Heart Disease Predictor

Kaustav Pal

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First, we load the required libraries

```
library(dplyr)
library(ggplot2)
library(caTools)
library(randomForest)
```

Data:

This database contains 14 physical attributes based on physical testing of a patient. Blood samples are taken and the patient also conducts a brief exercise test. The “goal” field refers to the presence of heart disease in the patient. It is integer (0 for no presence, 1 for presence). In general, to confirm 100% if a patient has heart disease can be quite an invasive process, so if we can create a model that accurately predicts the likelihood of heart disease, we can help avoid expensive and invasive procedures.

```
data<-read.csv('heart.csv')
head(data)
```

```
##   ï..age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal
## 1     63   1  3      145  233   1       0     150     0     2.3     0  0    1
## 2     37   1  2      130  250   0       1     187     0     3.5     0  0    2
## 3     41   0  1      130  204   0       0     172     0     1.4     2  0    2
## 4     56   1  1      120  236   0       1     178     0     0.8     2  0    2
## 5     57   0  0      120  354   0       1     163     1     0.6     2  0    2
## 6     57   1  0      140  192   0       1     148     0     0.4     1  0    1
##   target
## 1      1
## 2      1
## 3      1
## 4      1
## 5      1
## 6      1
```

Some information about the variables:

age age in years

sex (1 = male; 0 = female)

cp: chest pain type

trestbps: resting blood pressure (in mm Hg on admission to the hospital)

chol: serum cholestoral in mg/dl

fbs: (fasting blood sugar > 120 mg/dl) (1 = true; 0 = false)

restecg: resting electrocardiographic results

thalach: maximum heart rate achieved

exang: exercise induced angina (1 = yes; 0 = no)

oldpeak: ST depression induced by exercise relative to rest

slope: the slope of the peak exercise ST segment

ca: number of major vessels (0-3) colored by flourosopy

thal: 3 = normal; 6 = fixed defect; 7 = reversable defect

target: 1 or 0

Exploratory Data Analysis

We check for any missing values, the structure of the data, and then convert some of the variables into factors for better results.

```
any(is.na(data))
```

