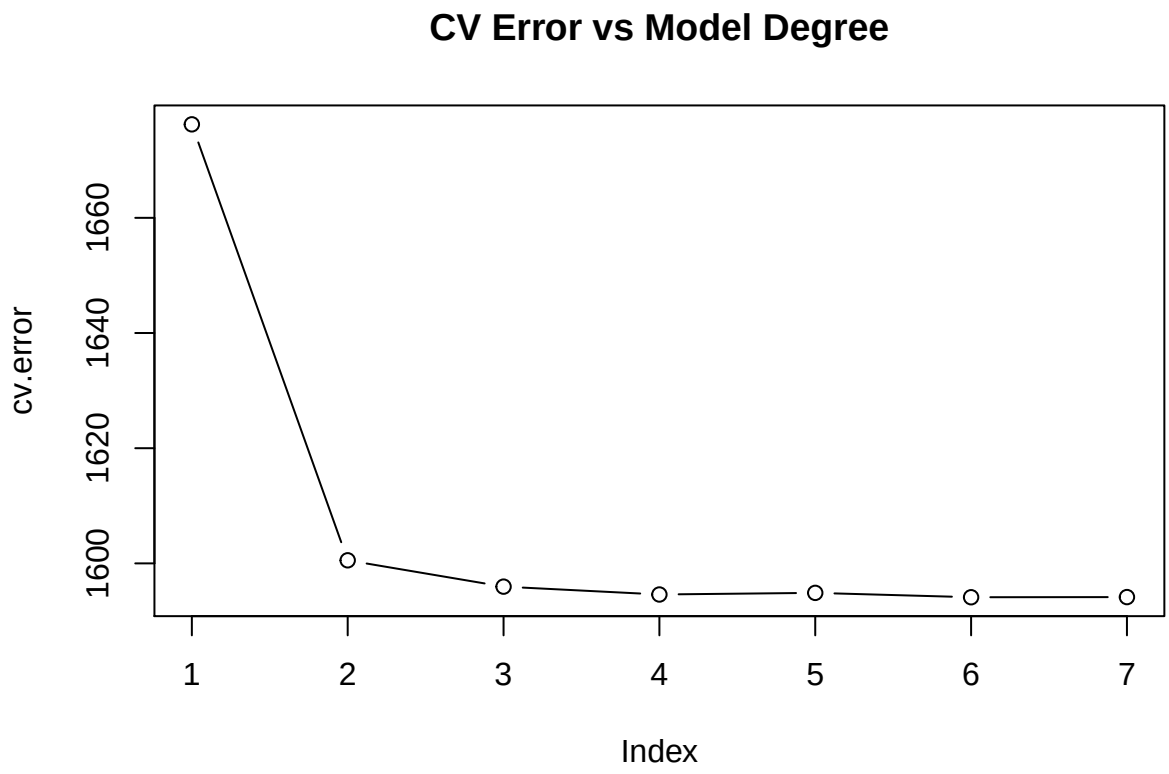
Question 3 (based on JWHT Chapter 7, Problem 6)

In this exercise, you will further analyze the `Wage` data set.

(a) Perform polynomial regression to predict `wage` using `age`. Use cross-validation to select the optimal degree d for the polynomial. What degree was chosen? Make a plot of the resulting polynomial fit to the data.

Testing polynomial models of degrees 1 through 7:

```
cv.error <- rep(Inf, 7)

for(i in 1:7){
  mdl <- glm(wage ~ poly(age, i), data = Wage)
  cv.error[i] = cv.glm(data = Wage, glmfit = mdl)$delta[1]
}

plot(cv.error, type="b", main = "CV Error vs Model Degree")
```




```
cv.error
```

```
## [1] 1676.235 1600.529 1595.960 1594.596 1594.879 1594.119 1594.145
```

```
idx <- which.min(cv.error)
idx
```

```
## [1] 6
```

