CS 5610 Project

Aaron Carr & Daniel Reardon

4/8/2022

Cardiovascular disease is the number 1 leading cause of death in the world, accounting for 31% of all deaths (17.9 million people every year.) Four fifths of these deaths are due to sudden episodes of heart attack and stroke, and one third of these occur in patients under 70 years old. As such, constructing a model which can predict these events prior to their occurrence has wide ranging potential benefits in the medical field.

```
library(boot)
library(MASS)
library(e1071)
library(caTools)
```

```
## Warning: package 'caTools' was built under R version 4.1.3
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:MASS':
##
##     select
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(tree)
```

```
## Warning: package 'tree' was built under R version 4.1.3
```

```
library(gbm)
```

```
## Warning: package 'gbm' was built under R version 4.1.3
```

```
## Loaded gbm 2.1.8
```

```
library(ggplot2)
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
library(randomForest)
```

```
## Warning: package 'randomForest' was built under R version 4.1.3
```

```
## randomForest 4.7-1
```

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

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:gridExtra':
##
##     combine
```

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

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

The dataset which we use was constructed using 5 different datasets from Cleveland, Hungary, Switzerland, Long Beach California, and the Stalog Heart Data from the UCI Machine Learning Repository. It contains 918 different observations of which 11 common features are abstracted. These features are Age, Sex, Type of Chest Pain (Typical Angina, Atypical Angina, Non-Anginal Pain, and Asymptomatic), Resting Blood Pressure, Cholesterol, Fasting Blood Sugar (a binary measurement (1 if $>$ 120 ml.dl, 0 otherwise), Resting Electrocardiogram Results (Normal, Having St-T wave abnormality, or showing at least probable left ventricular hypertrophy), Maximum Heart Rate achieved, Exercise Induced angina (yes or no), Oldpeak (as a numeric value), and ST-Slope (Up, down, or flat), and finally, the absence or presence of Heart Disease. The goal of our models is to predict the value of the Heart Disease variable using the values of the other variables as consistently and accurately as possible.

```
#Load Dataset
heart <- read.csv("heart.csv")
heart_copy = read.csv("heart.csv")
#View(heart)
heart <- mutate(heart, typical_angina = as.integer(ChestPainType == "TA")) %>%
  mutate(atypical_angina = as.integer(ChestPainType == "ATA")) %>%
  mutate(non_angina_pain = as.integer(ChestPainType == "NAP")) %>%
  mutate(st_abnorm =  as.integer(RestingECG == "ST")) %>%
  mutate(left_vent_hypertroph = as.integer(RestingECG == "LVH")) %>%
  mutate(ExerciseAngina = as.integer(ExerciseAngina == "Y")) %>%
  mutate(stslope_up = as.integer(ST_Slope == "Up")) %>%
  mutate(stslope_down = as.integer(ST_Slope == "Down")) %>%
  mutate(male = as.integer(Sex == "M")) %>%
  select(- c(ChestPainType, RestingECG, ST_Slope, Sex))

summary(heart)
```

```
##       Age          RestingBP      Cholesterol      FastingBS
##  Min.   :28.00   Min.   :  0.0   Min.   :  0.0   Min.   :0.0000
##  1st Qu.:47.00   1st Qu.:120.0   1st Qu.:173.2   1st Qu.:0.0000
##  Median :54.00   Median :130.0   Median :223.0   Median :0.0000
##  Mean   :53.51   Mean   :132.4   Mean   :198.8   Mean   :0.2331
##  3rd Qu.:60.00   3rd Qu.:140.0   3rd Qu.:267.0   3rd Qu.:0.0000
##  Max.   :77.00   Max.   :200.0   Max.   :603.0   Max.   :1.0000
```

```
##      MaxHR       ExerciseAngina      Oldpeak         HeartDisease
##  Min.   : 60.0   Min.   :0.0000   Min.   :-2.6000   Min.   :0.0000
##  1st Qu.:120.0   1st Qu.:0.0000   1st Qu.: 0.0000   1st Qu.:0.0000
##  Median :138.0   Median :0.0000   Median : 0.6000   Median :1.0000
##  Mean   :136.8   Mean   :0.4041   Mean   : 0.8874   Mean   :0.5534
##  3rd Qu.:156.0   3rd Qu.:1.0000   3rd Qu.: 1.5000   3rd Qu.:1.0000
##  Max.   :202.0   Max.   :1.0000   Max.   : 6.2000   Max.   :1.0000
##  typical_angina    atypical_angina  non_angina_pain    st_abnorm
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :0.00000   Median :0.0000   Median :0.0000   Median :0.0000
##  Mean   :0.05011   Mean   :0.1885   Mean   :0.2211   Mean   :0.1939
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.0000   3rd Qu.:0.0000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
##  left_vent_hypertroph   stslope_up      stslope_down          male
##  Min.   :0.0000       Min.   :0.0000   Min.   :0.00000   Min.   :0.0000
##  1st Qu.:0.0000       1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:1.0000
##  Median :0.0000       Median :0.0000   Median :0.00000   Median :1.0000
##  Mean   :0.2048       Mean   :0.4303   Mean   :0.06863   Mean   :0.7898
##  3rd Qu.:0.0000       3rd Qu.:1.0000   3rd Qu.:0.00000   3rd Qu.:1.0000
##  Max.   :1.0000       Max.   :1.0000   Max.   :1.00000   Max.   :1.0000
```

```
#There appear to be some gaps in the data, where Cholesterol and RestingBP are labeled as zero, which i
#We decided to construct small linear models to predict their values and replace them

lm.chol_fit <- lm(Cholesterol  ~ . - HeartDisease, data = dplyr::filter(heart, Cholesterol != 0))
lm.bp_fit <- lm(RestingBP ~ . - HeartDisease, data = dplyr::filter(heart, RestingBP != 0))

PredictedCholesterol <- predict(lm.chol_fit, dplyr::filter(heart, Cholesterol == 0))
PredictedBP <- predict(lm.bp_fit, dplyr::filter(heart, RestingBP == 0))

heart <- mutate(heart, Cholesterol = replace(Cholesterol, Cholesterol == 0, PredictedCholesterol))
heart <- mutate(heart, RestingBP = replace(RestingBP, RestingBP == 0, PredictedBP))

summary(heart)
```

```
##       Age          RestingBP      Cholesterol      FastingBS
##  Min.   :28.00   Min.   : 80.0   Min.   : 85.0   Min.   :0.0000
##  1st Qu.:47.00   1st Qu.:120.0   1st Qu.:214.0   1st Qu.:0.0000
##  Median :54.00   Median :130.0   Median :240.1   Median :0.0000
##  Mean   :53.51   Mean   :132.5   Mean   :244.2   Mean   :0.2331
##  3rd Qu.:60.00   3rd Qu.:140.0   3rd Qu.:268.0   3rd Qu.:0.0000
##  Max.   :77.00   Max.   :200.0   Max.   :603.0   Max.   :1.0000
##      MaxHR       ExerciseAngina      Oldpeak         HeartDisease
##  Min.   : 60.0   Min.   :0.0000   Min.   :-2.6000   Min.   :0.0000
##  1st Qu.:120.0   1st Qu.:0.0000   1st Qu.: 0.0000   1st Qu.:0.0000
##  Median :138.0   Median :0.0000   Median : 0.6000   Median :1.0000
##  Mean   :136.8   Mean   :0.4041   Mean   : 0.8874   Mean   :0.5534
##  3rd Qu.:156.0   3rd Qu.:1.0000   3rd Qu.: 1.5000   3rd Qu.:1.0000
##  Max.   :202.0   Max.   :1.0000   Max.   : 6.2000   Max.   :1.0000
##  typical_angina    atypical_angina  non_angina_pain    st_abnorm
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :0.00000   Median :0.0000   Median :0.0000   Median :0.0000
##  Mean   :0.05011   Mean   :0.1885   Mean   :0.2211   Mean   :0.1939
```

