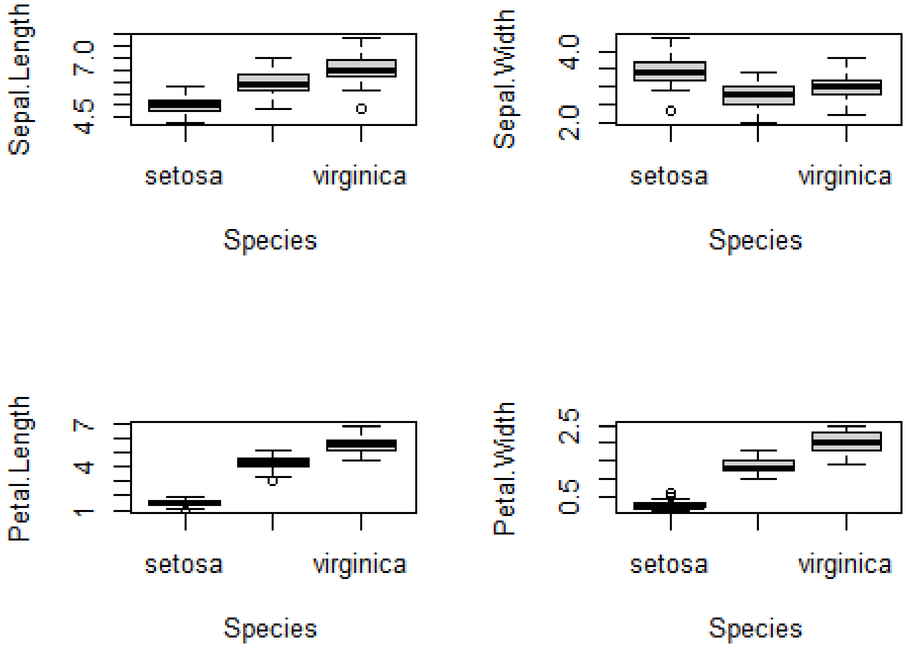
STAT318 Assignment 3
SJ/Katsu Lee
ID: 48792793

Question 1

```
# a)
library(caret)

## Loading required package: ggplot2

## Loading required package: lattice

dim(iris)

## [1] 150   5

summary(iris)

##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width   
##  Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100  
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300  
##  Median :5.800   Median :3.000   Median :4.350   Median :1.300  
##  Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199  
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800  
##  Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500  
##        Species  
##  setosa    :50  
##  versicolor:50  
##  virginica :50  
##                 
##                 
## 
```

There are 150 rows and 5 columns/variables. The variables are Sepal.length, Sepal.Width, Petal.Length, Petal.Width and Species.

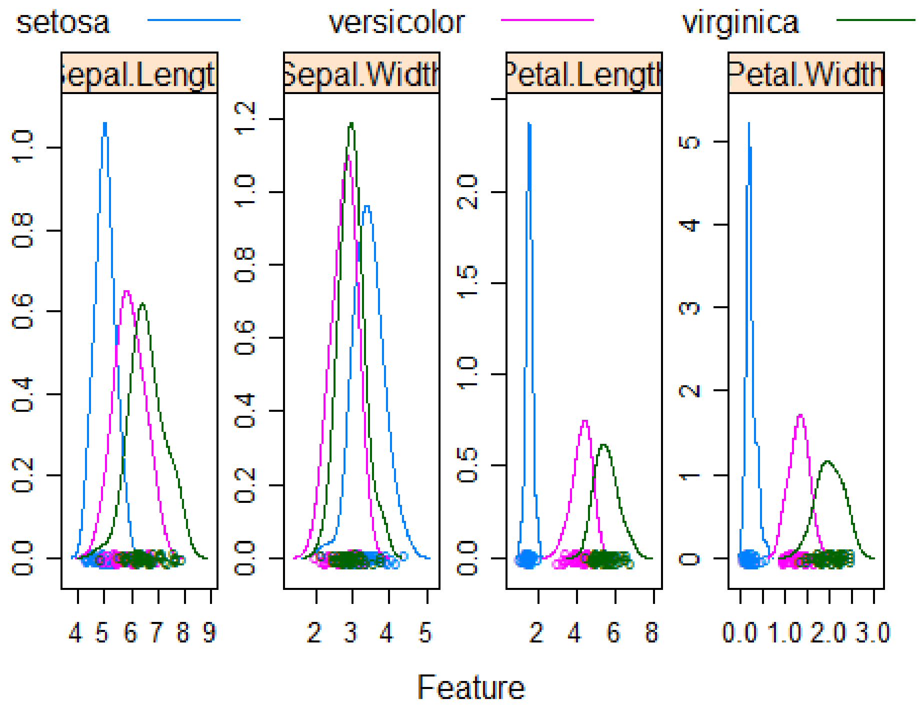
```
# b)
# Group by species
par(mfrow=c(2,2))
boxplot(Sepal.Length~Species, data = iris)
boxplot(Sepal.Width~Species, data = iris)
boxplot(Petal.Length~Species, data = iris)
boxplot(Petal.Width~Species, data = iris)
```



```
# c)
summary(iris)

##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width   
##  Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100  
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300  
##  Median :5.800   Median :3.000   Median :4.350   Median :1.300  
##  Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199  
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800  
##  Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500  
##        Species  
##  setosa    :50  
##  versicolor:50  
##  virginica :50  
##                 
##                 
## 
```

