RWorksheet_Gagante#4b.Rmd

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Using Loop Function for() loop 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. Hint: Use abs() function to get the absolute value

```
vectorA <- c(1, 2, 3, 4, 5)
matrix_5x5 <- matrix( nrow = 5, ncol = 5)

for (i in 1:5) {
  for (j in 1:5) {
    matrix_5x5[i, j] <- abs(i - j)
  }
}

print(matrix_5x5)
```

```
##      [,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. The output should be the same as shown in Figure

```
for (i in 1:5) {
  line <- rep('"*"', i)
  cat(line, sep = " ")
  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: "))

#a <- start
#b <- 1
#cat(a, b, sep = " ")
```

```
#repeat {
 # next_term <- a + b
 # if (!is.na(next_term) && next_term > 500) {
 #   break
#  }
#  cat(next_term, " ")
 # a <- b
#  b <- next_term
  #}
#cat("\n")
```

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_sizes.csv")

head(data)
```

```
##   Show.Size 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.

```
male_data <- subset(data, Gender == "M")
female_data <- subset(data, Gender == "F")

num_males <- nrow(male_data)
num_females <- nrow(female_data)

num_males
```

```
## [1] 14
```

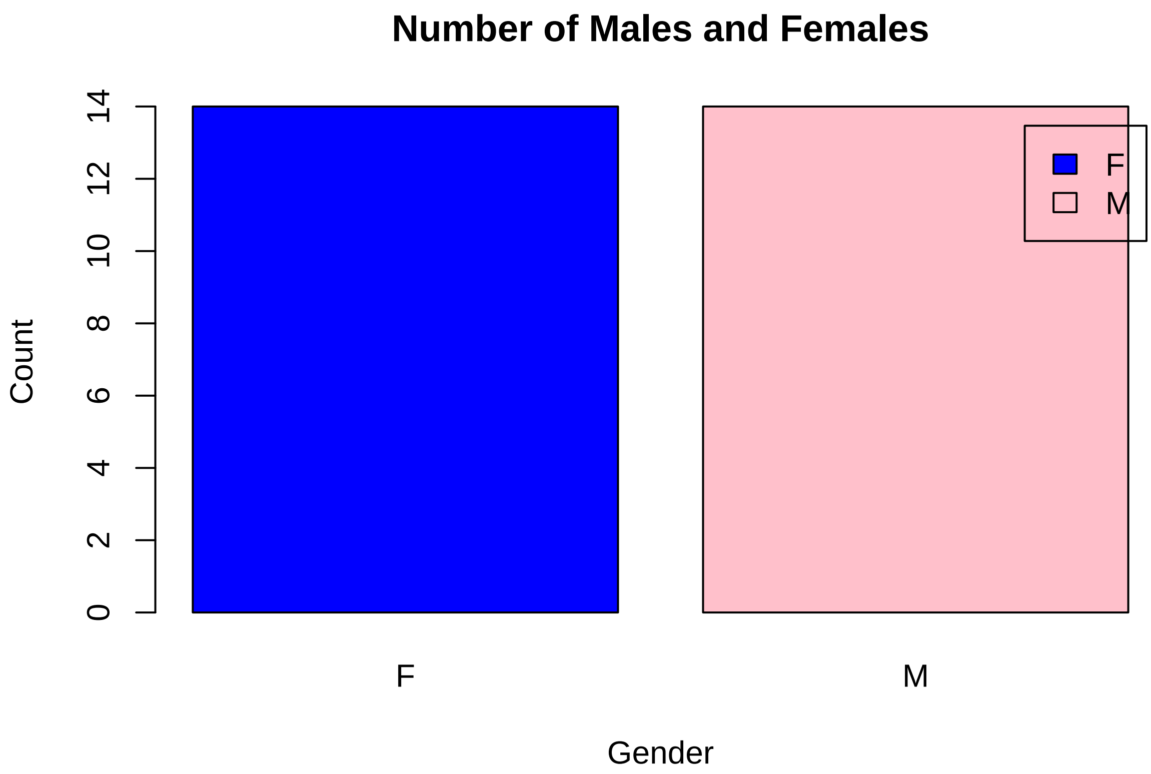
```
num_females
```

```
## [1] 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.

