Heart diseases features selection and exploratory data analysis

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# Introduction

The objective of this assignment is to prepare a dataset that can be used to predict heart disease, a common and serious health issue that affects a significant portion of the population. The dataset we will be working on is a subset of a larger real-world dataset collected by multiple healthcare institutions. It contains various attributes related to patients’ health, such as age, gender, blood pressure, and other clinical measurements. These attributes can be leveraged to predict the presence of heart disease.

Data mining plays a critical role in addressing challenges related to predicting disease spread and similar healthcare problems. By analyzing large and complex datasets, we can identify patterns and relationships that may not be immediately apparent. This, in turn, allows us to develop more accurate predictive models. In the context of heart disease, data mining techniques can help us extract insights and patterns from patient data. These insights can aid in identifying risk factors, predicting disease outcomes, and developing effective treatment strategies.

For example, by using data mining techniques on the given dataset, we can identify the most important predictors of heart disease. This knowledge can then be used to develop a classification model that accurately predicts the presence of the disease in patients. Moreover, data mining can also help us identify subpopulations that are more susceptible to the disease. We can then develop tailored prevention and treatment strategies for these subpopulations.

Overall, this assignment provides an opportunity to apply data mining techniques to a real-world dataset. It also allows us to gain hands-on experience with feature engineering, data exploration, and predictive modeling. The insights gained from this exploration can inform our work in subsequent assignments. This, in turn, can help us develop more accurate and effective predictive models for heart disease and other similar health challenges.

# Related Work

A recent academic paper titled “Application of Machine Learning Techniques for Heart Disease Prediction: A Systematic Review and Meta-Analysis,” authored by Muhammad Awais et al. (2021) was encountered. The paper aims to address the issue of predicting heart disease using machine learning techniques. The authors conducted a systematic review and meta-analysis of 55 studies to assess the performance of various machine learning algorithms in heart disease prediction. The studies used a range of risk factors such as age, sex, blood pressure, cholesterol level, smoking history, electrocardiogram (ECG) readings, echocardiography, and genetic factors. The predictive models used in the studies varied widely and included decision trees, random forests, support vector machines (SVMs), logistic regression, and artificial neural networks (ANNs). This study provides an overview of the different machine learning techniques used for heart disease prediction and highlights the importance of including novel risk factors in predictive models. It is a valuable resource for cardiovascular medicine research.

The paper “Predicting Heart Disease Using Data Mining Techniques” by Thangaraj et al. (2017) aims to predict the presence or absence of heart disease in patients using data mining techniques. The study uses the Cleveland Heart Disease dataset, which contains 303 instances and 14 features related to patient characteristics and medical history. The authors preprocess the data by handling missing values and normalizing the features, and then apply four different predictive models - decision tree, Naïve Bayes, support vector machine (SVM), and k-nearest neighbor (KNN) - to compare their performance. The study found that SVM had the highest accuracy in predicting heart disease (85.3%), followed by decision tree (81.2%), KNN (78.6%), and Naïve Bayes (70.3%). This study shows that data mining techniques can be effective in predicting heart disease, and provides insights into which models may be most appropriate for this task.

# Data Exploration

## Features Selection

The details of the original dataset are as follows.

| Variable | Description | Type |
| --- | --- | --- |
| id | A unique ID that identifies a participant in the study | Numerical |
| age | Age in years | Numerical |
| sex | Male and Female were recorded | Categorical |
| cp | Chest Pain type: typical angina; atypical angina; non-anginal pain; and asymptomatic | Categorical |
| trestbps | Resting blood pressure (in mm Hg on admission to the hospital) | Numerical |
| chol | Serum Cholestoral in mg/dl | Numerical |
| fbs | Fasting blood sugar > 120 mg/dl (True or False) | Boolean |
| restecg | Resting electrocardiographic results: normal; having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV) or showing probable or definite left ventricular hypertrophy by Estes’ criteria | Categorical |
| thalach | Maximum heart rate achieved | Numerical |
| exang | Exercise induced angina (True/False) | Boolean |
| oldpeak | ST depression induced by exercise relative to rest | Numerical |
| slope | The slope of the peak exercise ST segment: upsloping; flat; downsloping | Categorical |
| major\_vessels | Number of major vessels (0-3) colored by flourosopy | Numerical |
| restwm | Rest wall motion abnormality: none; mild or moderate; moderate or severe; akinesis or dyskmem | Categorical |
| target | Heart disease diagnosed (disease/no disease) | Categorical |

Import the dataset and view.

