Worksheet 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.

#Hint Use abs() function to get the absolute value

```
vectorA <- c(1:5)
mymatrix <- matrix(0, nrow = 5, ncol = 5)
mymatrix
```

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

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

mymatrix
```

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

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

```
triangle <- c()
for(i in 1:5){
  for(j in 1:i+1){
    triangle = c(triangle, "*")

}

print(triangle)
triangle <-c()
}
```

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

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.

```
n <- as.integer(readline(prompt = "Enter the number of terms: "))
```

```
## Enter the number of terms:
```

```
n
```

```
## [1] NA
```

```
a <- 0
b <- 1
cat("Fibonacci Sequence:", a, b)
```

```
## Fibonacci Sequence: 0 1
```

```
repeat {
  c <- a + b
  if (c > 500) {
    break
  }

  cat(", ",c)
  a <- b
  b <- c

}
```

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

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

```
Household <- read.csv("Household.csv", header = TRUE, sep = ",", as.is = TRUE)
```

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.

```
head(Household,6)
```

```
##   shoe_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_subset <- subset(Household, gender == 'M')
female_subset <- subset(Household, gender == 'F')
male_count <- nrow(male_subset)
male_count
```

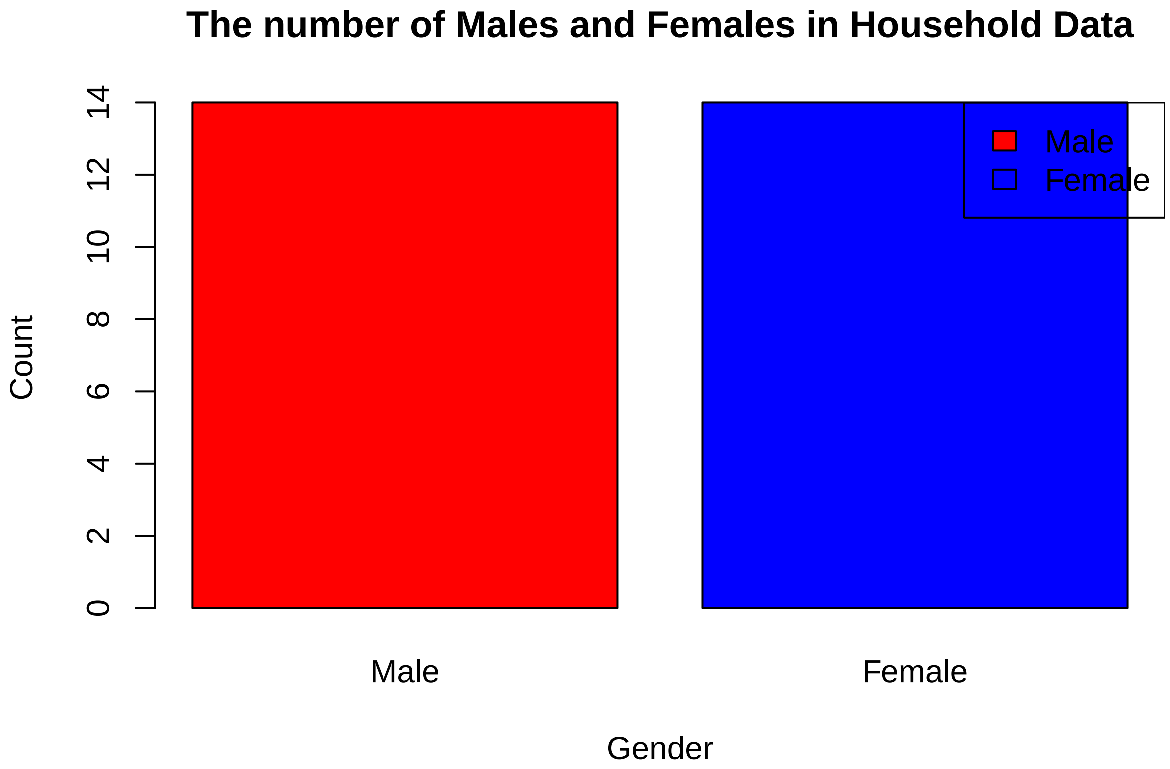
```
## [1] 14
```

```r
female_count <- nrow(female_subset)
female_count
```

```
## [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.

