Heart disease prediction using SVM

Anish Singh Walia

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Prediction of heart disease

Aim of analysis

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

Dataset:

The heart disease data are available at UCI The description of the database can be found here.

let's read the dataset from the URL in R.

```
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
```

```
heartdf <- read.csv("https://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/processed.
```

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

attach(heartdf)
```

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

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

Let's get a quick idea of data

```
head(heartdf,3)
```

```
##   age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal
## 1  63   1  1      145  233   1       2     150     0     2.3     3  0    6
```

```
## 2  67   1  4      160  286   0       2     108     1     1.5     2  3    3
## 3  67   1  4      120  229   0       2     129     1     2.6     2  2    7
##   num
## 1   0
## 2   2
## 3   1
```

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

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

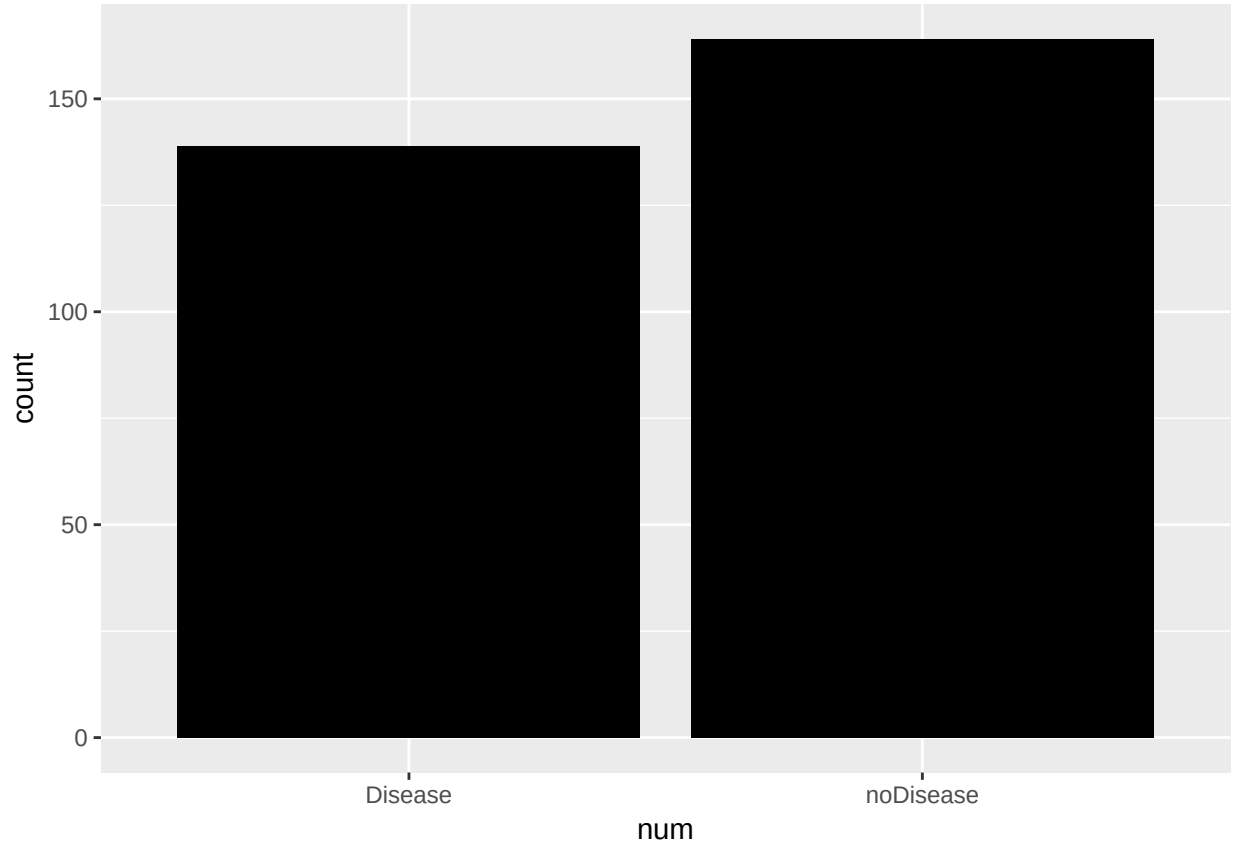
Let's explore the data and find how many had heart attacks, women or men have of a particular age?

Let's first convert the dependent(class variable) $Y - num$ to binary variable.

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

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

table(heartdf$num)
```

```
##
##   Disease noDisease
##       139       164
```

