Touray_FinalProject

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2023-10-15

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

```
##   age sex cp trtbps chol fbs restecg thalachh exng oldpeak slp caa thall output
## 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
## 6  57   1  0    140  192   0       1      148    0     0.4   1   0     1      1
```

Ckeck for missing and Null Values

```
nullv <- is.null(heart)
head(nullv)
```

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

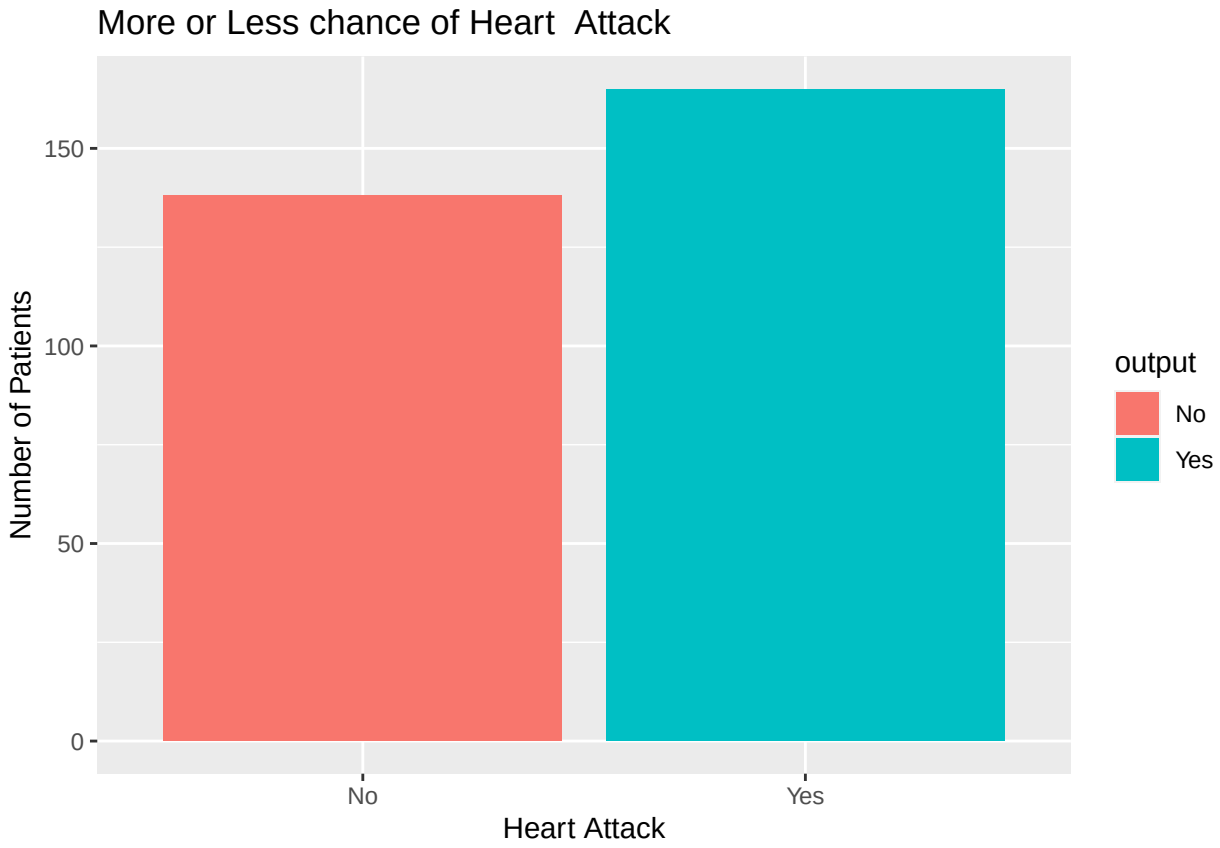
```
missnah <- is.na(heart)
head(missnah)
```

```
##        age   sex    cp trtbps  chol   fbs restecg thalachh  exng oldpeak   slp
## [1,] FALSE FALSE FALSE  FALSE FALSE FALSE   FALSE    FALSE FALSE   FALSE FALSE
## [2,] FALSE FALSE FALSE  FALSE FALSE FALSE   FALSE    FALSE FALSE   FALSE FALSE
## [3,] FALSE FALSE FALSE  FALSE FALSE FALSE   FALSE    FALSE FALSE   FALSE FALSE
## [4,] FALSE FALSE FALSE  FALSE FALSE FALSE   FALSE    FALSE FALSE   FALSE FALSE
## [5,] FALSE FALSE FALSE  FALSE FALSE FALSE   FALSE    FALSE FALSE   FALSE FALSE
## [6,] FALSE FALSE FALSE  FALSE FALSE FALSE   FALSE    FALSE FALSE   FALSE FALSE
##        caa thall output
## [1,] FALSE FALSE  FALSE
## [2,] FALSE FALSE  FALSE
## [3,] FALSE FALSE  FALSE
## [4,] FALSE FALSE  FALSE
## [5,] FALSE FALSE  FALSE
## [6,] FALSE FALSE  FALSE
```

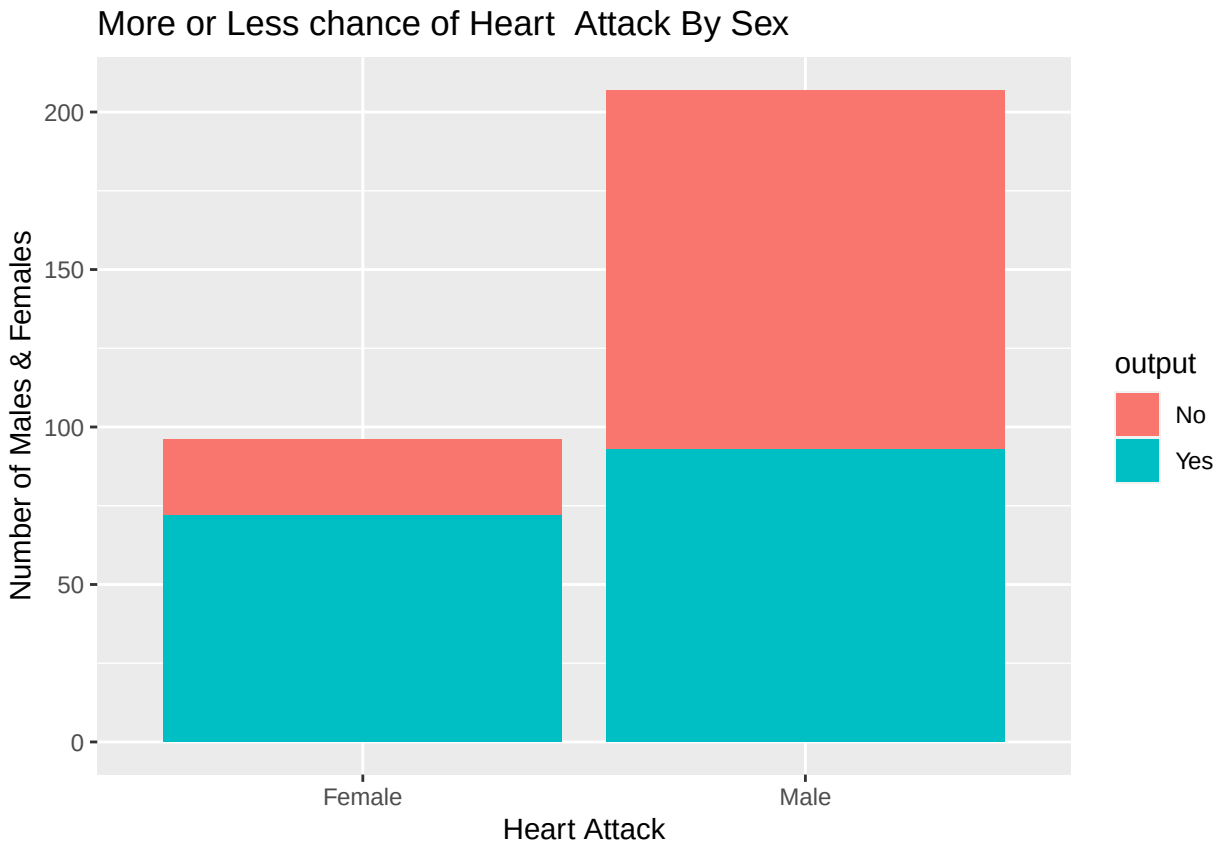
```
library(plyr)
heart$output <- as.factor(heart$output)
heart$output <- revalue(heart$output, c('1' = 'Yes', '0' = 'No'))
heart$sex <- as.factor(heart$sex)
heart$sex <- revalue(heart$sex, c('1' = 'Male', '0' = 'Female'))
heart$cp <- as.factor(heart$cp)
heart$cp <- revalue(heart$cp, c('0' = 'typical', '1' = 'atypical', '2' = 'non-aginal', '3'='Asymptomati
heart$restecg <- as.factor(heart$restecg)
heart$restecg <- revalue(heart$restecg, c('0' = 'Normal', '1' = 'Abnormal', '2' = 'LVH'))
```

```
heart$exng <- as.factor(heart$exng)
heart$exng <- revalue(heart$exng, c('1' = 'Yes', '0' = 'No'))
heart$slp <- as.factor(heart$slp)
heart$slp <- revalue(heart$slp, c('0' = 'Upsloping', '1' = 'Flat', '2' = 'Downsloping'))
heart$fbs <- as.factor(heart$fbs)
heart$fbs <- revalue(heart$fbs, c('1' = 'True', '0' = 'False'))
```

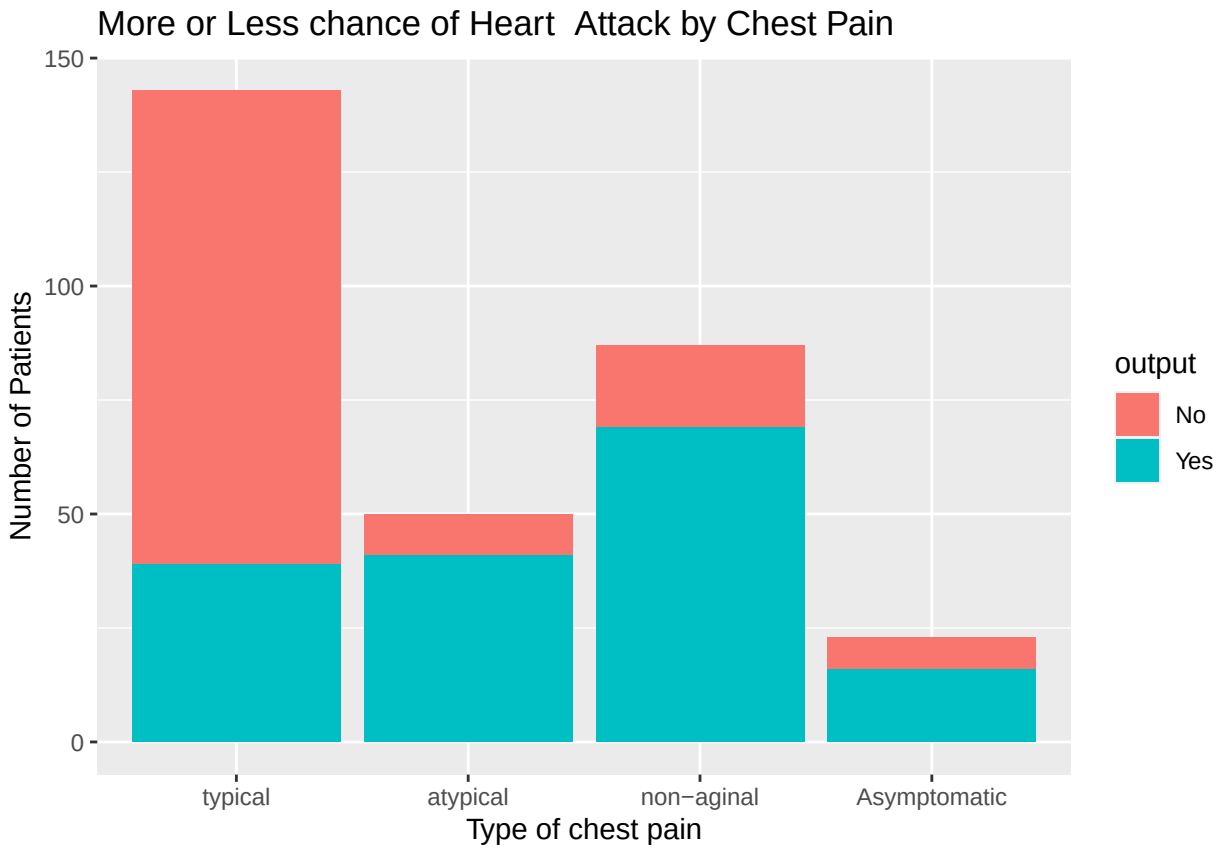
```
library(ggplot2)
par(mfrow=c(3,2))
classofpar <- ggplot(heart, aes(x=output, fill=output))+
  geom_bar()+
  xlab("Heart Attack")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack")
classofpar
```



