RWorksheet_Capaque#4b

shane capaque

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#1. Using the for loop, create an R script that will display a 5x5 matrix.

```
vectorA <- c(1, 2, 3, 4, 5)

matrixA <- matrix(c(0, 0, 0, 0, 0), nrow = 5, ncol = 5)

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

print(matrixA)
```

```
##      [,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.

for(i in 1:5) {
  numeric<- rep("*", i)
  print(numeric)
}
```

```
## [1] "*"
## [1] "*" "*"
## [1] "*" "*" "*"
## [1] "*" "*" "*" "*"
## [1] "*" "*" "*" "*" "*"
```

```
#3. Fibonacci

start_num <- as.numeric(readline("Enter the starting number for the Fibonacci sequence: "))
```

```
## Enter the starting number for the Fibonacci sequence:
```

```
if (is.na(start_num)) {
  cat("Please enter a valid numeric starting number.\n")
} else {
  num1 <- 0
  num2 <- 1

  repeat {
```

```
    if (!is.na(start_num) && num2 >= start_num) {
      cat(num2, " ")
    }

    fib_sum <- num1 + num2
    num1 <- num2
    num2 <- fib_sum

    if (num2 > 500) {
      break
    }
  }

  cat("\n")
}
```

```
## Please enter a valid numeric starting number.
```

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

```
library(readr)
Household <- read_csv("Worksheet#4/Household.csv")
```

```
## New names:
## Rows: 28 Columns: 4
## -- Column specification
## -------------------------------------------------------- Delimiter: "," chr
## (1): Gender dbl (3): ...1, ShoeSize, Height
## i Use `spec()` to retrieve the full column specification for this data. i
## Specify the column types or set `show_col_types = FALSE` to quiet this message.
## * `` -> `...1`
```

```
head(Household)
```

```
## # A tibble: 6 x 4
##    ...1 ShoeSize Height Gender
##   <dbl>    <dbl>  <dbl> <chr>
## 1     1      6.5   66   F
## 2     2      9     68   F
## 3     3      8.5   64.5 F
## 4     4      8.5   65   F
## 5     5     10.5   70   M
## 6     6      7     64   F
```

```
#4. 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.

library(readr)
Household <- read_csv("Worksheet#4/Household.csv")
```

```
## New names:
## Rows: 28 Columns: 4
## -- Column specification
## -------------------------------------------------------- Delimiter: "," chr
## (1): Gender dbl (3): ...1, ShoeSize, Height
## i Use `spec()` to retrieve the full column specification for this data. i
```

```
## Specify the column types or set `show_col_types = FALSE` to quiet this message.
## * `` -> `...1`
```

```
head(Household)
```

```
## # A tibble: 6 x 4
##    ...1 ShoeSize Height Gender
##   <dbl>    <dbl>  <dbl> <chr>
## 1     1      6.5   66   F
## 2     2      9     68   F
## 3     3      8.5   64.5 F
## 4     4      8.5   65   F
## 5     5     10.5   70   M
## 6     6      7     64   F
```

```
# Filter the data based on Gender
males <- Household[Household$Gender == "M",]
females <- Household[Household$Gender == "F",]

# Display the results
males
```

```
## # A tibble: 14 x 4
##     ...1 ShoeSize Height Gender
##    <dbl>    <dbl>  <dbl> <chr>
##  1     5     10.5   70   M
##  2     9     13     72   M
##  3    11     10.5   74.5 M
##  4    13     12     71   M
##  5    14     10.5   71   M
##  6    15     13     77   M
##  7    16     11.5   72   M
##  8    19     10     72   M
##  9    22      8.5   67   M
## 10    23     10.5   73   M
## 11    25     10.5   72   M
## 12    26     11     70   M
## 13    27      9     69   M
## 14    28     13     70   M
```

```
females
```

```
## # A tibble: 14 x 4
##     ...1 ShoeSize Height Gender
##    <dbl>    <dbl>  <dbl> <chr>
##  1     1      6.5   66   F
##  2     2      9     68   F
##  3     3      8.5   64.5 F
##  4     4      8.5   65   F
##  5     6      7     64   F
##  6     7      9.5   70   F
##  7     8      9     71   F
##  8    10      7.5   64   F
##  9    12      8.5   67   F
## 10    17      8.5   59   F
## 11    18      5     62   F
## 12    20      6.5   66   F
```

```
## 13    21      7.5   64   F
## 14    24      8.5   69   F
```