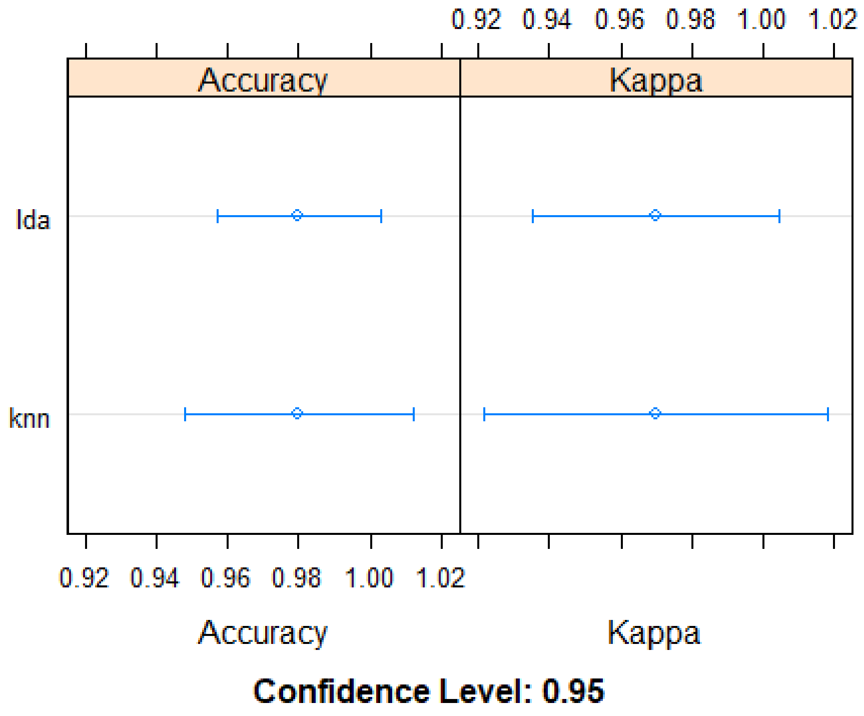
The data is not unbalanced as there are 3 classes in species (setosa, versicolor, virginica) with all equal ratios 50:50:50.

```
#d)

x <- iris[, 1:4]
y <- iris$Species
caret::featurePlot(x,
                   y,
                   plot="density",
                   scales = list(x = list(relation="free"),
                                 y = list(relation="free")),
                   adjust = 1.5,
                   pch = "o",
                   layout = c(4, 1),
                   auto.key = list(columns = 3))
```