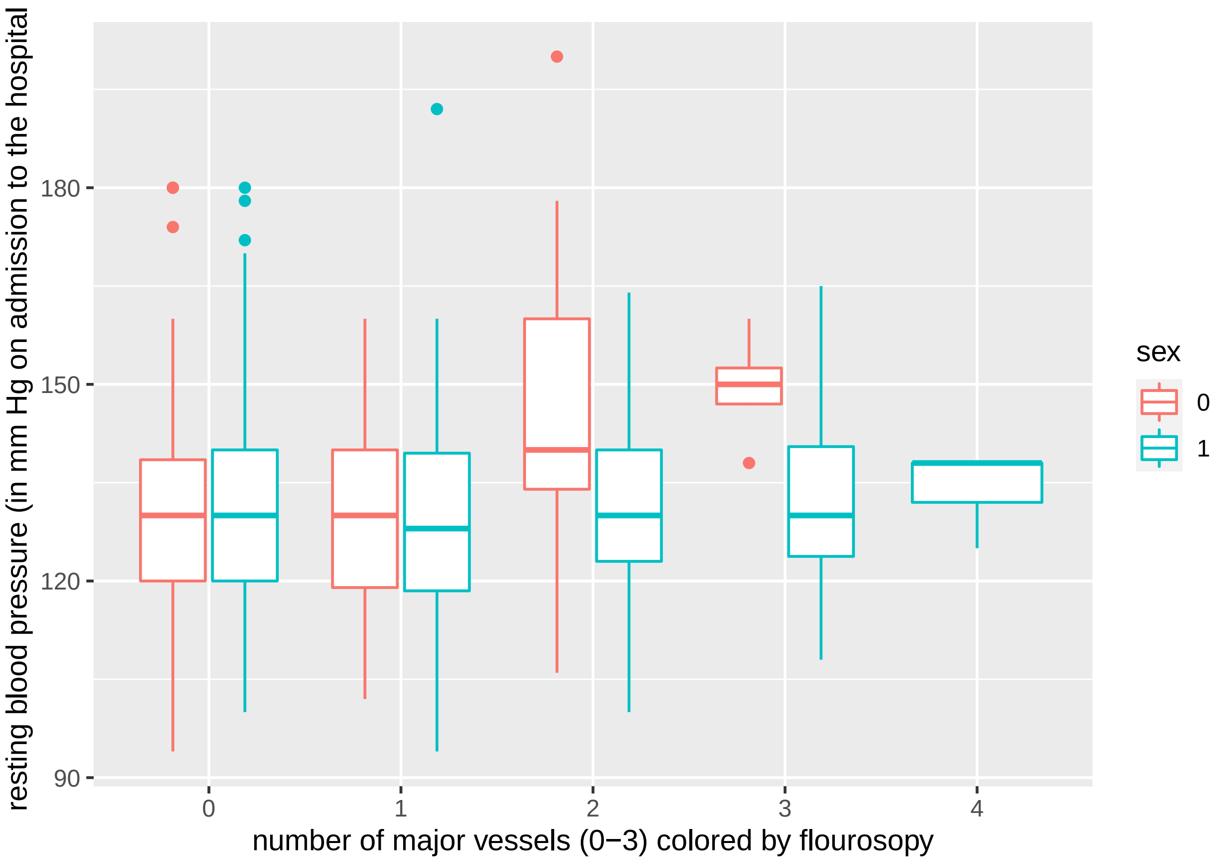
```
## [1] FALSE
```

```
str(data)
```

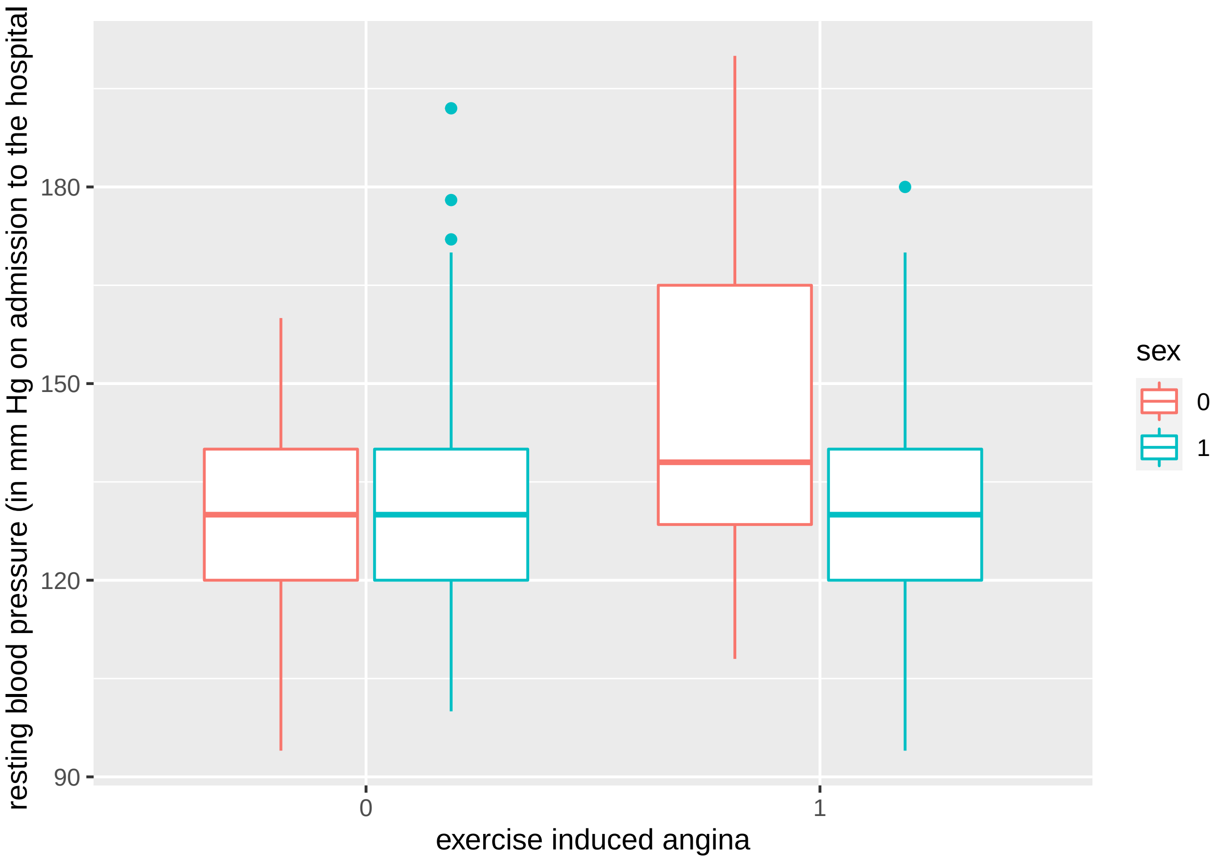
```
## 'data.frame':    303 obs. of  14 variables:
##  $ ï..age  : int  63 37 41 56 57 57 56 44 52 57 ...
##  $ sex     : int  1 1 0 1 0 1 0 1 1 1 ...
##  $ cp      : int  3 2 1 1 0 0 1 1 2 2 ...
##  $ trestbps: int  145 130 130 120 120 140 140 120 172 150 ...
##  $ chol    : int  233 250 204 236 354 192 294 263 199 168 ...
##  $ fbs     : int  1 0 0 0 0 0 0 0 1 0 ...
##  $ restecg : int  0 1 0 1 1 1 0 1 1 1 ...
##  $ thalach : int  150 187 172 178 163 148 153 173 162 174 ...
##  $ exang   : int  0 0 0 0 1 0 0 0 0 0 ...
##  $ oldpeak : num  2.3 3.5 1.4 0.8 0.6 0.4 1.3 0 0.5 1.6 ...
##  $ slope   : int  0 0 2 2 2 1 1 2 2 2 ...
##  $ ca      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ thal    : int  1 2 2 2 2 1 2 3 3 2 ...
##  $ target  : int  1 1 1 1 1 1 1 1 1 1 ...
```

```
data$sex<-factor(data$sex)
data$fbs<-factor(data$fbs)
data$restecg<-factor(data$restecg)
data$exang<-factor(data$exang)
data$slope<-factor(data$slope)
data$ca<-factor(data$ca)
data$target<-factor(data$target)
data$thal<-factor(data$thal)
```