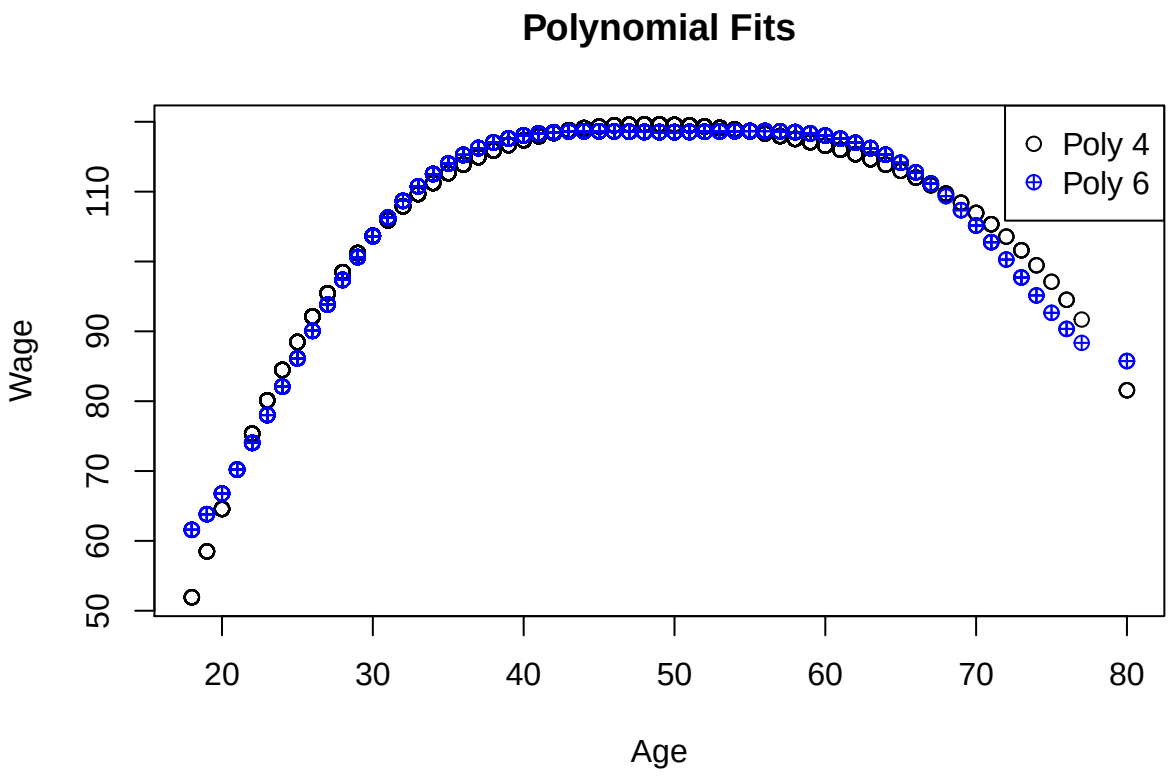
```
cv.error[idx]
```

```
## [1] 1594.119
```

The model that best minimizes the error via CV is the polynomial model of degree = 6. However, from the plot above we can see that this model is likely unnecessarily complicated as each extra term beyond the 3rd degree is only marginally decreasing the CV error.

Let's compare the plots of models of degree 4 and 6

```
m4 <- glm(wage ~ poly(age, 4), data = Wage)
m6 <- glm(wage ~ poly(age, 6), data = Wage)

{
  plot(y=m4$fitted.values, x=Wage$age, pch = 1, ylab = "Wage", xlab = "Age", main = "Polynomial Fits")
  points(y=m6$fitted.values, x=Wage$age, col = "blue", pch = 10)
  legend("topright", c("Poly 4", "Poly 6"), col = c("black", "blue"), pch = c(1, 10))
}
```



(b) Fit a step function to predict `wage` using `age`, and perform cross-validation to choose the optimal number of cuts. Make a plot of the fit obtained.

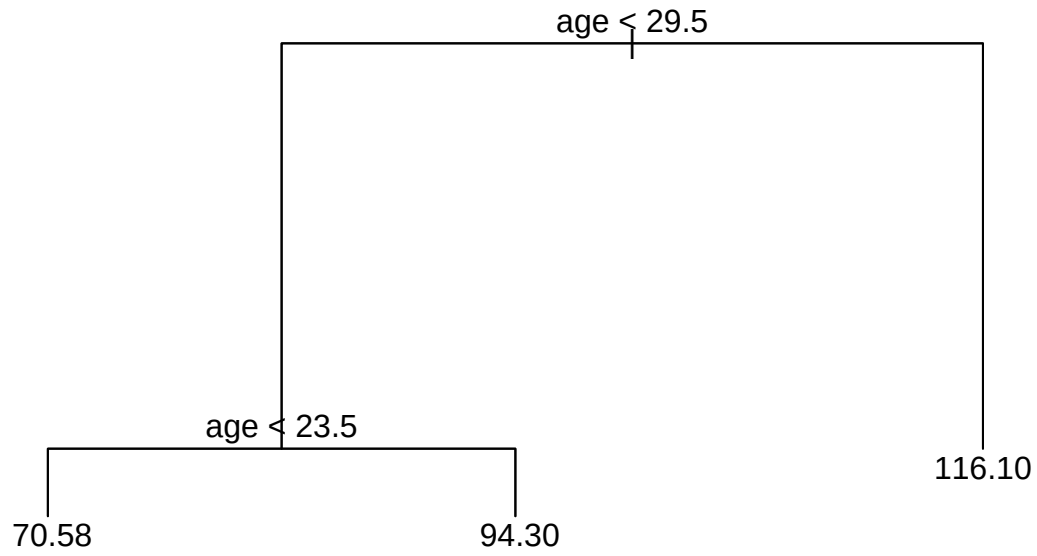
```
library(tree)
```

```
## Warning: package 'tree' was built under R version 3.4.4
```