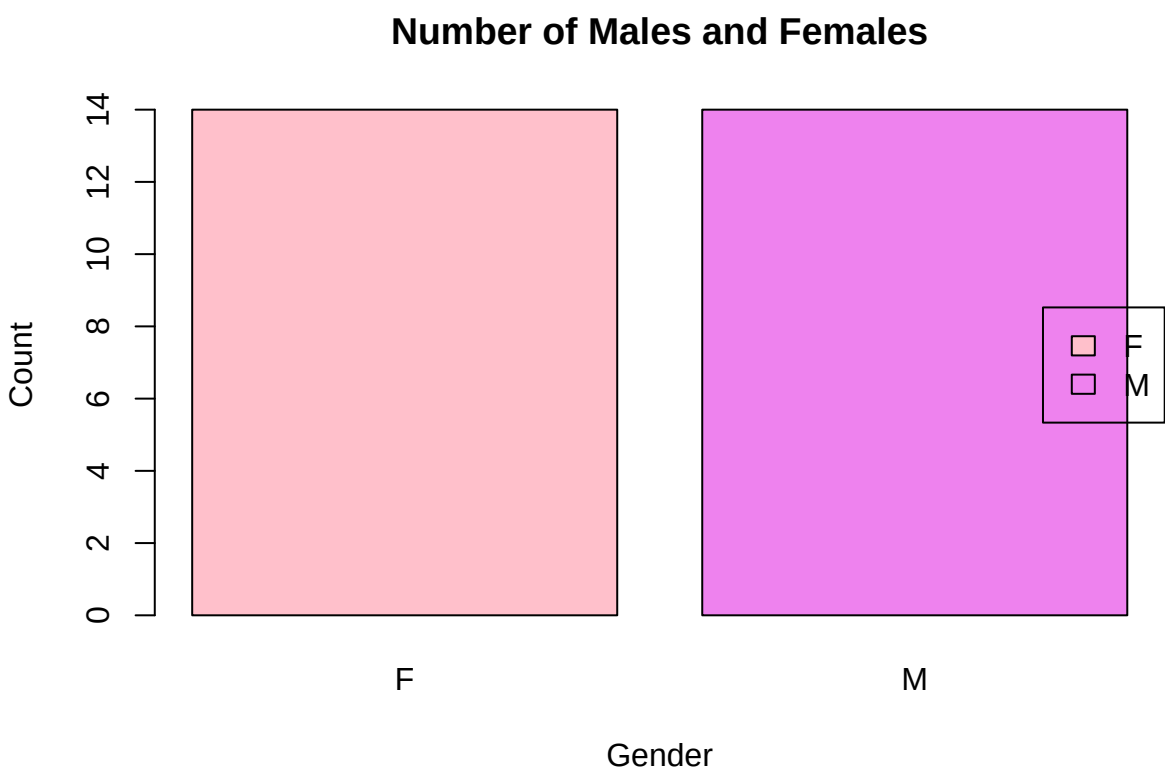
```
# Calculate the number of observations for each gender
observationF <- nrow(females)
observationM <- nrow(males)

# Display the number of observations
cat("Number of Female Observations:", observationF, "\n")
```

```
## Number of Female Observations: 14
```

```
cat("Number of Male Observations:", observationM, "\n")
```

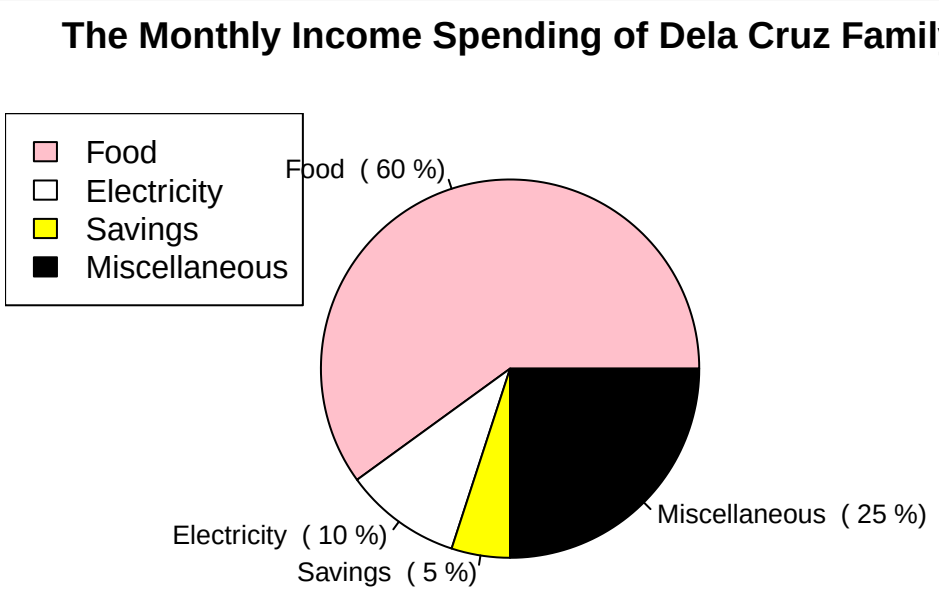
```
## Number of Male Observations: 14
```

```
#4. 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.

total <- table(Household$Gender)
barplot(total,
main = "Number of Males and Females",
xlab = "Gender", ylab = "Count", col = c("pink", "violet"))
legend("right", legend = rownames(total), fill = c("pink", "violet"))
```




