Lab 11

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INTRODUCTION

Aim of analysis

```
In the following document, I will be using SVM classification techinque to predict he
art disease (angiographic disease status). From a set of 14 variables, the most impor
tant to predict heart failure are whether or not there is a reversable defect in Thal
assemia followed by whether or not there is an occurrence of asymptomatic chest pain.
```

1. Load the necessary packages

```
require(ggplot2)
```

```
## Loading required package: ggplot2
```

```
require(pROC) #to plot the ROC curves
```

```
## Loading required package: pROC
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
require(caret)
```

```
## Loading required package: caret
```

```
## Loading required package: lattice
```

```
# Attach Packages
library(tidyverse)    # data manipulation and visualization
```

```
## ── Attaching packages ─────────────────────────────────────────────────────
──────────────────────────────── tidyverse 1.3.0 ──
```

```
## ✓ tibble  3.0.3     ✓ dplyr   1.0.4
## ✓ tidyr   1.1.1     ✓ stringr 1.4.0
## ✓ readr   1.4.0     ✓ forcats 0.5.1
## ✓ purrr   0.3.4
```

```
## ── Conflicts ────────────────────────────────────────────────────────────
────────────────────────── tidyverse_conflicts() ──
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x purrr::lift()   masks caret::lift()
```

```
library(kernlab)      # SVM methodology
```

```
##
## Attaching package: 'kernlab'
```

```
## The following object is masked from 'package:purrr':
##
##     cross
```

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

```
library(e1071)        # SVM methodology
library(ISLR)         # contains example data set "Khan"
library(RColorBrewer) # customized coloring of plots
```

2. Load the dataset

The heart disease data are available at UCI and Kaggle.

```
heartdf <- read.csv("heart.csv")
```

EXPLORATORY DATA ANALYSIS

1.Columns and shape of dataset

```
names(heartdf) <- c( "age", "sex", "cp", "trestbps", "chol","fbs", "restecg", "thalac
        h","exang", "oldpeak","slope", "ca", "thal", "num")
attach(heartdf)
```

```
# dimensions of the dataset
dim(heartdf)
```

```
## [1] 303  14
```

The variable we want to predict is num with Value 0: < 50% diameter narrowing and Val ue 1: > 50% diameter narrowing. We assume that every value with 0 means heart is oka y, and 1,2,3,4 means heart disease.

From the possible values the variables can take, it is evident that the following nee d to be dummified because the distances in the values is random: cp,thal, restecg, sl ope

