

1. Using the for loop, create an R script that will display a 5x5 matrix as shown in Figure 1. It must contain vectorA = [1,2,3,4,5] and a 5 x 5 zero matrix.

```
vectorA <- c(1, 2, 3, 4, 5)
matrixA <- matrix(0, nrow = 5, ncol = 5)
for (i in 1:5) {
  matrixA[i, i] <- vectorA[i]
}
matrixA
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    2    0    0    0
## [3,]    0    0    3    0    0
## [4,]    0    0    0    4    0
## [5,]    0    0    0    0    5
```

2. Print the string "*" using for() function.

```
n <- 5
for (i in 1:n) {
  for (j in 1:i) {
    cat(" * ")
  }
  cat("\n")
}
```

```
## *
## * *
## * * *
## * * * *
## * * * * *
```

3. Get an input from the user to print the Fibonacci sequence starting from the 1st input up to 500. Use repeat and break statements. Write the R Scripts and its output.

```
#start <- as.integer(readline(prompt = "Enter the starting number for the Fibonacci sequence: "))
start <- 5
a <- 0
b <- 1
repeat {
  fib <- a + b
  a <- b
  b <- fib
  if (fib >= start) {
    cat(fib, " ")
  }
  if (fib >= 500) {
    break
  }
}
```

```
## 5 8 13 21 34 55 89 144 233 377 610
```

4. Import the dataset as shown in Figure 1 you have created previously.

```
shoes <- read.csv("shoes.csv")
```

- a. What is the R script for importing an excel or a csv file? Display the first 6 rows of the dataset? Show

your codes and its result

```
head(shoes)
```

```
##   Shoesize Height Gender
## 1      6.5   66.0      F
## 2      9.0   68.0      F
## 3      8.5   64.5      F
## 4      8.5   65.0      F
## 5     10.5   70.0      M
## 6      7.0   64.0      F
```

- b. Create a subset for gender(female and male). How many observations are there in Male? How about in Female? Write the R scripts and its output.

```
female_subset <- subset(shoes, Gender == "F")
male_subset <- subset(shoes, Gender == "M")
female_count <- nrow(female_subset)
male_count <- nrow(male_subset)
cat("Female:", female_count, "\n")
```

```
## Female: 14
```

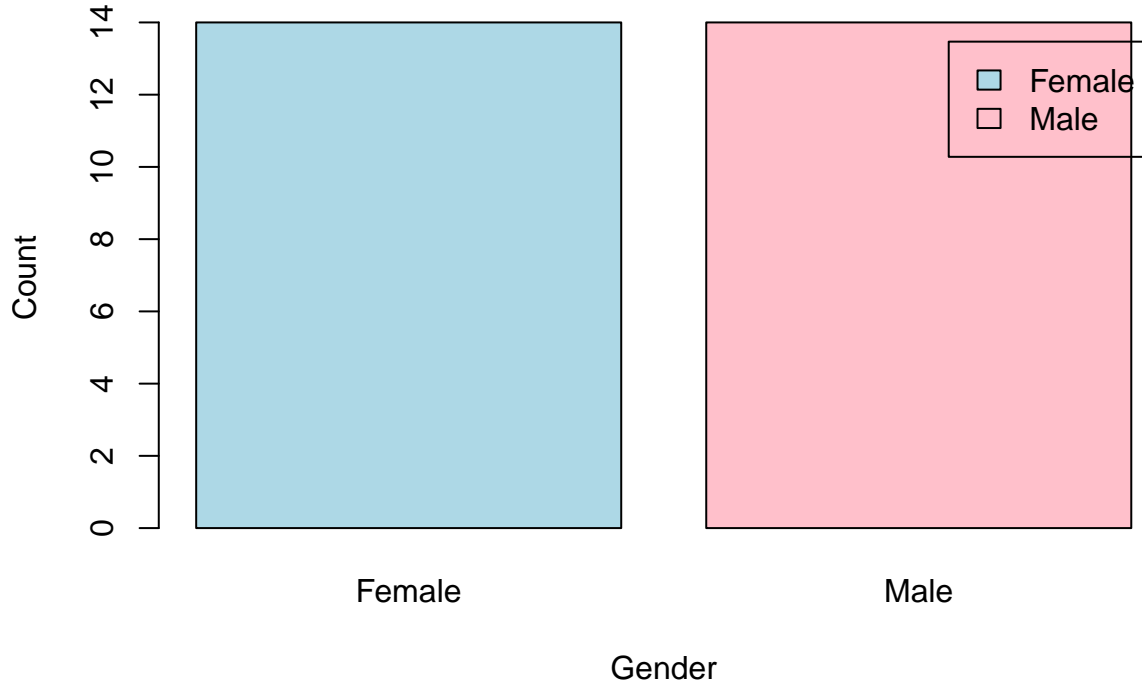
```
cat("Male:", male_count, "\n")
```

```
## Male: 14
```