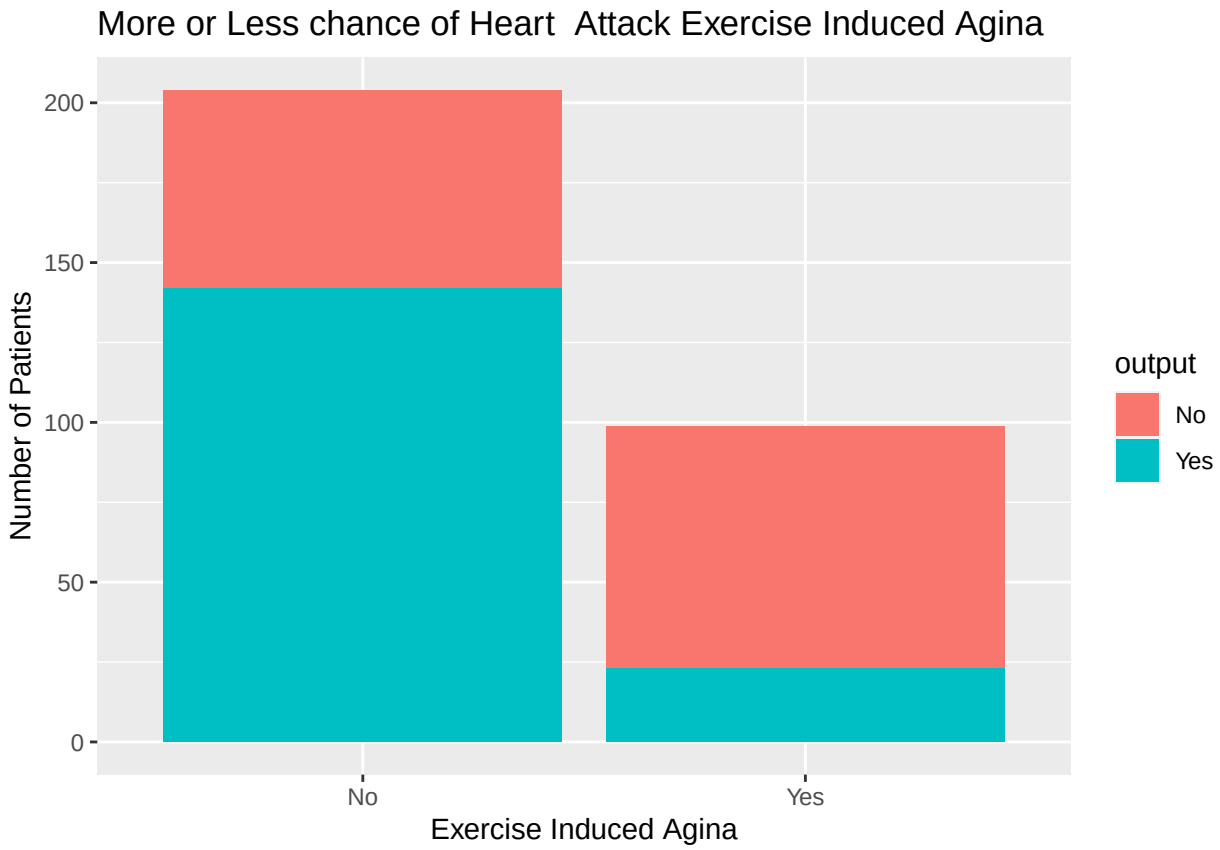

```
classofpar1 <- ggplot(heart, aes(x=sex, fill=output))+
  geom_bar()+
  xlab("Heart Attack")+
  ylab("Number of Males & Females")+
  ggtitle("More or Less chance of Heart  Attack By Sex")
classofpar1
```



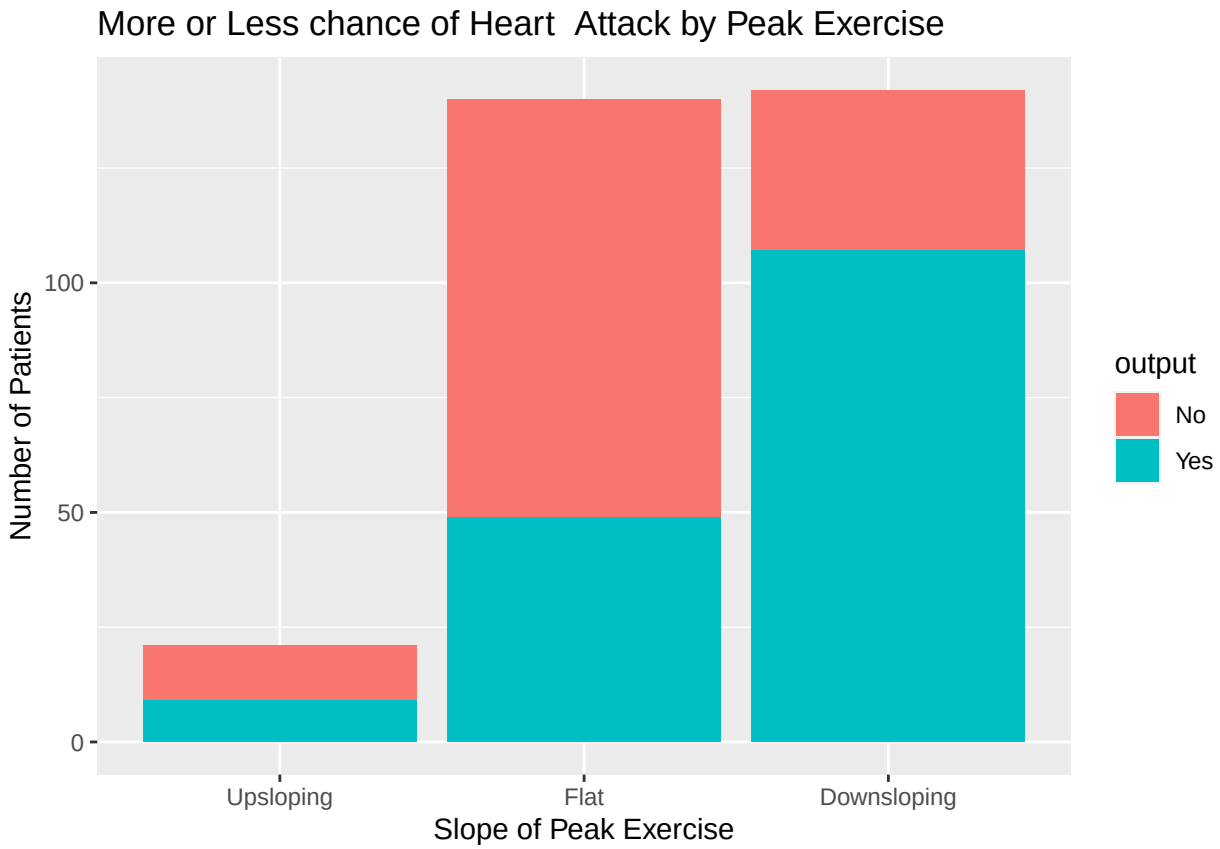

```
library(ggplot2)
classofpar2 <- ggplot(heart, aes(x=cp, fill=output))+
  geom_bar()+
  xlab("Type of chest pain")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack by Chest Pain")
classofpar2
```



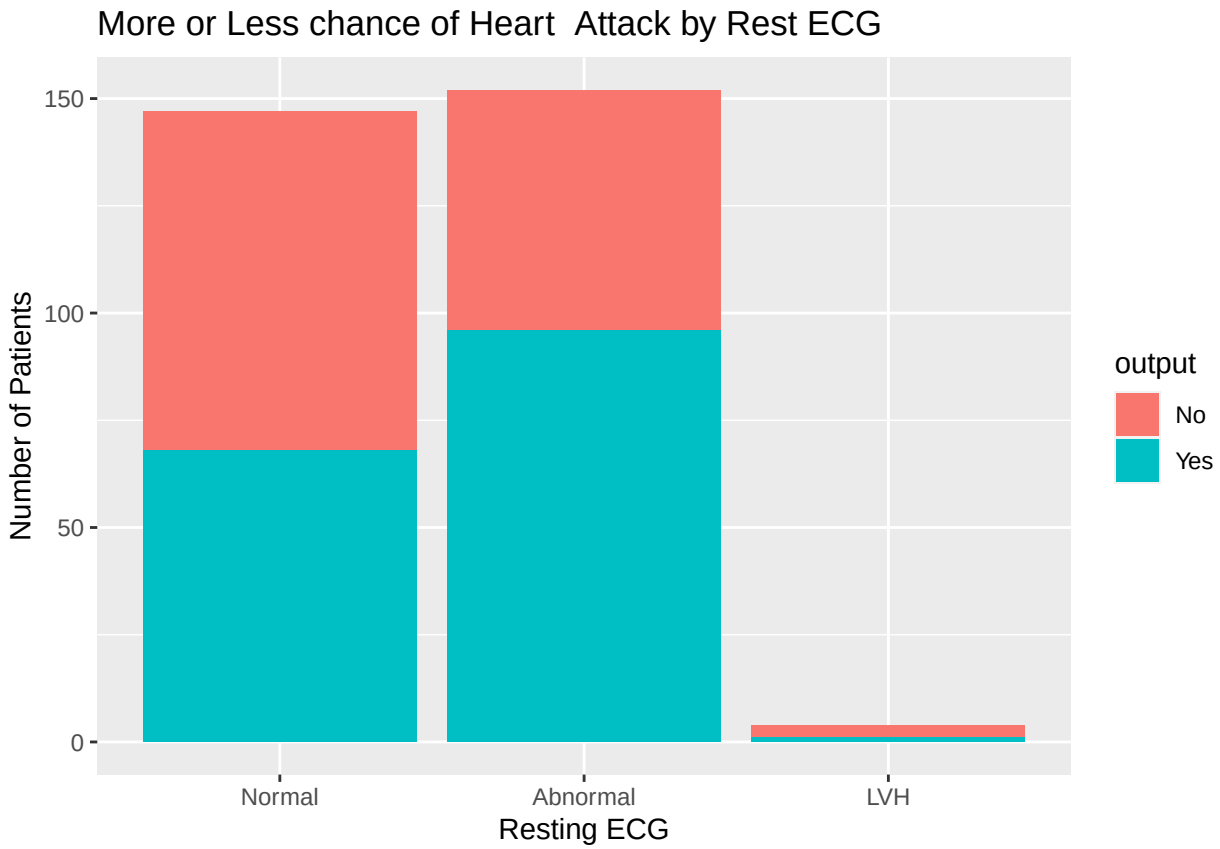

```
classofpar3 <- ggplot(heart, aes(x=exng, fill=output))+
  geom_bar()+
  xlab("Exercise Induced Agina")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack Exercise Induced Agina")
classofpar3
```




```
classofpar4 <- ggplot(heart, aes(x=slp, fill=output))+
  geom_bar()+
  xlab("Slope of Peak Exercise")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack by Peak Exercise")
classofpar4
```




```
classofpar5 <- ggplot(heart, aes(x=restecg, fill=output))+
  geom_bar()+
  xlab("Resting ECG")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack by Rest ECG")
classofpar5
```

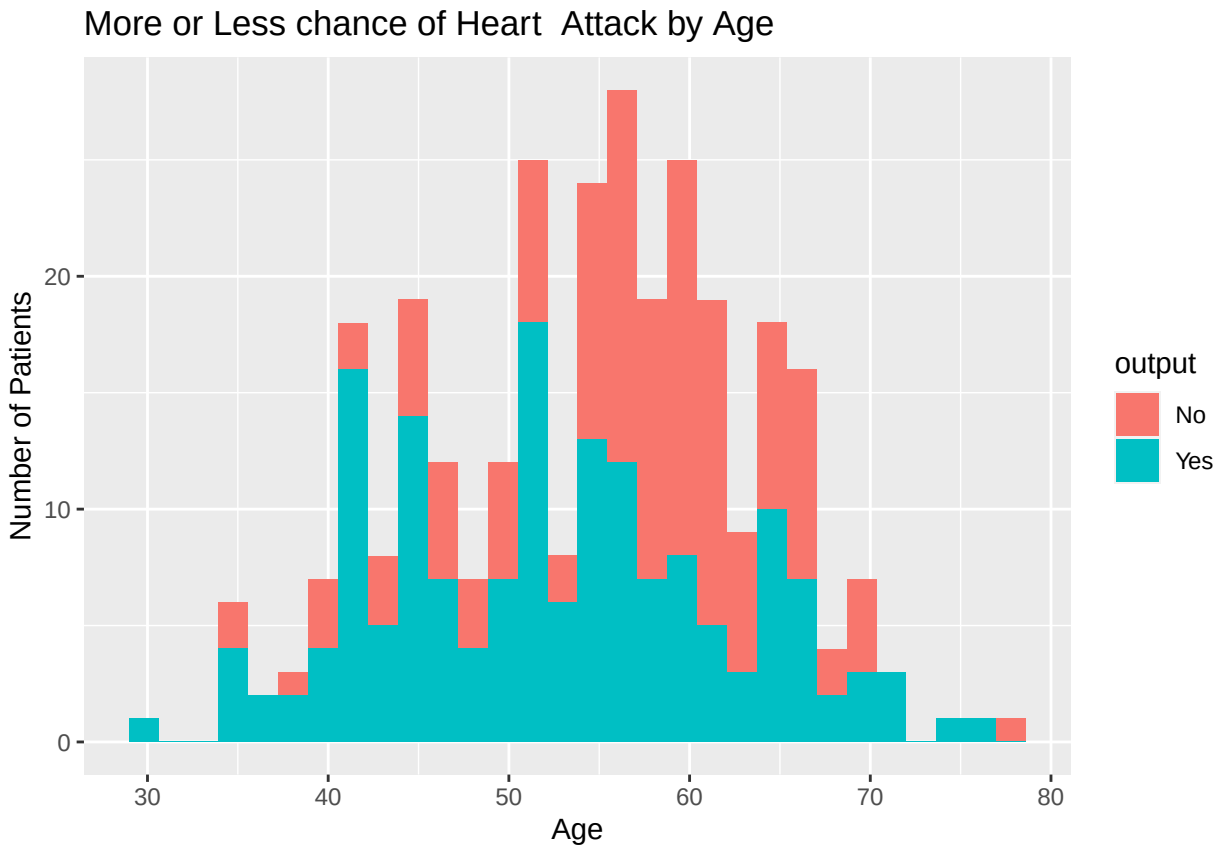



```
mfrow=par(c(2,3))
```

```
## Warning in par(c(2, 3)): argument 1 does not name a graphical parameter
```

