Project_Final

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2024-04-25

#https://www.kaggle.com/datasets/johnsmith88/heart-disease-dataset/data

#About Dataset

#Context This data set dates from 1988 and consists of four databases: Cleveland, Hungary, Switzerland, and Long Beach V. It contains 76 attributes, including the predicted attribute, but all published experiments refer to using a subset of 14 of them. The "target" field refers to the presence of heart disease in the patient. It is integer valued 0 = no disease and 1 = disease.

#Content Attribute Information:

library (PerformanceAnalytics)

Loading required package: xts

age sex chest pain type (4 values) resting blood pressure serum cholestoral in mg/dl fasting blood sugar > 120 mg/dl resting electrocardiographic results (values 0,1,2) maximum heart rate achieved exercise induced angina oldpeak = ST depression induced by exercise relative to rest the slope of the peak exercise ST segment number of major vessels (0-3) colored by flourosopy thal: 0 = normal; 1 = fixed defect; 2 = reversable defect The names and social security numbers of the patients were recently removed from the database, replaced with dummy values.

```
library(tidyverse)
## Warning: package 'ggplot2' was built under R version 4.3.3
## — Attaching core tidyverse packages —
                                                                    — tidyverse 2.0.0 —
    dplyr 1.1.4 readr 2.1.5
    forcats 1.0.0 stringr 1.5.1
##
    ggplot2 3.5.1 tibble 3.2.1
    lubridate 1.9.3 tidyr 1.3.1
##
    purrr 1.0.2
##
## — Conflicts —
                                                                     — tidyverse conflicts() —
    dplyr::filter() masks stats::filter()
##
    dplyr::lag() masks stats::lag()
## i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become errors
library(readr)
library (ROCR)
## Warning: package 'ROCR' was built under R version 4.3.3
```

Warning: package 'PerformanceAnalytics' was built under R version 4.3.3

```
## Loading required package: zoo
##
## Attaching package: 'zoo'
## The following objects are masked from 'package:base':
##
##
    as.Date, as.Date.numeric
##
##
## # The dplyr lag() function breaks how base R's lag() function is supposed to
## # work, which breaks lag(my xts). Calls to lag(my xts) that you type or
## # source() into this session won't work correctly.
## #
## # Use stats::lag() to make sure you're not using dplyr::lag(), or you can add #
## # conflictRules('dplyr', exclude = 'lag') to your .Rprofile to stop
## # dplyr from breaking base R's lag() function.
## #
## # Code in packages is not affected. It's protected by R's namespace mechanism #
## # Set `options(xts.warn dplyr breaks lag = FALSE)` to suppress this warning.
##
## Attaching package: 'xts'
## The following objects are masked from 'package:dplyr':
     first, last
##
##
##
## Attaching package: 'PerformanceAnalytics'
## The following object is masked from 'package:graphics':
##
##
      legend
```

library (e1071)

```
## Warning: package 'e1071' was built under R version 4.3.3
```

```
##
## Attaching package: 'e1071'
##
## The following objects are masked from 'package:PerformanceAnalytics':
##
## kurtosis, skewness
```

```
library(caret)
```

```
## Warning: package 'caret' was built under R version 4.3.3
## Loading required package: lattice
## Attaching package: 'caret'
## The following object is masked from 'package:purrr':
##
       lift
##
library(gbm)
## Warning: package 'gbm' was built under R version 4.3.3
## Loaded gbm 2.1.9
## This version of gbm is no longer under development. Consider transitioning to gbm3, https:/
/github.com/gbm-developers/gbm3
library(corrplot)
## corrplot 0.92 loaded
library (ggcorrplot)
## Warning: package 'ggcorrplot' was built under R version 4.3.3
library (MASS)
## Warning: package 'MASS' was built under R version 4.3.3
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##
       select
library(rpart)
library(caTools)
## Warning: package 'caTools' was built under R version 4.3.3
library (naivebayes)
```

```
## Warning: package 'naivebayes' was built under R version 4.3.3
## naivebayes 1.0.0 loaded
## For more information please visit:
## https://majkamichal.github.io/naivebayes/
library(class)
library(ISLR)
## Warning: package 'ISLR' was built under R version 4.3.3
library(glmnet)
## Warning: package 'glmnet' was built under R version 4.3.3
## Loading required package: Matrix
## Attaching package: 'Matrix'
## The following objects are masked from 'package:tidyr':
##
##
       expand, pack, unpack
##
## Loaded glmnet 4.1-8
library(Hmisc)
## Attaching package: 'Hmisc'
## The following object is masked from 'package:e1071':
##
##
       impute
##
## The following objects are masked from 'package:dplyr':
##
       src, summarize
##
##
## The following objects are masked from 'package:base':
##
##
       format.pval, units
library(funModeling)
## Warning: package 'funModeling' was built under R version 4.3.3
```

```
## funModeling v.1.9.5 :)
## Examples and tutorials at livebook.datascienceheroes.com
## / Now in Spanish: librovivodecienciadedatos.ai
```

```
library (pROC)
```

```
## Type 'citation("pROC")' for a citation.
##
## Attaching package: 'pROC'
##
## The following objects are masked from 'package:stats':
##
```

Warning: package 'pROC' was built under R version 4.3.3

library(randomForest)

cov, smooth, var

```
## Warning: package 'randomForest' was built under R version 4.3.3
```

```
## randomForest 4.7-1.1
## Type rfNews() to see new features/changes/bug fixes.
##
## Attaching package: 'randomForest'
##
## The following object is masked from 'package:dplyr':
##
## combine
##
## The following object is masked from 'package:ggplot2':
##
## margin
```

library(klaR)

```
## Warning: package 'klaR' was built under R version 4.3.3
```

library(scales)

```
##
## Attaching package: 'scales'
##
## The following object is masked from 'package:purrr':
##
## discard
##
## The following object is masked from 'package:readr':
```

```
##
       col factor
library(cluster)
## Warning: package 'cluster' was built under R version 4.3.3
library(factoextra)
## Warning: package 'factoextra' was built under R version 4.3.3
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
library(DataExplorer)
## Warning: package 'DataExplorer' was built under R version 4.3.3
library (ClustOfVar)
## Warning: package 'ClustOfVar' was built under R version 4.3.3
library (GGally)
## Registered S3 method overwritten by 'GGally':
##
   method from
##
   +.gg ggplot2
## Attaching package: 'GGally'
##
## The following object is masked from 'package:funModeling':
##
##
     range01
library(dplyr)
library(visdat)
## Warning: package 'visdat' was built under R version 4.3.3
library(naniar)
## Warning: package 'naniar' was built under R version 4.3.3
library(mice)
```

```
## Warning: package 'mice' was built under R version 4.3.3
 ##
 ## Attaching package: 'mice'
 ## The following object is masked from 'package:stats':
 ##
        filter
 ##
 ##
 ## The following objects are masked from 'package:base':
 ##
        cbind, rbind
 library (VIM)
 ## Warning: package 'VIM' was built under R version 4.3.3
 ## Loading required package: colorspace
 ## Attaching package: 'colorspace'
 ##
 ## The following object is masked from 'package:pROC':
 ##
 ##
        coords
 ##
 ## Loading required package: grid
 ## VIM is ready to use.
 ##
 ## Suggestions and bug-reports can be submitted at: https://github.com/statistikat/VIM/issues
 ##
 ## Attaching package: 'VIM'
 ##
 ## The following object is masked from 'package:datasets':
 ##
 ##
        sleep
(EDA) Exploratory Data Analysis:
 file path <- "D:/Multivariate Analysis/Final Project/heart.csv"</pre>
 data <- read.csv(file path)</pre>
 head (data)
      age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal
 ## 1 52
           1
               0
                      125 212
                                  0
                                          1
                                                168
                                                         0
                                                               1.0
 ## 2 53
          1 0
                      140 203
                                1
                                          0
                                                155
                                                               3.1
                                                         1
```

0

0

1

1

1

1

125

161

106

1

0

0

2.6

0.0

1.9

0 0

2 1

1 3

3

3

2

145 174

148 203

138 294

1 0

1 0

0 0

3 70

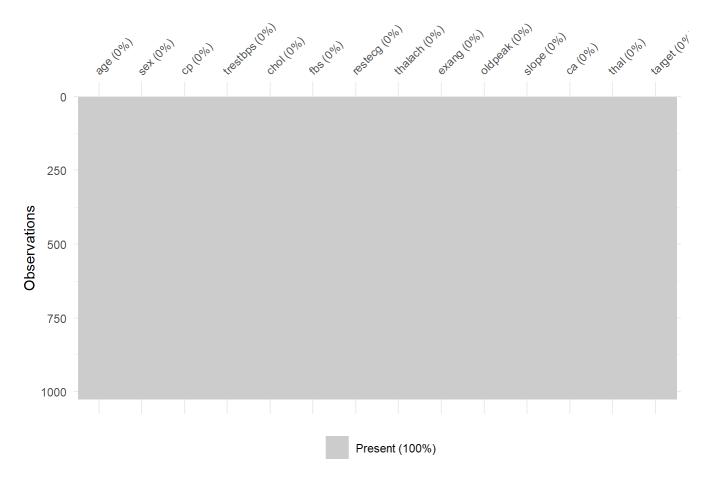
4 61

5 62

```
## 6 58
                    100 248
                                       0
                                               122
                                                      0
                                                              1.0
##
     target
## 1
## 2
          0
          0
## 4
          0
## 5
          0
## 6
          1
```

#Missing Values

```
#plot_missing(data)
vis_miss(data)
```



#Transformation

```
thal = as.factor(thal),
    target = if_else(target == 1, "YES", "NO")
    ) %>%
mutate_if(is.character, as.factor) %>%
dplyr::select(target, sex, fbs, exang, cp, restecg, slope, ca, thal, everything())
```

This code modifies the dataset data by recoding certain variables and converting them into factors or changing their labels. Here's what each line does: The changes made are: - Recoding binary variables into descriptive categories (e.g., sex, fbs, exang). - Recoding categorical variables into more readable labels (e.g., sp, resterg). - Converting certain variables into factors (e.g., stope, ca, that). - Converting the target variable into "YES" or "NO". - Converting all character variables into factors. - Rearranging columns so that target, sex, fbs, exang, cp, resterg, stope, ca, that, and other variables are selected in that order.

#Summary Statistics

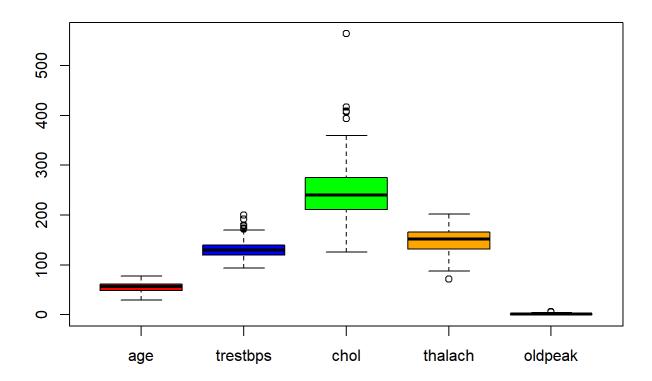
```
summary(data2)
```

```
fbs exang
##
  target
              sex
                                                     Ср
## NO:499 FEMALE:312
                     <=120:872 NO :680 ASYMPTOMATIC :574
  YES:526 MALE :713 >120 :153 YES:345 ATYPICAL ANGINA :167
##
##
                                        NON-ANGINAL PAIN:284
##
##
##
##
                restecg slope ca thal
                                                 age
                         0: 74 0:578 0: 7 Min. :29.00
##
  ABNORMALITY
                   :513
##
  NORMAL
                   :497 1:482 1:226 1: 64 1st Qu.:48.00
  PROBABLE OR DEFINITE: 15
                         2:469 2:134 2:544 Median :56.00
##
                                3: 69 3:410 Mean :54.43
##
##
                                4: 18
                                             3rd Qu.:61.00
##
                                             Max. :77.00
##
    trestbps
                   chol
                            thalach
                                           oldpeak
  Min. : 94.0 Min. :126
                            Min. : 71.0 Min. :0.000
##
  1st Qu.:120.0 1st Qu.:211 1st Qu.:132.0 1st Qu.:0.000
## Median:130.0 Median:240 Median:152.0 Median:0.800
## Mean :131.6 Mean :246 Mean :149.1 Mean :1.072
  3rd Qu.:140.0 3rd Qu.:275 3rd Qu.:166.0 3rd Qu.:1.800
##
## Max. :200.0 Max. :564 Max. :202.0 Max. :6.200
```

#Boxplot

```
# Define colors for boxplots
colors <- c("red", "blue", "green", "orange", "purple")

# Plot boxplots with different colors
boxplot(data2[, 10:14], col = colors)</pre>
```



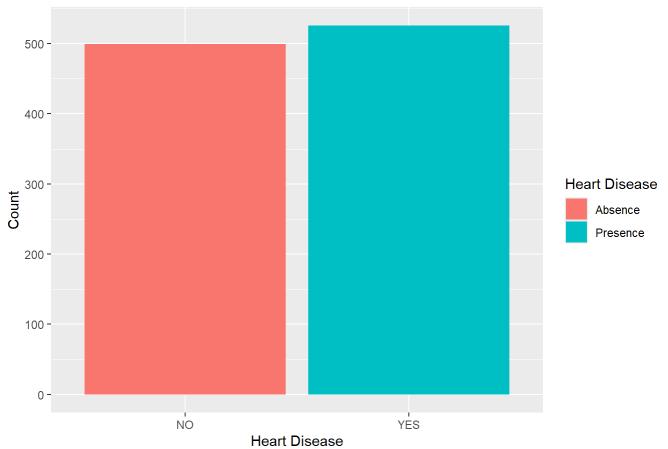
#Data Visualization

Bar plot for target (Heart disease)

```
ggplot(data2, aes(x=data2$target, fill=data2$target)) +
  geom_bar() +
  xlab("Heart Disease") +
  ylab("Count") +
  ggtitle("Analysis of Presence and Absence of Heart Disease") +
  scale_fill_discrete(name = "Heart Disease", labels = c("Absence", "Presence"))
```

```
## Warning: Use of `data2$target` is discouraged.
## i Use `target` instead.
## Use of `data2$target` is discouraged.
## i Use `target` instead.
```

Analysis of Presence and Absence of Heart Disease

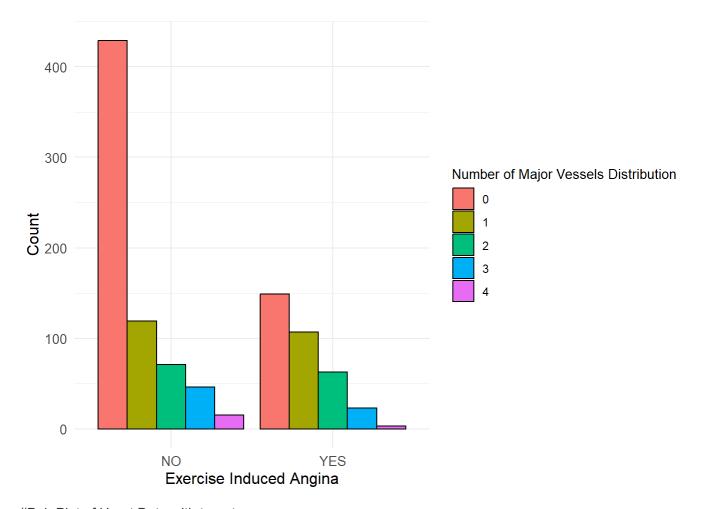


```
prop.table(table(data2$target))
```

```
##
## NO YES
## 0.4868293 0.5131707
```

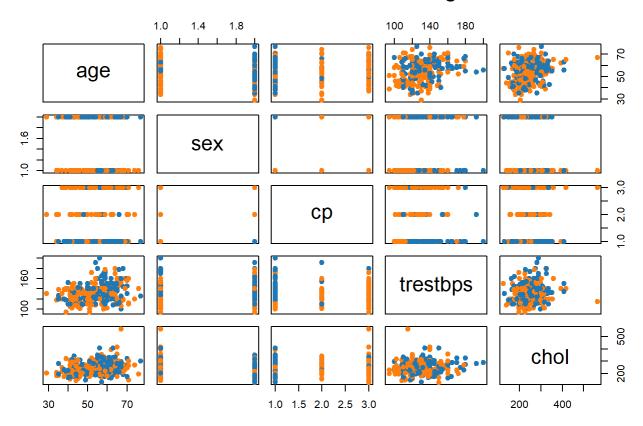
Bar chart of Number of Major Vessels Distribution based on Exercise Induced Angina

```
library(ggplot2)
ggplot(data2, aes(x = exang, fill = ca)) +
    geom_bar(position = "dodge", color = "black") +
    labs(x = "Exercise Induced Angina", y = "Count", fill = "Number of Major Vessels Distributio
n") +
    theme_minimal() +
    theme(legend.position = "right",
        axis.text = element_text(size = 10),
        axis.title = element_text(size = 12),
        legend.title = element_text(size = 10))
```



#Pair Plot of Heart Data with target

Pair Plot of Heart Data with target



This pair plot visualizes the pairwise relationships between five variables (age, sex, cp, trestbps, and chol) from a heart disease dataset, along with the target variable indicating the presence or absence of heart disease.

Age: The scatter plots involving age show a clear separation between the orange (healthy) and blue (unhealthy) points, with unhealthy individuals tending to be older. The density plot for age also exhibits a bimodal distribution, suggesting two distinct age groups in the data.

Sex: The scatter plots with sex, which is a binary variable (0 for female, 1 for male), show a higher concentration of unhealthy (blue) points for males compared to females, indicating a potential relationship between gender and heart disease risk.

Cp (chest pain type): The scatter plots with cp suggest a possible correlation between certain types of chest pain and the target variable, as indicated by the clustering of colors.

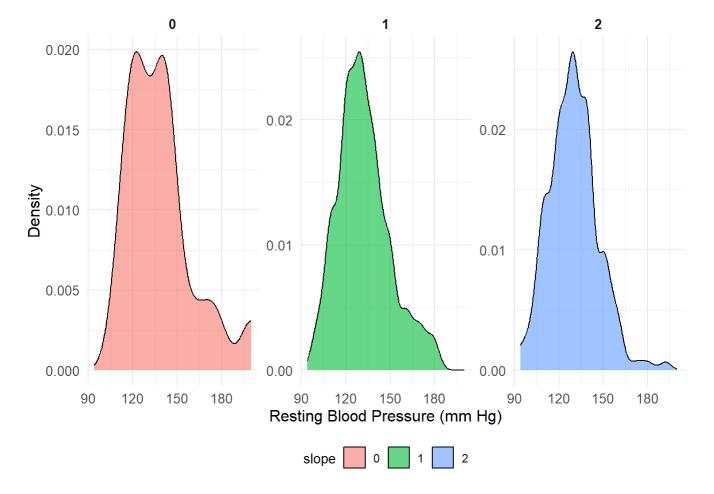
Trestbps (resting blood pressure): The scatter plots involving trestbps show a tendency for higher blood pressure values to be associated with the unhealthy (blue) points, implying a potential link between elevated blood pressure and heart disease risk.

Chol (cholesterol level): The scatter plots and density plot for chol exhibit a clear separation between healthy and unhealthy individuals, with higher cholesterol levels being more prevalent among the unhealthy (blue) points.

Density plot of resting blood pressure based on slope

library(ggplot2)

```
# Density plot of resting blood pressure based on slope
ggplot(data2, aes(x = trestbps, fill = slope)) +
    geom_density(alpha = 0.6, color = "black") +
    labs(x = "Resting Blood Pressure (mm Hg)", y = "Density") +
    facet_wrap(~ slope, scales = "free_y") +
    theme_minimal() +
    theme(legend.position = "bottom",
        axis.text = element_text(size = 10),
        axis.title = element_text(size = 12),
        legend.title = element_text(size = 10),
        strip.text = element_text(size = 10, face = "bold"))
```



Here are some observations about the individual plots:

The red plot (Category 0) shows a peak slightly lower than 120 mm Hg.

The green plot (Category 1) has its peak around 130 mm Hg and appears to have a broader spread than the red plot.

The blue plot (Category 2) has a peak just below 140 mm Hg and the narrowest spread of the three, indicating that the resting blood pressure for this group is more concentrated around the mean.

Counting the frequency of the values of the age

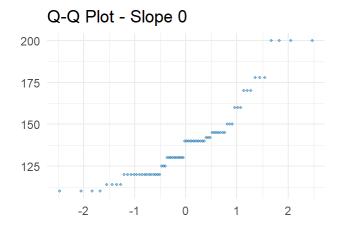
```
library(ggplot2)
library(gridExtra)
```

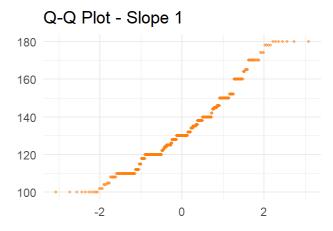
```
##
## Attaching package: 'gridExtra'
```

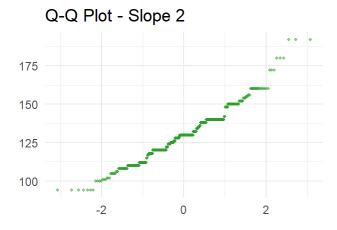
```
## The following object is masked from 'package:randomForest':
##
## combine
```

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

```
# Subset the data and convert 'slope' to character
df eda5 <- data2[, c('slope', 'trestbps')]</pre>
df eda5$slope <- as.character(df eda5$slope)</pre>
# Unique slope values and color palette
slope list <- sort(unique(df eda5$slope))</pre>
color palette <- c("#1f77b4", "#ff7f0e", "#2ca02c")</pre>
# Main KDE Plot
main plot \leftarrow ggplot(df eda5, aes(x = trestbps, fill = slope)) +
 geom_density(alpha = 0.4, bw = 0.4) +
 scale fill manual(values = color palette) +
 theme minimal() +
 labs(x = "\nResting Blood Pressure (in mm Hg)", y = "Density\n") +
  theme(legend.position = "none")
# Sub Q-Q Plot
sub plots <- lapply(seq along(slope list), function(i) {</pre>
  slope <- slope list[i]</pre>
 df slope <- df eda5[df eda5$slope == slope, ]</pre>
 qq plot <- ggplot(df slope, aes(sample = trestbps)) +
    stat qq(color = color palette[i], size = 0.8, alpha = 0.5) +
   geom abline(slope = 1, intercept = 0, linetype = "dashed", color = "black") +
    theme minimal() +
   labs(title = paste("Q-Q Plot - Slope", slope), x = "", y = "") +
    theme(legend.position = "none")
 return(qq plot)
})
# Combine plots
grid.arrange(main plot, grobs = sub plots, nrow = 2, align = "v")
```







```
# Note: Adjust plot settings (e.g., font sizes, titles, labels) as needed for your specific vi sualization.
```

Q-Q Plot - Slope 0: The blue dots represent the quantiles of the dataset for the category "Slope 0." The points do not align with a straight line, suggesting that the data for this category may not be normally distributed.

