RWorksheet#4b_Parrenas

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2023-11-08

```r
#Using Loop Function
#1. Using the for loop, create an R script that will display a 5x5 matrix as shown in Figure 1. It must
  vectorA <- c(1, 2, 3, 4, 5)
  zeroMatrix <- matrix(0, nrow = 5, ncol = 5)


  for (i in 1:5){
  for (j in 1:5){

    diff <- abs(vectorA[i] - j)

    cat(diff, " ")
  }
  cat("\n")
  }
```

```
## 0  1  2  3  4
## 1  0  1  2  3
## 2  1  0  1  2
## 3  2  1  0  1
## 4  3  2  1  0
```

```r
#2. Print the string "*" using for() function. The output should be the same as shown in Figure

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

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

```r
#3. Get an input from the user to print the Fibonacci sequence starting from the 1st input up to 500. U

user_input <- as.numeric(readline("Enter a number to start the Fibonacci sequence: "))
```

```
## Enter a number to start the Fibonacci sequence:
```

```r
a <- 0
b <- 1

cat("Fibonacci sequence starting from", user_input, ": ")
```

```
## Fibonacci sequence starting from NA :
```

```
cat(user_input, " ")
```

```
## NA
```

```
repeat {

  fiboSeq <- a + b


  if (fiboSeq > 500) {
    break
  }


  cat(fiboSeq, " ")


  a <- b
  b <- fiboSeq
}
```

```
## 1  2  3  5  8  13  21  34  55  89  144  233  377
```

```
#4a. Import the data set as shown in Figure 1 you have created previously.

library(readr)
shoeSizes <- read_csv("shoeSizes.csv")
```

```
## Rows: 28 Columns: 3
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (1): gender
## dbl (2): shoe_Size, 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.
```

```
View(shoeSizes)
```

```
## Warning in View(shoeSizes): unable to open display
```

```
## Error in .External2(C_dataviewer, x, title): unable to start data viewer
```

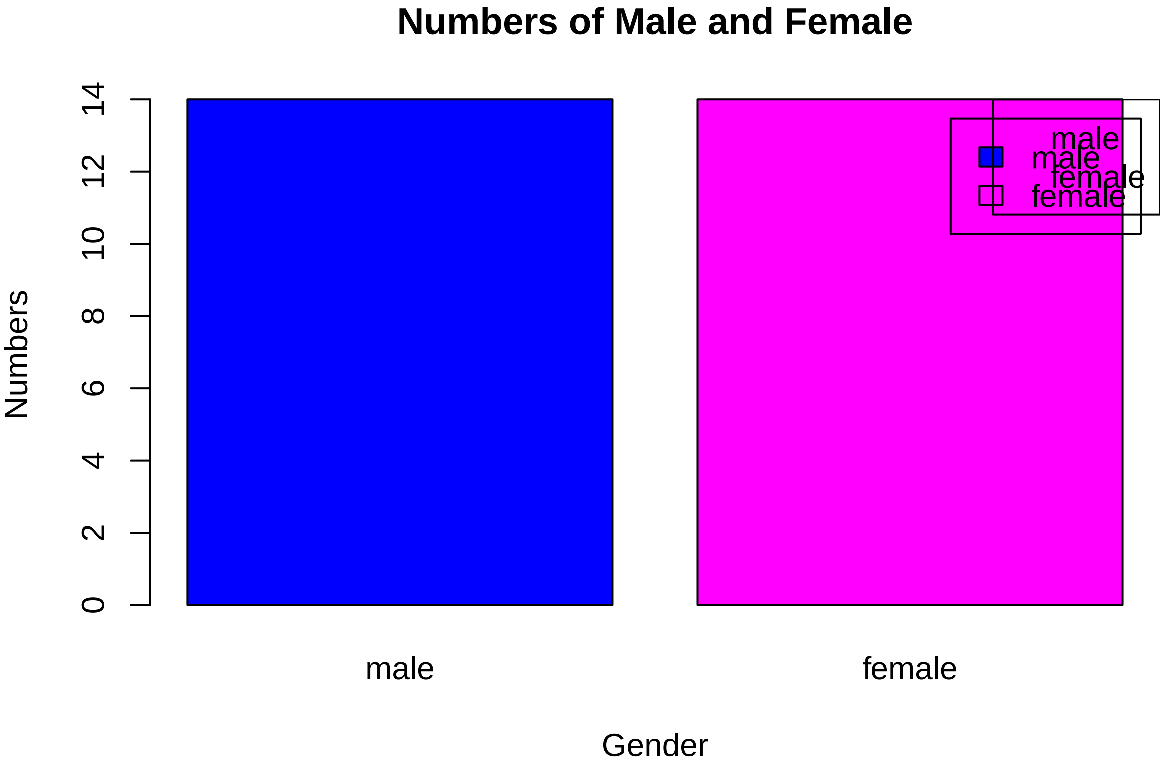
```
#b. Create a subset for gender(female and male). How many observations are there in Male? How about in 