```
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.0000   3rd Qu.:0.0000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
##  left_vent_hypertroph   stslope_up      stslope_down          male
##  Min.   :0.0000       Min.   :0.0000   Min.   :0.00000   Min.   :0.0000
##  1st Qu.:0.0000       1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:1.0000
##  Median :0.0000       Median :0.0000   Median :0.00000   Median :1.0000
##  Mean   :0.2048       Mean   :0.4303   Mean   :0.06863   Mean   :0.7898
##  3rd Qu.:0.0000       3rd Qu.:1.0000   3rd Qu.:0.00000   3rd Qu.:1.0000
##  Max.   :1.0000       Max.   :1.0000   Max.   :1.00000   Max.   :1.0000
```

```
#Give it a look over
#View(heart)
names(heart)
```

```
##  [1] "Age"                  "RestingBP"            "Cholesterol"
##  [4] "FastingBS"            "MaxHR"                "ExerciseAngina"
##  [7] "Oldpeak"              "HeartDisease"         "typical_angina"
## [10] "atypical_angina"      "non_angina_pain"      "st_abnorm"
## [13] "left_vent_hypertroph" "stslope_up"           "stslope_down"
## [16] "male"
```

```
dim(heart)
```

```
## [1] 918  16
```

```
summary(heart)
```

```
##       Age          RestingBP      Cholesterol      FastingBS
##  Min.   :28.00   Min.   : 80.0   Min.   : 85.0   Min.   :0.0000
##  1st Qu.:47.00   1st Qu.:120.0   1st Qu.:214.0   1st Qu.:0.0000
##  Median :54.00   Median :130.0   Median :240.1   Median :0.0000
##  Mean   :53.51   Mean   :132.5   Mean   :244.2   Mean   :0.2331
##  3rd Qu.:60.00   3rd Qu.:140.0   3rd Qu.:268.0   3rd Qu.:0.0000
##  Max.   :77.00   Max.   :200.0   Max.   :603.0   Max.   :1.0000
##      MaxHR       ExerciseAngina      Oldpeak         HeartDisease
##  Min.   : 60.0   Min.   :0.0000   Min.   :-2.6000   Min.   :0.0000
##  1st Qu.:120.0   1st Qu.:0.0000   1st Qu.: 0.0000   1st Qu.:0.0000
##  Median :138.0   Median :0.0000   Median : 0.6000   Median :1.0000
##  Mean   :136.8   Mean   :0.4041   Mean   : 0.8874   Mean   :0.5534
##  3rd Qu.:156.0   3rd Qu.:1.0000   3rd Qu.: 1.5000   3rd Qu.:1.0000
##  Max.   :202.0   Max.   :1.0000   Max.   : 6.2000   Max.   :1.0000
##  typical_angina    atypical_angina  non_angina_pain    st_abnorm
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :0.00000   Median :0.0000   Median :0.0000   Median :0.0000
##  Mean   :0.05011   Mean   :0.1885   Mean   :0.2211   Mean   :0.1939
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.0000   3rd Qu.:0.0000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
##  left_vent_hypertroph   stslope_up      stslope_down          male
##  Min.   :0.0000       Min.   :0.0000   Min.   :0.00000   Min.   :0.0000
##  1st Qu.:0.0000       1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:1.0000
##  Median :0.0000       Median :0.0000   Median :0.00000   Median :1.0000
##  Mean   :0.2048       Mean   :0.4303   Mean   :0.06863   Mean   :0.7898
##  3rd Qu.:0.0000       3rd Qu.:1.0000   3rd Qu.:0.00000   3rd Qu.:1.0000
##  Max.   :1.0000       Max.   :1.0000   Max.   :1.00000   Max.   :1.0000
```

```r
#Check to see if there's any missing values
any(is.na(heart))
```

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

```r
set.seed(97)
spl = sample.split(heart$HeartDisease, SplitRatio = 0.75)

heartTrain = subset(heart, spl==TRUE)
heartTest = subset(heart, spl==FALSE)

dim(heartTrain)
```

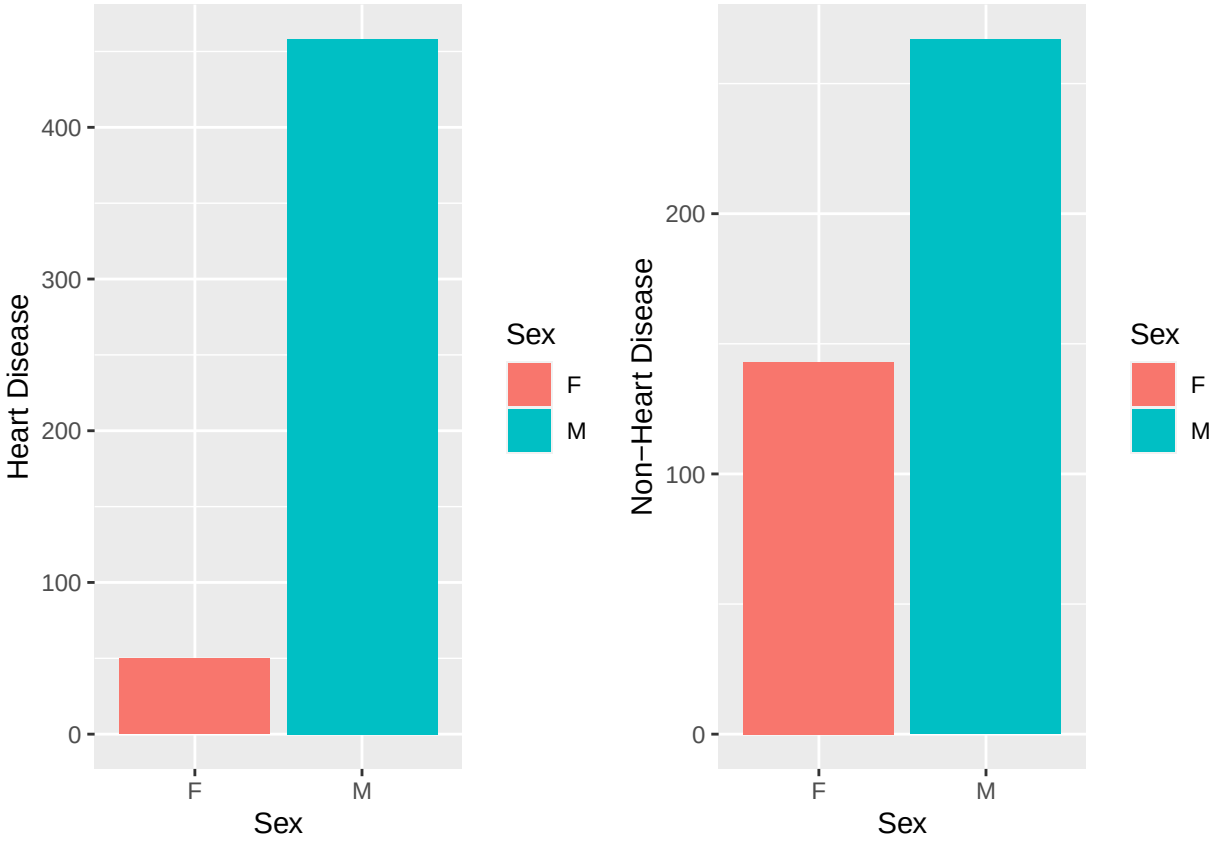
```
## [1] 689  16
```