Q-Q Plot - Slope 1: The orange dots for "Slope 1" show a clearer trend of the points lining up along an approximately straight diagonal line. This indicates that the data for "Slope 1" is closer to a normal distribution compared to "Slope 0."

Q-Q Plot - Slope 2: The green dots for "Slope 2" also line up closely with a straight diagonal line, similar to "Slope 1," suggesting that the data for "Slope 2" is also approximately normally distributed.

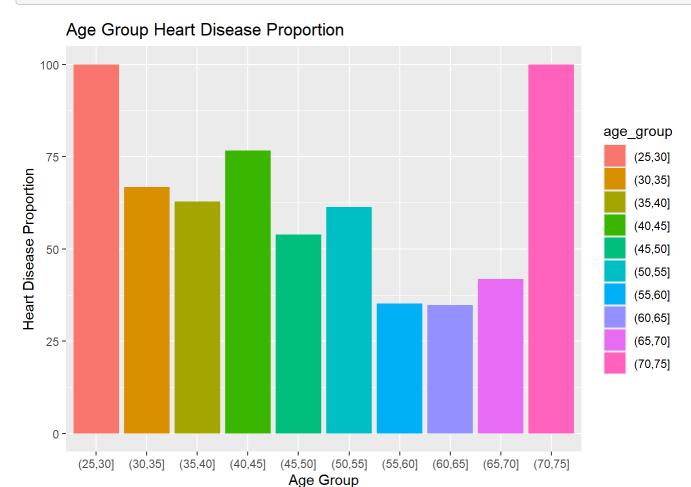
```
library(ggplot2)
library(dplyr)

# Group the age columns of the analysis by age_group
data2$age_group <- cut(data2$age, breaks = seq(25, 75, 5))

# Calculate heart disease proportion for each age group
age_group <- data2 %>%
    group_by(age_group) %>%
    summarise(heart_dis_prop = round(sum(target == "YES") / n(), 3) * 100) %>%
    na.omit()

# Plot the heart disease proportion by age group
ggplot(age_group, aes(x = age_group, y = heart_dis_prop, fill = age_group)) +
```

```
geom_col(position = "dodge") +
labs(x = "Age Group", y = "Heart Disease Proportion", title = "Age Group Heart Disease Propo
rtion")
```



This graph is a vertical bar chart titled "Age Group Heart Disease Proportion." It shows the proportion of heart disease across different age groups, where each age group is represented by a different color, as indicated in the legend on the right side of the graph.

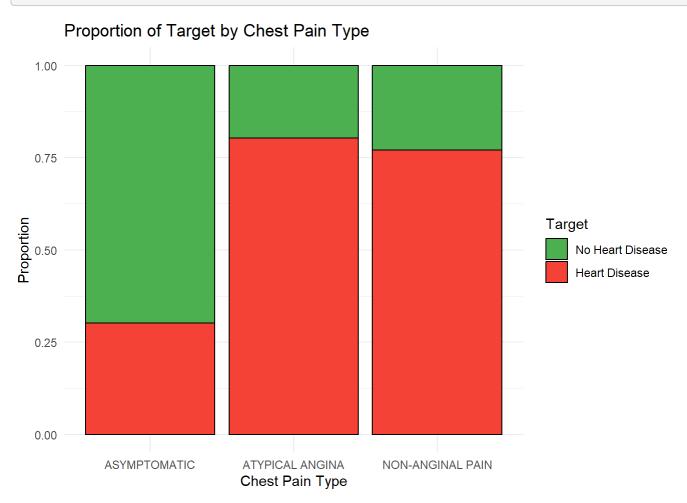
The y-axis indicates "Heart Disease Proportion" and is measured from 0 to 100, suggesting a percentage scale, although the actual units are not specified. The x-axis lists the age groups in intervals of 5 years.

The height of each bar represents the proportion of heart disease in that age group. While the graph lacks specific values on each bar, the visual representation shows an interesting trend: the proportion of heart disease generally increases with age, as the bars get taller in the higher age groups, with the (70,75) age group showing the highest proportion of all.

This graph could be used to analyze the prevalence of heart disease among different age demographics, potentially for use in public health planning, resource allocation, or to highlight the importance of preventive measures for certain age groups.

```
library(ggplot2)

# Modify the plot
ggplot(data2, aes(x = factor(cp), fill = factor(target))) +
  geom_bar(position = "fill", color = "black") +
  labs(x = "Chest Pain Type", y = "Proportion", fill = "Target") +
  ggtitle("Proportion of Target by Chest Pain Type") +
```



From the plot, we can observe the following:

In the ASYMPTOMATIC group, the proportion of individuals with heart disease (red) is less than the proportion without heart disease (green).

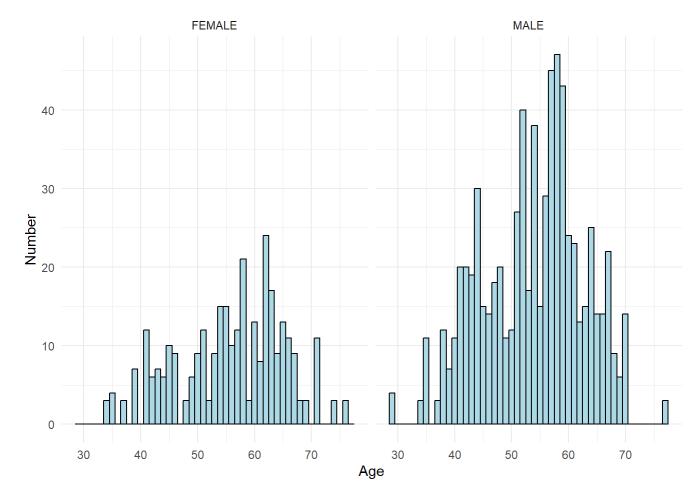
The ATYPICAL ANGINA group has a higher proportion of individuals with heart disease compared to those without.

The NON-ANGINAL PAIN group seems to have a roughly equal proportion of individuals with and without heart disease.

#Distribution of Male and Female population across Age parameter

```
library(ggplot2)

# Create separate plots for male and female populations
data2 %>%
    ggplot(aes(x = age)) +
    geom_histogram(binwidth = 1, color = "black", fill = "lightblue") +
    xlab("Age") +
    ylab("Number") +
    facet_wrap(~ sex, nrow = 1) + # Create separate plots for each sex
    theme_minimal() # Use minimal theme for cleaner appearance
```



For the "FEMALE" category, there are multiple bars of varying heights, indicating the frequency of different age groups. The ages appear to range from around 30 to over 70. The distribution seems fairly uniform with a slight concentration around the 50-60 age range.

For the "MALE" category, the ages also range from around 30 to over 70. However, there is a more pronounced peak in the distribution around the 50-60 age range, indicating a higher frequency of males in that age group compared to females.

The plot is designed to allow for easy comparison between the age distributions of females and males. It suggests that while both distributions cover similar age ranges, there are differences in the frequency of certain age groups between genders.

#Density plot of target with respect to variables

```
# Load necessary libraries
library(ggplot2)
library(gridExtra)

# Assuming your dataset is named data2
# Convert target variable to a factor with levels "NO" and "YES"
data2$target <- factor(data2$target, levels = c("NO", "YES"))

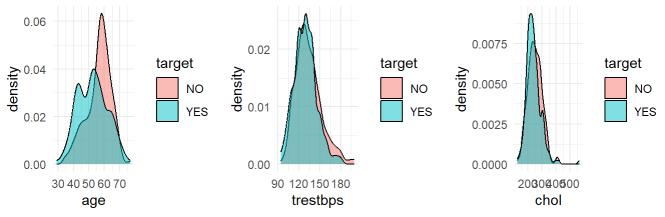
# Define a function to create density plots
plot_density <- function(data, var) {
    ggplot(data, aes(x = !!as.name(var), fill = target)) +
        geom_density(alpha = 0.5) +</pre>
```

```
labs(title = paste("Density plot of", var, "by target")) +
    theme_minimal()
}

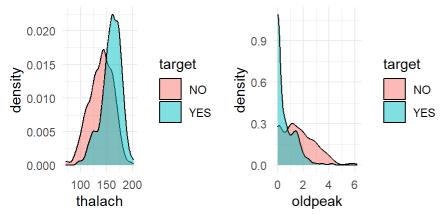
# Create density plots for all numeric variables
plots <- lapply(names(data2)[sapply(data2, is.numeric)], function(var) {
    plot_density(data2, var)
})

# Arrange plots in a grid layout
grid.arrange(grobs = plots, ncol = 3)</pre>
```

Density plot of age by target Density plot of trestbps by targeDensity plot of chol b



Density plot of thalach by target plot of oldpeak by target



Density plot of age by target: This plot shows the density distribution of 'age' for two groups. It appears that the group with 'target' value "YES" tends to have a slightly younger age distribution than the group with 'target' value "NO".

Density plot of trestbps by target: This plot represents the density distribution of 'trestbps', which could stand for resting blood pressure. Here, the distributions for both "YES" and "NO" categories are somewhat similar, with the "YES" group having a slightly higher density around the mode.

Density plot of chol by target: This plot shows the density distribution of 'chol', which may stand for cholesterol levels. Both groups have similar shapes, but the "NO" group seems to have a slightly higher density in the mid-range of cholesterol levels.

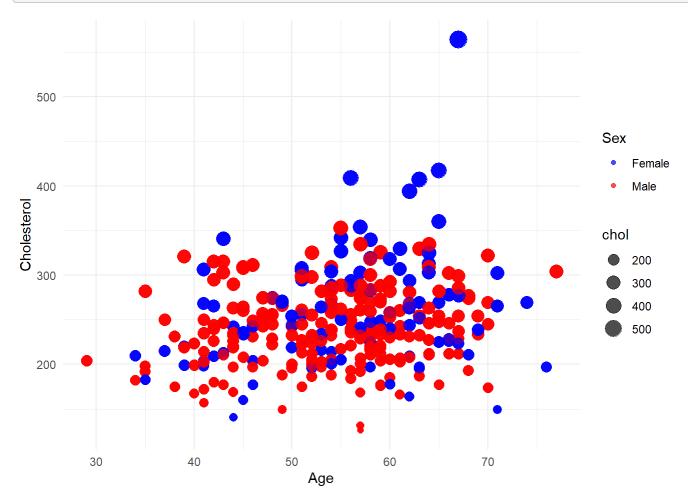
Density plot of thalach by target: Here, the variable 'thalach' could represent maximum heart rate achieved. The "YES" group shows a higher density for higher values of 'thalach', indicating that this group may have higher maximum heart rates.

Density plot of oldpeak by target: The variable 'oldpeak' might refer to ST depression induced by exercise relative to rest. In this plot, the "YES" group has a higher density at lower 'oldpeak' values, which could suggest less ST depression during exercise.

Representation of Cholesterol level

```
library(ggplot2)

# Modify the plot
data2 %>%
    ggplot(aes(x = age, y = chol, color = sex, size = chol)) +
    geom_point(alpha = 0.7) +
    labs(x = "Age", y = "Cholesterol", color = "Sex") + # Change axis and legend labels
    scale_color_manual(values = c("blue", "red"), labels = c("Female", "Male")) + # Customize c
    olor scale
    scale_size_continuous(range = c(2, 6)) + # Adjust point size range
    theme_minimal() # Use minimal theme for cleaner appearance
```

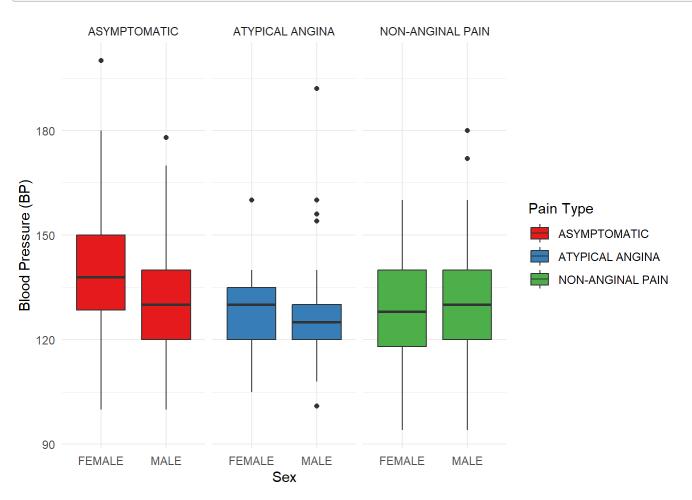


The image shows a scatter plot with "Age" on the x-axis and "Cholesterol" on the y-axis. The data points are color-coded to represent two different sexes: blue for female and red for male. Additionally, the size of each data point corresponds to different cholesterol levels, with larger dots indicating higher cholesterol levels.

Comparison of Blood pressure across pain type

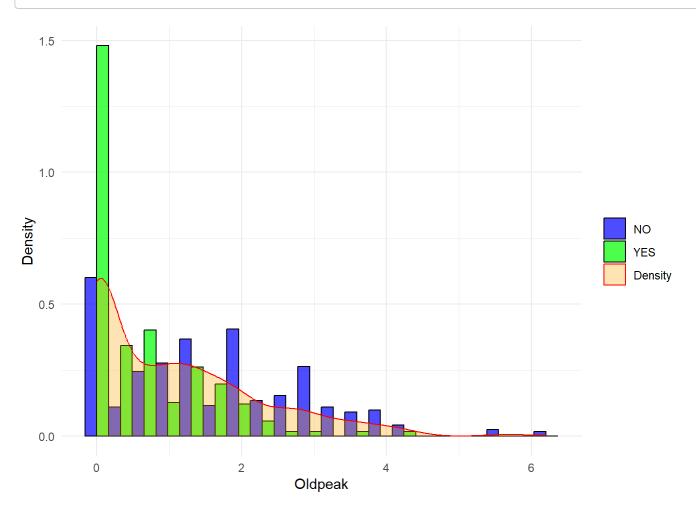
```
library(ggplot2)

# Modify the plot
data2 %>%
    ggplot(aes(x = sex, y = trestbps, fill = factor(cp))) +
    geom_boxplot() +
    scale_fill_brewer(palette = "Set1") + # Use a color palette for pain types
    labs(x = "Sex", y = "Blood Pressure (BP)", fill = "Pain Type") + # Change axis and legend 1
abels
    theme_minimal() + # Use minimal theme for a cleaner appearance
    facet_grid(~cp) # Facet by pain type
```



```
## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(density)` instead.
## This warning is displayed once every 8 hours.
```

Call `lifecycle::last_lifecycle_warnings()` to see where this warning was ## generated.



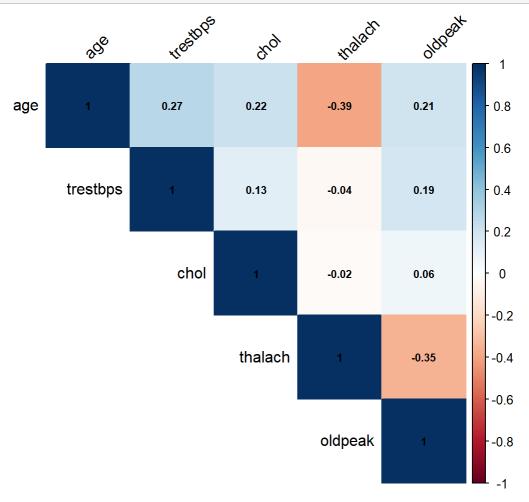
The histogram bars show the distribution of the Oldpeak values for two different groups (YES and NO). The height of each bar corresponds to the density (or frequency) of observations within that range of Oldpeak values. The density plot, which is represented by a red line, shows the probability density function of the Oldpeak variable, giving a sense of the continuous probability distribution across the values.

```
library(corrplot)
# Calculate the correlation matrix
cor_heart <- cor(data2[, 10:14])
# Display the correlation matrix
cor_heart</pre>
```

```
##
                      trestbps
                                    chol
                                           thalach
                                                      oldpeak
                age
## age
           1.0000000 0.27112141 0.21982253 -0.39022708 0.20813668
## trestbps 0.2711214 1.00000000 0.12797743 -0.03926407 0.18743411
## chol
           0.06488031
## thalach -0.3902271 -0.03926407 -0.02177209 1.00000000 -0.34979616
                              0.06488031 -0.34979616 1.00000000
## oldpeak
                    0.18743411
           0.2081367
```

```
# Plot the correlation matrix in a heatmap
corrplot(cor_heart, method = "color", type = "upper",
```

```
tl.col = "black", tl.srt = 45,
addCoef.col = "black", number.cex = 0.7)
```



The diagonal from the top left to the bottom right shows perfect correlations (1.0) because these are the variables correlated with themselves. 'age' has a moderate positive correlation with 'trestbps' (0.27) and a weak positive correlation with 'chol' (0.22). 'thalach' has a moderate negative correlation with 'age' (-0.39) and with 'oldpeak' (-0.35), indicating that as 'age' and 'oldpeak' increase, 'thalach' tends to decrease. 'trestbps' and 'chol' show very weak or no correlation with 'thalach' and 'oldpeak'.

```
library(ggplot2)

# Define colors for "NO" and "YES"
colors <- c("NO" = "green", "YES" = "red")

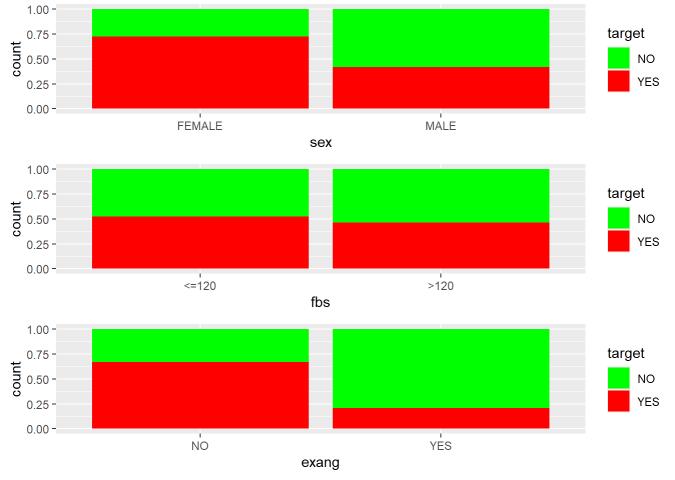
grid.arrange(
    ggplot(data2, aes(x = sex, fill = target)) +
        geom_bar(position = "fill") +
        scale_fill_manual(values = colors),

ggplot(data2, aes(x = fbs, fill = target)) +
        geom_bar(position = "fill") +
        scale_fill_manual(values = colors),

ggplot(data2, aes(x = fbs, fill = target)) +
        geom_bar(position = "fill") +
        geom_bar(position = "fill") +</pre>
```

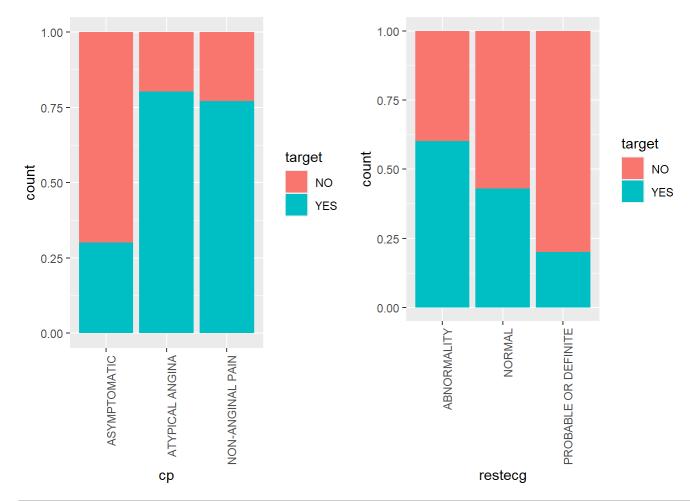
```
scale_fill_manual(values = colors),

nrow = 3
)
```



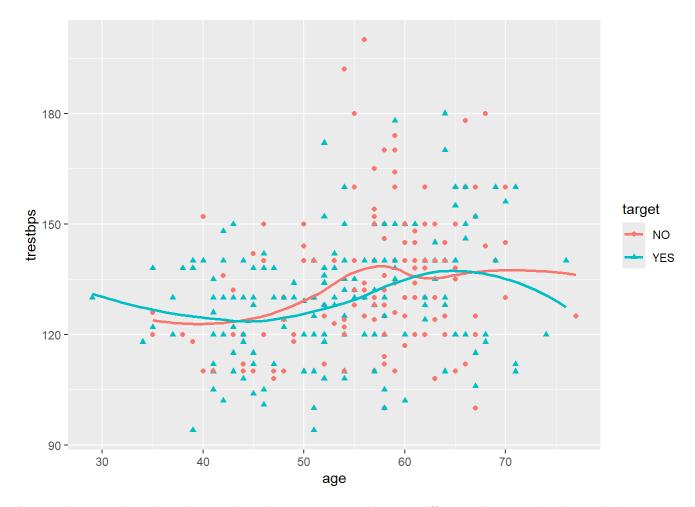
```
grid.arrange(
    ggplot(data2, aes(x = cp, fill = target))+
    geom_bar(position = "fill")+ theme(axis.text.x = element_text(angle = 90, hjust = 1)),

    ggplot(data2, aes(x = restecg, fill = target))+
    geom_bar(position = "fill")+ theme(axis.text.x = element_text(angle = 90, hjust = 1)), ncol
= 2
)
```



```
ggplot(data2, aes(x = age, y = trestbps, color = target, shape = target)) +
  geom_point() +
  geom_smooth(method = "auto", se = FALSE)
```

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



Data points are plotted on the graph and are represented by two different shapes: triangles and dots.