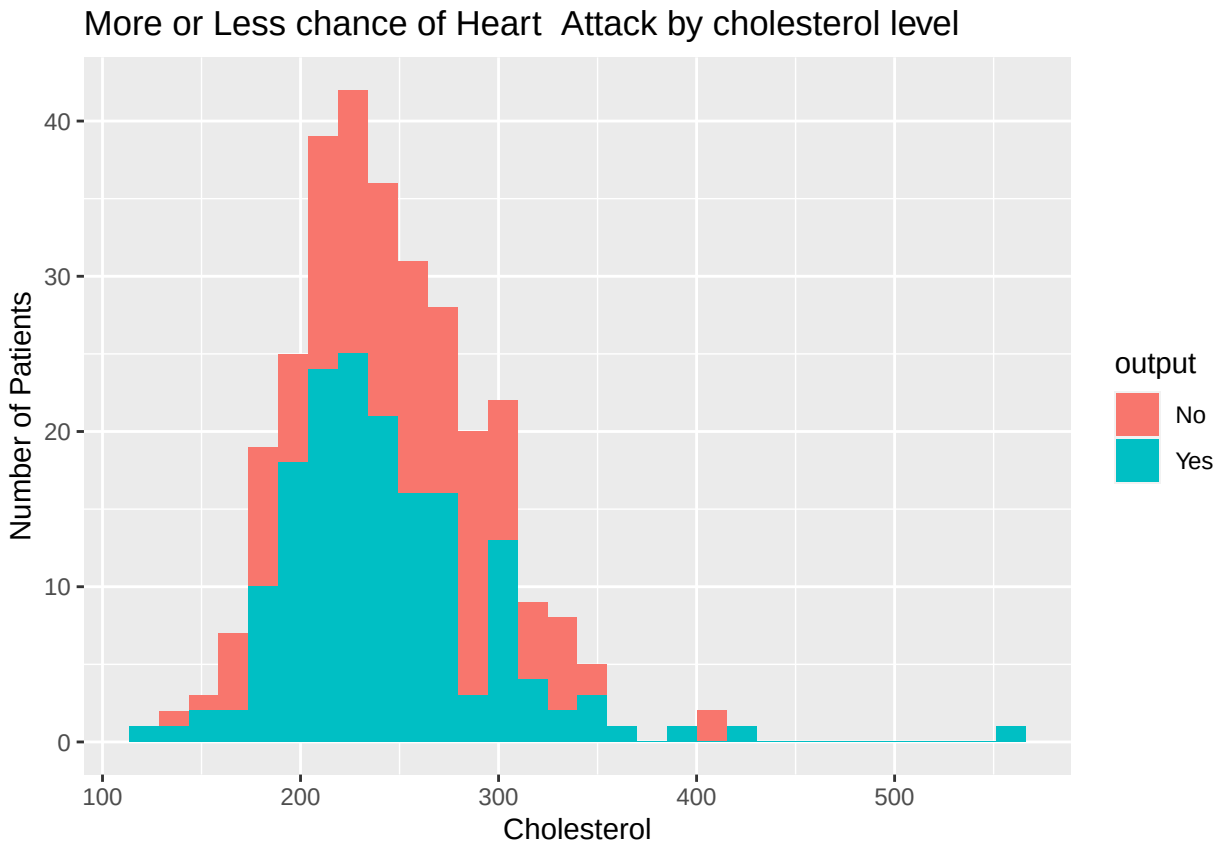
```
library(ggplot2)
hist1 <- ggplot(heart, aes(x=age, fill=output))+
  geom_histogram()+
  xlab("Age")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack by Age")
hist1
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



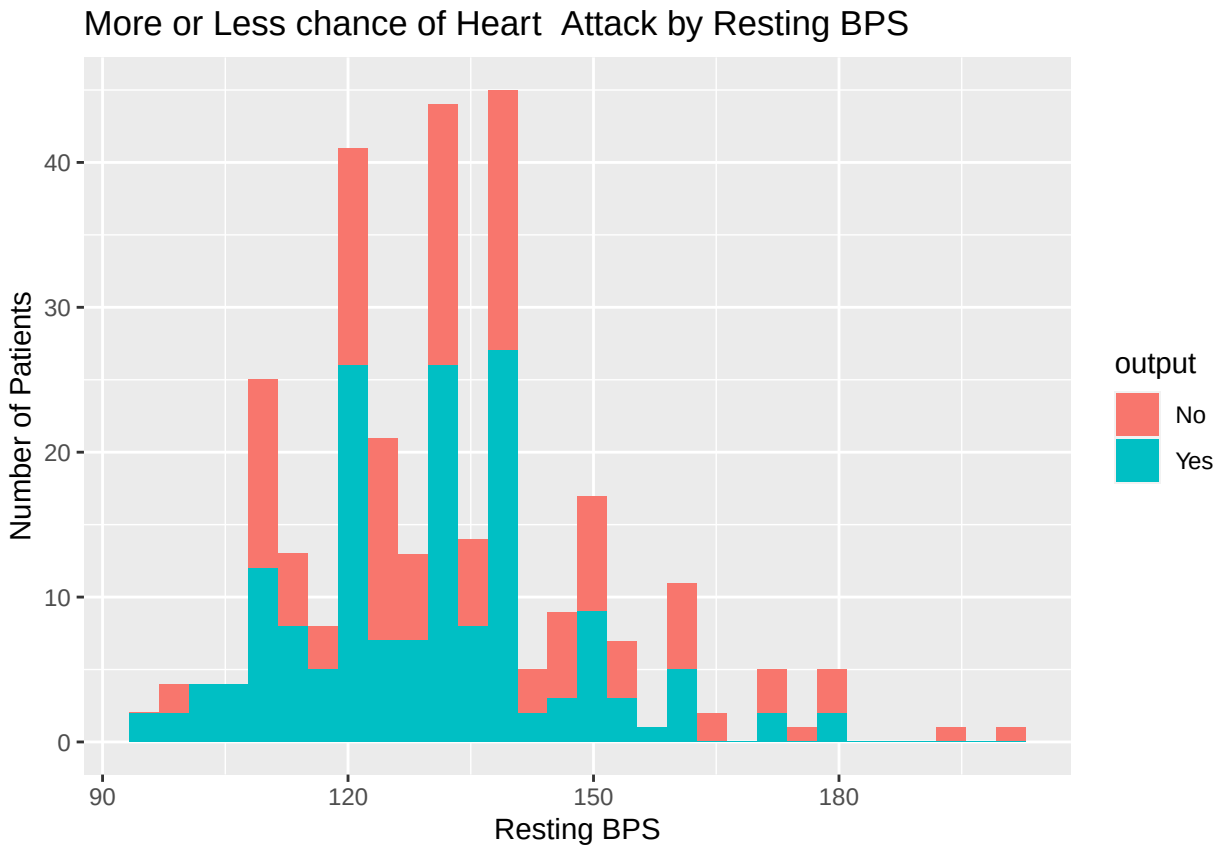

```
hist22 <- ggplot(heart, aes(x=chol, fill=output))+
  geom_histogram()+
  xlab("Cholesterol")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack by cholesterol level")
hist22
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



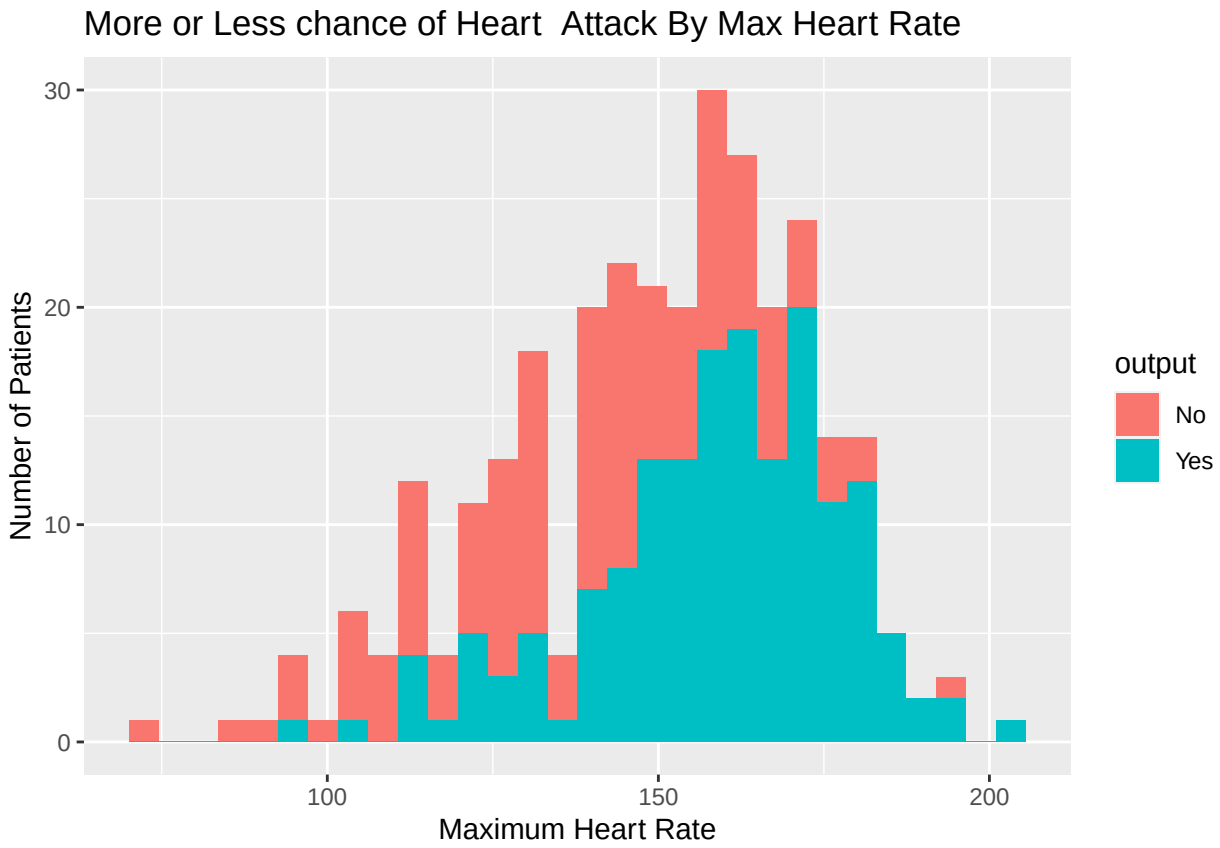

```
hist3 <- ggplot(heart, aes(x=trtbps, fill=output))+
  geom_histogram()+
  xlab("Resting BPS")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack by Resting BPS")
hist3
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



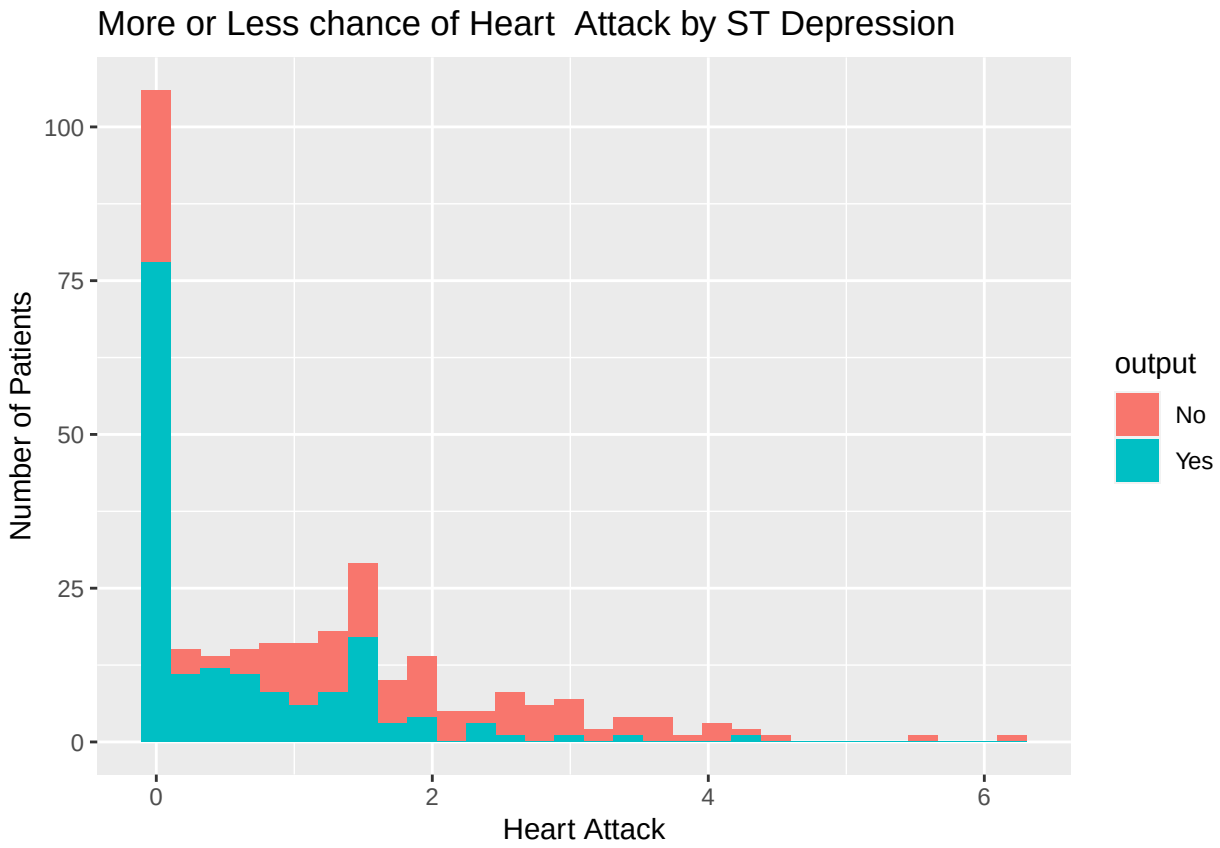