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

#5. 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.
```

```r
spend <- data.frame(
  Category = c("Food", "Electricity", "Savings", "Miscellaneous"),
  Value = c(60, 10, 5, 25)
)

spend$Percentage <- spend$Value / sum(spend$Value) * 100
colors <- c("pink", "white", "yellow", "black")

# Adjust the font size with the cex parameter
pie(spend$Value,
    labels = paste(spend$Category, " (", spend$Percentage, "%)"),
    col = colors,
    main = "The Monthly Income Spending of Dela Cruz Family",cex = 0.8)

legend("topleft", spend$Category, fill = colors)
```




```r
#6. Use the iris dataset.

#6 A. Check for the structure of the dataset using the str() function.
#Describe what youhave seen in the output.

str(iris)
```

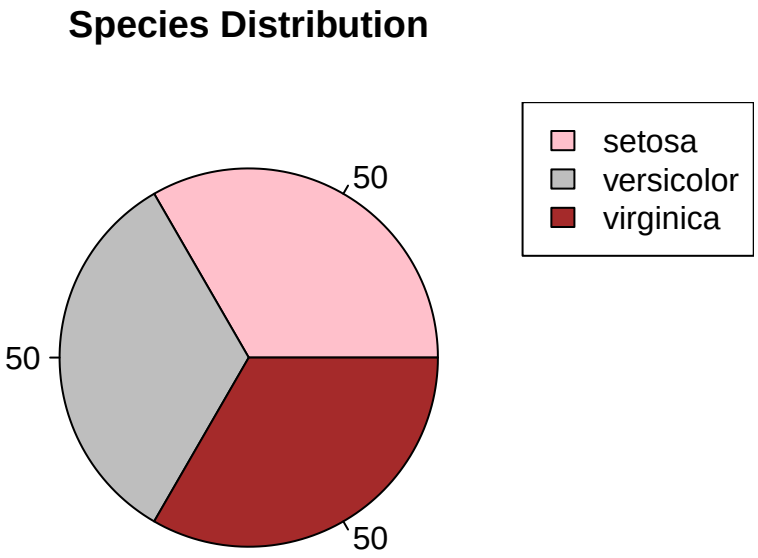
```
## 'data.frame':    150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3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

```r
#1. The dataset comprises 150 observations and 5 variables.
#2. 'Sepal.Length' represents the sepal length of iris flowers.
#3. 'Sepal.Width' represents the sepal width of iris flowers.
#4. 'Petal.Length' signifies the petal length of iris flowers.
#5. 'Petal.Width' signifies the petal width of iris flowers.
#6. 'Species' This is the categorized variables.
```

```r
#6 B. Create an R object that will contain the mean of the sepal.length,sepal.width,petal.length,and pe
#What is the R script and its result?

value_of_means <- c(
  Lsepal <- mean(iris$Sepal.Length),
  Wsepal <- mean(iris$Sepal.Width) ,
  Lpetal <- mean(iris$Petal.Length),
  Wpetal <- mean(iris$Petal.Width)
)
value_of_means
```

```
## [1] 5.843333 3.057333 3.758000 1.199333
```

```r
#6 C.Create a pie chart for the Species distribution.
#Add title, legends, and colors. Write the R script and its result.

# Assuming that I have a flower called the 'iris' and it  is the name of my dataset
species <- table(iris$Species)
colors <- c("pink", "gray", "brown")

# Create the pie chart
pie(species, col = colors, labels = species )
legend("topright", legend = levels(iris$Species), fill = colors)
title("Species Distribution")
```




```r
#6 D. Subset the species into setosa, versicolor, and virginica.
#Write the R scripts and show the last six (6) rows of each species.


#subset

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

#last 6 row each
```

```r
tail(setosa_subset, 6)
```

```
##    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
```

```r
tail(versicolor_subset, 6)
```