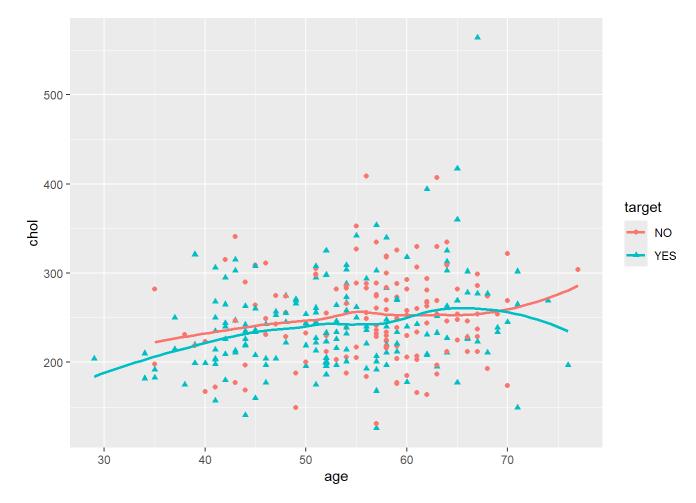
The legend in the top right corner shows that the triangles represent the category 'YES' and the dots represent 'NO,' which could be indicative of a binary target variable, like the presence or absence of a condition in a medical study.

There are two fitted lines, one for each category ('YES' and 'NO'), that suggest a trend or pattern within each group as age increases.

The trend lines indicate that for the 'YES' category, the measurement 'trestbps' tends to increase until about age 55 and then slightly decreases. For the 'NO' category, the measurement 'trestbps' remains relatively stable across ages, with a gentle rise and then a decline after age 60.

```
ggplot(data2, aes(x = age, y = chol, color = target, shape = target))+
  geom_point()+
  geom_smooth(se = FALSE)
```

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



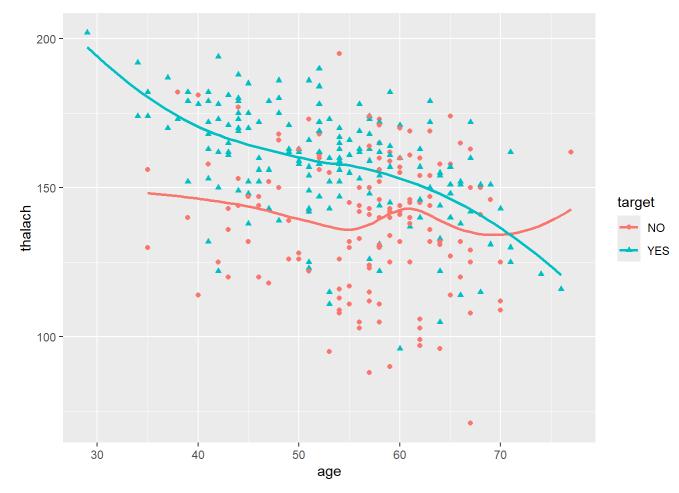
The legend in the top right corner indicates that triangles represent the category 'YES' and dots represent 'NO,' suggesting a binary classification similar to the previous graph.

There are two fitted lines that show the trend in cholesterol levels for each category across different ages. For the 'YES' category, the line indicates a gradual increase in cholesterol levels with age until about 55, then the trend levels off. For the 'NO' category, the line shows a more consistent increase in cholesterol levels with age.

The spread of the data points suggests there is a wide variation in cholesterol levels among individuals in both categories, and the trend lines are a simplified representation of this variation.

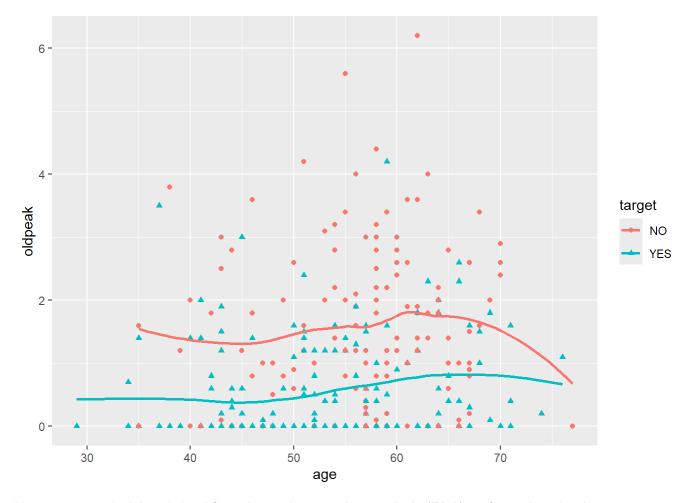
```
ggplot(data2, aes(x = age, y = thalach, color = target, shape = target))+
  geom_point()+
  geom_smooth(se = FALSE)
```

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



```
ggplot(data2, aes(x = age, y = oldpeak, color = target, shape = target))+
  geom_point()+
  geom_smooth(se = FALSE)
```

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



Here are some insights derived from the exploratory data analysis (EDA) performed on the dataset:

1. Data Overview:

• The dataset contains information related to heart disease, with various demographic and clinical variables such as age, sex, chest pain type, blood pressure, cholesterol levels, etc.

2. Missing Values:

• Visualization of missing values using vis miss () shows the presence of missing data in the dataset.

3. Data Transformation:

• The dataset was transformed by recoding certain variables and converting them into factors or changing their labels for better interpretability and analysis.

4. Summary Statistics:

Summary statistics provide an overview of the distribution of variables in the dataset.

5. Boxplots:

Boxplots show the distribution of variables across different categories, such as target variable (heart disease)
 and other categorical variables.

6. Bar Plot:

A bar plot visualizes the distribution of the target variable (heart disease) in the dataset.

7. Proportion of Heart Disease by Age Group:

 Analysis shows the proportion of heart disease across different age groups, providing insights into agerelated trends.

8. Proportion of Heart Disease by Chest Pain Type:

- A bar plot illustrates the proportion of heart disease based on different types of chest pain, revealing potential
 associations between chest pain and heart disease.
- 9. Distribution of Population by Age and Sex:

Histograms display the distribution of age for male and female populations separately.

- 10. Density Plots:
 - Density plots visualize the distribution of numeric variables by the target variable (heart disease), providing insights into their distributions.
- 11. Correlation Analysis:
 - Correlation matrix and heatmap visualize the relationships between variables, helping identify potential correlations among them.
- 12. Comparison of Heart Disease Across Different Variables:
 - Various plots compare heart disease across different categorical and numerical variables, such as blood pressure, cholesterol levels, etc., providing insights into potential relationships.

#PCA(Principal_Component_Analysis)

```
# prcomp is the principal component function
pca <- prcomp(data2[,10:14], scale = TRUE)
pca</pre>
```

This output represents the results of principal component analysis (PCA) applied to a dataset with five variables (age, trestbps, chol, thalach, oldpeak). The standard deviations indicate the variability explained by each principal component (PC), with PC1 explaining the most variability and PC5 the least. The rotation matrix shows the correlations between the original variables and the principal components. For example, in PC1, age and thalach have relatively high positive correlations, while trestbps and chol have lower positive correlations. This indicates how much each original variable contributes to each principal component.

```
# Variance of principal components
variance <- pca$sdev^2

# Proportion of variance explained by each principal component
variance_proportion <- variance / sum(variance)

# Print variance and proportion of variance explained
print(variance)</pre>
```

```
## [1] 1.8035898 1.0755283 0.8834962 0.7587172 0.4786685
```

```
summary(pca)
```

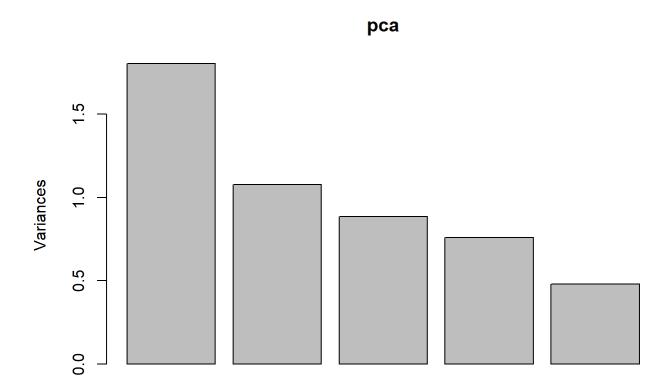
```
## Importance of components:
```

```
## PC1 PC2 PC3 PC4 PC5
## Standard deviation 1.3430 1.0371 0.9399 0.8710 0.69186
## Proportion of Variance 0.3607 0.2151 0.1767 0.1517 0.09573
## Cumulative Proportion 0.3607 0.5758 0.7525 0.9043 1.00000
```

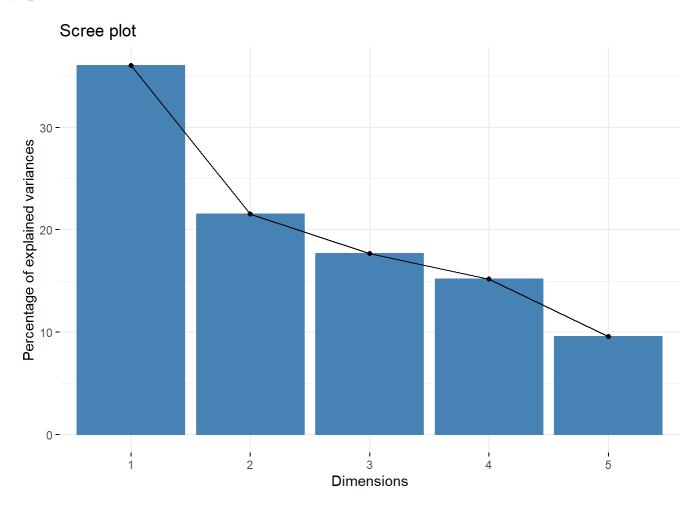
This result summarizes the importance of each principal component (PC) in a principal component analysis (PCA). The "Standard deviation" column represents the variability explained by each PC, with PC1 explaining the most and PC5 the least. "Proportion of Variance" indicates the proportion of total variance explained by each PC, with PC1 contributing the most variance and PC5 the least. "Cumulative Proportion" shows the cumulative proportion of variance explained by the PCs, indicating that the first PC alone explains 36.07% of the variance, while all five PCs combined explain 100% of the variance in the dataset.

```
PCs, indicating that the first PC alone explains 36.07% of the variance, while all five PCs combined explain 100% of the
variance in the dataset.
 pca$sdev
 ## [1] 1.3429780 1.0370768 0.9399448 0.8710437 0.6918587
 #Eigen vectors
 pca$rotation
 ##
                    PC1
                               PC2
                                          PC3
                                                     PC4
                                                                PC5
 ## age
              0.5635382 -0.1059946 -0.1692945 -0.5419762 0.5905854
 ## trestbps 0.3671043 -0.4530454 0.7306853 -0.1215011 -0.3336476
            0.2644374 -0.6602155 -0.5618229 0.3814106 -0.1818500
 ## chol
 ## thalach -0.5044408 -0.4968335 0.2629944 0.1778681 0.6307874
 ## oldpeak
            0.4725161 0.3174696 0.2294065 0.7172086 0.3300395
 #std deviation and mean of variables
 pca$center
                trestbps
                           chol
                                        thalach
                                                  oldpeak
           age
    54.434146 131.611707 246.000000 149.114146
                                                  1.071512
 pca$scale
 ##
                          chol
                                    thalach
                                              oldpeak
          age trestbps
    9.072290 17.516718 51.592510 23.005724 1.175053
 # Principal component scores (showing only first 5 rows)
 head(pca$x, 5)
                PC1
                           PC2
                                      PC3
                                                  PC4
                                                             PC5
 ## [1,] -0.9068936  0.2073491  0.3418077  0.04228957  0.5850594
 ## [2,] 0.5529602 0.7709982 1.3082301 0.99322312 0.6295568
 ## [3,] 2.0218277 1.3269638 1.0748005 -0.80854906 0.7802009
 ## [4,] -0.1605916 -0.4964952 0.9560288 -1.38592049 0.2917687
 ## [5,] 2.1283769 0.2870713 -0.7285281 0.03090104 -0.7477833
```

screeplot(pca)



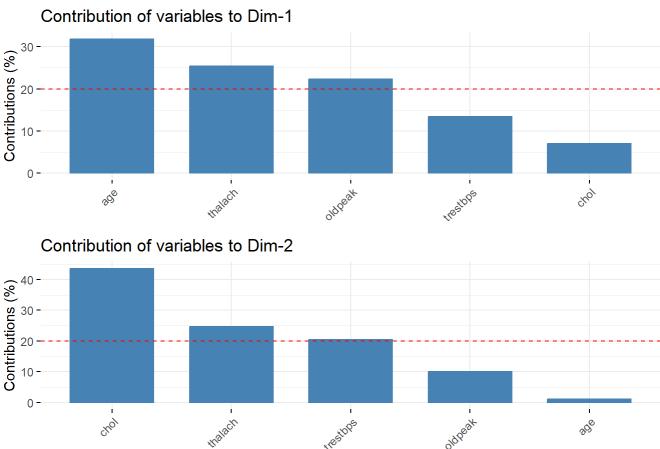
library(factoextra)
fviz_screeplot(pca)



In order to break into pieces each variable contribution on each Principal Component we can use fviz_contrib function.

```
var <- get_pca_var(pca)
a<-fviz_contrib(pca, "var", axes = 1)
b<-fviz_contrib(pca, "var", axes = 2)
grid.arrange(a,b,top='Contribution to the Principal Components')</pre>
```





In the first graph, "Contribution of variables to Dim-1," we see that several variables contribute to the first principal component, with their contributions shown in percentages. The variables are labeled along the x-axis (though the text is slightly obscured, possibly due to resolution issues), and the y-axis shows the percentage contribution. A dashed red line appears to indicate an average level of contribution across the variables. The first variable on the x-axis appears to contribute around 30%, which is the highest among all the variables shown.

In the second graph, "Contribution of variables to Dim-2," we see a similar setup with the same variables contributing to the second principal component. Again, the contributions are shown in percentages, and the same dashed red line indicates the average contribution level. In this case, the first variable on the x-axis also contributes the highest percentage to Dim-2, which is slightly over 30%.

Print variance and proportion_variance

```
# Variance of the first two principal components
variance <- (pca$sdev[1:2])^2

# Proportion of variance explained by the first two principal components
variance_proportion <- variance / sum(variance)

# Print variance and proportion of variance explained
print(variance)</pre>
```

```
## [1] 1.803590 1.075528
```

```
print (variance_proportion)
```

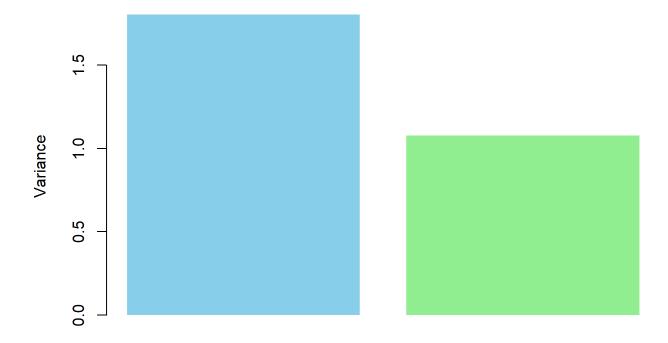
```
## [1] 0.6264383 0.3735617
```

Inference First 2 Principal components: 1st PC: 62% 2nd PC: 37%

Create a bar plot to visualize the variance of the first two principal components

```
barplot(variance,
    main = "Variance of First Two Principal Components",
    xlab = "Principal Component",
    ylab = "Variance",
    col = c("skyblue", "lightgreen"), # Adjusted color palette
    border = NA, # Remove border
    names.arg = NULL) # Remove labels for principal components
```

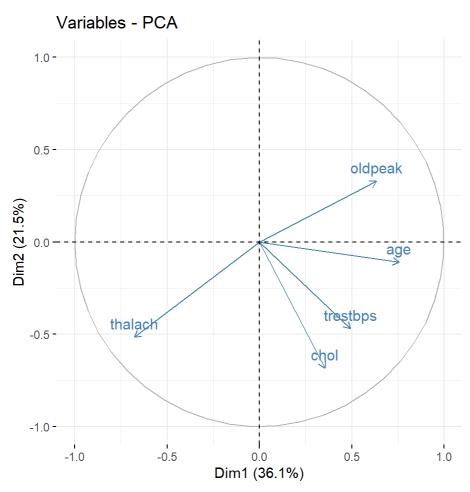
Variance of First Two Principal Components



Principal Component

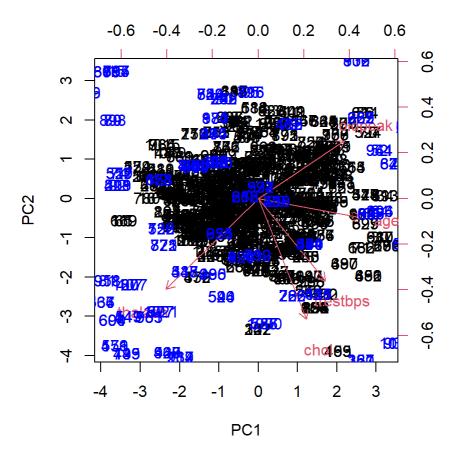
#PCA Biplot

```
fviz_pca_var(pca, col.var = "steelblue")
```



```
# Compute the biplot
biplot(pca, scale = 0)

# Add labels to the data points if needed
text(pca$x[, 1], pca$x[, 2], labels = rownames(data2), pos = 3, col = "blue")
```



From the plot, we can infer that:

Dimension 1 (Dim1):

"thalach" (maximum heart rate achieved): This variable has a strong positive loading on Dimension 1, suggesting it is an important variable in this component. In general, a higher maximum heart rate achieved during stress testing could be indicative of healthier heart function. However, in the context of predicting heart disease, the relationship might not be straightforward. Individuals with certain types of heart disease may also have a blunted heart rate response to exercise.

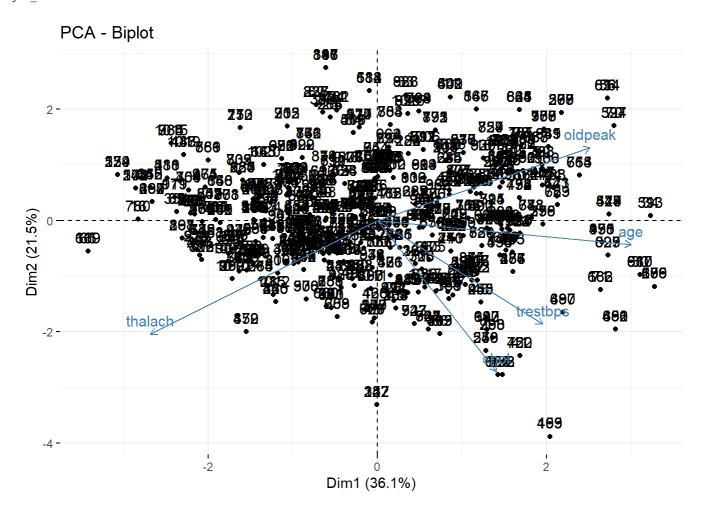
"trestbps" (resting blood pressure) and "chol" (cholesterol): These variables have a moderate negative and positive loading, respectively, on Dimension 1. High resting blood pressure and high cholesterol levels are known risk factors for heart disease. However, their influence on this component is not as strong as "thalach," suggesting that in this particular analysis, they may be less significant in explaining the variance captured by Dimension 1.

Dimension 2 (Dim2):

"oldpeak" (ST depression induced by exercise relative to rest): This variable has a strong positive loading on Dimension 2. ST depression is a sign of ischemia and can be an important predictor of coronary artery disease. Therefore, this variable might be relevant in predicting heart disease.

"age": This variable has a slight negative loading on Dimension 2. Age is a well-known risk factor for heart disease, with risk increasing as age increases. The direction and length of the vector for "age" suggest that it does have an influence on Dimension 2, but it might be explained in combination with other variables.

fviz_pca(pca)

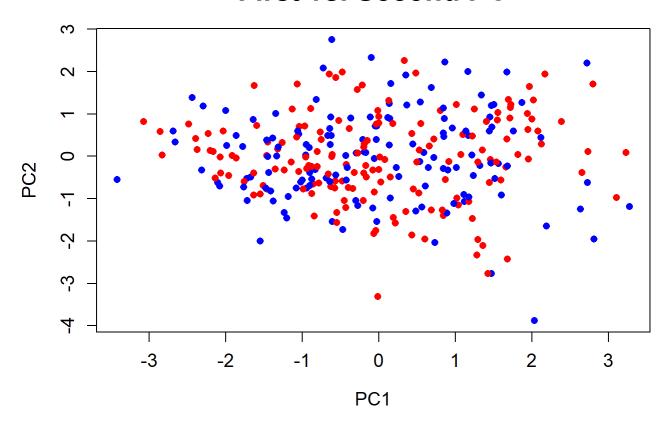


Plot the first vs. second principal component

```
# Define colors based on the first variable
colors <- c(rep("blue", 100), rep("red", 100)) # Adjust as per your actual data

# Plot the first vs. second principal component with dots
plot(x = pca$x[, 1], y = pca$x[, 2],
    pch = 16, # Use a solid dot for better visualization
    col = colors, # Use the defined colors
    xlab = "PC1", ylab = "PC2", main = "First vs. Second PC",
    cex.lab = 1.2, cex.axis = 1.2, cex.main = 1.8)</pre>
```

First vs. Second PC



Most of the patients with heart disease (the red ones), are predicted to have a high probability of having heart disease and most of the patients without heart disease (the blue ones) are predicted to have a low probability of having a heart disease. Thus logistic regression has done a pretty good job.