 male <- shoeSizes[shoeSizes$gender == "M",]
    female <- shoeSizes[shoeSizes$gender == "F",]

    maleCount <- nrow(male)
    femaleCount <- nrow(female)

    cat("Numbers of male: ", maleCount, "\n")
```

```
## Numbers of male:  14
```

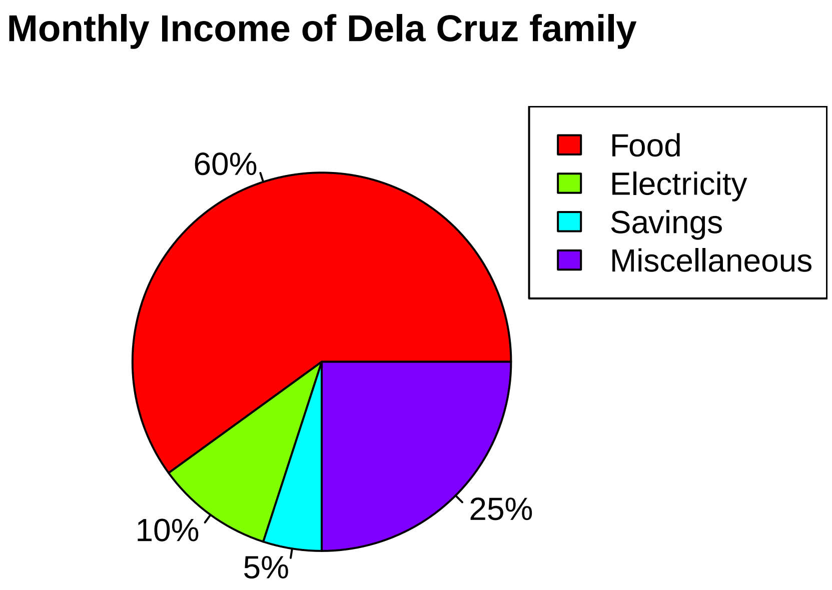
```
    cat("Numbers of female: ", femaleCount, "\n")
```

```
## Numbers of female:  14
```

```
#c. Create a graph for the number of males and females for Household Data. Use plot(),chart type = barp
genderCount <- c(male = maleCount, female = femaleCount)

      barplot(genderCount, main = "Numbers of Male and Female",
              xlab = "Gender", ylab = "Numbers", col = c("blue", "magenta"),
              legend.text = TRUE, width = c(0.2, 0.2))
      legend("topright", legend = names(genderCount), col =  c("blue", "magenta"))
```



```
#5. The monthly income of Dela Cruz family was spent
mypie <- c(60, 10, 5, 25)


pie(mypie,
    main = "Monthly Income of Dela Cruz family",
    col = rainbow(length(mypie)),
    labels = c("60%", "10%", "5%","25%"),

)
legend("topright", legend = c("Food", "Electricity", "Savings", "Miscellaneous"), fill = rainbow(length
```



```
#6.Use the iris data set

#a. Check for the structure of the data set using the str() function. Describe what you have seen in th

    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 ...
```

```
#The output shows the data's structure, which includes the variables and objects as well as the length,
```

