DPA Assignment 4

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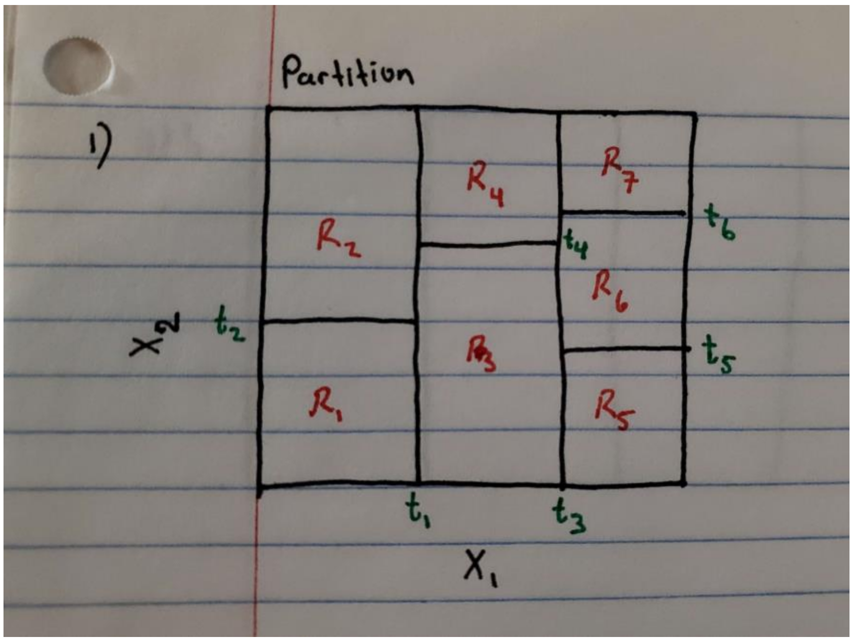
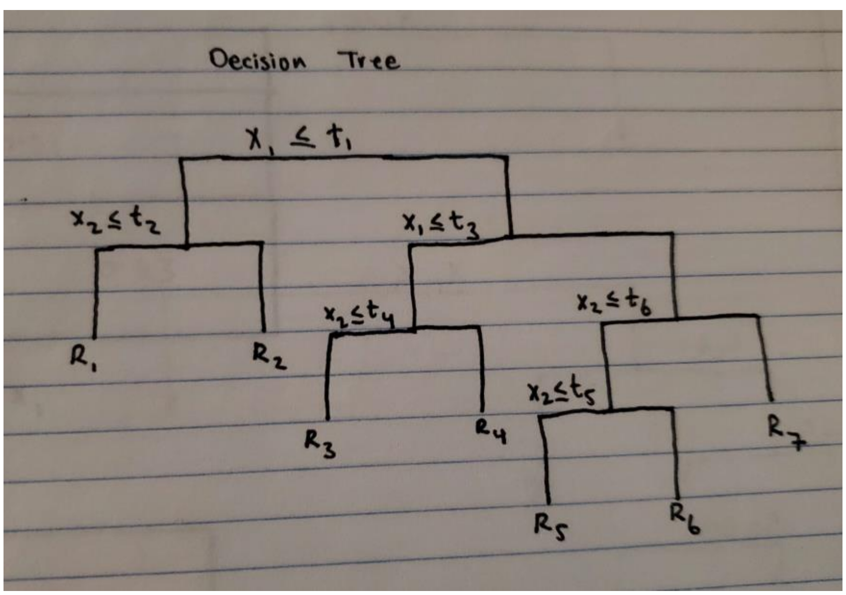
#Recitation Problems

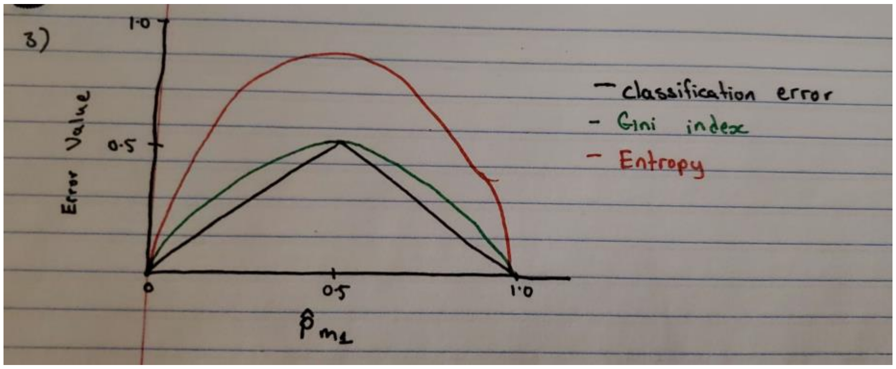
#Chapter 8

1)



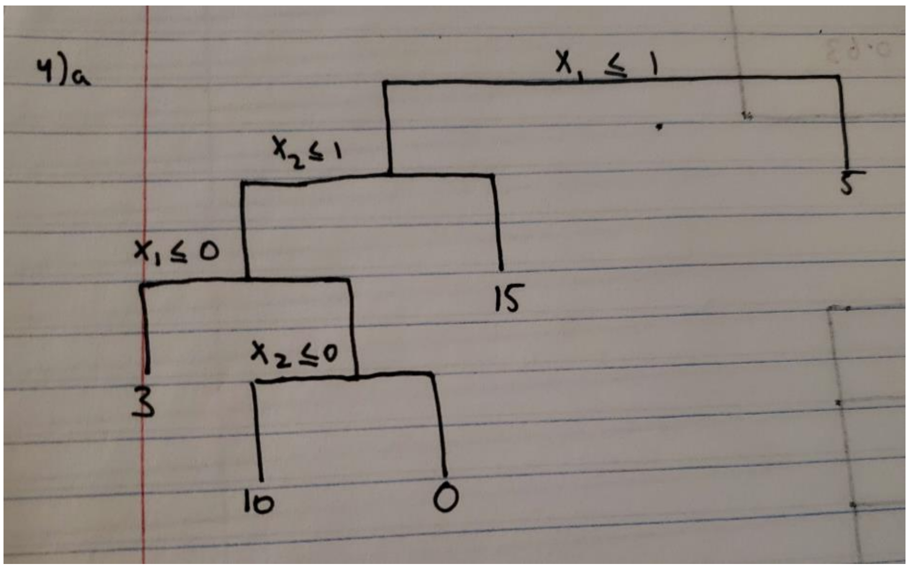


3)

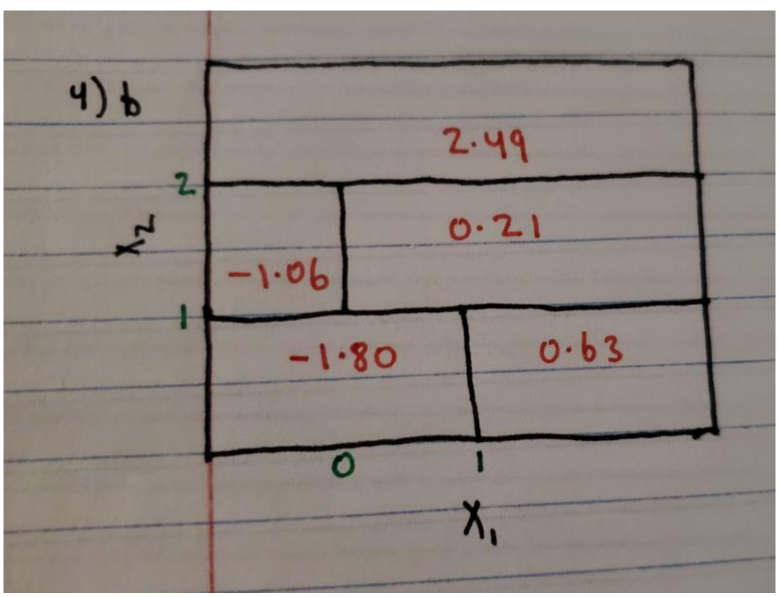


3)
1.0
0.5
Error Value
0
0.5
1.0
$\hat{p}_{m1}$
– classification error
– Gini index
– Entropy

4)



4) a
$X_1 \leq 1$
$X_2 \leq 1$
$X_1 \leq 0$
$X_2 \leq 0$
5
15
3
10
0



4) b
2.49
2
0.21
X_2
-1.06
1
-1.80
0.63
0
1
X_1

5)

Majority Vote Approach: Number of estimates for P(Class is Red | X) < 0.5 is 4 (4 estimates belong to Green class) Number of estimates for P(Class is Red | X) >= 0.5 is 6 (6 estimates belong to Red class)

Using majority vote, the specific value X would be classified as Red since majority of the estimates belong to Red Class

Average Probability Approach: Here, we calculate the average of the P(Class is Red | X) from the 10 estimates and if the average value is less than 0.5 we classify the specific value X as Green, else classify it as Red.

