RWorksheet_calvario#4b.Rmd

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2024-11-06

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)

zero_matrix <- matrix(0, nrow = 5, ncol = 5)

for (i in 1:5) {
  for (j in 1:5) {
    zero_matrix[i, j] <- abs(vectorA[i] - vectorA[j])
  }
}

zero_matrix
```

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

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

```
n <- 5

for (i in 1:n) {
  output <- paste(rep("*", i), collapse = " ")
  cat(output, "\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_value <- as.numeric(readline(prompt = "Enter a starting number for the Fibonacci sequence: "))

a <- 0
b <- 1

cat("Fibonacci sequence starting from", start_value, "up to 500:\n")

repeat {
   next_fib <- a + b

  if (next_fib > 500) {
    break
  }

  if (next_fib >= start_value) {
    cat(next_fib, "\n")
  }
   a <- b
   b <- next_fib
}
```

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

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

```
data <- read.csv("shoe_size.csv")

head(data)
```

```
##   Shoe.size Height Gender
## 1       6.5     66      F
## 2       9.0     68      F
## 3       8.5     64      F
## 4       8.5     65      F
## 5      10.5     70      M
## 6       7.0     64      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.

```r
male_data <- subset(data, Gender == "Male")
female_data <- subset(data, Gender == "Female")

num_male <- nrow(male_data)
num_female <- nrow(female_data)

cat("Number of Male observations:", num_male, "\n")
```

```
## Number of Male observations: 0
```

```r
cat("Number of Female observations:", num_female, "\n")
```

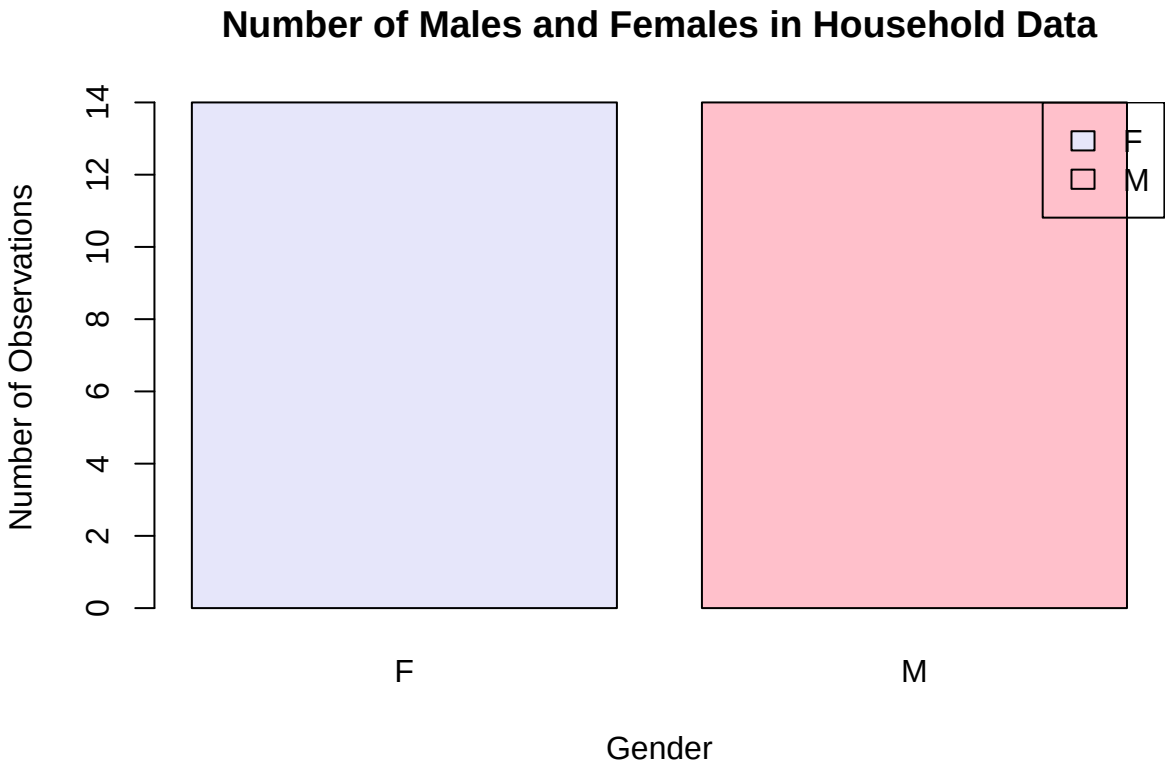
```
## Number of Female observations: 0
```