2. Viewing dataset

```
head(heartdf,5)
```

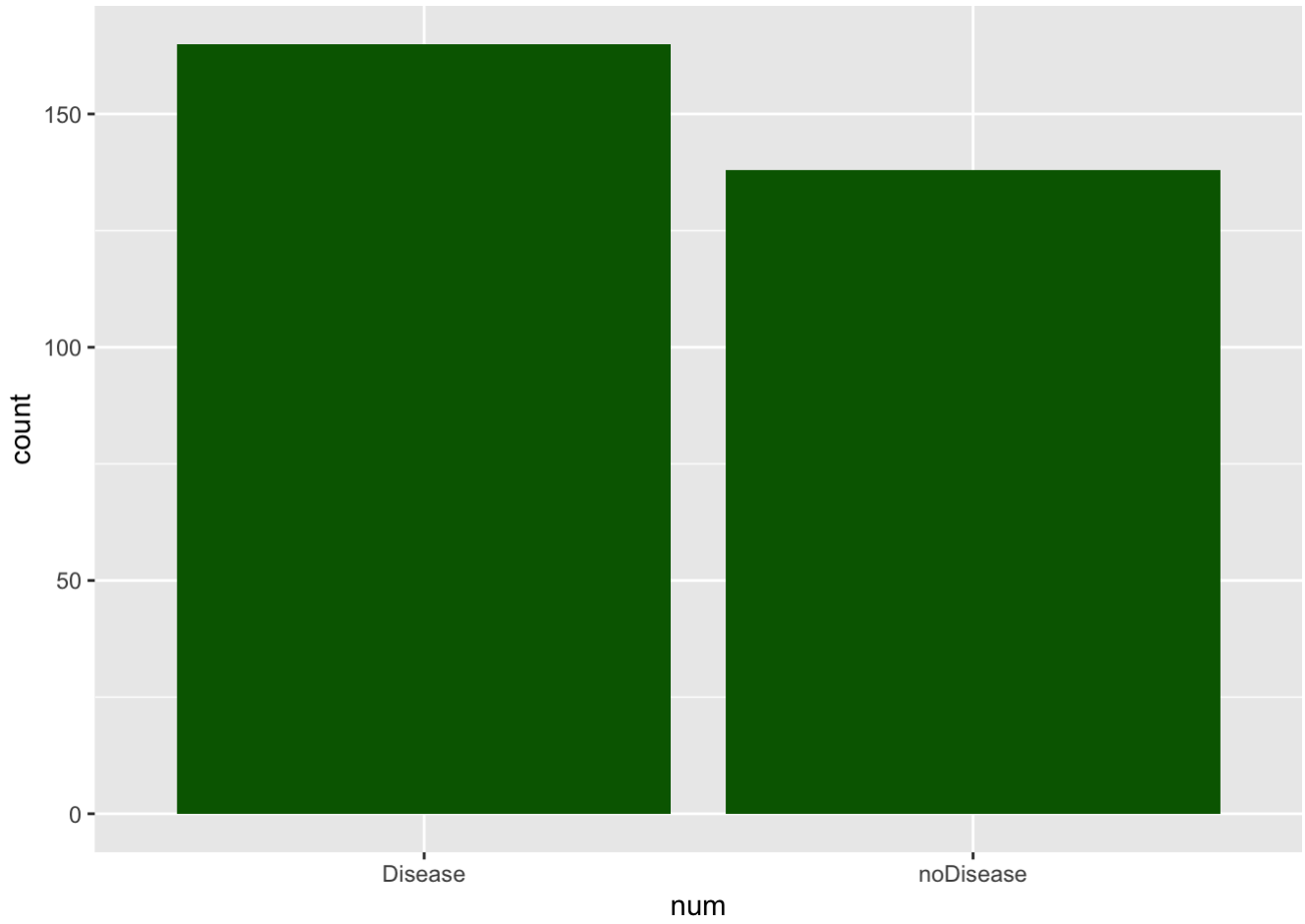
```
##   age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal num
## 1  63   1  3      145  233   1       0     150     0     2.3     0  0    1   1
## 2  37   1  2      130  250   0       1     187     0     3.5     0  0    2   1
## 3  41   0  1      130  204   0       0     172     0     1.4     2  0    2   1
## 4  56   1  1      120  236   0       1     178     0     0.8     2  0    2   1
## 5  57   0  0      120  354   0       1     163     1     0.6     2  0    2   1
```

Explore the data and find how many had heart attacks, women or men have of a particul ar age?

```
#converting the num variable to binary class variable

heartdf$num<-ifelse(heartdf$num > 0,"Disease","noDisease")
table(heartdf$num)
```

```
##
##   Disease noDisease
##       165       138
```

```
#distribution of the target variable
ggplot(heartdf,aes(x = num)) + geom_bar(fill="dark green")
```