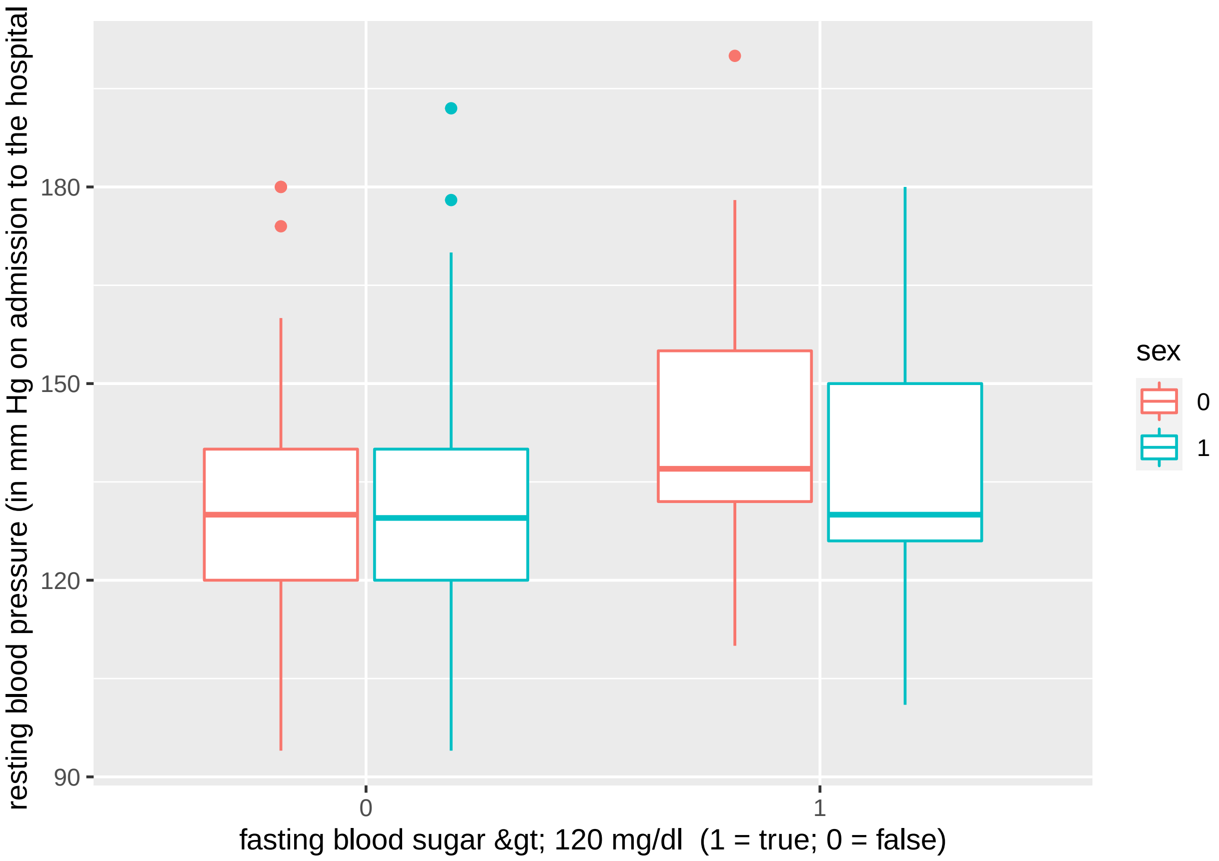
```
ggplot(data,aes(ca,trestbps))+geom_boxplot(aes(color=sex))+labs(x='number of major vessels (0-3) colore
```