Avg Probability = (0.1 + 0.15 + 0.2 + 0.2 + 0.55 + 0.6 + 0.6 + 0.65 + 0.7 + 0.75) / 10 = 4.5/10 = 0.45

Since the average probability is less than 0.5, the specific value X would be classified as Green

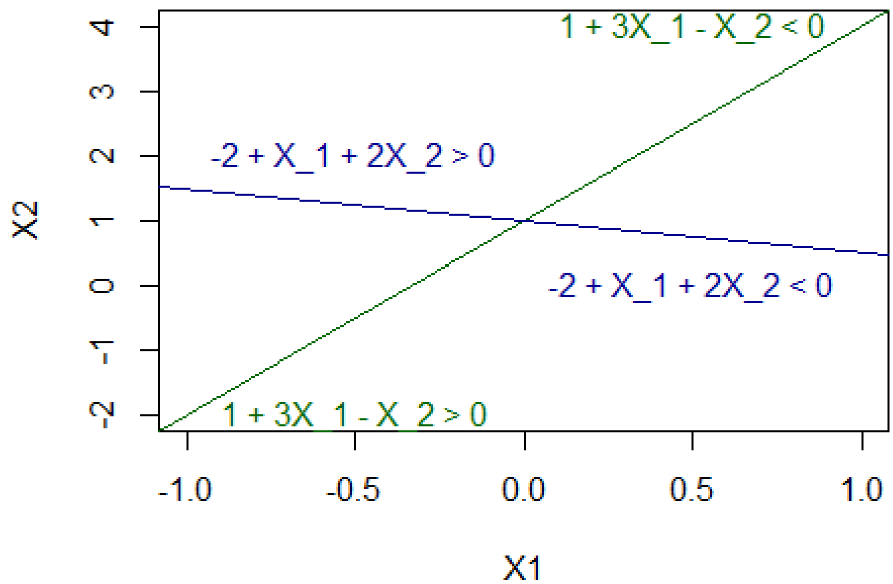
#Chapter 9

#1

1a. To sketch the hyperplane $1 + 3X_1 - X_2 = 0$ we can rewrite it in the form of $X_2 = mX_1 + c$ $(y = mx + c)$ which is $X_2 = 3X_1 + 1$

1b. To sketch the hyperplane $-2 + X_1 + 2X_2 = 0$ we can rewrite it in the form of $X_2 = mX_1 + c$ $(y = mx + c)$ which is $X_2 = -X_1/2 + 1$

```
#Create an empty plot
plot(0,0,xlab = "X1", ylab = "X2", xlim = c(-1, 1), ylim = c(-2, 4),type='l')

#Use abline to create the hyperplane using the intercept (1) and slope (3) in
X2 = 3X1 + 1
abline(a = 1, b = 3, col="darkgreen")

#Indicating the set of points / region for which 1 + 3X_1 - X_2 < 0 and 1 +
3X_1 - X_2 > 0
text(c(0.5), c(4), "1 + 3X_1 - X_2 < 0", col = "darkgreen")
text(c(-0.5), c(-2), "1 + 3X_1 - X_2 > 0", col = "darkgreen")

#Use abline to create the hyperplane using the intercept (1) and slope (-1/2)
in X_2 = - X_1 / 2 + 1
abline(a = 1, b = -1/2, col="darkblue")

#Indicating the set of points / region for which -2 + X_1 + 2X_2 < 0 and -2 +
X_1 + 2X_2 > 0
text(c(0.5), c(0), "-2 + X_1 + 2X_2 < 0", col = "darkblue")
text(c(-0.5), c(2), "-2 + X_1 + 2X_2 > 0", col = "darkblue")
```

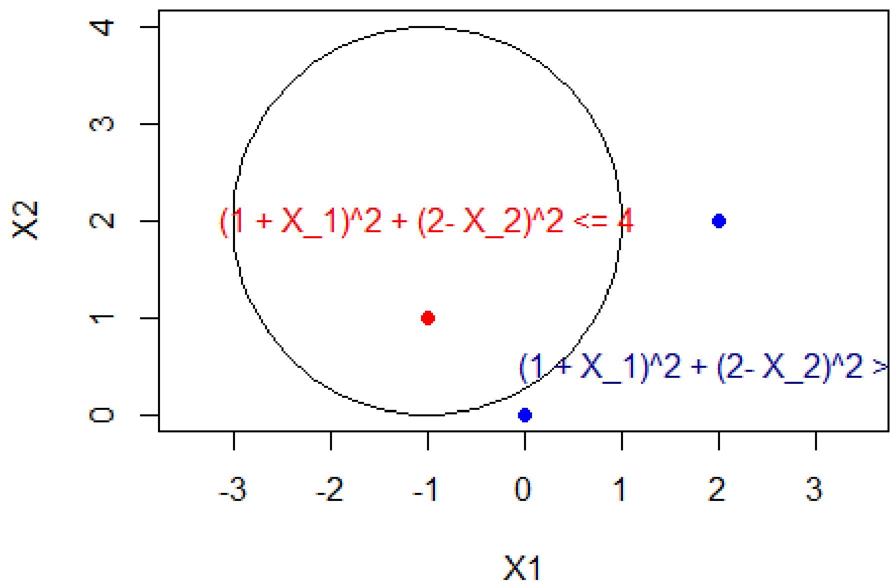


#2a and b

The curve $(1 + X_1)^2 + (2 - X_2)^2 = 4$ will be a circle and it can be rewritten in the form: $(x - h)^2 + (y - k)^2 = r^2$ where h and k are the coordinates of the center of the circle and r is the radius of the circle (these 3 parameters will be required to draw the circle)

Rewritten form: $\left(X_1 - (-1)\right)^2 + (-X_2 + 2)^2 = 2^2$ where the coordinates of the center is (-1,2) and radius is 2

```
#install.packages('plotrix')
library(plotrix)
plot(x=seq(-2,2), y=seq(0,4),type="n", xlab='X1', ylab='X2', asp =1)

#draw circle using coordinates of the center as (-1,2) and radius as 2
draw.circle(-1,2,2)

#Indicating the set of points / region for which (1 + X_1)^2 + (2- X_2)^2 > 4
and (1 + X_1)^2 + (2- X_2)^2 <= 4
text(c(2), c(0.5), "(1 + X_1)^2 + (2- X_2)^2 > 4", col = "darkblue")
text(c(-1), c(2), "(1 + X_1)^2 + (2- X_2)^2 <= 4", col = "red")
points(c(0,2,3),c(0,2,8), col="blue",pch=19)
points(-1,1, col="red",pch=19)
```



#2c

Blue class if $(1 + X_1)^2 + (2 - X_2)^2 > 4$ and red class otherwise

(0,0) –> $(1+0)^2 + (2-0)^2 = 5$ which is > 4 so it belongs to class blue

(-1,1) –> $\left(1+(-1)\right)^2 + (2-1)^2 = 1$ which is < 4 so it belongs to class red