From the density plot for petal length and petal width, we can see that the density of setosa flower does not overlap with the densities of the versicolor and virginica iris flowers.Because there is no overlap these might be better predictors for flower species. In the Sepal.Length and Sepal.Width plot all three densities (setosa, versicolor and virginica) have overlap which may mean they are not as significant for predictions. There is a a lot more overlap between all three species for the sepal length and sepal width features, so these variables are not as significant in predictions.

```
#e)
nfolds <- 10
traincontrol <- trainControl(method = "cv",
                             number = nfolds)
LDA <- train(Species ~ .,
             data = iris,
             method = "lda",
             trControl = traincontrol)

KNN <- train(Species ~ .,
             data = iris,
             method = "knn",
             tuneGrid   = expand.grid(k = c(1,2,3,4,5,6,7,8,9,10)),
             trControl = traincontrol,
             metric="Accuracy")

results <- resamples(list(lda=LDA, knn=KNN))
summary(results)

##
## Call:
## summary.resamples(object = results)
##
## Models: lda, knn
## Number of resamples: 10
##
## Accuracy
##          Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
## lda 0.9333333    0.95      1 0.98       1    1    0
## knn 0.8666667    1.00      1 0.98       1    1    0
##
## Kappa
##      Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
## lda  0.9   0.925      1 0.97       1    1    0
## knn  0.8   1.000      1 0.97       1    1    0

dotplot(results)
```



From the plot we can see that LDA is more accurate than knn. We can also see that knn has a larger 95% confidence interval compared to lda. Because of these two facts the lda should be used for better accuracy.

Question 2

```
#a
library(ISLR2)
summary(Credit)

##      Income           Limit           Rating          Cards      
##  Min.   : 10.35   Min.   :  855   Min.   : 93.0   Min.   :1.000  
##  1st Qu.: 21.01   1st Qu.: 3088   1st Qu.:247.2   1st Qu.:2.000  
##  Median : 33.12   Median : 4622   Median :344.0   Median :3.000  
##  Mean   : 45.22   Mean   : 4736   Mean   :354.9   Mean   :2.958  
##  3rd Qu.: 57.47   3rd Qu.: 5873   3rd Qu.:437.2   3rd Qu.:4.000  
##  Max.   :186.63   Max.   :13913   Max.   :982.0   Max.   :9.000  
##       Age          Education      Own      Student   Married     Region   
##  Min.   :23.00   Min.   : 5.00   No :193   No :360   No :155   East : 99  
##  1st Qu.:41.75   1st Qu.:11.00   Yes:207   Yes: 40   Yes:245   South:199  
##  Median :56.00   Median :14.00                                 West :102  
##  Mean   :55.67   Mean   :13.45                                            
##  3rd Qu.:70.00   3rd Qu.:16.00                                            
##  Max.   :98.00   Max.   :20.00                                            
##     Balance       
##  Min.   :   0.00  
##  1st Qu.:  68.75  
##  Median : 459.50  
##  Mean   : 520.01  
##  3rd Qu.: 863.00  
##  Max.   :1999.00

dim(Credit)

## [1] 400  11
```

There are 400 rows and 11 columns/variables. The variables are Income, Limit, Rating, Cards, Age, Education, Own, Student, Married, Region, Balance.

```
#b
creditBalanceMean <- mean(Credit$Balance)
creditBalanceMean

## [1] 520.015
```

Estimate for the population mean of the credit card balance is $520.015.

```
#c
n_observation <- nrow(Credit)
SE <- sd(Credit$Balance) / sqrt(n_observation)
SE
```

```
## [1] 22.98794
```

Estimate of the standard error is $22.98794.

```
#d
library(boot)

##
## Attaching package: 'boot'

## The following object is masked from 'package:lattice':
##
##     melanoma

meanfunc = function(x, index) {
  return(mean(x$Balance[index]))
}

bootSE <- boot(Credit, meanfunc, R=1000)
bootSE

##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
## boot(data = Credit, statistic = meanfunc, R = 1000)
##
##
## Bootstrap Statistics :
##     original    bias    std. error
## t1*  520.015 -0.850615    22.37525

bootSEval <- 22.23329
```

The standard error using bootstrap is $22.23329. Our standard error in c is a bit higher with value of $22.98794.

```
lower <- creditBalanceMean - 2*bootSEval
upper <- creditBalanceMean + 2*bootSEval
CI <- c(lower, upper)
CI

## [1] 475.5484 564.4816

t.test(Credit$Balance, conf.level = 0.95)

##
##  One Sample t-test
##
## data:  Credit$Balance
## t = 22.621, df = 399, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  474.8224 565.2076
## sample estimates:
## mean of x
##   520.015
```