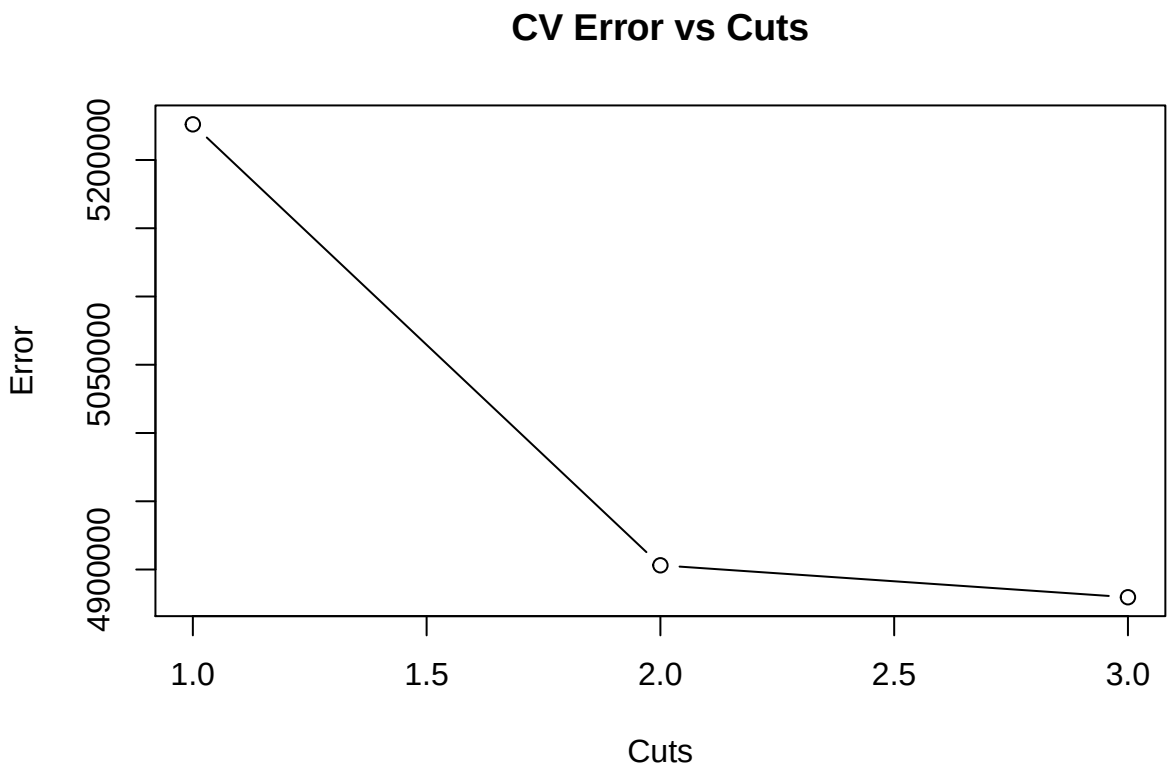
```
# Model regression tree
mdl <- tree(wage~age, data = Wage)
summary(mdl)
```

```
##
## Regression tree:
## tree(formula = wage ~ age, data = Wage)
## Number of terminal nodes:  3
## Residual mean deviance:  1615 = 4839000 / 2997
## Distribution of residuals:
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -96.000 -25.610  -6.254   0.000  15.530 202.300
```

```
# Plot the Tree
{
  plot(mdl)
  text(mdl, pretty = 1)
}
```




```
# Run K-Fold CV
cv.mdl <- cv.tree(mdl)
plot(cv.mdl$size, cv.mdl$dev, type="b", main="CV Error vs Cuts", ylab="Error", xlab="Cuts")
```



According to the plot above. Three cuts minimizes CV error, however this improvement is marginal beyond the second cut.

Question 4 (based on JWHT Chapter 8, Problem 8)

In the lab, a classification tree was applied to the `Carseats` data set after converting Sales into a qualitative response variable. Now we will seek to predict Sales using regression trees and related approaches, treating the response as a quantitative variable.