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



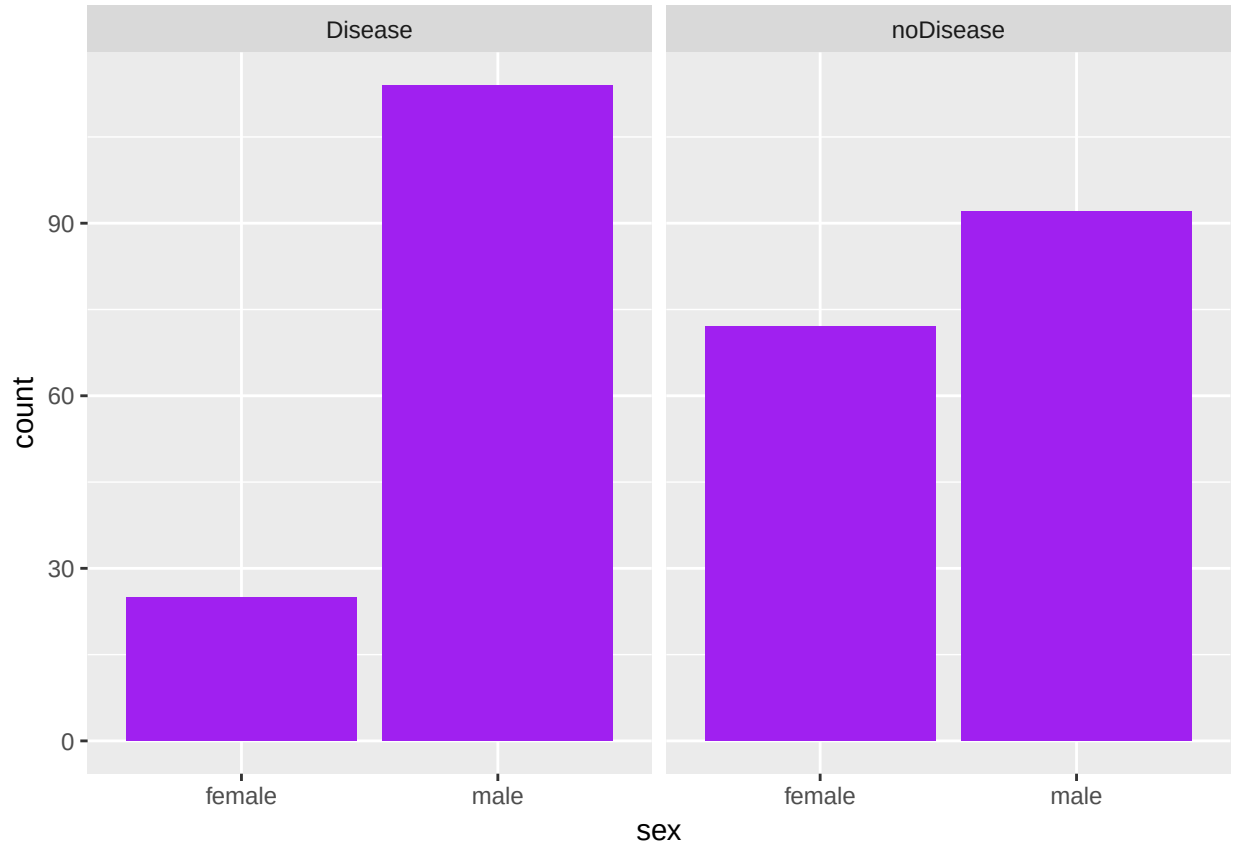
```r
#converting to factor variable
heartdf$sex<-ifelse(heartdf$sex==0,"female","male")

table(heartdf$sex)
```

```
##
## female   male
##     97    206
```