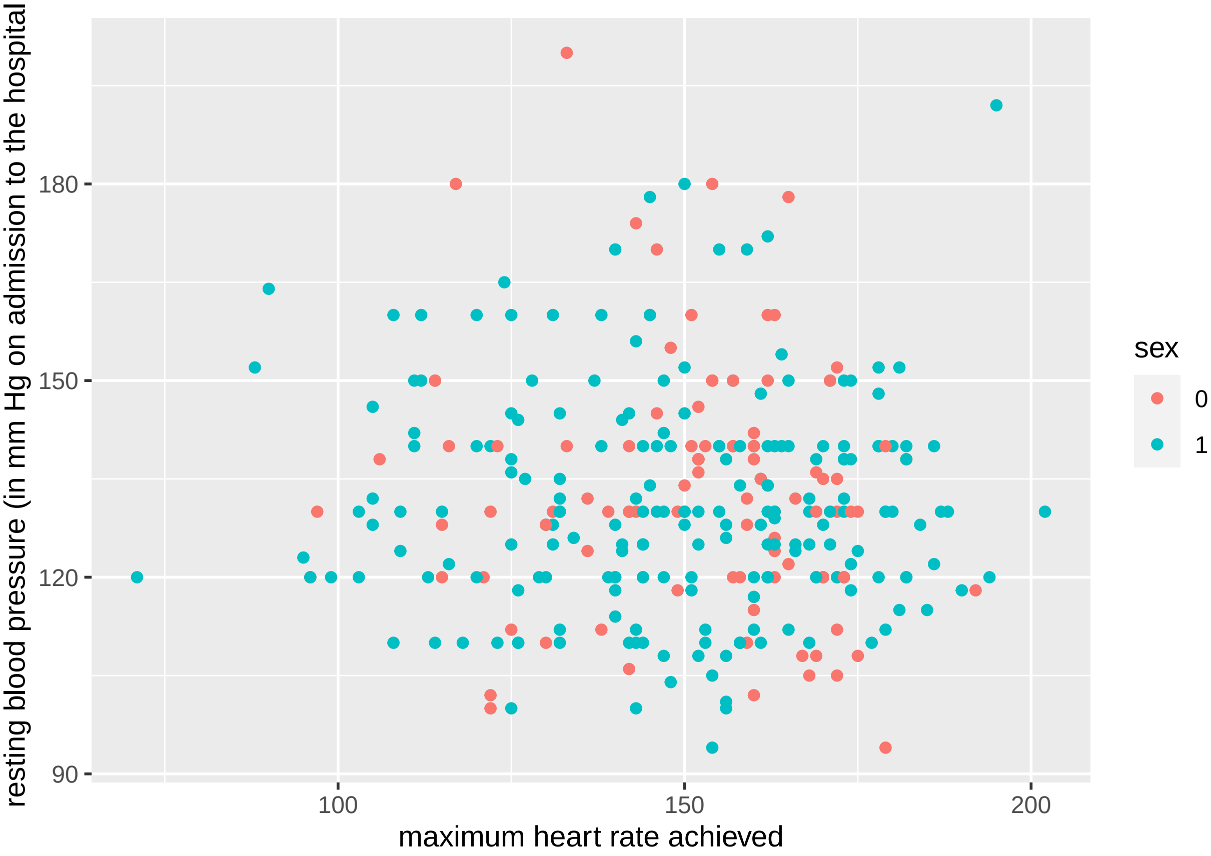
```
ggplot(data,aes(exang,trestbps))+geom_boxplot(aes(color=sex))+labs(x='exercise induced angina',y='restin
```