(a) Split the data set into a training set and a test set.

```
obs <- 1:nrow(Carseats)
train.idx <- sample(obs, size = round(length(obs)/2))
test.idx <- obs[!(obs %in% train.idx)]

intersect(train.idx, test.idx) # Should be Null
```

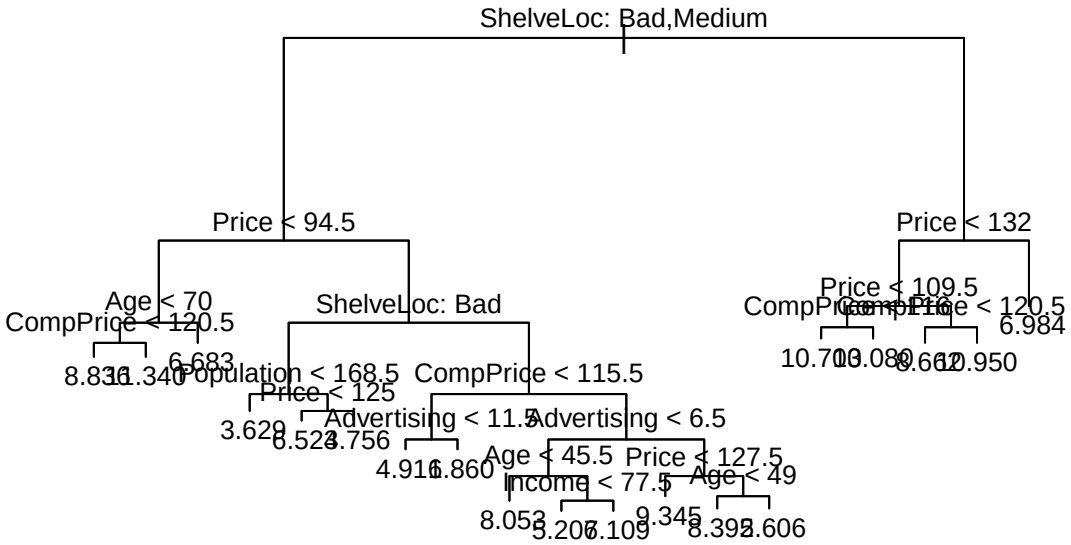
```
## integer(0)
```

```
train <- Carseats[train.idx,]
test <- Carseats[test.idx,]
```

(b) Fit a regression tree to the training set. Plot the tree, and interpret the results. What test MSE do you obtain?

```
mdl <- tree(Sales~., data = train)

{
```

```
  plot(mdl)
  text(mdl, pretty = 0, cex = 0.8)
}
```



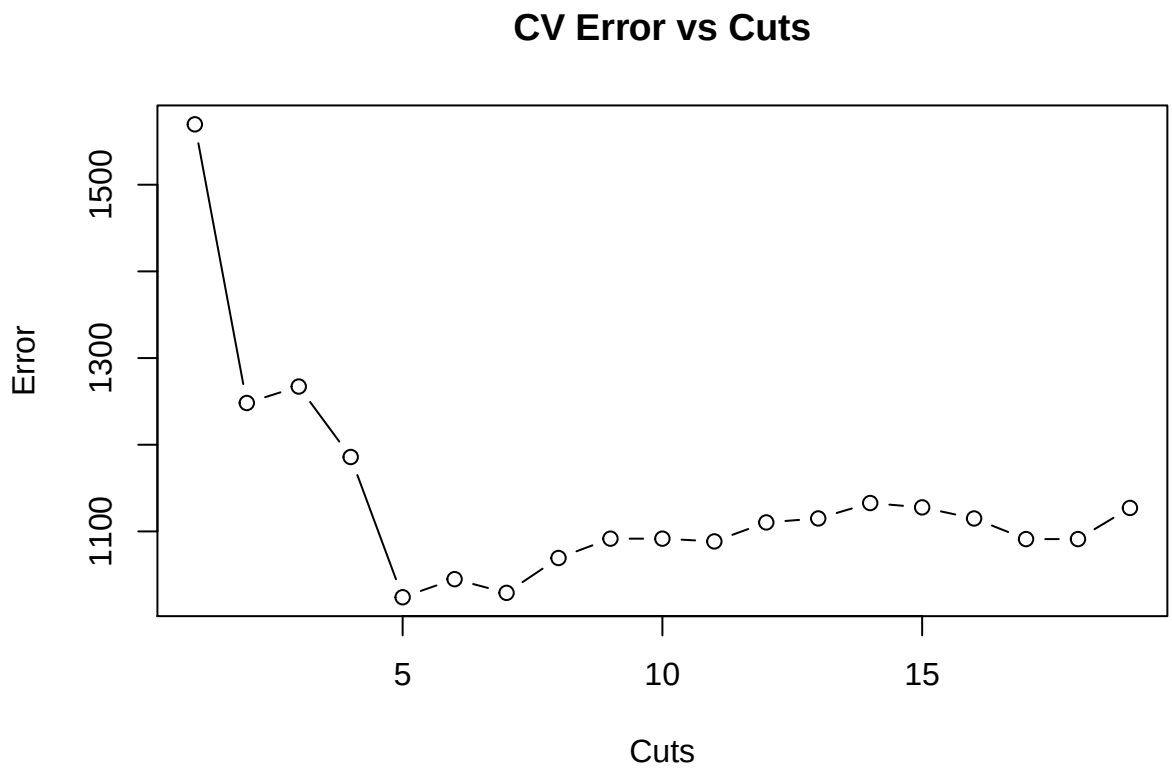

```
summary(mdl)
```

```
##
## Regression tree:
## tree(formula = Sales ~ ., data = train)
## Variables actually used in tree construction:
## [1] "ShelveLoc"   "Price"       "Age"         "CompPrice"   "Population"
## [6] "Advertising" "Income"
## Number of terminal nodes:  19
## Residual mean deviance:  1.943 = 351.6 / 181
## Distribution of residuals:
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
## -4.75100 -0.78590  0.03508  0.00000  0.82610  3.62600
```