```
#b. Create an R object that will contain the mean of the sepal.length,sepal.width,petal.length,and peta

  sepaleng <- mean(iris$Sepal.Length)

  sepalwid <- mean(iris$Sepal.Width)

  petlen <- mean(iris$Petal.Length)

  petwin <- mean(iris$Petal.Width)


  print(sepaleng)
```

```
## [1] 5.843333
```

```
  print(sepalwid)
```

```
## [1] 3.057333
```

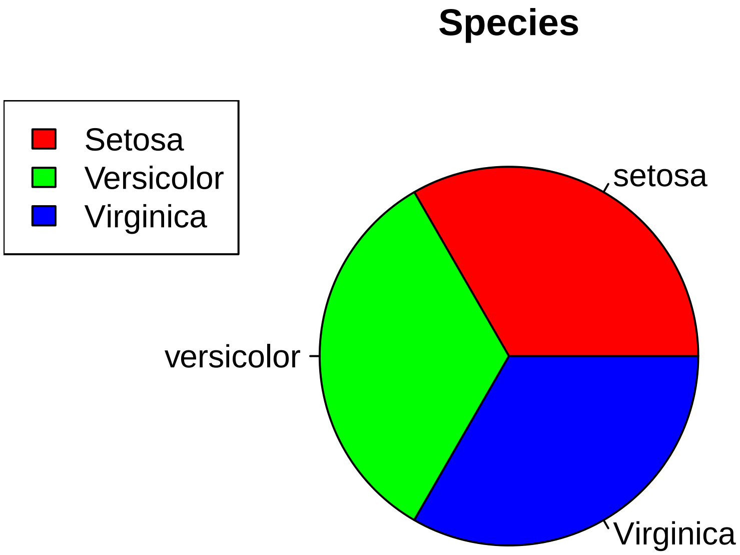
```
  print(petlen)
```

```
## [1] 3.758
```

```
    print(petwin)
```

```
## [1] 1.199333
```

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

      specCount <- table(iris$Species)

      pie(specCount,
          main = "Species",
          col = rainbow(length(specCount)),
          labels = c("setosa", "versicolor", "Virginica")
          )
      legend("topleft", legend = c("Setosa", "Versicolor", "Virginica"), fill = rainbow(length(specCoun
```