3. Conversion factor variable

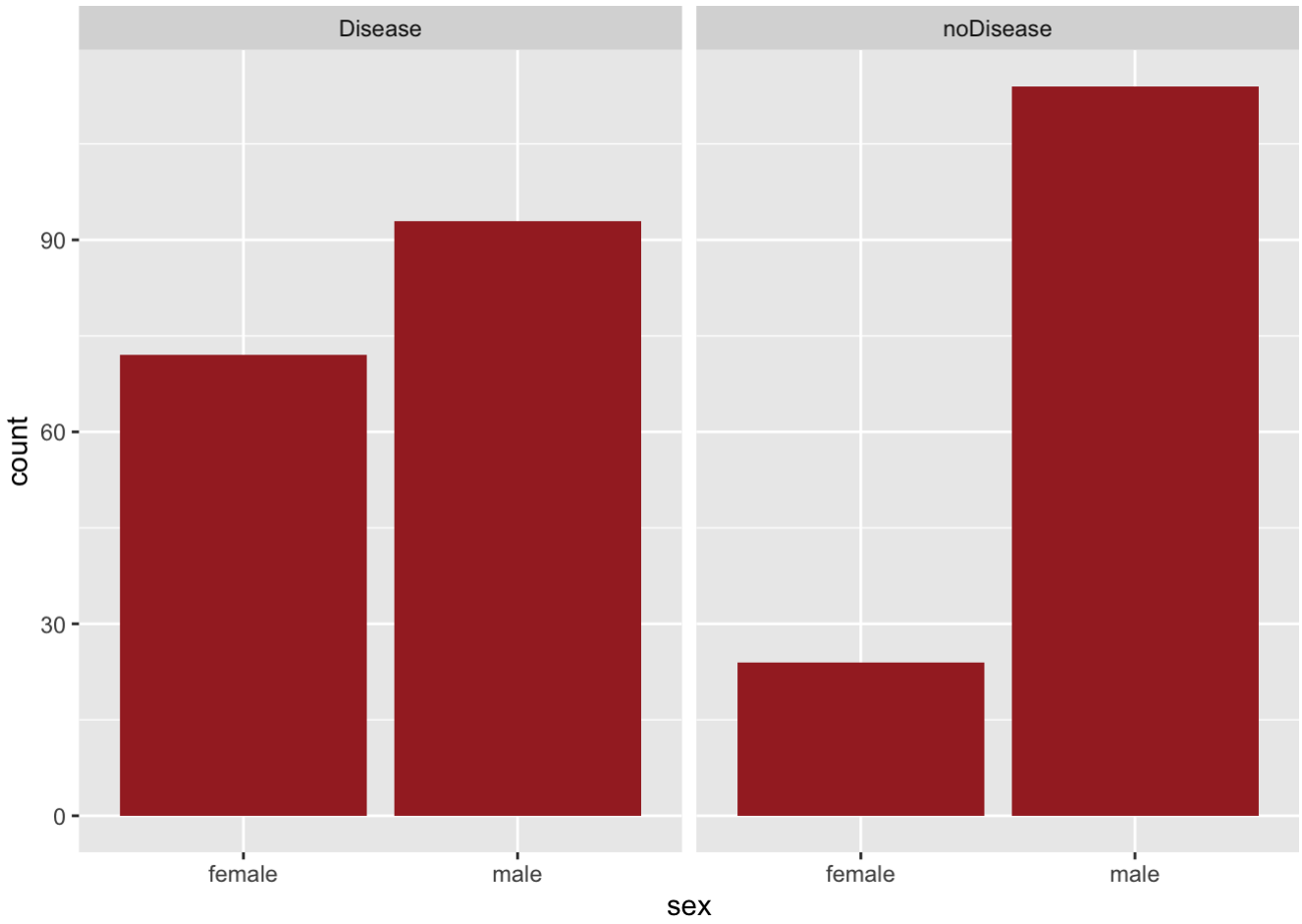
```
#converting to factor variable

heartdf$sex<-ifelse(heartdf$sex==0,"female","male")

table(heartdf$sex)
```

```
##
## female   male
##     96    207
```

```
table(sex=heartdf$sex,disease=heartdf$num)
```

```
##         disease
## sex      Disease noDisease
##   female      72        24
##   male        93       114
```

```
ggplot(heartdf,aes(x=sex)) + geom_bar(fill="brown") + facet_wrap(~num)
```