```r
dim(heartTest)
```

```
## [1] 229  16
```

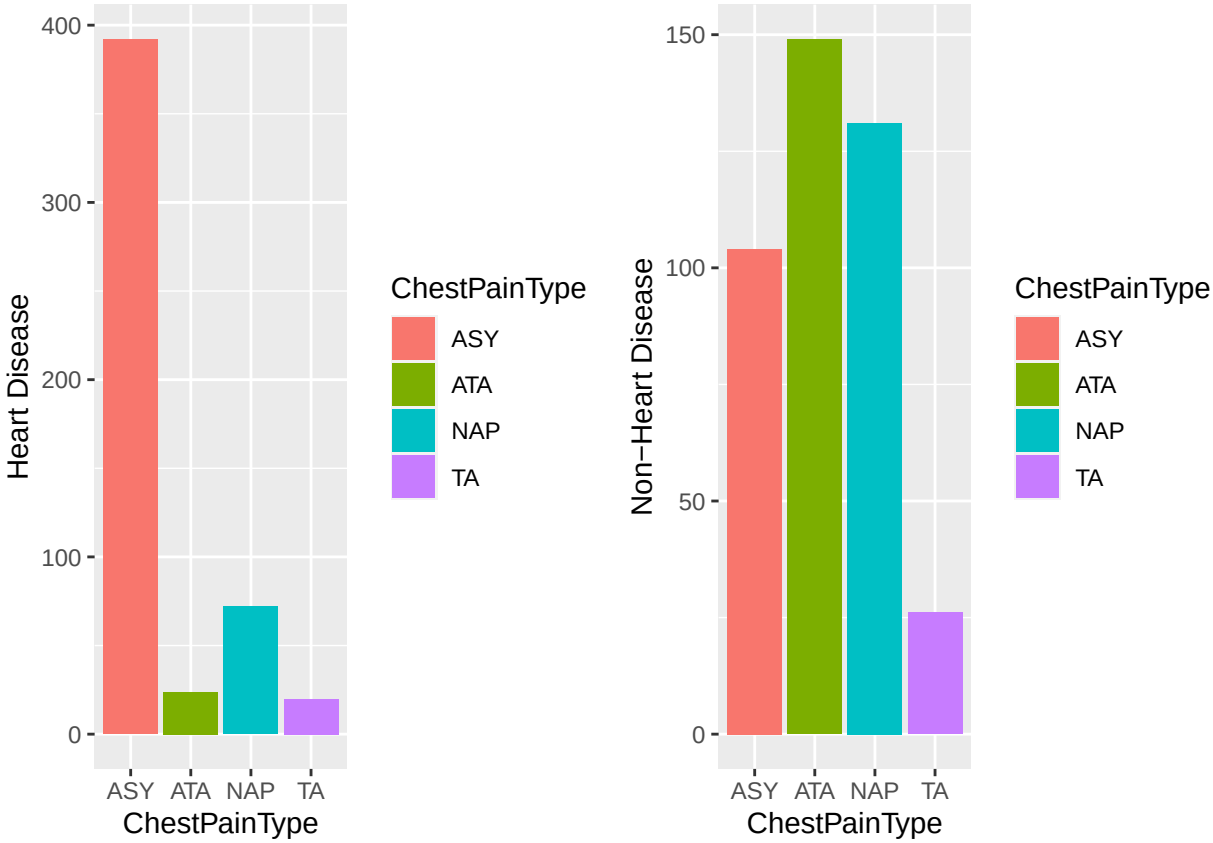
Our first task involves wrangling the dataset so that it optimal for use by the models. Glancing over the dataset, it is clear that the some of the variables are categorical and consist of three or more categories; in situations such as these, it is vital to split these categories into binary categories. For the sake of clarity, this is explicitly performed by the dplyr pipeline above and not left to the models themselves. The chest pain type, resting ECG type, exercised induced angina and patient sex have all been reformatted such that the baseline patient is a female with no resting chest pain, a standard ECG, and no exercised induced chest pain. Next, when looking over a summary of the original dataset, it becomes apparent that while there are technically no missing values, some Cholesterol values (and a single Resting Blood Pressure value) are listed as 0, which is clearly erroneous. In order to best address this without skewing the data or removing a large chunk of training data, toy linear regression models were constructed to predict the appropriate values for these variables. In situations where the data appeared to be erroneous, the erroneous value was replaced with the predicted value.

```r
#Heart Disease by sex
one = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = Sex, y = HeartDisease, fill = Sex)) + labs(y = "Heart Disease")
zero = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = Sex, y = 1 - HeartDisease, fill = Sex)) + labs(y = "Non-Heart Disease")

grid.arrange(one,zero, ncol= 2)
```



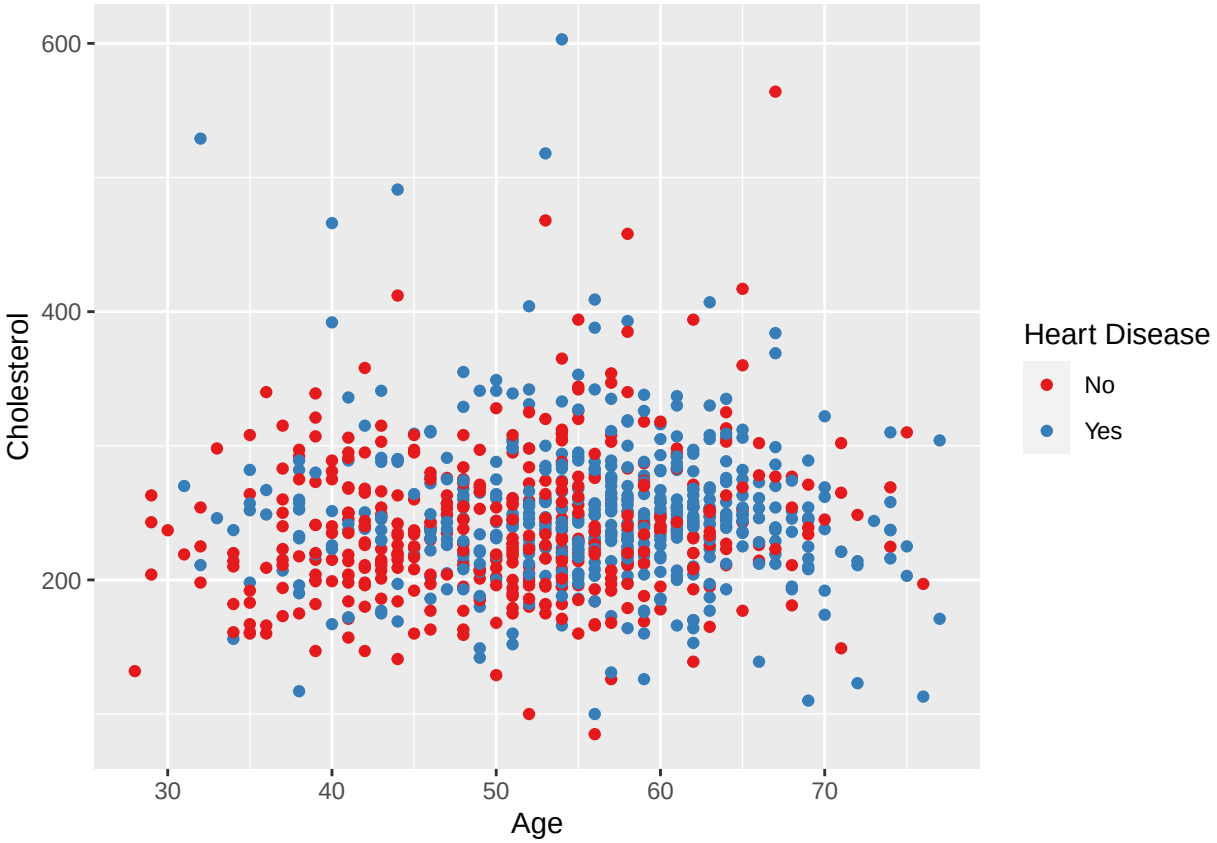
This dataset seems to suggest that Heart Disease is more common among men than women.