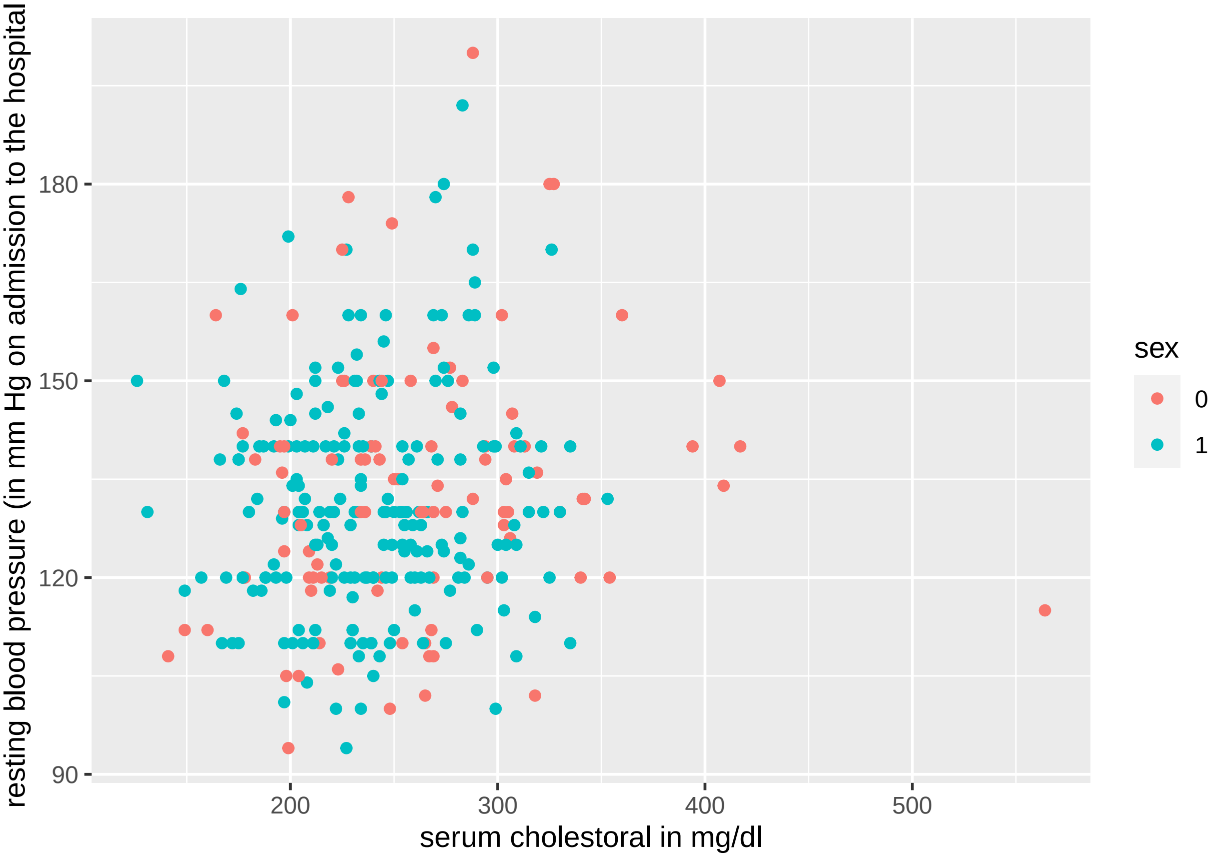
```
ggplot(data,aes(fbs,trestbps))+geom_boxplot(aes(color=sex))+labs(x='fasting blood sugar &gt; 120 mg/dl
```