- c. Create a graph for the number of males and females for Household Data. Use plot(), chart type = barplot. Make sure to place title, legends, and colors. Write the R scripts and its result.

```
gender_counts <- table(shoes$Gender)
barplot(gender_counts,
  main = "Number of Males and Females in Household Data",
  xlab = "Gender",
  ylab = "Count",
  col = c("lightblue", "pink"),
  legend = c("Female", "Male"),
  names.arg = c("Female", "Male"))
```

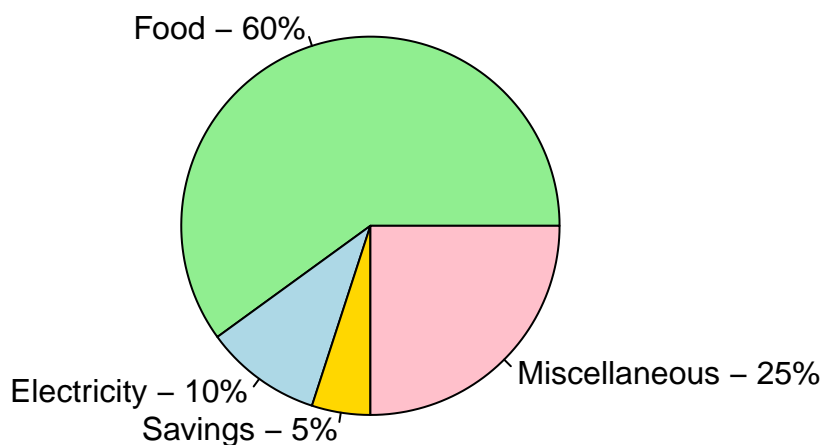
Number of Males and Females in Household Data



5. The monthly income of Dela Cruz family was spent on the following: a. Create a piechart that will include labels in percentage. Add some colors and title of the chart. Write the R scripts and show its output.

```
expenses <- c(Food = 60, Electricity = 10, Savings = 5, Miscellaneous = 25)
percent_labels <- paste0(names(expenses), " - ", round(expenses / sum(expenses) * 100), "%")
pie(expenses,
    labels = percent_labels,
    col = c("lightgreen", "lightblue", "gold", "pink"),
    main = "Dela Cruz Family Monthly Expenses")
```

Dela Cruz Family Monthly Expenses



6. Use the iris dataset. a. Check for the structure of the dataset using the `str()` function. Describe what you have seen in the output.

```
data(iris)
str(iris)
```

```
## 'data.frame': 150 obs. of 5 variables:
## $ Sepal.Length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ Petal.Length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ Petal.Width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
## $ Species : Factor w/ 3 levels "setosa","versicolor",...: 1 1 1 1 1 1 1 1 1 1 ...
```

- b. Create an R object that will contain the mean of the sepal.length, sepal.width, petal.length, and petal.width. What is the R script and its result?

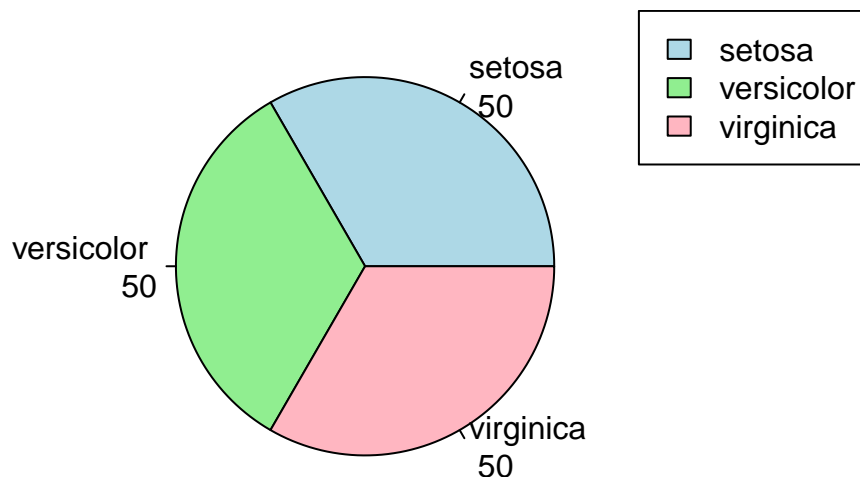
```
colMeans(iris[, 1:4])
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 5.843333 3.057333 3.758000 1.199333
```