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.

```r
gender_counts <- table(data$Gender)

barplot(gender_counts,
        main = "Number of Males and Females in Household Data",
        xlab = "Gender",
        ylab = "Number of Observations",
        col = c("lavender", "pink"),
        beside = TRUE)

legend("topright",
       legend = names(gender_counts),
       fill = c("lavender", "pink"))
```

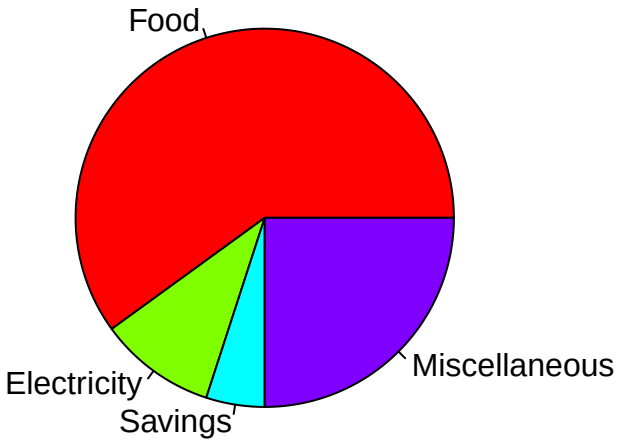


5. The monthly income of Dela Cruz family was spent on the following:

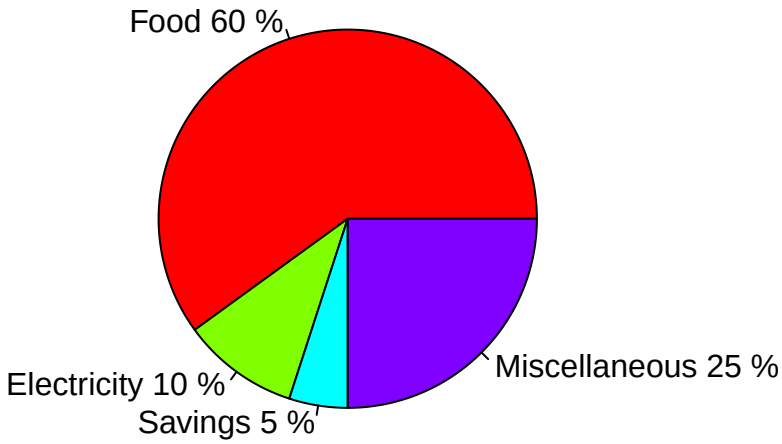
a. Create a piechart that will include labels in percentage.Add some colors and title of the chart. Write the R scripts and show its output.

```
expenses <- c(60, 10, 5, 25)
labels <- c("Food", "Electricity", "Savings", "Miscellaneous")

pie(expenses,
    labels = labels,
    main = "Monthly Income Distribution of Dela Cruz Family",
    col = rainbow(length(expenses)))
```




```
percentages <- round(expenses / sum(expenses) * 100, 1)
labels_with_percentages <- paste(labels, percentages, "%")
pie(expenses,
    labels = labels_with_percentages,
    main = "Monthly Income Distribution of Dela Cruz Family",
    col = rainbow(length(expenses)))
```



6. Use the iris dataset.

a. Check for the structure of the dataset using the str() function.

```
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 ...
```

Describe what you have seen in the output.