# load dataset first  
heart.full <- read.csv("heart.csv")  
  
# then check the dataset  
str(heart.full)

## 'data.frame': 1025 obs. of 15 variables:  
## $ id : int 1 2 3 4 5 6 7 8 9 10 ...  
## $ age : int 52 53 70 61 62 58 58 55 46 54 ...  
## $ sex : chr "male" "male" "male" "male" ...  
## $ cp : chr "typical angina" "typical angina" "typical angina" "typical angina" ...  
## $ trestbps : int 125 140 145 148 138 100 114 160 120 122 ...  
## $ chol : int 212 203 174 203 294 248 318 289 249 286 ...  
## $ fbs : logi FALSE TRUE FALSE FALSE TRUE FALSE ...  
## $ restecg : chr "ST-T wave abnormality" "normal" "ST-T wave abnormality" "ST-T wave abnormality" ...  
## $ thalach : int 168 155 125 161 106 122 140 145 144 116 ...  
## $ exang : logi FALSE TRUE TRUE FALSE FALSE FALSE ...  
## $ oldpeak : num 1 3.1 2.6 0 1.9 1 4.4 0.8 0.8 3.2 ...  
## $ slope : chr "downsloping" "upsloping" "upsloping" "downsloping" ...  
## $ major\_vessels: int 2 0 0 1 3 0 3 1 0 2 ...  
## $ restwm : chr "akinesis or dyskmem" "akinesis or dyskmem" "akinesis or dyskmem" "akinesis or dyskmem" ...  
## $ target : chr "no disease" "no disease" "no disease" "no disease" ...

From the output results, it can be found that the dataset contains 15 variables and 1025 observation. The details of each variable are consistent with the description.

Then check the distribution of missing values in the dataset.

sum(is.na(heart.full))

## [1] 0

There are not missing values in this data.

The dataset is undergoing a transformation from its original data types to appropriate data types required for analysis. Originally, the variables age, trestbps, chol, thalach, and oldpeak were imported as character vectors representing age, resting blood pressure, serum cholesterol, maximum heart rate achieved, and ST depression induced by exercise relative to rest, respectively. These variables have been converted to a numeric data type since they represent numerical measurements. Similarly, the variables sex, cp, restecg, slope, restwm, and target were originally imported as character vectors representing sex, chest pain type, resting electrocardiographic results, slope of the peak exercise ST segment, presence of a major vessels colored by fluoroscopy, and heart disease status, respectively. These variables have been converted to factor data type since they represent categorical variables. This transformation allows for easier data manipulation and analysis, especially when exploring relationships between variables.

# convert age, trestbps, chol, thalach, and oldpeak to numeric  
heart.full$age <- as.numeric(heart.full$age)  
heart.full$trestbps <- as.numeric(heart.full$trestbps)  
heart.full$chol <- as.numeric(heart.full$chol)  
heart.full$thalach <- as.numeric(heart.full$thalach)  
heart.full$oldpeak <- as.numeric(heart.full$oldpeak)  
  
  
# convert sex, cp, restecg, slope, restwm, and target to factor  
heart.full$sex <- as.factor(heart.full$sex)  
heart.full$cp <- as.factor(heart.full$cp)  
heart.full$restecg <- as.factor(heart.full$restecg)  
heart.full$slope <- as.factor(heart.full$slope)  
heart.full$restwm <- as.factor(heart.full$restwm)  
heart.full$target <- as.factor(heart.full$target)

Then use random forest to detect the importance of each feature. In order to understand whether these features differ between genders, the data will firstly be created based on the sub-dataset.

# dataset for each gender  
heart.male <- subset(heart.full, sex == "male")  
heart.female <- subset(heart.full, sex == "female")

Then use those two sub datasets to build the random forest.

For male sub-dataset.

# Random forest for male subset  
library(randomForest)

## Warning: package 'randomForest' was built under R version 4.2.2

## randomForest 4.7-1.1

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

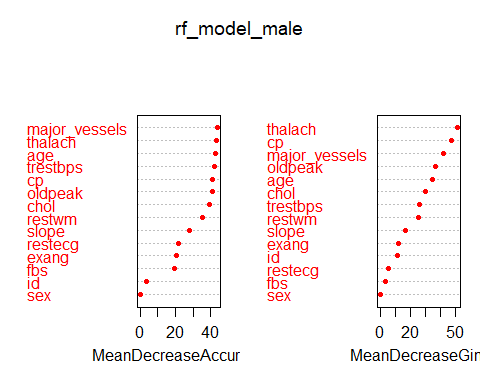
set.seed(123)  
rf\_model\_male <- randomForest(target ~ ., data = heart.male, importance = TRUE, ntree = 500)  
importance(rf\_model\_male)