The MSE (residual mean deviance in the summary above) is 2.053. The `ShelveLoc` and `Price` variables have the most significant impact on the outcome as they are the first and second variables to partition the space, respectively.

(c) Use cross-validation in order to determine the optimal level of tree complexity. Does pruning the tree improve the test MSE?

```
cv.mdl <- cv.tree(mdl)
plot(cv.mdl$size, cv.mdl$dev, type="b", main="CV Error vs Cuts", ylab="Error", xlab="Cuts")
```



Above we can see that the number of cuts locally minimizes the CV error at `nCuts` = 6. Error then increases, plateaus and steadily declines as the number of cuts increase. Thus, let's examine the tree with 6 cuts:

```
mdl.pruned <- prune.tree(mdl, best = 6)
mean( (test$Sales - predict(mdl, newdata = test))^2)        # MSE Non-Pruned Tree
```

```
## [1] 4.905835
```

```
mean( (test$Sales - predict(mdl.pruned, newdata = test))^2) # MSE Pruned Tree
```

```
## [1] 5.251832
```

Pruning does not improve the MSE of the model, which is intuitive since we are removing decision-making from the model. Though MSE is increased, we are reducing the amount of overfitting in the model.

(d) Use the bagging approach in order to analyze this data. What test MSE do you obtain? Use the `importance()` function to determine which variables are most important.

```
library(randomForest)
```

```
## Warning: package 'randomForest' was built under R version 3.4.4
```

```
## randomForest 4.6-14
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
mdl.bag <- randomForest(Sales ~ ., data = train, importance=TRUE)
mdl.bag
```

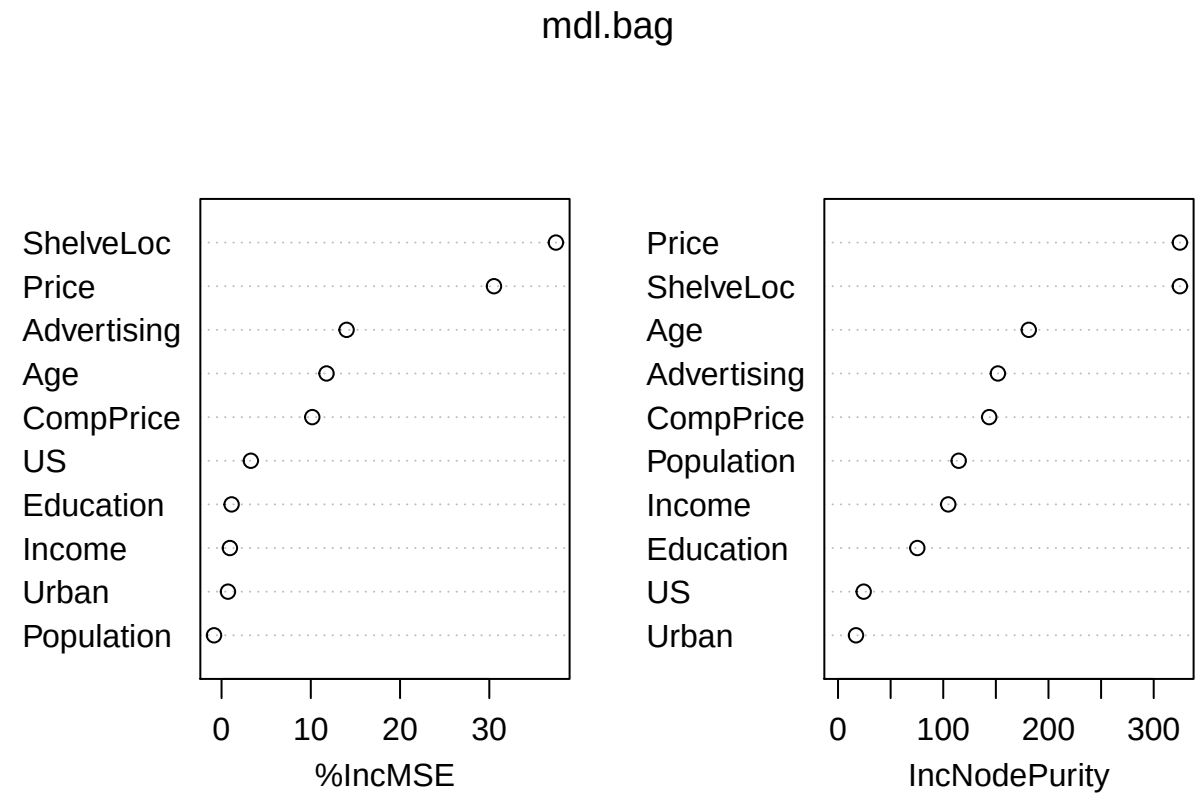
```
##
## Call:
```

```
##  randomForest(formula = Sales ~ ., data = train, importance = TRUE)
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 3
##
##           Mean of squared residuals: 3.357296
##                     % Var explained: 56.6
```

```
importance(mdl.bag)
```

```
##                %IncMSE IncNodePurity
## CompPrice   10.1626771     143.65510
## Income       0.9343679     104.73854
## Advertising 14.0104534     151.93162
## Population  -0.8421888     114.69947
## Price       30.5231982     324.91038
## ShelveLoc   37.4624584     324.88664
## Age         11.7611060     181.25809
## Education    1.1258044      75.36676
## Urban        0.7189220      17.07740
## US           3.2821644      24.38017
```

```
varImpPlot(mdl.bag)
```