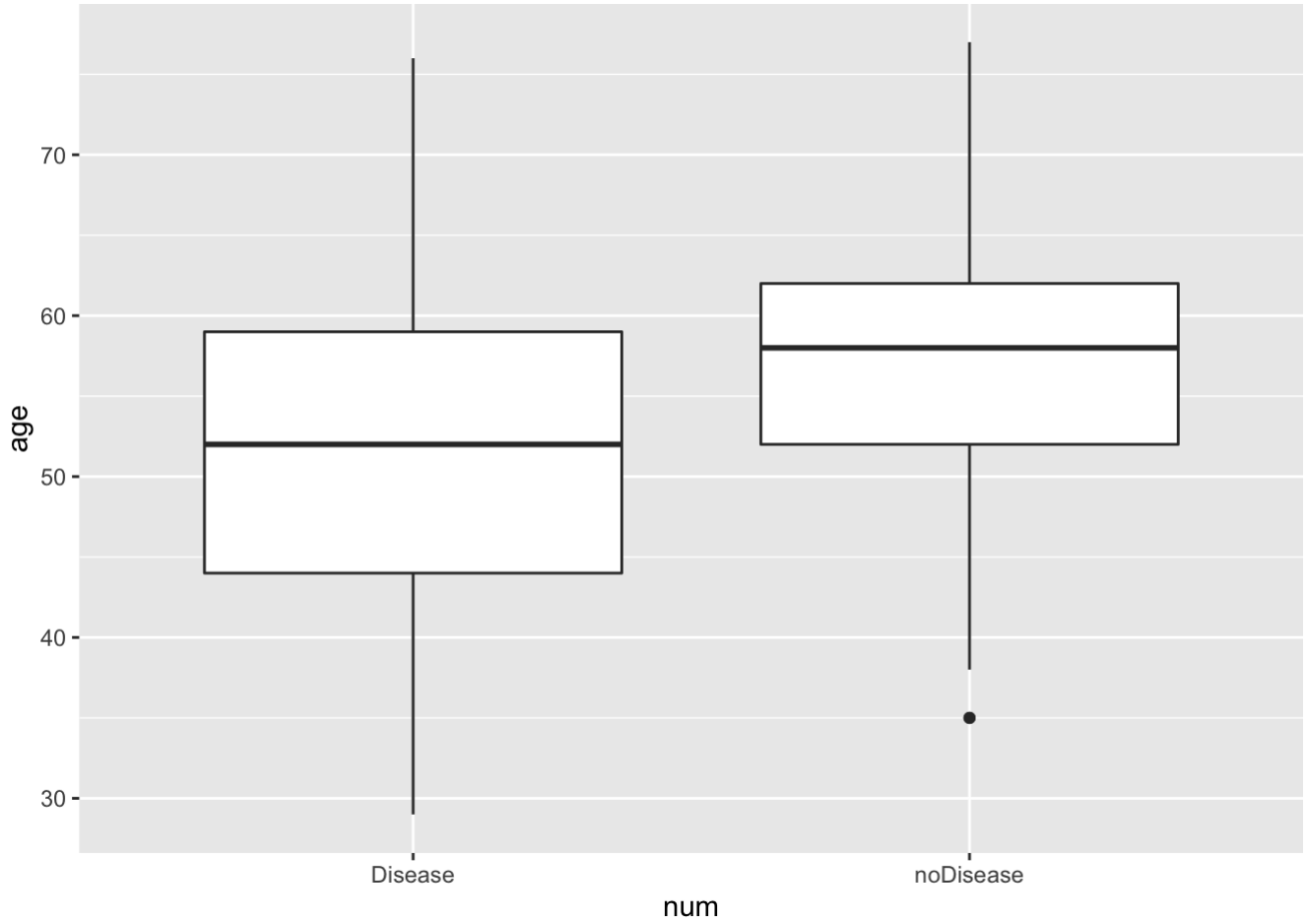
4. Box plot for statistical distribution

```
#heart disease and age

by(heartdf$age,heartdf$num,summary)
```

```
## heartdf$num: Disease
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    29.0    44.0    52.0    52.5    59.0    76.0
## ------------------------------------------------------------
## heartdf$num: noDisease
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    35.0    52.0    58.0    56.6    62.0    77.0
```

```
-So people who had heart disease for them the mean age is 52.5
```

```
ggplot(heartdf,aes(x = num,y = age)) + geom_boxplot()
```



5. Correlation analysis between some variables

```
#very low correlation
cor.test(age,chol)
```

```
##
##  Pearson's product-moment correlation
##
## data:  age and chol
## t = 3.7948, df = 301, p-value = 0.0001786
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.1034917 0.3186831
## sample estimates:
##      cor
## 0.213678
```

6. Confusion matrix

```
#confusion matrix of chest pain and heart disease

table(cp,num)
```

```
##    num
## cp    0   1
##   0 104  39
##   1   9  41
##   2  18  69
##   3   7  16
```

```
#confusuon matrix of exersice induced asthama and heart disease

table(exang,num)
```