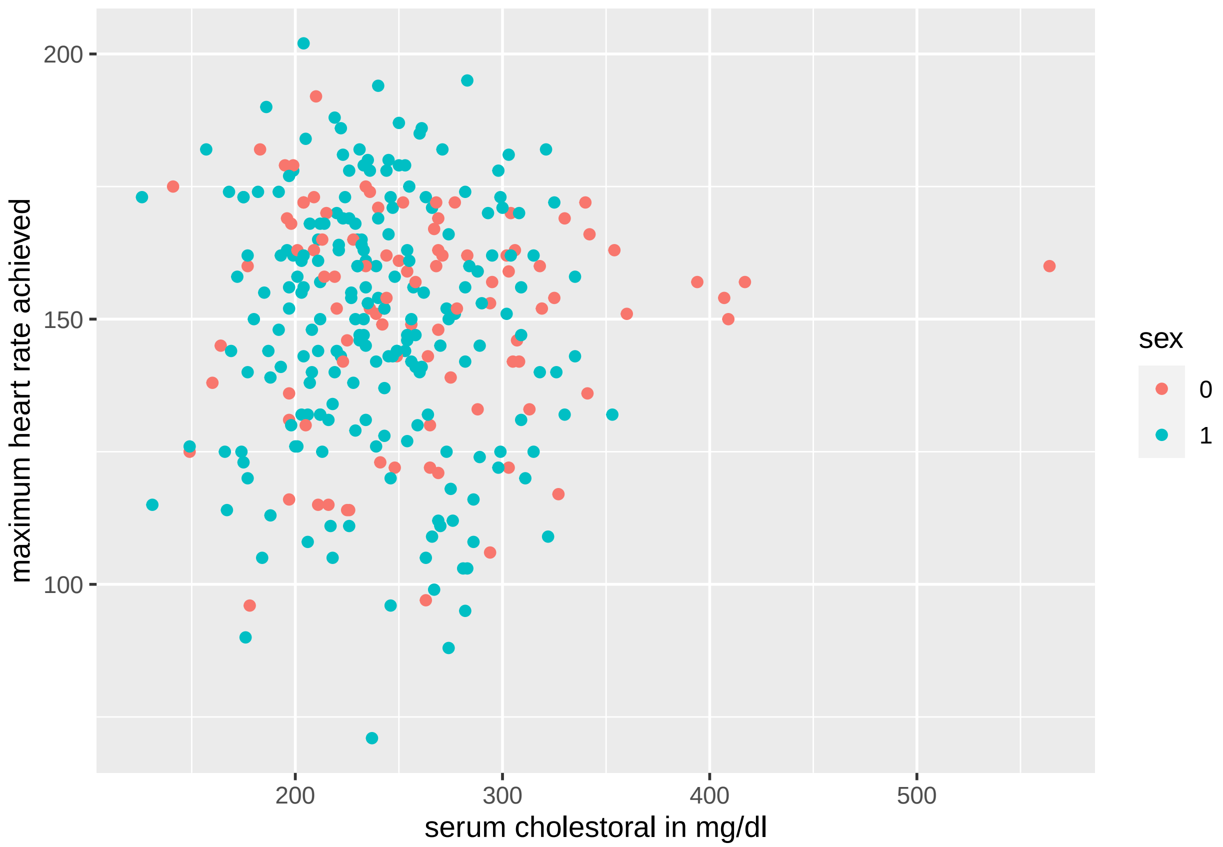
```
ggplot(data,aes(thalach,trestbps))+geom_point(aes(color=sex))+labs(x='maximum heart rate achieved',y='r
```



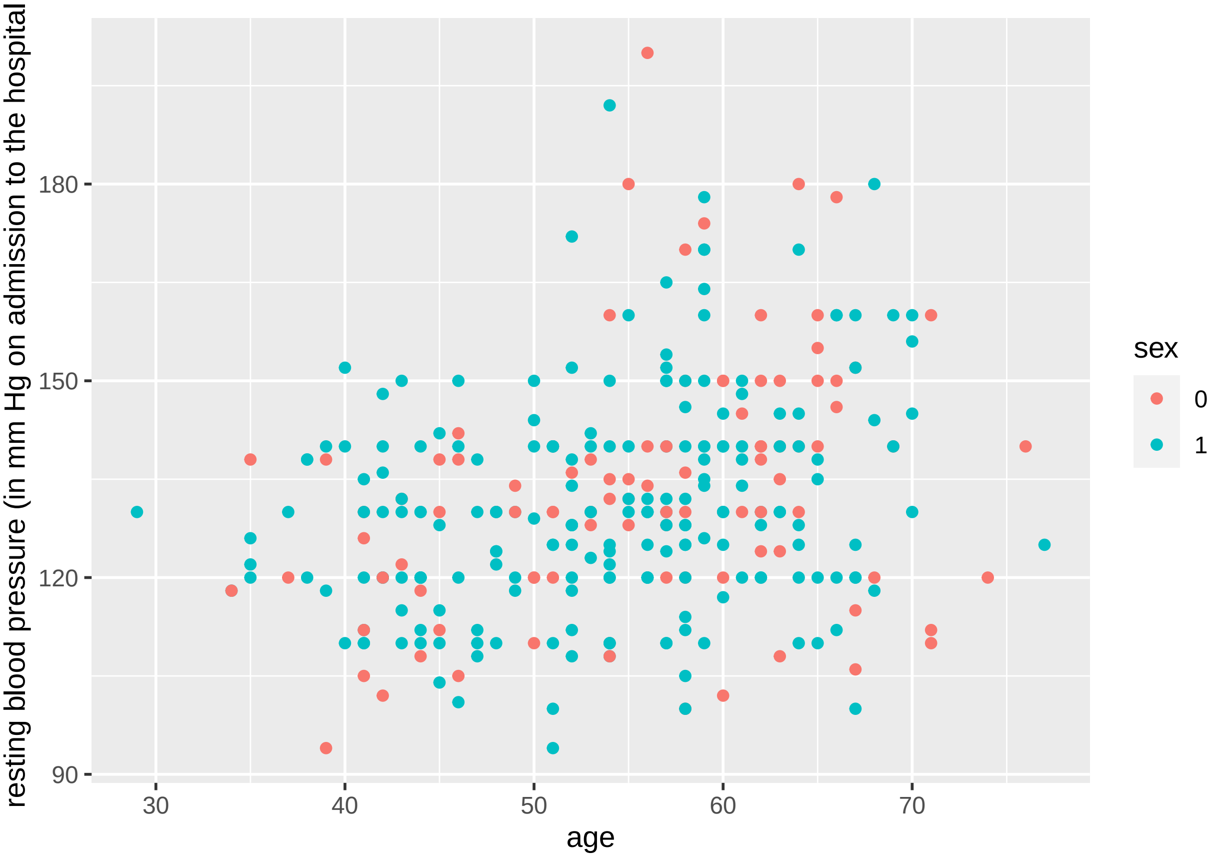
```
ggplot(data,aes(chol,trestbps))+geom_point(aes(color=sex))+labs(x='serum cholestoral in mg/dl',y='restin
```