```
hist4 <- ggplot(heart, aes(x=thalachh, fill=output))+
  geom_histogram()+
  xlab("Maximum Heart Rate")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack By Max Heart Rate")
hist4
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
hist5 <- ggplot(heart, aes(x=oldpeak, fill=output))+
  geom_histogram()+
  xlab("Heart Attack")+
  ylab("Number of Patients")+
  ggtitle("More or Less chance of Heart  Attack by ST Depression")
hist5
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
summary(heart)
```

```
##       age            sex                  cp          trtbps
##  Min.   :29.00   Female: 96   typical     :143   Min.   : 94.0
##  1st Qu.:47.50   Male  :207   atypical    : 50   1st Qu.:120.0
##  Median :55.00                non-aginal  : 87   Median :130.0
##  Mean   :54.37                Asymptomatic: 23   Mean   :131.6
##  3rd Qu.:61.00                                   3rd Qu.:140.0
##  Max.   :77.00                                   Max.   :200.0
##       chol          fbs          restecg       thalachh      exng
##  Min.   :126.0   False:258   Normal  :147   Min.   : 71.0   No :204
##  1st Qu.:211.0   True : 45   Abnormal:152   1st Qu.:133.5   Yes: 99
##  Median :240.0               LVH     :  4   Median :153.0
##  Mean   :246.3                              Mean   :149.6
##  3rd Qu.:274.5                              3rd Qu.:166.0
##  Max.   :564.0                              Max.   :202.0
##     oldpeak              slp           caa             thall       output
##  Min.   :0.00   Upsloping  : 21   Min.   :0.0000   Min.   :0.000   No :138
##  1st Qu.:0.00   Flat       :140   1st Qu.:0.0000   1st Qu.:2.000   Yes:165
##  Median :0.80   Downsloping:142   Median :0.0000   Median :2.000
##  Mean   :1.04                     Mean   :0.7294   Mean   :2.314
##  3rd Qu.:1.60                     3rd Qu.:1.0000   3rd Qu.:3.000
##  Max.   :6.20                     Max.   :4.0000   Max.   :3.000
```

```
str(heart)
```

```
## 'data.frame':    303 obs. of  14 variables:
##  $ age     : int  63 37 41 56 57 57 56 44 52 57 ...
```

```
##  $ sex     : Factor w/ 2 levels "Female","Male": 2 2 1 2 1 2 1 2 2 2 ...
##  $ cp      : Factor w/ 4 levels "typical","atypical",..: 4 3 2 2 1 1 2 2 3 3 ...
##  $ trtbps  : int  145 130 130 120 120 140 140 120 172 150 ...
##  $ chol    : int  233 250 204 236 354 192 294 263 199 168 ...
##  $ fbs     : Factor w/ 2 levels "False","True": 2 1 1 1 1 1 1 1 2 1 ...
##  $ restecg : Factor w/ 3 levels "Normal","Abnormal",..: 1 2 1 2 2 2 1 2 2 2 ...
##  $ thalachh: int  150 187 172 178 163 148 153 173 162 174 ...
##  $ exng    : Factor w/ 2 levels "No","Yes": 1 1 1 1 2 1 1 1 1 1 ...
##  $ oldpeak : num  2.3 3.5 1.4 0.8 0.6 0.4 1.3 0 0.5 1.6 ...
##  $ slp     : Factor w/ 3 levels "Upsloping","Flat",..: 1 1 3 3 3 2 2 3 3 3 ...
##  $ caa     : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ thall   : int  1 2 2 2 2 1 2 3 3 2 ...
##  $ output  : Factor w/ 2 levels "No","Yes": 2 2 2 2 2 2 2 2 2 2 ...
```

Assumptions 1. Normality 2. Positive Determinant for variance co-variance matrix 3. Equal variance between two groups

"'d) Providing univariate means and variances

```
df <- data.frame(heart$age,heart$trtbps,heart$chol,heart$thalachh,heart$oldpeak)
by(df, heart$output, colMeans)
```

```
## heart$output: No
##      heart.age   heart.trtbps     heart.chol heart.thalachh  heart.oldpeak
##      56.601449     134.398551     251.086957     139.101449       1.585507
## ------------------------------------------------------------
## heart$output: Yes
##      heart.age   heart.trtbps     heart.chol heart.thalachh  heart.oldpeak
##     52.4969697    129.3030303    242.2303030    158.4666667      0.5830303
```

```
by(df, heart$output, var)
```

```
## heart$output: No
##                 heart.age heart.trtbps   heart.chol heart.thalachh
## heart.age       63.394742    35.831535   44.3414789     -23.886279
## heart.trtbps    35.831535   350.810801  125.3592510       2.368031
## heart.chol      44.341479   125.359251 2445.7588067      50.297683
## heart.thalachh -23.886279     2.368031   50.2976833     510.704961
## heart.oldpeak    1.066445     3.128446   -0.6016503      -6.267132
##                heart.oldpeak
## heart.age          1.0664445
## heart.trtbps       3.1284460
## heart.chol        -0.6016503
## heart.thalachh    -6.2671321
## heart.oldpeak      1.6908833
## ------------------------------------------------------------
## heart$output: Yes
##                 heart.age heart.trtbps  heart.chol heart.thalachh heart.oldpeak
## heart.age       91.214930    42.421656  131.525092     -96.288211     1.3017775
## heart.trtbps    42.421656   261.456393   80.783444       8.693089     2.2911493
## heart.chol     131.525092    80.783444 2867.910052      14.843089     2.4130783
## heart.thalachh -96.288211     8.693089   14.843089     367.652846    -2.7249593
## heart.oldpeak    1.301778     2.291149    2.413078      -2.724959     0.6094664
```

```
by(df, heart$output, cor)
```

```
## heart$output: No
```

```
##                 heart.age heart.trtbps  heart.chol heart.thalachh heart.oldpeak
## heart.age       1.0000000   0.24027153  0.11260994    -0.13275071    0.10300417
## heart.trtbps    0.2402715   1.00000000  0.13533593     0.00559456    0.12845037
## heart.chol      0.1126099   0.13533593  1.00000000     0.04500452   -0.00935579
## heart.thalachh -0.1327507   0.00559456  0.04500452     1.00000000   -0.21326864
## heart.oldpeak   0.1030042   0.12845037 -0.00935579    -0.21326864    1.00000000
## ------------------------------------------------------------
## heart$output: Yes
##                 heart.age heart.trtbps heart.chol heart.thalachh heart.oldpeak
## heart.age       1.0000000   0.27469770 0.25715377    -0.52580074    0.17459385
## heart.trtbps    0.2746977   1.00000000 0.09329105     0.02803855    0.18150094
## heart.chol      0.2571538   0.09329105 1.00000000     0.01445515    0.05771833
## heart.thalachh -0.5258007   0.02803855 0.01445515     1.00000000   -0.18203973
## heart.oldpeak   0.1745938   0.18150094 0.05771833    -0.18203973    1.00000000
```

```
library(mvnormtest)
multv <- t(df)

mshapiro.test(multv)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  Z
## W = 0.93989, p-value = 9.335e-10
```

Highly significant P value we might have to reject the null hypothesis, does not pass normality test.

```
covheart <- cov(df, method = 'spearman')
det(covheart)
```

```
## [1] 1.476375e+19
```

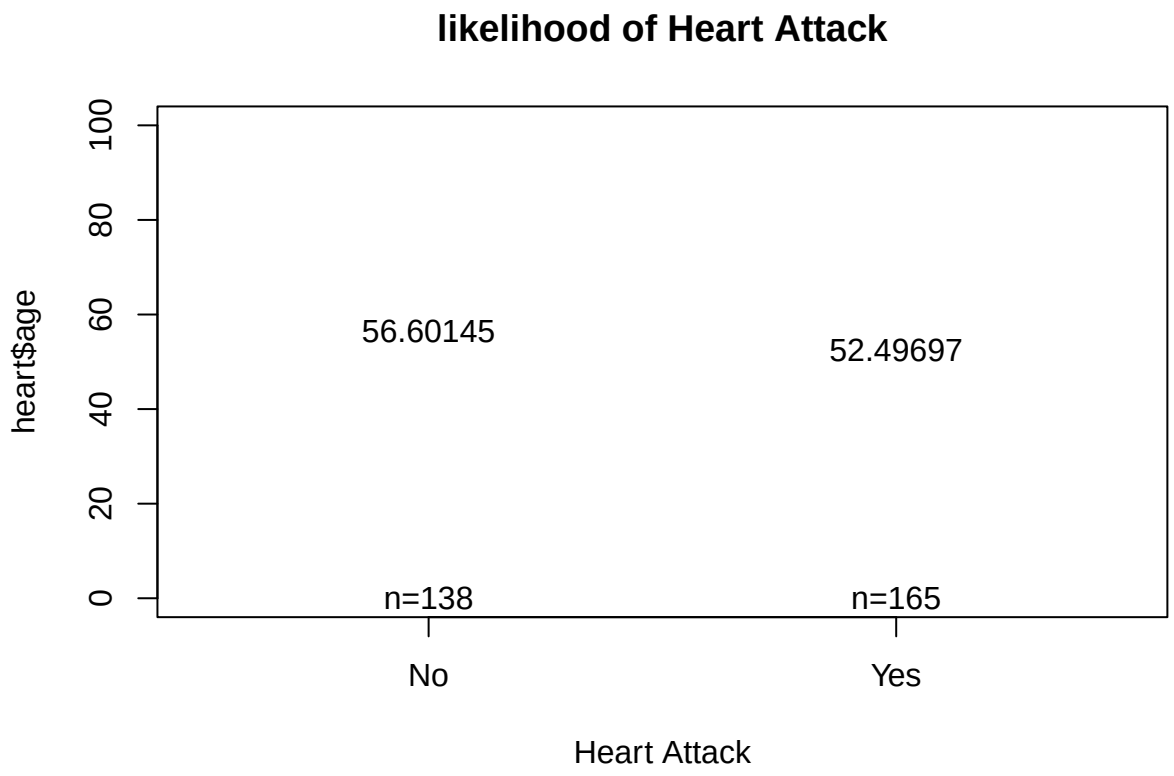
It passes the positive determinant test of variance-covariance matrix.

