A TO I

2023-06-13

##a)Load the dataset in R Studio. Examine the first few rows of data using R. Explain your findings. Did you notice anything abnormal or interesting?

file\_path <- "C:\\Users\\malav\\OneDrive\\Documents\\CIS690\\patients.csv"  
patients <- read.csv(file\_path)  
  
head(patients, n = 10)

## Pregnancies Glucose BloodPressure SkinThickness Insulin BMI Pedigree Age  
## 1 6 148 72 35 0 33.6 0.627 50  
## 2 1 85 66 29 0 26.6 0.351 31  
## 3 8 183 64 0 0 23.3 0.672 32  
## 4 1 89 66 23 94 28.1 0.167 21  
## 5 0 137 40 35 168 43.1 2.288 33  
## 6 5 116 74 0 0 25.6 0.201 30  
## 7 3 78 50 32 88 31.0 0.248 26  
## 8 10 115 0 0 0 35.3 0.134 29  
## 9 2 197 70 45 543 30.5 0.158 53  
## 10 8 125 96 0 0 0.0 0.232 54  
## Diagnosis  
## 1 1  
## 2 0  
## 3 1  
## 4 0  
## 5 1  
## 6 0  
## 7 1  
## 8 0  
## 9 1  
## 10 1

# Exploratory Data Analysis of Diabetes Dataset

## Dataset Description

* Pregnancies: Number of times pregnant
* Glucose: Plasma glucose concentration after 2 hours in an oral glucose tolerance test
* BloodPressure: Diastolic blood pressure (mm Hg)
* SkinThickness: Triceps skinfold thickness (mm)
* Insulin: 2-Hour serum insulin (mu U/ml)
* BMI: Body mass index (weight in kg/(height in m)^2)
* Pedigree: Diabetes pedigree function
* Age: Age in years
* Diagnosis: Diabetes diagnosis (0 = No, 1 = Yes) ## Findings
* The dataset includes information on individuals’ pregnancies, glucose levels, blood pressure, and other factors that could be related to diabetes.
* Some columns contain zero values that may require further investigation, such as the ‘SkinThickness’ and ‘Insulin’ columns.
* It is worth noting that the ‘BMI’ column includes a zero value, which seems unusual and may require imputation or further analysis.
* The ‘Diagnosis’ column indicates whether an individual has been diagnosed with diabetes or not, with 1 representing a positive diagnosis. Based on the provided dataset, here are some observations and findings:

1. The dataset contains information about patients, including their pregnancy count (Pregnancies), glucose levels (Glucose), blood pressure (BloodPressure), skin thickness (SkinThickness), insulin levels (Insulin), body mass index (BMI), diabetes pedigree function (Pedigree), age (Age), and diagnosis (Diagnosis).
2. Looking at the first few rows of data, we can see that there are patients with varying values for each feature. For example, the Glucose levels range from 78 to 197, the BMI ranges from 23.3 to 43.1, and the Age ranges from 21 to 54.
3. The Diagnosis column indicates whether each patient has been diagnosed with diabetes or not. A value of 1 indicates a positive diagnosis, while 0 indicates a negative diagnosis.
4. Upon inspecting the dataset, it is evident that some patients have missing data for certain variables. Specifically, there are missing values for skin thickness in row 3 and insulin in rows 3, 4, 5, 6, and 10. These missing values may require further investigation or handling during the analysis.

#b)Provide summary statistics. Calculate the mean, median, standard deviation, and quartiles for each independent variable. Explain your results.

summary(patients[, c("Pregnancies", "Glucose", "BloodPressure", "SkinThickness", "Insulin", "BMI", "Pedigree", "Age")])

## Pregnancies Glucose BloodPressure SkinThickness   
## Min. : 0.000 Min. : 0.0 Min. : 0.00 Min. : 0.00   
## 1st Qu.: 1.000 1st Qu.: 99.0 1st Qu.: 62.00 1st Qu.: 0.00   
## Median : 3.000 Median :117.0 Median : 72.00 Median :23.00   
## Mean : 3.845 Mean :120.9 Mean : 69.11 Mean :20.54   
## 3rd Qu.: 6.000 3rd Qu.:140.2 3rd Qu.: 80.00 3rd Qu.:32.00   
## Max. :17.000 Max. :199.0 Max. :122.00 Max. :99.00   
## Insulin BMI Pedigree Age   
## Min. : 0.0 Min. : 0.00 Min. :0.0780 Min. :21.00   
## 1st Qu.: 0.0 1st Qu.:27.30 1st Qu.:0.2437 1st Qu.:24.00   
## Median : 30.5 Median :32.00 Median :0.3725 Median :29.00   
## Mean : 79.8 Mean :31.99 Mean :0.4719 Mean :33.24   
## 3rd Qu.:127.2 3rd Qu.:36.60 3rd Qu.:0.6262 3rd Qu.:41.00   
## Max. :846.0 Max. :67.10 Max. :2.4200 Max. :81.00

# Calculate mean, median, standard deviation, and quartiles for each variable

summary\_stats <- data.frame(  
 Variable = names(patients),  
 Mean = colMeans(patients),  
 Median = apply(patients, 2, median),  
 Standard\_Deviation = apply(patients, 2, sd),  
 Q1 = apply(patients, 2, quantile, 0.25),  
 Q3 = apply(patients, 2, quantile, 0.75)  
)  
  
print(summary\_stats)