(2,2) –> $(1+2)^2 + (2-2)^2 = 9$ which is > 4 so it belongs to class blue

(3,8) –> $(1+3)^2 + (2-8)^2 = 52$ which is > 4 so it belongs to class blue

#2d

We can expand on $(1 + X_1)^2 + (2 - X_2)^2 = 4$ equation to include X_1^2 and X_2^2:

$$(1 + X_1)^2$$
$$(1 + X_1)(1 + X_1)$$
$$1 + X_1 + X_1 + X_1^2$$
$$= 1 + 2X_1 + X_1^2$$

$$(2 - X_2)^2$$
$$(2 - X_2)(2 - X_2)$$
$$4 - 2X_2 - 2X_2 + X_2^2$$
$$= 4 - 4X_2 + X_2^2$$

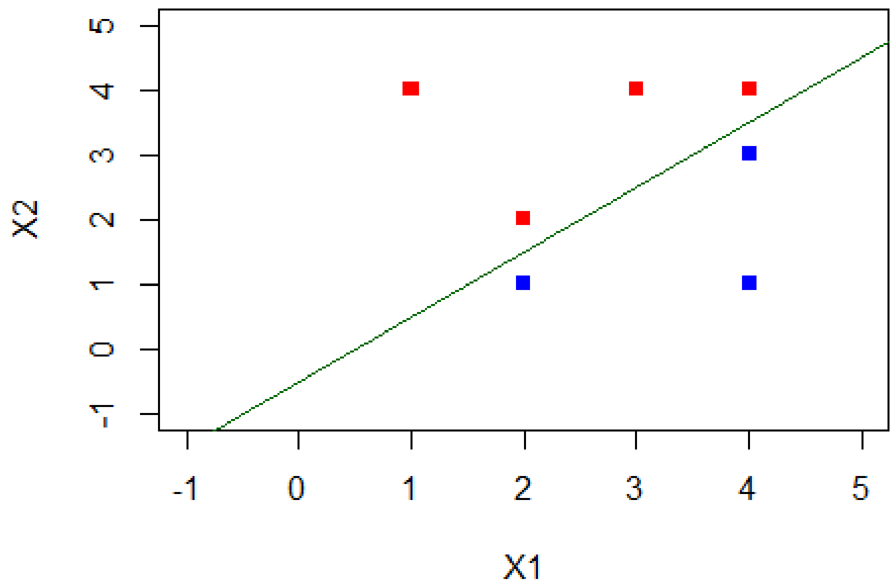
Combine to get:

$$(1 + 2X_1 + X_1^2) + (4 - 4X_2 + X_2^2) = 4$$
$$1 + 2X_1 - 4X_2 + X_1^2 + X_2^2 = 0$$

As we can see from above, when we include X_1^2 and X_2^2, the decision boundary in (c) results in a linear equation

#3a and b

```
plot(-1:5,-1:5,type="n",xlab='X1', ylab='X2')
points(c(3,2,4,1),c(4,2,4,4), col="red", pch=15)
points(c(2,4,4),c(1,3,1), col="blue", pch=15)

#3b plotting the optimal separating hyperplane
abline(a = -0.5, b = 1, col="darkgreen")
```



#3b continued Using the format $y = mx + c$, the equation for the hyperplane above would be $y = x - 0.5$

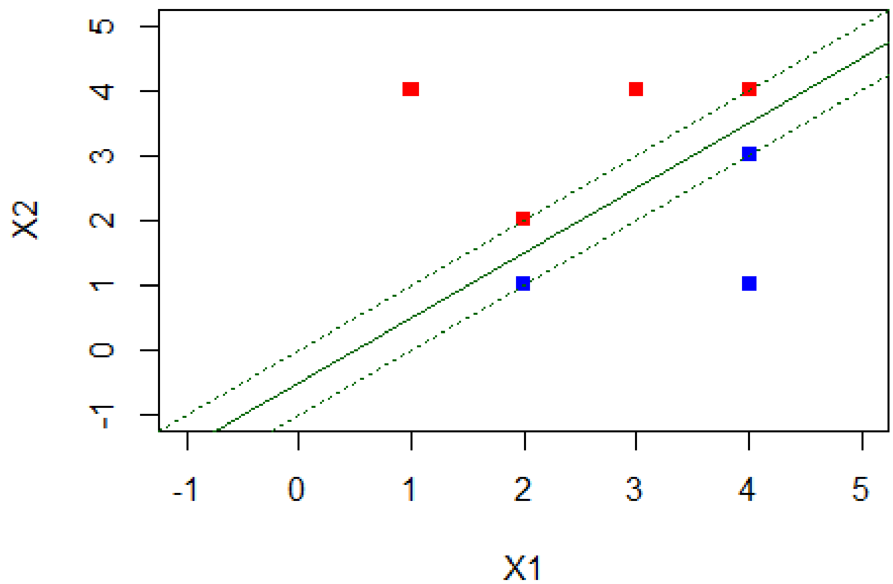
In the form of 9.1 with X_1 and X_2, we get $X_2 = X_1 - 0.5$ or $X_2 - X_1 + 0.5 = 0$

#3c Classify to red if $X_2 - X_1 + 0.5 > 0$ else blue otherwise where $\beta_0 = 0.5, \beta_1 = -1$, and $\beta_2 = 1$

#3d

```
plot(-1:5,-1:5,type="n",xlab='X1', ylab='X2')
points(c(3,2,4,1),c(4,2,4,4), col="red", pch=15)
points(c(2,4,4),c(1,3,1), col="blue", pch=15)
```

```
#3b plotting the optimal separating hyperplane
abline(a = -0.5, b = 1, col="darkgreen")

#3d margin for maximal margin hyperplane
abline(-1, 1, col='darkgreen',lty='dotted')
abline(0, 1, col='darkgreen',lty='dotted')
```

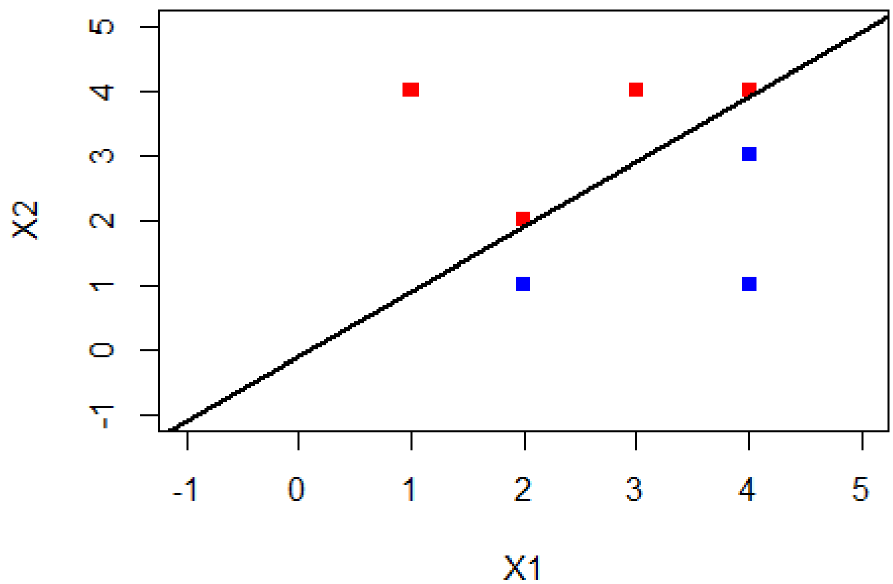


#3e the support vectors for the maximal margin classifier:(2,1), (2,2), (4,3) and (4,4)

#3f A slight movement of the seventh observation (4,1) would not affect the maximal margin hyperplane because it is not a support vector (only those mentioned in 3e are). Since only movements in support vectors will affect the maximal margin hyperplane, a slight movement in the seventh observation will not affect the maximal margin hyperplane.