The variable importance plots affirm that `Price` and `ShelveLoc` are again the most important features as removing them would subject the model to a high % increase in MSE.

The new MSE is:

```
mean((test$Sales - predict(mdl.bag, newdata = test))^2)
```

```
## [1] 3.246154
```

Question 5 (based on JWTH Chapter 8, Problem 10)

Use boosting (and bagging) to predict Salary in the Hitters data set

(a) Remove the observations for which salary is unknown, and then log-transform the salaries

```
library(gbm)
```

```
## Warning: package 'gbm' was built under R version 3.4.4
```

```
## Loaded gbm 2.1.4
```

```
df <- Hitters[!is.na(Hitters$Salary),]
df$Salary <- log(df$Salary)
```

(b) Split the data into training and testing sets for cross validation purposes.

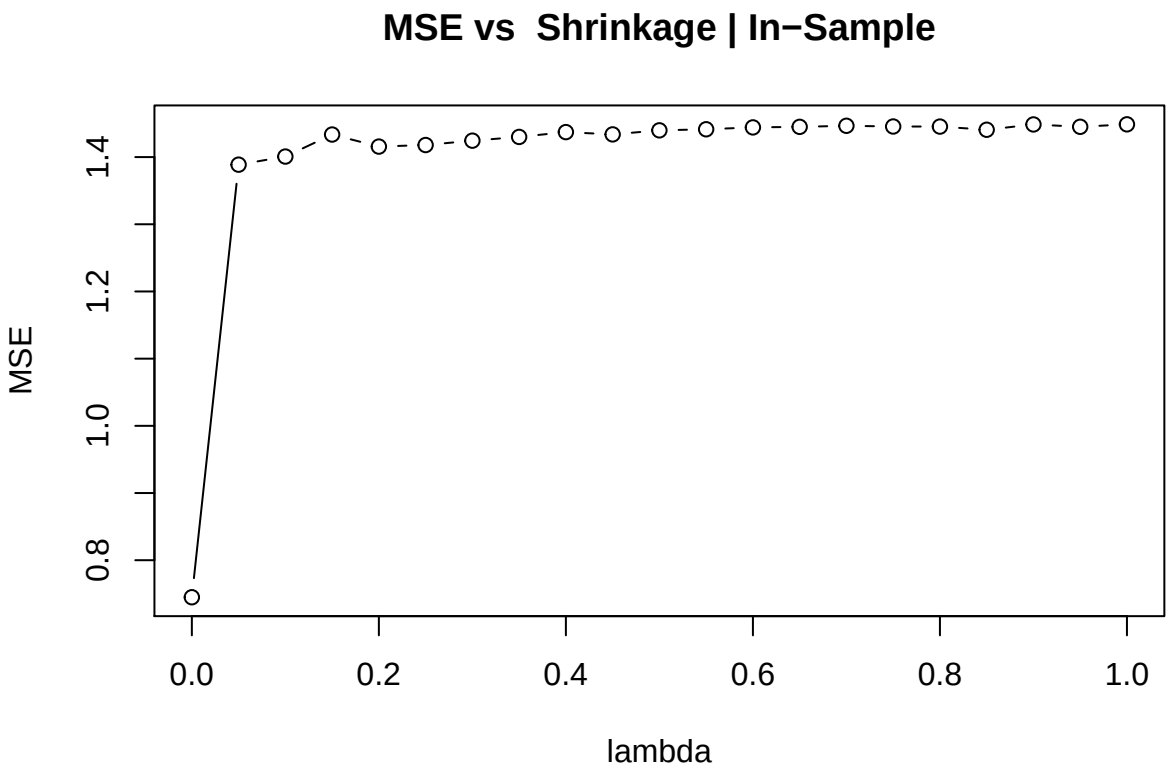
```
obs <- 1:nrow(df)
train.idx <- sample(obs, size = round(length(obs)/2))
test.idx <- obs[!(obs %in% train.idx)]

intersect(train.idx, test.idx) # Should be Null
```

```
## integer(0)
```

```
train <- df[train.idx,]
test <- df[test.idx,]
```