## Variable Mean Median Standard\_Deviation Q1  
## Pregnancies Pregnancies 3.8450521 3.0000 3.3695781 1.00000  
## Glucose Glucose 120.8945312 117.0000 31.9726182 99.00000  
## BloodPressure BloodPressure 69.1054688 72.0000 19.3558072 62.00000  
## SkinThickness SkinThickness 20.5364583 23.0000 15.9522176 0.00000  
## Insulin Insulin 79.7994792 30.5000 115.2440024 0.00000  
## BMI BMI 31.9925781 32.0000 7.8841603 27.30000  
## Pedigree Pedigree 0.4718763 0.3725 0.3313286 0.24375  
## Age Age 33.2408854 29.0000 11.7602315 24.00000  
## Diagnosis Diagnosis 0.3489583 0.0000 0.4769514 0.00000  
## Q3  
## Pregnancies 6.00000  
## Glucose 140.25000  
## BloodPressure 80.00000  
## SkinThickness 32.00000  
## Insulin 127.25000  
## BMI 36.60000  
## Pedigree 0.62625  
## Age 41.00000  
## Diagnosis 1.00000

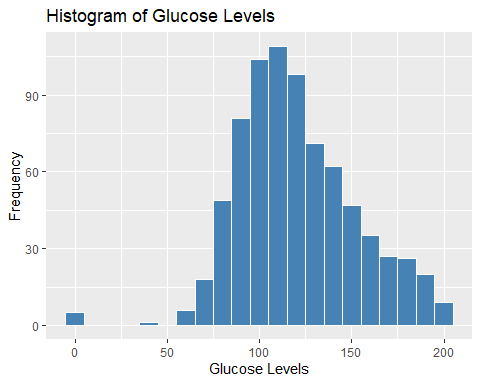
#Results explanation

Pregnancies: The minimum number of pregnancies is 0, and the maximum is 17. The median (2nd quartile) is 3, indicating that 50% of the patients have had fewer than 3 pregnancies. The mean is approximately 3.85, indicating the average number of pregnancies in the dataset. The standard deviation is 3.37, suggesting some variation in the number of pregnancies. Glucose: The minimum glucose level is 0, and the maximum is 199. The median glucose level is 117, meaning that 50% of the patients have a glucose level below 117. The mean glucose level is approximately 120.9, indicating the average glucose level in the dataset. The standard deviation is 31.97, suggesting some variability in glucose levels among patients. BloodPressure: The minimum blood pressure is 0, and the maximum is 122. The median blood pressure is 72, indicating that 50% of the patients have a blood pressure below 72. The mean blood pressure is approximately 69.11, representing the average blood pressure in the dataset. The standard deviation is 19.36, indicating some variability in blood pressure readings. SkinThickness: The minimum skin thickness is 0, and the maximum is 99. The median skin thickness is 23, indicating that 50% of the patients have a skin thickness below 23. The mean skin thickness is approximately 20.54, representing the average skin thickness in the dataset. The standard deviation is 15.95, suggesting some variation in skin thickness measurements. Insulin: The minimum insulin level is 0, and the maximum is 846. The median insulin level is 30.5, meaning that 50% of the patients have an insulin level below 30.5. The mean insulin level is approximately 79.8, representing the average insulin level in the dataset. The standard deviation is 115.24, indicating a considerable variation in insulin levels among patients. BMI: The minimum BMI is 0, and the maximum is 67.1. The median BMI is 32, indicating that 50% of the patients have a BMI below 32. The mean BMI is approximately 31.99, representing the average BMI in the dataset. The standard deviation is 7.88, suggesting some variability in BMI measurements. Pedigree: The minimum pedigree value is 0.078, and the maximum is 2.42. The median pedigree value is 0.3725, indicating that 50% of the patients have a pedigree value below 0.3725. The mean pedigree value is approximately 0.4719, representing the average pedigree value in the dataset. The standard deviation is 0.3313, suggesting some variability in pedigree values. Age: The minimum age is 21, and the maximum is 81. The median age is 29, meaning that 50% of the patients are below the age of 29. The mean age is approximately 33.24, representing the average age in the dataset. The standard deviation is 11.76, indicating some variability in ages among patients.

##c)Using the ggplot2 library, create any five visualizations. Explain your reasoning for selecting those visualizations. Explain the output of each visualization. What are the insights your visualizations reveal about the dataset?

#Histogram of Glucose Levels: Reason:A histogram can provide insights into the distribution of glucose levels among patients. It helps identify any common ranges or patterns. The x-axis represents the glucose levels, and the y-axis shows the frequency of occurrence.