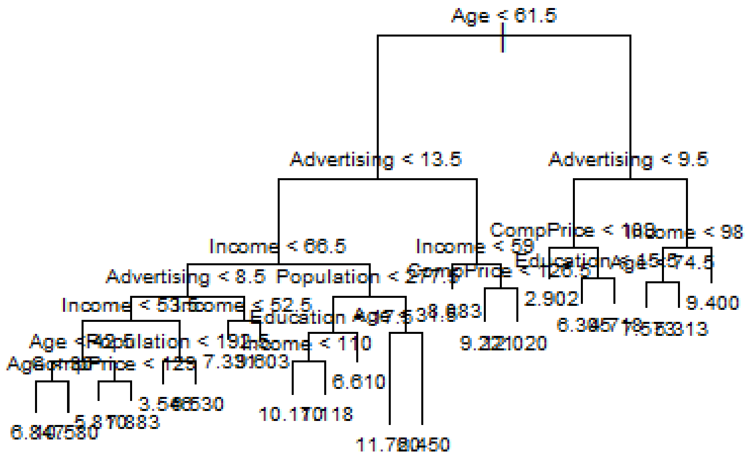
From the results we can see that they are very similar/values are very close to each other.

Question 3

```
library(tree)
library(gbm)

## Loaded gbm 2.1.8

library(randomForest)

## randomForest 4.6-14

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

##
## Attaching package: 'randomForest'

## The following object is masked from 'package:ggplot2':
##
##     margin

setwd("H:/Documents/STAT318/Assignments/Assignment3")
training = read.csv("carseatsTrain.csv")
testing = read.csv("carseatsTest.csv")

library(tree)
library(gbm)
library(randomForest)
library(MASS)

##
## Attaching package: 'MASS'

## The following object is masked from 'package:ISLR2':
##
##     Boston

setwd("H:/Documents/STAT318/Assignments/Assignment3")
training = read.csv("carseatsTrain.csv")
testing = read.csv("carseatsTest.csv")

#a)
plot.new()
train_tree <- tree(Sales~., data=training)
```

```
## Warning in tree(Sales ~ ., data = training): NAs introduced by coercion
```

```
plot(train_tree)
text(train_tree,
     cex=0.6)
```



```
trainingMSE <- (mean((predict(train_tree,
                newdata=training) - training$Sales) ^ 2))
```

```
## Warning in pred1.tree(object, tree.matrix(newdata)): NAs introduced by coe
rcion
```

```
testingMSE <- (mean((predict(train_tree,
               newdata=testing) - testing$Sales) ^ 2))
```

```
## Warning in pred1.tree(object, tree.matrix(newdata)): NAs introduced by coe
rcion
```

```
trainingMSE
```

```
## [1] 4.224765
```

```
testingMSE
```

```
## [1] 9.758961
```

From the tree we can see that there are 22 terminal nodes. We can also see that Age and Advertising are the most useful predictors as age is at the top and advertising is in the second level.

The training MSE is 4.224765 and the testing MSE is 9.758961.

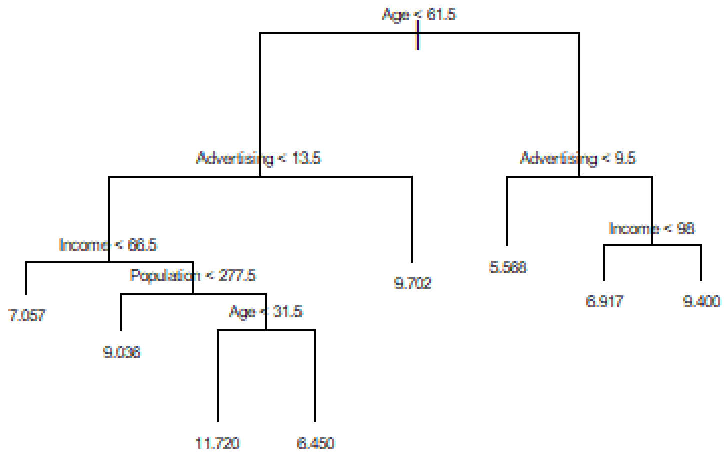
```
#b)
prune <- cv.tree(train_tree)
```

```
## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion

## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion

## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion

## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion

## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion

## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion

## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion

## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion

## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion
## Warning in tree(model = m[rand != i, , drop = FALSE]): NAs introduced by
## coercion

## Warning in pred1.tree(tree, tree.matrix(nd)): NAs introduced by coercion
```

```
prune
```

```
## $size
##  [1] 22 21 20 19 18 17 15 13 11 10  8  7  4  3  2  1
##
## $dev
##  [1] 2679.833 2640.129 2634.543 2663.411 2648.710 2637.552 2637.552 2488.7
73
##  [9] 2438.603 2438.603 2392.426 2371.598 2194.845 2185.154 2268.638 2355.0
73
##
## $k
##  [1]      -Inf  23.48884  23.54946  28.77311  32.44689  32.60524  32.75497
##  [8]  37.40522  38.43426  38.54855  41.61580  43.01071  69.00835  89.56740
## [15] 109.43976 185.42861
##
## $method
## [1] "deviance"
##
## attr(,"class")
## [1] "prune"         "tree.sequence"
```

```
tree_prune <- prune.tree(train_tree, best=8)
plot(tree_prune)
text(tree_prune,
     cex=0.5)
```



```
pruneMSE <- (mean((predict(tree_prune,
                  newdata=testing) - testing$Sales)^2))

## Warning in pred1.tree(object, tree.matrix(newdata)): NAs introduced by coe
rcion

pruneMSE

## [1] 7.004235
```