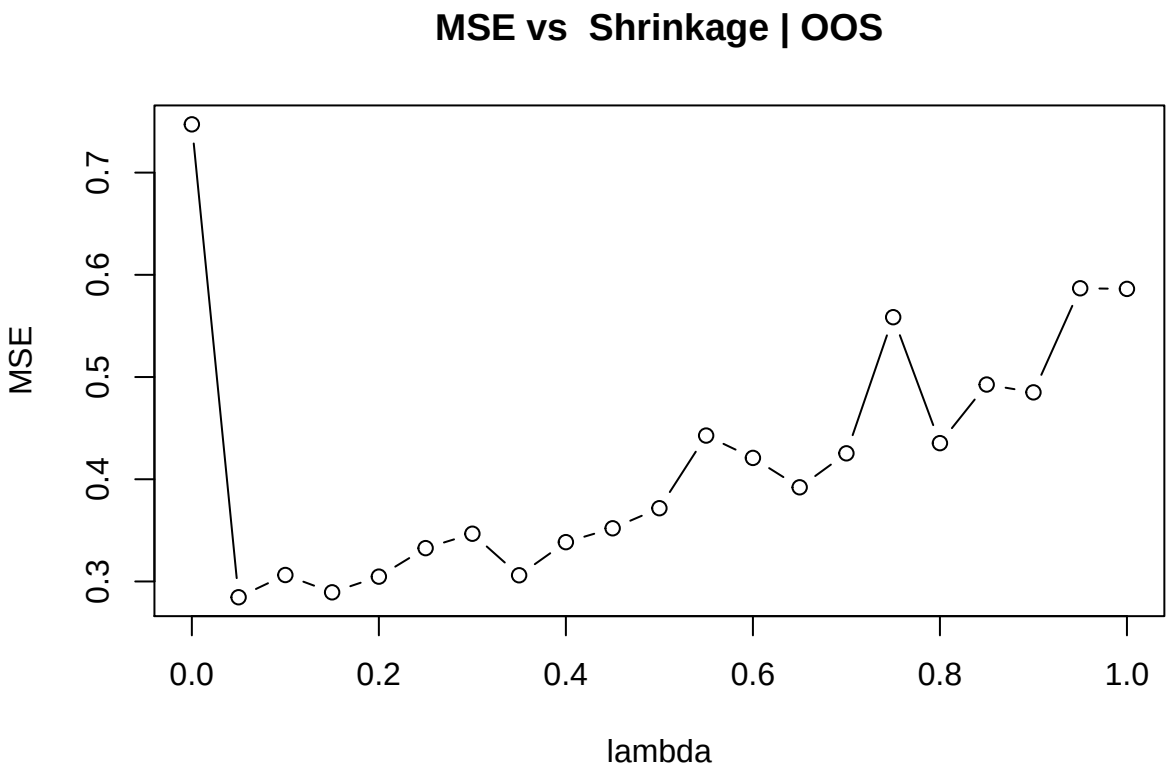
(c) Perform boosting on the training set with 1000 trees for a range of values of the shrinkage parameter λ. Produce a plot with different shrinkage parameters on the x-axis and the corresponding training set MSE on the y-axis

```
lambda <- seq(0, 1, by = 0.05)
MSE <- rep(Inf, 20)

for(i in 1:length(lambda)){
  mdl.boost <- gbm(Salary~., data = train, n.trees = 1000, shrinkage = lambda[i], distribution = "gauss
  MSE[i] <- mean( (test$Salary - predict(mdl.boost, newdata = train, n.trees = 1000))^2)
}

plot(y = MSE, x = lambda, main = "MSE vs  Shrinkage | In-Sample", type = "b")
```