```
#Graph the means of the 5 variables for presence or absence of heart attack
library(gplots)
```

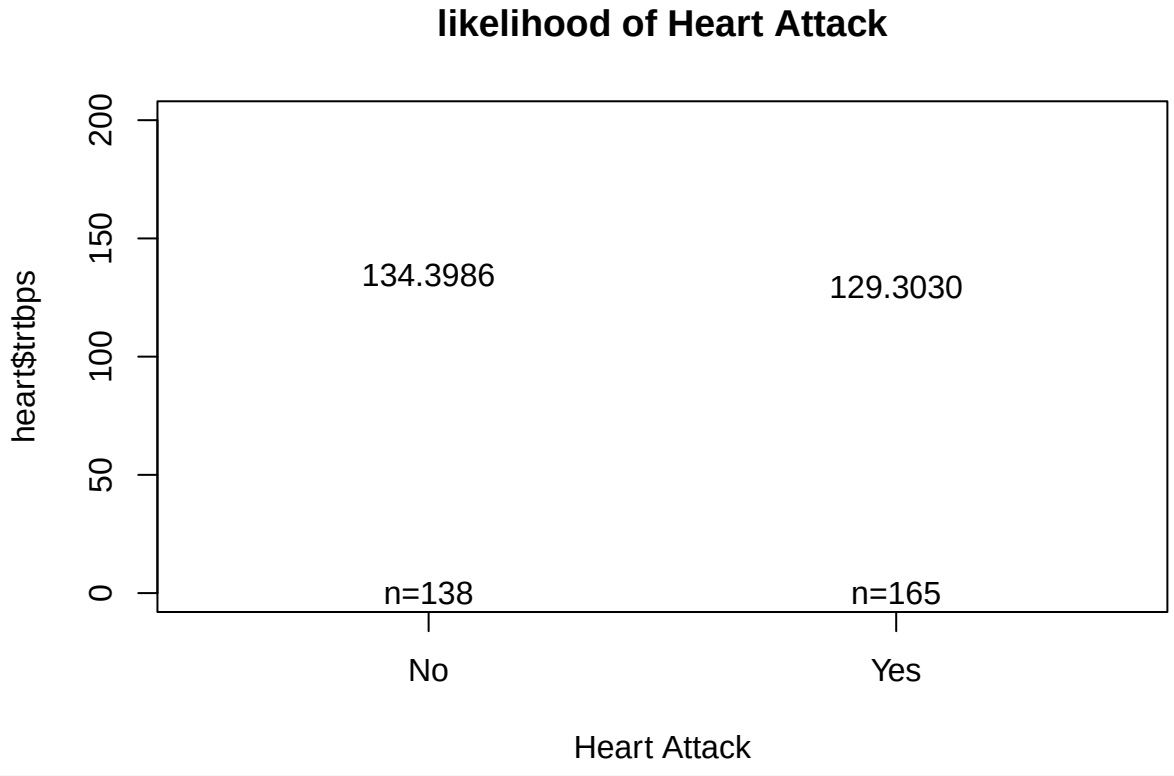
```
##
## Attaching package: 'gplots'
```

```
## The following object is masked from 'package:stats':
##
##     lowess
```

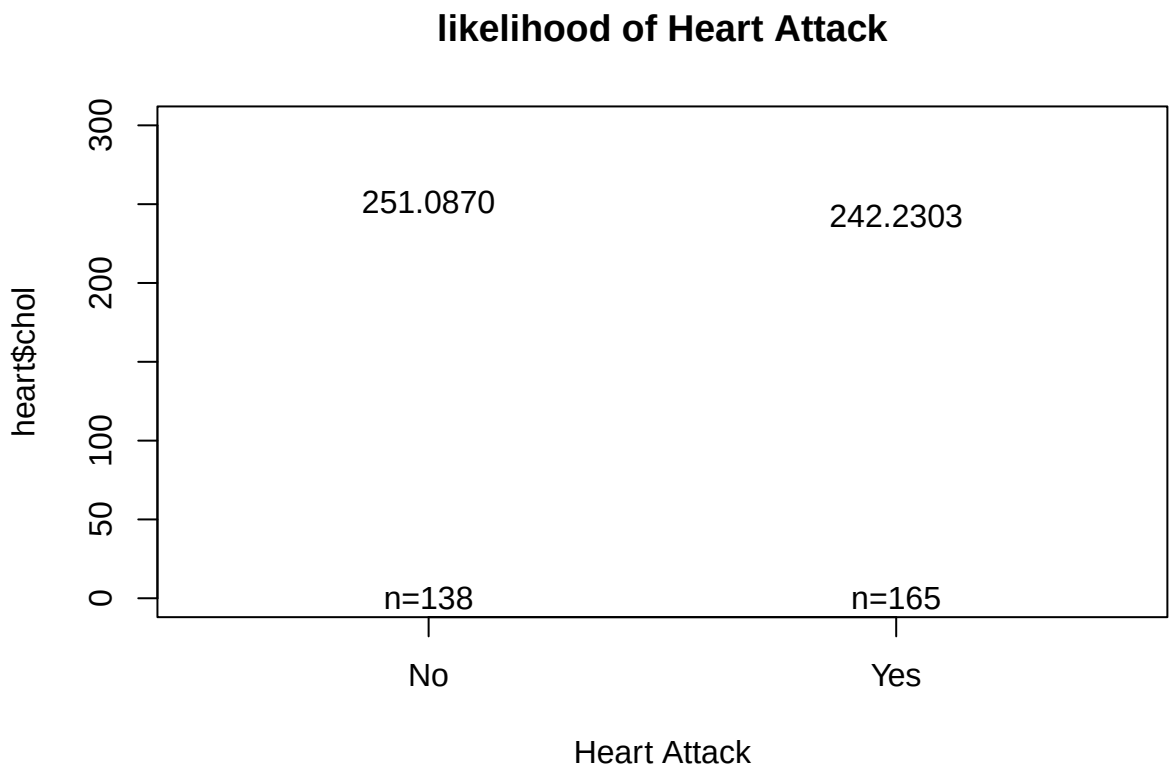
```
plotmeans(heart$age~heart$output, data=heart,ylim=c(0,100),xlab="Heart Attack",legends = c("No","Yes"),n
```



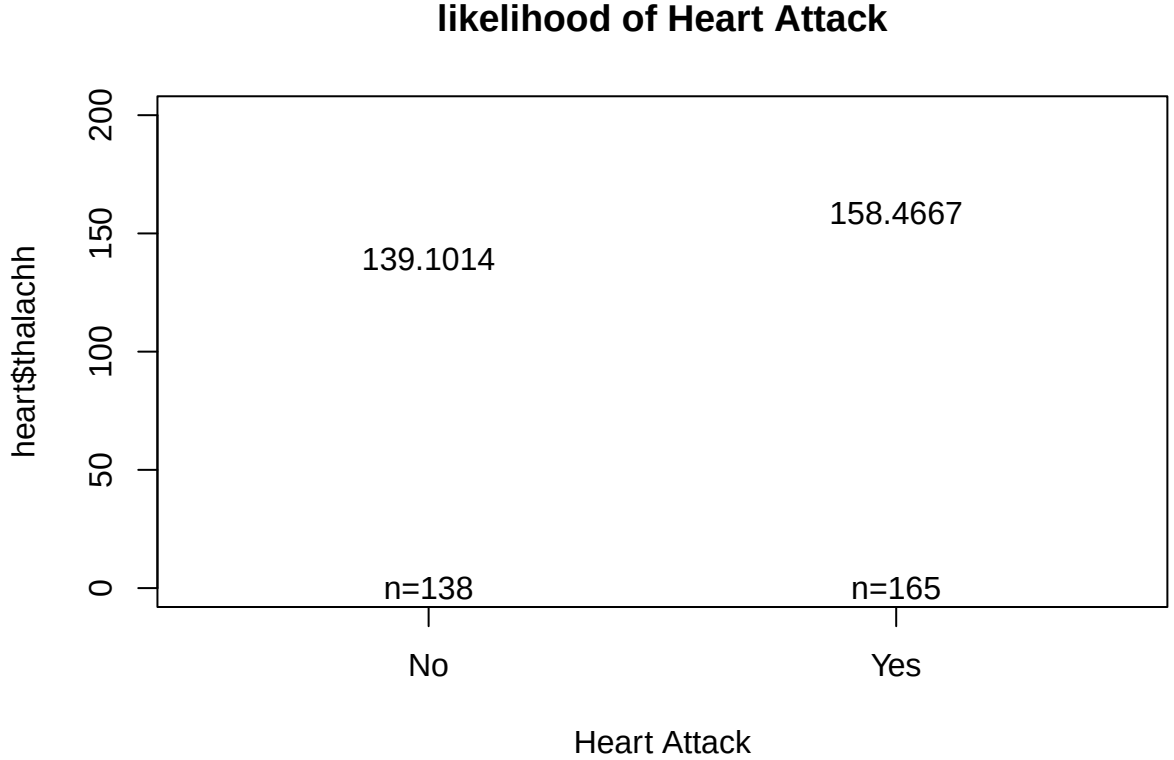

```
plotmeans(heart$trtbps~heart$output, data=heart,ylim=c(0,200),xlab="Heart Attack",legends = c("No","Yes
```



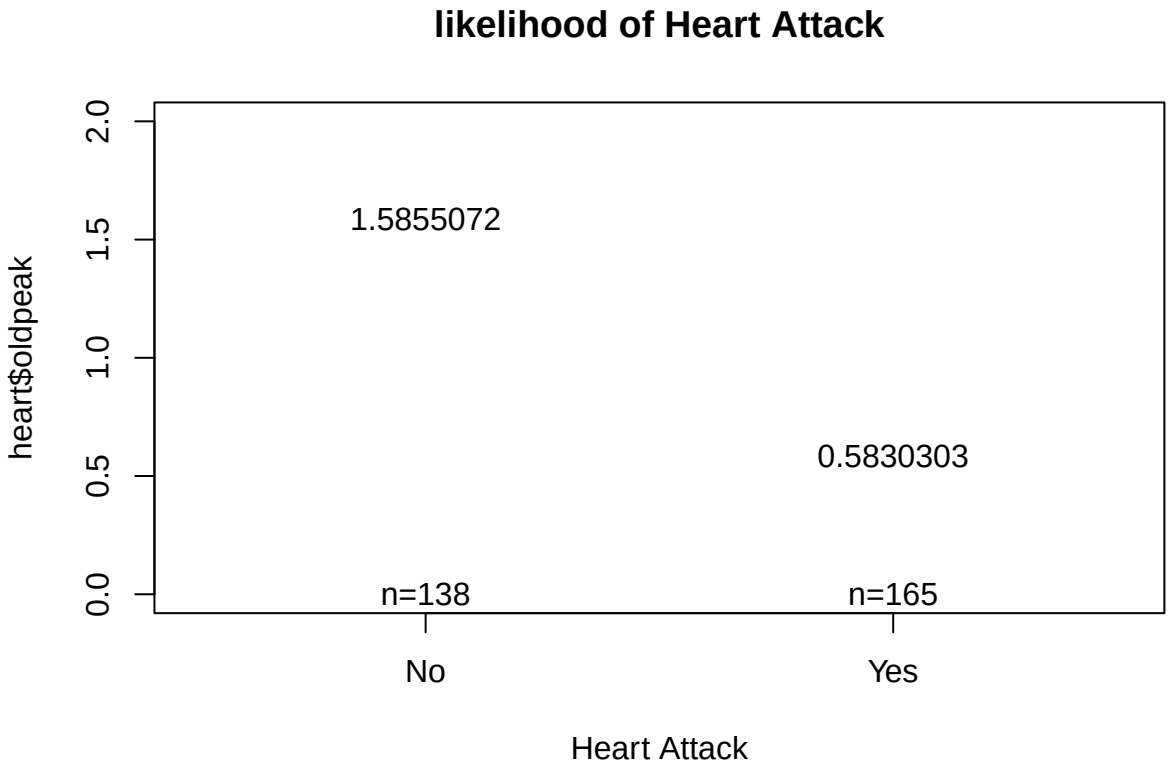

```
plotmeans(heart$chol~heart$output, data=heart,ylim=c(0,300),xlab="Heart Attack",legends = c("No","Yes")
```




```
plotmeans(heart$thalachh~heart$output, data=heart,ylim=c(0,200),xlab="Heart Attack",legends = c("No","Ye
```




```
plotmeans(heart$oldpeak~heart$output, data=heart,ylim=c(0,2),xlab="Heart Attack",legends = c("No","Yes"
```




```
library(ICSNP)
```

```
## Loading required package: mvtnorm
```

```
## Loading required package: ICS
```

```
library(mvtnorm)
```

```
result <- HotellingsT2(df[1:165,], df[166:303,])

# Print the test result
print(result)
```

```
##
##  Hotelling's two sample T2-test
##
## data:  df[1:165, ] and df[166:303, ]
## T.2 = 22.924, df1 = 5, df2 = 297, p-value < 2.2e-16
## alternative hypothesis: true location difference is not equal to c(0,0,0,0,0)
```

```
library(caTools)
set.seed(1028)
total_rows <- nrow(heart)

# Calculate the number of rows for the training and testing sets
train_rows <- round(0.8 * total_rows)  # 80% for training
test_rows <- total_rows - train_rows  # 20% for testing

# Generate random indices for the training set
train_indices <- sample(1:total_rows, train_rows)

# Create the training and testing datasets
```

```
train_data <- heart[train_indices, ]
test_data <- heart[-train_indices, ]
```

```
set.seed(1130)
dim(train_data)
```

```
## [1] 242  14
```

```
dim(test_data)
```

```
## [1] 61 14
```

(d) Perform Random Forest on the training data in order to predict origin2. Evaluate performance on the test data. What test error do you obtain?