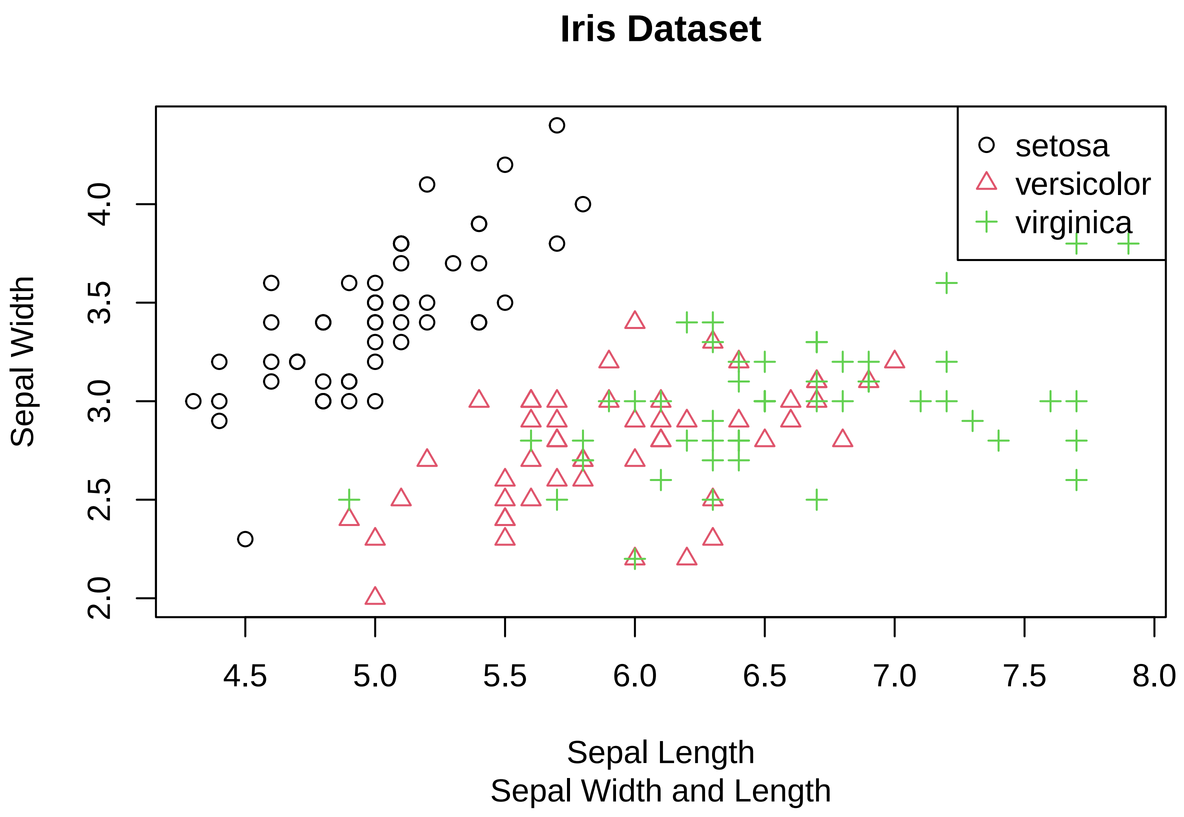
```
#d. Subset the species into setosa, versicolor, and virginica. Write the R scripts and show the last si

      setsub <- iris[iris$Species == "setosa" | iris$Species == "Versicolor" | iris$Species == "virgini
      setsub
```

```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 1            5.1         3.5          1.4         0.2    setosa
## 2            4.9         3.0          1.4         0.2    setosa
## 3            4.7         3.2          1.3         0.2    setosa
## 4            4.6         3.1          1.5         0.2    setosa
## 5            5.0         3.6          1.4         0.2    setosa
## 6            5.4         3.9          1.7         0.4    setosa
## 7            4.6         3.4          1.4         0.3    setosa
## 8            5.0         3.4          1.5         0.2    setosa
## 9            4.4         2.9          1.4         0.2    setosa
## 10           4.9         3.1          1.5         0.1    setosa
## 11           5.4         3.7          1.5         0.2    setosa
## 12           4.8         3.4          1.6         0.2    setosa
## 13           4.8         3.0          1.4         0.1    setosa
## 14           4.3         3.0          1.1         0.1    setosa
## 15           5.8         4.0          1.2         0.2    setosa
## 16           5.7         4.4          1.5         0.4    setosa
## 17           5.4         3.9          1.3         0.4    setosa
## 18           5.1         3.5          1.4         0.3    setosa
## 19           5.7         3.8          1.7         0.3    setosa
## 20           5.1         3.8          1.5         0.3    setosa
## 21           5.4         3.4          1.7         0.2    setosa
## 22           5.1         3.7          1.5         0.4    setosa
## 23           4.6         3.6          1.0         0.2    setosa
## 24           5.1         3.3          1.7         0.5    setosa
## 25           4.8         3.4          1.9         0.2    setosa
## 26           5.0         3.0          1.6         0.2    setosa
## 27           5.0         3.4          1.6         0.4    setosa
## 28           5.2         3.5          1.5         0.2    setosa
## 29           5.2         3.4          1.4         0.2    setosa
## 30           4.7         3.2          1.6         0.2    setosa
## 31           4.8         3.1          1.6         0.2    setosa
## 32           5.4         3.4          1.5         0.4    setosa
## 33           5.2         4.1          1.5         0.1    setosa
## 34           5.5         4.2          1.4         0.2    setosa
## 35           4.9         3.1          1.5         0.2    setosa
## 36           5.0         3.2          1.2         0.2    setosa
## 37           5.5         3.5          1.3         0.2    setosa
## 38           4.9         3.6          1.4         0.1    setosa
## 39           4.4         3.0          1.3         0.2    setosa
## 40           5.1         3.4          1.5         0.2    setosa
## 41           5.0         3.5          1.3         0.3    setosa
## 42           4.5         2.3          1.3         0.3    setosa
## 43           4.4         3.2          1.3         0.2    setosa
## 44           5.0         3.5          1.6         0.6    setosa
## 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
## 101          6.3         3.3          6.0         2.5 virginica
## 102          5.8         2.7          5.1         1.9 virginica
## 103          7.1         3.0          5.9         2.1 virginica
## 104          6.3         2.9          5.6         1.8 virginica
## 105          6.5         3.0          5.8         2.2 virginica
## 106          7.6         3.0          6.6         2.1 virginica
## 107          4.9         2.5          4.5         1.7 virginica
## 108          7.3         2.9          6.3         1.8 virginica
## 109          6.7         2.5          5.8         1.8 virginica
## 110          7.2         3.6          6.1         2.5 virginica
## 111          6.5         3.2          5.1         2.0 virginica
## 112          6.4         2.7          5.3         1.9 virginica
## 113          6.8         3.0          5.5         2.1 virginica
## 114          5.7         2.5          5.0         2.0 virginica
## 115          5.8         2.8          5.1         2.4 virginica
## 116          6.4         3.2          5.3         2.3 virginica
## 117          6.5         3.0          5.5         1.8 virginica
## 118          7.7         3.8          6.7         2.2 virginica
## 119          7.7         2.6          6.9         2.3 virginica
## 120          6.0         2.2          5.0         1.5 virginica
## 121          6.9         3.2          5.7         2.3 virginica
## 122          5.6         2.8          4.9         2.0 virginica
## 123          7.7         2.8          6.7         2.0 virginica
## 124          6.3         2.7          4.9         1.8 virginica
## 125          6.7         3.3          5.7         2.1 virginica
## 126          7.2         3.2          6.0         1.8 virginica
## 127          6.2         2.8          4.8         1.8 virginica
## 128          6.1         3.0          4.9         1.8 virginica
## 129          6.4         2.8          5.6         2.1 virginica
## 130          7.2         3.0          5.8         1.6 virginica
## 131          7.4         2.8          6.1         1.9 virginica
## 132          7.9         3.8          6.4         2.0 virginica
## 133          6.4         2.8          5.6         2.2 virginica
## 134          6.3         2.8          5.1         1.5 virginica
## 135          6.1         2.6          5.6         1.4 virginica
## 136          7.7         3.0          6.1         2.3 virginica
## 137          6.3         3.4          5.6         2.4 virginica
## 138          6.4         3.1          5.5         1.8 virginica
## 139          6.0         3.0          4.8         1.8 virginica
## 140          6.9         3.1          5.4         2.1 virginica
## 141          6.7         3.1          5.6         2.4 virginica
## 142          6.9         3.1          5.1         2.3 virginica
## 143          5.8         2.7          5.1         1.9 virginica
## 144          6.8         3.2          5.9         2.3 virginica
## 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
```

```
      tail(setsub, 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
```

```
#e. Create a scatterplot of the sepal.length and sepal.width using the different species(setosa,versico

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

legend("topright", legend = levels(iris$Species), col = unique(as.numeric(iris$Species)), pch = unique(
```



```
#6f. The scatterplot displays the relationship between the sepal length and width.
```

```
#Basic Cleaning and Transformation of Objects
#7. Import the alexa-file.xlsx. Check on the variations. Notice that there are extra whitespaces among

library(readxl)
alexa_file <- read_excel("alexa_file.xlsx")
```

```
## Error: `path` does not exist: 'alexa_file.xlsx'
```

```
View(alexa_file)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
  library(readxl)
alexa_file$variation <- gsub("Black  Dot", "BlackDot", alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
alexa_file$variation <- gsub("Black  Plus", "BlackPlus", alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
  alexa_file$variation <- gsub("Black  Show", "BlackShow", alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
  alexa_file$variation <- gsub("Black  Spot", "BlackSpot", alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
alexa_file$variation <- gsub("White  Dot", "WhiteDot", alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
alexa_file$variation <- gsub("White  Plus", "WhitePlus",alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
alexa_file$variation <- gsub("White  Show", "WhiteShow", alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
alexa_file$variation <- gsub("White  Spot", "WhiteSpot", alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
alexa_file
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
#b. Get the total number of each variations and save it into another object. Save the object as variati

library("dplyr")
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
vari <- alexa_file
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
  count(alexa_file$variation)
```

```
## Error in eval(expr, envir, enclos): object 'alexa_file' not found
```

```
vari
```

```
## Error in eval(expr, envir, enclos): object 'vari' not found
```