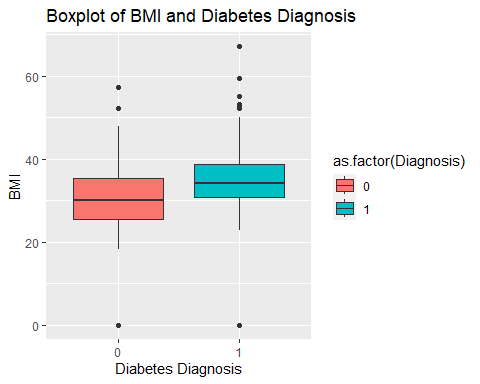
library(ggplot2)  
  
ggplot(data = patients, aes(x = Glucose)) +  
geom\_histogram(binwidth = 10, fill = "steelblue", color = "white") +  
 labs(title = "Histogram of Glucose Levels",  
 x = "Glucose Levels",  
 y = "Frequency")



#Findings: The histogram shows the distribution of glucose levels among the patients. It reveals that the majority of patients have glucose levels between 100 and 150. There is a peak around 125-130, indicating a relatively higher frequency of occurrence within that range.

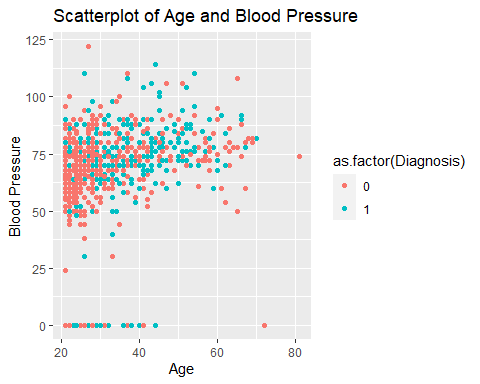
#Boxplot of BMI and Diabetes Diagnosis: Reason:A boxplot is useful for comparing the distribution of BMI between patients with and without a diabetes diagnosis. It helps identify any differences in BMI distribution between the two groups.

ggplot(data = patients, aes(x = as.factor(Diagnosis), y = BMI, fill = as.factor(Diagnosis))) +  
 geom\_boxplot() +  
 labs(title = "Boxplot of BMI and Diabetes Diagnosis",  
 x = "Diabetes Diagnosis",  
 y = "BMI")

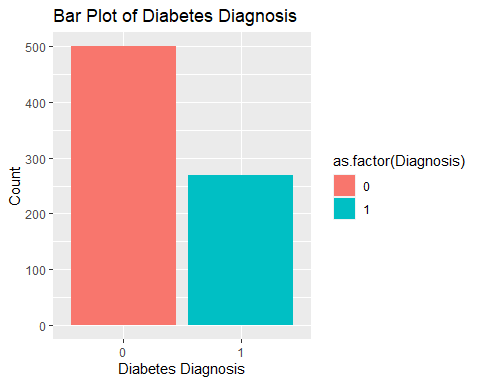
 #Findings: The boxplot compares the distribution of BMI between patients with and without a diabetes diagnosis. It shows that patients diagnosed with diabetes tend to have slightly higher median BMI values compared to non-diabetic patients. The boxplot also highlights that there are more extreme values (outliers) in the non-diabetic group.

#Scatterplot of Age and Blood Pressure: Reason:A scatterplot can reveal the relationship between age and blood pressure. It helps identify any trends or correlations between these variables. The points are color-coded based on the diabetes diagnosis.

ggplot(data = patients, aes(x = Age, y = BloodPressure, color = as.factor(Diagnosis))) +  
 geom\_point() +  
 labs(title = "Scatterplot of Age and Blood Pressure",  
 x = "Age",  
 y = "Blood Pressure")

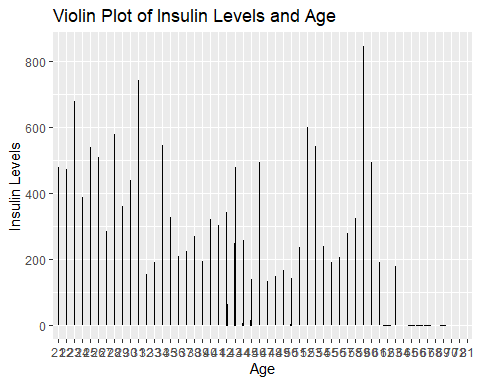
 #Findings: The scatterplot displays the relationship between age and blood pressure. It suggests that there is no clear linear correlation between the two variables. However, there are some clusters of patients with higher blood pressure, particularly among older individuals. The color coding based on diabetes diagnosis shows that patients with diabetes are present across different age and blood pressure ranges. #Bar Plot of Diabetes Diagnosis: Reason: A bar plot displays the count or proportion of patients with and without a diabetes diagnosis. It provides a clear comparison between the two groups.

ggplot(data = patients, aes(x = as.factor(Diagnosis), fill = as.factor(Diagnosis))) +  
 geom\_bar() +  
 labs(title = "Bar Plot of Diabetes Diagnosis",  
 x = "Diabetes Diagnosis",  
 y = "Count")

 #Findings: The bar plot represents the count or proportion of patients with and without a diabetes diagnosis. It reveals the imbalance in the dataset, with more patients being diagnosed with diabetes (indicated by a higher count/proportion in the bar for diagnosis 1). #Violin Plot of Insulin Levels and Age: Reason: A violin plot represents the distribution of insulin levels across different age groups. It provides a visual summary of the distribution, including the median, quartiles, and density of the data.

