

RWorksheet_guion#4b

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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)
matri <- matrix(0, nrow = 5, ncol = 5)
  for(i in 1:5) {
    for(j in 1:5) {
      matri[i,j] <- abs(vectorA[i] - vectorA[j])
    }
    print(matri[i,j])
  }
```

```
## [1] 4
## [1] 3
## [1] 2
## [1] 1
## [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.

4.

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

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.

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.

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.

6.

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

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?

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

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

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.

f. Interpret the result.

7.