## disease no disease MeanDecreaseAccuracy MeanDecreaseGini  
## id 1.606825 3.213858 3.376221 11.154653  
## age 33.928469 40.857084 42.838250 34.448119  
## sex 0.000000 0.000000 0.000000 0.000000  
## cp 38.745483 36.059468 41.121602 47.161819  
## trestbps 33.903759 37.024285 41.751265 25.962476  
## chol 34.122660 35.756098 39.121768 29.972875  
## fbs 16.795603 16.203869 19.636756 3.761825  
## restecg 19.083360 19.416802 21.509917 5.531215  
## thalach 37.581333 37.899592 43.252118 51.572260  
## exang 17.532815 19.401905 20.468760 11.933409  
## oldpeak 32.589020 38.902000 40.817055 37.108368  
## slope 24.318522 24.566740 27.686364 17.111266  
## major\_vessels 37.680805 40.115231 43.835239 42.184090  
## restwm 31.201322 32.398437 34.984151 25.367047

According to the provided correlation matrix, the most important features for predicting the presence of heart disease are: cp, thalach, major\_vessels, oldpeak, trestbps, and age. These features have the highest correlation with the target variable (disease/no disease), as well as high values for MeanDecreaseAccuracy and MeanDecreaseGini, indicating that they are crucial predictors for a machine learning model.

To facilitate observation, data can be visualized.

varImpPlot(rf\_model\_male, col = "red", pch = 20)



The feature chest pain type (cp) has high values for both MeanDecreaseAccuracy and MeanDecreaseGini, suggesting that it is a strong predictor for heart disease. Maximum heart rate achieved (thalach) and the number of major vessels colored by fluoroscopy (major\_vessels) also have high correlations and values for MeanDecreaseAccuracy and MeanDecreaseGini, making them strong predictors as well. Though ST depression induced by exercise relative to rest (oldpeak) and resting blood pressure (trestbps) have lower correlations, they still have high values for MeanDecreaseAccuracy and MeanDecreaseGini, indicating their importance in predicting the presence of heart disease. Finally, age is also an important feature as it has a moderate correlation with the target variable and a relatively high value for MeanDecreaseAccuracy.

In conclusion, these six features can be considered the most important for predicting the presence of heart disease in males in this dataset.

For female sub-dataset.

# Random forest for female subset  
set.seed(123)  
rf\_model\_female <- randomForest(target ~ ., data = heart.female, importance = TRUE, ntree = 500)  
importance(rf\_model\_female)

## disease no disease MeanDecreaseAccuracy MeanDecreaseGini  
## id 1.932703 -3.148355 -0.5202009 2.590325  
## age 23.376089 24.724758 28.2364781 12.018921  
## sex 0.000000 0.000000 0.0000000 0.000000  
## cp 19.702221 20.271296 22.9715941 12.537614  
## trestbps 18.409296 18.651176 22.1370717 8.429236  
## chol 19.941082 22.898914 25.6314494 8.321454  
## fbs 7.611649 9.737944 10.2944996 1.418907  
## restecg 14.299858 15.552097 17.3754050 2.982791  
## thalach 19.430050 20.969639 24.2566433 8.272732  
## exang 18.303884 21.574578 22.6248431 9.167964  
## oldpeak 20.677704 21.784792 24.3639560 16.486048  
## slope 17.218824 19.973871 21.5111294 8.150365  
## major\_vessels 19.573486 20.510840 22.7582749 10.407631  
## restwm 22.156482 24.907233 26.5256308 22.290165

According to the provided correlation matrix, the following features are significant in predicting the presence of heart disease in women:

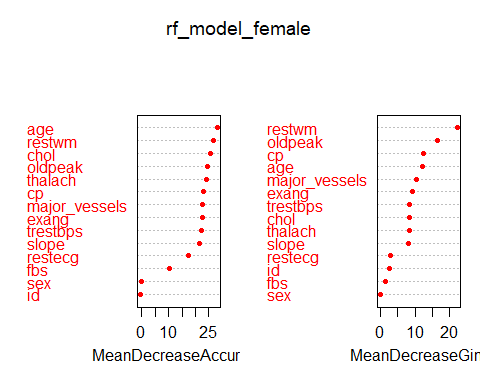
* Age: It exhibits a high correlation with both disease and non-disease and has high values for MeanDecreaseAccuracy and MeanDecreaseGini.
* cp (Chest pain type): It exhibits a moderate correlation with disease and non-disease, and has high values for MeanDecreaseAccuracy and MeanDecreaseGini.
* thalach (Maximum heart rate achieved): It exhibits a moderate correlation with disease and non-disease and has high values for MeanDecreaseAccuracy and MeanDecreaseGini.
* oldpeak (ST depression induced by exercise relative to rest): It exhibits a moderate correlation with disease and non-disease and has a high value for MeanDecreaseAccuracy.
* major\_vessels (Number of major vessels (0-3) colored by flourosopy): It exhibits a moderate correlation with disease and non-disease and has high values for MeanDecreaseAccuracy and MeanDecreaseGini.
* restwm (resting wall motion abnormalities): It exhibits a moderate correlation with disease and non-disease and has high values for MeanDecreaseAccuracy and MeanDecreaseGini.
* exang (exercise-induced angina): It exhibits a moderate correlation with both disease and non-disease and has a high value for MeanDecreaseGini.