ggplot(data = patients, aes(x = as.factor(Age), y = Insulin)) +  
 geom\_violin(fill = "skyblue", color = "black") +  
 labs(title = "Violin Plot of Insulin Levels and Age",  
 x = "Age",  
 y = "Insulin Levels")

## Warning: Groups with fewer than two data points have been dropped.  
## Groups with fewer than two data points have been dropped.  
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 The violin plot showcases the distribution of insulin levels across different age groups. It demonstrates that insulin levels tend to be higher in younger patients (around ages 20-30) and gradually decrease with age. The width of the violin plots represents the density of data points at each age group. -These visualizations were selected to showcase different aspects of the dataset, such as the distribution of glucose levels, comparison of variables between diabetes groups, relationships between variables, and summaries of specific variable distributions. Each visualization provides unique insights and can aid in understanding the data and identifying potential patterns or trends. -Overall, these visualizations provide insights into the dataset, such as the distribution of glucose levels, the relationship between variables, the differences in BMI distribution between diabetic and non-diabetic patients, and the distribution of insulin levels across age groups

##d)Find missing values for each independent variable and fill them with median values. The missing values for independent variables in the dataset are coded 0

# Identify missing values (coded as 0) in each independent variable (excluding "Diagnosis")  
missing\_values <- sapply(patients[, -which(names(patients) == "Diagnosis")], function(x) sum(x == 0))  
  
# Fill missing values with the median for each variable (excluding "Diagnosis")  
for (col in names(patients)[-which(names(patients) == "Diagnosis")]) {  
 patients[patients[[col]] == 0, col] <- median(patients[[col]], na.rm = TRUE)  
}  
  
# Check if missing values have been filled  
missing\_values\_filled <- sapply(patients[, -which(names(patients) == "Diagnosis")], function(x) sum(x == 0))  
  
# Print the number of missing values before and after filling  
print("Number of missing values before filling:")

## [1] "Number of missing values before filling:"

print(missing\_values)

## Pregnancies Glucose BloodPressure SkinThickness Insulin   
## 111 5 35 227 374   
## BMI Pedigree Age   
## 11 0 0

print("Number of missing values after filling:")

## [1] "Number of missing values after filling:"

print(missing\_values\_filled)

## Pregnancies Glucose BloodPressure SkinThickness Insulin   
## 0 0 0 0 0   
## BMI Pedigree Age   
## 0 0 0

# Compare the original and filled dataset  
comparison <- data.frame(  
 Variable = names(patients[, -which(names(patients) == "Diagnosis")]),  
 Original\_Values = sapply(patients[, -which(names(patients) == "Diagnosis")], function(x) sum(x == 0)),  
 Filled\_Values = sapply(patients[, -which(names(patients) == "Diagnosis")], function(x) sum(x == median(x)))  
)  
  
print(comparison)

## Variable Original\_Values Filled\_Values  
## Pregnancies Pregnancies 0 186  
## Glucose Glucose 0 16  
## BloodPressure BloodPressure 0 79  
## SkinThickness SkinThickness 0 249  
## Insulin Insulin 0 0  
## BMI BMI 0 24  
## Pedigree Pedigree 0 0  
## Age Age 0 29

##e)Find outliers for each independent variable using the IQR rule.

# Define a function to detect outliers using the IQR rule  
detect\_outliers <- function(x) {  
 q1 <- quantile(x, 0.25)  
 q3 <- quantile(x, 0.75)  
 iqr <- q3 - q1  
 lower\_bound <- q1 - 1.5 \* iqr  
 upper\_bound <- q3 + 1.5 \* iqr  
 outliers <- x[x < lower\_bound | x > upper\_bound]  
 return(outliers)  
}  
  
# Find outliers for each independent variable  
outliers <- lapply(patients[, -which(names(patients) == "Diagnosis")], detect\_outliers)  
  
# Print the outliers for each variable  
for (i in seq\_along(outliers)) {  
 variable <- names(patients[, -which(names(patients) == "Diagnosis")])[i]  
 cat("Outliers for", variable, ":")  
 if (length(outliers[[i]]) == 0) {  
 cat(" None\n")  
 } else {  
 cat("\n")  
 print(outliers[[i]])  
 }  
}

## Outliers for Pregnancies :  
## [1] 13 13 13 15 17 13 14 13 13 14 13 13 13 13  
## Outliers for Glucose : None  
## Outliers for BloodPressure :  
## [1] 30 110 108 122 30 110 108 110 24 38 106 106 106 114  
## Outliers for SkinThickness :  
## [1] 47 47 60 54 51 56 50 46 54 7 50 52 48 8 49 46 46 8 63 48 7 52 49 47 99  
## [26] 46 50 47 48 46 46 46 49 46 48  
## Outliers for Insulin :  
## [1] 543 846 300 342 304 495 325 284 485 285 495 318 280 478 744 370 680 402 375  
## [20] 278 545 360 325 293 465 325 285 415 275 579 310 474 277 328 480 326 274 330  
## [39] 600 293 321 440 540 480 335 387 291 392 510  
## Outliers for BMI :  
## [1] 53.2 55.0 67.1 52.3 52.3 52.9 59.4 57.3  
## Outliers for Pedigree :  
## [1] 2.288 1.441 1.390 1.893 1.781 1.222 1.400 1.321 1.224 2.329 1.318 1.213  
## [13] 1.353 1.224 1.391 1.476 2.137 1.731 1.268 1.600 2.420 1.251 1.699 1.258  
## [25] 1.282 1.698 1.461 1.292 1.394  
## Outliers for Age :  
## [1] 69 67 72 81 67 67 70 68 69