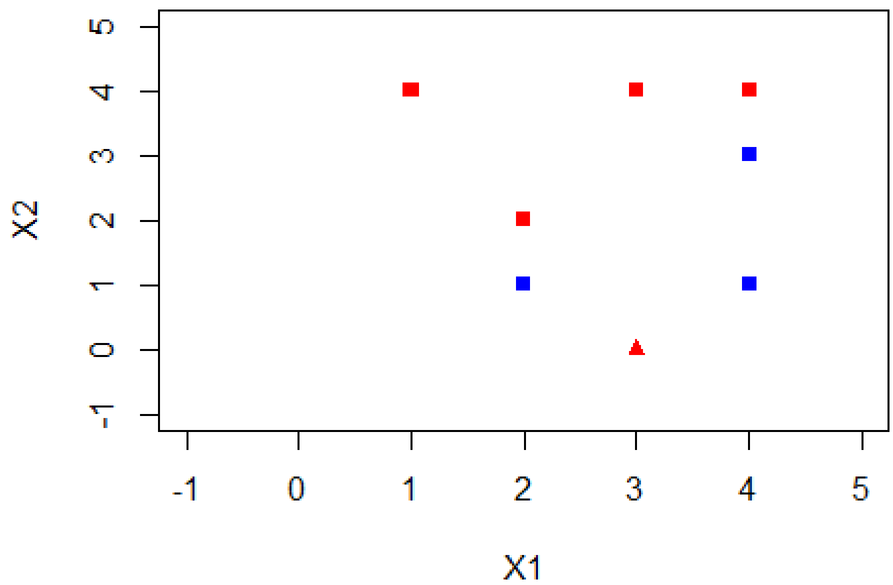
#3g

```
plot(-1:5,-1:5,type="n",xlab='X1', ylab='X2')
points(c(3,2,4,1),c(4,2,4,4), col="red", pch=15)
points(c(2,4,4),c(1,3,1), col="blue", pch=15)

#3g plotting non optimal separating hyperparameter where intercept a is -0.1
and slope b is 1 which results in $-0.1 + X_1 - X_2 = 0$ as the equation for
the hyperplane
abline(-0.1,1, col="black", lwd=2)
```



#3h

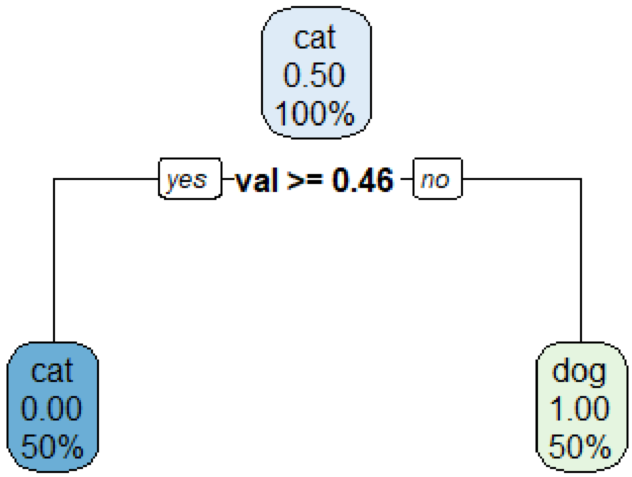
```
plot(-1:5,-1:5,type="n",xlab='X1', ylab='X2')
points(c(3,2,4,1),c(4,2,4,4), col="red", pch=15)
points(c(2,4,4),c(1,3,1), col="blue", pch=15)

#3h (additional observation represented by red triangle)
points(3,0, col="red", pch=17)
```



#Question 1

```
#install.packages("rpart.plot")
#install.packages("randomForest")
library(rpart)
library(rpart.plot)

## Warning: package 'rpart.plot' was built under R version 4.2.3

library(caret)

## Loading required package: ggplot2

## Loading required package: lattice

library(randomForest)

## Warning: package 'randomForest' was built under R version 4.2.3

## randomForest 4.7-1.1

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

##
## Attaching package: 'randomForest'

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

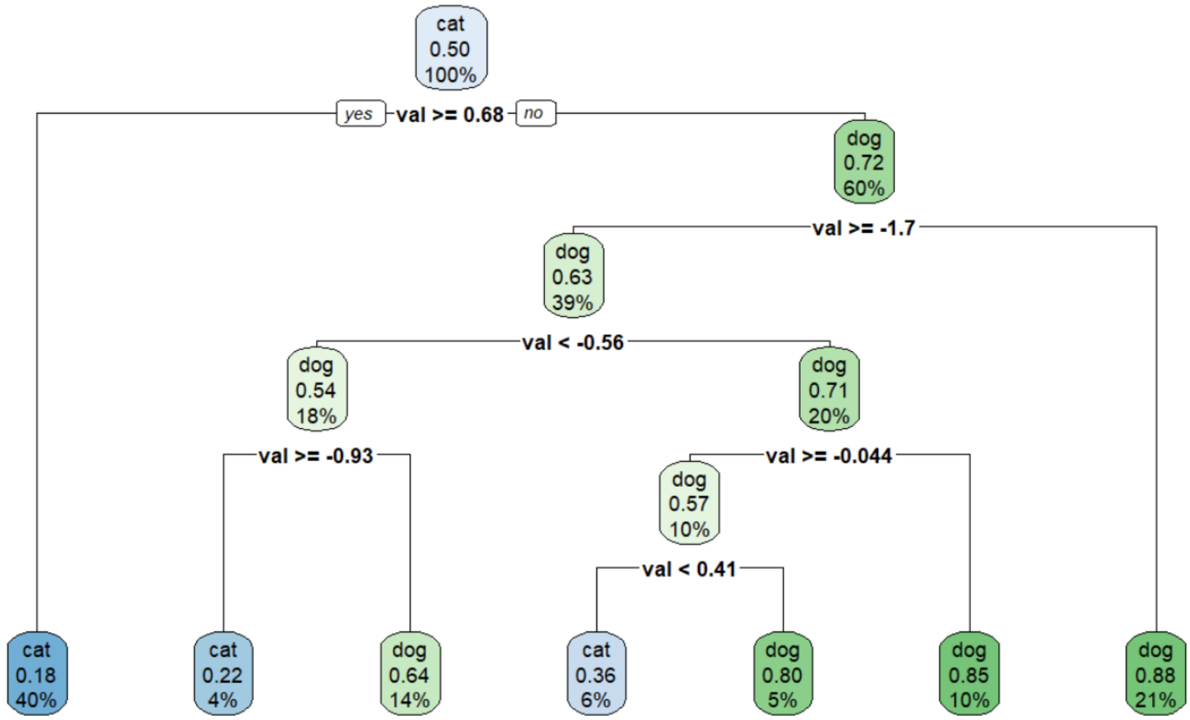
```r
set.seed(100)

#Use rnorm to simulate the normal distributions for the 2 datasets
normal_dist_1 <- rnorm(n = 200, mean = 5, sd = 2)
normal_dist_2 <- rnorm(n = 200, mean = -5, sd = 2)

#Use the normal distribution to simulate dataframes with a class label then
combine them together
data_frame1 <- data.frame(val = normal_dist_1, label = rep("cat",200))
data_frame2 <- data.frame(val = normal_dist_2, label = rep("dog",200))
dataset1 <- rbind(data_frame1, data_frame2)

#Convert the label feature to a categorical variable
dataset1$label <- as.factor(dataset1$label)

head(dataset1)

##        val label
## 1 3.995615   cat
## 2 5.263062   cat
## 3 4.842166   cat
## 4 6.773570   cat
## 5 5.233943   cat
## 6 5.637260   cat

summary(dataset1)

##       val             label
##  Min.   :-11.0416   cat:200
##  1st Qu.: -5.0323   dog:200
##  Median :  0.5916
##  Mean   : -0.0282
##  3rd Qu.:  4.8694
##  Max.   : 10.1639

#Inducing a binary decision tree using rpart then plotting it using
rpart.plot
binary_decision_tree <- rpart(label~val, dataset1, method = "class")
rpart.plot(binary_decision_tree)
```



The threshold value for the feature in the first split is 0.46 as shown above. Since the tree is able to classify both classes, it follows an empirical distribution. The tree above has three nodes (1 root node and 2 leaf nodes).

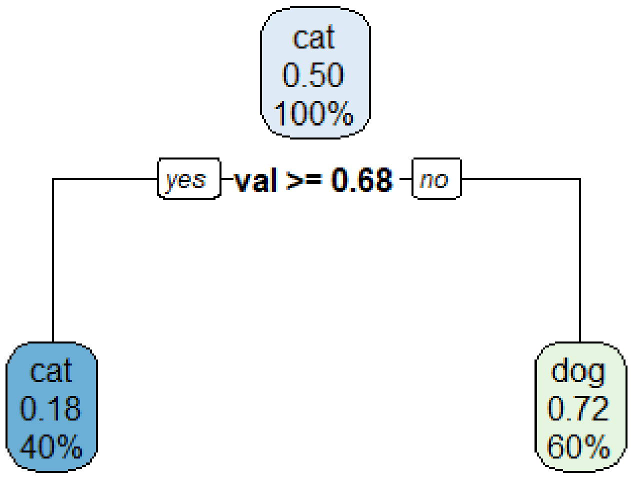
```
#Write our functions to calculate gini and entropy
entropy_func <- function(p){
entropy = (p*log(p) + (1-p) * log(1-p))
return (entropy)}

gini_func <- function(p){
gini = 2 * p * (1-p)
return (gini)}

#Use the above entropy and gini functions to compute the entropy and gini at
each node
p_tree1 <- c(0.5, 0, 1)

entropy_tree1 <- sapply(p_tree1, entropy_func)
cat("Entropy at each node of tree 1: ",entropy_tree1)

