Project

Group 7

2023-05-01

Importing the dataset from local

```
setwd("/Users/prathyushavajinepally/Downloads")

# Import CSV file
data <- read.csv("UA.csv")

head(data)
```

```
##   Gender  Age Height Weight      BMI  L1.4 L1.4T     FN   FNT     TL   TLT
ALT
## 1      2 61.9    164     47 17.47472 0.894  -2.4 0.6895 -2.95 0.7130 -2.90
17.0
## 2      2 55.0    162     54 20.57613 1.333   1.3 0.9130 -1.30 1.0675 -0.15
34.0
## 3      2 44.0    160     54 21.09375 1.157  -0.2 0.5190 -3.85 0.5770 -3.55
11.0
## 4      1 64.7    158     59 23.63403 0.948  -2.3 0.7920 -2.15 0.9050 -1.40
4.1
## 5      1 88.5    167     60 21.51386 1.114  -0.9 0.8250 -1.90 0.9385 -1.15
32.0
## 6      1 73.0    169     65 22.75831 0.956  -2.2 0.6965 -2.35 0.7550 -2.05
17.0
##   AST   BUN  CREA  URIC  FBG HDL.C LDL.C   Ca    P   Mg Calsium Calcitriol
## 1  21  8.10  84.8 265.4 4.55  1.16  2.06 2.15 1.04 0.76       1          1
## 2  25  7.64  85.0 466.0 3.89  1.22  2.35 2.15 1.11 0.96       1          0
## 3  21  5.14  76.2 479.1 4.66  1.54  1.65 2.18 1.10 0.89       1          1
## 4  28 12.99 104.0 473.1 6.84  0.93  1.39 2.35 0.87 0.78       0          0
## 5  19  4.10  72.4 429.8 5.07  1.25  1.85 1.98 0.93 0.86       1          1
## 6  23  5.09  81.6 366.1 6.65  1.16  3.13 2.43 1.09 0.78       1          1
##   Bisphosphonate Calcitonin HTN COPD DM Hyperlipidaemia Hyperuricemia AS
VT VD
## 1              0          0   1    1  0               0             1  1
0  1
## 2              0          0   1    0  1               0             1  1
0  1
## 3              0          1   1    1  1               0             1  1
0  1
## 4              0          1   1    1  1               0             1  1
0  1
## 5              0          0   1    0  1               0             1  1
```

```
0  1
## 6              1          1   1    1  1               0             1  1
0  1
##   OP CAD CKD Fracture Smoking Drinking
## 1  1   1   0        0       1        0
## 2  1   0   1        0       0        0
## 3  1   1   0        0       0        0
## 4  1   1   0        0       1        1
## 5  1   1   0        0       1        0
## 6  1   0   1        0       0        0
```

Selecting columns of dataframe

```
# Select columns "A" and "C"
data <- data[, c("Age", "Gender", "BMI", "Ca", "P", "Mg", "OP", "Smoking",
"Drinking")]
head(data)
```

```
##    Age Gender      BMI   Ca    P   Mg OP Smoking Drinking
## 1 61.9      2 17.47472 2.15 1.04 0.76  1       1        0
## 2 55.0      2 20.57613 2.15 1.11 0.96  1       0        0
## 3 44.0      2 21.09375 2.18 1.10 0.89  1       0        0
## 4 64.7      1 23.63403 2.35 0.87 0.78  1       1        1
## 5 88.5      1 21.51386 1.98 0.93 0.86  1       1        0
## 6 73.0      1 22.75831 2.43 1.09 0.78  1       0        0
```

Structure of dataframe

```
str(data)
```

```
## 'data.frame':    1537 obs. of  9 variables:
##  $ Age     : num  61.9 55 44 64.7 88.5 73 61.5 52.9 53.1 86 ...
##  $ Gender  : int  2 2 2 1 1 1 1 2 2 2 ...
##  $ BMI     : num  17.5 20.6 21.1 23.6 21.5 ...
##  $ Ca      : num  2.15 2.15 2.18 2.35 1.98 2.43 2.74 2.08 1.91 2.21 ...
##  $ P       : num  1.04 1.11 1.1 0.87 0.93 1.09 0.76 0.94 0.93 0.94 ...
##  $ Mg      : num  0.76 0.96 0.89 0.78 0.86 0.78 0.92 0.87 0.84 0.87 ...
##  $ OP      : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ Smoking : int  1 0 0 1 1 0 0 0 1 1 ...
##  $ Drinking: int  0 0 0 1 0 0 0 0 1 1 ...
```

Summary of the data

```
summary(data)
```

```
##       Age            Gender           BMI               Ca
##  Min.   :28.60   Min.   :1.000   Min.   : 9.213   Min.   :1.780
##  1st Qu.:51.00   1st Qu.:1.000   1st Qu.:22.066   1st Qu.:2.160
##  Median :57.00   Median :1.000   Median :24.219   Median :2.230
```

```
##  Mean   :59.85   Mean   :1.385   Mean   :24.313   Mean   :2.238
##  3rd Qu.:67.30   3rd Qu.:2.000   3rd Qu.:26.356   3rd Qu.:2.310
##  Max.   :99.80   Max.   :2.000   Max.   :37.261   Max.   :5.840
##  NA's   :36                      NA's   :34       NA's   :2
##        P              Mg               OP            Smoking
##  Min.   :0.56   Min.   :0.0970   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.92   1st Qu.:0.8100   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :1.02   Median :0.8700   Median :0.0000   Median :0.0000
##  Mean   :1.04   Mean   :0.8686   Mean   :0.3696   Mean   :0.2576
##  3rd Qu.:1.13   3rd Qu.:0.9300   3rd Qu.:1.0000   3rd Qu.:1.0000
##  Max.   :4.41   Max.   :1.7300   Max.   :1.0000   Max.   :1.0000
##  NA's   :5      NA's   :3
##     Drinking
##  Min.   :0.0000
##  1st Qu.:0.0000
##  Median :0.0000
##  Mean   :0.2277
##  3rd Qu.:0.0000
##  Max.   :1.0000
##
```

Check for null values

```
# Check for null values
sum(is.na(data))
```

```
## [1] 80
```

Replacing null values with mean values of the column

#It will not disturb overall structure of the data.

```
library(dplyr)
```

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

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

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

```
# Replace null values with mean value of each column in df: data
data <- select(data, -ncol(data)) %>%
  mutate_all(~ifelse(is.na(.), mean(., na.rm = TRUE), .)) %>%
  bind_cols(select(data, ncol(data)) %>% rename(Drinking = everything()))
```

```
sum(is.na(data))
```