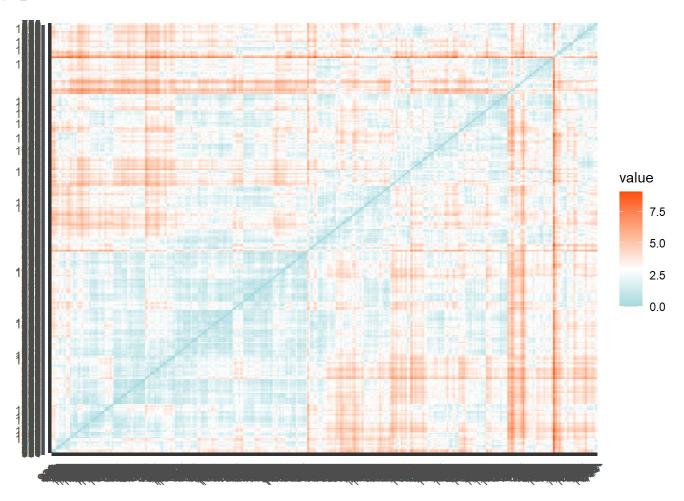
#Cluster_Analysis #K-Means Clustering

```
uns_df <- scale(data2[,10:14])
head(as_tibble(uns_df))</pre>
```

```
\# A tibble: 6 \times 5
    age trestbps
                   chol thalach oldpeak
  <dbl>
         <dbl>
                 <dbl> <dbl>
                                 <dbl>
1 -0.268 -0.377 -0.659 0.821 -0.0609
2 -0.158
         0.479 -0.833
                       0.256 1.73
          0.764 - 1.40
  1.72
                        -1.05
                                1.30
4 0.724 0.936 -0.833 0.517 -0.912
                                0.705
  0.834
         0.365 0.930
                         -1.87
  0.393
          -1.80
                 0.0388 -1.18 -0.0609
```

```
# Calculate distances between observations using the standardized data
distance <- dist(uns_df)

# Visualize the distance matrix
fviz_dist(distance, gradient = list(low = "#00AFBB", mid = "white", high = "#FC4E07"))</pre>
```



```
## List of 9
                  : int [1:1025] 1 2 2 1 2 1 2 2 1 2 ...
   $ cluster
                 : num [1:2, 1:5] -0.518 0.708 -0.358 0.49 -0.268 ...
   ..- attr(*, "dimnames")=List of 2
   .. ..$ : chr [1:2] "1" "2"
##
    ....$ : chr [1:5] "age" "trestbps" "chol" "thalach" ...
##
   $ totss
                  : num 5120
##
##
   $ withinss
                 : num [1:2] 1796 2057
   $ tot.withinss: num 3854
   $ betweenss : num 1266
   $ size
                : int [1:2] 592 433
   $ iter
                 : int 1
##
##
   $ ifault
                : int 0
   - attr(*, "class") = chr "kmeans"
```

The output is from a k-means clustering analysis performed on a dataset with 1025 observations and 5 variables (age, trestbps, chol, thalach, and oldpeak). Two clusters were identified, labeled 1 and 2, with respective cluster centers indicating the average values of each variable within each cluster. The total sum of squares (totss) represents the total variability in the data, while withinss and betweenss denote the variability within and between clusters, respectively. The size of each cluster indicates the number of observations assigned to it. The iter parameter indicates the number of

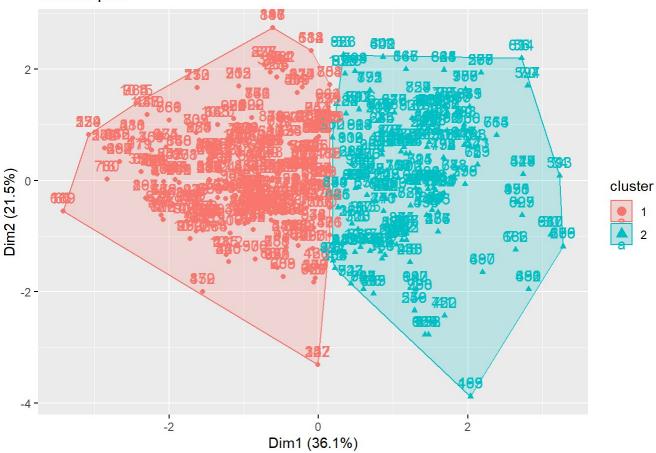
iterations performed during the clustering process, and ifault suggests no errors occurred during execution.

```
k2
```

```
## K-means clustering with 2 clusters of sizes 592, 433
##
## Cluster means:
##
        age trestbps chol thalach
                                   oldpeak
## 1 -0.5179893 -0.3580682 -0.2681813 0.4769983 -0.4557517
## 2 0.7081978 0.4895529 0.3666590 -0.6521547 0.6231062
##
## Clustering vector:
##
   [38] 1 2 1 2 1 1 1 2 1 1 2 2 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 2 2 1 1
##
##
  [75] 1 1 1 2 1 1 1 1 2 1 1 1 1 2 2 2 1 1 2 1 1 1 1 2 1 2 1 1 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 1 2 1 1 1
  ##
  ##
  [186] 2 1 1 2 2 1 1 2 2 2 2 1 1 1 2 1 1 1 2 2 1 2 1 2 1 2 2 2 2 1 1 1 2 2 1 2
##
##
  ##
  [260] 2 1 1 1 2 2 1 2 2 2 2 1 1 1 1 2 2 1 1 2 1 1 1 1 2 2 2 2 2 2 1 1 1 2 2 2 2 2
  [297] 2 2 1 1 1 1 2 2 1 2 1 1 2 2 2 1 2 2 1 2 2 1 1 2 1 1 1 1 1 1 2 1 2 1 2 2 1 1 1 1
  [334] 1 2 2 1 1 1 2 1 1 2 1 1 2 2 1 1 2 2 2 2 1 1 1 2 2 2 1 1 1 2 1 1 1 1 1 1 1 1 1
##
##
  [371] 2 2 1 2 1 2 1 2 2 1 2 2 1 2 2 1 2 1 1 1 2 2 2 2 1 1 2 2 2 2 1 2 2 1 2 2 1 2 1 1 1
  ##
##
  [445] 1 1 1 2 1 1 2 1 2 1 2 2 1 1 1 1 2 1 1 1 2 2 1 2 1 2 1 1 1 2 2
  [482] 2 2 1 1 2 1 2 1 2 1 1 2 2 1 1 2 1 1 1 2 1 1 1 1 1 2 1 2 2 1 1 1 1 1 2 1
##
  [519] 1 1 1 1 2 1 1 1 2 1 2 2 2 2 1 1 1 2 1 1 1 2 2 1 2 1 1 1 2 1 1 2 2 2 2 1 1
##
  [556] 1 1 1 1 2 1 2 1 1 2 1 1 1 1 1 1 1 2 1 1 2 1 1 2 2 2 1 1 1 1 2 1 2 2 2 2 1
##
  ##
##
  [667] 1 1 1 2 1 1 2 1 2 1 2 2 1 2 1 2 2 1 2 2 1 2 2 1 1 2 1 1 1 2 1 1 1 1 2 1 1 1 1 2
##
##
  [704] 1 1 2 1 2 2 1 1 1 1 2 1 2 2 1 1 1 2 2 2 2 1 1 2 2 2 2 1 1 2 1 1 1 1 1 1 1 1 1 2 1 1
  [741] 1 1 2 1 1 1 2 1 1 1 1 2 1 1 1 1 2 2 1 1 2 2 1 1 2 2 2 2 2 2 2 1 2 1 1 2 2 1 1 2
##
  [778] 2 1 1 1 2 2 1 1 2 1 2 2 2 2 2 2 2 2 1 1 2 2 1 2 2 1 1 1 2 2 1 1 1 1 2 2
##
##
  ##
  ##
  ##
## [1000] 1 2 1 1 1 2 2 1 1 1 1 1 1 1 2 1 2 2 2 1 1 1 2 2 2 2 3 1 1 1 2 1 1 2
##
## Within cluster sum of squares by cluster:
## [1] 1796.23 2057.36
  (between SS / total SS = 24.7 %)
##
##
## Available components:
##
## [1] "cluster"
                                              "tot.withinss"
               "centers"
                         "totss"
                                    "withinss"
## [6] "betweenss"
              "size"
                         "iter"
                                    "ifault"
```

```
fviz_cluster(k2, data = uns_df)
```

Cluster plot



The image displays a scatter plot titled "Cluster plot," which is used to visualize the clustering of data points in a two-dimensional space. The axes are labeled "Dim1 (36.1%)" and "Dim2 (25.1%)" which likely represent the first two principal components from a Principal Component Analysis (PCA). The percentages indicate how much of the variance in the data is explained by each principal component.

In the plot, there are two distinct clusters of data points, each highlighted with a different color and labeled as "1" and "2" in the legend under the label "cluster." Cluster 1 is colored red and Cluster 2 is colored blue. These clusters are also enclosed within their respective convex hulls, which are the smallest convex polygons that can contain all the points of a cluster. This visual aid helps to emphasize the separation between the clusters.

```
k3 <- kmeans(uns_df, centers = 3, nstart = 25)
k4 <- kmeans(uns_df, centers = 4, nstart = 25)
k5 <- kmeans(uns_df, centers = 5, nstart = 25)

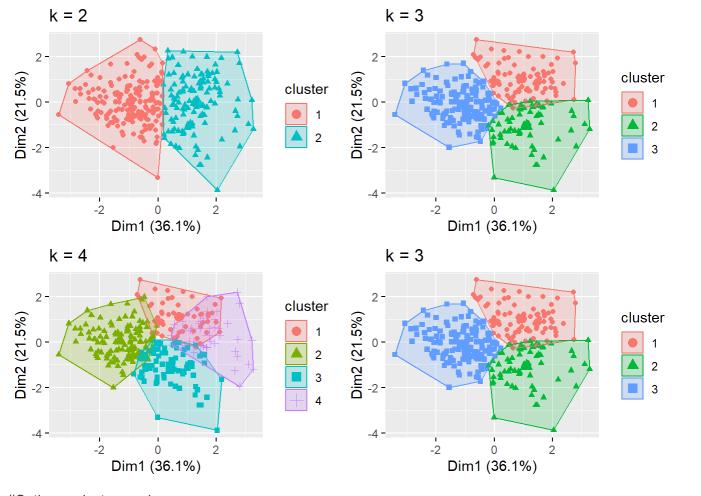
p1 <- fviz_cluster(k2, geom = "point", data = uns_df)+
    ggtitle("k = 2")

p2 <- fviz_cluster(k3, geom = "point", data = uns_df)+
    ggtitle("k = 3")

p3 <- fviz_cluster(k4, geom = "point", data = uns_df)+
    ggtitle("k = 4")

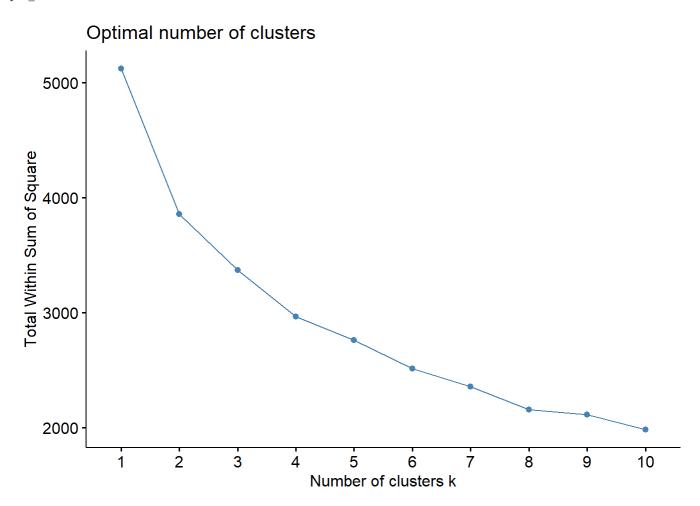
p4 <- fviz_cluster(k5, geom = "point", data = uns_df)+
    ggtitle("k = 5")

library(gridExtra)
grid.arrange(p1,p2,p3,p2, nrow = 2)</pre>
```



#Optimum cluster numbers

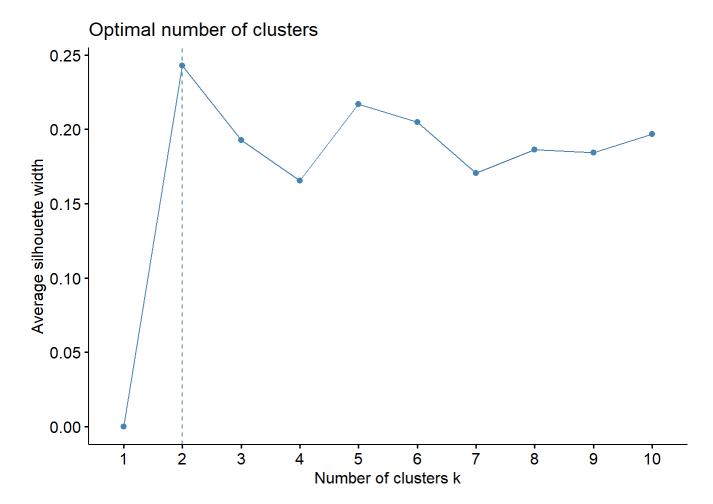
```
# Elbow Method
set.seed(123)
fviz_nbclust(uns_df, kmeans, method = "wss")
```



In this plot, you can observe that as the number of clusters increases, the total WSS decreases. This is expected because when you increase the number of clusters, the clusters themselves become smaller and the points are closer to their respective centroids.

To find the optimal number of clusters, you look for the "elbow" point in the plot, which is the point after which the rate of decrease of WSS slows down significantly. This point represents a balance between minimizing the WSS and having a smaller number of clusters. In this plot, the elbow seems to appear around the 3 or 4 cluster mark, suggesting that 3 or 4 might be the optimal number of clusters for this particular dataset.

```
# Average Silouette Method
fviz_nbclust(uns_df, kmeans, method = "silhouette")
```



#Gap Statistics

```
library(cluster)
set.seed(123)

gap_stat <- clusGap(uns_df, FUN = kmeans, nstart = 25, K.max = 10, B = 50)</pre>
```

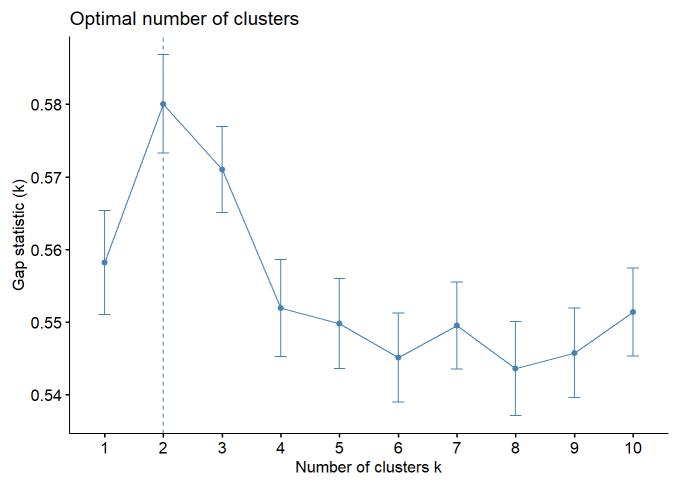
```
## Warning: did not converge in 10 iterations
```

```
print(gap_stat, method = "firstmax")
```

```
## Clustering Gap statistic ["clusGap"] from call:
## clusGap(x = uns df, FUNcluster = kmeans, K.max = 10, B = 50, nstart = 25)
\#\# B=50 simulated reference sets, k = 1..10; spaceH0="scaledPCA"
   --> Number of clusters (method 'firstmax'): 2
             logW E.logW
##
                                 gap
##
   [1,] 6.631293 7.189493 0.5581999 0.007180497
   [2,] 6.484217 7.064241 0.5800238 0.006775992
   [3,] 6.407674 6.978675 0.5710010 0.005937317
   [4,] 6.353428 6.905347 0.5519184 0.006685759
   [5,] 6.299485 6.849281 0.5497963 0.006182010
   [6,] 6.253780 6.798893 0.5451135 0.006117756
   [7,] 6.211680 6.761185 0.5495051 0.005998341
##
    [8,] 6.184648 6.728249 0.5436015 0.006480379
```

```
## [9,] 6.156408 6.702161 0.5457528 0.006160733
## [10,] 6.126893 6.678288 0.5513945 0.006073452
```

```
fviz_gap_stat(gap_stat)
```



```
set.seed(123)
final <- kmeans(uns_df, 2, nstart = 25)
final</pre>
```

```
## K-means clustering with 2 clusters of sizes 430, 595
##
## Cluster means:
     age
       trestbps
              chol
                 thalach
                      oldpeak
  0.7165487 0.4880342 0.3754376 -0.6496950
 2 - 0.5178419 - 0.3526970 - 0.2713246 0.4695275 - 0.4541897
 Clustering vector:
##
  ##
  ##
##
 ##
 [223] 1 2 2 2 2 2 2 1 2 2 1 2 2 1 2 2 1 2 2 1 2 1 2 1 2 1 2 1 2 2 2 1 2 2 2 1 2 2 2 1 1 2 1 2 1 2
```

```
[260] 1 2 2 2 1 1 2 1 1 1 1 2 2 2 2 1 1 2 2 1 2 2 2 2 1 1 1 1 1 1 2 2 2 2 1 1 1 1 1
 [297] 1 1 2 2 2 2 1 1 2 1 2 2 1 1 1 2 1 1 2 2 1 2 2 2 2 2 2 2 1 2 1 2 1 1 2 2 2 2
 [371] 1 1 2 1 2 1 2 1 1 2 1 1 2 1 2 2 2 1 1 1 1 2 2 1 1 1 1 2 1 1 2 1 1 2 1 2 2 2
 [445] 2 2 2 1 2 2 1 2 1 2 1 2 1 2 2 2 2 1 2 2 2 1 2 2 2 1 1 2 1 2 2 2 2 1 2 2 1 1
 [556] 2 2 2 2 1 2 1 2 2 1 2 2 2 2 2 2 2 1 2 2 1 2 2 1 1 1 2 2 2 2 1 2 1 1 1 1 2 2
 [630] 1 2 2 2 1 2 2 1 2 1 2 1 2 2 1 1 2 2 1 2 1 2 2 1 2 1 1 2 1 2 2 2 2 1 2 1 1 2 2 1 1
 [741] 2 2 1 2 2 2 1 2 2 2 2 1 2 2 2 2 1 1 2 2 2 1 1 2 2 1 2 1 1 1 1 1 1 2 1 2 2 1 1 2 2 1
 [815] 2 2 1 2 2 1 1 1 1 2 1 2 2 2 2 1 2 2 1 1 1 2 2 2 2 2 1 2 2 1 1 1 2 1 2 1 2 1
 ## Within cluster sum of squares by cluster:
## [1] 2045.944 1807.620
 (between SS / total SS = 24.7 %)
## Available components:
## [1] "cluster"
         "centers"
                "totss"
                        "withinss"
                               "tot.withinss"
## [6] "betweenss" "size"
                       "ifault"
                 "iter"
```

Descriptive Statistics for Clusters

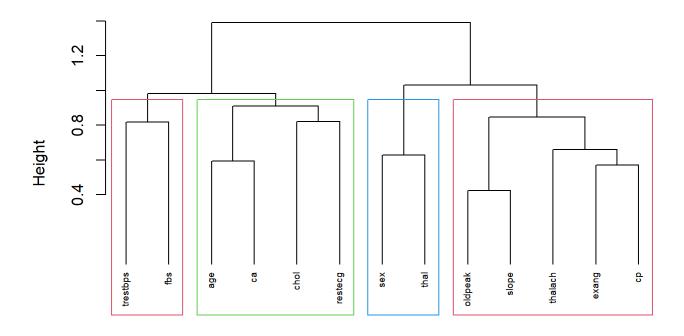
```
data2[,10:14] %>%
  mutate(Cluster = final$cluster) %>%
  group_by(Cluster) %>%
  summarise_all("mean")
```

HIERARCHICAL CLUSTERING

```
xquant <- data2[10:14] # Numeric variables
xqual <- data2[2:9] # Categorical variables
tree <- hclustvar(xquant, xqual)</pre>
```

```
plot(tree, cex = 0.6)
rect.hclust(tree, k = 4, border = 2:4)
```

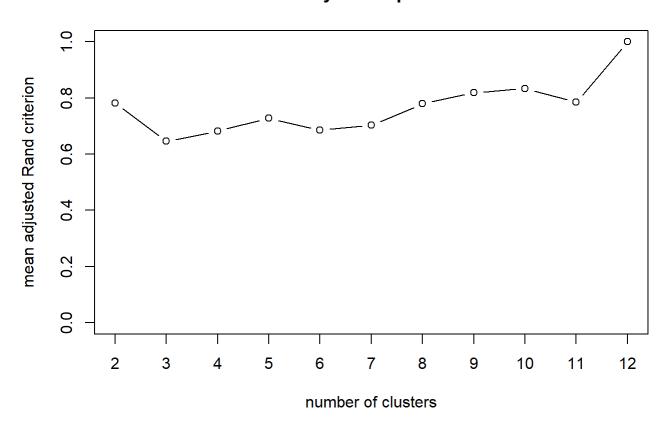
Cluster Dendrogram



In the dendrogram shown, you can see several clusters being merged at different heights. The decision on the number of clusters can be made by cutting the dendrogram at a certain height, which will define clusters as the number of vertical lines that are intersected by the horizontal line.

stab < - stability(tree, B=50) # "B=50" refers to the number of bootstrap samples to use in the estimation.