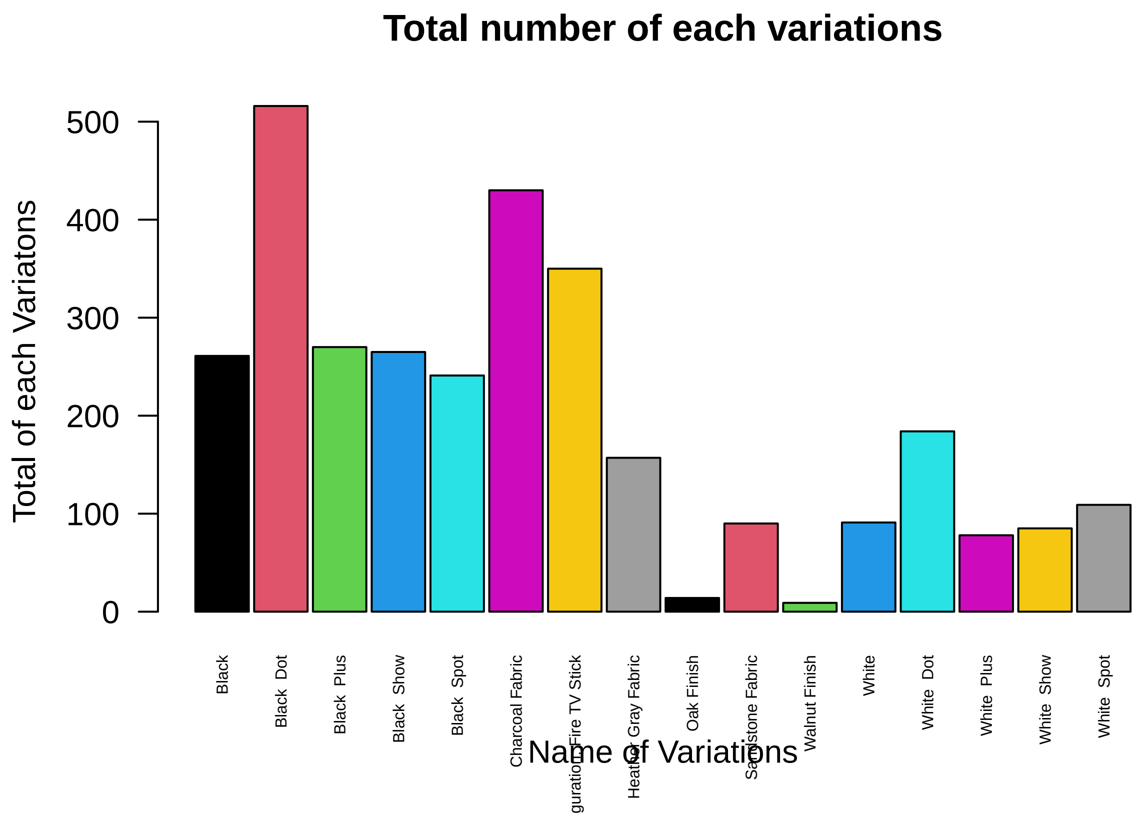
```
save(vari, file = "variations.RData")
```

```
## Error in save(vari, file = "variations.RData"): object 'vari' not found
```

```
#c. From the variations.RData, create a barplot(). Complete the details of the chart which include the
    load("variations.RData")
  vari
```