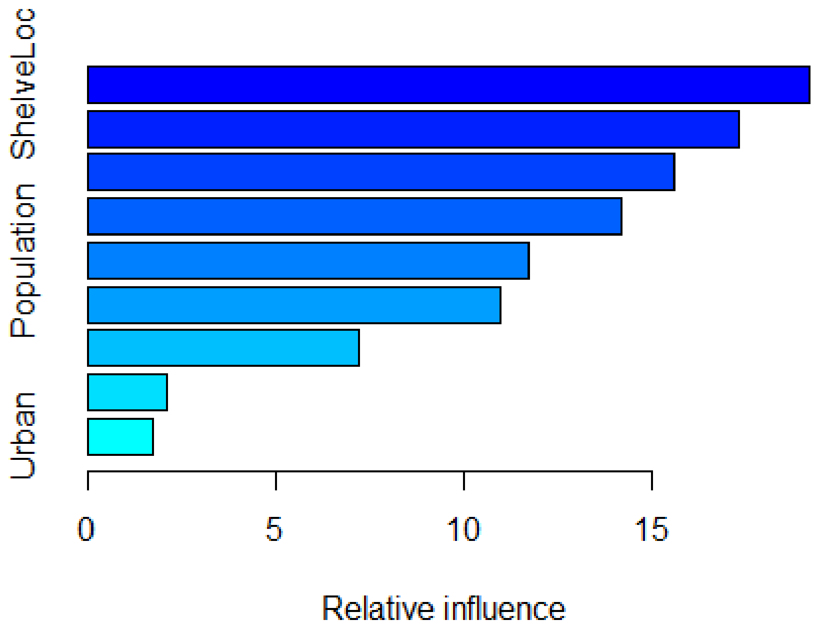
When we compare the pruned tree MSE and the non pruned tree MSE we can see that the pruned tree MSE (7.004235) is less than the non pruned tree (9.758961). So therefore the pruned tree does perform better.

```
#c)
randForest <- randomForest(Sales~.,data=training,importance=TRUE)

RF_train_MSE <- (mean((predict(randForest, newdata=training) - training$Sales
)^2))
RF_test_MSE <- (mean((predict(randForest, newdata=testing) - testing$Sales)^2
))

RF_train_MSE

## [1] 1.158755

RF_test_MSE
```

```
## [1] 5.039522

bagged <- randomForest(Sales~.,data=training,mtry=9,importance=TRUE)

bagged_train_MSE <- (mean((predict(bagged, newdata=training) - training$Sales
)^2))
bagged_test_MSE <- (mean((predict(bagged, newdata=testing) - testing$Sales)^2
))

bagged_train_MSE

## [1] 0.967346

bagged_test_MSE

## [1] 5.049298
```

The random forest training MSE had a value of 1.157876 and the random forest testing MSE had a value of 4.981077. The bagged training MSE is 0.9528967 and the bagged testing MSE is 4.968944. Because bagging has smaller MSE values in both training and testing decorrelating was not a good strategy for this problem.