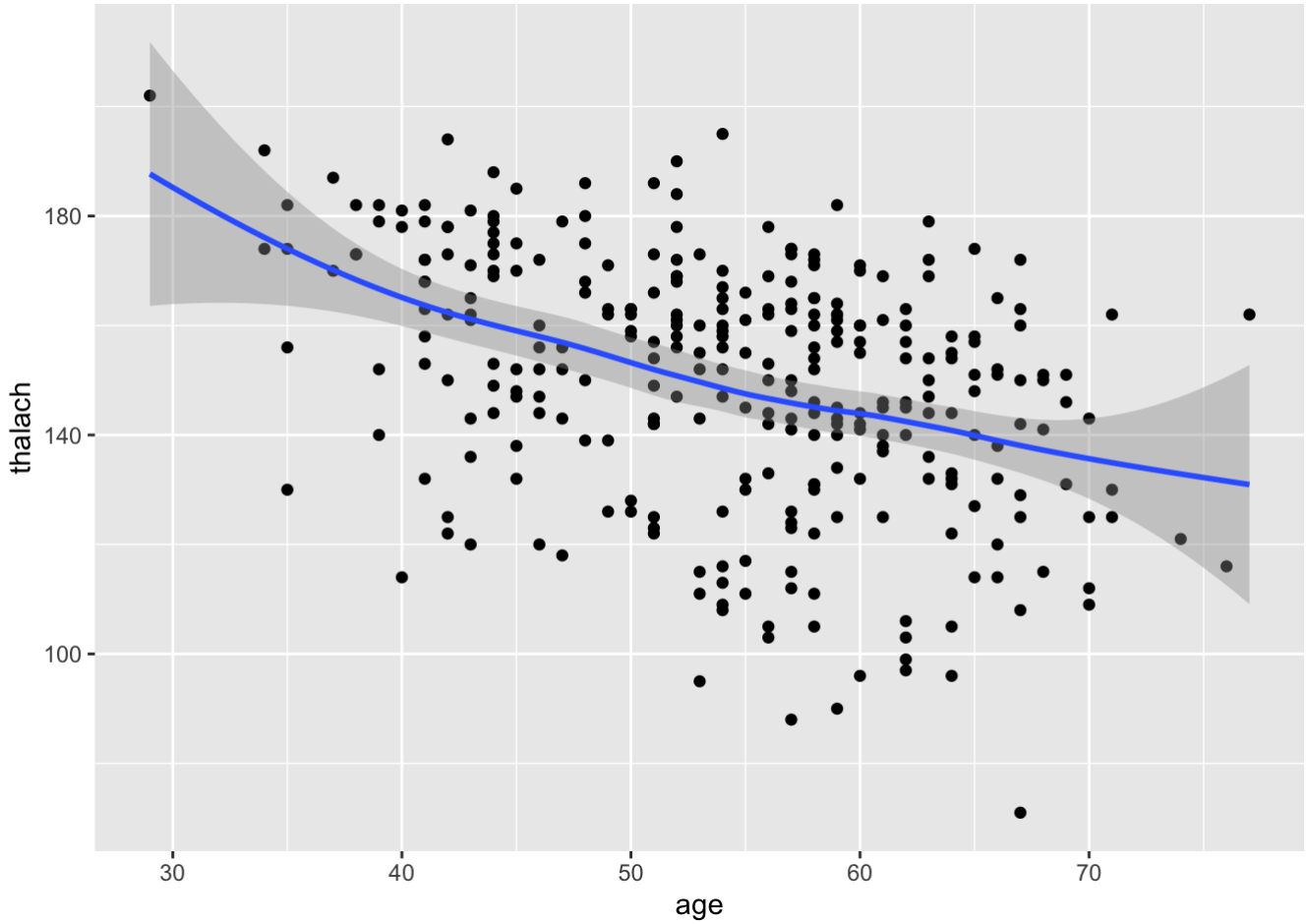
```
##      num
## exang   0   1
##     0  62 142
##     1  76  23
```

```
cor.test(age,thalach)
```

```
##
##  Pearson's product-moment correlation
##
## data:  age and thalach
## t = -7.5386, df = 301, p-value = 5.628e-13
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.4892312 -0.2992831
## sample estimates:
##        cor
## -0.3985219
```

```
ggplot(heartdf,aes(x = age,y = thalach )) + geom_point() + geom_smooth()
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```