Stability of the partitions

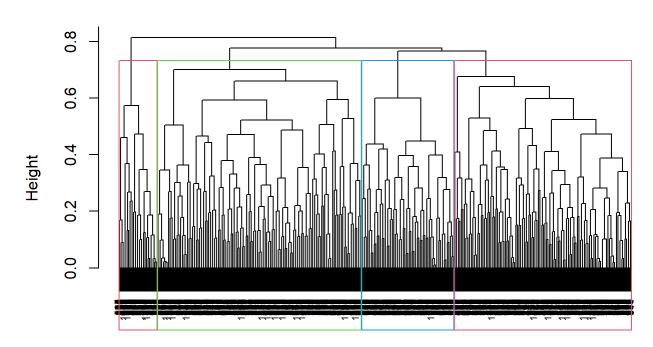


```
d <- daisy(data2[-1], metric="gower")

fit <- hclust(d=d, method="complete")  # Also try: method="ward.D"

plot(fit, cex = 0.6)
 rect.hclust(fit, k = 4, border = 2:4)</pre>
```

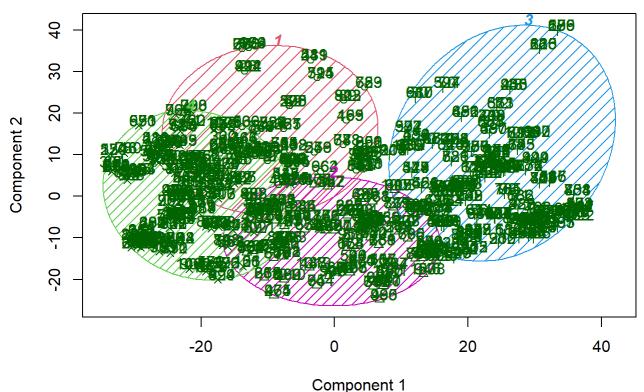
Cluster Dendrogram



d hclust (*, "complete")

```
kfit <- kmeans(d, 4)
clusplot(as.matrix(d), kfit$cluster, color=T, shade=T, labels=2, lines=0)</pre>
```

CLUSPLOT(as.matrix(d))



These two components explain 51.8 % of the point variability.

Plot the first two principal components with cluster assignments

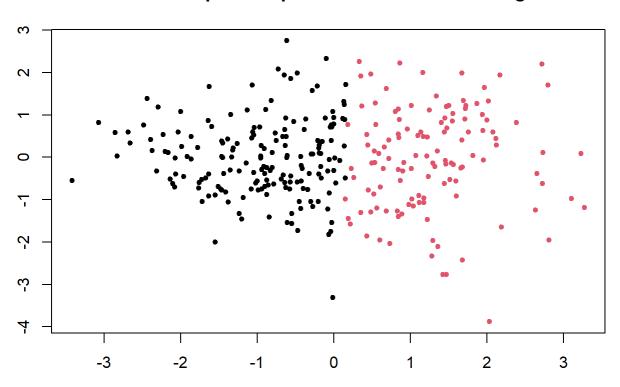
```
# Perform PCA
pc <- prcomp(uns_df)

# Extract the first two principal components
pc_first_two <- pc$x[, 1:2]

# Perform K-means clustering on the first two principal components
set.seed(12)  # For reproducibility
k <- 2  # Number of clusters
km_clusters <- kmeans(pc_first_two, centers = k)

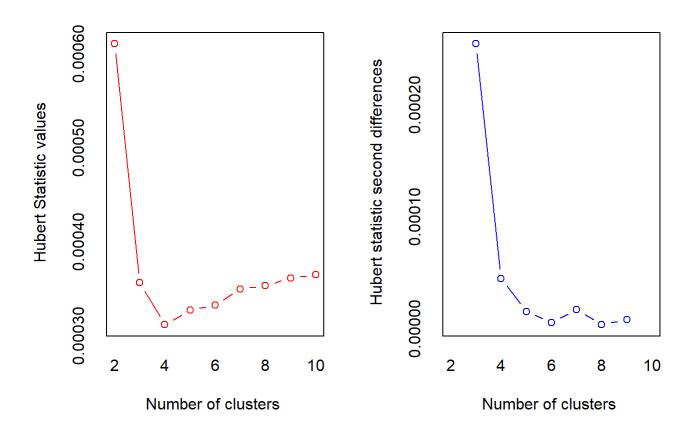
# Plot the first two principal components with cluster assignments
plot(pc_first_two, col = km_clusters$cluster,
    main = "First Two Principal Components with Cluster Assignments",
    xlab = "", ylab = "", pch = 20)</pre>
```

First Two Principal Components with Cluster Assignments

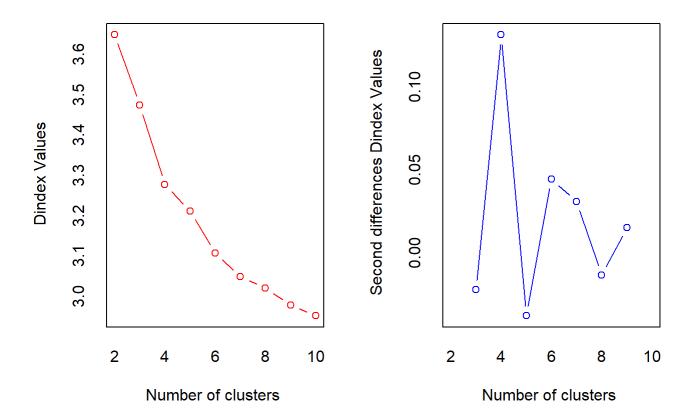


The plot displays a scatterplot of data points reduced to two dimensions using Principal Component Analysis (PCA), where the first two principal components are plotted along the x and y axes, respectively. The data points are colored to represent two distinct clusters, as identified by a clustering algorithm, with black and red dots indicating the separate groupings. The plot's purpose is to illustrate the variance captured by PCA and the natural groupings within the data as determined by the clustering, enabling visualization and analysis of patterns within a high-dimensional dataset in a simplified two-dimensional space.

```
library(NbClust)
res.nbclust <- data %>% scale() %>% NbClust(distance = "euclidean", min.nc = 2, max.nc = 10, m
ethod = "complete", index ="all")
```



```
## ***: The Hubert index is a graphical method of determining the number of clusters.
## In the plot of Hubert index, we seek a significant knee that corresponds to
a
## significant increase of the value of the measure i.e the significant peak i
n Hubert
## index second differences plot.
##
```



```
## *** : The D index is a graphical method of determining the number of clusters.
##
                  In the plot of D index, we seek a significant knee (the significant peak in
Dindex
##
                  second differences plot) that corresponds to a significant increase of the
value of
##
                  the measure.
##
   ***********
  * Among all indices:
  * 9 proposed 2 as the best number of clusters
  * 2 proposed 3 as the best number of clusters
  * 7 proposed 4 as the best number of clusters
\#\# * 1 proposed 5 as the best number of clusters
\#\# * 1 proposed 6 as the best number of clusters
  * 4 proposed 7 as the best number of clusters
##
                     ***** Conclusion *****
##
##
   * According to the majority rule, the best number of clusters is 2
```

#Factor_Analysis

```
# Load necessary library
```

```
library (psych)
## Attaching package: 'psych'
## The following objects are masked from 'package:scales':
##
##
      alpha, rescale
## The following object is masked from 'package:randomForest':
##
##
       outlier
## The following object is masked from 'package:Hmisc':
##
##
      describe
## The following objects are masked from 'package:ggplot2':
##
       %+%, alpha
##
# Subset the dataset to include only columns 10 to 14
subset data <- data2[, 10:14]</pre>
# Perform Factor Analysis
fit.pc <- principal(subset data, nfactors = 3, rotate = "varimax")</pre>
# View factor analysis results
fit.pc
## Principal Components Analysis
## Call: principal(r = subset data, nfactors = 3, rotate = "varimax")
## Standardized loadings (pattern matrix) based upon correlation matrix
             RC1 RC2 RC3 h2
                                  u2 com
           0.58 0.47 0.24 0.61 0.390 2.3
## age
## trestbps 0.08 0.10 0.96 0.94 0.064 1.0
## chol
        -0.03 0.93 0.05 0.87 0.126 1.0
## thalach -0.87 -0.06 0.16 0.79 0.214 1.1
## oldpeak 0.68 -0.11 0.28 0.56 0.442 1.4
##
##
                         RC1 RC2 RC3
## SS loadings
                       1.57 1.11 1.08
## Proportion Var
                        0.31 0.22 0.22
## Cumulative Var
                       0.31 0.54 0.75
## Proportion Explained 0.42 0.30 0.29
## Cumulative Proportion 0.42 0.71 1.00
##
## Mean item complexity = 1.4
## Test of the hypothesis that 3 components are sufficient.
```

```
##
## The root mean square of the residuals (RMSR) is 0.14
## with the empirical chi square 400.78 with prob < NA
##
## Fit based upon off diagonal values = 0.61</pre>
```

Variables (Rows): The rows represent different variables included in the factor analysis. These are 'age', 'trestbps' (resting blood pressure), 'chol' (cholesterol), 'thalach' (maximum heart rate achieved), and 'oldpeak' (ST depression induced by exercise relative to rest).

Factors (RC1, RC2, RC3): The columns labeled RC1, RC2, and RC3 represent the factor loadings on three extracted factors. Factor loadings can be interpreted similarly to correlation coefficients between the observed variables and the latent factors. For example, 'age' has a loading of 0.58 on RC1, indicating a moderate positive association with the first factor.

Communalities (h2): This column represents the communalities (h2), which are estimates of the proportion of each variable's variance that is accounted for by the common factors. For instance, the communality for 'age' is 0.6101805, suggesting that approximately 61% of the variance in age can be explained by the three factors together.

Uniqueness (u2): This column shows the uniqueness (u2), which is the proportion of variance that is unique to the variable and not shared with other variables in the analysis. It is the variance that is not explained by the extracted factors. For 'age', the uniqueness is 0.39881951, meaning around 39.9% of the variance in age is unique to it.

Complexity (com): The last column represents the complexity (com) of the variables. Complexity indicates how many factors significantly load on a variable. A complexity value close to 1 suggests that the variable is primarily associated with one factor, while a higher value indicates that the variable is complexly determined by multiple factors. For example, 'age' has a complexity of 2.267834, indicating that it's influenced by more than one factor.

#Factor Loadings

```
round(fit.pc$values, 3)
```

```
## [1] 1.804 1.076 0.883 0.759 0.479
```

```
fit.pc$loadings
```

```
##
## Loadings:
##
        RC1 RC2 RC3
## age 0.581 0.466 0.235
## trestbps
                     0.959
## chol
                0.933
## thalach -0.871 0.156
## oldpeak 0.684 -0.113 0.277
##
##
                RC1 RC2 RC3
## SS loadings 1.570 1.113 1.079
## Proportion Var 0.314 0.223 0.216
## Cumulative Var 0.314 0.537 0.753
```

The output represents the results of a factor analysis or principal component analysis (PCA). The first line provides the standard deviations of the principal components, indicating their importance in explaining the variance within the data. The

"Loadings" section displays the correlation coefficients between the original variables and the extracted components. For example, the loading of age on RC1 is 0.581, indicating a strong positive correlation. The "SS loadings" section shows the sum of squares loadings for each component, representing the proportion of variance explained by each component. In this case, RC1 explains 31.4% of the total variance, followed by RC2 and RC3. The "Proportion Var" and "Cumulative Var" sections provide the proportion and cumulative proportion of variance explained by each component, respectively.

Communalities

```
## age trestbps chol thalach oldpeak
## 0.6101805 0.9355137 0.8737971 0.7855377 0.5575853
```

```
# Rotated factor scores, Notice the columns ordering: RC1, RC3, RC2 and RC4 fit.pc$scores
```

```
##
                  RC1
                                RC2
                                             RC3
##
      [1,] -0.48496963 -0.621396151 -0.083036723
      [2,] 0.60745480 -1.203041549 0.918186630
##
##
      [3,] 1.83373196 -0.999177042 0.922091583
##
      [4,] -0.46937513 -0.334755852 0.972438909
##
      [5,] 1.54310620 0.894367840 -0.089135614
##
     [6,] 0.97698050 0.282485542 -1.994612785
##
     [7,] 1.51161155 0.788561508 -0.596296505
      [8,] -0.23624868  0.698468187  1.329404050
##
##
     [9,] -0.19651722 -0.175795538 -0.799769779
##
     [10,] 1.59721663 0.273832375 -0.648080374
     [11,] 1.74168413 -1.073925394 -0.931962326
##
##
     [12,] 0.43174536 0.811464252 -0.096812658
##
    [13,] -1.79585392 -1.236266649 -0.351655312
    [14,] 1.57846773 0.111176073 0.495477322
##
##
     [15,] -0.16633077 -0.777346110 -0.060260527
    [16,] -1.79585392 -1.236266649 -0.351655312
##
##
     [17,] 0.02880827 0.810856586 0.281976409
##
     [18,] 1.44959201 0.110990701 -0.758631345
##
     [19,] -0.41001842 -0.155041499 -0.481442969
##
    [20,] -0.65228656 -0.278923485 0.559704227
##
     [21,] 0.85329357 -1.226696837 0.994362013
##
    [22,] 0.52743916 0.320536088 -1.420103897
##
    [23,] 0.66837103 -1.271060107 -1.165164071
##
    [24,] -0.74003152  0.633608586  0.350937156
##
    [25,] -1.29183135 -0.837661396 -0.529490629
     [26,] 0.05389925 1.251241017 0.600854098
##
##
    [27,] -1.34802971 -0.461953094 0.113129230
##
     [28,] -0.55606177 1.571352509 -0.012066806
##
    [29,] 0.04988701 0.321158003 -0.257042200
##
    [30,] 1.25740445 0.757250077 2.394851035
##
    [31,] 0.67375321 -1.999177003 -0.340270586
##
    [32,] -0.41001842 -0.155041499 -0.481442969
##
     [33,] 1.32519415 -1.908249125 -0.258995954
```

```
[34,] 1.96834650 0.500782105 1.427315612
##
##
    [35,] -0.77417591 -0.797666988 -0.087271469
##
    [36,] 0.63995884 -1.127813491 1.317781718
    [37,] 0.75665612 -0.747595209 -0.566070333
##
##
    [38,] -1.20261149 0.802380915 0.565786401
    [39,] 1.14026065 0.801873016 -0.836791835
##
##
    [40,] -0.12243410 -0.050993981 -0.237550631
##
    [41,] -0.22941968 2.292880233 1.360024201
##
    [42,] -0.17339040 0.358676190 -0.776405067
##
    [43,] -0.89487171 1.906540179 -0.110559782
##
    [44,] -0.19651722 -0.175795538 -0.799769779
##
    [45,] -0.61689605 1.646061025 0.082453286
##
    [46,] -1.57570271 -0.618813458 0.558550277
##
    [47,] -0.31623662 -1.061790526 -0.248320972
    [48,] -0.26167298 -0.019268537 2.769344583
##
    [49,] -0.23738530 1.136273862 0.659489329
##
##
    [50,] 0.14518118 -0.063477652 -0.504471231
##
    [51,] -0.43686055 0.720164729 1.083734250
##
    [52,] 0.41720826 0.128910741 0.003118411
##
    [53,] -1.44308895 -1.636755874 0.449429384
##
    [54,] 0.63221046 -1.336421922 -0.527074241
    [55,] 2.72247916 -1.395391918 0.771153448
##
##
    [56,] 2.72247916 -1.395391918 0.771153448
##
    [57,] 0.21660756 -0.951773118 -0.204835563
##
    [58,] -1.34190233 -0.066992187 0.104824977
##
    [59,] 0.27566123 -0.129390652 1.212757882
    [60,] -0.78930760 -0.011194742 1.239770585
##
##
    [61,] -2.53927762 -1.432223141 0.260258313
    [62,] -0.23738530 1.136273862 0.659489329
##
##
    [63,] 1.04114436 1.514649973 -1.990029065
    [64,] 0.12650245 -0.572285784 1.258595759
##
##
    [65,] -2.53927762 -1.432223141 0.260258313
##
    [66,] -0.74279746 0.919201214 1.969963751
##
    [67,] 0.05315472 -0.907437903 0.049640935
##
    [68,] 0.28501504 0.536356664 -0.182402944
##
    [69,] -1.39803721 -0.926248596 -0.620732253
##
    [70,] 2.31015170 -2.202086742 2.509396102
##
    [71,] 0.84673784 0.944363547 2.190717516
##
    [72,] 0.87251722 -0.614782904 0.568059380
##
    [73,] 0.26430985 0.107160247 -0.384245502
    [74,] -0.45518990 -0.823708961 0.592864832
##
    [75,] -0.65472464 0.138695174 -0.324163542
##
##
    [76,] -0.89307064 0.092105960 0.163241394
##
    [77,] -1.27617649 0.160994701 -0.326083366
##
    [78,] 1.60964575 -1.277475150 1.043599806
##
    [79,] -0.31858939 -0.811485196 0.254216474
##
    [80,] -0.31858939 -0.811485196 0.254216474
##
    [81,] -0.70445933 -0.321564957 0.525167328
##
    [82,] 0.63738753 -1.774614891 -0.922350535
##
    [83,] 0.63995884 -1.127813491 1.317781718
##
    [84,] -1.44308895 -1.636755874 0.449429384
##
    [85,] -1.39803721 -0.926248596 -0.620732253
##
    [86,] -1.17215745 -0.576263712 -0.570129573
##
    [87,] -0.65228656 -0.278923485 0.559704227
```

```
[88,] -0.32178620 0.265648618 2.019153143
    [89,] 0.80643737 0.154999413 1.021270104
##
##
    [90,] 1.59968785 -0.888482448 1.149958782
##
    [91,] -0.80313581 0.647139272 -1.242252919
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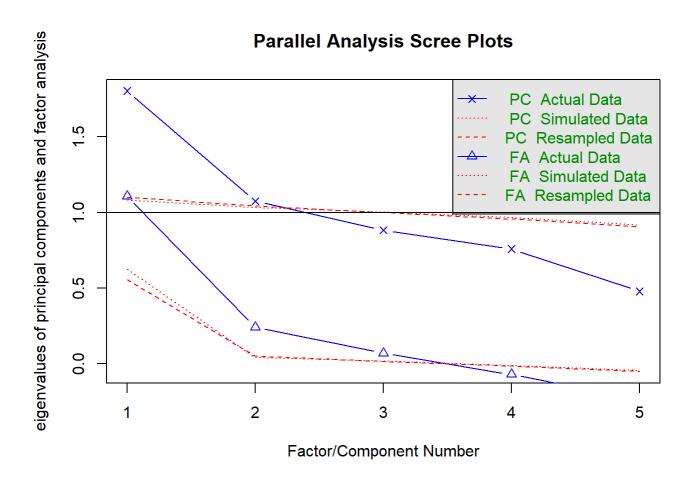
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##
   [963,] -0.22435835 -0.041650836 -1.431167428
## [964,] 0.41720826 0.128910741 0.003118411
  [965,] -0.81961719 -1.991455364 -0.897788721
##
## [966,] 1.68996644 -0.080706600 0.306697623
## [967,] 1.32517741 -0.010778763 -0.105210730
   [968,] 1.42130242 -0.738712017 -1.283787254
##
##
  [969,] 0.60745480 -1.203041549 0.918186630
   [970,] -1.13847343 1.482215445 -0.635882767
##
## [971,] -1.44308895 -1.636755874 0.449429384
##
   [972,] -0.73946851 -0.927811436 2.265818110
## [973,] -1.33023381 -0.833382915 -0.294722567
##
  [974,] -0.03004647 -0.364308492 0.054129746
  [975,] -0.89219176 -0.736428357 -1.203203573
##
##
  [976,] -0.09627427 -1.024239798 -0.894354012
   [977,] 0.11186182 0.679265703 -0.846856150
##
##
   [978,] -1.27478476 -0.550426041 0.123597610
   [979,] -1.24398033 -0.926843996 -0.968602966
##
## [980,] -0.87548343 0.883353353 0.149574797
##
   [981,] -0.04444006 -0.729018407 0.438994214
## [982,] -0.09627427 -1.024239798 -0.894354012
##
   [983,] 0.52743916 0.320536088 -1.420103897
## [984,] 1.14026065 0.801873016 -0.836791835
## [985,] -0.35745407 0.072159770 0.294468192
##
   [986,] 0.65502665 -0.105264191 0.088145324
## [987,] 1.25740445 0.757250077 2.394851035
   [988,] -0.78930760 -0.011194742 1.239770585
##
## [989,] -0.47460768 0.971167612 0.687501050
##
  [990,] -0.31866751 1.613131741 1.589130105
## [991,] -0.71750873 0.003265292 -0.264670616
## [992,] 0.14518118 -0.063477652 -0.504471231
  [993,] -0.70787134  0.261057919 -1.247184736
##
  [994,] -0.59267725 -0.235298007 -0.315912006
##
## [995,] 0.52652264 0.104569971 -1.157776053
## [996,] -1.35750846 0.159999438 -0.611221395
   [997,] -0.08027550 2.675962448 -0.010829013
##
## [998,] 1.26365830 -1.050492590 -0.909184048
## [999,] 0.28501504 0.536356664 -0.182402944
## [1000,] -0.24310358  0.812100466 -0.226564266
## [1001,] 1.12935504 -0.457858675 0.789986209
## [1002,] -1.57570271 -0.618813458 0.558550277
## [1003,] 0.67633518 0.103868087 -1.249862315
## [1004,] -0.22435835 -0.041650836 -1.431167428
## [1005,] 0.02880827 0.810856586 0.281976409
```

```
## [1006,] 0.98671980 -0.855357567 -0.197114258
## [1007,] -0.65228656 -0.278923485 0.559704227
## [1008,] 0.21660756 -0.951773118 -0.204835563
## [1009,] -1.21574900 0.623352515 -0.824651634
  [1010,] -1.78140594 -0.788499312 1.218454811
  [1011,] -0.72661435  0.659085063  0.703323814
  [1012,] -1.40022967 0.934224741 -0.300003184
  [1013,] -0.58046027 -0.426212036 -0.940663423
  [1014,] 1.51161155 0.788561508 -0.596296505
  [1015,] -0.81961719 -1.991455364 -0.897788721
  [1016,] 1.10932512 -0.591626449 -0.146085330
  [1017,] -0.29724367
                      0.944361147 0.727788319
  [1018,] 1.67536237 0.378828493 -1.057680079
  [1019,] -0.78482386 -1.479993504 -1.186502186
  [1020,] -0.23966265 -0.743508698 -1.259597477
  [1021,] -0.61673638 -0.071047858 0.537415254
  [1022,] 1.04916820 0.104596899 -0.139995878
  [1023,] 0.58563622 0.287583700 -1.659768378
  [1024,] -0.70787134
                      0.261057919 -1.247184736
## [1025,] 1.26365830 -1.050492590 -0.909184048
```

Play with FA utilities

fa.parallel(data2[, 10:14]) # See factor recommendation



```
\#\# Parallel analysis suggests that the number of factors = 3 and the number of components = 2
```

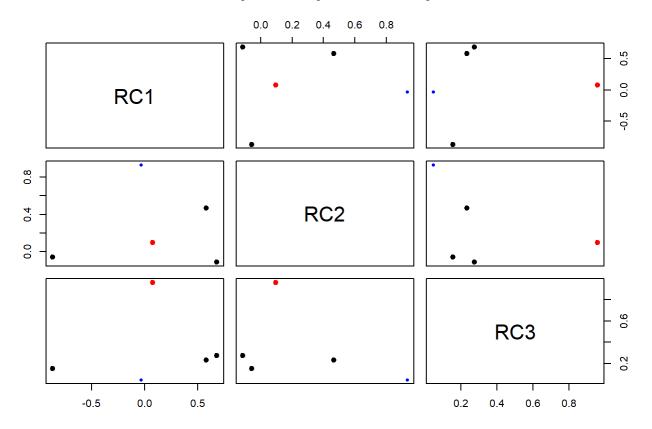
In the plot, there are six lines representing different data:

- "PC Actual Data" (marked with 'X') shows the eigenvalues for each principal component from the actual dataset.
- "PC Simulated Data" (dotted line) represents the average eigenvalues for each component from the simulated datasets.
- "PC Resampled Data" (dashed line) represents the eigenvalues from a resampling of the actual data (e.g., bootstrapping).
- "FA Actual Data" (marked with ' Δ ') shows the eigenvalues for each factor from the actual dataset using factor analysis.
- "FA Simulated Data" (dotted line) represents the average eigenvalues for each factor from the simulated datasets using factor analysis.
- "FA Resampled Data" (dashed line) represents the eigenvalues from a resampling of the actual data using factor analysis.