- c. Create a pie chart for the Species distribution. Add title, legends, and colors. Write the R script and its result.

```
species_counts <- table(iris$Species)
pie(species_counts,
    main = "Species Distribution in Iris Dataset",
    col = c("lightblue", "lightgreen", "lightpink"),
    labels = paste(names(species_counts), "\n", species_counts))
legend("topright",
    legend = names(species_counts),
    fill = c("lightblue", "lightgreen", "lightpink"))
```

Species Distribution in Iris Dataset



- d. Subset the species into setosa, versicolor, and virginica. Write the R scripts and show the last six (6) rows of each species.

```
setosa <- subset(iris, Species == "setosa")
versicolor <- subset(iris, Species == "versicolor")
virginica <- subset(iris, Species == "virginica")
tail(setosa)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 45 5.1 3.8 1.9 0.4 setosa
```

```
## 46      4.8      3.0      1.4      0.3 setosa
## 47      5.1      3.8      1.6      0.2 setosa
## 48      4.6      3.2      1.4      0.2 setosa
## 49      5.3      3.7      1.5      0.2 setosa
## 50      5.0      3.3      1.4      0.2 setosa
```

```
tail(versicolor)
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width  Species
## 95          5.6        2.7        4.2        1.3 versicolor
## 96          5.7        3.0        4.2        1.2 versicolor
## 97          5.7        2.9        4.2        1.3 versicolor
## 98          6.2        2.9        4.3        1.3 versicolor
## 99          5.1        2.5        3.0        1.1 versicolor
## 100         5.7        2.8        4.1        1.3 versicolor
```

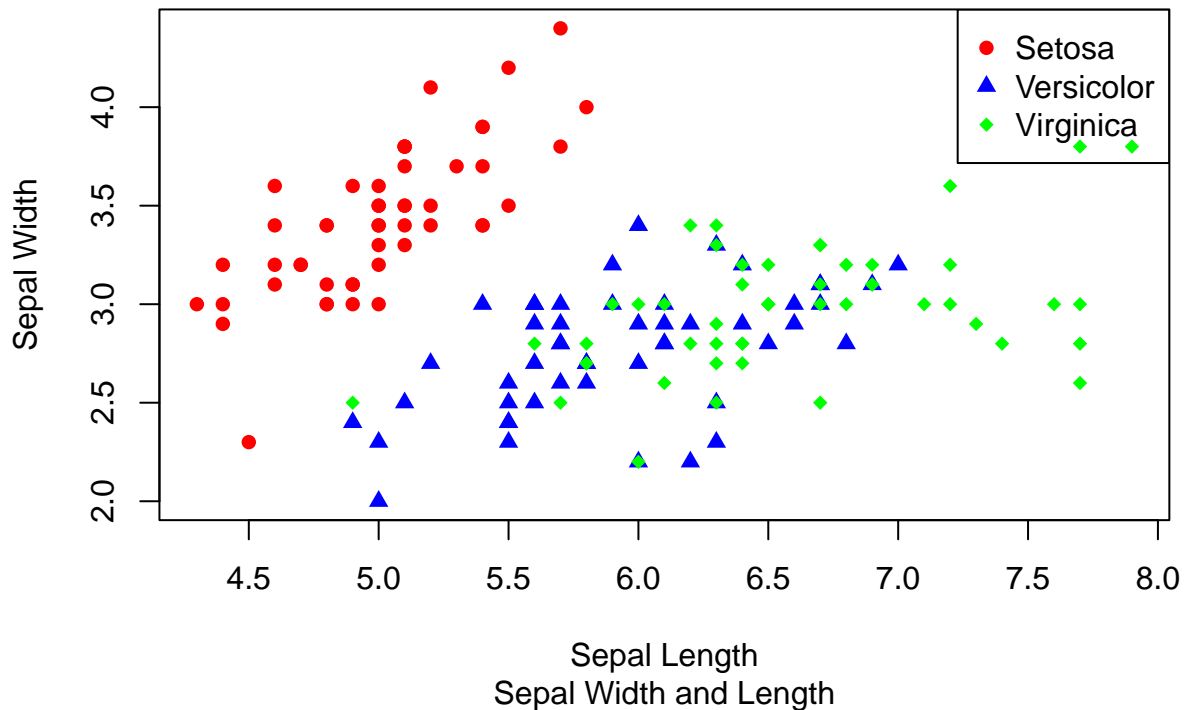
```
tail(virginica)
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width  Species
## 145          6.7        3.3        5.7        2.5 virginica
## 146          6.7        3.0        5.2        2.3 virginica
## 147          6.3        2.5        5.0        1.9 virginica
## 148          6.5        3.0        5.2        2.0 virginica
## 149          6.2        3.4        5.4        2.3 virginica
## 150          5.9        3.0        5.1        1.8 virginica
```