```
#Heart disease by chest pain type
two = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = ChestPainType, y = HeartDisease, fill = ChestPainType)) + labs(y = "Heart D
three = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = ChestPainType, y = 1 - HeartDisease, fill = ChestPainType)) + labs(y = "Non

grid.arrange(two,three, ncol= 2)
```



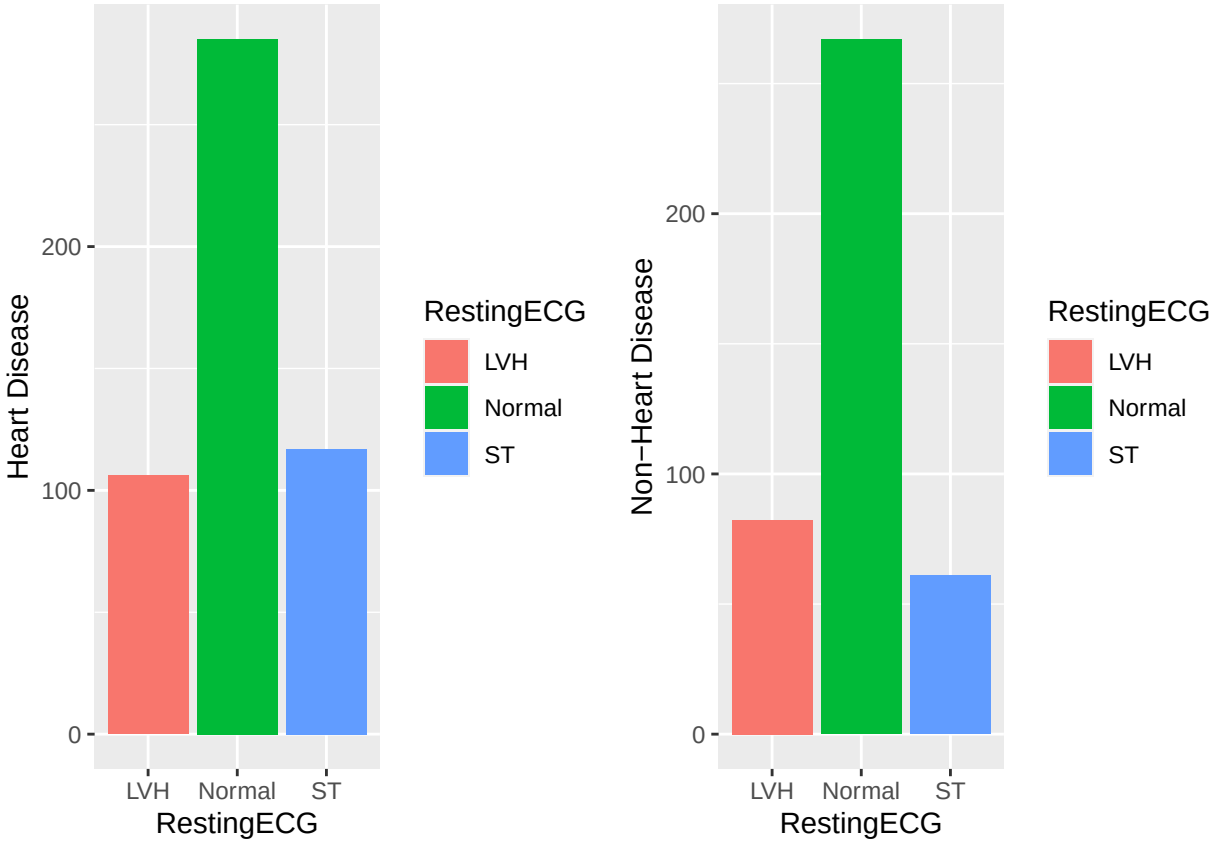
Asymptomatic individuals seem to dominate the heart disease group. There is a condition known as silent ischemia which restricts blood flow to the heart while the person feels no pain.

```
#Heart disease by age and cholesterol
ggplot(data = heart) +
  geom_point(mapping = aes(y = Cholesterol, x = Age, color = factor(HeartDisease, labels = c("No","Yes")
      scale_color_brewer(palette = "Set1") +
      labs(color = "Heart Disease")
```



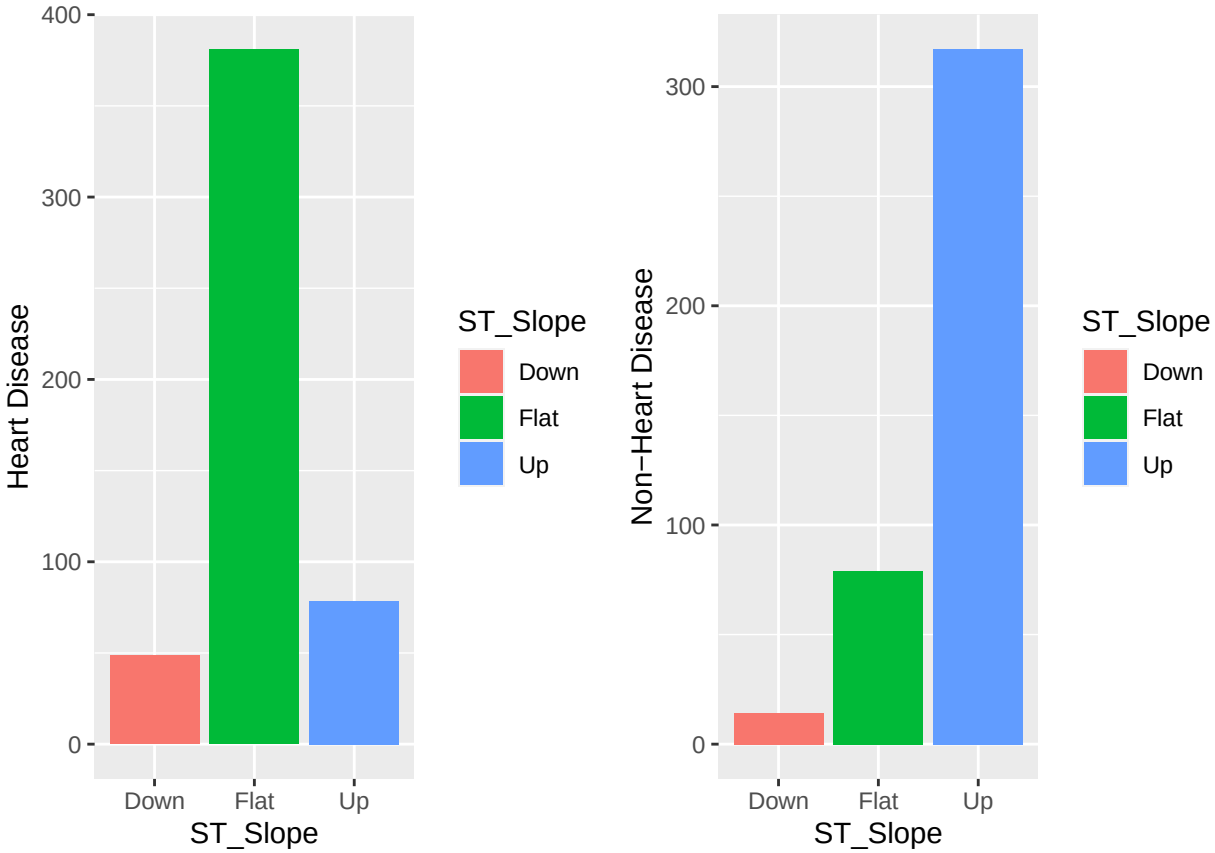
It is difficult to establish a relationship of age, cholesterol, and heart disease based on this scatterplot. It does appear that there that heart disease risk increases with age.