See Correlations within Factors

fa.plot(fit.pc)

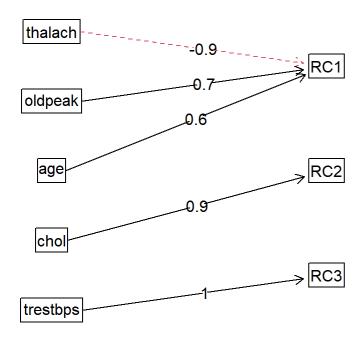
Principal Component Analysis



Visualize the relationship

fa.diagram(fit.pc)

Components Analysis



Interpreting the plot:

'thalach' has a strong negative correlation with RC1, as indicated by the loading score of -0.9 and the dashed line.

'oldpeak' has a somewhat strong positive correlation with RC1, with a loading score of 0.7.

'age' has a moderate positive correlation with RC1, indicated by the loading score of 0.6.

'chol' has a strong positive correlation with RC2, with a loading score of 0.9.

'trestbps' has a perfect positive correlation with RC3, as the loading score is 1.

RC1 might represent some form of heart health factor, given that 'thalach' (maximum heart rate achieved) is negatively correlated (as heart rate might decrease with certain heart conditions) and 'oldpeak' (ST depression induced by exercise relative to rest) is positively correlated with it, as higher values of ST depression can be associated with heart issues. RC2 and RC3 could represent other underlying factors or components that describe different dimensions of variation in the data.

See Factor recommendations for a simple structure

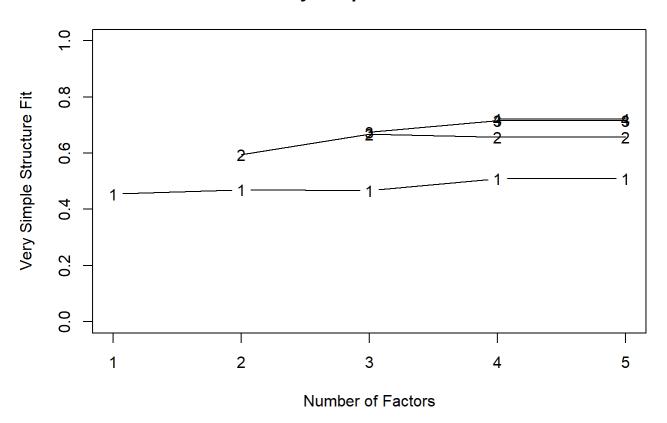
Warning in fa.stats(r = r, f = f, phi = phi, n.obs = n.obs, np.obs = np.obs, :

```
vss(data2[, 10:14])
```

```
## The estimated weights for the factor scores are probably incorrect. Try a ## different factor score estimation method.
```

```
## Warning in fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate = rotate, : An
## ultra-Heywood case was detected. Examine the results carefully
```

Very Simple Structure



```
## Very Simple Structure
## Call: vss(x = data2[, 10:14])
## Although the VSS complexity 1 shows 4 factors, it is probably more reasonable to think ab
out 2 factors
## VSS complexity 2 achieves a maximimum of 0.67 with 3 factors
## The Velicer MAP achieves a minimum of 0.08 with 1
## BIC achieves a minimum of 10.21 with 2 factors
## Sample Size adjusted BIC achieves a minimum of 13.39 with 2
##
## Statistics by number of factors
    vss1 vss2
                map dof chisq
                                  prob sqresid fit RMSEA BIC SABIC complex
  1 0.45 0.00 0.081
                    5 1.2e+02 8.5e-24
                                            3.3 0.45 0.15
                                                           83
                                                                 99
                                                                        1.0
## 2 0.47 0.60 0.180
                                                                        1.3
                    1 1.7e+01 3.5e-05
                                            2.4 0.60 0.13
                                                           10
                                                                 13
## 3 0.47 0.67 0.380 -2 9.6e-11
                                                                        1.5
                                     NA
                                            1.9 0.67
                                                           NA
                                                                 NA
                                                       NA
## 4 0.51 0.66 1.000 -4 0.0e+00
                                            1.7 0.72
                                                                        1.6
                                     NA
                                                       NA
                                                           NA
                                                                 NA
## 5 0.51 0.66
                                            1.7 0.72
                 NA -5 0.0e+00
                                     NA
                                                       NA
                                                           NA
                                                                 NA
                                                                        1.6
     eChisq
               SRMR eCRMS eBIC
```

```
## 1 1.3e+02 7.9e-02 0.112 94

## 2 1.7e+01 2.9e-02 0.091 10

## 3 9.9e-11 6.9e-08 NA NA

## 4 2.6e-14 1.1e-09 NA NA

## 5 2.6e-14 1.1e-09 NA NA
```

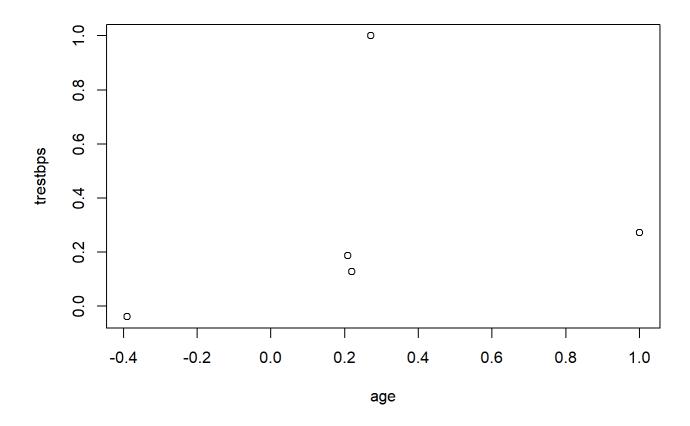
Computing Correlation Matrix

```
corrm.data <- cor(data2[, 10:14])
corrm.data</pre>
```

```
## age trestbps chol thalach oldpeak
## age 1.0000000 0.27112141 0.21982253 -0.39022708 0.20813668
## trestbps 0.2711214 1.00000000 0.12797743 -0.03926407 0.18743411
## chol 0.2198225 0.12797743 1.00000000 -0.02177209 0.06488031
## thalach -0.3902271 -0.03926407 -0.02177209 1.00000000 -0.34979616
## oldpeak 0.2081367 0.18743411 0.06488031 -0.34979616 1.00000000
```

This is a correlation matrix showing the pairwise correlations between the variables: age, trestbps (resting blood pressure), chol (serum cholesterol), thalach (maximum heart rate achieved), and oldpeak (ST depression induced by exercise relative to rest). Each cell in the matrix represents the correlation coefficient between two variables. For example, the correlation between age and trestbps is 0.271, indicating a weak positive correlation, while the correlation between thalach and oldpeak is -0.350, indicating a moderate negative correlation. This matrix helps understand how each variable is related to the others in the dataset, providing insights into potential relationships and dependencies between variables.

```
plot(corrm.data)
```



#importance of each principal component

```
data2_pca <- prcomp(data2[, 10:14], scale = TRUE)
summary(data2_pca)</pre>
```

```
## Importance of components:

## PC1 PC2 PC3 PC4 PC5

## Standard deviation 1.3430 1.0371 0.9399 0.8710 0.69186

## Proportion of Variance 0.3607 0.2151 0.1767 0.1517 0.09573

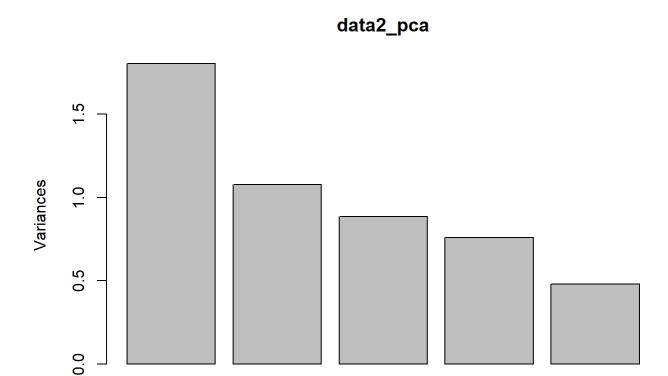
## Cumulative Proportion 0.3607 0.5758 0.7525 0.9043 1.00000
```

This result summarizes the importance of each principal component (PC) extracted from a dimensionality reduction technique like Principal Component Analysis (PCA).

Standard Deviation: It represents the variability of the data captured by each principal component. Larger standard deviations indicate that the corresponding PCs explain more variance in the original data. Proportion of Variance: It shows the proportion of the total variance in the data explained by each principal component. For example, PC1 explains 36.07% of the total variance, PC2 explains 21.51%, and so on. Cumulative Proportion: It represents the cumulative proportion of variance explained by the principal components. In this case, the first PC alone explains 36.07% of the variance, while the first two PCs combined explain 57.58%, and so on. These values help in understanding the relative importance of each principal component in capturing the variability of the original dataset.

#Plotting Variances of PCs

```
plot(data2_pca)
```



```
# A table containing eigenvalues and %'s accounted, follows. Eigenvalues are the sdev^2 (eigen_data2 <- round(data2_pca$sdev^2,3))
```

```
## [1] 1.804 1.076 0.883 0.759 0.479
```

```
round(fit.pc$values, 3)
```

```
## [1] 1.804 1.076 0.883 0.759 0.479
```

#Eigen values

```
eigen_data2 <- data2_pca$sdev^2
names(eigen_data2) <- paste("PC", 1:5, sep = "")
eigen_data2</pre>
```

```
## PC1 PC2 PC3 PC4 PC5
## 1.8035898 1.0755283 0.8834962 0.7587172 0.4786685
```

#Sum of eigen values

```
sumlambdas <- sum(eigen_data2)
sumlambdas</pre>
```

```
## [1] 5
```

```
#calculates the proportion of variance
 propvar <- round(eigen data2/sumlambdas,2)</pre>
 propvar
 ## PC1 PC2 PC3 PC4 PC5
 ## 0.36 0.22 0.18 0.15 0.10
 cumvar data2 <- cumsum(propvar)</pre>
 cumvar data2
 ## PC1 PC2 PC3 PC4 PC5
 ## 0.36 0.58 0.76 0.91 1.01
 matlambdas <- rbind(eigen data2,propvar,cumvar data2)</pre>
 matlambdas
                                      PC3
                    PC1
                             PC2
                                               PC4
 ## propvar 0.36000 0.220000 0.1800000 0.1500000 0.1000000
 ## cumvar data2 0.36000 0.580000 0.7600000 0.9100000 1.0100000
 rownames(matlambdas) <- c("Eigenvalues", "Prop. variance", "Cum. prop. variance")</pre>
 rownames (matlambdas)
 ## [1] "Eigenvalues"
                             "Prop. variance"
                                                  "Cum. prop. variance"
 eigvec.data2 <- data2 pca$rotation
 print(data2 pca)
 ## Standard deviations (1, ..., p=5):
 ## [1] 1.3429780 1.0370768 0.9399448 0.8710437 0.6918587
 ##
 ## Rotation (n \times k) = (5 \times 5):
                  PC1 PC2 PC3
                                              PC4
 ##
 ## age 0.5635382 -0.1059946 -0.1692945 -0.5419762 0.5905854
 ## trestbps 0.3671043 -0.4530454 0.7306853 -0.1215011 -0.3336476
            0.2644374 -0.6602155 -0.5618229 0.3814106 -0.1818500
 ## chol
 ## thalach -0.5044408 -0.4968335 0.2629944 0.1778681 0.6307874
 ## oldpeak 0.4725161 0.3174696 0.2294065 0.7172086 0.3300395
```

This output is from a principal component analysis (PCA) of a dataset. The first section provides the standard deviations of the principal components, indicating their respective magnitudes of variability. The second section, the rotation matrix, displays the loadings of each original variable on each principal component. Each row represents an original variable,

while each column corresponds to a principal component. The values in the matrix indicate the correlation between the original variables and the principal components.

Taking the first four PCs to generate linear combinations for all the variables with four factors

```
pcafactors.data2 <- eigvec.data2[,1:4]
pcafactors.data2</pre>
```

Multiplying each column of the eigenvector's matrix by the square-root of the corresponding eigenvalue in order to get the factor loadings

```
unrot.fact.data2 <- sweep(pcafactors.data2,MARGIN=2,data2_pca$sdev[1:4],`*`)
unrot.fact.data2</pre>
```

Computing communalities

```
communalities.data2 <- rowSums(unrot.fact.data2^2)
communalities.data2</pre>
```

```
## age trestbps chol thalach oldpeak
## 0.8330447 0.9467143 0.9841707 0.8095413 0.9478605
```

Performing the varimax rotation. The default in the varimax function is norm=TRUE thus, Kaiser

normalization is carried out

```
rot.fact.data2 <- varimax(unrot.fact.data2)
rot.fact.data2</pre>
```

```
## $loadings
## Loadings:
## PC1 PC2 PC3 PC4
## age 0.832 -0.205 0.310
## trestbps 0.962 0.112
## chol -0.988
## thalach -0.793 0.167 -0.380
## oldpeak 0.141
                  0.125 0.954
##
               PC1 PC2 PC3
## SS loadings 1.351 1.031 1.068 1.072
## Proportion Var 0.270 0.206 0.214 0.214
## Cumulative Var 0.270 0.476 0.690 0.904
## $rotmat
  [,1] [,2] [,3] [,4]
## [1,] 0.7308539 -0.2732704 0.3836183 0.4939766
## [2,] 0.2609835 0.7008221 -0.5235769 0.4081707
## [3,] -0.3179240 0.5551585 0.7417030 0.2014945
## [4,] -0.5446692 -0.3549236 -0.1690590 0.7407994
```

This output represents the results of a factor analysis, specifically the loadings matrix and rotation matrix. The loadings matrix displays the correlations between the original variables and the extracted factors (PCs). Each row corresponds to an original variable, while each column represents a factor. For instance, in the first column (PC1), 'age' has a high loading (0.832), indicating a strong correlation with PC1. In contrast, 'trestbps' has a high loading (0.962) in PC2, suggesting it contributes most to the variance explained by PC2. The rotation matrix displays the rotated loadings after applying an orthogonal transformation to simplify interpretation. Each column represents a factor, and each row represents a variable. The values in the matrix indicate the correlation between the rotated factors and the original variables.

The print method of varimax omits loadings less than abs(0.1). In order to display all the loadings, it is necessary to ask explicitly the contents of the object \$loadings

```
fact.load.data2 <- rot.fact.data2$loadings
fact.load.data2</pre>
```

```
## ## Loadings:
## PC1 PC2 PC3 PC4
```

```
## age
      0.832 -0.205 0.310
## trestbps
                       0.962 0.112
## chol
                -0.988
## thalach -0.793 0.167 -0.380
                       0.125 0.954
## oldpeak 0.141
##
##
                  PC1 PC2 PC3
                                  PC4
## SS loadings
               1.351 1.031 1.068 1.072
## Proportion Var 0.270 0.206 0.214 0.214
## Cumulative Var 0.270 0.476 0.690 0.904
```

This output presents the loadings and variance explained by each principal component (PC) obtained from a factor analysis or principal component analysis (PCA). The loadings represent the correlation between the original variables and the PCs. For instance, in PC1, 'age' has a loading of 0.832, indicating a strong positive correlation, while 'chol' has a loading of -0.988, suggesting a strong negative correlation. The "SS loadings" row shows the sum of squared loadings for each PC, indicating the amount of variance explained by each component. The "Proportion Var" row displays the proportion of total variance explained by each PC, while the "Cumulative Var" row shows the cumulative proportion of variance explained up to each PC.

```
# Computing the rotated factor scores for the data. Notice that signs are reversed for factors
F2, F3, and F4
scale.emp <- scale(data2[, 10:14])
factor_scores <- as.matrix(scale.emp) %*% fact.load.data2 %*% solve(t(fact.load.data2) %*% fact.load.data2)
factor_scores</pre>
```

```
##
                   PC1
                                PC2
                                             PC3
##
     [1,] -0.583410927  0.509304952 -0.102224021 -0.142728313
     [2,] -0.568613357 0.776468666 0.608248296 1.631991709
##
     [3,] 1.576274729 1.449581871 0.912647290 0.808690135
##
     [4,] 0.330921550 0.826540668 1.228172201 -1.228224704
##
##
     [5,] 1.457605903 -0.681971775 -0.117838092 0.765955603
     [6,] 1.135473711 -0.065448151 -1.946863759 -0.000729923
##
##
     [7,] -0.044908176 -1.553313522 -1.081131817 2.699355953
##
     [8,] -0.004231532 -0.628717353 1.380594592 -0.160288722
     [9,] -0.399110908 -0.020731857 -0.864284319 0.121315256
##
##
    [10,] 0.480508696 -0.670469191 -0.978131312 2.027211683
    [11,] 2.006824867 1.764570990 -0.787417120 -0.081985052
##
##
    [12,] -0.952660302 -1.710387474 -0.545988804 2.165347060
    [13,] -2.465487022 0.490435071 -0.552753097 0.084212830
##
    [14,] -0.164568508 -0.847285459 -0.018381056 2.926764424
##
##
    [15,] -0.274251022 0.757914116 -0.071397572 -0.056958882
    [16,] -2.465487022  0.490435071 -0.552753097  0.084212830
    [17,] -0.265292605 -1.081105100 0.165829088 0.582983058
##
##
    [18,] 0.841517867 -0.197975316 -0.928631283 1.249901186
##
    [19,] -0.611628044 -0.081261037 -0.548630189 0.079933534
##
    [20,] 0.031092815 0.623212349 0.772003119 -1.146870544
    [21,] -0.006139267 1.073657021 0.788280551 1.280137011
##
    [22,] 1.402503798 0.274555411 -1.156489954 -1.067772425
##
##
    [23,] -0.797636451  0.581517618 -1.571899968  1.879117249
##
    [24,] 0.189456211 -0.271698183 0.606920917 -1.352422790
##
    [25,] -1.269706571  0.610233808 -0.520819064 -0.635303426
```

```
[26,] 0.433174432 -1.115305102 0.681189196 -0.218287910
##
   [27,] -1.423048448 0.141547450 0.081369899 -0.402612489
##
   [28,] 0.241472781 -1.381310101 0.173564407 -0.964569775
##
   [29,] 0.372165409 -0.150010825 -0.167960629 -0.380890051
    [30,] 0.157837776 -1.143420245 2.062870511 2.212209730
##
    [31,] -0.760276159 1.459174714 -0.708943700 1.760680365
##
##
    [32,] -0.611628044 -0.081261037 -0.548630189 0.079933534
    [33,] 1.225334024 2.391340834 -0.204435674 0.175004534
##
##
    [34,] 1.663578280 -0.207277746 1.358580171 1.235997990
##
    [35,] -0.438833762  0.918070084  0.028771604 -0.857649756
    [36,] -1.049345884  0.384336065  0.848589550  2.383973410
##
##
    [37,] 0.397284897 0.765146264 -0.642083970 0.544880118
##
    [38,] -0.410018794 -0.654541691 0.766429948 -1.264631379
    [39,] 1.997455280 -0.098415346 -0.580733554 -0.716023709
##
##
    [40,] 0.317076364 0.302249625 -0.102809955 -0.663587845
##
    [41,] 0.487365200 -2.098598472 1.509346858 -0.514179166
    [42,] 0.170947067 -0.257190288 -0.688262858 -0.512625749
##
##
    [43,] 0.036078504 -1.758782971 0.098844095 -1.197018468
##
    [44,] -0.399110908 -0.020731857 -0.864284319 0.121315256
##
    [45,] -0.552144416 -1.953251932 0.037537396 0.033941373
##
    [46,] -1.520854091  0.366720204  0.570346116  -0.647925295
##
    ##
    [48,] 0.257910572 0.424979993 2.940027366 -0.588768471
    [49,] 0.845158663 -0.597290765 0.956945973 -1.284180427
##
##
    [50,] 0.171372463 0.100586054 -0.494090301 -0.038949415
    [51,] -0.199000403 -0.710316645 1.131214900 -0.245616517
##
##
    [52,] 0.978150312 0.324148727 0.180500691 -0.606590147
##
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## [1007,] 0.031092815 0.623212349 0.772003119 -1.146870544
## [1008,] -0.223242881   0.825202912 -0.307055220   0.471854029
## [1009,] -1.100814391 -0.963503442 -0.835445431 -0.483429198
## [1011,] -1.077169037 -1.114609552 0.563114168 0.423581799
## [1012,] -1.142587839 -1.240369786 -0.277525553 -0.638414101
## [1013,] -0.831703780 0.127052412 -1.019613770 0.008549275
## [1014,] -0.044908176 -1.553313522 -1.081131817 2.699355953
## [1015,] -1.117606795 1.795653004 -0.943701213 -0.295763095
## [1016,] 0.615158207 0.609108255 -0.260690288 0.900018094
## [1017,] 0.005422172 -0.901763547 0.788766872 -0.273578448
## [1018,] 1.147067538 -0.404677539 -1.209146414 1.241219804
## [1019,] -0.853748960 1.366174153 -1.178970451 -0.521047274
## [1021,] 0.117987703 0.431183024 0.759323711 -1.167872441
## [1022,] 0.364078930 -0.311030503 -0.337885453 1.272584475
## [1023,] 0.334148204 -0.419390270 -1.744855390 0.458929381
## [1024,] -0.321416184 -0.274319923 -1.154662881 -0.791866763
## [1025,] 0.992339289 1.271630009 -0.940417264 0.502769701
```

#Multiple Rgression

```
correlation_matrix <- cor(data2[c("age", "trestbps", "chol", "thalach", "oldpeak")])
# Display correlation matrix
print(correlation_matrix)</pre>
```

```
## age trestbps chol thalach oldpeak
## age 1.0000000 0.27112141 0.21982253 -0.39022708 0.20813668
## trestbps 0.2711214 1.00000000 0.12797743 -0.03926407 0.18743411
## chol 0.2198225 0.12797743 1.00000000 -0.02177209 0.06488031
## thalach -0.3902271 -0.03926407 -0.02177209 1.00000000 -0.34979616
## oldpeak 0.2081367 0.18743411 0.06488031 -0.34979616 1.00000000
```

This table represents the correlation matrix between the variables 'age', 'trestbps', 'chol', 'thalach', and 'oldpeak'. Each cell in the table contains the correlation coefficient between the corresponding pair of variables.