The output of str(iris) reveals that the iris dataset is a data frame with 150 observations and 5 variables. Four of the variables—Sepal.Length, Sepal.Width, Petal.Length, and Petal.Width—are numeric, representing various measurements of the flower's sepal and petal dimensions. The fifth variable, Species, is a factor with three levels: "setosa", "versicolor", and "virginica", indicating the species of the iris flower. This dataset is commonly used for statistical analysis and machine learning tasks.

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?

```r
mean_values <- colMeans(iris[, 1:4])
mean_values
```

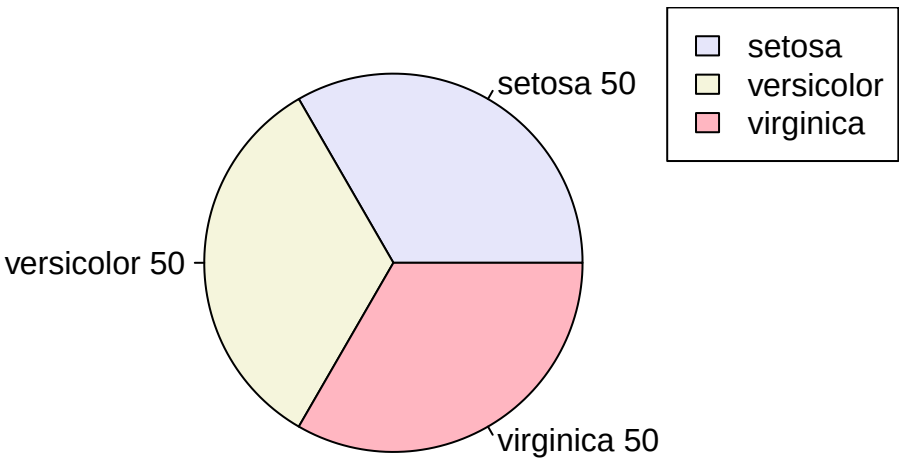
```
## Sepal.Length  Sepal.Width Petal.Length  Petal.Width
##     5.843333     3.057333     3.758000     1.199333
```

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

```r
species_counts <- table(iris$Species)

pie(species_counts,
    main = "Species Distribution in Iris Dataset",
    col = c("lavender", "beige", "lightpink"),
    labels = paste(names(species_counts), species_counts))

legend("topright", legend = names(species_counts), fill = c("lavender", "beige", "lightpink"))
```



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

```
setosa_subset <- iris[iris$Species == "setosa", ]
versicolor_subset <- iris[iris$Species == "versicolor", ]
virginica_subset <- iris[iris$Species == "virginica", ]

setosa_last_six <- tail(setosa_subset, 6)
versicolor_last_six <- tail(versicolor_subset, 6)
virginica_last_six <- tail(virginica_subset, 6)

print("Last six rows of Setosa:")
```

```
## [1] "Last six rows of Setosa:"
```

```
print(setosa_last_six)
```

```
##    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
```

```
print("Last six rows of Versicolor:")
```

```
## [1] "Last six rows of Versicolor:"
```

```
print(versicolor_last_six)
```

```
##     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
```

```
print("Last six rows of Virginica:")
```

```
## [1] "Last six rows of Virginica:"
```

```
print(virginica_last_six)
```