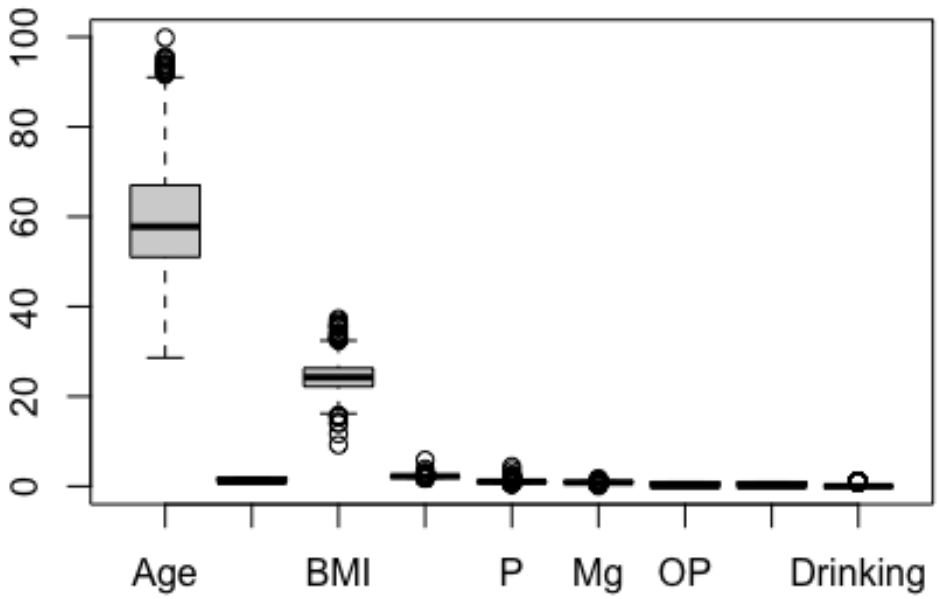
```
## [1] 0
```

```
head(data)
```

```
##    Age Gender      BMI   Ca    P   Mg OP Smoking Drinking
## 1 61.9      2 17.47472 2.15 1.04 0.76  1       1        0
## 2 55.0      2 20.57613 2.15 1.11 0.96  1       0        0
## 3 44.0      2 21.09375 2.18 1.10 0.89  1       0        0
## 4 64.7      1 23.63403 2.35 0.87 0.78  1       1        1
## 5 88.5      1 21.51386 1.98 0.93 0.86  1       1        0
## 6 73.0      1 22.75831 2.43 1.09 0.78  1       0        0
```

Checking the outliers with Boxplot

```
boxplot(data, outline = TRUE)
```



Print the outliers

```
# Load the required packages
library(dplyr)
```

```r
# Calculate the number of outliers in df
outliers <- apply(data, 2, function(x) {
  qnt <- quantile(x, probs=c(.25, .75), na.rm = TRUE)
  H <- 1.5 * IQR(x, na.rm = TRUE)
  sum(x < (qnt[1] - H) | x > (qnt[2] + H), na.rm = TRUE)
})

# Print the number of outliers for each column
print(outliers)
```

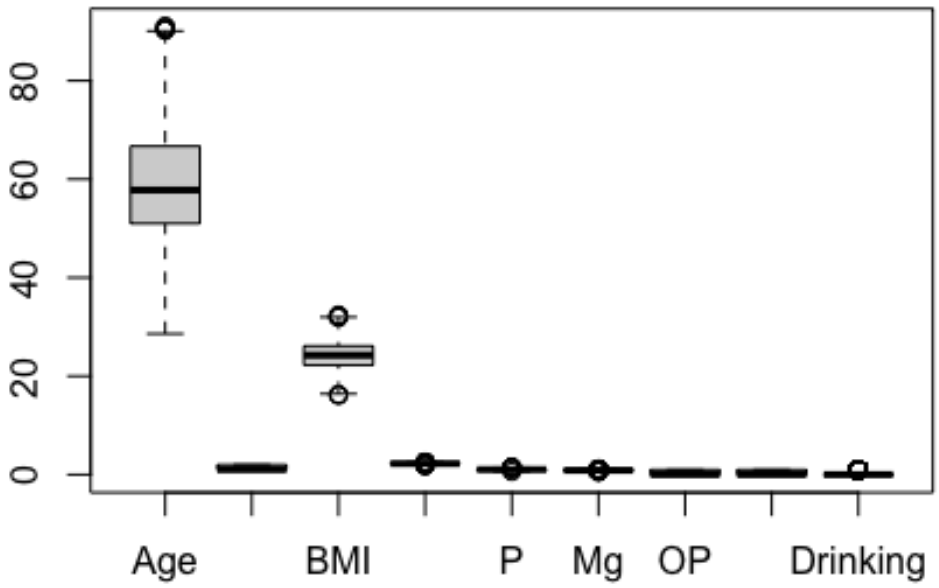
```
##      Age   Gender      BMI       Ca        P       Mg       OP  Smoking
##       16        0       30       32       42       28        0        0
## Drinking
##      350
```

Function to replace outliers with median values

```r
# Define a function to replace outliers with the median value of a vector
replace_outliers <- function(x) {
  q1 <- quantile(x, 0.25, na.rm = TRUE)
  q3 <- quantile(x, 0.75, na.rm = TRUE)
  iqr <- q3 - q1
  upper <- q3 + 1.5 * iqr
  lower <- q1 - 1.5 * iqr
  replace(x, x > upper | x < lower, median(x, na.rm = TRUE))
}

# Replace outlier values with median value of each column in df
data <- select(data, -last_col()) %>%
  mutate_all(replace_outliers) %>%
  bind_cols(select(data, last_col()) %>% rename_with(~"Drinking", .cols =
everything()))
```

Checking outliers after cleaning

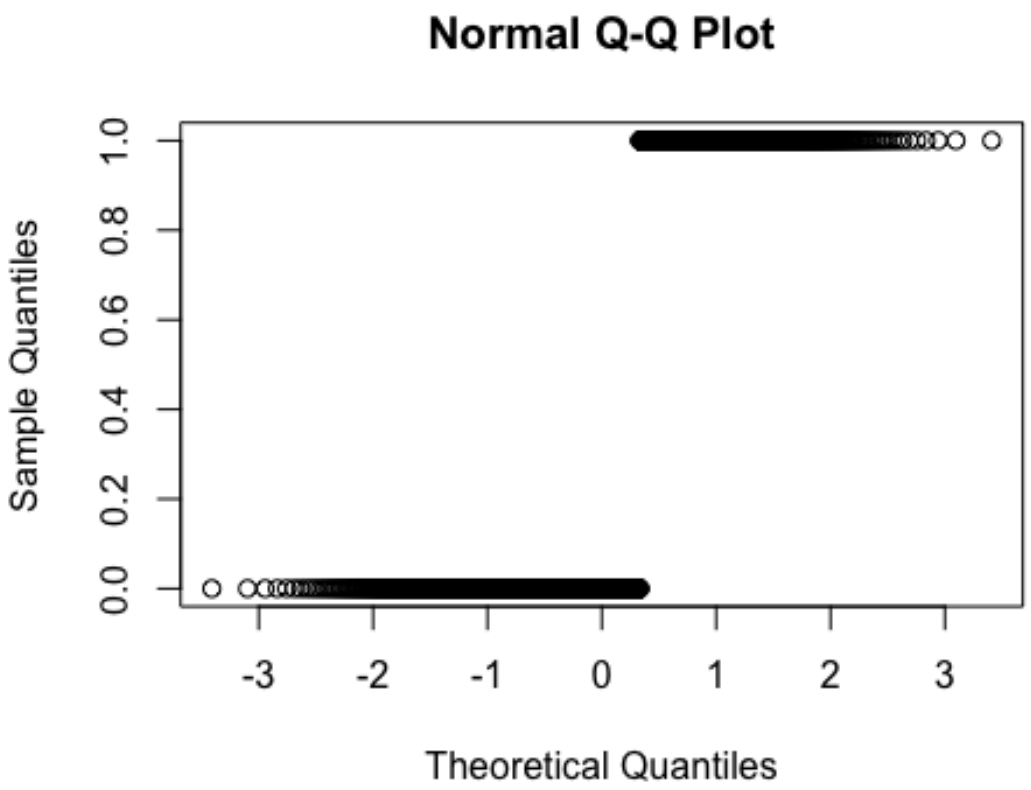
```r
boxplot(data, outline = TRUE)
```



Q-Q Plot

#to check normality

```
qqnorm(data$OP)
```



#the distribution of the data is approximately normal. The straight line means that the quantiles of the dataset are linearly related to the quantiles of the standard normal distribution.