The correlation coefficient between 'age' and 'trestbps' is approximately 0.271, indicating a weak positive correlation. The correlation coefficient between 'age' and 'thalach' is approximately -0.390, indicating a moderate negative correlation. The correlation coefficient between 'chol' and 'thalach' is approximately -0.022, indicating a very weak negative correlation. The correlation coefficient between 'thalach' and 'oldpeak' is approximately -0.350, indicating a moderate negative correlation.

```
df <- as.data.frame(data2)

# Create a linear regression model
model <- lm(thalach ~ age , data = df)

# Display the summary of the regression model
summary(model)</pre>
```

```
##
## Call:
## lm(formula = thalach ~ age, data = df)
## Residuals:
    Min 1Q Median 3Q
##
## -65.680 -11.680 4.373 16.394 45.456
## Coefficients:
##
             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 202.9793 4.0283 50.39 <2e-16 ***
             -0.9896 0.0730 -13.56 <2e-16 ***
## age
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 21.19 on 1023 degrees of freedom
## Multiple R-squared: 0.1523, Adjusted R-squared: 0.1514
## F-statistic: 183.8 on 1 and 1023 DF, p-value: < 2.2e-16
```

Residuals: These are the differences between the observed and predicted values of the target variable. They show the variability that is not explained by the model. The minimum residual is -65.680, and the maximum is 45.456. Coefficients: The 'Estimate' column provides the estimated coefficients of the linear regression model. The intercept is 202.9793, indicating the expected value of 'thalach' when 'age' is 0. The coefficient for 'age' is -0.9896, indicating that for each one-unit increase in 'age', the 'thalach' decreases by approximately 0.9896 units.

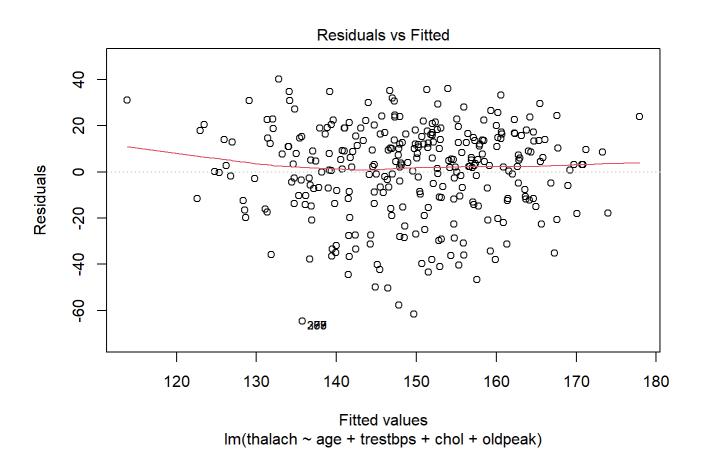
```
df <- as.data.frame(data2)

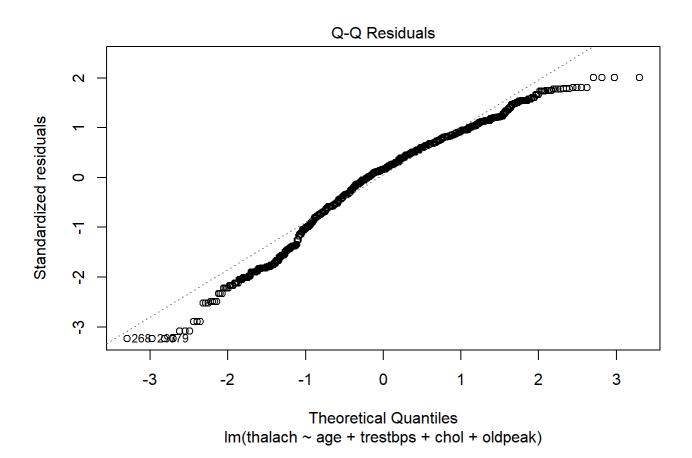
# Create a multiple linear regression model
fit <- lm(thalach ~ age + trestbps + chol + oldpeak, data = df)

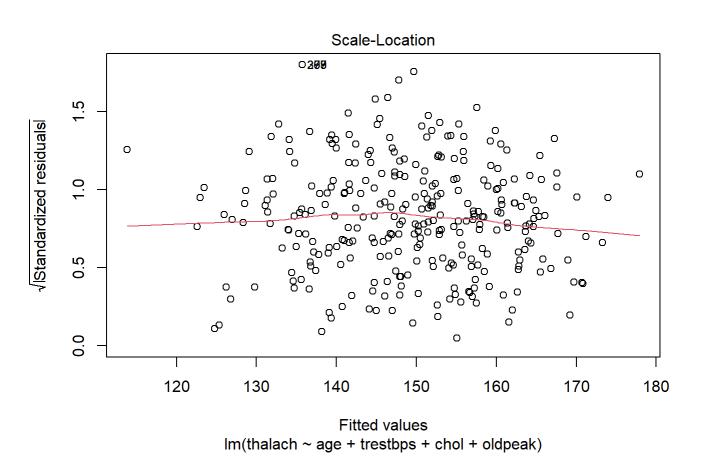
# Display the summary of the regression model
summary(fit)</pre>
```

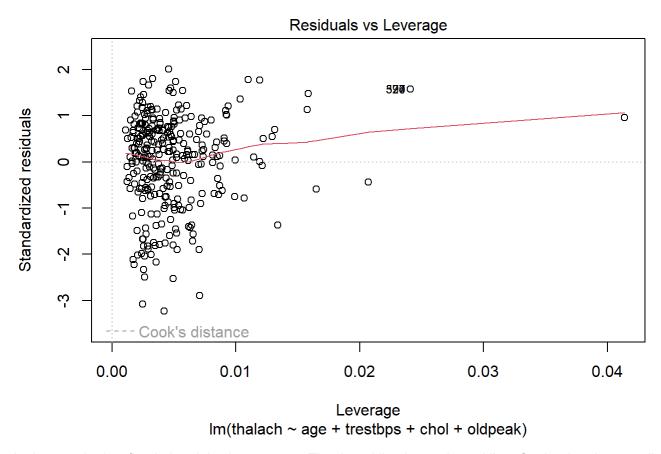
```
-0.94419
                            0.07411 -12.741
## age
                                             < 2e-16 ***
## trestbps
                 0.14313
                            0.03762
                                      3.805
                                             0.00015 ***
## chol
                0.02916
                            0.01248
                                      2.336
                                             0.01967 *
                            0.55052 -10.561
                                             < 2e-16 ***
## oldpeak
                -5.81417
  Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
  Residual standard error: 20.05 on 1020 degrees of freedom
## Multiple R-squared: 0.2435, Adjusted R-squared: 0.2405
## F-statistic: 82.07 on 4 and 1020 DF, p-value: < 2.2e-16
```

```
plot(fit)
```









In the resudual vs fitted plot, it is almost same. The dotted line is nearby red line. So the data is normally distributed.

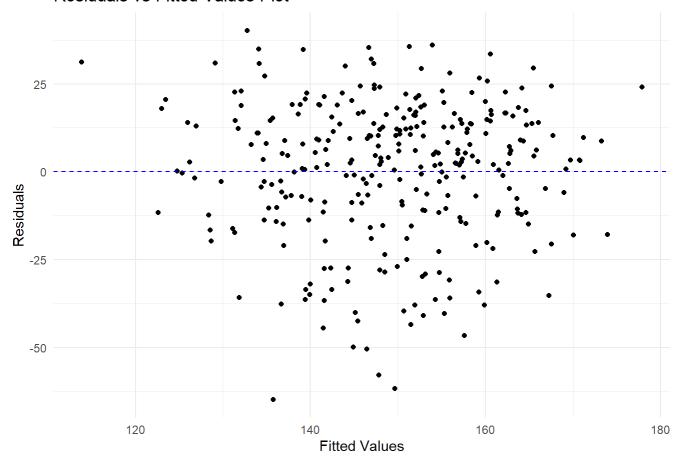
The Q-Q plot indicates that the residuals of the model are not perfectly normal, particularly at the tails, the central portion of the data follows the expected pattern closely. This might be acceptable in many practical situations,

This is the homoscedasticity, the values are equally scattered.

residuals_df <- data.frame(
 fitted values = fitted(fit),</pre>

```
coefficients(fit)
    (Intercept)
                          age
                                  trestbps
                                                    chol
                                                              oldpeak
## 180.72923414
                                0.14312658
                 -0.94418609
                                             0.02916137
                                                         -5.81417065
confint(fit,level=0.95)
                       2.5 %
                                   97.5 %
##
  (Intercept) 169.358462168 192.1000061
                -1.089609092 -0.7987631
  age
  trestbps
                 0.069306756
                                0.2169464
## chol
                 0.004667538
                                0.0536552
## oldpeak
                              -4.7338843
                -6.894456984
# Create a dataframe with fitted values and residuals
```

Residuals vs Fitted Values Plot



In this plot:

The horizontal axis is labeled "Fitted Values," which represent the values predicted by the regression model.

The vertical axis is labeled "Residuals," which are the differences between the observed values and the fitted (predicted) values for each observation in the dataset.

The points on the plot are the individual observations. Each point represents one observation's residual corresponding to its fitted value.

A horizontal dashed line at zero on the residuals axis represents the ideal case where the residuals would be if the model

perfectly predicted the observed values.

#Prediction

```
new_data <- data.frame(predict.lm(fit, data.frame( age= 70, trestbps=145, chol=300 , oldpeak=
3)))
new_data</pre>
```

```
## predict.lm.fit..data.frame.age...70..trestbps...145..chol...300..
## 1
```

Model Accuracy

```
rsquared <- summary(fit)$r.squared
cat("R-squared:", rsquared, "\n")</pre>
```

```
## R-squared: 0.2434723
```

```
adjusted_rsquared <- summary(fit)$adj.r.squared
cat("Adjusted R-squared:", adjusted_rsquared, "\n")</pre>
```

```
## Adjusted R-squared: 0.2405055
```

#Nonlinearity # component + residual plot

```
library(car)
```

```
## Warning: package 'car' was built under R version 4.3.3
```

```
## Loading required package: carData
```

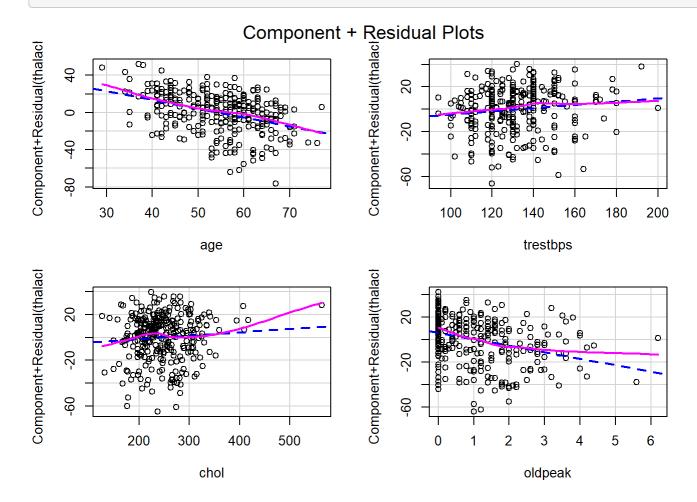
```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:psych':
##
## logit
```

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

```
## The following object is masked from 'package:purrr':
##
## some
```

crPlots(fit)



The top left plot shows the relationship between "age" and the dependent variable. The solid purple line represents the fitted values, showing a general negative trend, indicating that as age increases, the dependent variable tends to decrease. The blue dashed line is the zero line, which helps to assess the distribution of residuals.

The top right plot is for "trestbps" (which might stand for resting blood pressure) against the dependent variable. Again, there's a general negative trend indicated by the purple line.

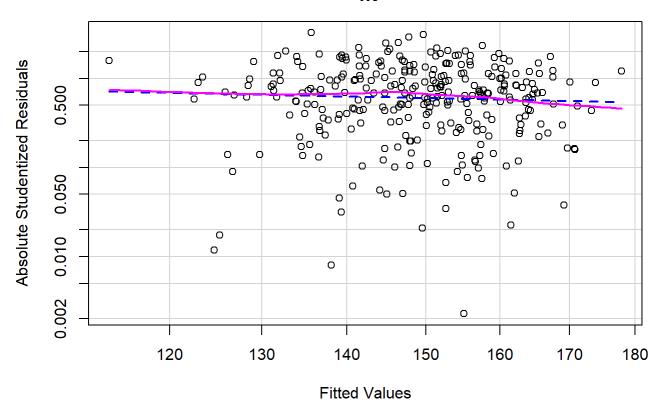
The bottom left plot shows the relationship for "chol" (possibly cholesterol levels) with the dependent variable. This plot reveals a slight positive trend, suggesting that higher cholesterol levels might be associated with an increase in the dependent variable.

The bottom right plot represents the variable "oldpeak" (which might relate to ST depression induced by exercise relative to rest) against the dependent variable. There is a noticeable negative trend, as the purple line slopes downwards.

plot studentized residuals vs. fitted values

```
library(car)
spreadLevelPlot(fit)
```

Spread-Level Plot for fit



```
## ## Suggested power transformation: 1.608289
```

In the plot:

The x-axis represents the fitted values (the predicted values from the regression model). The y-axis shows the absolute standardized residuals (the absolute value of the residuals, which are the differences between the observed values and the fitted values, standardized by dividing by an estimate of the standard deviation of the residuals).

#LDA(Linear Discrimination Analysis)

```
Ldata <- as.matrix(data2[, c(10:14)])
row.names(Ldata) <- row.names(data2)
Lraw <- cbind(Ldata, as.numeric(as.factor(data2$target)) - 1)
colnames(Lraw)[ncol(Lraw)] <- "diagnosis"
smp_size_raw <- floor(0.75 * nrow(Lraw))
train_ind_raw <- sample(nrow(Lraw), size = smp_size_raw)
train_raw.df <- as.data.frame(Lraw[train_ind_raw, ])
test_raw.df <- as.data.frame(Lraw[-train_ind_raw, ])
Lraw.lda <- lda(formula = diagnosis ~ ., data = train_raw.df)
Lraw.lda</pre>
```

```
## Call:
## lda(diagnosis ~ ., data = train_raw.df)
##
```

```
## Prior probabilities of groups:

## 0 1

## 0.4765625 0.5234375

##

## Group means:

## age trestbps chol thalach oldpeak

## 0 56.28142 134.6557 250.7131 138.0519 1.5838798

## 1 52.46766 129.3483 240.9055 158.0398 0.5597015

##

## Coefficients of linear discriminants:

## LD1

## age 0.0004021632

## trestbps -0.0068421073

## chol -0.0029050167

## thalach 0.0304184498

## oldpeak -0.5848674985
```

Prior probabilities: These are the probabilities of belonging to each group (0 and 1) before considering any information from the predictor variables. Here, the prior probability of group 0 is 0.4974, and the prior probability of group 1 is 0.5026. Group means: These are the mean values of each predictor variable for each group. For example, for group 0, the mean age is 56.62, mean 'trestbps' is 133.71, mean 'chol' is 250.87, mean 'thalach' is 139.46, and mean 'oldpeak' is 1.58. Coefficients of linear discriminants: These coefficients represent the weights assigned to each predictor variable in the linear combination that maximizes the separation between the groups. In this case, the linear discriminant function (LD1) is constructed using these coefficients. For example, a one-unit increase in 'thalach' corresponds to an increase of 0.0307 units in LD1, while a one-unit increase in 'oldpeak' corresponds to a decrease of 0.5746 units in LD1.

#Summary

```
summary(Lraw.lda)
```

```
##
       Length Class Mode
## prior 2 -none- numeric
## counts 2
             -none- numeric
## means 10
             -none- numeric
## scaling 5
             -none- numeric
## lev 2
             -none- character
             -none- numeric
## svd
        1
## N
        1
             -none- numeric
## call
             -none- call
        3
## terms 3
             terms call
## xlevels 0
             -none- list
```

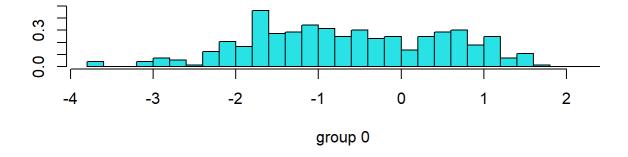
```
print(Lraw.lda)
```

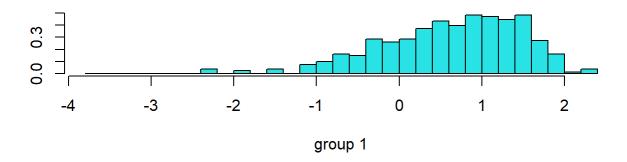
```
## Call:
## lda(diagnosis ~ ., data = train_raw.df)
##
## Prior probabilities of groups:
## 0 1
## 0.4765625 0.5234375
##
```

```
## Group means:
##
          age trestbps
                           chol thalach
                                            oldpeak
  0 56.28142 134.6557 250.7131 138.0519 1.5838798
  1 52.46766 129.3483 240.9055 158.0398 0.5597015
##
  Coefficients of linear discriminants:
##
                      LD1
             0.0004021632
##
  age
  trestbps -0.0068421073
  chol
            -0.0029050167
             0.0304184498
  thalach
  oldpeak
           -0.5848674985
```

Prior probabilities: These are the probabilities of belonging to each group (0 and 1) before considering any predictor variables. Group means: These represent the average values of predictor variables for each group. For instance, group 0 has a mean age of 56.62, mean 'trestbps' of 133.71, mean 'chol' of 250.87, mean 'thalach' of 139.46, and mean 'oldpeak' of 1.58, while group 1 has lower means for all variables. Coefficients of linear discriminants: These coefficients are used to form a linear combination of predictor variables that best separates the groups. For example, 'thalach' has a positive coefficient, indicating that higher values of 'thalach' contribute to the prediction of group 1, while 'oldpeak' has a negative coefficient, suggesting that higher values of 'oldpeak' contribute to the prediction of group 0.

```
plot(Lraw.lda)
```





These histograms represent the distributions of Linear Discriminant Analysis (LDA) scores for two different groups or classes in a dataset. LDA is a technique used in statistics and machine learning for pattern classification and

dimensionality reduction. It projects the data onto a lower-dimensional space where the classes are most separable.

In the context of LDA:

Levels: 0 1

Classes (groups) are typically predefined based on the labels in the dataset.

LDA tries to find a linear combination of features that best separates the different classes.

The resulting histograms show the distribution of the projected data along the LDA component axis for each class.