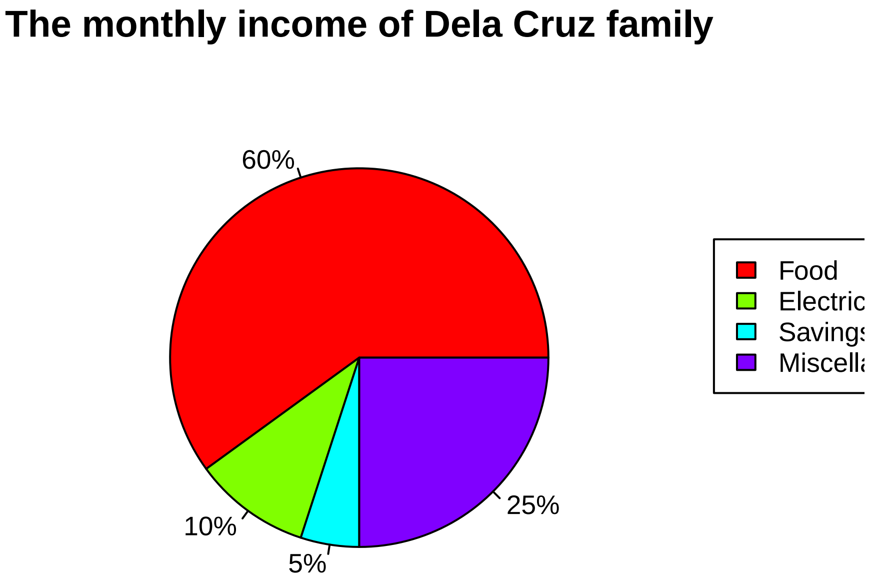
```r
count <- c(male_count, female_count)
gender <- c("Male", "Female")
barplot(count,
        names.arg = gender,
        main = "The number of Males and Females in Household Data",
        xlab = "Gender",
        ylab = "Count",
        col = c("red", "blue"))
legend("topright",
       legend = gender,
       fill = c("red", "blue"))
```



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

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
monthly_income <- c(60,10,5,25)
month_labels <- round(monthly_income/sum(monthly_income)*100,1)
month_labels <- paste(month_labels,"%", sep ="")
pie(monthly_income , main = "The monthly income of Dela Cruz family", col = rainbow(length(monthly_inco
legend(1.5,0.5, c("Food", "Electricity", "Savings", "Miscellaneous"), cex = 0.8, fill =rainbow(length(m
```



6. Use the iris dataset.

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

```
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 ...
```

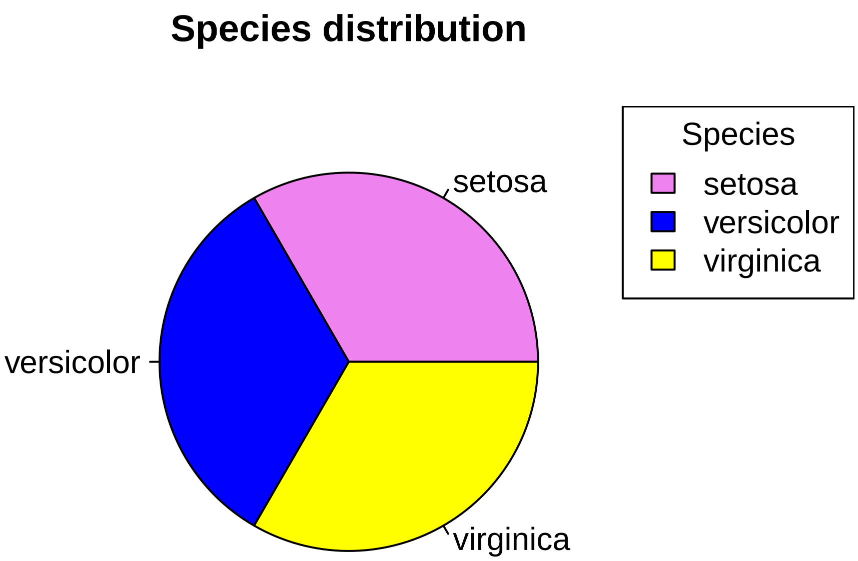
b. Create an R object that will contain the mean of the sepal.length, sepal.width,petal.length,and petal.width. What is the R script and its result?