#shapiro-wilk test #to check normality for each column

```
library(dplyr)
data <- select_if(data, is.numeric)
# Perform Shapiro-Wilk test on each column
for (col in names(data)) {
  test_result <- shapiro.test(data[[col]])
  print(paste("Shapiro-Wilk test for column", col))
  print(test_result)
}
```

```
## [1] "Shapiro-Wilk test for column Age"
##
##  Shapiro-Wilk normality test
##
## data:  data[[col]]
## W = 0.97815, p-value = 1.545e-14
##
## [1] "Shapiro-Wilk test for column Gender"
##
##  Shapiro-Wilk normality test
```

```
##
## data:  data[[col]]
## W = 0.61714, p-value < 2.2e-16
##
## [1] "Shapiro-Wilk test for column BMI"
##
##  Shapiro-Wilk normality test
##
## data:  data[[col]]
## W = 0.99699, p-value = 0.004661
##
## [1] "Shapiro-Wilk test for column Ca"
##
##  Shapiro-Wilk normality test
##
## data:  data[[col]]
## W = 0.99595, p-value = 0.0004033
##
## [1] "Shapiro-Wilk test for column P"
##
##  Shapiro-Wilk normality test
##
## data:  data[[col]]
## W = 0.99329, p-value = 1.916e-06
##
## [1] "Shapiro-Wilk test for column Mg"
##
##  Shapiro-Wilk normality test
##
## data:  data[[col]]
## W = 0.99627, p-value = 0.0008455
##
## [1] "Shapiro-Wilk test for column OP"
##
##  Shapiro-Wilk normality test
##
## data:  data[[col]]
## W = 0.61138, p-value < 2.2e-16
##
## [1] "Shapiro-Wilk test for column Smoking"
##
##  Shapiro-Wilk normality test
##
## data:  data[[col]]
## W = 0.54489, p-value < 2.2e-16
##
## [1] "Shapiro-Wilk test for column Drinking"
##
##  Shapiro-Wilk normality test
##
```

```
## data:  data[[col]]
## W = 0.5184, p-value < 2.2e-16
```

#none of the columns in our dataset have a normal distribution.

Correlation

```
cor(data)
```

```
##                   Age       Gender            BMI           Ca             P
## Age       1.000000000 -0.025185924  0.0367214161 -0.06893962  0.0037652633
## Gender   -0.025185924  1.000000000 -0.2433608838  0.02464990  0.0438763440
## BMI       0.036721416 -0.243360884  1.0000000000 -0.00443306 -0.0001982793
## Ca       -0.068939623  0.024649895 -0.0044330597  1.00000000  0.2172390220
## P         0.003765263  0.043876344 -0.0001982793  0.21723902  1.0000000000
## Mg       -0.104387459 -0.224082708  0.2099576475  0.06646473 -0.0543005275
## OP        0.055422445  0.003395221  0.0040782647 -0.03776777  0.0112742873
## Smoking   0.024180666 -0.007721263  0.0242814301 -0.04188546 -0.0849766112
## Drinking  0.008769412 -0.012140662 -0.0021391965 -0.01135212 -0.0453782737
##                   Mg           OP      Smoking     Drinking
## Age       -0.104387459  0.055422445  0.024180666  0.008769412
## Gender    -0.224082708  0.003395221 -0.007721263 -0.012140662
## BMI        0.209957647  0.004078265  0.024281430 -0.002139196
## Ca         0.066464725 -0.037767766 -0.041885462 -0.011352121
## P         -0.054300528  0.011274287 -0.084976611 -0.045378274
## Mg         1.000000000  0.008308790  0.004678726  0.002864552
## OP         0.008308790  1.000000000 -0.010301088 -0.103957796
## Smoking    0.004678726 -0.010301088  1.000000000  0.524408834
## Drinking   0.002864552 -0.103957796  0.524408834  1.000000000
```

Spearman Correlation

```
# Calculate the Spearman correlation matrix
cor(data, method = "spearman")
```

```
##                   Age       Gender           BMI           Ca             P
## Age       1.000000000 -0.010631750  0.054427140 -0.050837223 -0.004496005
## Gender   -0.010631750  1.000000000 -0.257175375  0.028577861  0.042703248
## BMI       0.054427140 -0.257175375  1.000000000  0.008806547  0.007583249
## Ca       -0.050837223  0.028577861  0.008806547  1.000000000  0.192135098
## P        -0.004496005  0.042703248  0.007583249  0.192135098  1.000000000
## Mg       -0.129500641 -0.211954050  0.220823297  0.064020829 -0.054805644
## OP        0.051667692  0.003395221 -0.003232426 -0.044172827  0.010144822
## Smoking   0.011338926 -0.007721263  0.015982038 -0.029030032 -0.089295242
## Drinking  0.004138680 -0.012140662 -0.006923549 -0.003804442 -0.049830261
##                   Mg           OP      Smoking     Drinking
## Age       -0.129500641  0.051667692  0.011338926  0.004138680
## Gender    -0.211954050  0.003395221 -0.007721263 -0.012140662
## BMI        0.220823297 -0.003232426  0.015982038 -0.006923549
## Ca         0.064020829 -0.044172827 -0.029030032 -0.003804442
```

```
## P         -0.054805644  0.010144822 -0.089295242 -0.049830261
## Mg         1.000000000  0.003133075  0.007011499  0.008185209
## OP         0.003133075  1.000000000 -0.010301088 -0.103957796
## Smoking    0.007011499 -0.010301088  1.000000000  0.524408834
## Drinking   0.008185209 -0.103957796  0.524408834  1.000000000
```

#there is a slight correlation between Age and OP .