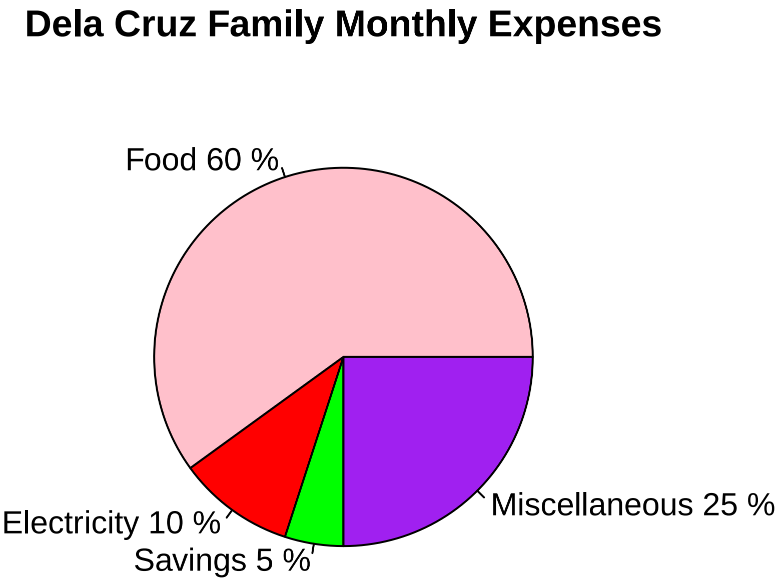
```
gender_counts <- table(data$Gender)

barplot(gender_counts,
        main = "Number of Males and Females",
        xlab = "Gender",
        ylab = "Count",
        col = c("blue", "pink"),
        legend = rownames(gender_counts))
```



5. The monthly income of Dela Cruz family was spent on the following: Food Electricity Savings Miscellaneous 60 10 5 25 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)
percentages <- round(expenses / sum(expenses) * 100)
labels <- paste(names(expenses), percentages, "%")
colors <- c("pink", "red", "green", "purple")
pie(expenses,
    labels = labels,
    col = colors,
    main = "Dela Cruz Family Monthly Expenses")
```



6. Use the iris dataset. data(iris) a.

Check for the structure of the dataset using the str() function. Describe what you have seen in the output.

```r
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 ...
```

#It will show that iris is a data frame with 150 observations and 5 variables: Sepal.Length: Numeric, lengths of sepals (in cm). Sepal.Width: Numeric, widths of sepals (in cm). Petal.Length: Numeric, lengths of petals (in cm). Petal.Width: Numeric, widths of petals (in cm). Species: Factor with 3 levels - setosa, versicolor, virginica. This gives us an idea of what data types are present in each column and how many levels the Species factor has.

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
means <- colMeans(subset(iris, select = -Species))
means
```

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

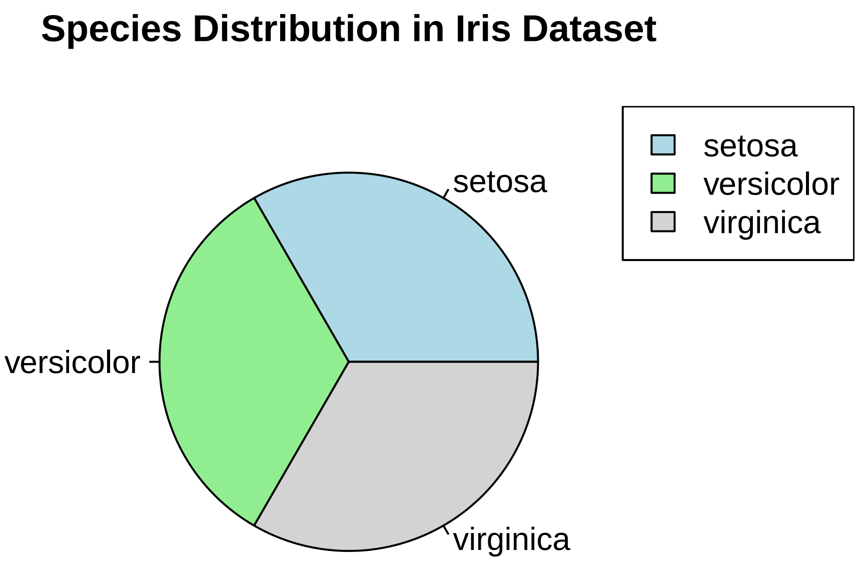
c. Create a pie chart for the Species distribution. Add title, legends, and colors. Write the R script and its result.