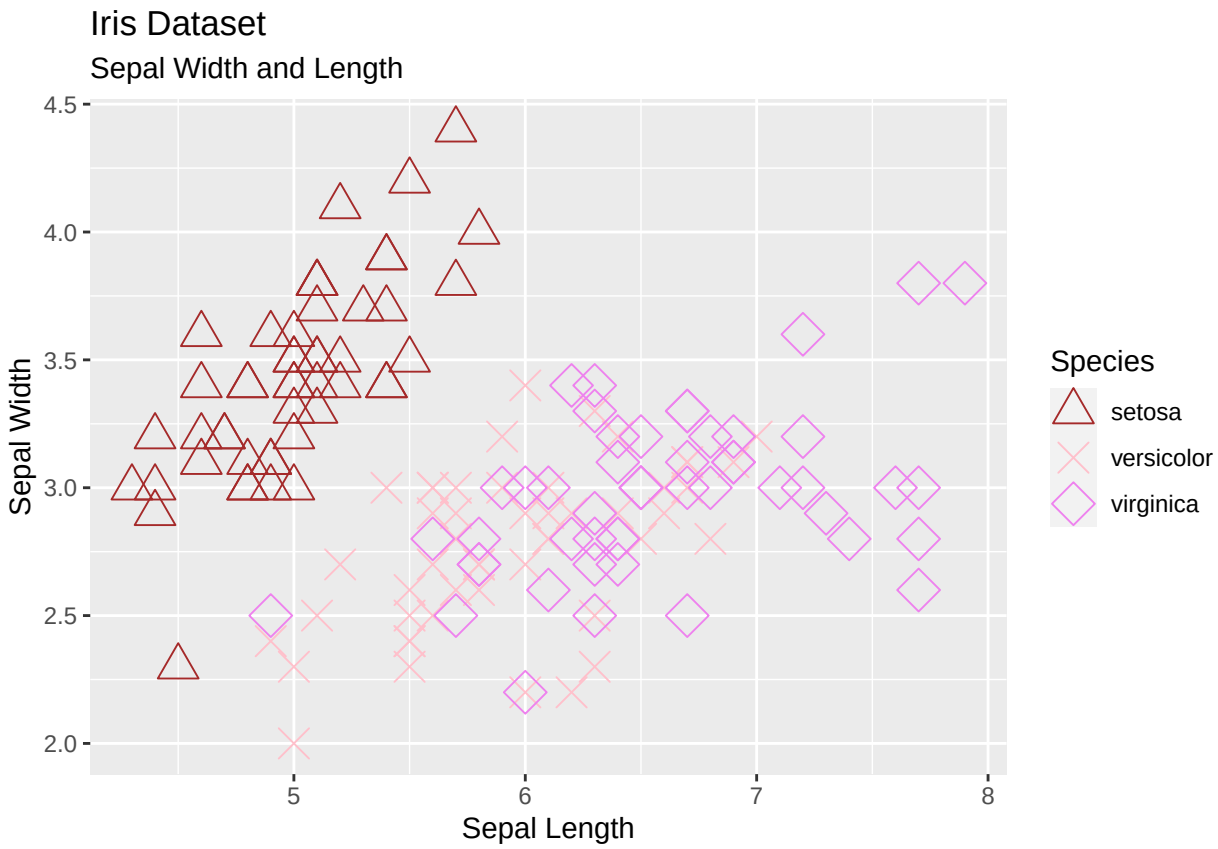
```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
## 95           5.6         2.7          4.2         1.3 versicolor
## 96           5.7         3.0          4.2         1.2 versicolor
## 97           5.7         2.9          4.2         1.3 versicolor
## 98           6.2         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
```

```r
tail(virginica_subset, 6)
```

```
##     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
```

```r
#6 E.
#Create a scatterplot of the sepal.length and sepal.width using the differentspecies(setosa,versicolor,
#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)

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

# Create a scatterplot
scatterplot <- ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, color = Species, shape = Species)) +
  geom_point(size = 5) +
  labs(
    title = "Iris Dataset",
    subtitle = "Sepal Width and Length",
    x = "Sepal Length",
    y = "Sepal Width"
  ) +
  scale_color_manual(values = c("setosa" = "brown", "versicolor" = "pink", "virginica" = "violet")) +
  scale_shape_manual(values = c("setosa" = 2, "versicolor" = 4, "virginica" = 5))
```

```
print(scatterplot)
```




```
#6 F. Interpret the result.

#The plot shows a visual representation
#of the Sepal Length and Sepal Width for
#each Iris flower species. Each species is
#represented by a different color and shape.

#Setosa flowers are brown and have a cross-like shape.
#Versicolor flowers are pink and have a circle shape.
#Virginica flowers are violet and have a diamond shape.

#This plot allows you to easily compare and differentiate between
#different species based on their sepal
#length and sepal width, offering a comprehensive
#and visually appealing representation of the data.
```