Pearson Correlation

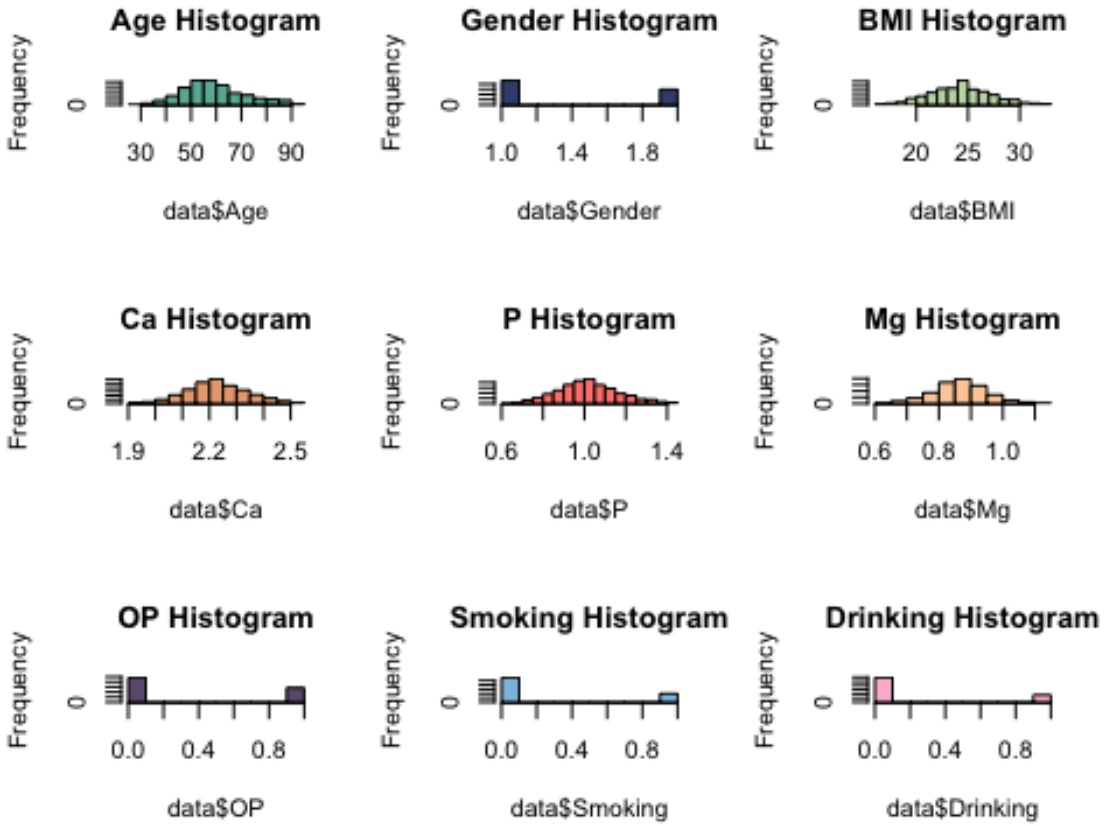
```
# Calculate the Pearson correlation matrix
cor(data, method = "pearson")
```

```
##                   Age       Gender          BMI           Ca            P
## Age        1.000000000 -0.025185924  0.036721416 -0.06893962  0.003765263
## Gender    -0.025185924  1.000000000 -0.243360884  0.02464990  0.043876344
## BMI        0.036721416 -0.243360884  1.000000000 -0.00443306 -0.000198279
## Ca        -0.068939623  0.024649895 -0.004433059  1.00000000  0.217239022
## P          0.003765263  0.043876344 -0.000198279  0.21723902  1.000000000
## Mg        -0.104387459 -0.224082708  0.209957647  0.06646473 -0.054300528
## OP         0.055422445  0.003395221  0.004078265 -0.03776777  0.011274287
## Smoking    0.024180666 -0.007721263  0.024281430 -0.04188546 -0.084976611
## Drinking   0.008769412 -0.012140662 -0.002139196 -0.01135212 -0.045378274
##                   Mg           OP      Smoking     Drinking
## Age        -0.104387459  0.055422445  0.024180666  0.008769412
## Gender     -0.224082708  0.003395221 -0.007721263 -0.012140662
## BMI         0.209957647  0.004078265  0.024281430 -0.002139196
## Ca          0.066464725 -0.037767766 -0.041885462 -0.011352121
## P          -0.054300528  0.011274287 -0.084976611 -0.045378274
## Mg         1.000000000  0.008308790  0.004678726  0.002864552
## OP         0.008308790  1.000000000 -0.010301088 -0.103957796
## Smoking    0.004678726 -0.010301088  1.000000000  0.524408834
## Drinking   0.002864552 -0.103957796  0.524408834  1.000000000
```

#there is a slight correlation between Age and OP .

Histogram

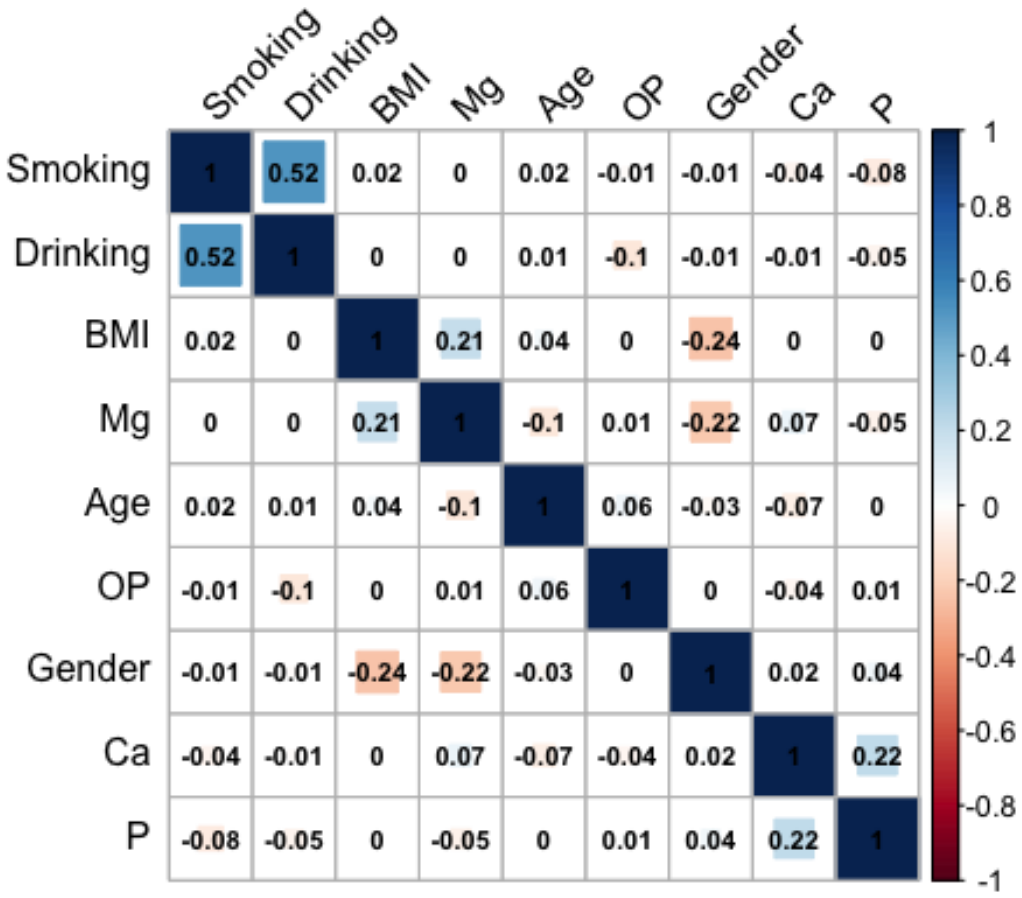
```
par(mfrow=c(3,3))
hist(data$Age, col = "#69b3a2", main="Age Histogram")
hist(data$Gender,col = "#404e7c", main="Gender Histogram")
hist(data$BMI,col = "#c2d9b1", main="BMI Histogram")
hist(data$Ca,col = "#e8a87c", main="Ca Histogram")
hist(data$P,col = "#ff847c", main="P Histogram")
hist(data$Mg,col = "#fecea8", main="Mg Histogram")
hist(data$OP,col = "#6c5b7b", main="OP Histogram")
hist(data$Smoking,col = "#8fbfe0", main="Smoking Histogram")
hist(data$Drinking,col = "#fcbad3", main="Drinking Histogram")
```



#we found Gender, OP, Smoking and Drinking has highly skewed data.

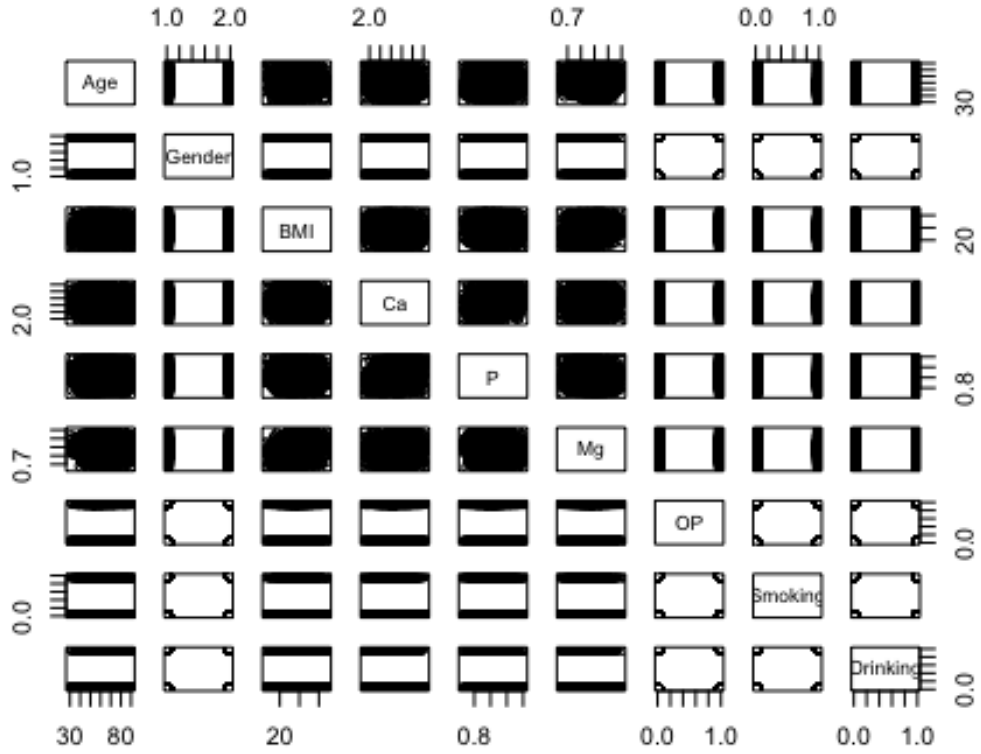
Correlation plot

```
library(corrplot)

## corrplot 0.92 loaded

corrplot(cor(data), method = "square", order = "hclust",
         tl.col = "black", tl.srt = 45,
         addCoef.col = "black", number.cex = 0.7)
```