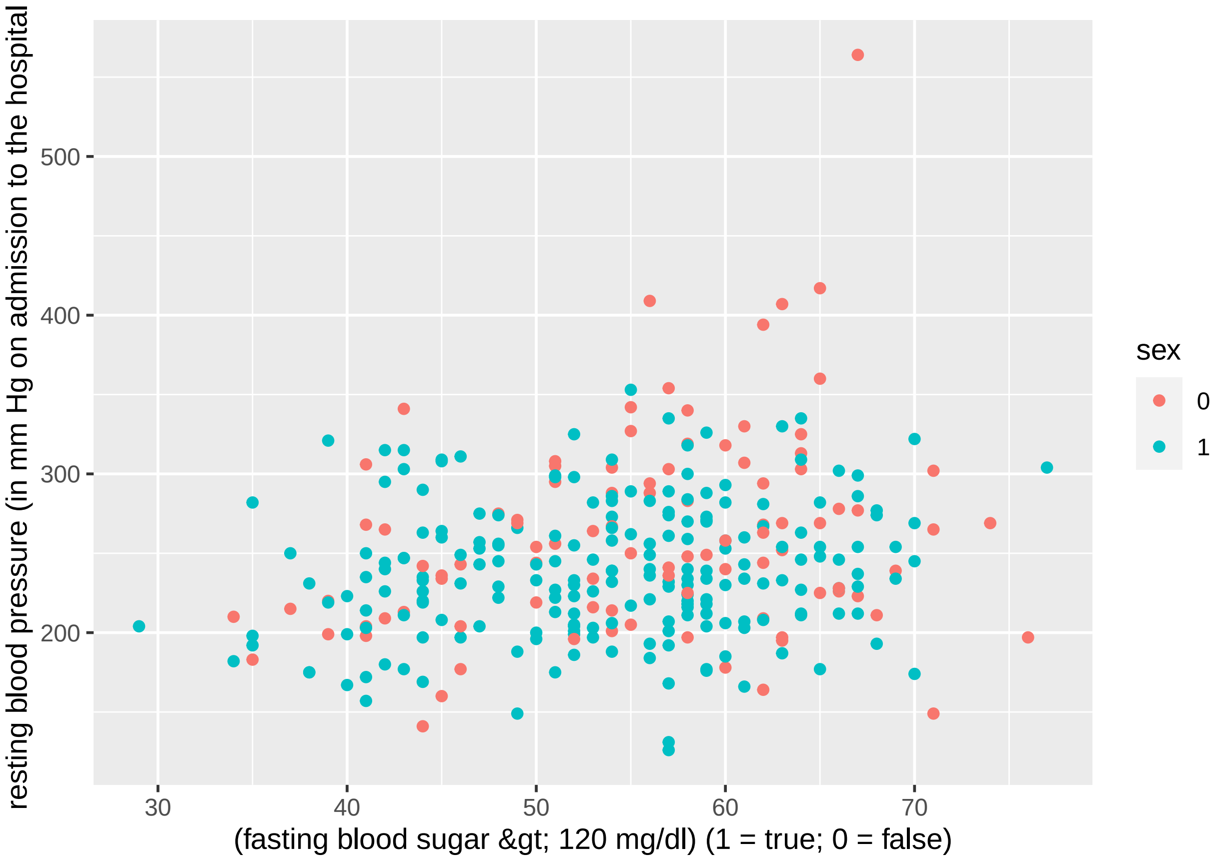
```
ggplot(data,aes(chol,thalach))+geom_point(aes(color=sex))+labs(x='serum cholestoral in mg/dl',y='maximu
```



```
ggplot(data,aes(ï..age,trestbps))+geom_point(aes(color=sex))+labs(x='age',y='resting blood pressure (in
```