```
#Heart disease by Resting ECG
four = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = RestingECG, y = HeartDisease, fill = RestingECG)) + labs(y = "Heart Disease
five = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = RestingECG, y = 1 - HeartDisease, fill = RestingECG)) + labs(y = "Non-Heart

grid.arrange(four,five, ncol= 2)
```



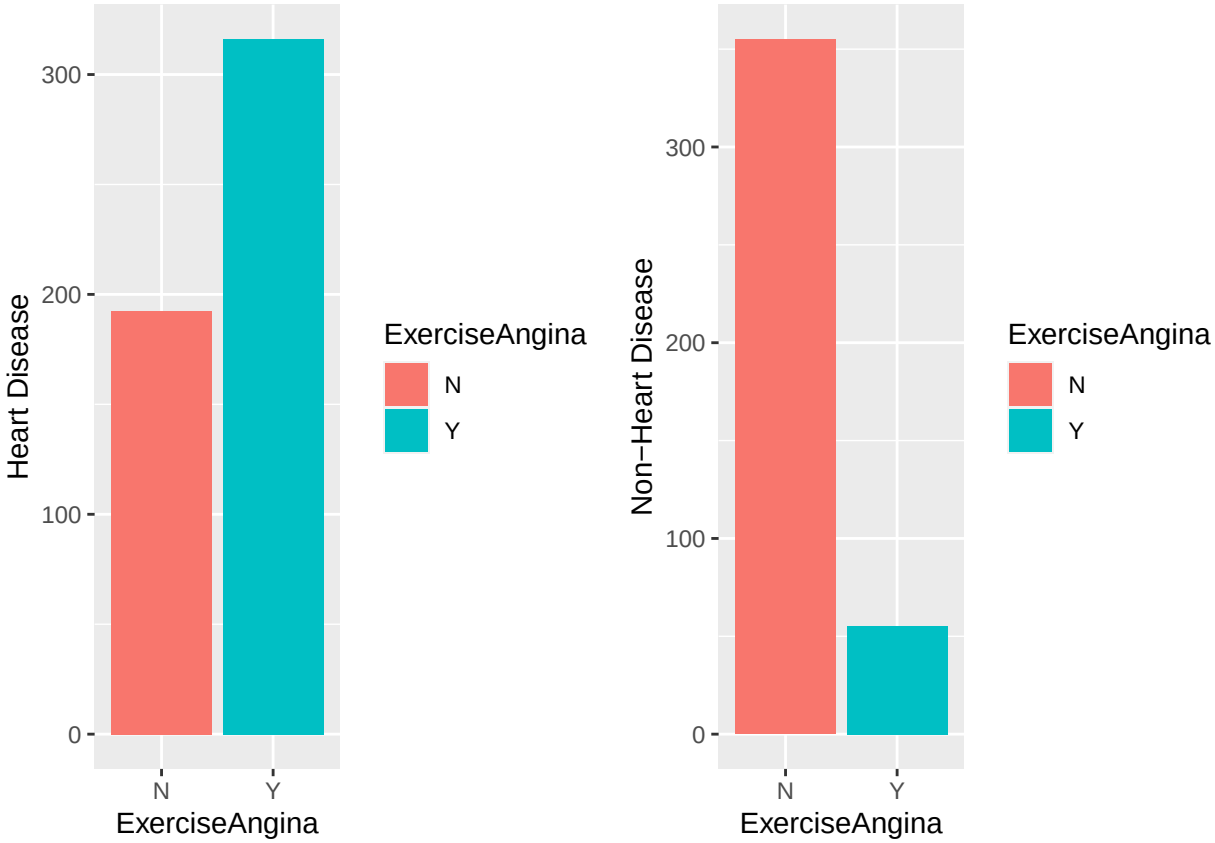
RestingECG seems to have no affect on heart disease risk.

```
#Heart Disease by ST_slope
six = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = ST_Slope, y = HeartDisease, fill = ST_Slope)) + labs(y = "Heart Disease")
seven = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = ST_Slope, y = 1 - HeartDisease, fill = ST_Slope)) + labs(y = "Non-Heart Dis

grid.arrange(six,seven, ncol= 2)
```



A flat ST_slope seems to be a risk factor for heart disease.

```
eight = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = ExerciseAngina, y = HeartDisease, fill = ExerciseAngina)) + labs(y = "Heart
nine = ggplot(data = heart_copy) +
 geom_col(mapping = aes(x = ExerciseAngina, y = 1 - HeartDisease, fill = ExerciseAngina)) + labs(y = "N

grid.arrange(eight,nine, ncol= 2)
```



The presence of exercise angina appears to be an indicator of heart disease.

```
#Logistic Regression (87%)
glm.fits <- glm(HeartDisease ~ .,
  family = binomial, data = heartTrain
)
summary(glm.fits)
```

```
##
## Call:
## glm(formula = HeartDisease ~ ., family = binomial, data = heartTrain)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.8350  -0.4045   0.1933   0.5045   2.5901
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -0.788478   1.611022  -0.489 0.624539
## Age                   0.011393   0.014997   0.760 0.447443
## RestingBP             0.004111   0.007047   0.583 0.559639
## Cholesterol           0.002555   0.002384   1.071 0.283995
## FastingBS             1.065646   0.302524   3.523 0.000427 ***
## MaxHR                -0.008234   0.005573  -1.477 0.139546
## ExerciseAngina        0.938880   0.274380   3.422 0.000622 ***
## Oldpeak               0.357433   0.130584   2.737 0.006197 **
## typical_angina       -1.192704   0.461671  -2.583 0.009782 **
```

```
## atypical_angina      -1.824644   0.365610  -4.991 6.02e-07 ***
## non_angina_pain      -1.611619   0.297733  -5.413 6.20e-08 ***
## st_abnorm             0.267192   0.334449   0.799 0.424346
## left_vent_hypertroph  0.221632   0.305032   0.727 0.467479
## stslope_up           -2.302289   0.273953  -8.404  < 2e-16 ***
## stslope_down         -1.346388   0.498025  -2.703 0.006862 **
## male                  1.654871   0.340736   4.857 1.19e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 947.41  on 688  degrees of freedom
## Residual deviance: 463.91  on 673  degrees of freedom
## AIC: 495.91
##
## Number of Fisher Scoring iterations: 5
```