```
-Here we can notice as age increase maximum heart rate achived descreases, as the cor
-relation is negetive.
```

Model Building

1. Data splitting

```
set.seed(5)

inTrainRows <- createDataPartition(heartdf$num,p=0.8,list=FALSE)

trainData <- heartdf[inTrainRows,]
testData <- heartdf[-inTrainRows,]

nrow(trainData)/(nrow(testData)+nrow(trainData))
```

```
## [1] 0.8019802
```

2. Feature selections

```
# for this to work add names to all levels (numbers not allowed)
feature.names=names(heartdf)
for (f in feature.names) {
  if (class(heartdf[[f]])=="factor") {
      levels <- unique(c(heartdf[[f]]))
      heartdf[[f]] <- factor(heartdf[[f]],
      labels=make.names(levels))
  }
}
```

```
#converting to factor variable with 2 levels

heartdf$num<-as.factor(heartdf$num)
levels(heartdf$num) <- c("Notdisease","Disease")

table(heartdf$num)
```

```
##
## Notdisease    Disease
##        165        138
```

3. Building a SVM classifier

```
Now SVM classifier tends to generate hyperplanes which separate the classes with maxi
mum margins i.e in simpler terms it aims to generate maximum marginal hyperplane.
```

```
set.seed(10)
inTrainRows <- createDataPartition(heartdf$num,p=0.7,list=FALSE)
trainData2 <- heartdf[inTrainRows,]
testData2 <- heartdf[-inTrainRows,]

#cross validation
fitControl <- trainControl(method = "repeatedcv",
                           number = 10,
                           repeats = 10,
                           ## Estimate class probabilities
                           classProbs = TRUE,
                           ## Evaluate performance using
                           ## the following function
                           summaryFunction = twoClassSummary)
```

```
svmModel <- train(num ~ ., data = na.omit(trainData2),
                  method = "svmRadial",
                  trControl = fitControl,
                  preProcess = c("center", "scale"),
                  tuneLength = 8,
                  metric = "ROC")

svmModel
```

```
## Support Vector Machines with Radial Basis Function Kernel
##
## 213 samples
##  13 predictor
##   2 classes: 'Notdisease', 'Disease'
##
## Pre-processing: centered (13), scaled (13)
## Resampling: Cross-Validated (10 fold, repeated 10 times)
## Summary of sample sizes: 191, 192, 192, 192, 191, 192, ...
## Resampling results across tuning parameters:
##
##   C      ROC        Sens       Spec
##    0.25  0.8934646  0.8569697  0.7500000
##    0.50  0.8929621  0.8697727  0.7461111
##    1.00  0.8941759  0.8534848  0.7697778
##    2.00  0.8891439  0.8408333  0.7674444
##    4.00  0.8805833  0.8246970  0.7380000
##    8.00  0.8785909  0.8303788  0.7130000
##   16.00  0.8678897  0.8192424  0.7103333
##   32.00  0.8589891  0.8083333  0.7010000
##
## Tuning parameter 'sigma' was held constant at a value of 0.05165118
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were sigma = 0.05165118 and C = 1.
```

```
#prediction on test data-class labels
svmPrediction <- predict(svmModel, testData2)


#probability of no heart disease-finding probabilities value
svmPredictionprob <- predict(svmModel, testData2, type='prob')[2]


#generating a confusion matrix
ConfMatrixPrediction <- confusionMatrix(svmPrediction, na.omit(testData2)$num)
ConfMatrixPrediction$table
```

```
##             Reference
## Prediction   Notdisease Disease
##   Notdisease         43       7
##   Disease             6      34
```

```
-In the confusion matrix the diagonals represent the correctly classified examples, w
hereas the offdiagonals are incorrectly classifier examples.
-To find the ROC curver and the AUC value to better understand the accuracy and perfo
rmance
-ROC curve is the plot of True positive rate vs the false positive rate.
```

4. ROC and AUC value

```
#ROC and AUC value

AUC<- roc(na.omit(testData2)$num,as.numeric(as.matrix((svmPredictionprob))))$auc
```