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

```
##         disease
## sex      Disease noDisease
##   female      25        72
##   male       114        92
```

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



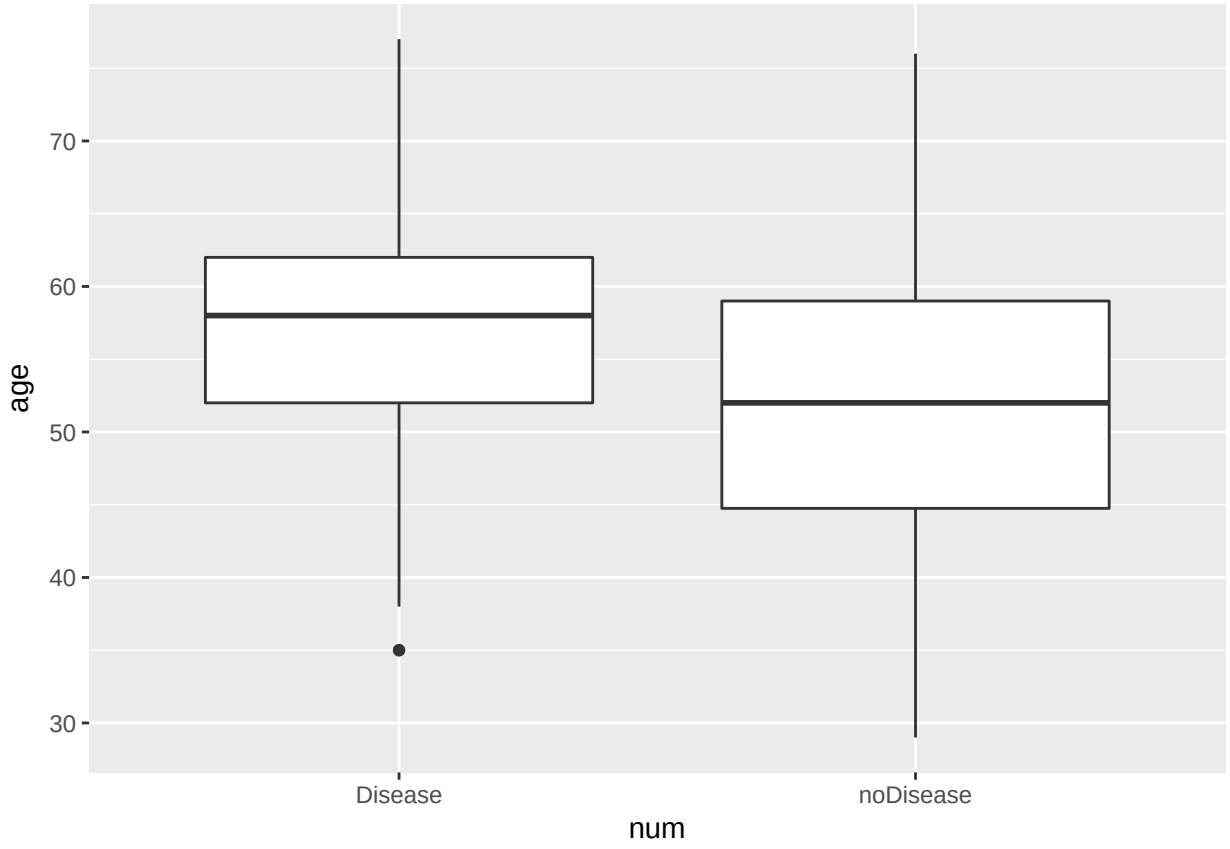

```r
#heart disease and age
#making a box plot to unserstand the statistical distribution

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