```
glm.probs <- predict(glm.fits, type = "response")
glm.pred <- rep(0, 689)
glm.pred[glm.probs > .5] = 1

table(glm.pred, heartTrain$HeartDisease)
```

```
##
## glm.pred   0   1
##        0 253  42
##        1  55 339
```

```
mean(glm.pred == heartTrain$HeartDisease)
```

```
## [1] 0.8592163
```

```
glm.probs <- predict(glm.fits, type = "response", newdata = heartTest)
glm.predTest <- rep(0, 229)
glm.predTest[glm.probs > .5] = 1

table(glm.predTest, heartTest$HeartDisease)
```

```
##
## glm.predTest   0   1
##            0  86  13
##            1  16 114
```

```
mean(glm.predTest == heartTest$HeartDisease)
```

```
## [1] 0.8733624
```

```
##Feature Selection algorithm
i <- glm(HeartDisease ~ 1,
                family = binomial, data = heartTrain)

glm.new <- step(i, direction='both', scope=formula(glm.fits), trace=0)

summary(glm.new)
```

```
##
## Call:
```

```
## glm(formula = HeartDisease ~ stslope_up + ExerciseAngina + male +
##     non_angina_pain + atypical_angina + FastingBS + typical_angina +
##     Oldpeak + stslope_down + MaxHR, family = binomial, data = heartTrain)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.8268  -0.4138   0.1946   0.5056   2.7572
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       1.376374   0.797648   1.726 0.084430 .
## stslope_up       -2.316734   0.270974  -8.550  < 2e-16 ***
## ExerciseAngina    0.988086   0.270632   3.651 0.000261 ***
## male              1.557620   0.332344   4.687 2.78e-06 ***
## non_angina_pain  -1.620591   0.293086  -5.529 3.21e-08 ***
## atypical_angina  -1.824558   0.362917  -5.027 4.97e-07 ***
## FastingBS         1.130285   0.294911   3.833 0.000127 ***
## typical_angina   -1.152981   0.450237  -2.561 0.010442 *
## Oldpeak           0.393905   0.127162   3.098 0.001950 **
## stslope_down     -1.406604   0.493726  -2.849 0.004386 **
## MaxHR            -0.010062   0.005077  -1.982 0.047503 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 947.41  on 688  degrees of freedom
## Residual deviance: 467.97  on 678  degrees of freedom
## AIC: 489.97
##
## Number of Fisher Scoring iterations: 5
```

```
glm.probs <- predict(glm.new, type = "response", newdata = heartTest)
glm.predTest <- rep(0, 229)
glm.predTest[glm.probs > .5] = 1

table(glm.predTest, heartTest$HeartDisease)
```

```
##
## glm.predTest   0   1
##            0  86  11
##            1  16 116
```

```
mean(glm.predTest == heartTest$HeartDisease)
```

```
## [1] 0.8820961
```

The Logistic function models the probability of the outcome being a "success" (in this case success means that a patient has heart disease). The estimates return the log odds of a success given a value. For example, the estimate for the sex of the patient is 1.642. Meaning that a male has e^1.642 higher odds (or about 5 times higher odds) of having heart disease than a female.

For a continuous variable like cholesterol, the interpretation is similar except it relates to an increase of one unit. For example if a patient has one cholesterol unit higher than another patient, that patient with have an increase in odds of e^0.003597 (or about 1.0036 times higher odds).

The algorithm used to select the features used in the model was the stepwise regression algorithm. The

algorithm begins with nothing in the model but the intercept, and adds the most significant variable. It continues this step until there are no more significant variables. However, at each step it also looks to see that no variables have been made insignificant by the addition of new variables. While this method is not foolproof, it does generally give a good idea of what features to include.

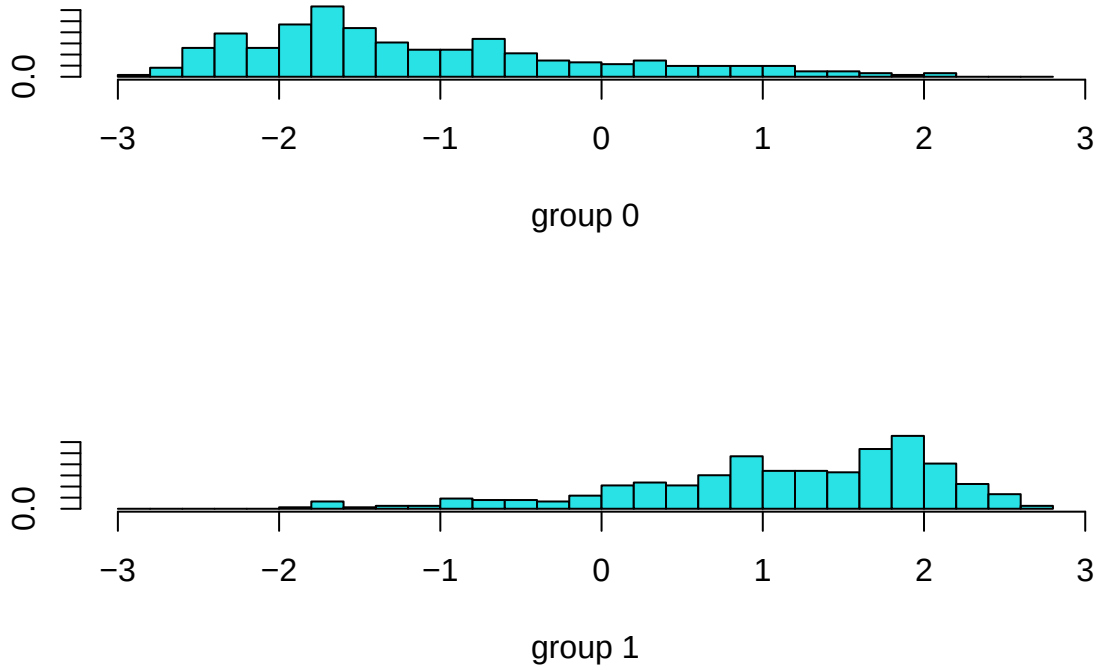
The model seems to agree that the variables we identified as significant in the visualization stage should be included in the model. It also agrees with not including RestingECG in the model as that seemed to have no effect when looking at the bar chart.

The feature selected model performs almost identically to the model which includes all features, each having an accuracy score of around 88%. (In fact, on the test data, the feature selection model performs slightly better).