## Entropy at each node of tree 1:  -0.6931472 NaN NaN

gini_tree1 <- sapply(p_tree1, gini_func)
cat("\nGini at each node of tree 1: ",gini_tree1)

##
## Gini at each node of tree 1:  0.5 0 0
```

```r
#Repeat the same process using normal distributions of (1,2) and (-1,2)
set.seed(200)
#Use rnorm to simulate the normal distributions for the 2 datasets
normal_dist_1 <- rnorm(n = 100, mean = 1, sd = 2)
normal_dist_2 <- rnorm(n = 100, mean = -1, sd = 2)

#Use the normal distribution to simulate dataframes with a class label then
combine them together
data_frame1 <- data.frame(val = normal_dist_1, label = rep("cat",100))
data_frame2 <- data.frame(val = normal_dist_2, label = rep("dog",100))
dataset2 <- rbind(data_frame1, data_frame2)

#Convert the label feature to a categorical variable
dataset2$label <- as.factor(dataset2$label)

head(dataset2)

##         val label
## 1 1.1695127   cat
## 2 1.4529207   cat
## 3 1.8651130   cat
## 4 2.1161305   cat
## 5 1.1195105   cat
## 6 0.7707183   cat

summary(dataset2)

##       val              label
##  Min.   :-5.461128   cat:100
##  1st Qu.:-1.421417   dog:100
##  Median : 0.009538
##  Mean   :-0.012207
##  3rd Qu.: 1.313753
##  Max.   : 7.175955

#Inducing a binary decision tree using rpart then plotting it using
rpart.plot
binary_decision_tree2 <- rpart(label~val, dataset2, method = "class")
rpart.plot(binary_decision_tree2)
```



The threshold value for the feature in the first split is 0.68 as shown above. The tree above has 13 nodes. Due to this large size of decision tree, there are overlapping of labels. This means that the decision tree is more likely to overfit and be less interpretable.

```
#Use the above entropy and gini functions to compute the entropy and gini at each node
p_tree2 <- c(0.5,0.18,0.72,0.63,0.54,0.22,0.64,0.71,0.57,0.36,0.80,0.85,0.88)

entropy_tree2 <- sapply(p_tree2, entropy_func)
cat("Entropy at each node of tree 2: ",entropy_tree2)

## Entropy at each node of tree 2:  -0.6931472 -0.4713935 -0.5929533 -0.6589557 -0.6899438 -0.526908 -0.6534182 -0.6021517 -0.6833149 -0.6534182 -0.5004024 -0.4227091 -0.366925

gini_tree2 <- sapply(p_tree2, gini_func)
cat("\nGini at each node of tree 2: ",gini_tree2)

##
## Gini at each node of tree 2:  0.5 0.2952 0.4032 0.4662 0.4968 0.3432 0.4608 0.4118 0.4902 0.4608 0.32 0.255 0.2112

#Pruning the tree

binary_decision_tree2_prune <- prune.rpart(binary_decision_tree2, cp = 0.1)
rpart.plot(binary_decision_tree2_prune)
```



From above, we can see that the pruned tree has a lot less nodes, in this case, 3 nodes (1 root and 2 leaf nodes). We can observe that the results of the pruned tree is better than the initial tree due to less nodes and less overlapping labels. This means that parts of the tree that do not contribute to the classifier have been removed. This decreases the risk of overfitting.

```
#Use the entropy and gini functions to compute the entropy and gini at each
node
p_tree3 <- c(0.5,0.18,0.72)

entropy_tree3 <- sapply(p_tree3, entropy_func)
cat("Entropy at each node of tree 3: ",entropy_tree3)

## Entropy at each node of tree 3:  -0.6931472 -0.4713935 -0.5929533

gini_tree3 <- sapply(p_tree3, gini_func)
cat("\nGini at each node of tree 3: ",gini_tree3)

##
## Gini at each node of tree 3:  0.5 0.2952 0.4032
```

#Question 2

```
set.seed(2)
white_wine_data <- read.csv('https://archive.ics.uci.edu/ml/machine-learning-
databases/wine-quality/winequality-white.csv', header = TRUE, sep = ";")
summary(white_wine_data)
```

```
##  fixed.acidity    volatile.acidity  citric.acid     residual.sugar
##  Min.   : 3.800   Min.   :0.0800   Min.   :0.0000   Min.   : 0.600
##  1st Qu.: 6.300   1st Qu.:0.2100   1st Qu.:0.2700   1st Qu.: 1.700
##  Median : 6.800   Median :0.2600   Median :0.3200   Median : 5.200
##  Mean   : 6.855   Mean   :0.2782   Mean   :0.3342   Mean   : 6.391
##  3rd Qu.: 7.300   3rd Qu.:0.3200   3rd Qu.:0.3900   3rd Qu.: 9.900
##  Max.   :14.200   Max.   :1.1000   Max.   :1.6600   Max.   :65.800
##    chlorides        free.sulfur.dioxide total.sulfur.dioxide    density
##  Min.   :0.00900   Min.   :  2.00      Min.   :  9.0        Min.   :0.9871
##  1st Qu.:0.03600   1st Qu.: 23.00      1st Qu.:108.0        1st Qu.:0.9917
##  Median :0.04300   Median : 34.00      Median :134.0        Median :0.9937
##  Mean   :0.04577   Mean   : 35.31      Mean   :138.4        Mean   :0.9940
##  3rd Qu.:0.05000   3rd Qu.: 46.00      3rd Qu.:167.0        3rd Qu.:0.9961
##  Max.   :0.34600   Max.   :289.00      Max.   :440.0        Max.   :1.0390
##        pH          sulphates         alcohol         quality
##  Min.   :2.720   Min.   :0.2200   Min.   : 8.00   Min.   :3.000
##  1st Qu.:3.090   1st Qu.:0.4100   1st Qu.: 9.50   1st Qu.:5.000
##  Median :3.180   Median :0.4700   Median :10.40   Median :6.000
##  Mean   :3.188   Mean   :0.4898   Mean   :10.51   Mean   :5.878
##  3rd Qu.:3.280   3rd Qu.:0.5500   3rd Qu.:11.40   3rd Qu.:6.000
##  Max.   :3.820   Max.   :1.0800   Max.   :14.20   Max.   :9.000
```

```
head(white_wine_data)
```

```
##   fixed.acidity volatile.acidity citric.acid residual.sugar chlorides
## 1           7.0             0.27        0.36           20.7     0.045
## 2           6.3             0.30        0.34            1.6     0.049
## 3           8.1             0.28        0.40            6.9     0.050
## 4           7.2             0.23        0.32            8.5     0.058
## 5           7.2             0.23        0.32            8.5     0.058
## 6           8.1             0.28        0.40            6.9     0.050
##   free.sulfur.dioxide total.sulfur.dioxide density   pH sulphates alcohol
## 1                  45                  170  1.0010 3.00      0.45     8.8
## 2                  14                  132  0.9940 3.30      0.49     9.5
## 3                  30                   97  0.9951 3.26      0.44    10.1
## 4                  47                  186  0.9956 3.19      0.40     9.9
## 5                  47                  186  0.9956 3.19      0.40     9.9
## 6                  30                   97  0.9951 3.26      0.44    10.1
##   quality
## 1       6
## 2       6
## 3       6
## 4       6
## 5       6
## 6       6
```