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

colors <- c("lightblue", "lightgreen", "lightgray")

pie(species_counts,
    main = "Species Distribution in Iris Dataset",
    col = colors,
    labels = names(species_counts))


legend("topright", legend = names(species_counts), fill = colors)
```



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
```

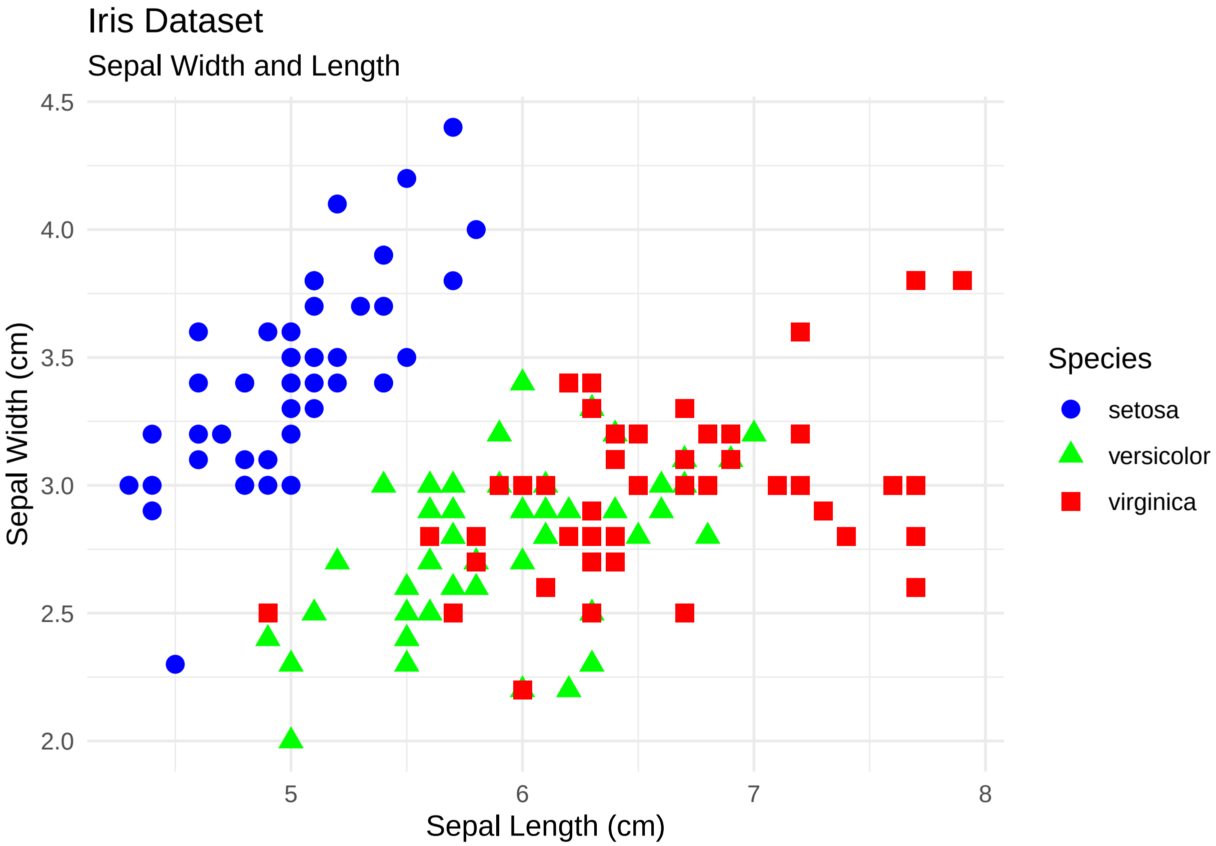
```
tail(virginica)
```

```
##     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. Hint: Need to convert to factors the species to store categorical variables.

```
library(ggplot2)

ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width, color = Species, shape = Species)) +
  geom_point(size = 3) +
  labs(
    title = "Iris Dataset",
    subtitle = "Sepal Width and Length",
    x = "Sepal Length (cm)",
    y = "Sepal Width (cm)"
  ) +
  theme_minimal() +
  scale_color_manual(values = c("setosa" = "blue", "versicolor" = "green", "virginica" = "red"))
```



f. Interpret the result. #The scatter plot of Sepal.Length vs. Sepal.Width shows the relationship between these two measurements for each species:

#Setosa: Typically has smaller sepal lengths and widths, clustering separately from the other two species. #Versicolor and Virginica: Overlap more in their sepal dimensions, but Virginica generally has the largest sepal dimensions. #Overall Pattern: The species are distinguishable based on sepal size, with Setosa forming a distinct cluster. Versicolor and Virginica have some overlap, but Virginica tends to have larger sepal lengths and widths on average. This plot illustrates how sepal dimensions vary by species and how these features can help differentiate the species.