```
## heartdf$num: Disease
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   35.00   52.00   58.00   56.63   62.00   77.00
```

```
## ------------------------------------------------------------
## heartdf$num: noDisease
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   29.00   44.75   52.00   52.59   59.00   76.00
```

So people who had heart disease for them the mean age is 56.6

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



Let's do some correlation analysis between some variables-

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

```
##
##  Pearson's product-moment correlation
##
## data:  age and chol
## t = 3.707, df = 301, p-value = 0.0002496
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.09859353 0.31423005
## sample estimates:
##       cor
## 0.2089503
```

We can see that age and cholestrol levlels have very low cor-relation.

```r
#confusion matrix of chest pain and heart disease
table(cp,num)
```

```
##    num
## cp   0  1  2  3  4
##   1 16  5  1  0  1
##   2 41  6  1  2  0
##   3 68  9  4  4  1
##   4 39 35 30 29 11
```

```r
#confusuon matrix of exersice induced asthama and heart disease
table(exang,num)
```

```
##      num
## exang   0   1   2   3   4
##     0 141  30  14  12   7
##     1  23  25  22  23   6
```

We can notice from the table that people who had heart diseases had severe level of chest pain. Also people who had heart diseases had exercise induced asthama.

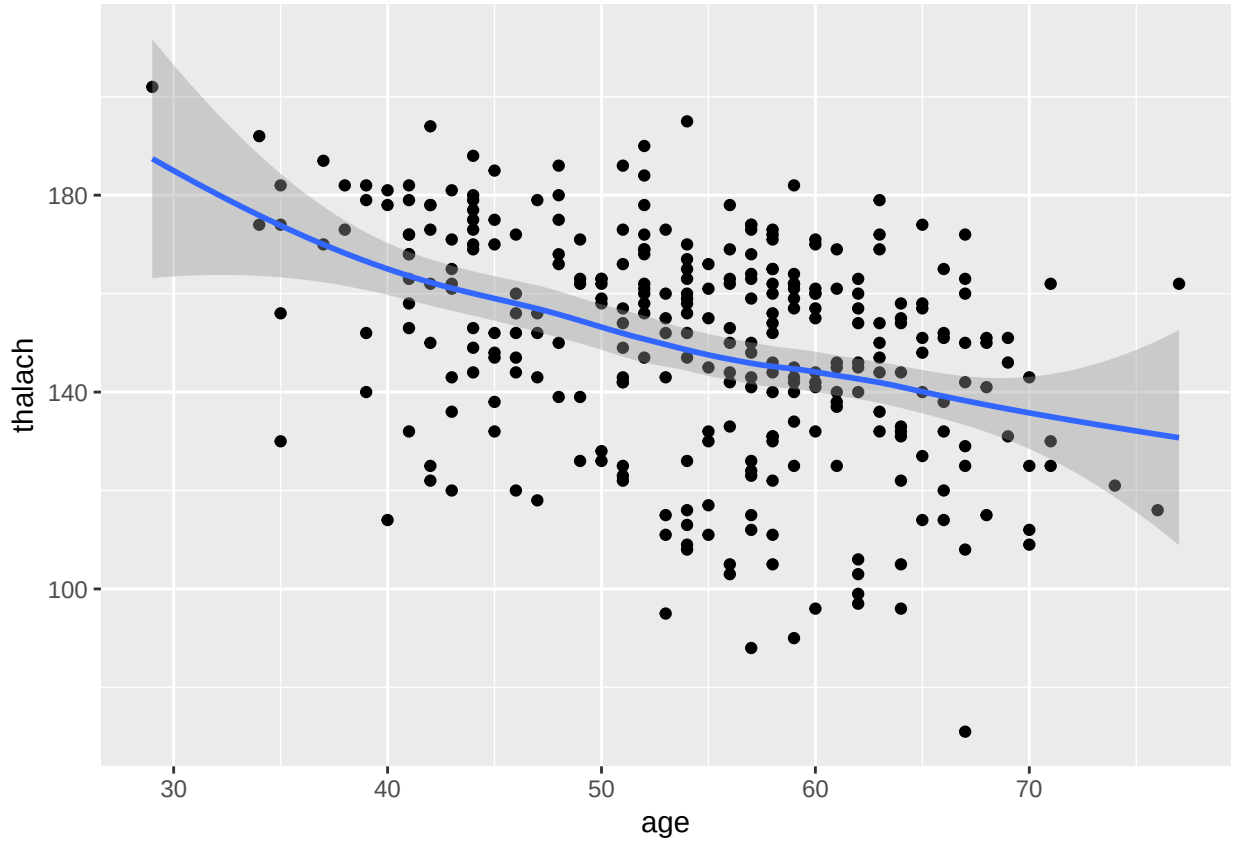
Correlation between age and maximum heart rate achieved-

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