```
red_wine_data <- read.csv('https://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/winequality-red.csv', header = TRUE, sep = ";")
#str(red_wine_data)
summary(red_wine_data)
```

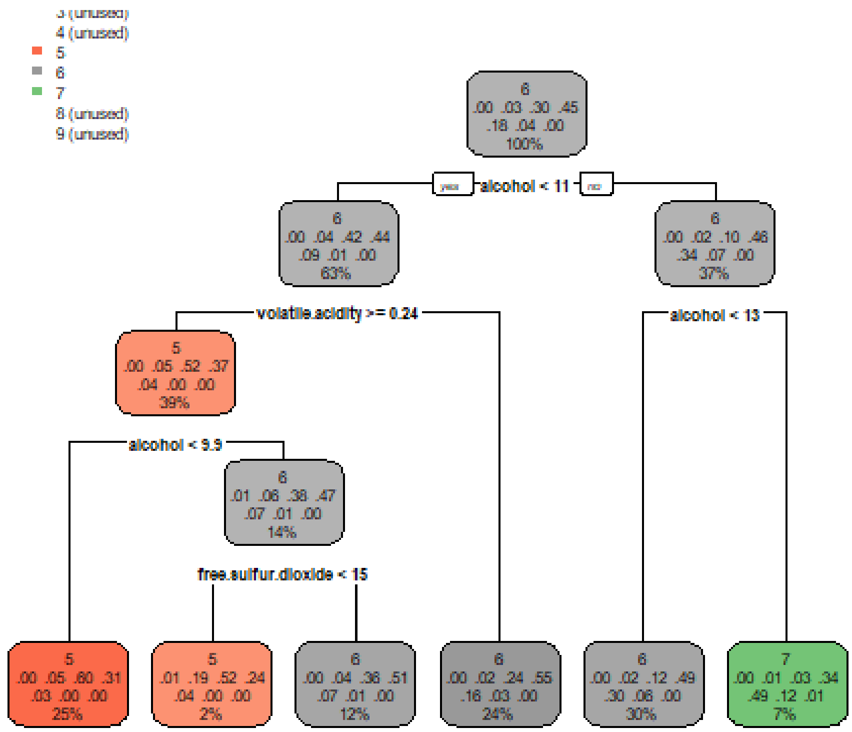
```
##  fixed.acidity   volatile.acidity  citric.acid    residual.sugar  
##  Min.   : 4.60   Min.   :0.1200   Min.   :0.000   Min.   : 0.900  
##  1st Qu.: 7.10   1st Qu.:0.3900   1st Qu.:0.090   1st Qu.: 1.900  
##  Median : 7.90   Median :0.5200   Median :0.260   Median : 2.200  
##  Mean   : 8.32   Mean   :0.5278   Mean   :0.271   Mean   : 2.539  
##  3rd Qu.: 9.20   3rd Qu.:0.6400   3rd Qu.:0.420   3rd Qu.: 2.600  
##  Max.   :15.90   Max.   :1.5800   Max.   :1.000   Max.   :15.500  
##    chlorides       free.sulfur.dioxide total.sulfur.dioxide    density      
##  Min.   :0.01200   Min.   : 1.00       Min.   :  6.00       Min.   :0.9901  
##  1st Qu.:0.07000   1st Qu.: 7.00       1st Qu.: 22.00       1st Qu.:0.9956  
##  Median :0.07900   Median :14.00       Median : 38.00       Median :0.9968  
##  Mean   :0.08747   Mean   :15.87       Mean   : 46.47       Mean   :0.9967  
##  3rd Qu.:0.09000   3rd Qu.:21.00       3rd Qu.: 62.00       3rd Qu.:0.9978  
##  Max.   :0.61100   Max.   :72.00       Max.   :289.00       Max.   :1.0037  
##        pH          sulphates         alcohol         quality     
##  Min.   :2.740   Min.   :0.3300   Min.   : 8.40   Min.   :3.000  
##  1st Qu.:3.210   1st Qu.:0.5500   1st Qu.: 9.50   1st Qu.:5.000  
##  Median :3.310   Median :0.6200   Median :10.20   Median :6.000  
##  Mean   :3.311   Mean   :0.6581   Mean   :10.42   Mean   :5.636  
##  3rd Qu.:3.400   3rd Qu.:0.7300   3rd Qu.:11.10   3rd Qu.:6.000  
##  Max.   :4.010   Max.   :2.0000   Max.   :14.90   Max.   :8.000
```

```
head(red_wine_data)
```

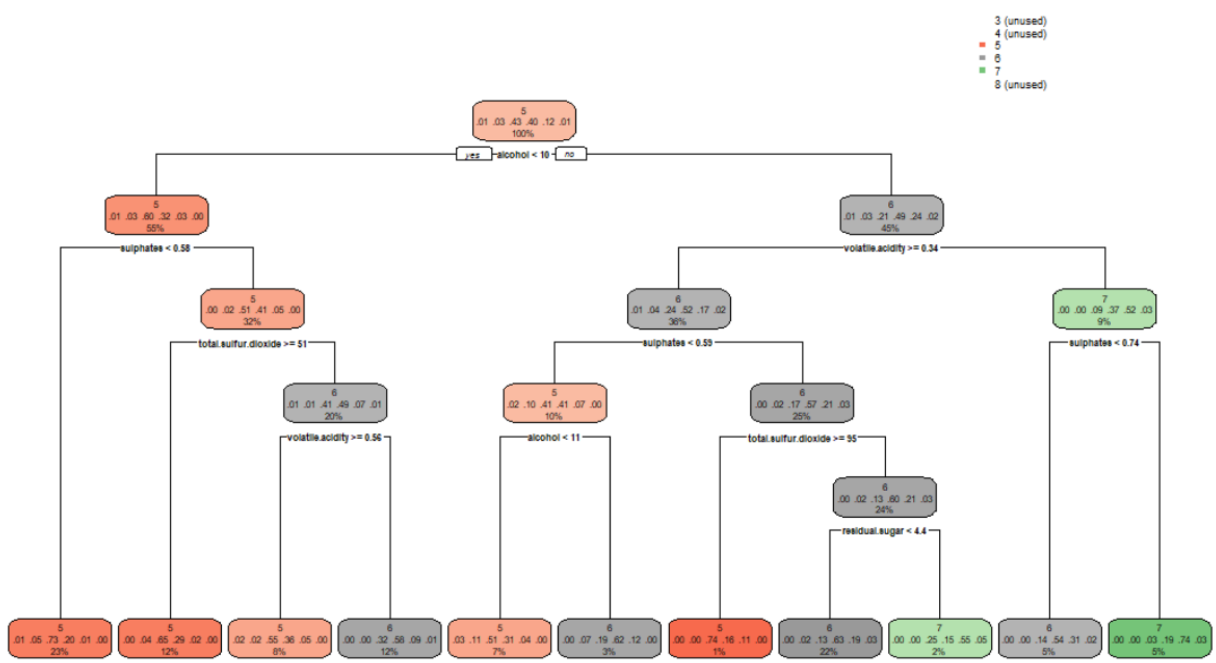
```
##   fixed.acidity volatile.acidity citric.acid residual.sugar chlorides
## 1           7.4             0.70        0.00            1.9     0.076
## 2           7.8             0.88        0.00            2.6     0.098
## 3           7.8             0.76        0.04            2.3     0.092
## 4          11.2             0.28        0.56            1.9     0.075
## 5           7.4             0.70        0.00            1.9     0.076
## 6           7.4             0.66        0.00            1.8     0.075
##   free.sulfur.dioxide total.sulfur.dioxide density   pH sulphates alcohol
## 1                  11                   34  0.9978 3.51      0.56     9.4
## 2                  25                   67  0.9968 3.20      0.68     9.8
## 3                  15                   54  0.9970 3.26      0.65     9.8
## 4                  17                   60  0.9980 3.16      0.58     9.8
## 5                  11                   34  0.9978 3.51      0.56     9.4
## 6                  13                   40  0.9978 3.51      0.56     9.4
##   quality
## 1       5
## 2       5
## 3       5
## 4       6
## 5       5
## 6       5
```

```
#Using createDataPartition to perform 80/20 train-test split on white wine data