On the other hand, “trestbps”, “chol”, “fbs”, and “restecg” display moderate correlations with disease and non-disease but have relatively lower values for MeanDecreaseAccuracy and MeanDecreaseGini. As a result, they are not included in the list of important features.

Overall, these seven features are the most significant in predicting the presence of heart disease in women using this dataset.

To facilitate observation, this is a visualization of the results.

varImpPlot(rf\_model\_female, col = "red", pch = 20)



Therefore, after comprehensive consideration, we have decided to retain the following features: age, cp, thalach, oldpeak, major\_vessels, restwm, exang, and sex.

Now create a new data set with those selected features.

# Create new dataset with selected features and target variable  
heart\_features\_selected <- heart.full[, c("id", "age", "sex", "cp", "thalach", "exang", "oldpeak", "major\_vessels", "restwm", "target")]  
  
# Save new dataset as CSV file  
write.csv(heart\_features\_selected, "heart\_features\_selected.csv", row.names = FALSE)

## Descriptive Statistics

Import the new data set and check the details of that new data set:

heart.selected <- read.csv("heart\_features\_selected.csv")  
  
str(heart.selected)

## 'data.frame': 1025 obs. of 10 variables:  
## $ id : int 1 2 3 4 5 6 7 8 9 10 ...  
## $ age : int 52 53 70 61 62 58 58 55 46 54 ...  
## $ sex : chr "male" "male" "male" "male" ...  
## $ cp : chr "typical angina" "typical angina" "typical angina" "typical angina" ...  
## $ thalach : int 168 155 125 161 106 122 140 145 144 116 ...  
## $ exang : logi FALSE TRUE TRUE FALSE FALSE FALSE ...  
## $ oldpeak : num 1 3.1 2.6 0 1.9 1 4.4 0.8 0.8 3.2 ...  
## $ major\_vessels: int 2 0 0 1 3 0 3 1 0 2 ...  
## $ restwm : chr "akinesis or dyskmem" "akinesis or dyskmem" "akinesis or dyskmem" "akinesis or dyskmem" ...  
## $ target : chr "no disease" "no disease" "no disease" "no disease" ...

Summarize the selected data set.

library(tidyverse)

## Warning: package 'tidyverse' was built under R version 4.2.3

## Warning: package 'ggplot2' was built under R version 4.2.3

## Warning: package 'tibble' was built under R version 4.2.3

## Warning: package 'tidyr' was built under R version 4.2.2

## Warning: package 'readr' was built under R version 4.2.2

## Warning: package 'purrr' was built under R version 4.2.2

## Warning: package 'dplyr' was built under R version 4.2.3

## Warning: package 'stringr' was built under R version 4.2.2

## Warning: package 'forcats' was built under R version 4.2.3

## Warning: package 'lubridate' was built under R version 4.2.3

## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──  
## ✔ dplyr 1.1.1 ✔ readr 2.1.4  
## ✔ forcats 1.0.0 ✔ stringr 1.5.0  
## ✔ ggplot2 3.4.2 ✔ tibble 3.2.1  
## ✔ lubridate 1.9.2 ✔ tidyr 1.3.0  
## ✔ purrr 1.0.1   
## ── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
## ✖ dplyr::combine() masks randomForest::combine()  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ dplyr::lag() masks stats::lag()  
## ✖ ggplot2::margin() masks randomForest::margin()  
## ℹ Use the ]8;;http://conflicted.r-lib.org/conflicted package]8;; to force all conflicts to become errors

heart.selected$id <- as.numeric(heart.selected$id)  
heart.selected$age <- as.numeric(heart.selected$age)  
heart.selected$sex <- as.factor(heart.selected$sex)  
heart.selected$cp <- as.factor(heart.selected$cp)  
heart.selected$thalach <- as.numeric(heart.selected$thalach)  
heart.selected$oldpeak <- as.numeric(heart.selected$oldpeak)  
heart.selected$major\_vessels <- as.numeric(heart.selected$major\_vessels)  
heart.selected$target <- as.factor(heart.selected$target)  
  
  
summary(heart.selected[, -1])

## age sex cp thalach   
## Min. :29.00 female:312 asymptomatic : 77 Min. : 71.0   
## 1st Qu.:48.00 male :713 atypical angina :167 1st Qu.:132.0   
## Median :56.00 non-anginal pain:284 Median :152.0   
## Mean :54.43 typical angina :497 Mean :149.1   
## 3rd Qu.:61.00 3rd Qu.:166.0   
## Max. :77.00 Max. :202.0   
## exang oldpeak major\_vessels restwm   
## Mode :logical Min. :0.000 Min. :0.0000 Length:1025   
## FALSE:680 1st Qu.:0.000 1st Qu.:0.0000 Class :character   
## TRUE :345 Median :0.800 Median :0.0000 Mode :character   
## Mean :1.072 Mean :0.7541   
## 3rd Qu.:1.800 3rd Qu.:1.0000   
## Max. :6.200 Max. :4.0000   
## target   
## disease :526   
## no disease:499   
##   
##   
##   
##

This result shows the statistical summary of a dataset related to heart disease. The dataset consists of 1025 observations and several variables, including age, sex, chest pain type, maximum heart rate, exercise-induced angina, ST depression induced by exercise relative to rest, number of major vessels colored by fluoroscopy, and the presence or absence of heart disease.