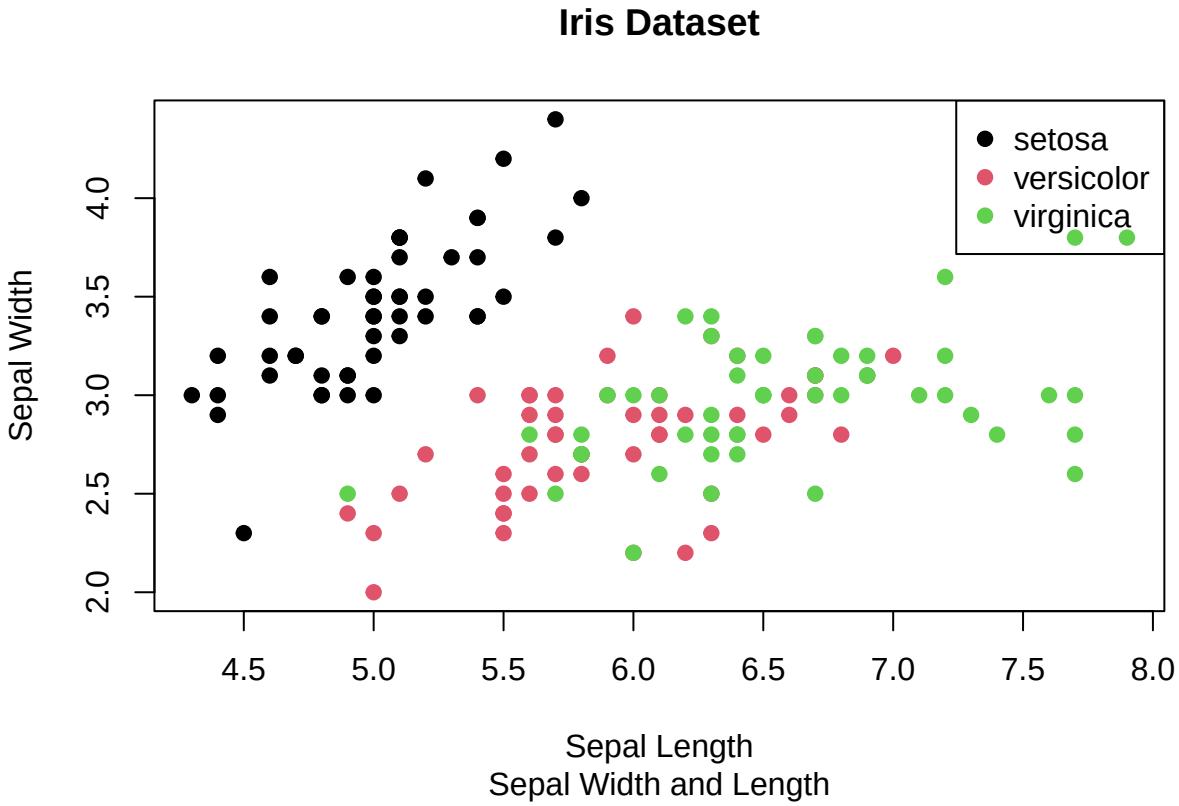
```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 145          6.7         3.3          5.7         2.5 virginica
## 146          6.7         3.0          5.2         2.3 virginica
## 147          6.3         2.5          5.0         1.9 virginica
## 148          6.5         3.0          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.

```
iris$Species <- as.factor(iris$Species)

plot(iris$Sepal.Length, iris$Sepal.Width,
     col = iris$Species,
     pch = 19,
     main = "Iris Dataset",
     sub = "Sepal Width and Length",
     xlab = "Sepal Length",
     ylab = "Sepal Width")

legend("topright", legend = levels(iris$Species), col = 1:3, pch = 19)
```



f. Interpret the result.

The resulting plot visually displays the relationship between sepal length and sepal width for the different species of iris. Each species will appear in distinct colors, allowing for easy visual differentiation. This can help in understanding how sepal dimensions vary among the species.You may observe clustering of points by species, indicating differences in sepal dimensions that could be useful for classification or further analysis. For instance, Setosa typically has smaller sepals compared to the other two species.

7. Import the alexa-file.xlsx. Check on the variations. Notice that there are ex- tra 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")
str(alexa_data)
```

```
## tibble [3,150 x 5] (S3: tbl_df/tbl/data.frame)
```

```
##  $ rating          : num [1:3150] 5 5 4 5 5 5 3 5 5 5 ...
##  $ date            : POSIXct[1:3150], format: "2018-07-31" "2018-07-31" ...
##  $ variation       : chr [1:3150] "Charcoal Fabric" "Charcoal Fabric" "Walnut Finish" "Charcoal Fabri
##  $ verified_reviews: chr [1:3150] "Love my Echo!" "Loved it!" "Sometimes while playing a game, you ca
##  $ feedback        : num [1:3150] 1 1 1 1 1 1 1 1 1 1 ...
```