#Changing our response variable quality to a categorical value
```

```r
white_wine_data$quality <- as.factor(white_wine_data$quality)

datasetPartition <- createDataPartition(white_wine_data$quality, p = 0.8,
list = FALSE)
train_white <- white_wine_data[datasetPartition,]
test_white <- white_wine_data[-datasetPartition,]

cat("Dimensions of training data: ", dim(train_white))

## Dimensions of training data:  3920 12

cat("\nDimensions of testing data: ", dim(test_white))

##
## Dimensions of testing data:  978 12

#Using createDataPartition to perform 80/20 train-test split on red wine data

#Changing our response variable quality to a categorical value
red_wine_data$quality <- as.factor(red_wine_data$quality)

datasetPartition1 <- createDataPartition(red_wine_data$quality, p = 0.8, list
= FALSE)
train_red <- red_wine_data[datasetPartition1,]
test_red <- red_wine_data[-datasetPartition1,]

cat("Dimensions of training data: ", dim(train_red))

## Dimensions of training data:  1282 12

cat("\nDimensions of testing data: ", dim(test_red))

##
## Dimensions of testing data:  317 12

#Decision tree for white wine
decision_tree_white <- rpart(quality~., train_white, method = "class")
rpart.plot(decision_tree_white)
```




```
#Decision tree for red wine
decision_tree_red <- rpart(quality~., train_red, method = "class")
rpart.plot(decision_tree_red)
```



```r
#using the caret package confusionMatrix method to determine the
#decision tree accuracy on the white wine test set

predict_white <- predict(decision_tree_white, test_white, type = 'class')
confusionMatrix(predict_white, test_white$quality)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   3   4   5   6   7   8   9
##          3   0   0   0   0   0   0   0
##          4   0   0   0   0   0   0   0
##          5   1  14 161  77   7   0   0
##          6   2  17 129 339 132  23   1
##          7   1   1   1  23  37  12   0
##          8   0   0   0   0   0   0   0
##          9   0   0   0   0   0   0   0
##
## Overall Statistics
##
##                Accuracy : 0.5491
##                  95% CI : (0.5173, 0.5806)
##     No Information Rate : 0.4489
##     P-Value [Acc > NIR] : 2.093e-10
##
##                   Kappa : 0.2632
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: 3 Class: 4 Class: 5 Class: 6 Class: 7 Class: 8
## Sensitivity           0.00000  0.00000   0.5533   0.7722  0.21023  0.00000
## Specificity           1.00000  1.00000   0.8559   0.4360  0.95262  1.00000
## Pos Pred Value            NaN      NaN   0.6192   0.5272  0.49333      NaN
## Neg Pred Value        0.99591  0.96728   0.8189   0.7015  0.84607  0.96421
## Prevalence            0.00409  0.03272   0.2975   0.4489  0.17996  0.03579
## Detection Rate        0.00000  0.00000   0.1646   0.3466  0.03783  0.00000
## Detection Prevalence  0.00000  0.00000   0.2658   0.6575  0.07669  0.00000
## Balanced Accuracy     0.50000  0.50000   0.7046   0.6041  0.58142  0.50000
##                      Class: 9
## Sensitivity          0.000000
## Specificity          1.000000
## Pos Pred Value            NaN
## Neg Pred Value       0.998978
## Prevalence           0.001022
## Detection Rate       0.000000
## Detection Prevalence 0.000000
## Balanced Accuracy    0.500000
```

```r
#using the caret package confusionMatrix method to determine the
#decision tree accuracy on the red wine test set

predict_red <- predict(decision_tree_red, test_red, type = 'class')
confusionMatrix(predict_red, test_red$quality)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   3   4   5   6   7   8
##          3   0   0   0   0   0   0
##          4   0   0   0   0   0   0
##          5   1   9 108  44   3   0
##          6   1   1  25  74  26   3
##          7   0   0   3   9  10   0
##          8   0   0   0   0   0   0
##
## Overall Statistics
##
##                Accuracy : 0.6057
##                  95% CI : (0.5495, 0.6598)
##     No Information Rate : 0.429
##     P-Value [Acc > NIR] : 1.938e-10
##
##                   Kappa : 0.347
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: 3 Class: 4 Class: 5 Class: 6 Class: 7 Class: 8
## Sensitivity          0.000000  0.00000   0.7941   0.5827  0.25641 0.000000
## Specificity          1.000000  1.00000   0.6851   0.7053  0.95683 1.000000
## Pos Pred Value            NaN      NaN   0.6545   0.5692  0.45455      NaN
## Neg Pred Value       0.993691  0.96845   0.8158   0.7166  0.90169 0.990536
## Prevalence           0.006309  0.03155   0.4290   0.4006  0.12303 0.009464
## Detection Rate       0.000000  0.00000   0.3407   0.2334  0.03155 0.000000
## Detection Prevalence 0.000000  0.00000   0.5205   0.4101  0.06940 0.000000
## Balanced Accuracy    0.500000  0.50000   0.7396   0.6440  0.60662 0.500000
```

It can be seen that the decision tree for white wine had an accuracy of 54.91% while the decision tree for the red wine had an accuracy of 60.57%.

For the white wine decision tree, it was observed that the first split on alcohol < 11 while the red wine decision tree performed the first split on alcohol < 10

In terms of variables of interest:

The white wine decision tree utilized the free sulfur dioxide variable while the red wine decision tree did not

On the flip side, the red wine decision tree utilized the total sulfur dioxide, sulphates, and residual sugar variable while the white wine decision tree did not.

```
#Repeat with a random forest tree model for white wine data
random_forest_white <- train(quality ~ ., data = train_white, method = "rf",
preProcess = c("center","scale"))

predict_white_random_forest <- predict(random_forest_white, test_white)
confusionMatrix(predict_white_random_forest, test_white$quality)

## Confusion Matrix and Statistics
##
##           Reference
## Prediction   3   4   5   6   7   8   9
##          3   0   0   0   0   0   0   0
##          4   0   7   1   0   0   0   0
##          5   1  14 201  52   1   0   0
##          6   3  11  87 358  80   7   1
##          7   0   0   2  28  94  11   0
##          8   0   0   0   1   1  17   0
##          9   0   0   0   0   0   0   0
##
## Overall Statistics
##
##                Accuracy : 0.6922
##                  95% CI : (0.6622, 0.7211)
##     No Information Rate : 0.4489
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.5201
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: 3 Class: 4 Class: 5 Class: 6 Class: 7 Class: 8
## Sensitivity           0.00000 0.218750   0.6907   0.8155  0.53409  0.48571
## Specificity           1.00000 0.998943   0.9010   0.6494  0.94888  0.99788
## Pos Pred Value            NaN 0.875000   0.7472   0.6545  0.69630  0.89474
## Neg Pred Value        0.99591 0.974227   0.8731   0.8121  0.90273  0.98123
## Prevalence            0.00409 0.032720   0.2975   0.4489  0.17996  0.03579
## Detection Rate        0.00000 0.007157   0.2055   0.3661  0.09611  0.01738
## Detection Prevalence  0.00000 0.008180   0.2751   0.5593  0.13804  0.01943
## Balanced Accuracy     0.50000 0.608846   0.7959   0.7324  0.74148  0.74180
##                      Class: 9
## Sensitivity          0.000000
## Specificity          1.000000
## Pos Pred Value            NaN
## Neg Pred Value       0.998978
## Prevalence           0.001022
```

```
## Detection Rate       0.000000
## Detection Prevalence 0.000000
## Balanced Accuracy    0.500000
```

From above, we can see that when we use random forest tree model on the white wine data we get an accuracy of 69.22% which when compared to the decision tree model accuracy of 54.91%, shows an improvement.