```
mean<- colMeans(iris[, c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")])
mean
```

```
## 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.

```
pie(table(iris$Species),
    main = "Species distribution",
    labels = levels(iris$Species),
    col = c("violet","blue","yellow"))
legend("topright", legend = levels(iris$Species), fill = c("violet","blue","yellow"), title = "Species"
```



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

```
setosa_lastsix<- tail(subset(iris, Species == "setosa"), n = 6)
versicolor_lastsix <- tail(subset(iris, Species == "versicolor"), n = 6)
virginica_lastsix<- tail(subset(iris, Species == "virginica"), n = 6)
setosa_lastsix
```

```
##    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
```

```
versicolor_lastsix
```

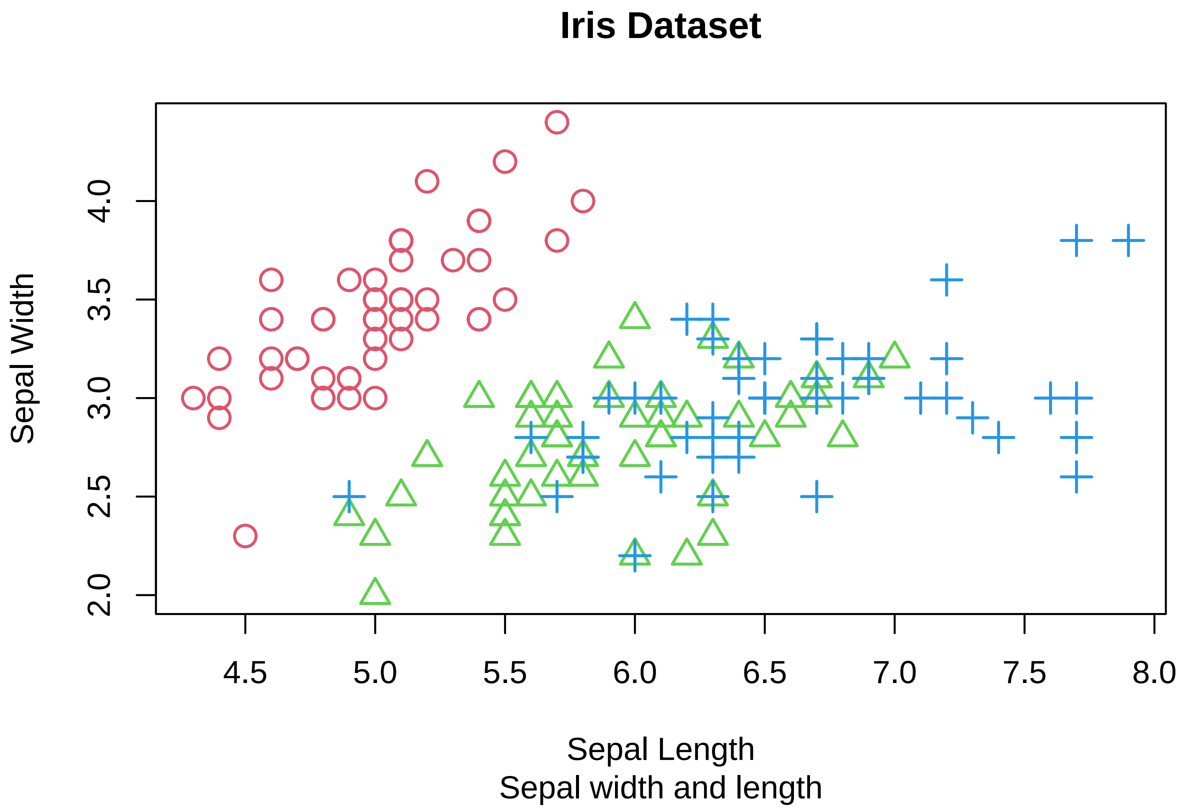
```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
## 95           5.6         2.7          4.2         1.3 versicolor
## 96           5.7         3.0          4.2         1.2 versicolor
## 97           5.7         2.9          4.2         1.3 versicolor
## 98           6.2     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