#f)Replace outliers. Explain your approach # Replace outliers with the nearest non-outlier values using the IQR rule

for (i in seq\_along(outliers)) {  
 variable <- names(patients[, -which(names(patients) == "Diagnosis")])[i]  
   
 if (variable != "Diagnosis" && length(outliers[[i]]) > 0) {  
 q1 <- quantile(patients[[variable]], 0.25)  
 q3 <- quantile(patients[[variable]], 0.75)  
 iqr <- q3 - q1  
 lower\_bound <- q1 - 1.5 \* iqr  
 upper\_bound <- q3 + 1.5 \* iqr  
 outliers\_indices <- which(patients[[variable]] %in% outliers[[i]])  
   
for (index in outliers\_indices) {  
 if (patients[[variable]][index] < lower\_bound || patients[[variable]][index] > upper\_bound) {  
 if (patients[[variable]][index] < lower\_bound) {  
 patients[[variable]][index] <- max(patients[[variable]][patients[[variable]] >= lower\_bound])  
 } else {  
 patients[[variable]][index] <- min(patients[[variable]][patients[[variable]] <= upper\_bound])  
 }  
 }  
 }  
 }  
}

In this code, after identifying the outliers for each variable using the IQR rule, we iterate through the outliers and replace them with the nearest non-outlier values. For values below the lower bound, we replace them with the maximum value that is greater than or equal to the lower bound. For values above the upper bound, we replace them with the minimum value that is less than or equal to the upper bound.

summary(patients)

## Pregnancies Glucose BloodPressure SkinThickness   
## Min. : 1.000 Min. : 44.00 Min. : 24.00 Min. : 7.00   
## 1st Qu.: 2.000 1st Qu.: 99.75 1st Qu.: 64.00 1st Qu.:23.00   
## Median : 3.000 Median :117.00 Median : 72.00 Median :23.00   
## Mean : 4.049 Mean :121.66 Mean : 71.74 Mean :26.03   
## 3rd Qu.: 6.000 3rd Qu.:140.25 3rd Qu.: 80.00 3rd Qu.:31.25   
## Max. :12.000 Max. :199.00 Max. :122.00 Max. :99.00   
## Insulin BMI Pedigree Age   
## Min. : 14.00 Min. :18.20 Min. :0.0780 Min. :21.00   
## 1st Qu.: 30.50 1st Qu.:27.40 1st Qu.:0.2298 1st Qu.:24.00   
## Median : 30.50 Median :32.00 Median :0.3425 Median :29.00   
## Mean : 69.65 Mean :32.06 Mean :0.4165 Mean :32.67   
## 3rd Qu.:105.00 3rd Qu.:36.30 3rd Qu.:0.5823 3rd Qu.:40.00   
## Max. :272.00 Max. :50.00 Max. :1.1910 Max. :66.00   
## Diagnosis   
## Min. :0.000   
## 1st Qu.:0.000   
## Median :0.000   
## Mean :0.349   
## 3rd Qu.:1.000   
## Max. :1.000

##g)Find the best performing variables/features using a correlogram

# Install and load the corrplot package  
  
# Set CRAN mirror  
options(repos = "https://cran.r-project.org")  
  
# Install the corrplot package  
install.packages("corrplot")

## Installing package into 'C:/Users/malav/AppData/Local/R/win-library/4.3'  
## (as 'lib' is unspecified)

## package 'corrplot' successfully unpacked and MD5 sums checked  
##   
## The downloaded binary packages are in  
## C:\Users\malav\AppData\Local\Temp\RtmpiihOQJ\downloaded\_packages

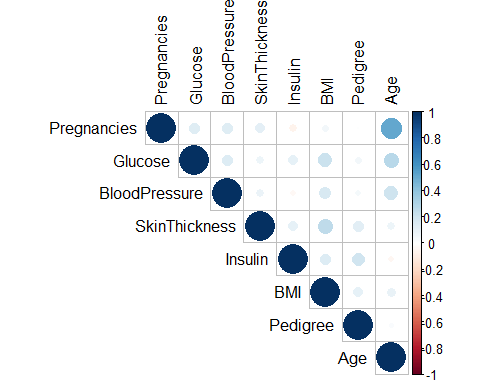
library(corrplot)