a. Rename the white and black variants by using gsub() function.

```
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)
# Fix "White" variants
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)
alexa_data$variation[1052:2000]
```

```
##   [1] "White  Spot" "Black  Spot" "Black  Spot" "Black  Spot" "Black  Spot"
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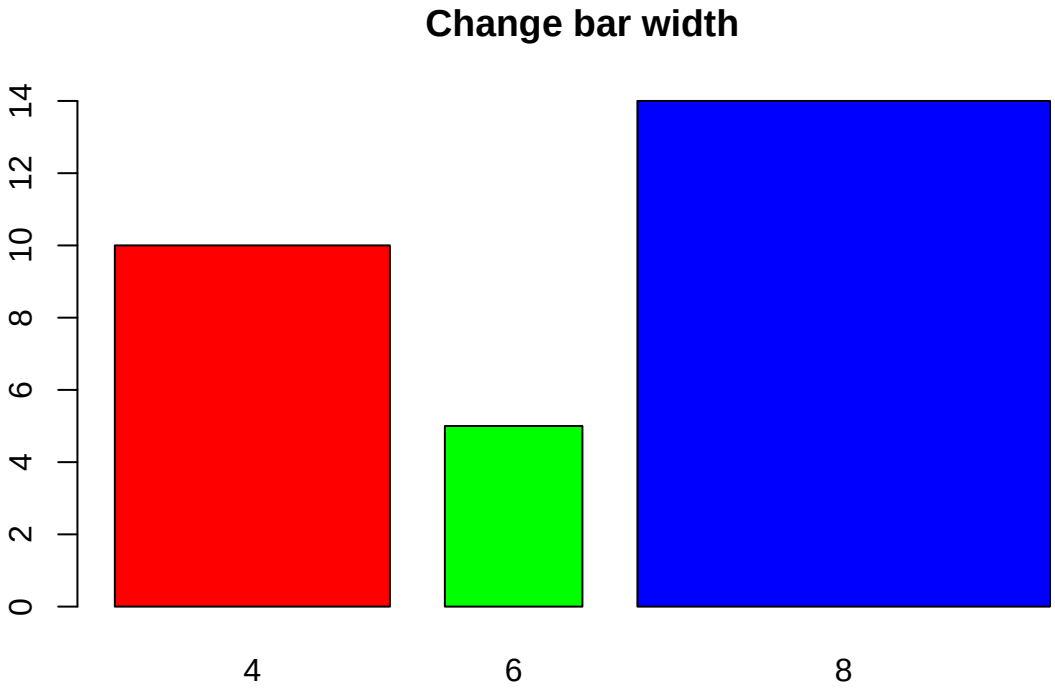
b. Get the total number of each variations and save it into another object. Save theobject as variations.RData. Write the R scripts. What is its result? Hint: Use the dplyr package. Make sure to install it before loading the package. Syntax for dplyr RObject %>% count(RObject$columnName)

```
library(knitr)
values <- c(10, 5, 14)
names <- c(4, 6, 8)
colors <- c("red", "green", "blue")
barplot(values, names.arg=names, col=colors, main="Change bar width", width=c(1, 0.5, 1.5))
```



c. From the variations.RData, create a barplot(). Complete the details of the chart which include the title, color, labels of each bar.

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

asdgjhfbjgfkhasdfghjkl