there is correlation between drinking and smoking, BMI and Mg, Ca and P. # Pairplot

```
pairs(data)
```



#One-sample t-test

```
# Loop through each column and perform t-test
for (col in colnames(data)) {
  t.test_result <- t.test(data[,col], mu = 0)
  if (t.test_result$p.value < 0.05) {
    print(paste("Null hypothesis for", col, "rejected with p-value =",
t.test_result$p.value))
  } else {
    print(paste("Null hypothesis for", col, "not rejected with p-value =",
t.test_result$p.value))
  }
}
```

```
## [1] "Null hypothesis for Age rejected with p-value = 0"
## [1] "Null hypothesis for Gender rejected with p-value = 0"
## [1] "Null hypothesis for BMI rejected with p-value = 0"
## [1] "Null hypothesis for Ca rejected with p-value = 0"
## [1] "Null hypothesis for P rejected with p-value = 0"
## [1] "Null hypothesis for Mg rejected with p-value = 0"
## [1] "Null hypothesis for OP rejected with p-value = 4.52362573006446e-156"
## [1] "Null hypothesis for Smoking rejected with p-value =
1.70686014534895e-101"
```

```
## [1] "Null hypothesis for Drinking rejected with p-value =
2.7646881617891e-88"
```

t-test with OP as target variable

```
# Loop through each column (except OP) and perform t-test with OP as target
variable
for (col in colnames(data)) {
  t.test_result <- t.test(data[,col], data$OP)
  if (t.test_result$p.value < 0.05) {
    print(paste("Null hypothesis for", col, "rejected with p-value =",
t.test_result$p.value))
  } else {
    print(paste("Null hypothesis for", col, "not rejected with p-value =",
t.test_result$p.value))
  }
}
```

```
## [1] "Null hypothesis for Age rejected with p-value = 0"
## [1] "Null hypothesis for Gender rejected with p-value = 0"
## [1] "Null hypothesis for BMI rejected with p-value = 0"
## [1] "Null hypothesis for Ca rejected with p-value = 0"
## [1] "Null hypothesis for P rejected with p-value = 0"
## [1] "Null hypothesis for Mg rejected with p-value = 3.00304774759658e-244"
## [1] "Null hypothesis for OP not rejected with p-value = 1"
## [1] "Null hypothesis for Smoking rejected with p-value =
1.97224248413668e-11"
## [1] "Null hypothesis for Drinking rejected with p-value =
5.66641836262055e-18"
```

Wilcoxon rank-sum test

#to test significance of subgroups with OP variable

```
# Subset data by gender
group1 <- subset(data, Gender == 1)
group2 <- subset(data, Gender == 2)

# Perform Wilcoxon rank-sum test on Score column
wilcox.test(group1$OP, group2$OP)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  group1$OP and group2$OP
## W = 278778, p-value = 0.8942
## alternative hypothesis: true location shift is not equal to 0
```

This result indicates that there is no significant difference between the median of "OP" for group 1 and group 2. The p-value is greater than 0.05, which suggests that we cannot reject the null hypothesis that the true location shift is equal to 0.

Kruskal-Wallis test

```
# subset the data into two groups based on Gender
group1 <- subset(data, Gender == 1)
group2 <- subset(data, Gender == 2)

# create a data frame with the combined groups
Kruskal_test <- data.frame(value = c(group1$OP, group2$OP),
                           group = factor(rep(c("Group 1", "Group 2"),
                                              c(nrow(group1),
nrow(group2)))))

# perform the Kruskal-Wallis test
kruskal.test(value ~ group, data = Kruskal_test)

##
##  Kruskal-Wallis rank sum test
##
## data:  value by group
## Kruskal-Wallis chi-squared = 0.017706, df = 1, p-value = 0.8941
```

The Kruskal-Wallis test was performed successfully, with a chi-squared value of 0.017706 and a p-value of 0.8941. This suggests that there is no significant difference in the median values of the "value" variable between the two groups.

Kruskal-Wallis test by age groups

```
# subset the data into 4 groups based on Age
age1 <- subset(data, Age >= 28.6 & Age < 51)
age2 <- subset(data, Age >= 51  & Age < 57)
age3 <- subset(data, Age >= 57  & Age < 67.3)
age4 <- subset(data, Age >= 67.3  & Age < 100)

# create a data frame with the combined groups
Kruskal_test <- data.frame(value = c(age1$OP, age2$OP, age3$OP, age4$OP),
                           group = factor(rep(c("age1", "age2"," age3",
"age4"),
                                              c(nrow(age1), nrow(age2),
nrow(age3), nrow(age4) ))))

# perform the Kruskal-Wallis test
kruskal.test(value ~ group, data = Kruskal_test)

##
##  Kruskal-Wallis rank sum test
```

```
##
## data:  value by group
## Kruskal-Wallis chi-squared = 7.5839, df = 3, p-value = 0.05544
```

The Kruskal-Wallis test suggests that there might be a significant difference between the groups based on Age. However, the p-value is just above the usual significance level of 0.05. Therefore, further investigation with post-hoc tests such as Dunn's test or pairwise Wilcoxon rank-sum tests should be performed to identify which groups are significantly different from each other.

Mann-Whitney U test

```
# subset the data into 4 groups based on Age
age1 <- subset(data, Age >= 28.6 & Age < 51)
age2 <- subset(data, Age >= 51  & Age < 57)
age3 <- subset(data, Age >= 57  & Age < 67.3)
age4 <- subset(data, Age >= 67.3  & Age < 100)

# perform pairwise Wilcoxon rank-sum tests
mann_test <- pairwise.wilcox.test(x = data$OP, g = data$Age_group,
p.adjust.method = "bonferroni")

mann_test

##
##  Pairwise comparisons using
##
## data:  data$OP and data$Age_group
##
## <0 x 0 matrix>
##
## P value adjustment method: bonferroni
```

The output of the pairwise Wilcoxon rank-sum test suggests that there are no significant differences between the "OP" values for the different age groups. The p-values are all greater than 0.05 after Bonferroni correction for multiple comparisons. Therefore, we cannot reject the null hypothesis that there are no differences in "OP" values between the age groups.

Based on the output of the Kruskal-Wallis test and the pairwise comparison results, there is no significant difference between the groups in terms of the variable "x". The p-value for the Kruskal-Wallis test is 0.4, which is greater than the significance level of 0.05, indicating that there is no significant difference between the groups. Furthermore, the pairwise comparison results also show that all the p-values are greater than the adjusted significance level (0.05/15 = 0.0033 using the Bonferroni correction), suggesting that there are no significant differences between any pairs of groups. Therefore, we can conclude that there is no significant difference between the groups in terms of the variable "x".