The average age of the patients in the dataset is 54.43 years, with a minimum age of 29 years and a maximum age of 77 years. Out of the 1025 patients, 312 are female and 713 are male. Chest pain type is categorized into four types, namely asymptomatic, atypical angina, non-anginal pain, and typical angina. The most frequent type is typical angina, with 497 occurrences. The maximum heart rate (thalach) ranges from 71 to 202 beats per minute, with a mean of 149.1 beats per minute. Exercise-induced angina (exang) is a binary variable, with 345 patients experiencing it during exercise and 680 patients not experiencing it. ST depression induced by exercise relative to rest (oldpeak) ranges from 0 to 6.2, with an average value of 1.072. The number of major vessels colored by fluoroscopy (major\_vessels) ranges from 0 to 4, with a mean of 0.7541. The dataset is labeled with the presence or absence of heart disease (target). Out of the 1025 patients, 526 have heart disease and 499 do not have heart disease.

After examining the results, it is clear that there is room for further analysis. For example, while the report provides some information about the results, it does not provide a complete picture. In order to gain a deeper understanding, it would be helpful to explore additional metrics such as standard deviation, skewness, and kurtosis. This would allow us to better understand the distribution of the data and identify any outliers or patterns that may be present. By conducting a more thorough analysis, we can gain a more comprehensive understanding of the data and make more informed decisions based on the results.

library(psych)

## Warning: package 'psych' was built under R version 4.2.3

##   
## Attaching package: 'psych'

## The following objects are masked from 'package:ggplot2':  
##   
## %+%, alpha

## The following object is masked from 'package:randomForest':  
##   
## outlier

describe(heart.selected[, -1])

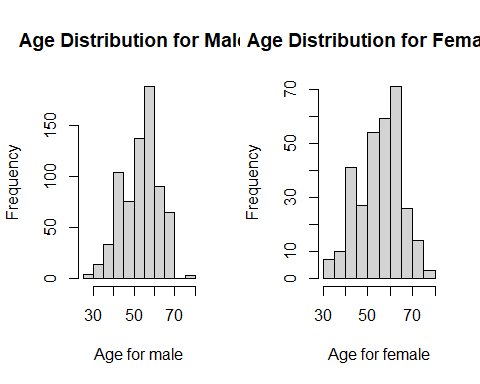
## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf

## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf

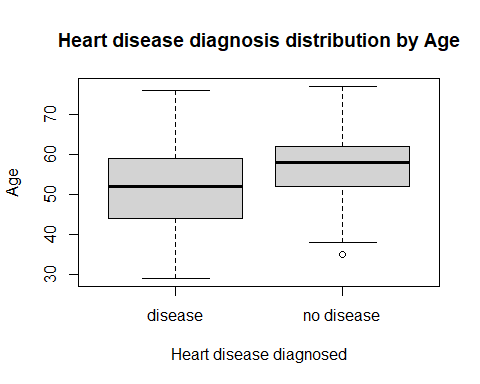
## vars n mean sd median trimmed mad min max range skew  
## age 1 1025 54.43 9.07 56.0 54.66 8.90 29 77.0 48.0 -0.25  
## sex\* 2 1025 1.70 0.46 2.0 1.74 0.00 1 2.0 1.0 -0.85  
## cp\* 3 1025 3.17 0.96 3.0 3.31 1.48 1 4.0 3.0 -0.86  
## thalach 4 1025 149.11 23.01 152.0 150.40 23.72 71 202.0 131.0 -0.51  
## exang 5 1025 NaN NA NA NaN NA Inf -Inf -Inf NA  
## oldpeak 6 1025 1.07 1.18 0.8 0.89 1.19 0 6.2 6.2 1.21  
## major\_vessels 7 1025 0.75 1.03 0.0 0.57 0.00 0 4.0 4.0 1.26  
## restwm\* 8 1025 2.14 0.97 3.0 2.17 0.00 1 4.0 3.0 -0.25  
## target\* 9 1025 1.49 0.50 1.0 1.48 0.00 1 2.0 1.0 0.05  
## kurtosis se  
## age -0.53 0.28  
## sex\* -1.28 0.01  
## cp\* -0.39 0.03  
## thalach -0.10 0.72  
## exang NA NA  
## oldpeak 1.29 0.04  
## major\_vessels 0.68 0.03  
## restwm\* -1.81 0.03  
## target\* -2.00 0.02