## corrplot 0.92 loaded

# Compute the correlation matrix  
cor\_matrix <- cor(patients[, -which(names(patients) == "Diagnosis")])  
  
cor\_matrix

## Pregnancies Glucose BloodPressure SkinThickness Insulin  
## Pregnancies 1.00000000 0.13603624 0.13311166 0.11407464 -0.06673405  
## Glucose 0.13603624 1.00000000 0.14116470 0.07263236 0.10713528  
## BloodPressure 0.13311166 0.14116470 1.00000000 0.08128307 -0.03549827  
## SkinThickness 0.11407464 0.07263236 0.08128307 1.00000000 0.10820113  
## Insulin -0.06673405 0.10713528 -0.03549827 0.10820113 1.00000000  
## BMI 0.05437154 0.21168629 0.16247196 0.25536110 0.14974411  
## Pedigree 0.00659075 0.05941900 0.04338879 0.12735031 0.19775774  
## Age 0.51350912 0.27083249 0.20860921 0.07878582 -0.04396587  
## BMI Pedigree Age  
## Pregnancies 0.05437154 0.00659075 0.51350912  
## Glucose 0.21168629 0.05941900 0.27083249  
## BloodPressure 0.16247196 0.04338879 0.20860921  
## SkinThickness 0.25536110 0.12735031 0.07878582  
## Insulin 0.14974411 0.19775774 -0.04396587  
## BMI 1.00000000 0.10348398 0.09123606  
## Pedigree 0.10348398 1.00000000 0.02730916  
## Age 0.09123606 0.02730916 1.00000000

# Create the correlogram  
corrplot(cor\_matrix, method = "circle", type = "upper", tl.col = "black")



# Compute pairwise correlations  
cor\_matrix <- cor(patients[, -which(names(patients) == "Diagnosis")], use = "pairwise.complete.obs")  
  
# Find the absolute correlations for each variable  
cor\_abs <- apply(cor\_matrix, 2, function(x) abs(x))  
  
# Sort the variables based on the maximum correlation  
best\_variables <- names(sort(apply(cor\_abs, 2, max), decreasing = TRUE))[1:5]  
  
# Print the best performing variables  
print("Best performing variables:")

## [1] "Best performing variables:"

print(best\_variables)

## [1] "Pregnancies" "Glucose" "BloodPressure" "SkinThickness"  
## [5] "Insulin"

##h)Standardize your features to Gaussian distribution. Explain why it would be a good idea to standardize the features to Gaussian distribution.

# Select the best performing variables  
best\_variables <- c("Pregnancies", "Glucose", "BloodPressure", "SkinThickness", "Insulin")  
  