```
#Repeat with a random forest tree model for red wine data
random_forest_red <- train(quality ~ ., data = train_red, method = "rf",
preProcess = c("center","scale"))
predict_red_random_forest <- predict(random_forest_red, test_red)
confusionMatrix(predict_red_random_forest, test_red$quality)

## Confusion Matrix and Statistics
##
##           Reference
## Prediction   3   4   5   6   7   8
##          3   0   0   0   0   0   0
##          4   0   0   0   0   0   0
##          5   1   7 111  21   0   0
##          6   1   3  25 102  18   1
##          7   0   0   0   4  21   2
##          8   0   0   0   0   0   0
##
## Overall Statistics
##
##                Accuracy : 0.7382
##                  95% CI : (0.6861, 0.7857)
##     No Information Rate : 0.429
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.5711
##
##  Mcnemar's Test P-Value : NA
##
## Statistics by Class:
##
##                      Class: 3 Class: 4 Class: 5 Class: 6 Class: 7 Class: 8
## Sensitivity          0.000000  0.00000   0.8162   0.8031  0.53846 0.000000
## Specificity          1.000000  1.00000   0.8398   0.7474  0.97842 1.000000
## Pos Pred Value            NaN      NaN   0.7929   0.6800  0.77778      NaN
## Neg Pred Value       0.993691  0.96845   0.8588   0.8503  0.93793 0.990536
## Prevalence           0.006309  0.03155   0.4290   0.4006  0.12303 0.009464
## Detection Rate       0.000000  0.00000   0.3502   0.3218  0.06625 0.000000
## Detection Prevalence 0.000000  0.00000   0.4416   0.4732  0.08517 0.000000
## Balanced Accuracy    0.500000  0.50000   0.8280   0.7753  0.75844 0.500000
```

From above, we can see that when we use random forest tree model on the red wine data we get an accuracy of 73.82% which when compared to the decision tree model accuracy of 60.57%, shows an improvement.

#Question 3

```
#install.packages("tm")
library(tm)

## Warning: package 'tm' was built under R version 4.2.3

## Loading required package: NLP

##
## Attaching package: 'NLP'

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

library(e1071)

sms_data <- read.csv("D:\\Users\\giris\\Downloads\\SMSSpamCollection",header
= FALSE,sep = "\t", quote = "", stringsAsFactors=FALSE)
colnames(sms_data) <- c("Class", "Message")

#Changing our response variable quality to a categorical value
sms_data$Class <- as.factor(sms_data$Class)

summary(sms_data)

##   Class        Message
##  ham :4827   Length:5574
##  spam: 747   Class :character
##              Mode  :character

head(sms_data)

##   Class
## 1   ham
## 2   ham
## 3  spam
## 4   ham
## 5   ham
## 6  spam
##
Message
## 1                                             Go until jurong point,
crazy.. Available only in bugis n great world la e buffet... Cine there got
amore wat...
## 2
Ok lar... Joking wif u oni...
```

```
## 3 Free entry in 2 a wkly comp to win FA Cup final tkts 21st May 2005. Text
FA to 87121 to receive entry question(std txt rate)T&C's apply
08452810075over18's
## 4
U dun say so early hor... U c already then say...
## 5
Nah I don't think he goes to usf, he lives around here though
## 6         FreeMsg Hey there darling it's been 3 week's now and no word
back! I'd like some fun you up for it still? Tb ok! XxX std chgs to send,
£1.50 to rcv
```

```
corpusVectorSource <- VCorpus(VectorSource(sms_data$Message))

#Convert lowercase
corpusVectorSource <- tm_map(corpusVectorSource,
content_transformer(tolower))

#Remove stopwords
corpusVectorSource <- tm_map(corpusVectorSource, removeWords,
stopwords("en"))

#Strip whitespace
corpusVectorSource <- tm_map(corpusVectorSource, stripWhitespace)

#Remove punctuation
corpusVectorSource <- tm_map(corpusVectorSource, removePunctuation)

#Create DocumentTermMatrix
doc_term_matrix <- DocumentTermMatrix(corpusVectorSource)
doc_term_matrix
```

```
## <<DocumentTermMatrix (documents: 5574, terms: 8879)>>
## Non-/sparse entries: 44937/49446609
## Sparsity           : 100%
## Maximal term length: 51
## Weighting          : term frequency (tf)
```

```
#Use findFreqTerms to contruct features from words occuring more than 10
times
const_features <- findFreqTerms(doc_term_matrix, 10)

#split the data into a training and test set
doc_term_matrix_train = doc_term_matrix[1:3999,]
doc_term_matrix_test = doc_term_matrix[4000:5574,]

train_labels <- sms_data[1:3999, ]$Class
train_labels <- as.factor(train_labels)
test_labels <- sms_data[4000:5574, ]$Class
test_labels <- as.factor(test_labels)
```

```
#create a DocumentTermMatrix for each
freq_doc_term_matrix_train <- doc_term_matrix_train[, const_features]
freq_doc_term_matrix_test <- doc_term_matrix_test[, const_features]

freq_doc_term_matrix_train

## <<DocumentTermMatrix (documents: 3999, terms: 855)>>
## Non-/sparse entries: 20999/3398146
## Sparsity           : 99%
## Maximal term length: 15
## Weighting          : term frequency (tf)

#Convert the DocumentTermMatrix train/test matrices to a Boolean
representation (counts greater than zero are converted to a 1)
count_func <- function(x) {x <- ifelse(x > 0, "1", "0")}

#Apply boolean representation function to train/test matrices
train <- apply(freq_doc_term_matrix_train, MARGIN = 2,count_func)
test <- apply(freq_doc_term_matrix_test, MARGIN = 2, count_func)
train <- as.data.frame(train)
test <- as.data.frame(test)

#fit a naiveBayes model for both training and testing data
fit_nb_train = naiveBayes(train,train_labels)
fit_nb_test = naiveBayes(test,test_labels)

#Perform prediction using training and testing data
nb_train_pred = predict(fit_nb_train,train)
nb_test_pred = predict(fit_nb_test,test)

#Show confusion matrix for training data after prediction to observe accuracy
train_confusion_matrix <- confusionMatrix(nb_train_pred,train_labels)
train_confusion_matrix

## Confusion Matrix and Statistics
##
##             Reference
## Prediction   ham spam
##       ham  3457   54
##       spam    9  479
##
##                Accuracy : 0.9842
##                  95% CI : (0.9799, 0.9879)
##     No Information Rate : 0.8667
##     P-Value [Acc > NIR] : < 2.2e-16
##
##                   Kappa : 0.9293
##
##  Mcnemar's Test P-Value : 2.965e-08
##
##             Sensitivity : 0.9974
```

```
##              Specificity : 0.8987
##           Pos Pred Value : 0.9846
##           Neg Pred Value : 0.9816
##               Prevalence : 0.8667
##           Detection Rate : 0.8645
##     Detection Prevalence : 0.8780
##        Balanced Accuracy : 0.9480
##
##         'Positive' Class : ham
##
```

#Train accuracy of naiveBayes model is 98.42%

```
#Show confusion matrix for testing data after prediction to observe accuracy
test_confusion_matrix <- confusionMatrix(nb_test_pred,test_labels)
test_confusion_matrix

## Confusion Matrix and Statistics
##
##           Reference
## Prediction  ham spam
##       ham  1357   20
##       spam    4  194
##
##                 Accuracy : 0.9848
##                   95% CI : (0.9774, 0.9902)
##      No Information Rate : 0.8641
##      P-Value [Acc > NIR] : <2e-16
##
##                    Kappa : 0.933
##
##   Mcnemar's Test P-Value : 0.0022
##
##              Sensitivity : 0.9971
##              Specificity : 0.9065
##           Pos Pred Value : 0.9855
##           Neg Pred Value : 0.9798
##               Prevalence : 0.8641
##           Detection Rate : 0.8616
##     Detection Prevalence : 0.8743
##        Balanced Accuracy : 0.9518
##
##         'Positive' Class : ham
##
```

#Test accuracy of naiveBayes model is 98.48%

```
# fit a SVM using the e1071 package
fit_svm_train = svm(train_labels~., data= train, kernel = "linear")

pred_svm_train = predict(fit_svm_train, train)
```

```r
train_acc = mean(pred_svm_train == train_labels)
cat("The train accuracy of SVM is :", train_acc*100, "%")
```

```
## The train accuracy of SVM is : 99.54989 %
```

```r
pred_svm_test = predict(fit_svm_train, test)
test_acc = mean(pred_svm_test == test_labels)
cat("The test accuracy of SVM is :", test_acc*100, "%")
```

```
## The test accuracy of SVM is : 98.43182 %
```