```
#Linear Discriminant Analysis (87%)
lda.fit <- lda(HeartDisease ~ ., data = heartTrain)
lda.fit
```

```
## Call:
## lda(HeartDisease ~ ., data = heartTrain)
##
## Prior probabilities of groups:
##         0         1
## 0.4470247 0.5529753
##
## Group means:
##        Age RestingBP Cholesterol FastingBS    MaxHR ExerciseAngina   Oldpeak
## 0 50.72727  130.3442    240.4317 0.1201299 148.0227      0.1331169 0.4123377
## 1 55.92388  135.3390    251.4317 0.3307087 128.2756      0.6246719 1.2958005
##   typical_angina atypical_angina non_angina_pain st_abnorm left_vent_hypertroph
## 0     0.06493506      0.36038961       0.3344156 0.1493506            0.1948052
## 1     0.05249344      0.04986877       0.1548556 0.2309711            0.2125984
##   stslope_up stslope_down      male
## 0  0.7889610   0.03246753 0.6623377
## 1  0.1653543   0.09711286 0.9160105
##
## Coefficients of linear discriminants:
##                                LD1
## Age                    0.007225944
## RestingBP              0.001151866
## Cholesterol            0.001079759
## FastingBS              0.515764906
## MaxHR                 -0.004872809
## ExerciseAngina         0.554412550
## Oldpeak                0.164861467
## typical_angina        -0.584059677
## atypical_angina       -1.020089731
## non_angina_pain       -0.903042790
## st_abnorm              0.150132055
## left_vent_hypertroph   0.101949823
## stslope_up            -1.510016605
## stslope_down          -0.595821588
## male                   0.718177361
```

```
plot(lda.fit)
```




```
lda.pred <- predict(lda.fit, newdata = heartTest)
lda.class <- lda.pred$class
table(lda.class, heartTest$HeartDisease)
```

```
##
## lda.class   0   1
##         0  85  12
##         1  17 115
```

```
mean(lda.class == heartTest$HeartDisease)
```

```
## [1] 0.8733624
```

The linear discriminant analysis model also displays a relatively high level of accuracy, at 87%.

```
#Quadratic Discriminant Analysis (86%)

qda.fit <- qda(HeartDisease ~ ., data = heartTrain)
qda.fit
```

```
## Call:
## qda(HeartDisease ~ ., data = heartTrain)
##
## Prior probabilities of groups:
##         0         1
## 0.4470247 0.5529753
```

```
##
## Group means:
##        Age RestingBP Cholesterol FastingBS    MaxHR ExerciseAngina   Oldpeak
## 0 50.72727  130.3442    240.4317 0.1201299 148.0227      0.1331169 0.4123377
## 1 55.92388  135.3390    251.4317 0.3307087 128.2756      0.6246719 1.2958005
##   typical_angina atypical_angina non_angina_pain st_abnorm left_vent_hypertroph
## 0     0.06493506      0.36038961       0.3344156 0.1493506            0.1948052
## 1     0.05249344      0.04986877       0.1548556 0.2309711            0.2125984
##   stslope_up stslope_down      male
## 0  0.7889610   0.03246753 0.6623377
## 1  0.1653543   0.09711286 0.9160105
```

```
qda.class <- predict(qda.fit, newdata = heartTest)$class
table(qda.class, heartTest$HeartDisease)
```

```
##
## qda.class   0   1
##         0  83  16
##         1  19 111
```

```
mean(qda.class == heartTest$HeartDisease)
```

```
## [1] 0.8471616
```

The quandradic discriminant model has an accuracy of only around 85%, close to the other models but slightly weaker. This might be an indication that the boundary between categories can be represented linearly.

```
#Naive Bayes (87%)
nb.fit <- naiveBayes(HeartDisease ~ ., data = heartTrain)
nb.fit
```

```
##
## Naive Bayes Classifier for Discrete Predictors
##
## Call:
## naiveBayes.default(x = X, y = Y, laplace = laplace)
##
## A-priori probabilities:
## Y
##         0         1
## 0.4470247 0.5529753
##
## Conditional probabilities:
##    Age
## Y       [,1]     [,2]
##   0 50.72727 9.347628
##   1 55.92388 8.595102
##
##    RestingBP
## Y       [,1]     [,2]
##   0 130.3442 16.68305
##   1 135.3390 19.15541
##
##    Cholesterol
## Y       [,1]     [,2]
##   0 240.4317 53.19314
##   1 251.4317 54.68725
```

```
##
##    FastingBS
## Y        [,1]      [,2]
##   0 0.1201299 0.3256424
##   1 0.3307087 0.4710870
##
##    MaxHR
## Y       [,1]     [,2]
##   0 148.0227 22.91983
##   1 128.2756 23.67989
##
##    ExerciseAngina
## Y        [,1]      [,2]
##   0 0.1331169 0.3402538
##   1 0.6246719 0.4848442
##
##    Oldpeak
## Y        [,1]     [,2]
##   0 0.4123377 0.720055
##   1 1.2958005 1.175779
##
##    typical_angina
## Y         [,1]      [,2]
##   0 0.06493506 0.2468122
##   1 0.05249344 0.2233132
##
##    atypical_angina
## Y         [,1]      [,2]
##   0 0.36038961 0.4808948
##   1 0.04986877 0.2179600
##
##    non_angina_pain
## Y        [,1]      [,2]
##   0 0.3344156 0.4725535
##   1 0.1548556 0.3622427
##
##    st_abnorm
## Y        [,1]      [,2]
##   0 0.1493506 0.3570138
##   1 0.2309711 0.4220082
##
##    left_vent_hypertroph
## Y        [,1]      [,2]
##   0 0.1948052 0.3966952
##   1 0.2125984 0.4096839
##
##    stslope_up
## Y        [,1]      [,2]
##   0 0.7889610 0.4087100
##   1 0.1653543 0.3719885
##
##    stslope_down
## Y         [,1]      [,2]
##   0 0.03246753 0.1775267
```

```
##   1 0.09711286 0.2965008
##
##    male
## Y        [,1]      [,2]
##   0 0.6623377 0.4736824
##   1 0.9160105 0.2777368
```

```
nb.class <- predict(nb.fit, newdata = heartTest)
table(nb.class, heartTest$HeartDisease)
```

```
##
## nb.class   0   1
##        0  84  18
##        1  18 109
```

```
mean(nb.class == heartTest$HeartDisease)
```

```
## [1] 0.8427948
```

The Naive Bayes model performs about as well as the quadradic discriminant model, at around 84%.

```
#Classification Tree 85%
tree.heart <- tree(as.factor(HeartDisease) ~ ., data = heartTrain)
summary(tree.heart)
```

```
##
## Classification tree:
## tree(formula = as.factor(HeartDisease) ~ ., data = heartTrain)
## Variables actually used in tree construction:
##  [1] "stslope_up"           "MaxHR"                "Oldpeak"
##  [4] "ExerciseAngina"       "male"                 "Cholesterol"
##  [7] "left_vent_hypertroph" "atypical_angina"      "non_angina_pain"
## [10] "RestingBP"
## Number of terminal nodes:  17
## Residual mean deviance:  0.6075 = 408.2 / 672
## Misclassification error rate: 0.1277 = 88 / 689
```

```
tree:::print.tree(tree.heart)
```

```
## node), split, n, deviance, yval, (yprob)
##       * denotes terminal node
##
##  1) root 689 947.400 1 ( 0.44702 0.55298 )
##    2) stslope_up < 0.5 383 348.900 1 ( 0.16971 0.83029 )
##      4) MaxHR < 140.5 260 145.900 1 ( 0.08077 0.91923 )
##        8) Oldpeak < 0.05 59   0.000 1 ( 0.00000 1.00000 ) *
##        9) Oldpeak > 0.05 201 134.600 1 ( 0.10448 0.89552 )
##         18) Oldpeak < 1.65 101  97.660 1 ( 0.18812 0.81188 )
##           36) ExerciseAngina < 0.5 23  31.490 1 ( 0.43478 0.56522 )
##             72) male < 0.5 5   0.000 0 ( 1.00000 0.00000 ) *
##             73) male > 0.5 18  21.270 1 ( 0.27778 0.72222 ) *
##           37) ExerciseAngina > 0.5 78  55.790 1 ( 0.11538 0.88462 ) *
##         19) Oldpeak > 1.65 100  19.610 1 ( 0.02000 0.98000 ) *
##      5) MaxHR > 140.5 123 160.400 1 ( 0.35772 0.64228 )
##       10) Cholesterol < 245.153 62  85.950 0 ( 0.50000 0.50000 )
##         20) Oldpeak < 2.4 51  69.100 0 ( 0.58824 0.41176 ) *
##         21) Oldpeak > 2.4 11   6.702 1 ( 0.09091 0.90909 ) *
```