```
library(randomForest)
```

```
## 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
```

```
set.seed(937)
#random forest model
randori <- randomForest(output~.-output, train_data, mtry =5, importance = TRUE)
```

```
#predicting new data on the random forest model
pred.randori <- predict(randori,newdata = test_data)
mean(pred.randori!=test_data$output)
```

```
## [1] 0.147541
```

```
mean(pred.randori==test_data$output)
```

```
## [1] 0.852459
```

```
#confusion matrix
table(pred.randori,test_data$output)
```

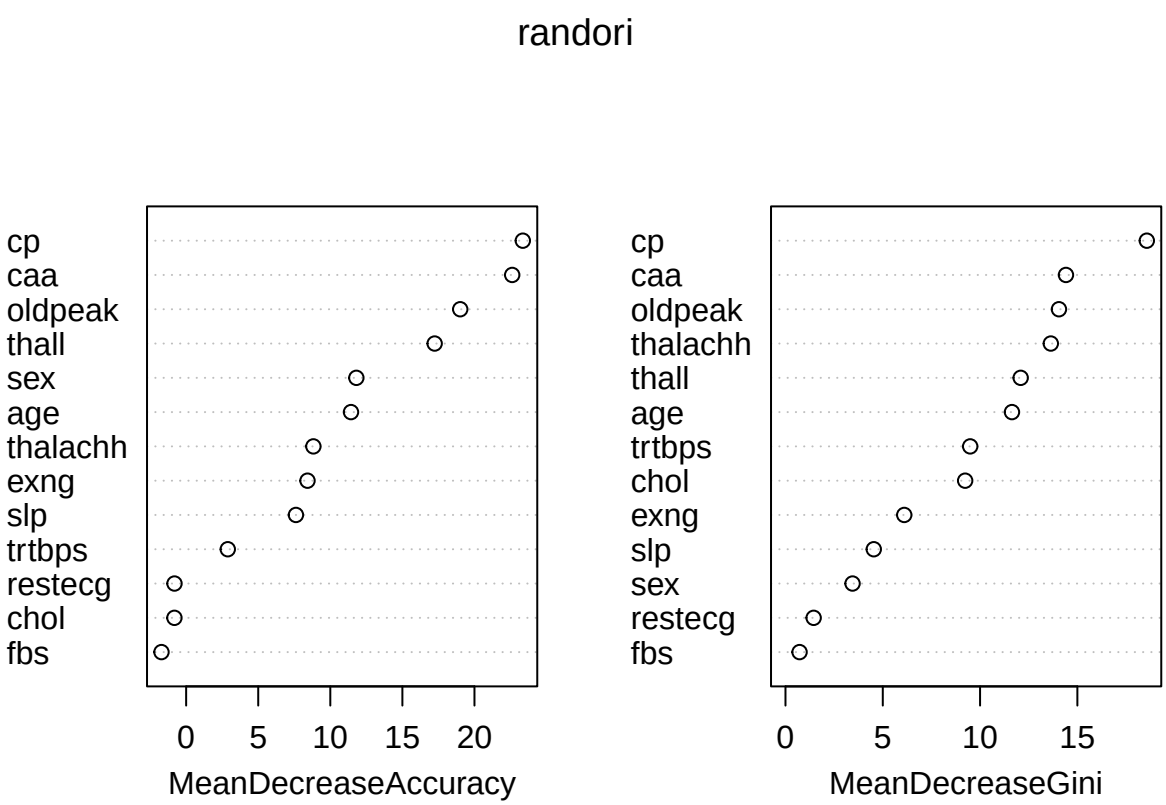
```
##
## pred.randori No Yes
##          No  21   2
##          Yes  7  31
```

```
#importance of variables
importance(randori)
```

```
##                 No        Yes MeanDecreaseAccuracy MeanDecreaseGini
## age       4.3857870 11.4440591           11.4348948       11.6390449
## sex       6.4744027 10.5151711           11.8072660        3.4463238
## cp       19.2109285 15.4486309           23.3534498       18.5684786
## trtbps    0.1017973  3.7541518            2.8876303        9.4932074
## chol     -2.1180602  0.7002795           -0.8142109        9.2332600
## fbs      -2.3740169 -0.3350165           -1.7114196        0.7235888
## restecg  -0.9285768 -0.1308484           -0.8094133        1.4471774
```

```
## thalachh  4.7758225  7.2811953            8.8259248       13.6352038
## exng      9.0476382  3.6010811            8.4185208        6.1034752
## oldpeak  14.2753390 11.8247450           19.0113823       14.0534116
## slp       6.3329648  4.1100172            7.6159437        4.5372944
## caa      15.0044316 18.9716049           22.6166979       14.4132533
## thall     9.9129996 15.7886058           17.2388402       12.0861334
```

```
#plot of variables based on importance
varImpPlot(randori)
```



These plots above show important variables and cp variable shows up as the most important variable.

(c) Perform Classification Tree on the training data in order to predict output. Use cross- validation to prune the tree. Plot the resulting tree. Evaluate performance on the test data. What test error do you obtain?

```
library(tree)
attach(heart)
#change this to factors so that it can make a classification tree without having level issues
output= factor(output)
tree_output <- tree(output~.-output,train_data)
```

```
summary(tree_output)#gives summary statistics of tree
```

```
##
## Classification tree:
## tree(formula = output ~ . - output, data = train_data)
## Variables actually used in tree construction:
## [1] "cp"       "caa"      "oldpeak"  "thall"    "thalachh" "chol"     "age"
## [8] "sex"
## Number of terminal nodes:  19
```

```
## Residual mean deviance:  0.4743 = 105.8 / 223
## Misclassification error rate: 0.1116 = 27 / 242
```

```
set.seed(4399)
#perform prediction on test data
tree_pred = predict(tree_output, test_data, type = "class")

table(tree_pred,test_data$output) #confusion matrix
```

```
##
## tree_pred No Yes
##       No  22   4
##       Yes  6  29
```

```
mean(tree_pred != test_data$output) #test error
```

```
## [1] 0.1639344
```

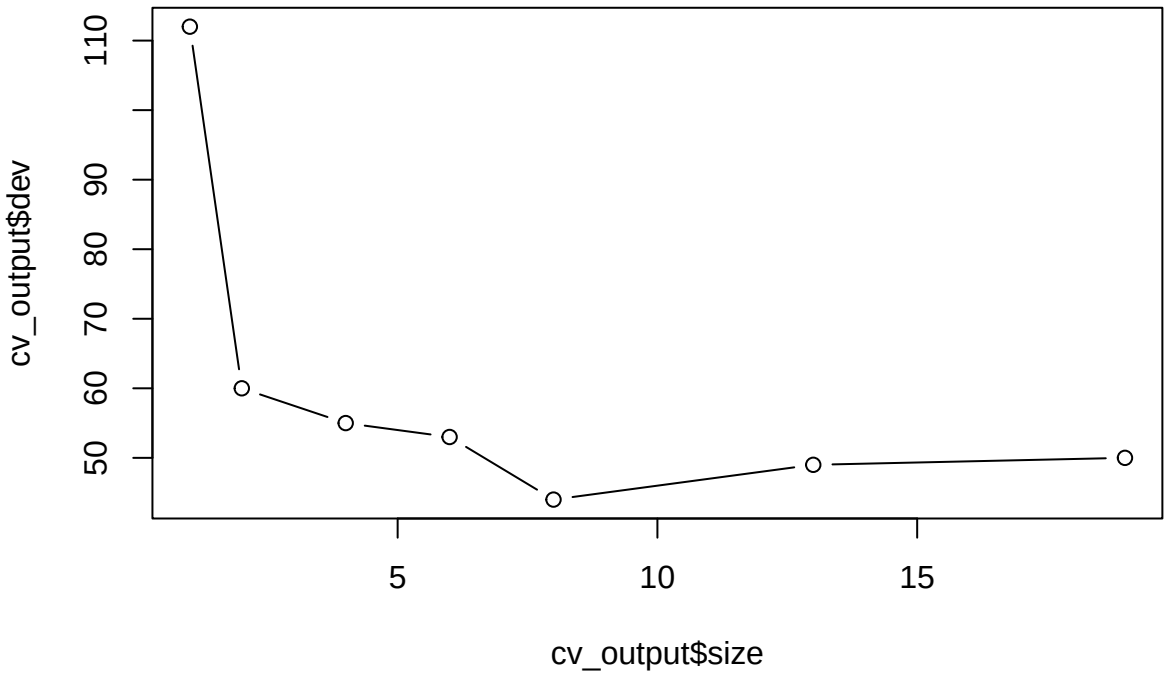
```
mean(tree_pred == test_data$output) #test accuracy
```

```
## [1] 0.8360656
```

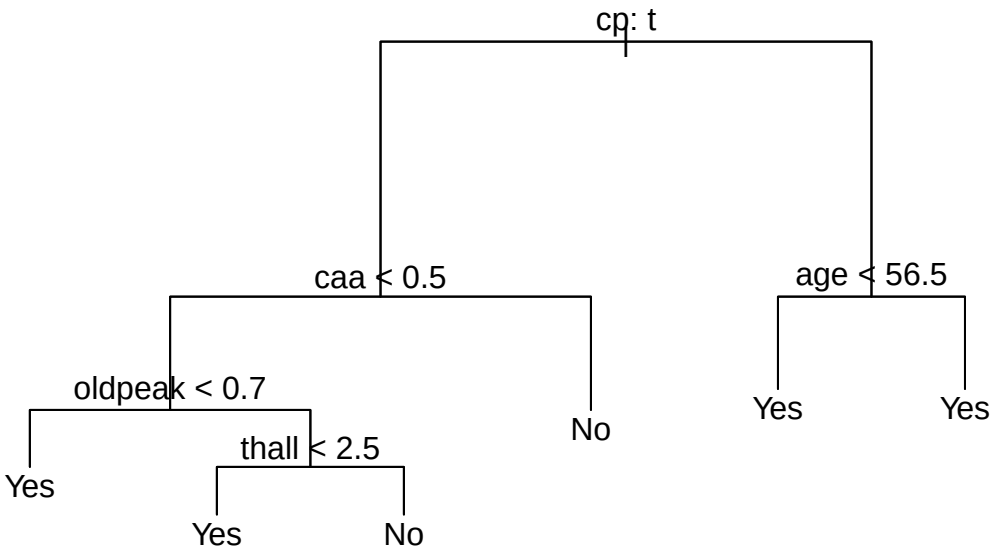
```
set.seed(1111)
#perform cross validation
cv_output = cv.tree(tree_output, FUN = prune.misclass)

cv_output
```

```
## $size
## [1] 19 13  8  6  4  2  1
##
## $dev
## [1]  50  49  44  53  55  60 112
##
## $k
## [1] -Inf    0    1    3    4    7   50
##
## $method
## [1] "misclass"
##
## attr(,"class")
## [1] "prune"         "tree.sequence"
```

```
#plot the CV
plot(cv_output$size, cv_output$dev, type = "b")
text(tree_output, pretty=TRUE, cex=0.8)
```




```
#prune tree and plot resulting tree
prune.output <- prune.tree(tree_output, best = 6)
plot(prune.output)
text(prune.output,pretty=TRUE)
```



find below the test terror for my pruned classification tree

```
#predict test data on pruned tree
prune.pred = predict(prune.output, test_data,type="class")
table(prune.pred,test_data$output)
```

```
##
## prune.pred No Yes
##        No  20   0
##        Yes  8  33
```

```r
mean(prune.pred != test_data$output) #test error
```

```
## [1] 0.1311475
```

```r
mean(prune.pred == test_data$output) #test accuracy for pruned tree
```

```
## [1] 0.8688525
```

e) Fit a Support Vector Classifier to the data with various values of cost, in order to predict the likelihood of a heart attack or not . Report the cross-validation errors associated with different values of this parameter. Comment on your results.

```r
library(e1071)

set.seed(821)
# SV classifier model
svmlinear =  svm(output ~ .-output, data = train_data, kernel = "linear", ranges = list(cost = c(0.001,
summary(svmlinear)
```

```
##
## Call:
## svm(formula = output ~ . - output, data = train_data, kernel = "linear",
##     ranges = list(cost = c(0.001, 0.01, 1, 5, 10, 100)))
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  linear
##        cost:  1
##
## Number of Support Vectors:  107
##
##  ( 52 55 )
##
##
## Number of Classes:  2
##
## Levels:
##  No Yes
```

```r
#prediction of SV classifier, table and error
pred.svmlinear <- predict(svmlinear,newdata = test_data)
table(test_data$output,pred.svmlinear)
```

```
##      pred.svmlinear
##       No Yes
##   No  21   7
##   Yes  1  32
```

```r
mean(pred.svmlinear!=test_data$output)#test error
```

```
## [1] 0.1311475
```

```r
mean(pred.svmlinear==test_data$output)#test accuracy
```

```
## [1] 0.8688525
```

As can be seen above the cross-validation gives a better error than just the classifier model

```r
set.seed(433)
#cv on SV classifier
svmlineart =  tune(svm,output ~ .-output, data = train_data, kernel = "linear", ranges = list(cost = c(
summary(svmlineart)
```

```
##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  cost
##   100
##
## - best performance: 0.1946667
##
## - Detailed performance results:
##    cost     error dispersion
## 1 1e-03 0.4545000 0.06114166
## 2 1e-02 0.2151667 0.05860229
## 3 1e+00 0.1986667 0.07286805
## 4 5e+00 0.2030000 0.08022268
## 5 1e+01 0.1988333 0.07857547
## 6 1e+02 0.1946667 0.07664170
```

The lowest error was achieved by using a cost of 100, which was 0.194. The highest error was 0.4545 which was when cost was set to 0.001.

f) Now repeat (e), this time using Support Vector Machines (SVMs) with radial and polynomial basis kernels, with different values of gamma and degree and cost. Comment on your results.