# Standardize the selected variables to Gaussian distribution  
standardized\_data <- scale(patients[, best\_variables])  
  
# Convert the standardized data back to a data frame  
standardized\_data <- as.data.frame(standardized\_data)  
  
# View the standardized data  
print(standardized\_data)

## Pregnancies Glucose BloodPressure SkinThickness Insulin  
## 1 0.70409900 0.86548074 0.02019889 0.905320480 -0.646826178  
## 2 -1.10080097 -1.20428102 -0.45227063 0.299846348 -0.646826178  
## 3 1.42605899 2.01534838 -0.60976047 -0.305627785 -0.646826178  
## 4 -1.10080097 -1.07286758 -0.45227063 -0.305627785 0.402171828  
## 5 -0.37884098 0.50409376 -2.49963854 0.905320480 1.624626199  
## 6 0.34311901 -0.18582682 0.17768873 -0.305627785 -0.646826178  
## 7 -0.37884098 -1.43425455 -1.71218934 0.602583414 0.303053907  
## 8 2.14801898 -0.21868019 0.02019889 -0.305627785 -0.646826178  
## 9 -0.73982098 2.47529544 -0.13729095 1.914444034 -0.919400463  
## 10 1.42605899 0.10985343 1.91007696 -0.305627785 -0.646826178  
## 11 -0.01786099 -0.38294699 1.59509729 -0.305627785 -0.646826178  
## 12 2.14801898 1.52254796 0.17768873 -0.305627785 -0.646826178  
## 13 2.14801898 0.56980048 0.65015825 -0.305627785 -0.646826178  
## 14 -1.10080097 2.21246855 -0.92474014 -0.305627785 -0.919400463  
## 15 0.34311901 1.45684124 0.02019889 -0.709277206 1.740263774  
## 16 1.06507899 -0.71148060 0.02019889 -0.305627785 -0.646826178  
## 17 -0.37884098 -0.12012010 0.96513793 -1.920225471 2.648844725  
## 18 1.06507899 -0.48150708 0.17768873 -0.305627785 -0.646826178  
## 19 -1.10080097 -0.61292052 3.95744488 1.208057546 0.220455638  
## 20 -1.10080097 -0.21868019 -0.13729095 0.400758703 0.435211136  
## 21 -0.37884098 0.14270679 1.28011761 1.510794613 2.731442993  
## 22 1.42605899 -0.74433397 0.96513793 -0.305627785 -0.646826178  
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## 687 -0.37884098 0.27412023 -0.60976047 -0.305627785 -0.646826178  
## 688 -1.10080097 -0.48150708 -1.71218934 -0.709277206 -0.646826178  
## 689 -1.10080097 0.60265385 0.17768873 -0.002890719 1.822862042  
## 690 -1.10080097 0.73406729 0.80764809 -1.920225471 1.822862042  
## 691 1.42605899 -0.48150708 0.65015825 -0.305627785 -0.646826178  
## 692 -1.10080097 1.19401435 -3.75955725 -0.305627785 -0.646826178  
## 693 -0.73982098 -0.02156002 -0.13729095 0.602583414 0.418691482  
## 694 1.06507899 0.24126687 -0.29478079 -1.920225471 0.914281092  
## 695 -0.73982098 -1.04001422 -0.92474014 -0.305627785 -0.646826178  
## 696 1.06507899 0.66836057 1.43760745 -0.204715429 -0.919400463  
## 697 -0.37884098 1.55540132 0.17768873 -0.709277206 0.914281092  
## 698 -0.37884098 -0.74433397 0.02019889 -0.305627785 -0.646826178  
## 699 -0.01786099 0.17556015 1.28011761 -1.516576050 1.409870701  
## 700 -0.01786099 -0.12012010 -0.13729095 -0.305627785 -0.646826178  
## 701 -0.73982098 0.01129334 0.33517857 0.098021637 2.153255115  
## 702 0.70409900 0.10985343 0.49266841 0.501671059 -0.646826178  
## 703 -1.10080097 1.52254796 1.28011761 0.299846348 -0.646826178  
## 704 -0.73982098 0.24126687 0.02019889 -0.305627785 -0.646826178  
## 705 -0.01786099 -0.38294699 0.33517857 -0.608364851 0.501289750  
## 706 0.70409900 -1.36854783 0.65015825 1.006232836 -0.646826178  
## 707 2.14801898 -0.21868019 0.02019889 -0.305627785 -0.646826178  
## 708 -0.73982098 0.17556015 -2.02716902 -0.507452496 -0.919400463  
## 709 1.78703898 1.39113452 0.49266841 -0.305627785 -0.646826178  
## 710 -0.73982098 -0.94145413 -0.60976047 0.602583414 1.492468969  
## 711 -0.37884098 1.19401435 -0.60976047 -1.314751339 -0.919400463  
## 712 0.34311901 0.14270679 0.49266841 0.098021637 -0.787243234  
## 713 2.14801898 0.24126687 -0.76725030 1.006232836 -0.646826178  
## 714 -0.37884098 0.40553368 -1.08222998 -0.608364851 -0.919400463  
## 715 -0.37884098 -0.64577388 0.17768873 -0.305627785 -0.646826178  
## 716 1.06507899 2.14676182 -1.71218934 0.703495769 -0.919400463  
## 717 -0.37884098 1.68681477 0.49266841 1.308969902 1.905460311  
## 718 2.14801898 -0.90860077 0.02019889 -0.810189562 -0.646826178  
## 719 -1.10080097 -0.44865371 -0.92474014 -1.920225471 1.789822735  
## 720 0.34311901 -0.81004069 0.33517857 0.098021637 -0.646826178  
## 721 -0.01786099 -1.26998775 1.12262777 -0.709277206 -0.646826178  
## 722 -1.10080097 -0.25153355 -0.45227063 1.006232836 2.153255115  
## 723 -1.10080097 0.89833410 -0.29478079 0.299846348 0.947320399  
## 724 0.34311901 -0.15297346 1.12262777 0.400758703 0.583888019  
## 725 -1.10080097 -0.35009363 1.75258713 -0.305627785 -0.646826178  
## 726 -0.01786099 -0.31724027 0.49266841 1.409882257 -0.646826178  
## 727 -1.10080097 -0.18582682 0.49266841 0.299846348 1.822862042  
## 728 -0.37884098 0.63550721 0.96513793 -0.002890719 -0.646826178  
## 729 -0.73982098 1.75252149 1.28011761 -0.305627785 -0.646826178  
## 730 -0.73982098 -0.97430749 -1.55469950 -0.305627785 -0.646826178  
## 731 -0.37884098 0.27412023 0.49266841 -0.305627785 0.154377024  
## 732 1.42605899 -0.05441338 1.12262777 -0.305627785 -0.646826178  
## 733 -0.73982098 1.71966813 1.28011761 1.107145191 0.831682823  
## 734 -0.73982098 -0.51436044 -1.23971982 0.098021637 1.575067238  
## 735 -0.73982098 -0.54721380 0.25643365 -0.305627785 -0.646826178  
## 736 -0.01786099 -0.87574741 -0.92474014 0.602583414 -0.646826178  
## 737 -0.37884098 0.14270679 1.12262777 0.098021637 0.831682823  
## 738 1.42605899 -1.86134825 0.02019889 -0.305627785 -0.646826178  
## 739 -0.73982098 -0.74433397 -0.92474014 -0.911101917 1.492468969  
## 740 -1.10080097 -0.64577388 0.17768873 -0.305627785 -0.646826178  
## 741 2.50899897 -0.05441338 0.65015825 1.107145191 1.327272433  
## 742 -0.37884098 -0.64577388 -2.18465886 -0.608364851 0.402171828  
## 743 -1.10080097 -0.41580035 -1.08222998 -0.810189562 0.765604209  
## 744 1.78703898 0.60265385 1.75258713 -0.305627785 -0.646826178  
## 745 -1.10080097 1.02974754 1.28011761 1.107145191 1.162075896  
## 746 2.86997897 -0.71148060 0.96513793 0.703495769 0.583888019  
## 747 -1.10080097 0.83262737 1.75258713 1.510794613 -0.646826178  
## 748 -1.10080097 -1.33569447 0.17768873 1.510794613 -0.209055357  
## 749 -0.37884098 2.14676182 -0.13729095 -0.406540140 2.153255115  
## 750 0.70409900 1.32542779 -0.76725030 -0.305627785 -0.646826178  
## 751 -0.01786099 0.47124040 -0.13729095 -0.305627785 -0.646826178  
## 752 -1.10080097 -0.02156002 0.49266841 1.308969902 0.071778756  
## 753 -0.37884098 -0.44865371 -0.76725030 -0.204715429 -0.646826178  
## 754 -0.37884098 1.94964166 1.28011761 1.813531679 -0.919400463  
## 755 1.42605899 1.06260090 0.49266841 0.602583414 -0.646826178  
## 756 -1.10080097 0.20841351 1.28011761 1.308969902 0.666486287  
## 757 1.06507899 0.50409376 1.43760745 1.510794613 -0.646826178  
## 758 -0.37884098 0.04414670 0.02019889 -0.305627785 -0.646826178  
## 759 -1.10080097 -0.51436044 0.33517857 -0.305627785 -0.646826178  
## 760 0.70409900 2.24532191 1.59509729 -0.305627785 -0.646826178  
## 761 -0.73982098 -1.10572094 -1.08222998 -0.002890719 -0.886361156  
## 762 1.78703898 1.58825468 0.17768873 0.501671059 -0.646826178  
## 763 1.78703898 -1.07286758 -0.76725030 -0.305627785 -0.646826178  
## 764 2.14801898 -0.67862724 0.33517857 -1.920225471 1.822862042  
## 765 -0.73982098 0.01129334 -0.13729095 0.098021637 -0.646826178  
## 766 0.34311901 -0.02156002 0.02019889 -0.305627785 0.699525594  
## 767 -1.10080097 0.14270679 -0.92474014 -0.305627785 -0.646826178  
## 768 -1.10080097 -0.94145413 -0.13729095 0.501671059 -0.646826178