- e. Create a scatterplot of the sepal.length and sepal.width using the different species(setosa,versicolor,virginica). Add a title = "Iris Dataset", subtitle = "Sepal width and length, labels for the x and y axis, the pch symbol and colors should be based on the species.

```
colors <- c("setosa" = "red", "versicolor" = "blue", "virginica" = "green")
symbols <- c("setosa" = 16, "versicolor" = 17, "virginica" = 18)
plot(iris$Sepal.Length, iris$Sepal.Width,
     col = colors[iris$Species],
     pch = symbols[iris$Species],
     main = "Iris Dataset",
     sub = "Sepal Width and Length",
     xlab = "Sepal Length",
     ylab = "Sepal Width")
legend("topright", legend = c("Setosa", "Versicolor", "Virginica"),
     col = c("red", "blue", "green"),
     pch = c(16, 17, 18))
```

Iris Dataset



f. Overall Interpretation —The data structure showed that it is appropriate for both exploratory data analysis and more advanced statistical modeling. —The mean values provided a quick overview of the characteristics of the iris flowers. —The pie chart effectively visualized the distribution of species, highlighting the predominance of setosa. —Subsetting the data allowed for a more granular examination of individual species, which can be crucial for targeted analysis. —The scatterplot illustrated the interdependence of sepal length and width while visually distinguishing between species, facilitating further exploration into their relationships.

7. Import the alexa-file.xlsx. Check on the variations. Notice that there are extra whitespaces among black variants (Black Dot, Black Plus, Black Show, Black Spot). Also on the white variants (White Dot, White Plus, White Show, White Spot).

```
library(readxl)
alexa_data <- read_excel("alexa_file.xlsx")
unique(alexa_data$variation)

## [1] "Charcoal Fabric"      "Walnut Finish"
## [3] "Heather Gray Fabric" "Sandstone Fabric"
## [5] "Oak Finish"          "Black"
## [7] "White"               "Black Spot"
## [9] "White Spot"          "Black Show"
## [11] "White Show"          "Black Plus"
## [13] "White Plus"          "Configuration: Fire TV Stick"
## [15] "Black Dot"           "White Dot"

alexa_data$variation <- gsub("Black Dot", "BlackDot", alexa_data$variation)
alexa_data$variation <- gsub("Black Plus", "BlackPlus", alexa_data$variation)
alexa_data$variation <- gsub("Black Show", "BlackShow", alexa_data$variation)
alexa_data$variation <- gsub("Black Spot", "BlackSpot", alexa_data$variation)
alexa_data$variation <- gsub("White Dot", "WhiteDot", alexa_data$variation)
```

```

alexa_data$variation <- gsub("White Plus", "WhitePlus", alexa_data$variation)
alexa_data$variation <- gsub("White Show", "WhiteShow", alexa_data$variation)
alexa_data$variation <- gsub("White Spot", "WhiteSpot", alexa_data$variation)
unique(alexa_data$variation)

```

```

## [1] "Charcoal Fabric"      "Walnut Finish"
## [3] "Heather Gray Fabric"  "Sandstone Fabric"
## [5] "Oak Finish"           "Black"
## [7] "White"                "Black Spot"
## [9] "White Spot"           "Black Show"
## [11] "White Show"           "Black Plus"
## [13] "White Plus"           "Configuration: Fire TV Stick"
## [15] "Black Dot"            "White Dot"

```

- b. Get the total number of each variations and save it into another object. Save the object as variations.RData. Write the R scripts. What is its result?

```

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

```

```

variation_counts <- alexa_data %>%
  count(variation)
print(variation_counts)

```

```

## # A tibble: 16 x 2
##   variation      n
##   <chr>      <int>
## 1 Black      261
## 2 Black Dot  516
## 3 Black Plus 270
## 4 Black Show 265
## 5 Black Spot 241
## 6 Charcoal Fabric 430
## 7 Configuration: Fire TV Stick 350
## 8 Heather Gray Fabric 157
## 9 Oak Finish  14
## 10 Sandstone Fabric 90
## 11 Walnut Finish 9
## 12 White      91
## 13 White Dot  184
## 14 White Plus 78
## 15 White Show 85
## 16 White Spot 109