This study provides a summary of the results obtained from a sample of subjects with different variables related to heart disease. The subjects had an average age of 54.43 years, with a standard deviation of 9.07. The majority of subjects were male, with an average value of 1.70 and a standard deviation of 0.46. The average level of chest pain experienced by the subjects was 3.17, with a standard deviation of 0.96. The average maximum heart rate achieved by the subjects was 149.11 bpm, with a standard deviation of 23.01 bpm. The average ST depression induced by exercise was 1.07 mm, with a standard deviation of 1.18 mm. The average number of major vessels colored by fluoroscopy was 0.75, with a standard deviation of 1.03. The average resting wall motion score index was 2.14, with a standard deviation of 0.97. The majority of subjects did not have heart disease, with a mean value of 1.49 and a standard deviation of 0.50. These findings provide important insights into the characteristics of the sample and may inform future research on heart disease.

par(mfrow=c(1,2)) # To plot the histograms side by side  
hist(heart.selected$age[heart.selected$sex == "male"], main = "Age Distribution for Males", xlab = "Age for male")  
hist(heart.selected$age[heart.selected$sex == "female"], main = "Age Distribution for Females", xlab = "Age for female")

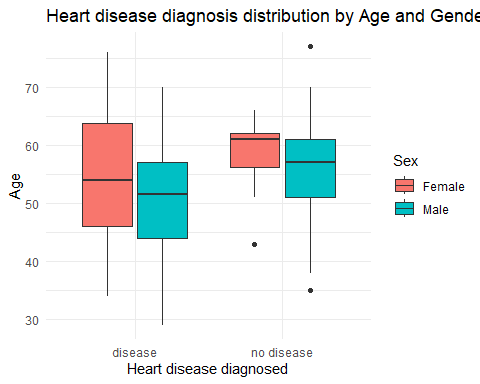
 In terms of male age, the distribution is generally symmetric, or slightly left-skewed. When compared to the male age distribution, the female age distribution is more left-skewed. Additionally, it’s worth noting that there are more females over the age of 70 than males.

boxplot(heart.selected$age ~ heart.selected$target,  
 main="Heart disease diagnosis distribution by Age",  
 ylab="Age",xlab="Heart disease diagnosed")



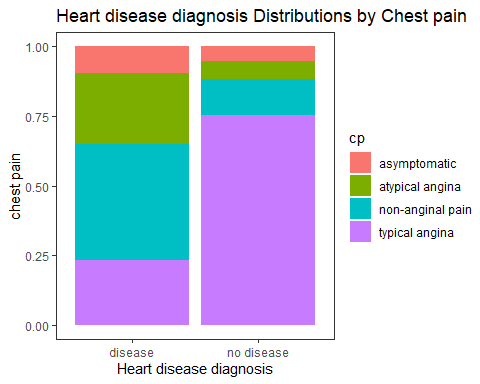
According to our findings, the median age of individuals without disease is higher than that of those with disease. Moreover, the range in age is relatively smaller for those without disease. Though there is an outlier among the no disease group, it is not considered an extreme outlier and therefore can be retained rather than removed.

ggplot(heart.selected, aes(x = target, y = age, fill = sex)) +  
 geom\_boxplot() +  
 labs(title = "Heart disease diagnosis distribution by Age and Gender",  
 x = "Heart disease diagnosed",  
 y = "Age") +  
 scale\_fill\_discrete(name = "Sex",  
 labels = c("Female", "Male")) +  
 theme\_minimal()



Females have higher median ages than males, regardless of disease status. Additionally, it’s worth noting that individuals without disease have a higher average age than those with disease. This may be due to the fact that individuals with heart disease tend to have shorter lifespans.

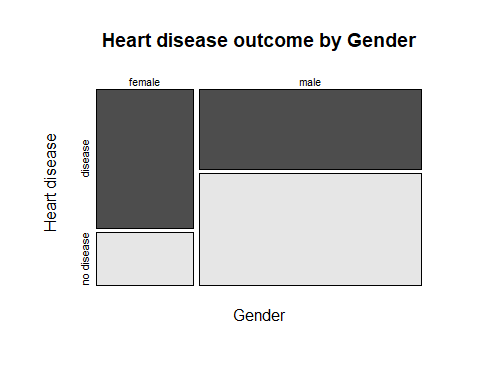
ggplot(data = heart.selected, aes(x = target, fill = cp)) +   
 geom\_bar(position = "fill") +  
 labs(title = "Heart disease diagnosis Distributions by Chest pain",  
 x = "Heart disease diagnosis",  
 y = "chest pain") +  
 theme\_test()



There are four possible outcomes for chest pain (CP), with varying proportions between individuals with and without the disease. For individuals with the disease, non-anginal pain has the highest proportion, followed by atypical angina, while asymptomatic has the lowest proportion. Conversely, for individuals without the disease, typical angina has the highest proportion, which is significantly higher than the proportion in those with the disease, while the other three types have smaller proportions.