```
##       11) Cholesterol > 245.153 61  63.200 1 ( 0.21311 0.78689 ) *
##    3) stslope_up > 0.5 306 311.200 0 ( 0.79412 0.20588 )
##      6) Oldpeak < 0.45 233 163.000 0 ( 0.88841 0.11159 )
##       12) left_vent_hypertroph < 0.5 196 105.900 0 ( 0.92347 0.07653 )
##         24) atypical_angina < 0.5 112  84.400 0 ( 0.87500 0.12500 )
##           48) non_angina_pain < 0.5 54  57.210 0 ( 0.77778 0.22222 ) *
##           49) non_angina_pain > 0.5 58  17.400 0 ( 0.96552 0.03448 ) *
##         25) atypical_angina > 0.5 84  10.850 0 ( 0.98810 0.01190 ) *
##       13) left_vent_hypertroph > 0.5 37  45.030 0 ( 0.70270 0.29730 )
##         26) non_angina_pain < 0.5 26  35.430 0 ( 0.57692 0.42308 ) *
##         27) non_angina_pain > 0.5 11   0.000 0 ( 1.00000 0.00000 ) *
##      7) Oldpeak > 0.45 73 101.200 1 ( 0.49315 0.50685 )
##       14) male < 0.5 19   7.835 0 ( 0.94737 0.05263 ) *
##       15) male > 0.5 54  68.740 1 ( 0.33333 0.66667 )
##         30) MaxHR < 124.5 13   0.000 1 ( 0.00000 1.00000 ) *
##         31) MaxHR > 124.5 41  56.230 1 ( 0.43902 0.56098 )
##           62) RestingBP < 146.5 31  37.350 1 ( 0.29032 0.70968 ) *
##           63) RestingBP > 146.5 10   6.502 0 ( 0.90000 0.10000 ) *
```

```
tree.pred <- predict(tree.heart, heartTest, type = "class")
table(tree.pred, heartTest$HeartDisease)
```

```
##
## tree.pred   0   1
##         0  78  17
##         1  24 110
```

```
(78+110)/229
```

```
## [1] 0.8209607
```

The single decision tree model was relatively inaccurate, at only 82% accuracy.

```
#Random Forest 84%
rf.heart <- randomForest(as.factor(HeartDisease) ~ ., data = heartTrain, importance = TRUE)
rf.pred <- predict(rf.heart, heartTest, type = "class")
table(rf.pred, heartTest$HeartDisease)
```

```
##
## rf.pred   0   1
##       0  85  11
##       1  17 116
```

```
(86 + 114)/229
```

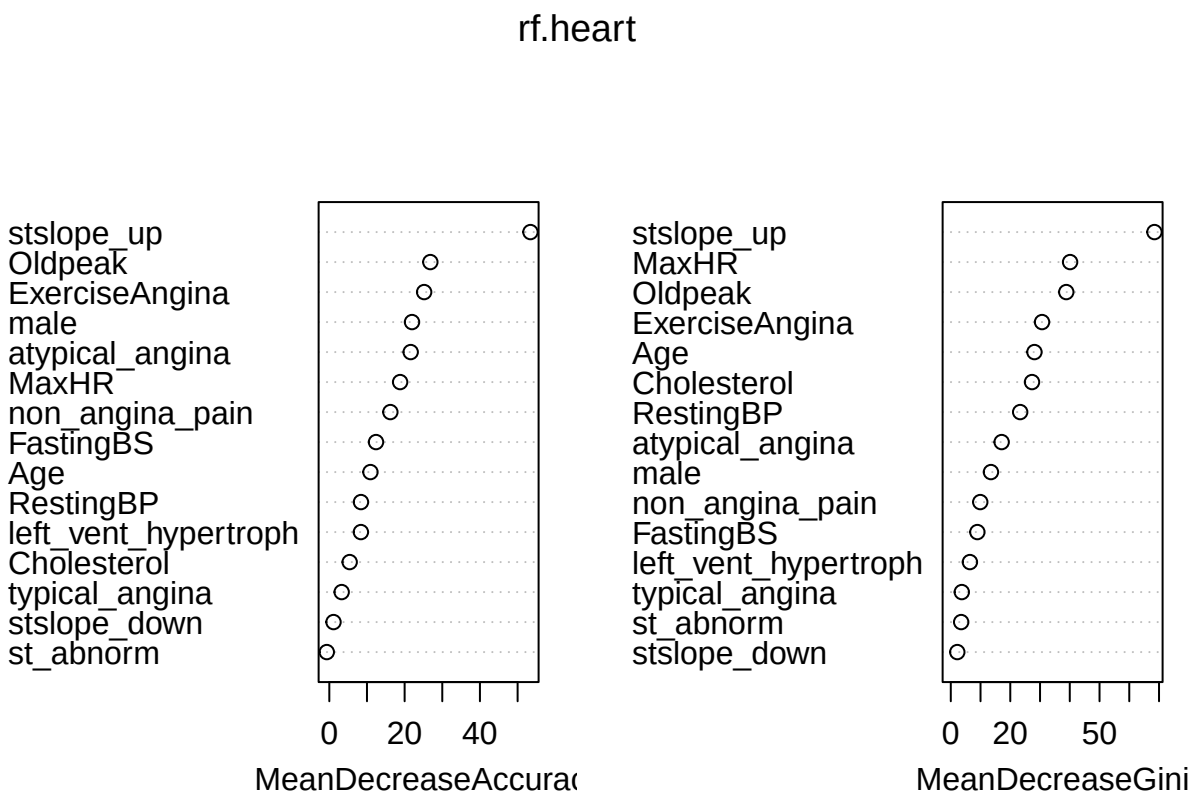
```
## [1] 0.8733624
```

```
importance(rf.heart)
```

```
##                              0          1 MeanDecreaseAccuracy MeanDecreaseGini
## Age                 13.824741  1.2336320           10.9172439        28.118585
## RestingBP            4.839518  7.0998126            8.4058077        23.326737
## Cholesterol          2.986400  4.6324464            5.4056095        27.306245
## FastingBS           10.043454  7.9555532           12.4024993         8.934894
## MaxHR                9.512849 16.8482427           18.8029124        40.103336
## ExerciseAngina      21.358172 15.3484944           25.1797255        30.679202
## Oldpeak             29.769385  5.3210615           26.8222659        38.824826
## typical_angina       3.860771  1.2198604            3.2771607         3.704032
```

```
## atypical_angina      14.997631 15.8600948          21.6066217        17.098950
## non_angina_pain      13.883831  9.3832491          16.2090330         9.907325
## st_abnorm             2.383083 -2.9399912          -0.6736414         3.494780
## left_vent_hypertroph  6.561548  5.8332081           8.3881652         6.432005
## stslope_up           48.107553 33.9892617          53.4126063        68.461485
## stslope_down          2.685078 -0.8650802           1.1154627         2.194090
## male                 14.447781 19.2995568          21.9599960        13.500637
```

```
varImpPlot(rf.heart)
```



But the random forest model pushed the accuracy back up to around 87%. The random forest model also seems to indicate that upward sloping ST region is overwhelmingly indicative of the absence of heart disease, in agreement with the linear model.