```
##
##  Pearson's product-moment correlation
##
## data:  age and thalach
## t = -7.4329, df = 301, p-value = 1.109e-12
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.4849644 -0.2941816
## sample estimates:
##        cor
## -0.3938058
```

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

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



We can notice that as age increase maximum heart rate achived descreases, as the cor-relation is negetive.

---

predictive Modelling

let's now predict who is likely to have a hear disease and who is not?

Separating training and testing data

```
library(caret)
```

```
## Warning: package 'caret' was built under R version 3.4.3
```

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

```
set.seed(20)


inTrainRows <- createDataPartition(heartdf$num,p=0.7,list=FALSE)


trainData <- heartdf[inTrainRows,]
testData <-  heartdf[-inTrainRows,]
nrow(trainData)/(nrow(testData)+nrow(trainData)) #checking whether really 70% -> OK
```

```
## [1] 0.7029703
```

Building a SVM classifier

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

So amongst a set of competing hypothesis $h_i(x)$ we want to choose the one which maximizes the margin between both the classes on either side of the separating hyperplane, i.e our main goal is to separate the classes on either sides of hyperplane with **maximum margin** using the *support vectors*(which help us define the maximum margins).

So a linear SVM classifier will generate a simple linear hyperplane for linearlly separable data.

```
# 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
##        139        164
```

```
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
##
## 209 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: 188, 189, 189, 187, 189, 188, ...
## Resampling results across tuning parameters:
##
##   C      ROC        Sens       Spec
##    0.25  0.8903140  0.7963333  0.8625758
##    0.50  0.8907567  0.7860000  0.8634091
##    1.00  0.8888721  0.7857778  0.8625000
##    2.00  0.8912214  0.7941111  0.8680303
##    4.00  0.8887837  0.7942222  0.8740152
##    8.00  0.8792062  0.7970000  0.8594697
##   16.00  0.8593729  0.7680000  0.8406818
##   32.00  0.8329242  0.7380000  0.7964394
##
## Tuning parameter 'sigma' was held constant at a value of 0.05051126
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were sigma = 0.05051126 and C = 2.
```

```
#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         32       7
##   Disease             9      40
```

In the confusion matrix the diagonals represent the correctly classified examples, whereas the offdiagonals are incorrectly classifier examples.

Let's find the ROC curver and the AUC value to better understand the accuracy and performance-

ROC curve is the plot of True positive rate vs the false positive rate.

```
#ROC and AUC value


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

Accuracy<- ConfMatrixPrediction$overall['Accuracy']

svmPerformance<-cbind(AUC,Accuracy)

svmPerformance
```

```
##                AUC  Accuracy
## Accuracy 0.8993254 0.8181818
```

Hence we get an **AUC** value of 0.911 and overall **prediction** accuracy of 0.89.

Plotting the ROC curve-

We will use the **roc()** function to find the parameters which contain all the sensitivity(TPR) and specificity(FPR) and other predictive parameters for a classifier.

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

plot(auc_roc)
```