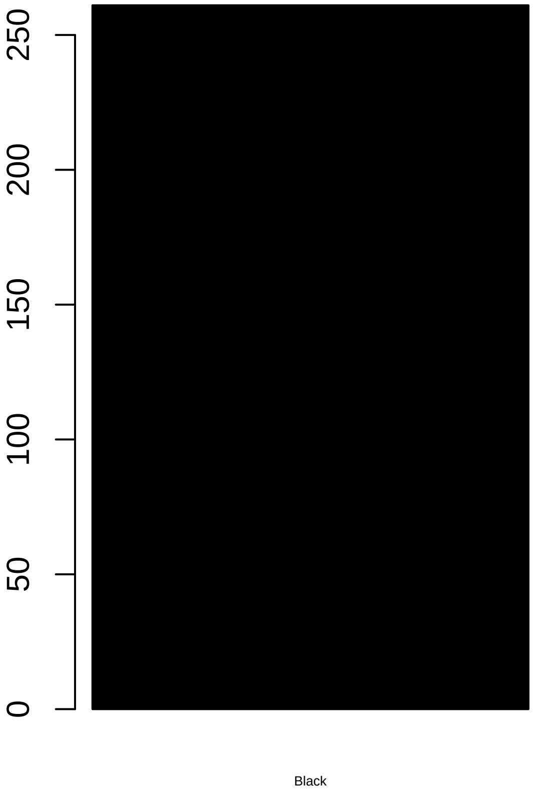
```
## # A tibble: 16 x 2
##    `alexa_file$variation`           n
##    <chr>                        <int>
##  1 Black                          261
##  2 Black  Dot                     516
##  3 Black  Plus                    270
##  4 Black  Show                    265
##  5 Black  Spot                    241
##  6 Charcoal Fabric                430
##  7 Configuration: Fire TV Stick   350
##  8 Heather Gray Fabric          157
##  9 Oak Finish                    14
## 10 Sandstone Fabric              90
## 11 Walnut Finish                  9
## 12 White                         91
## 13 White  Dot                   184
## 14 White  Plus                   78
## 15 White  Show                   85
## 16 White  Spot                  109
```

```
  namevari <- vari$`alexa_file$variation`

  ploto <- barplot(vari$n,
                   names.arg = namevari,
                   main = "Total number of each variations",
                   xlab = "Name of Variations",
                   ylab = "Total of each Variatons",
                   col = 1:16,
                   space = 0.1,
                   cex.names = 0.5,
                   las = 2)
```