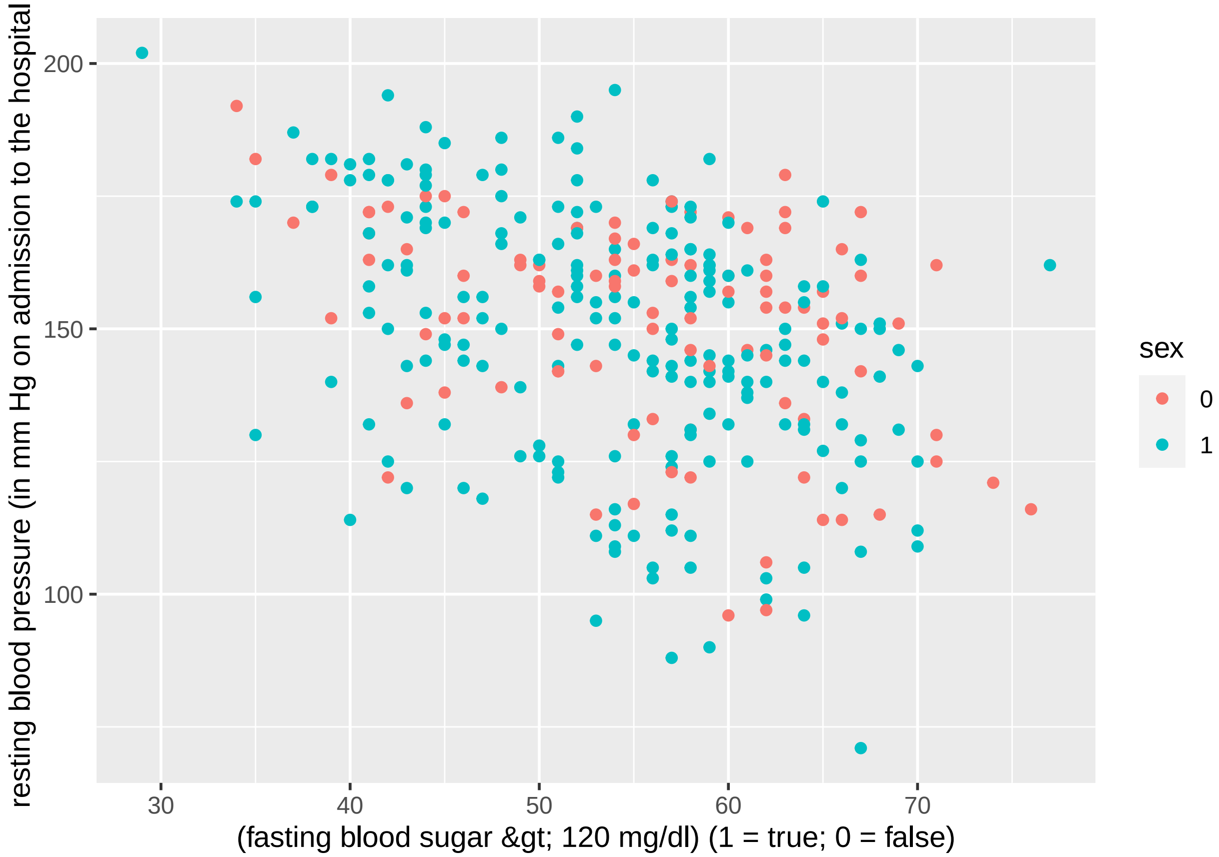


```
ggplot(data,aes(ï..age,chol))+geom_point(aes(color=sex))+labs(x='(fasting blood sugar &gt; 120 mg/dl) (
```



Till now, we see that most of the data is pretty much random.

```
ggplot(data,aes(ï..age,thalach))+geom_point(aes(color=sex))+labs(x='(fasting blood sugar &gt; 120 mg/dl
```



Here, we can see that there is somewhat negative relationship between the age and maximum heart rate achieved.

Train-Test Split

We split the data into training and test sets, with 70% of the data going to training and 30% going for testing.

```
sample<-sample.split(data,SplitRatio=0.7)
train<-subset(data,sample=T)
test<-subset(data,sample=F)
```

Model Building:

We build a random forest model and make predictions based on the model:

```
model<-randomForest(target~., train, importance = T, ntree=500)
predictions<-predict(model,test)
```

We check for the confusion matrix:

```
cm<-table(predictions,test$target)
cm
```

```
##
## predictions   0   1
##           0 138   0
##           1   0 165
```

Hence, we see that the random forest model works perfectly on the test set.