Multiple regression model on BMI, Smoking, Drinking

```
# Fit the multiple regression model
reg_model <- lm(OP ~ BMI + Smoking + Drinking, data = data)

summary(reg_model)

##
## Call:
## lm(formula = OP ~ BMI + Smoking + Drinking, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4580 -0.3879 -0.2992  0.6116  0.7703
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.3787067  0.1014464   3.733 0.000196 ***
## BMI          0.0003774  0.0041491   0.091 0.927529
## Smoking      0.0672212  0.0328963   2.043 0.041181 *
## Drinking    -0.1564128  0.0342966  -4.561 5.51e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.48 on 1533 degrees of freedom
## Multiple R-squared:  0.01351,    Adjusted R-squared:  0.01158
## F-statistic: 6.998 on 3 and 1533 DF,  p-value: 0.0001127
```

Smoking and Drinking are significant predictors of OP, but BMI is not. The model overall is not a strong predictor of OP, as indicated by the low R-squared value.

Multiple Regression on OP vs Ca, Mg, P

```
# Fit the multiple regression model
reg_model <- lm(OP ~ Ca + Mg + P, data = data)

summary(reg_model)

##
## Call:
## lm(formula = OP ~ Ca + Mg + P, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4316 -0.3749 -0.3512  0.6180  0.7035
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.66023    0.27984   2.359   0.0184 *
## Ca          -0.19114    0.11597  -1.648   0.0995 .
```

```
## Mg           0.07265    0.15093   0.481   0.6303
## P            0.07103    0.08724   0.814   0.4157
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4828 on 1533 degrees of freedom
## Multiple R-squared:  0.001975,   Adjusted R-squared:  2.239e-05
## F-statistic: 1.011 on 3 and 1533 DF,  p-value: 0.3867
```

only the intercept has a statistically significant relationship with the response variable, while the three predictor variables do not have significant relationships. The R-squared value indicates that the predictor variables explain very little of the variance in the response variable, and the F-statistic and p-value suggest that the overall model is not significant.

Multiple regression model on Age, Gender

```
# Fit the multiple regression model
reg_model <- lm(OP ~ Age + Gender, data = data)

summary(reg_model)

##
## Call:
## lm(formula = OP ~ Age + Gender, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4390 -0.3719 -0.3471  0.6181  0.6863
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.233286   0.070913   3.290  0.00103 **
## Age         0.002180   0.001001   2.178  0.02955 *
## Gender      0.004755   0.025294   0.188  0.85090
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4824 on 1534 degrees of freedom
## Multiple R-squared:  0.003095,   Adjusted R-squared:  0.001795
## F-statistic: 2.381 on 2 and 1534 DF,  p-value: 0.09281
```

Logistic regression model on BMI, Gender

```
# Fit a logistic regression model
model <- glm(OP ~ BMI + Gender, data = data, family = binomial)

# Print the model summary
summary(model)
```

```
##
## Call:
## glm(formula = OP ~ BMI + Gender, family = binomial, data = data)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9769  -0.9616  -0.9570   1.4087   1.4270
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.650242   0.510309  -1.274    0.203
## BMI          0.003657   0.018449   0.198    0.843
## Gender       0.019846   0.111909   0.177    0.859
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2024.9  on 1536  degrees of freedom
## Residual deviance: 2024.8  on 1534  degrees of freedom
## AIC: 2030.8
##
## Number of Fisher Scoring iterations: 4
```

The results indicate that neither “BMI” nor “Gender” has a statistically significant effect on “OP” (both p-values > 0.05).

Logistic Regression on OP vs BMI, Smoking, Drinking

```
# Fit a logistic regression model
model <- glm(OP ~ BMI + Smoking  + Drinking, data = data, family = binomial)

# Print the summary of the model
summary(model)
```

```
##
## Call:
## glm(formula = OP ~ BMI + Smoking + Drinking, family = binomial,
##     data = data)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.1153  -0.9898  -0.8382   1.3764   1.6989
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.503516   0.441361  -1.141   0.2539
## BMI          0.001827   0.018050   0.101   0.9194
## Smoking      0.297149   0.144074   2.062   0.0392 *
## Drinking    -0.705845   0.156887  -4.499 6.83e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2024.9  on 1536  degrees of freedom
## Residual deviance: 2003.5  on 1533  degrees of freedom
## AIC: 2011.5
##
## Number of Fisher Scoring iterations: 4
```

the model suggests that Smoking and Drinking are significant predictors of OP, while BMI is not.

Logistic Regression on OP vs Ca, Mg, P

```
# Fit a logistic regression model
model2 <- glm(OP ~ Ca  + Mg + P, data = data, family = binomial)

# Print the summary of the model
summary(model2)
```

```
##
## Call:
## glm(formula = OP ~ Ca + Mg + P, family = binomial, data = data)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.0658  -0.9690  -0.9301   1.3876   1.5528
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.7166     1.2027   0.596   0.5513
## Ca           -0.8228     0.4994  -1.648   0.0994 .
## Mg            0.3121     0.6482   0.481   0.6302
## P             0.3058     0.3750   0.816   0.4148
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2024.9  on 1536  degrees of freedom
## Residual deviance: 2021.9  on 1533  degrees of freedom
## AIC: 2029.9
##
## Number of Fisher Scoring iterations: 4
```

Ca may have a weak negative relationship with the outcome variable, while Mg and P may not be significant predictors

Logistic Regression on OP vs BMI, Gender

```
# Fit a logistic regression model
model <- glm(OP ~ BMI + Gender, data = data, family = binomial)

# Print the summary of the model
summary(model)

##
## Call:
## glm(formula = OP ~ BMI + Gender, family = binomial, data = data)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9769  -0.9616  -0.9570   1.4087   1.4270
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.650242   0.510309  -1.274    0.203
## BMI          0.003657   0.018449   0.198    0.843
## Gender       0.019846   0.111909   0.177    0.859
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2024.9  on 1536  degrees of freedom
## Residual deviance: 2024.8  on 1534  degrees of freedom
## AIC: 2030.8
##
## Number of Fisher Scoring iterations: 4
```

None of the predictors are statistically significant at the 0.05 level, as all their p-values are greater than 0.05.

Random Forest Regression

```
# Load required library
library(randomForest)

## randomForest 4.7-1.1

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

##
## Attaching package: 'randomForest'

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

library(caret)
```

```
## Loading required package: ggplot2

##
## Attaching package: 'ggplot2'

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

## Loading required package: lattice

data$OP <- as.factor(data$OP)

# Split data into training and testing sets
set.seed(123)
train_idx <- sample(1:nrow(data), size = 0.7*nrow(data))
train_data <- data[train_idx,]
test_data <- data[-train_idx,]


rf_model <- randomForest(OP ~ ., data = train_data, importance = TRUE, ntree
= 500, mtry = 3)

# Predict using the fitted model and test data
rf_pred <- predict(rf_model, newdata = test_data)

# Create contingency table
tab <- table(rf_pred, test_data$OP)

# Convert to confusion matrix
cm <- confusionMatrix(tab)

# Print confusion matrix
print(cm)

## Confusion Matrix and Statistics
##
##
## rf_pred   0   1
##       0 248 137
##       1  47  30
##
##                Accuracy : 0.6017
##                  95% CI : (0.5555, 0.6467)
##     No Information Rate : 0.6385
##     P-Value [Acc > NIR] : 0.9542
##
##                   Kappa : 0.023
##
##  Mcnemar's Test P-Value : 5.339e-11
```