```r
set.seed(439)
#SVM polynomial model
svmpol =  svm(output ~ .-output, data = train_data, kernel = "polynomial", ranges = list(cost = c(0.1,
summary(svmpol)
```

```
##
## Call:
## svm(formula = output ~ . - output, data = train_data, kernel = "polynomial",
##     ranges = list(cost = c(0.1, 1, 5, 10), degree = c(2, 3, 4)))
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  polynomial
##        cost:  1
##      degree:  3
##      coef.0:  0
##
## Number of Support Vectors:  192
##
##  ( 95 97 )
##
##
## Number of Classes:  2
```

```
##
## Levels:
##  No Yes
```

```
#predicting new data on the SVM model polynonial model
pred.svmpol <- predict(svmpol,newdata = test_data)
#confusion matrix
table(test_data$output,pred.svmpol)
```

```
##      pred.svmpol
##       No Yes
##   No  16  12
##   Yes  0  33
```

```
#computing test error obtained
mean(pred.svmpol!=test_data$output)
```

```
## [1] 0.1967213
```

```
#computing test Accuracy obtained
mean(pred.svmpol==test_data$output)
```

```
## [1] 0.8032787
```

```
set.seed(1145)
svmpolt =  tune(svm,output ~ .-output, data = train_data, kernel = "polynomial", ranges = list(cost = c
summary(svmpolt)
```

```
##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  cost degree
##    10      3
##
## - best performance: 0.2021667
##
## - Detailed performance results:
##    cost degree     error dispersion
## 1   0.1      2 0.4298333 0.08117748
## 2   1.0      2 0.2025000 0.07964524
## 3   5.0      2 0.2105000 0.07795238
## 4  10.0      2 0.2228333 0.07521184
## 5   0.1      3 0.4381667 0.08838555
## 6   1.0      3 0.2855000 0.05503114
## 7   5.0      3 0.2148333 0.06421150
## 8  10.0      3 0.2021667 0.07073272
## 9   0.1      4 0.4548333 0.09699322
## 10  1.0      4 0.3885000 0.07872224
## 11  5.0      4 0.2938333 0.07067160
## 12 10.0      4 0.3100000 0.09032178
```

The lowest error was achieved by using a cost of 1 and degree of 2, which was 0.2025. The highest error was 0.4548 which was when cost was set to 0.1 and a degree 4.

```r
set.seed(1146)
svmrad =  svm(output ~ .-output, data = train_data, kernel = "radial", ranges = list(cost = c(0.1, 1, 5
summary(svmrad)
```

```
##
## Call:
## svm(formula = output ~ . - output, data = train_data, kernel = "radial",
##     ranges = list(cost = c(0.1, 1, 5, 10), gamma = c(0.01, 0.1, 1,
##         5, 10, 100)))
##
##
## Parameters:
##    SVM-Type:  C-classification
##  SVM-Kernel:  radial
##        cost:  1
##
## Number of Support Vectors:  139
##
##  ( 70 69 )
##
##
## Number of Classes:  2
##
## Levels:
##  No Yes
```

```r
#prediction of SVM radial classifier, table and error
pred.svmrad <- predict(svmrad,newdata = test_data)
table(test_data$output,pred.svmrad)
```

```
##      pred.svmrad
##       No Yes
##   No  24   4
##   Yes  1  32
```

```r
mean(pred.svmrad!=test_data$output)
```

```
## [1] 0.08196721
```

```r
mean(pred.svmrad==test_data$output)
```

```
## [1] 0.9180328
```

```r
set.seed(934)
svmradt =  tune(svm,output ~ .-output, data = train_data, kernel = "radial", ranges = list(cost = c(0.1
summary(svmradt)
```

```
##
## Parameter tuning of 'svm':
##
## - sampling method: 10-fold cross validation
##
## - best parameters:
##  cost gamma
##    10  0.01
##
## - best performance: 0.2061667
```

```
##
## - Detailed performance results:
##    cost gamma     error dispersion
## 1   0.1 1e-02 0.3760000 0.17869935
## 2   1.0 1e-02 0.2185000 0.07370884
## 3   5.0 1e-02 0.2103333 0.05470347
## 4  10.0 1e-02 0.2061667 0.06543327
## 5   0.1 1e-01 0.2473333 0.09171278
## 6   1.0 1e-01 0.2145000 0.05944211
## 7   5.0 1e-01 0.2271667 0.05885245
## 8  10.0 1e-01 0.2556667 0.08875059
## 9   0.1 1e+00 0.4546667 0.14808614
## 10  1.0 1e+00 0.3926667 0.14146980
## 11  5.0 1e+00 0.3926667 0.12451932
## 12 10.0 1e+00 0.3926667 0.12451932
## 13  0.1 5e+00 0.4546667 0.14808614
## 14  1.0 5e+00 0.4546667 0.14808614
## 15  5.0 5e+00 0.4546667 0.14808614
## 16 10.0 5e+00 0.4546667 0.14808614
## 17  0.1 1e+01 0.4546667 0.14808614
## 18  1.0 1e+01 0.4546667 0.14808614
## 19  5.0 1e+01 0.4546667 0.14808614
## 20 10.0 1e+01 0.4546667 0.14808614
## 21  0.1 1e+02 0.4546667 0.14808614
## 22  1.0 1e+02 0.4546667 0.14808614
## 23  5.0 1e+02 0.4546667 0.14808614
## 24 10.0 1e+02 0.4546667 0.14808614
```

The lowest error was achieved by using a cost of 5 and gamma of 0.01, which was 0.2103. The highest error was 0.4547 which was when cost was set to 0.1 and a gamma of 1. And the lowest CV error is not lower than that of the regular model which was not expected.

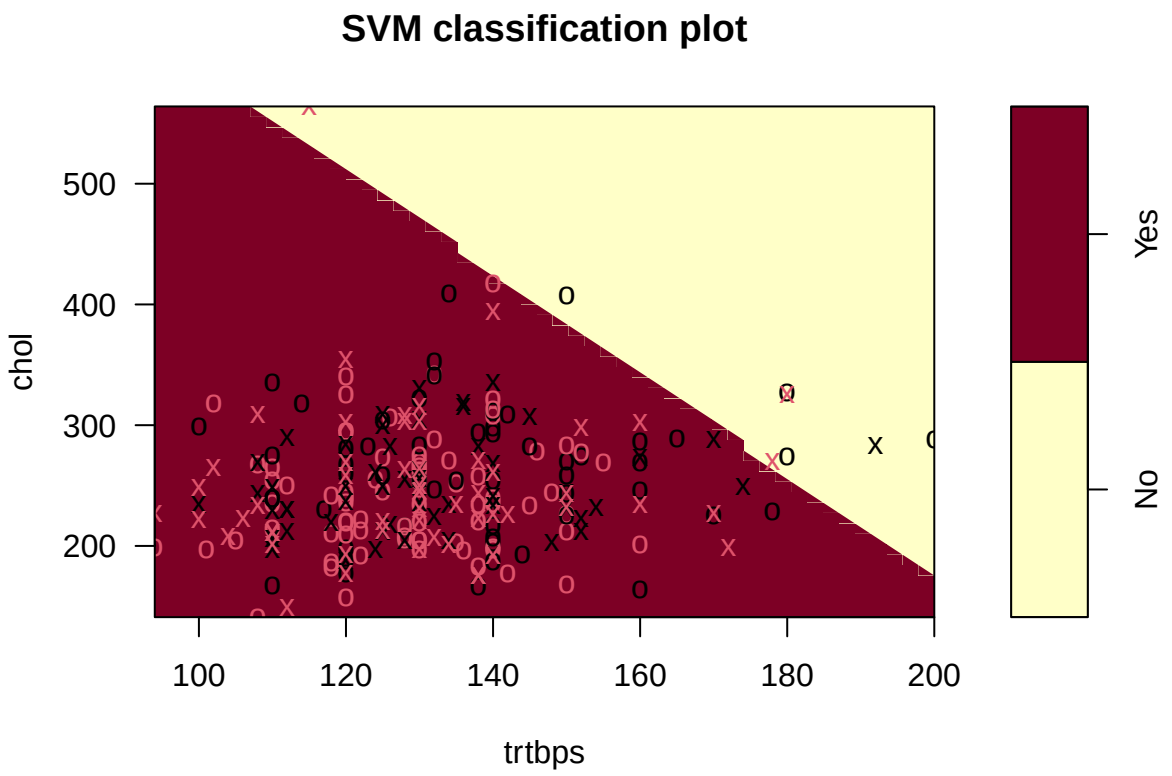
(g) Make some plots to back up your assertions in (e) and (f).

```
library(kernlab)
```

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

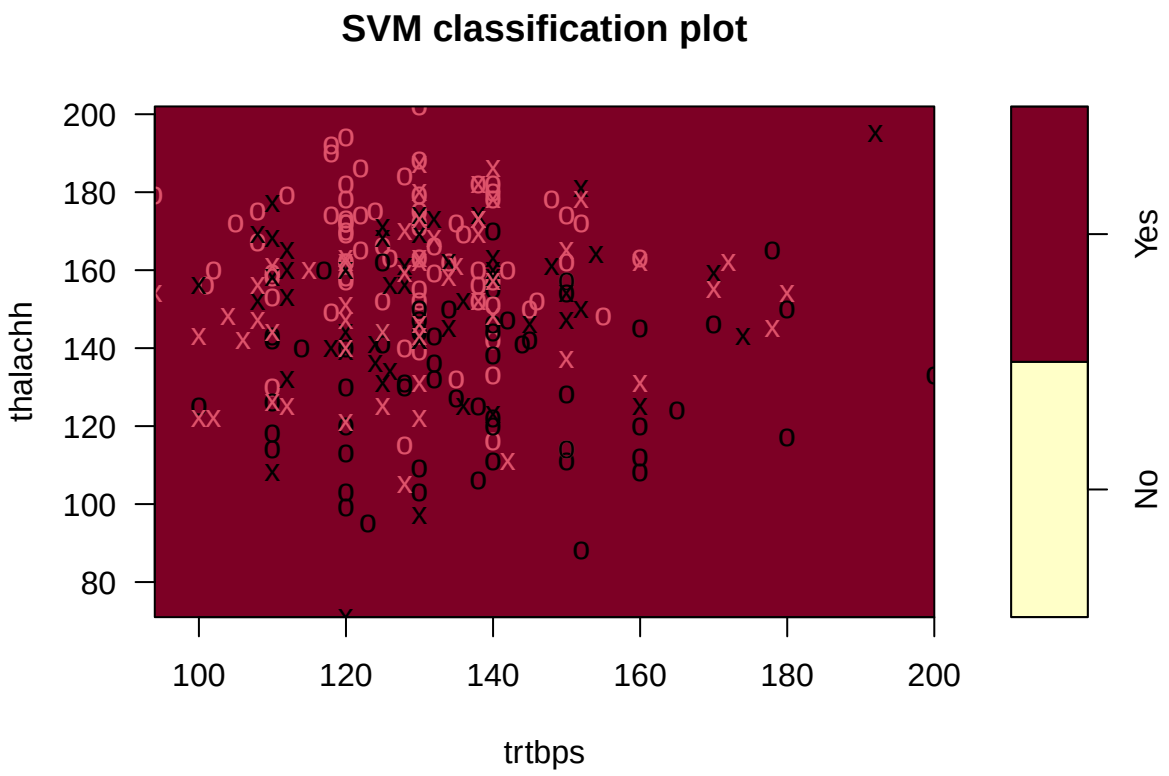
```
## The following object is masked from 'package:ggplot2':
##
##     alpha
```

```
plot(svmlinear,train_data,chol~trtbps)
```

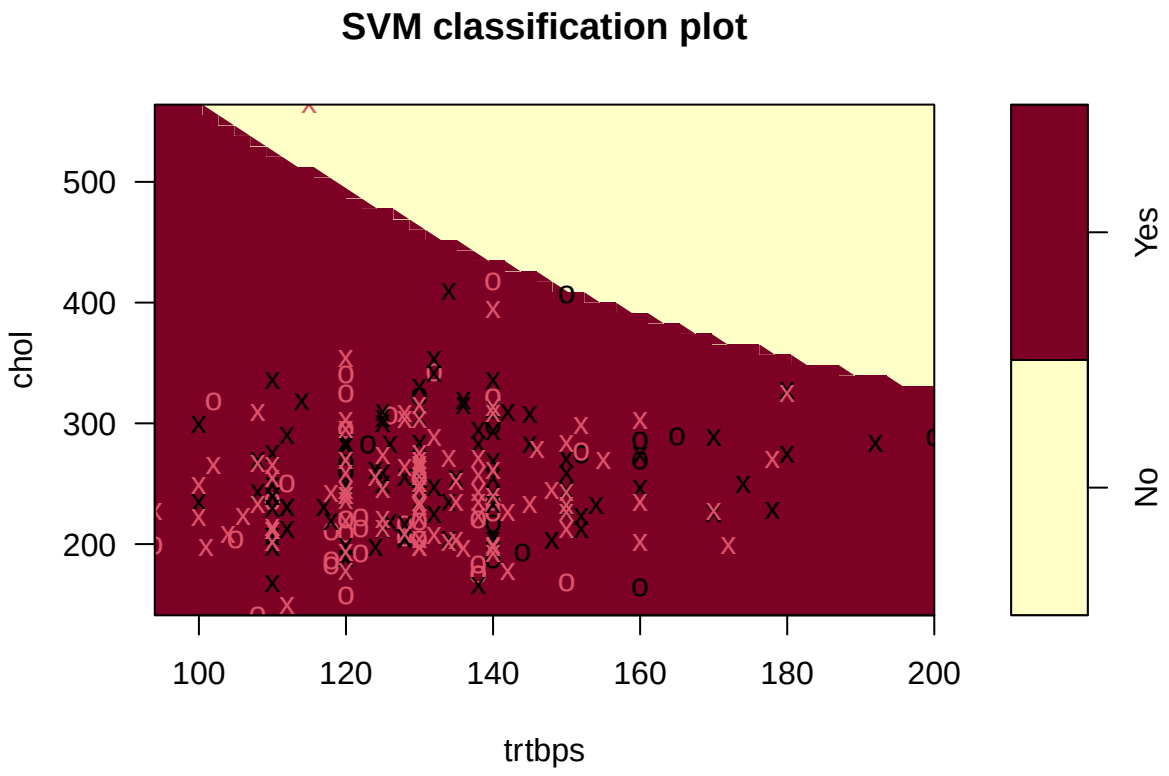