```
## Setting levels: control = Notdisease, case = Disease
```

```
## Setting direction: controls < cases
```

```
Accuracy<- ConfMatrixPrediction$overall['Accuracy']

svmPerformance<-cbind(AUC,Accuracy)
svmPerformance
```

```
##                AUC  Accuracy
## Accuracy 0.9133897 0.8555556
```

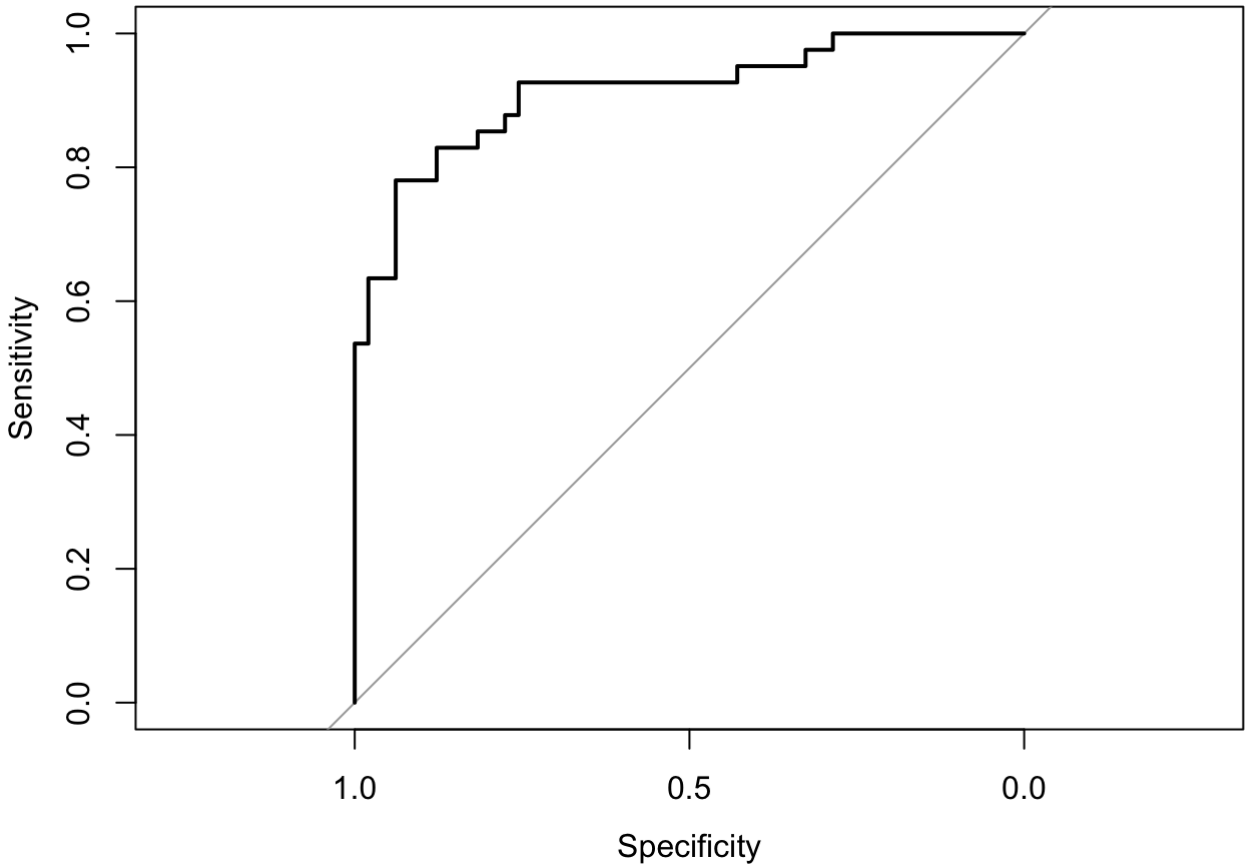
```
Hence we get an AUC value of 0.9133897 and overall prediction accuracy of 0.8555556.
```

```
auc_roc<-roc(na.omit(testData2)$num,as.numeric(as.matrix((svmPredictionprob))))
```

```
## Setting levels: control = Notdisease, case = Disease
```

```
## Setting direction: controls < cases
```

```
plot(auc_roc)
```


Sensitivity
0.0
0.2
0.4
0.6
0.8
1.0
1.0
0.5
0.0
Specificity