This finding is intriguing because individuals with typical angina should logically have a higher likelihood of having the disease. Therefore, further exploration is necessary in subsequent research to fully understand this relationship.

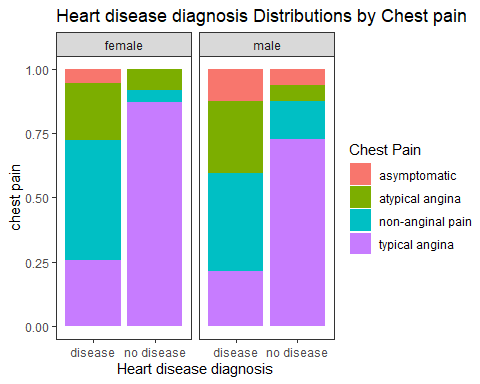
mosaicplot(heart.selected$sex ~ heart.selected$target,  
 main="Heart disease outcome by Gender", shade=FALSE,color=TRUE,  
 xlab="Gender", ylab="Heart disease")



Based on the figure above, it is evident that the proportion of disease is higher among females, while it is relatively low among males. Hence, it can be inferred that the probability of an observed individual being classified as having the disease is higher if they are female.

The relationship between CP and disease was examined in different genders.

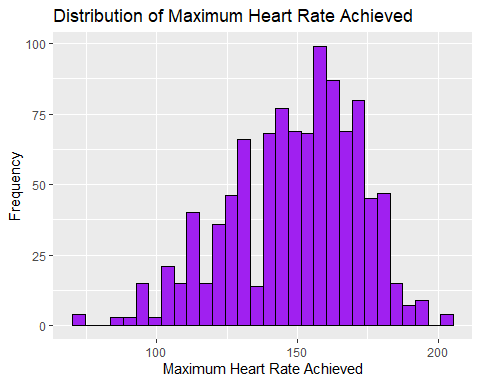
# Create barplot by chest pain and gender  
ggplot(heart.selected, aes(x = target, fill = cp)) +  
 geom\_bar(position = "fill") +  
 facet\_wrap(~sex) +  
 labs(title = "Heart disease diagnosis Distributions by Chest pain",  
 x = "Heart disease diagnosis",  
 y = "chest pain") +  
 scale\_fill\_discrete(name = "Chest Pain") +  
 theme\_test()



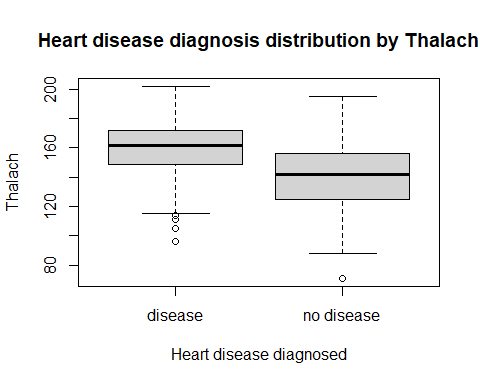
The figure above shows the situation of four types of chest pain under different genders, which is basically consistent with the overall results. Therefore, we can conclude that during classification, regardless of gender, if the observed individual has typical angina, they are more likely to be classified as having no disease.

The next step involves exploring the Thalach variable visually.

# Exploratory data analysis of thalach  
ggplot(data = heart.selected, aes(x = thalach)) +  
 geom\_histogram(bins = 30, fill = "purple", color = "black") +  
 labs(title = "Distribution of Maximum Heart Rate Achieved",  
 x = "Maximum Heart Rate Achieved", y = "Frequency")

 According to the results, the distribution of Thalach exhibits a slightly skewed left distribution, indicating the possible presence of an outlier on the left side. However, further analysis is required to confirm this observation.

boxplot(heart.selected$thalach ~ heart.selected$target,  
 main="Heart disease diagnosis distribution by Thalach",  
 ylab="Thalach",xlab="Heart disease diagnosed")

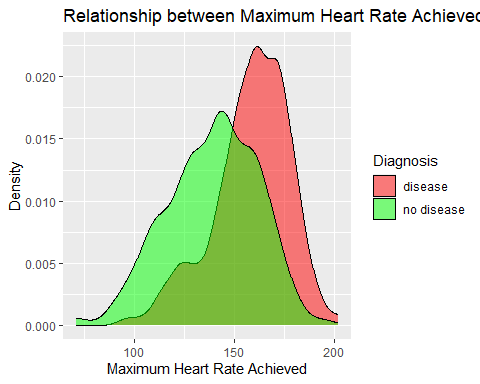


Based on the figure above, it is evident that the proportion of disease is higher among females, while it is relatively low among males. Therefore, it can be inferred that the probability of an observed individual being classified as having the disease is higher if they are female.