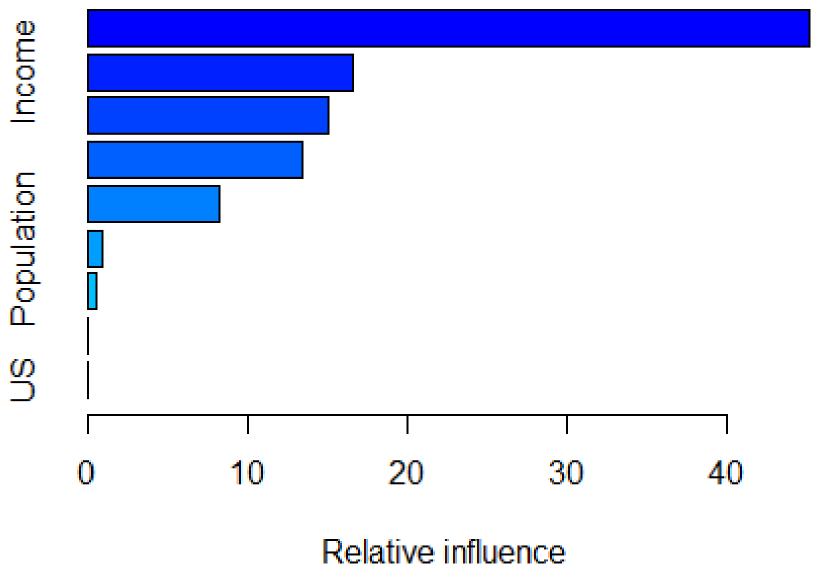
```
train <- sample(1:nrow(training), nrow(training)/2)

training$ShelveLoc <- as.factor(training$ShelveLoc)
training$Urban  <- as.factor(training$Urban)
training$US  <- as.factor(training$US)

boost_tree <- gbm(Sales~.,
                  data=training[train,],
                  distribution="gaussian",
                  n.trees=5000,
                  interaction.depth=4,
                  shrinkage=0.05)


summary(boost_tree)
```



```
##                     var   rel.inf
## ShelveLoc     ShelveLoc 19.188549
## Income           Income 17.291850
## Age                 Age 15.569253
## CompPrice     CompPrice 14.196259
## Population   Population 11.730603
## Advertising Advertising 10.975132
## Education     Education  7.197264
## US                   US  2.099280
## Urban             Urban  1.751811
```

```
MSE_calc <- function(x) {
  MSE_train_calc <- (mean((predict(x,
                                 newdata=training) - training$Sales)^2))
  MSE_test_calc <- (mean((predict(x,
                                newdata=testing) - testing$Sales)^2))

  return(c(MSE_train_calc, MSE_test_calc))
}

boost_tree <- gbm(Sales~.,
                  data=training[train,],
                  distribution="gaussian",
                  n.trees=1000,
                  interaction.depth=1,
                  shrinkage=0.005)
```

```
summary(boost_tree)
```



```
##                     var     rel.inf
## ShelveLoc     ShelveLoc 45.20723529
## Income           Income 16.64560868
## Advertising Advertising 15.05036241
## Age                 Age 13.38673548
## CompPrice     CompPrice  8.24190860
## Population   Population  0.93082999
## Education     Education  0.52189258
## Urban             Urban  0.01542698
## US                   US  0.00000000

boost_train_MSE <- MSE_calc(boost_tree)[1]

## Using 1000 trees...
##
## Using 1000 trees...

## Warning in predict.gbm(x, newdata = testing): NAs introduced by coercion

boost_test_MSE <- MSE_calc(boost_tree)[2]

## Using 1000 trees...
##
## Using 1000 trees...
## Warning in predict.gbm(x, newdata = testing): NAs introduced by coercion

boost_train_MSE

## [1] 4.41582

boost_test_MSE

## [1] 6.774848
```

After trying different depths, shrinkage and number of trees I have found that 1000 trees with depth 1 and shrinkage gave me a training MSE of 4.311855 and testing MSE of 6.474855 which was my best one. When I tested different values I found that increasing the depth, number of trees and shrinkage would increase the MSE values.

e) I believe bagging model performed the best as it had a testing MSE of 4.968944 which was the smallest. The Sales were the most important for the predictors.