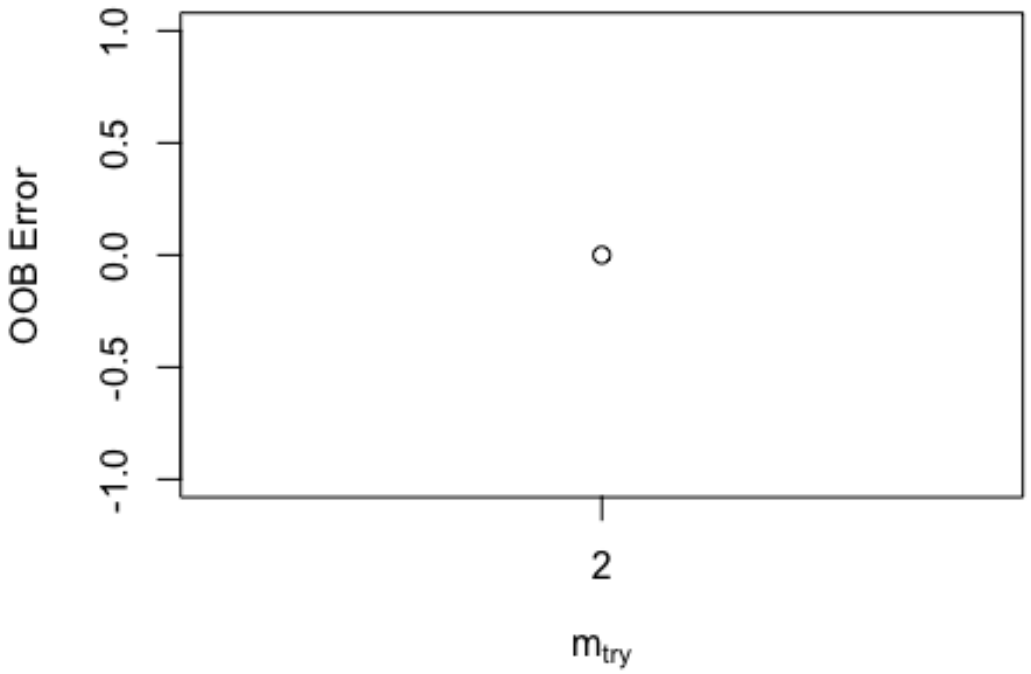
```
##
##             Sensitivity : 0.8407
##             Specificity : 0.1796
##          Pos Pred Value : 0.6442
##          Neg Pred Value : 0.3896
##              Prevalence : 0.6385
##          Detection Rate : 0.5368
##    Detection Prevalence : 0.8333
##       Balanced Accuracy : 0.5102
##
##        'Positive' Class : 0
##
```

Based on this confusion matrix, we can evaluate the performance of the random forest model. We can see that the model predicted 295 observations as category 0, out of which 248 were correctly classified (true negatives) and 47 were incorrectly classified (false positives). The model predicted 167 observations as category 1, out of which only 30 were correctly classified (true positives) and 137 were incorrectly classified (false negatives), which gives an overall accuracy of approximately 60.17%.

Tuning the hyperparameters using grid search to improve the accuracy of the model

```
# Load required library
library(randomForest)

# Split data into training and testing sets
set.seed(123)
train_idx <- sample(1:nrow(data), size = 0.7*nrow(data))
train_data <- data[train_idx,]
test_data <- data[-train_idx,]

# Define grid for tuning
rf_grid <- expand.grid(ntree = c(500, 1000),
                       mtry = c(2, 4))

# Define the grid of ntree and mtry values
ntree_vals <- c(500, 1000)
mtry_vals <- c(2, 4)

# Tune random forest model
rf_tune <- tuneRF(x = train_data[, -1], y = train_data$OP,
                  ntreeTry = ntree_vals[1],
                  mtryStart = mtry_vals[1],
                  stepFactor = 1.2,
                  improve = 0.01)
```

```
## mtry = 2  OOB error = 0%
## Searching left ...
## Searching right ...
```




```
# Train random forest model with optimal hyperparameters
rf_model <- randomForest(OP ~ ., data = train_data[-1], ntree = 1000, mtry =
rf_tune[1, "mtry"])

# Predict on test data
rf_pred <- predict(rf_model, test_data)

# Evaluate model performance
confusionMatrix(table(rf_pred, test_data$OP))

## Confusion Matrix and Statistics
##
##
## rf_pred   0   1
##       0 272 149
##       1  23  18
##
##                Accuracy : 0.6277
##                  95% CI : (0.5818, 0.6719)
```

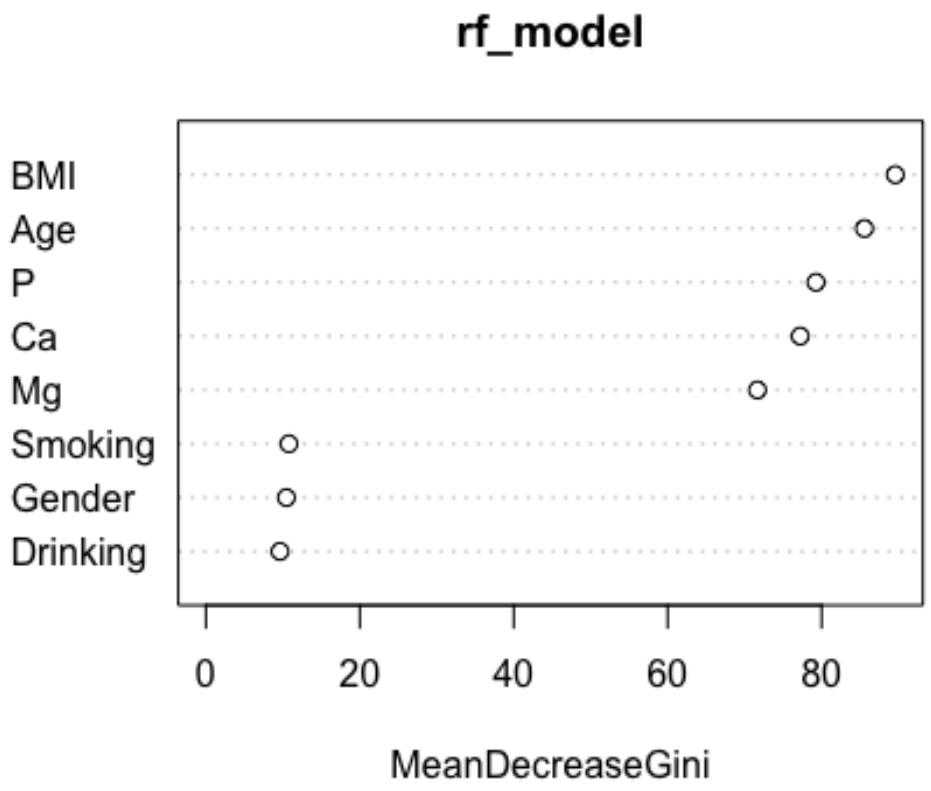
```
##     No Information Rate : 0.6385
##     P-Value [Acc > NIR] : 0.7039
##
##                   Kappa : 0.0357
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.9220
##             Specificity : 0.1078
##          Pos Pred Value : 0.6461
##          Neg Pred Value : 0.4390
##              Prevalence : 0.6385
##          Detection Rate : 0.5887
##    Detection Prevalence : 0.9113
##       Balanced Accuracy : 0.5149
##
##        'Positive' Class : 0
##
```

```r
# Load required libraries
library(caret)
library(randomForest)

# Split data into training and testing sets
set.seed(123)
train_idx <- sample(1:nrow(data), size = 0.7*nrow(data))
train_data <- data[train_idx,]
test_data <- data[-train_idx,]

# Set up a grid of hyperparameters to tune
rf_grid <- expand.grid(mtry = c(2, 3, 4, 5))

# Tune random forest model
rf_tune <- train(OP ~ ., data = train_data, method = "rf",
                 trControl = trainControl(method = "cv", number = 10),
                 tuneGrid = rf_grid, importance = TRUE)

# Train random forest model with optimal hyperparameters
rf_model <- randomForest(train_data$OP ~ ., data = train_data, mtry =
rf_tune$bestTune$mtry)

# Predict on test data
rf_pred <- predict(rf_model, test_data)

# Evaluate model performance
table(rf_pred, test_data$OP)
```

```
##
## rf_pred   0   1
```

```
##       0 269 150
##       1  26  17
```

```
# Variable importance measures
varImpPlot(rf_model)
```




```
# Evaluate model performance
confusionMatrix(rf_pred, test_data$OP)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 269 150
##          1  26  17
##
##                Accuracy : 0.619
##                  95% CI : (0.573, 0.6635)
##     No Information Rate : 0.6385
##     P-Value [Acc > NIR] : 0.8214
##
##                   Kappa : 0.0163
##
##  Mcnemar's Test P-Value : <2e-16
```

```
##
##             Sensitivity : 0.9119
##             Specificity : 0.1018
##          Pos Pred Value : 0.6420
##          Neg Pred Value : 0.3953
##              Prevalence : 0.6385
##          Detection Rate : 0.5823
##    Detection Prevalence : 0.9069
##       Balanced Accuracy : 0.5068
##
##        'Positive' Class : 0
##
```