For "group 0," the histogram shows a fairly normal distribution of LDA scores centered around zero. For "group 1," the distribution is also roughly normal but appears to be slightly skewed towards the right.

```
Lraw.lda.predict$x
```

[223] 0 1 1 0 1 1 0 0 0 1 1 1 1 1 0 1 0 0 0 1 0 1 1 1 1 1 1 0 1 0 0

```
##
              LD1
## 2 -0.93538596
## 4
      1.00869443
## 6
      -0.56600370
## 10 -2.29774854
## 14 -2.85932996
       0.40205235
## 15
## 18 -1.88139407
## 21
     -0.82179377
       1.54022363
## 25
## 28
       0.47884525
## 38
      1.51755749
## 43
      1.00626285
## 44
       0.07560258
      0.16220910
## 45
       0.20695335
## 51
## 54 -0.59991816
## 55
     -3.77583240
## 57
      0.14648299
## 60
       0.97304300
## 69
       1.42952737
## 79
       0.54752515
## 83 -1.62374399
```

```
## 86
       1.41781743
## 88
       0.14883245
## 93
       -1.74586776
## 94
     -0.86253541
## 101
      1.15500042
      0.76252207
## 104
## 106 -0.83895781
## 107
       0.20976146
## 108 -1.60900028
## 110 -0.35501352
## 113 0.63805541
## 114 -1.41851093
## 115 -0.99316542
## 117 -0.26017195
## 127
       0.37655611
## 130
       0.46439097
## 131
       0.66492619
## 137
       0.16220910
## 142
        0.43067819
## 153
       1.18725429
## 159 -0.77802051
## 160
       1.96464838
## 162
       0.02852554
## 164
       0.82107920
## 173
       1.33412460
## 175 -1.54097597
## 178 -2.18734352
## 179
       1.76598303
## 180 -0.94181151
## 183
       0.37350268
## 185 1.10784126
## 189 -0.26017195
## 190 -1.10597737
## 192 1.13838815
## 194 -0.13128931
## 196 -0.08940106
## 198
       1.79250621
## 200 -0.55067237
## 203
       0.51700260
## 206
       0.93116729
## 230
       0.26962291
## 232
       1.15161672
## 240 -0.15543695
## 241
        0.80758969
## 244 -0.82179377
## 249
       0.74511658
## 250
       0.85642370
## 252
       0.67386706
## 253 -0.90397337
## 262 0.09383539
## 263
       1.88662703
## 281
       1.11030003
## 285 -0.45059829
## 286
       0.14963317
```

```
## 288
       0.43948558
## 298 -1.18964888
## 299
       1.60352801
## 300
       1.05987138
## 303
       0.16220910
## 304 -1.41625727
## 305
       1.29237622
## 313 -2.44814227
## 315
       0.76490508
## 316
       0.93116729
## 319
       1.16857585
## 320 -0.29469463
## 322
       0.13128365
## 323
       0.30952240
## 326 -0.20661139
## 327
       1.50665253
## 331
       1.42952737
## 332
       0.28203805
## 333 -0.27049189
## 338
       0.39369679
## 343 -0.09265661
## 345
       1.96464838
## 348
       1.27615321
## 351
       0.37655611
## 353 -1.41851093
## 361
       1.88662703
## 364
       1.36874074
## 367 -0.16512659
## 371 -1.80502683
## 376 -1.18884505
## 379 -2.21861213
## 380
       2.14185851
## 381 -1.89557128
## 390 -0.73692361
## 392 -0.49892216
## 393 -0.16080825
## 400 -0.73692361
## 407
       1.16065847
## 418
       1.25874330
## 420 -0.29996832
## 423
       0.46992367
## 426 -0.44827251
## 429
       0.37708963
## 435
       1.39274389
## 437
       0.14883245
## 438 -1.36688991
## 440 -0.11941935
## 449
       0.45639597
## 453
       0.26962291
## 460
       1.65137994
## 461 -0.70751900
## 463
       2.14185851
## 464
       1.23821544
## 472 -0.22360415
```

```
## 474
        0.13504807
## 475
       0.81599760
## 476
       1.46513575
## 480 -1.09269712
## 482
      -2.14920800
## 485
       0.69740156
## 493 -1.10597737
## 502
       0.94473254
## 505
       0.88678172
## 506
       0.55334358
## 507 -1.70962295
## 517 -1.16308189
## 524
       1.00869443
## 531 -0.80749716
## 536 -0.92529065
## 537
       0.12232603
## 539
       0.07560258
## 541 -1.71592528
## 548
       0.48696479
## 550
       0.11274956
## 554
       0.17045811
## 560 -2.21861213
## 565 -1.76030228
## 566
       0.95342423
## 571
       1.07518605
       0.51700260
## 577
## 578 -2.19566653
## 587
      -1.10597737
## 589 -0.31404522
## 590 -2.29774854
## 593 -2.44814227
## 595 -1.04758795
## 610 -2.89984933
## 613 -1.30085453
## 624 -0.99292227
## 633
       1.11030003
## 635
       0.76435993
## 659 -1.10597737
## 660
       1.51755749
## 661 -2.01598606
## 663
       0.64045615
## 664 -0.56600370
## 665 -2.02011698
## 668
       0.21897614
## 669
       2.36323456
## 671
        1.00626285
       0.76435993
## 672
## 677
       -0.34972878
## 681
       0.95578925
## 688
       1.18725429
## 693 -0.93538596
## 697
       0.12232603
## 699
        0.29025417
## 707
        0.49984755
```

```
## 716
        0.28803425
## 722
        1.79250621
## 727
        0.82107920
## 735
        0.40205235
## 742
        1.39274389
## 749
        1.36996888
## 750
       0.36441048
## 756
       1.44247432
## 757
       -2.18734352
       1.62857053
## 759
## 767
       -1.41851093
## 768
       -1.52899032
## 769
       1.18957888
## 771
       0.20746352
## 773 -0.15543695
## 777 -0.31404522
## 789 -1.97110183
## 790 -1.60900028
## 793 -1.52899032
## 800
       0.84327137
## 802 -0.73692361
## 804
       1.14253693
## 805
       -0.11539802
## 807 -1.06008919
## 809
       1.09149705
## 810
       0.20688084
## 811 -1.23457245
## 815
       0.49262621
## 817
       0.28803425
## 823 -0.34972878
## 825 -2.01598606
## 826
       1.29070328
## 828
       0.49984755
## 843 -0.16512659
## 844 -0.37263054
## 845
       0.37350268
## 847
       0.94473254
## 849
       0.20695335
## 851
      -0.11941935
## 853
       0.99085624
## 874
       0.46439097
## 876 -1.16308189
## 878
       1.15500042
## 880
       1.51755749
## 890 -2.14920800
## 899 -0.40156081
## 903 -1.26093407
## 907
       1.50608845
## 908
       0.46380816
## 915
       0.29025417
## 916
       0.07560258
## 919
       0.66329904
## 921 -0.18199865
## 924
        0.22377610
```

```
## 926 -0.76168478
## 930 -1.16308189
## 931 -1.72076166
## 932 1.52314924
## 933 -0.70086888
## 938 0.58992023
## 954 0.58407580
## 962 -0.56600370
## 963 0.70726371
## 965 1.53059078
## 972 0.59046915
## 973
       2.14185851
## 979 1.76598303
## 986 -0.45812418
## 988 0.97304300
## 992 0.29272920
## 1008 0.14648299
## 1014 -2.30616176
## 1022 -1.24011317
```

#Accuracy

```
# Get the predicted classes
predicted_classes <- predict(Lraw.lda, newdata = test_raw.df)$class

# Calculate accuracy
accuracy <- mean(predicted_classes == test_raw.df$diagnosis)
accuracy</pre>
```

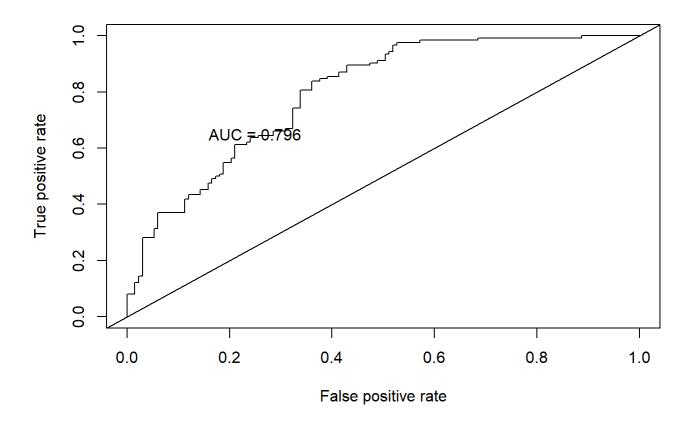
```
## [1] 0.7315175
```

#ROC Plot

```
# Get the posteriors as a dataframe
Lraw.lda.predict.posteriors <- as.data.frame(predict(Lraw.lda, newdata = test_raw.df)$posterio
r)

# Calculate the performance metrics
pred <- prediction(Lraw.lda.predict.posteriors[, 2], test_raw.df$diagnosis)
roc.perf <- performance(pred, measure = "tpr", x.measure = "fpr")
auc.train <- performance(pred, measure = "auc")@y.values

# Plot the ROC curve
plot(roc.perf)
abline(a = 0, b = 1)
text(x = 0.25, y = 0.65, paste("AUC = ", round(auc.train[[1]], 3), sep = ""))</pre>
```



In this ROC curve:

The x-axis represents the False Positive Rate (FPR): the proportion of negative instances that are incorrectly classified as positive. The y-axis represents the True Positive Rate (TPR): the proportion of positive instances that are correctly classified. The plot also includes a diagonal line, which represents the performance of a completely random classifier (AUC = 0.5). An ideal classifier would yield a point in the upper left corner of the ROC space, corresponding to a TPR of 1 (perfect sensitivity) and an FPR of 0 (perfect specificity).

The Area Under the Curve (AUC) value is a measure of the overall performance of the classifier and is shown in the plot as "AUC = 0.821". An AUC of 1 represents a perfect classifier, and an AUC of 0.5 represents a worthless classifier. An AUC of 0.821 suggests that the classifier has a good discriminatory ability to distinguish between the positive class and the negative class.

#Logistic Regression

```
library(tidyverse)
library(readr)
library(ROCR)
library(PerformanceAnalytics)
library(e1071)
library(caret)
library(gbm)
library(corrplot)
library(ggcorrplot)
library(mass)
library(rpart)
```

```
library(caTools)
library(naivebayes)
library(class)
library (ISLR)
library(glmnet)
library(Hmisc)
library(funModeling)
library(pROC)
library(randomForest)
library(klaR)
library(scales)
library(cluster)
library(factoextra)
library(DataExplorer)
library(ClustOfVar)
library (GGally)
library(dplyr)
library(visdat)
```

```
file_path <- "D:/Multivariate Analysis/Final_Project/heart.csv"
data <- read.csv(file_path)
head(data)</pre>
```

```
age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal
## 1 52 1 0 125 212 0 1 168 0 1.0 2 2
                                      3.1
## 2 53 1 0
            140 203 1
                        0
                             155
                                           0 0
                                  1
## 3 70 1 0
            145 174 0
                        1
                            125
                                  1
                                      2.6
                                           0 0
                                                 3
                        1 161
1 106
## 4 61 1 0
                                  0
                                           2 1
            148 203 0
                                     0.0
                                                3
                                     1.9
                                           1 3
## 5 62 0 0
            138 294 1
                                  0
                                                2
            100 248 0 0 122
## 6 58 0 0
                                     1.0
                                           1 0
                                                 2
                                 0
## target
## 1
## 2
     0
     0
## 3
## 4
     0
     0
## 5
     1
## 6
```

#Transformation

```
target = if_else(target == 1, "UNHEALTHY", "HEALTHY")
) %>%
mutate_if(is.character, as.factor) %>%
dplyr::select(target, sex, fbs, exang, cp, restecg, slope, ca, thal, everything())
```

```
str(data2)
```

```
## 'data.frame':
                   1025 obs. of 14 variables:
## $ target : Factor w/ 2 levels "HEALTHY", "UNHEALTHY": 1 1 1 1 1 2 1 1 1 1 ...
           : Factor w/ 2 levels "FEMALE", "MALE": 2 2 2 2 1 1 2 2 2 2 ...
## $ fbs
           : Factor w/ 2 levels "<=120",">120": 1 2 1 1 2 1 1 1 1 ...
## $ exang : Factor w/ 2 levels "NO", "YES": 1 2 2 1 1 1 1 2 1 2 ...
  $ cp : Factor w/ 3 levels "ASYMPTOMATIC",..: 1 1 1 1 1 1 1 1 1 1 ...
## $ restecg : Factor w/ 3 levels "ABNORMALITY",..: 1 2 1 1 1 2 3 2 2 2 ...
## $ slope : Factor w/ 3 levels "0","1","2": 3 1 1 3 2 2 1 2 3 2 ...
           : Factor w/ 5 levels "0","1","2","3",...: 3 1 1 2 4 1 4 2 1 3 ...
            : Factor w/ 4 levels "0","1","2","3": 4 4 4 4 3 3 2 4 4 3 ...
## $ thal
## $ age : int 52 53 70 61 62 58 58 55 46 54 ...
## $ trestbps: int 125 140 145 148 138 100 114 160 120 122 ...
          : int 212 203 174 203 294 248 318 289 249 286 ...
## $ thalach : int 168 155 125 161 106 122 140 145 144 116 ...
## $ oldpeak : num 1 3.1 2.6 0 1.9 1 4.4 0.8 0.8 3.2 ...
```

Now we see how many rows of data have NA values

```
nrow(data2[is.na(data2$ca) | is.na(data2$thal), ])
```

```
## [1] 0
```

There is no rows of data having NAs in them.

It is now necessary to ensure that samples of both healthy and diseased individuals are taken from each gender (male and female). We should presumably eliminate every female from the model if heart disease is limited to male samples.

```
xtabs(~ target + sex, data=data2)
```

```
## sex
## target FEMALE MALE
## HEALTHY 86 413
## UNHEALTHY 226 300
```

Healthy and Unhealthy patients are both represented by a lot of female and male samples.

For all 3 levels of chest pain reported by patients

```
xtabs(~ target + cp, data=data2)
```

```
##
## target ASYMPTOMATIC ATYPICAL ANGINA NON-ANGINAL PAIN
## HEALTHY
                                  33
               401
                                                 65
## UNHEALTHY
                   173
                                 134
                                                219
xtabs(~ target + fbs, data=data2)
           fbs
##
## target <=120 >120
## HEALTHY 417 82
## UNHEALTHY 455 71
xtabs(~ target + restecg, data=data2)
##
          restecg
## target ABNORMALITY NORMAL PROBABLE OR DEFINITE
## HEALTHY 204 283
## UNHEALTHY 309 214
                                             3
xtabs(~ target + exang, data=data2)
##
           exang
## target NO YES
## HEALTHY 225 274
## UNHEALTHY 455 71
xtabs(~ target + slope, data=data2)
          slope
## slope
## target 0 1 2
##
## HEALTHY 46 324 129
## UNHEALTHY 28 158 340
xtabs(~ target + ca, data=data2)
##
          са
## target 0 1 2 3 4
## HEALTHY 163 160 113 60 3
## UNHEALTHY 415 66 21 9 15
xtabs(~ target + thal, data=data2)
##
           thal
## target 0 1 2 3
## HEALTHY 4 43 132 320
## UNHEALTHY 3 21 412 90
```

#Applying Rgression model A simple model in which we will try to predict heart disease only using the gender of eah patient.

```
logistic <- glm(target ~ sex, data = data2, family = "binomial")
summary(logistic)</pre>
```

```
##
## Call:
## glm(formula = target ~ sex, family = "binomial", data = data2)
## Coefficients:
##
            Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.9662 0.1267 7.626 2.42e-14 ***
## sexMALE -1.2859
                         0.1477 -8.707 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 1420.2 on 1024 degrees of freedom
##
## Residual deviance: 1337.8 on 1023 degrees of freedom
## AIC: 1341.8
##
## Number of Fisher Scoring iterations: 4
```

Here the glm() function that performs Generalized Linear Models. we used formula syntax(hd~sex) to predict heart disease(target). Then we specify the data(data=data2) that we are using for this model. In last, we specify that we want the binomial family of generalized linear models. This makes the glm() function do logistic regression, as apposed to some other type of generalized linear model. we are storing the output from glm() in a variable called "logistic". Then use the summary function to get details about the logistic regression.

summary output: The first line has the original call to the glm() function. Then it gives the summary of the deviance residuals. They look good since they are close to being centered on 0 and are roughly symmetrical.

Then we have the coefficients. They corresponding to the following model: Heart disease = 0.9662 - 1.2859 x the patient is male. The variable(the patient is male, is equal to 2 when the patient is female and 1 when the patient is male). Thus if are predicting heart disease for a female patient, we get the following equation: Heart disease = 0.9662 - 1.2859 x 2 = -1.6056. Thus the log (odds) that a female has heart disease = -1.6056 If are predicting heart disease for a male patient, we get the following equation: Heart disease = 0.9662 - 1.2859 x 1 = -0.3197. Since the first term(0.9662) is the log(odds) of a female having heart disease and the second term(-1.2859) indicates the increase in the log(odds) that a male has of having heart disease. In other words, the second term(-1.2859) is the log(odds ratio) of the odds that a male will have heart disease.

The output std.error and z value shows how the Walds test was computed for both coefficients.

The p-values(Pr(>|z|)) are well below 0.05 and thus, the log(odds) and the log(odd ratio) are both statistically significant.

When we do "normal linear regression, we estimate both the mean and variance from the data". In contrast, with logistic regression, we estimate the mean of the data, and the variance is derived from the mean. Since we are not estimating the variance from the data(instead of just deriving it from the mean), it is possible that the variance is underestimated. If so, you can adjust the dispersion parameter in the summary command.

The null deviance and residuals deviance can be used to compare models, compute R^2 and an overall P-value.

Lastly, we have the number of Fisher Scoring iterations, which just tell us how quickly the glm() function converged on the maximum likelihood estimates for the coefficients

```
median(data2$age)

## [1] 56

logistic <- glm(target~ sex, data=data2, family= "binomial")</pre>
```

we have done a simple logistic regression using just one of the variables (sex) to predict heart disease, we can create a fancy model that uses all of the variables to predict heart disease.

```
logistic <- glm(target~ ., data=data2, family= "binomial")
summary(logistic)</pre>
```

```
##
## Call:
## qlm(formula = target \sim ., family = "binomial", data = data2)
## Coefficients:
##
                    Estimate Std. Error z value Pr(>|z|)
                    -1.217015 1.731518 -0.703 0.48214
## (Intercept)
## sexMALE
                    ## fbs>120
                    0.557247 0.303949 1.833 0.06675 .
                    ## exangYES
## cpATYPICAL ANGINA
                    0.405498 0.297009 1.365 0.17217
## cpNON-ANGINAL PAIN
                    ## restecgNORMAL
## slope1
                    ## slope2
                     0.743280 0.473771 1.569 0.11668
                    -2.216707 0.271674 -8.159 3.37e-16 ***
## ca1
## ca2
                    -2.546774 0.508091 -5.012 5.37e-07 ***
## ca3
                    1.184139 0.873710 1.355 0.17532
## ca4
                     2.418942 1.138722 2.124 0.03365 *
## thall
## thal2
                    2.470571 1.091652 2.263 0.02363 *
## thal3
                     1.010352 1.095374 0.922 0.35633
                    ## age
                    -0.017261 0.006220 -2.775 0.00552 **
## trestbps
                    ## chol
## thalach
                    0.024631 0.006031 4.084 4.43e-05 ***
                    ## oldpeak
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##
    Null deviance: 1420.24 on 1024 degrees of freedom
```

```
## Residual deviance: 648.79 on 1003 degrees of freedom
## AIC: 692.79
##
## Number of Fisher Scoring iterations: 6
```

This formula syntax, target~., means that we want to model heart disease(target) using all of the remaining variables in our data.frame called "data2".

From the above result, we will just talk about a few of the coefficients: We see that age is not a useful predictor because it has a large P-value. However the median age in our dataset was 56, so most of the folks were pretty old and that explains why its was not very useful.

The predictors with p-values less than 0.05 are: sexMALE, exangYES, cpNON-ANGINAL PAIN, ca1, ca2, ca3, thal1, thal2, age, trestbps, chol, thalach, oldpeak.

On the bottom of the output, we see that the Residual Deviance and the AIC are much smaller for this fancy model than they were for the simple model, when we only used gender to predict heart disease.

If we want to calculate the McFadden's Pseudo R^2, we can pull the log-likelihood of the null model out of the logistic variable by getting the value for the null deviance and dividing by -2 and we can pull the log-likelihood for the fancy model out of the logistic variable by getting the value for the residual deviance and dividing by -2.

```
ll.null <- logistic$null.deviance/-2
ll.proposed <- logistic$deviance/-2

## McFadden's Pseudo R^2 = [ LL(Null) - LL(Proposed) ] / LL(Null)
(ll.null - ll.proposed) / ll.null</pre>
```

```
## [1] 0.5431804
```

Then we just do the math and ended up with a Pseudo $R^2 = 0.54$. This can ne interpreted as the overall effect size. And we can use the same log likelihoods to calculate a P value for that R^2 using a Chi-square distribution.

```
1 - pchisq(2*(ll.proposed - ll.null), df=(length(logistic$coefficients)-1))
```

```
## [1] 0
```

In this case, the tiny P-value indicates that the R² value is not a result of random chance.

Lastly, we can draw a graph that shows the predicted probabilities that each patient has heart disease along with their actual heart disease status.

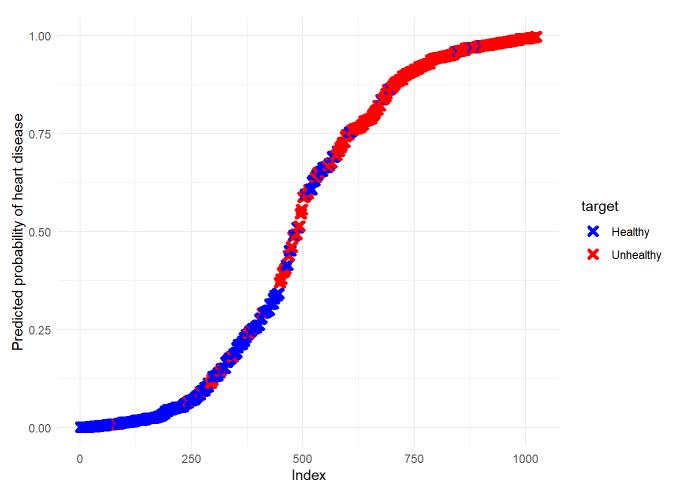
```
## Load necessary libraries
library(ggplot2)
library(cowplot)
```

```
##
## Attaching package: 'cowplot'
```

```
## The following object is masked from 'package:lubridate':
##
```

stamp

```
## Create a data frame with predicted probabilities and actual heart disease status
predicted.data <- data.frame(</pre>
 probability.of.target = logistic$fitted.values,
 target = ifelse(data$target == 0, "Healthy", "Unhealthy")
## Order the predicted data by probability of target, and add a rank column (sort the data.fra
me from low probabilities to high probabilities)
predicted.data <- predicted.data[order(predicted.data$probability.of.target, decreasing = FALS</pre>
E), ]
# Then we add a new column to the data.frame that is rank of each sample , from low probababil
ity to high probability.
predicted.data$rank <- 1:nrow(predicted.data)</pre>
## Plot the predicted probabilities for each sample, color by actual heart disease status
ggplot(data = predicted.data, aes(x = rank, y = probability.of.target)) +
 geom point(aes(color = target), alpha = 1, shape = 4, stroke = 2) +
 scale color manual(values = c("Healthy" = "blue", "Unhealthy" = "red")) + ## Customize colo
 xlab("Index") +
 ylab("Predicted probability of heart disease") +
  theme minimal()
```



```
## Save the plot as a PDF
ggsave("heart_disease_probabilities.pdf")
```

```
## Saving 7 x 5 in image
```

Most of the patients with heart disease (the red ones), are predicted to have a high probability of having heart disease and most of the patients without heart disease (the blue ones) are predicted to have a low probability of having a heart disease. Thus logistic regression has done a pretty good job.