Moreover, the distribution of thalach for disease appears to be higher overall than that of no disease, which aligns with common knowledge. Additionally, there are more outliers for thalach in disease. Thus, it can be assumed that, in the case of an individual having a relatively high value of thalach, the probability of them having the disease is higher, making it easier for them to be classified into the disease category during classification.

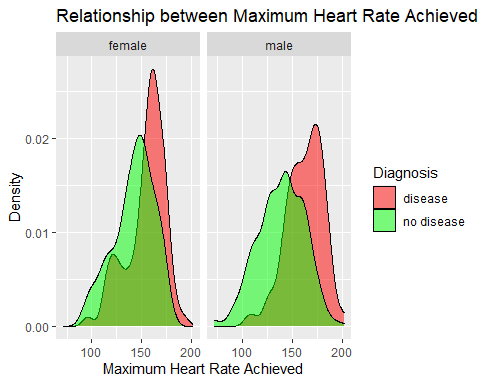
The density diagram below illustrates the distribution of maximum heart rate achieved for individuals with and without heart disease.

# Relationship between thalach and target  
ggplot(data = heart.selected, aes(x = thalach, fill = target)) +  
 geom\_density(alpha = 0.5) +  
 labs(title = "Relationship between Maximum Heart Rate Achieved and Heart Disease Diagnosis",  
 x = "Maximum Heart Rate Achieved", y = "Density", fill = "Diagnosis") +  
 scale\_fill\_manual(values = c("red", "green"))



The density diagram reveals that, under the condition of having the disease, the maximum heart rate achieved has higher values and proportion, which is significantly higher than that of the condition of no disease. It is suggested that individuals with a higher maximum heart rate achieved value are more likely to be classified as having the disease during classification.

# Relationship between thalach and target divided into gender  
ggplot(data = heart.selected, aes(x = thalach, fill = target)) +  
 geom\_density(alpha = 0.5) +  
 labs(title = "Relationship between Maximum Heart Rate Achieved and Heart Disease Diagnosis by Gender",  
 x = "Maximum Heart Rate Achieved", y = "Density", fill = "Diagnosis") +  
 scale\_fill\_manual(values = c("red", "green")) +  
 facet\_wrap(~ sex)



Regardless of gender, the density of maximum heart rate achieved is very similar to the overall situation. However, among females with disease, the proportion of higher maximum heart rate achieved values is very significant.

Overall, no single variable can make highly accurate predictions, so combining all variables is necessary for classification.

## Correlation Between Variables

To examine the relationship between variables, you can use the cor function to perform calculations and display the results with a corplot.

# calculate the correlation matrix  
library(corrplot)

## Warning: package 'corrplot' was built under R version 4.2.3

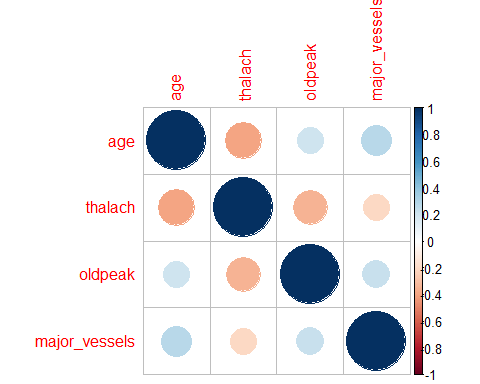
## corrplot 0.92 loaded

heart.selected$age <- as.numeric(heart.selected$age)  
heart.selected$thalach <- as.numeric(heart.selected$thalach)  
heart.selected$oldpeak <- as.numeric(heart.selected$oldpeak)  
heart.selected$major\_vessels <- as.numeric(heart.selected$major\_vessels)  
  
  
cor.matrix <- cor(heart.selected[, c("age", "thalach", "oldpeak", "major\_vessels")])  
cor.matrix

## age thalach oldpeak major\_vessels  
## age 1.0000000 -0.3902271 0.2081367 0.2715505  
## thalach -0.3902271 1.0000000 -0.3497962 -0.2078884  
## oldpeak 0.2081367 -0.3497962 1.0000000 0.2218160  
## major\_vessels 0.2715505 -0.2078884 0.2218160 1.0000000

Age has a positive correlation with major\_vessels (0.2715) and a weak positive correlation with oldpeak (0.2081). Thalach has a negative correlation with oldpeak (-0.3498). Finally, oldpeak and major\_vessels have a moderate positive correlation (0.2218).

corrplot(cor.matrix)



From the figure, it appears that thalach is negatively correlated with both age and oldpeak. In terms of positive correlation, major\_vessels and age appear to be positively correlated.

# References