```
plot(svmlinear,train_data,trtbps~age)
```

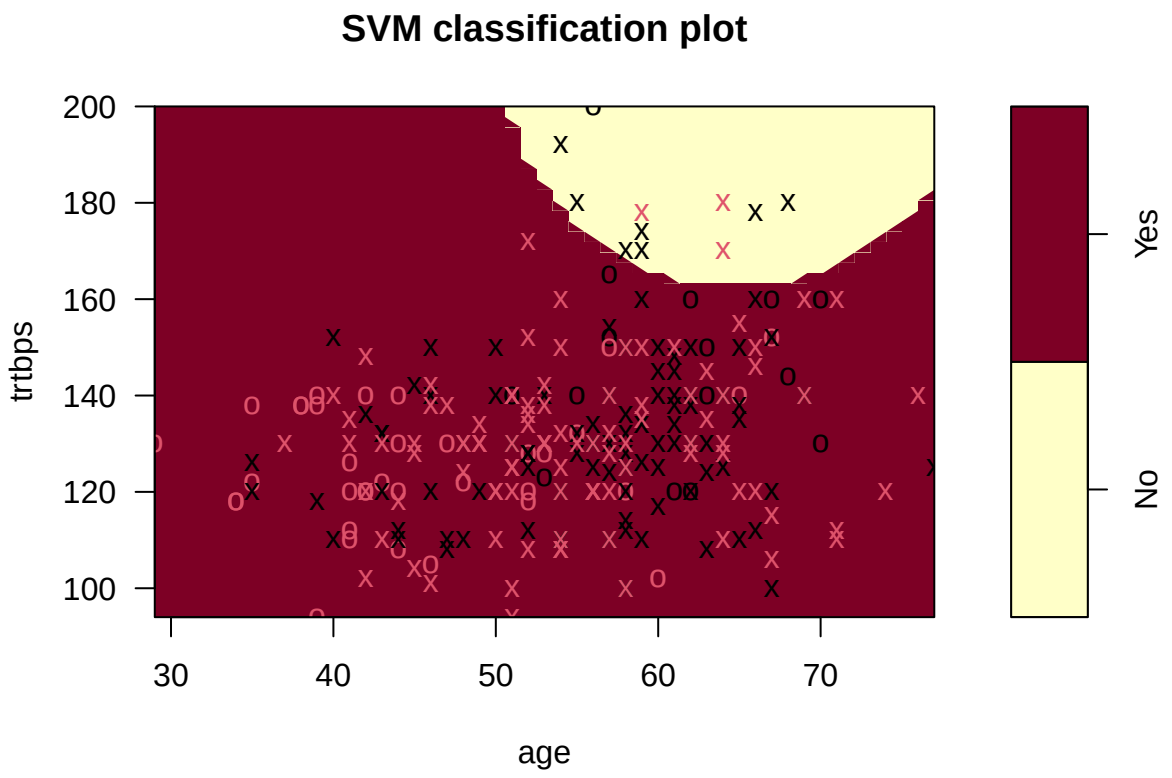

```
plot(svmlinear,train_data,thalachh~trtbps)
```



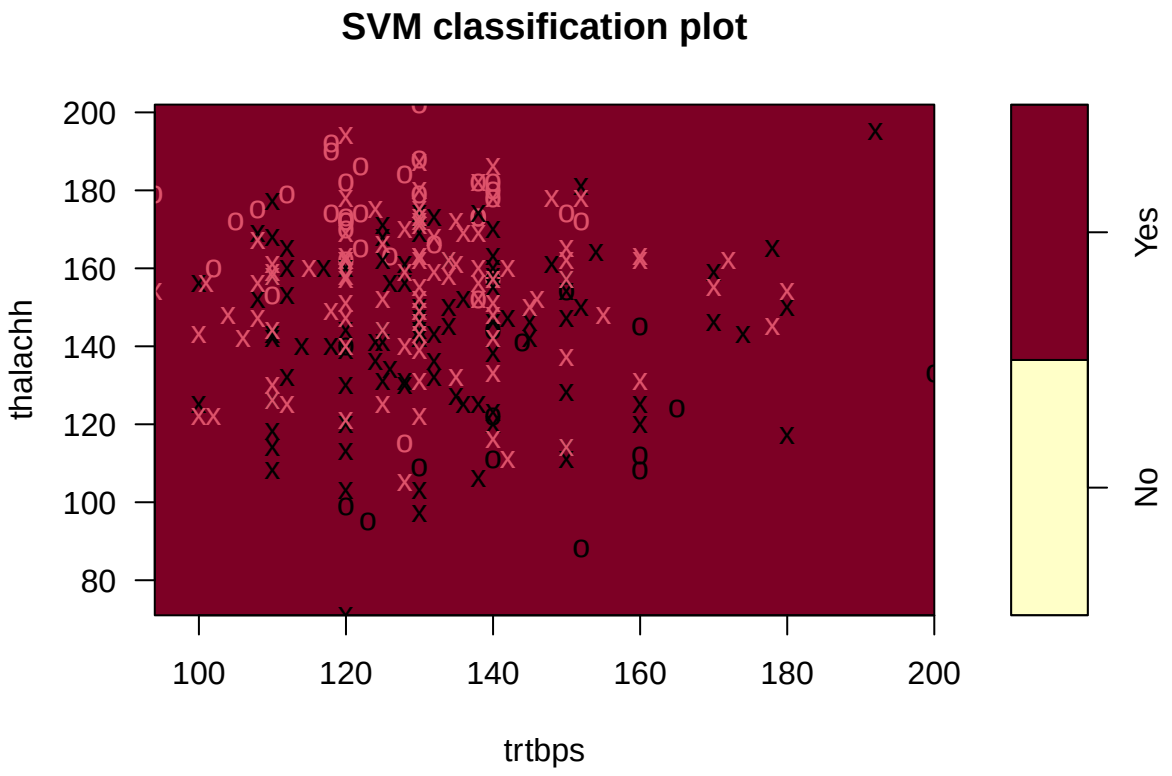

```
plot(svmpol,train_data,chol~trtbps)
```



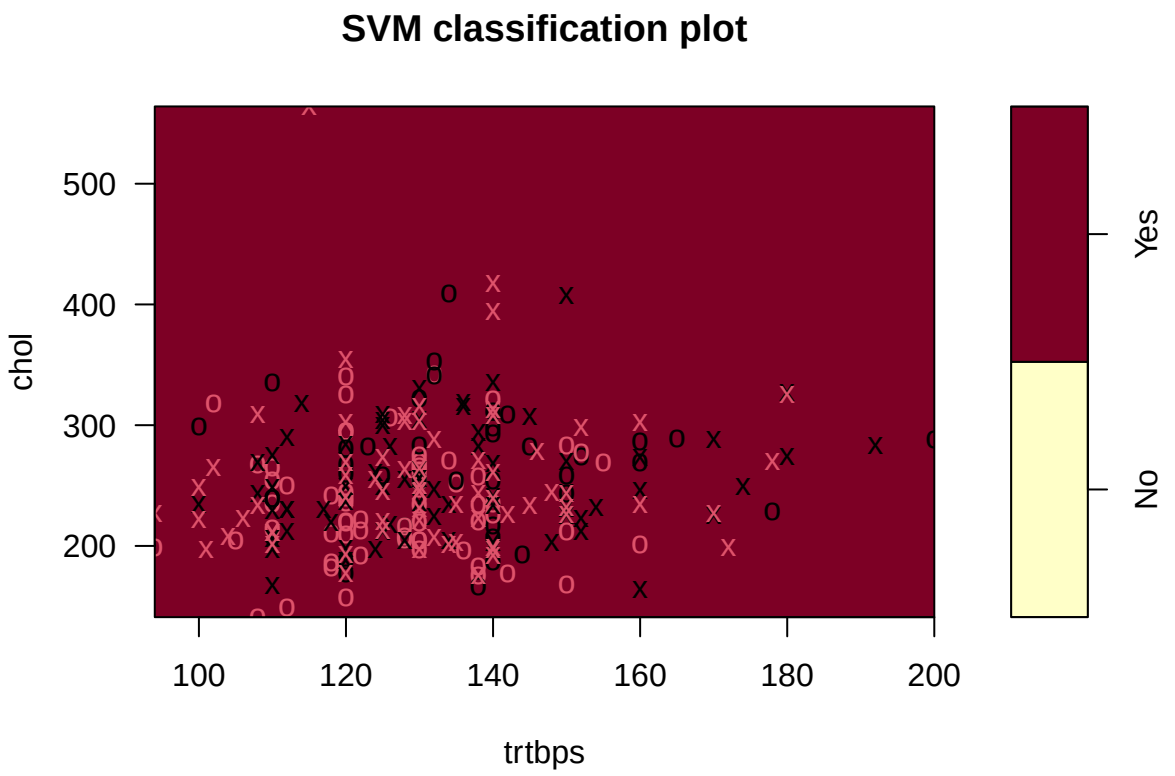

```
plot(svmpol,train_data,trtbps~age)
```




```
plot(svmpol,train_data,thalachh~trtbps)
```

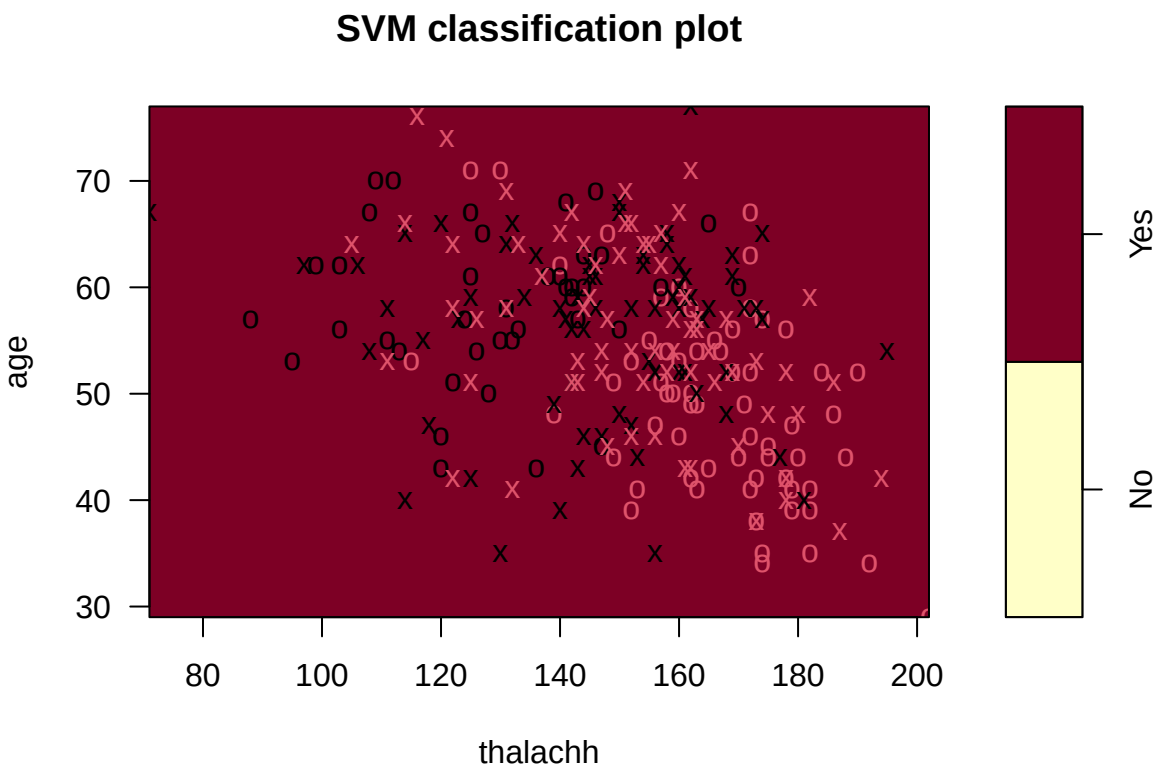



```
plot(svmrad,train_data,chol~trtbps)
```




```
plot(svmrad,train_data,trtbps~age)
```


```
plot(svmrad,train_data,age~thalachh)
```


SVM classification plot
age
thalachh
70
60
50
40
30
80
100
120
140
160
180
200
Yes
No