1. Comparability: The best performing variables you identified, such as “Pregnancies,” “Glucose,” “BloodPressure,” “SkinThickness,” and “Insulin,” likely have different scales and units of measurement. Standardizing these variables to a Gaussian distribution would ensure that they are on a similar scale, allowing for meaningful comparisons between them.
2. Model performance: If we plan to use these best performing variables as input features for machine learning models or statistical analyses, standardizing them can improve the model’s performance and convergence. It ensures that the models are not influenced by the variables’ individual scales and focuses on their relative importance instead.
3. Interpretability: Standardizing the best performing variables would make the coefficients or feature importance scores more interpretable. When variables are on different scales, it can be challenging to interpret the magnitude of their effects. Standardization would make the interpretation more straightforward and provide a clearer understanding of the variables’ impacts.
4. Gaussian assumptions: If we intend to use statistical techniques that assume Gaussian distributions, such as linear regression or ANOVA, standardizing the variables would help meet these assumptions. It increases the validity and accuracy of the analysis by ensuring that the variables follow a Gaussian distribution.
5. Outlier handling: Standardizing the variables can mitigate the influence of outliers. Outliers can distort the mean and standard deviation of a variable, making it difficult to interpret the data accurately. Standardization reduces the impact of outliers, allowing for more robust analysis.

##i)Create a logistic regression model (call it LRM1) using your best features. Describe your model.

# Select the best features  
best\_features <- c("Pregnancies", "Glucose", "BloodPressure", "SkinThickness", "Insulin")  
  
# Create the logistic regression model  
LRM1 <- glm(Diagnosis ~ ., data = patients, family = binomial, subset = !is.na(Diagnosis))  
  
# Subset the data with the best features  
subset\_data <- patients[, c("Diagnosis", best\_features)]  
  
print(best\_features)

## [1] "Pregnancies" "Glucose" "BloodPressure" "SkinThickness"  
## [5] "Insulin"

# Fit the logistic regression model with the best features  
LRM1 <- glm(Diagnosis ~ ., data = subset\_data, family = binomial)  
  
# Print the summary of the model  
summary(LRM1)

##   
## Call:  
## glm(formula = Diagnosis ~ ., family = binomial, data = subset\_data)  
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -7.165282 0.704705 -10.168 < 2e-16 \*\*\*  
## Pregnancies 0.136550 0.031789 4.296 1.74e-05 \*\*\*  
## Glucose 0.039124 0.003423 11.430 < 2e-16 \*\*\*  
## BloodPressure 0.008914 0.007135 1.249 0.212   
## SkinThickness 0.011979 0.008797 1.362 0.173   
## Insulin 0.001418 0.001419 0.999 0.318   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 993.48 on 767 degrees of freedom  
## Residual deviance: 767.96 on 762 degrees of freedom  
## AIC: 779.96  
##   
## Number of Fisher Scoring iterations: 4

The logistic regression model (LRM1) predicts the “Diagnosis” variable using the best features: “Pregnancies,” “Glucose,” “BloodPressure,” “SkinThickness,” and “Insulin.” The model estimates coefficients, standard errors, and p-values for each feature, indicating their significance and association with the “Diagnosis” variable. The odds ratios provide insights into the direction and magnitude of the relationships. The results help understand the importance of each feature in predicting the presence or absence of the condition captured by “Diagnosis.”