RWorksheet_calvario#4b.Rmd

Jolien

2024-10-30

1. Using the for loop, create an R script that will display a 5x5 matrix as shown in Figure 1. It must contain vector A = [1,2,3,4,5] and a 5×5 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</pre>
```

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

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

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

- 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")</pre>
head(data)
##
   Shoe.Size Height Gender
## 1 6.5 66.0
## 2
         9.0 68.0
                        F
## 3
         8.5 64.5
                        F
## 4
         8.5 65.0
                        F
## 5
        10.5 70.0
                        М
## 6
         7.0 64.0
```

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 == "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")

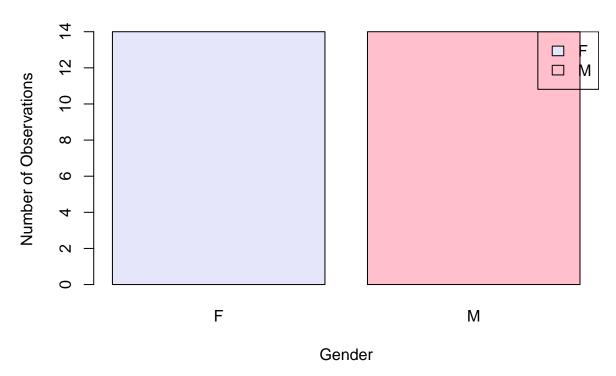
## Number of Male observations: 0

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

## Number of Female observations: 0</pre>
```

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.

Number of Males and Females in Household Data



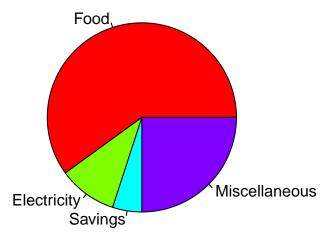
5. The monthly income of Dela Cruz family was spent on the following:

a.

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

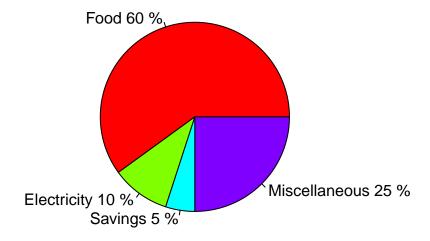
pie(expenses,
    labels = labels,
    main = "Monthly Income Distribution of Dela Cruz Family",
    col = rainbow(length(expenses)))</pre>
```

Monthly Income Distribution of Dela Cruz Family



```
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)))</pre>
```

Monthly Income Distribution of Dela Cruz Family



6. Use the iris dataset.

a.

```
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 1 ...
```

b.

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

## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 5.843333 3.057333 3.758000 1.199333</pre>
```

c.

```
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"))</pre>
```

Species Distribution in Iris Dataset