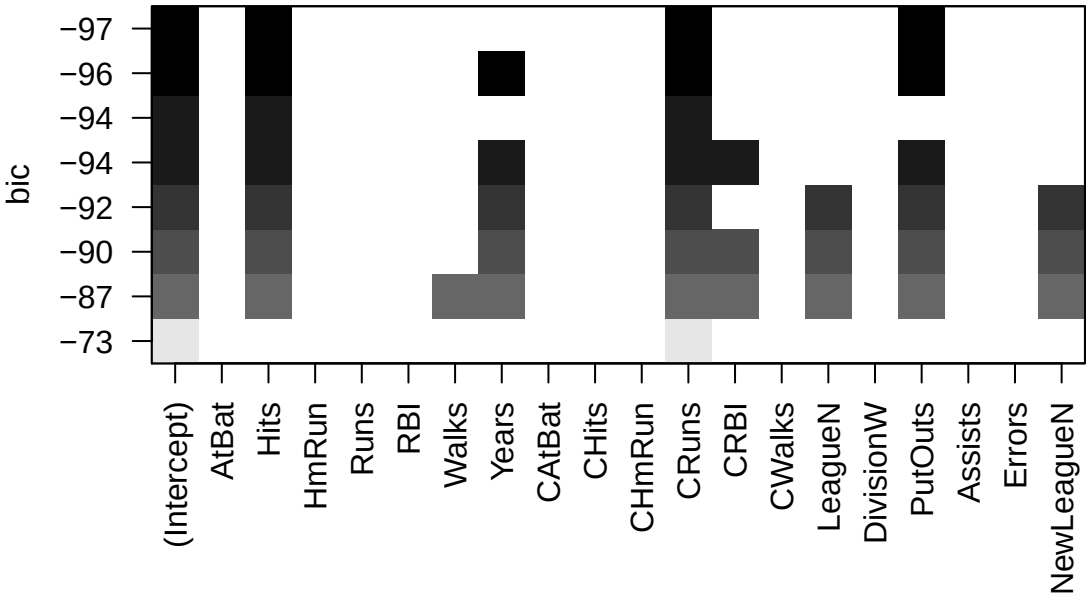
(d) Produce a plot similar to the last one, but this time using the test set MSE

```
MSE <- rep(Inf, 20)

for(i in 1:length(lambda)){
  mdl.boost <- gbm(Salary~., data = train, n.trees = 1000, shrinkage = lambda[i], distribution = "gauss
  MSE[i] <- mean( (test$Salary - predict(mdl.boost, newdata = test, n.trees = 1000))^2)
}

plot(y = MSE, x = lambda, main = "MSE vs  Shrinkage | OOS", type = "b")
```



(e) Fit the model using two other regression techniques (from previous classes) and compare the MSE of those techniques to the results of these boosted trees.

```
rsubs <- regsubsets(Salary ~ ., data = train)
plot(rsubs)
```



Utilizing regression subsets to select features based on the best linear regression model, the best model is:

$$Salary = \beta_0 + \beta_1 Runs + \beta_2 CHits$$

Let's build an OLS and GAM from this selected model:

```
mdl.lm <- lm(Salary ~ Runs + CHits, data = train)
mdl.gam <- gam(Salary ~ s(Runs, 5) + s(CHits, 5), data = train)
```

Now testing on OOS, we have MSEs

```
mean((test$Salary - predict(mdl.lm, newdata = test))^2) # OLS MSE
```

```
## [1] 0.4652213
```

```
mean((test$Salary - predict(mdl.gam, newdata = test))^2)# GAM MSE
```

```
## [1] 0.2897559
```

```
min(MSE)  # GBM MSE
```

```
## [1] 0.2845555
```

Despite utilizing feature selection before building OLS and GAMs, the OOS MSE of the boosted trees is still superior. This is given that we use the MSE of the error minimizing λ-shrinkage parameter.

(f) Reproduce (c) and (d), but this time use bagging instead of boosting and compare to the boosted MSE's and the MSE's from (e)

```
mdl.bag <- randomForest(Salary ~ ., data = train, importance=TRUE)
mdl.bag
```

```
##
## Call:
##  randomForest(formula = Salary ~ ., data = train, importance = TRUE)
##                Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 6
##
##           Mean of squared residuals: 0.1970462
##                     % Var explained: 76.24
```

Now we have:

```
mean((test$Salary - predict(mdl.lm, newdata = test))^2) # OLS MSE
```

```
## [1] 0.4652213
```

```
mean((test$Salary - predict(mdl.gam, newdata = test))^2)# GAM MSE
```

```
## [1] 0.2897559
```

```
min(MSE)                                                # GBM MSE
```

```
## [1] 0.2845555
```

```
mean((test$Salary - predict(mdl.bag, newdata = test))^2)# RF MSE
```

```
## [1] 0.2203611
```

Finally, we see that the bagging method (randomForest) outdoes the previously superior boosting method with the lowest MSE.