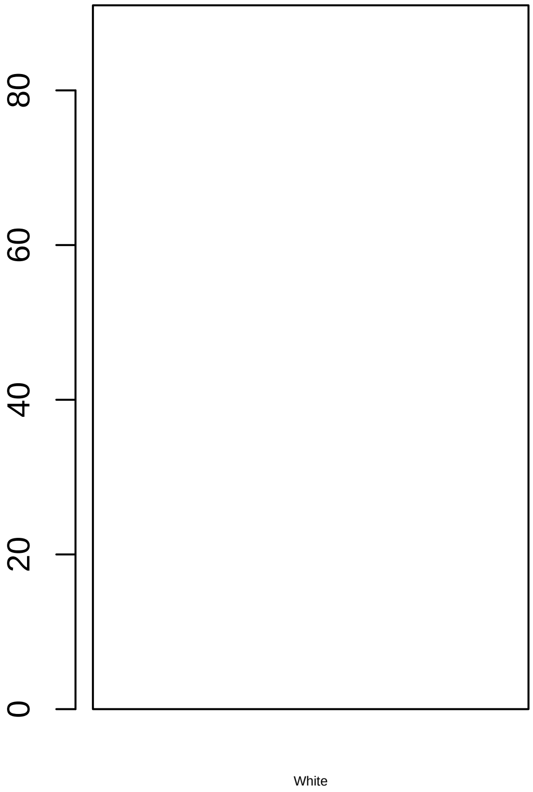


```
#d. Create a barplot() for the black and white variations. Plot it in 1 frame, side byside. Complete th

library(ggplot2)
library(magrittr)

#layout one frame
par(mfrow = c(1, 2), mar = c(2, 2, 2, 2))
```

```
Blackplot <- vari[vari$`alexa_file$variation` %in% c("Black", "BlackDot", "BlackShow", "BlackPlus", "Bla

Whiteplot <- vari[vari$`alexa_file$variation` %in% c("White", "WhiteDot", "WhiteShow", "WhitePlus", "Whi

# Barplot for Black variations
Black <- barplot(height = Blackplot$n,
                names.arg = Blackplot$`alexa_file$variation`,
                col = "Black",
                main = "Black Variations",
                xlab = "Number of Variation",
                ylab = "Count",
                las = 0.0,
                cex.names = 0.4,
        space = 0.2
)

# Barplot for White variations
White <- barplot(height = Whiteplot$n,
                 names.arg = Whiteplot$`alexa_file$variation`,
                 col = "White",
                 main = "White Variations",
                 xlab = "Number of Variation",
                 ylab = "Count",
                 las = 0.0,
                 cex.names = 0.4,
                 space = 0.2
)
```



Black Variations



White Variations