```

```

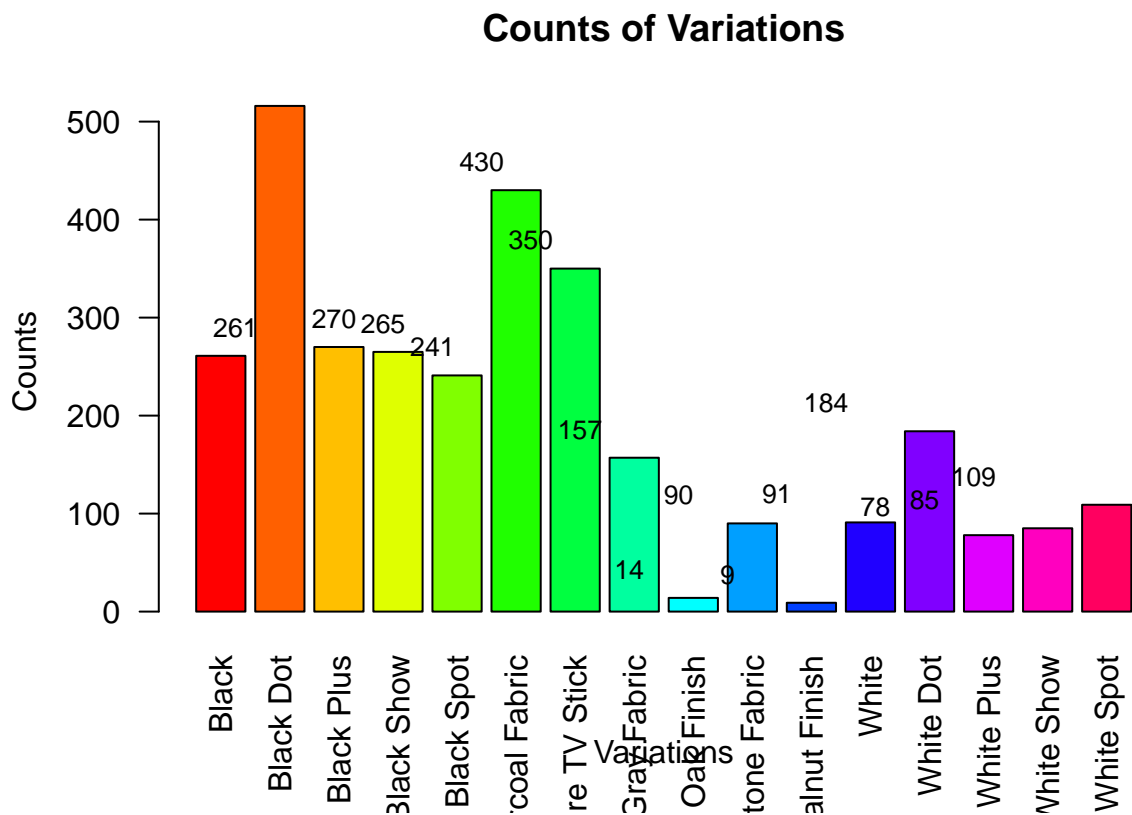
save(variation_counts, file = "variations.RData")

```

- c. From the variations.RData, create a barplot(). Complete the details of the chart which include the

title, color, labels of each bar.

```
library(dplyr)
load("variations.RData")
variation_counts$variation <- gsub(" +", " ", variation_counts$variation)
variation_counts$variation <- trimws(variation_counts$variation)
bar_data <- variation_counts$n
bar_names <- variation_counts$variation
barplot(
  bar_data,
  main = "Counts of Variations",
  col = rainbow(length(bar_data)),
  names.arg = bar_names,
  xlab = "Variations",
  ylab = "Counts",
  las = 2,
  border = "black"
)
text(x = seq_along(bar_data), y = bar_data, labels = bar_data, pos = 3, cex = 0.8, col = "black")
```



d. Create a barplot() for the black and white variations. Plot it in 1 frame, side by side. Complete the details of the chart.

```
library(ggplot2)
library(dplyr)
load("variations.RData")
variation_counts$variation <- gsub(" +", " ", variation_counts$variation)
variation_counts$variation <- trimws(variation_counts$variation)
bw_variations <- variation_counts %>%
  filter(grepl("Black|White", variation))
```



```

bar_data <- as.matrix(bw_variations$n)
bar_names <- bw_variations$variation
barplot(
  bar_data,
  beside = TRUE,
  main = "Counts of Black and White Variations",
  col = c("black", "gray", "lightgray", "white"),
  names.arg = bar_names,
  xlab = "Variations",
  ylab = "Counts",
  las = 2,
  border = "black"
)
text(x = seq_along(bar_data), y = bar_data, labels = bar_data, pos = 3, cex = 0.8, col = "black")

```