The confusion matrix shows the performance of the random forest model. The model correctly predicted 269 out of 395 samples with true negative cases (TN) and 17 out of 43 samples with true positive cases (TP). However, it misclassified 150 samples with false positive cases (FP) and 26 samples with false negative cases (FN).

The accuracy of the model is 0.619, which means that the model correctly classified 61.9% of the samples. The kappa value of 0.0163 indicates that the model's agreement with the actual class is very low.

The sensitivity of the model is 0.9119, which means that the model correctly identified 91.19% of the true positive cases. The specificity of the model is 0.1018, which means that the model correctly identified only 10.18% of the true negative cases. The balanced accuracy, which is the average of sensitivity and specificity, is 0.5068.

The positive predictive value (PPV) of the model is 0.6420, which means that among the samples predicted as positive, only 64.2% were actually positive. The negative predictive value (NPV) is 0.3953, which means that among the samples predicted as negative, only 39.53% were actually negative.

The prevalence of the positive class in the dataset is 0.6385, which means that 63.85% of the samples are actually positive. The detection rate, which is the proportion of true positive cases detected by the model, is 0.5823. The detection prevalence, which is the proportion of samples predicted as positive by the model, is 0.9069.

Overall, the random forest model's performance is suboptimal and needs further improvement.

```
rf_pred
```

```
##    3   12   14   15   20   21   22   23   27   30   33   43   47   50   53
54
##    0    0    0    0    0    0    1    0    0    0    0    0    0    0    0
0
##   57   59   60   62   63   65   66   70   73   82   85   87   92   97  101
102
##    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
0
```

```
##  104  107  109  113  114  116  118  123  125  128  131  132  133  135  136
138
##    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
0
##  140  146  147  149  150  154  157  173  175  176  181  182  183  184  187
188
##    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
0
##  192  198  203  213  214  216  219  225  226  228  231  232  233  244  245
246
##    0    0    0    1    0    0    0    0    0    0    1    0    1    0    0
0
##  249  252  254  257  260  267  268  272  273  276  283  284  288  295  296
299
##    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
0
##  300  301  302  305  306  307  308  313  314  317  322  324  325  333  334
336
##    0    1    1    1    0    0    0    0    0    0    0    0    0    0    0
0
##  338  340  342  345  346  351  353  354  356  359  360  361  362  364  368
369
##    0    0    0    0    0    0    0    1    1    1    0    0    0    0    0
1
##  371  377  388  389  390  395  399  404  405  408  410  412  414  417  418
427
##    0    0    0    0    0    0    0    0    0    1    0    1    0    0    0
0
##  428  429  437  438  439  440  442  443  453  454  465  472  476  483  486
491
##    0    1    0    0    0    0    1    0    0    0    0    0    0    0    0
0
##  492  495  497  501  506  509  510  511  513  514  518  521  527  532  543
546
##    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
0
##  550  552  553  558  563  568  569  570  571  573  574  580  582  583  585
590
##    0    0    0    0    0    0    0    0    0    0    1    0    0    0    0
0
##  607  614  624  629  630  632  634  636  638  644  645  652  659  661  663
664
##    0    1    0    1    0    0    0    0    1    0    0    0    0    0    0
0
##  681  689  693  695  697  704  707  716  717  718  721  723  725  727  735
736
##    0    0    0    0    0    0    0    0    0    0    0    0    1    0    0
0
##  739  745  754  761  762  764  770  771  773  777  780  781  782  790  795
798
```

```
##    0    0    0    0    0    1    0    0    0    0    0    0    0    0    0
0
##  799  800  801  805  809  816  823  824  830  833  837  849  852  854  862
863
##    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
0
##  864  867  868  871  874  875  880  881  882  883  884  885  887  895  897
909
##    0    0    0    0    0    1    0    0    0    1    0    0    0    0    0
0
##  911  912  913  914  918  925  934  936  942  943  948  954  958  961  962
963
##    0    0    0    0    0    1    0    1    0    1    0    1    0    0    0
0
##  964  967  968  969  972  980  984  998 1000 1001 1003 1004 1008 1010 1012
1018
##    0    0    0    0    1    0    0    0    0    0    0    0    0    0    0
0
## 1019 1024 1025 1026 1027 1037 1039 1041 1042 1045 1049 1050 1051 1052 1053
1058
##    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
0
## 1059 1061 1067 1074 1084 1085 1086 1089 1092 1094 1095 1104 1106 1111 1114
1116
##    0    0    0    0    0    1    0    0    0    0    0    0    0    0    0
0
## 1119 1138 1144 1145 1147 1148 1150 1151 1152 1156 1157 1160 1162 1170 1173
1179
##    0    0    0    1    0    0    0    0    0    0    0    0    0    0    0
0
## 1186 1189 1190 1191 1192 1194 1197 1198 1200 1206 1208 1209 1210 1211 1213
1214
##    0    0    0    0    0    0    0    0    0    0    1    0    0    0    0
0
## 1215 1217 1218 1223 1225 1226 1227 1228 1229 1232 1237 1243 1252 1254 1264
1265
##    1    0    0    0    0    0    0    0    0    0    0    0    1    0    0
0
## 1266 1267 1271 1272 1287 1292 1295 1297 1303 1305 1311 1312 1325 1330 1335
1339
##    0    0    0    1    0    0    0    0    0    0    0    0    0    0    0
0
## 1341 1342 1345 1346 1347 1350 1354 1358 1360 1362 1367 1375 1383 1385 1388
1394
##    0    0    1    1    0    0    0    0    1    0    0    0    1    0    0
0
## 1395 1400 1402 1404 1405 1409 1413 1414 1419 1424 1425 1432 1434 1437 1443
1447
##    0    0    0    0    0    0    0    1    1    0    0    0    0    0    0
0
```

```
## 1449 1458 1460 1461 1465 1470 1471 1473 1480 1481 1482 1485 1487 1490 1495
1498
##    0    0    0    0    0    0    0    1    0    0    1    0    0    0    0
0
## 1500 1502 1504 1506 1509 1513 1514 1518 1522 1526 1527 1529 1534 1535
##    0    0    0    0    0    0    0    1    0    0    0    0    0    0
## Levels: 0 1
```