```
virginica_lastsix
```

```
##     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. 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.

```r
plot(iris$Sepal.Length, iris$Sepal.Width,
     pch = as.integer(iris$Species),
     col = as.integer(iris$Species) + 1,
     main = "Iris Dataset",
     sub = "Sepal width and length",
     xlab = "Sepal Length",
     ylab = "Sepal Width",
     cex = 1.5,
     lwd = 1.5)
```



```r
as.factor(iris$Species)
```

```
##   [1] setosa     setosa     setosa     setosa     setosa     setosa
##   [7] setosa     setosa     setosa     setosa     setosa     setosa
##  [13] setosa     setosa     setosa     setosa     setosa     setosa
##  [19] setosa     setosa     setosa     setosa     setosa     setosa
##  [25] setosa     setosa     setosa     setosa     setosa     setosa
##  [31] setosa     setosa     setosa     setosa     setosa     setosa
##  [37] setosa     setosa     setosa     setosa     setosa     setosa
##  [43] setosa     setosa     setosa     setosa     setosa     setosa
##  [49] setosa     setosa     versicolor versicolor versicolor versicolor
##  [55] versicolor versicolor versicolor versicolor versicolor versicolor
##  [61] versicolor versicolor versicolor versicolor versicolor versicolor
##  [67] versicolor versicolor versicolor versicolor versicolor versicolor
##  [73] versicolor versicolor versicolor versicolor versicolor versicolor
##  [79] versicolor versicolor versicolor versicolor versicolor versicolor
##  [85] versicolor versicolor versicolor versicolor versicolor versicolor
##  [91] versicolor versicolor versicolor versicolor versicolor versicolor
##  [97] versicolor versicolor versicolor versicolor virginica  virginica
## [103] virginica  virginica  virginica  virginica  virginica  virginica
## [109] virginica  virginica  virginica  virginica  virginica  virginica
## [115] virginica  virginica  virginica  virginica  virginica  virginica
## [121] virginica  virginica  virginica  virginica  virginica  virginica
## [127] virginica  virginica  virginica  virginica  virginica  virginica
## [133] virginica  virginica  virginica  virginica  virginica  virginica
## [139] virginica  virginica  virginica  virginica  virginica  virginica
## [145] virginica  virginica  virginica  virginica  virginica  virginica
## Levels: setosa versicolor virginica
```

7. Import the alexa-file.xlsx. Check on the variations. Notice that there are extra whitespaces among black variants (Black Dot, Black Plus, Black Show, Black Spot). Also on the white variants (White Dot, White Plus, White Show, White Spot).

a. Rename the white and black variants by using gsub() function.

```
library(readxl)
alexa_file <- read_excel("/cloud/project/RWorksheet 4/Worksheet 4B/alexa_file.xlsx")

alexaVaration <- gsub("Black Plus", "Black Plus", alexa_file$variation)
alexa_file$variation <- gsub("Black Show", "Black Show", alexa_file$variation)
alexa_file$variation <- gsub("Black Spot", "Black Spot", alexa_file$variation)
alexa_file$variation <- gsub("Black Dot", "Black Dot", alexa_file$variation)
alexa_file$variation <- gsub("White Dot", "White Dot", alexa_file$variation)
alexa_file$variation <- gsub("White Plus", "White Plus", alexa_file$variation)
alexa_file$variation <- gsub("White Show", "White Show", alexa_file$variation)
alexa_file$variation <- gsub("White Spot", "White Spot", alexa_file$variation)
```

b. Get the total number of each variations and save it into another object. Save the object as variations.RData. Write the R scripts. What is its result? Hint: Use the dplyr package. Make sure to install it before loading the package.

```
library(dplyr)
```

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

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

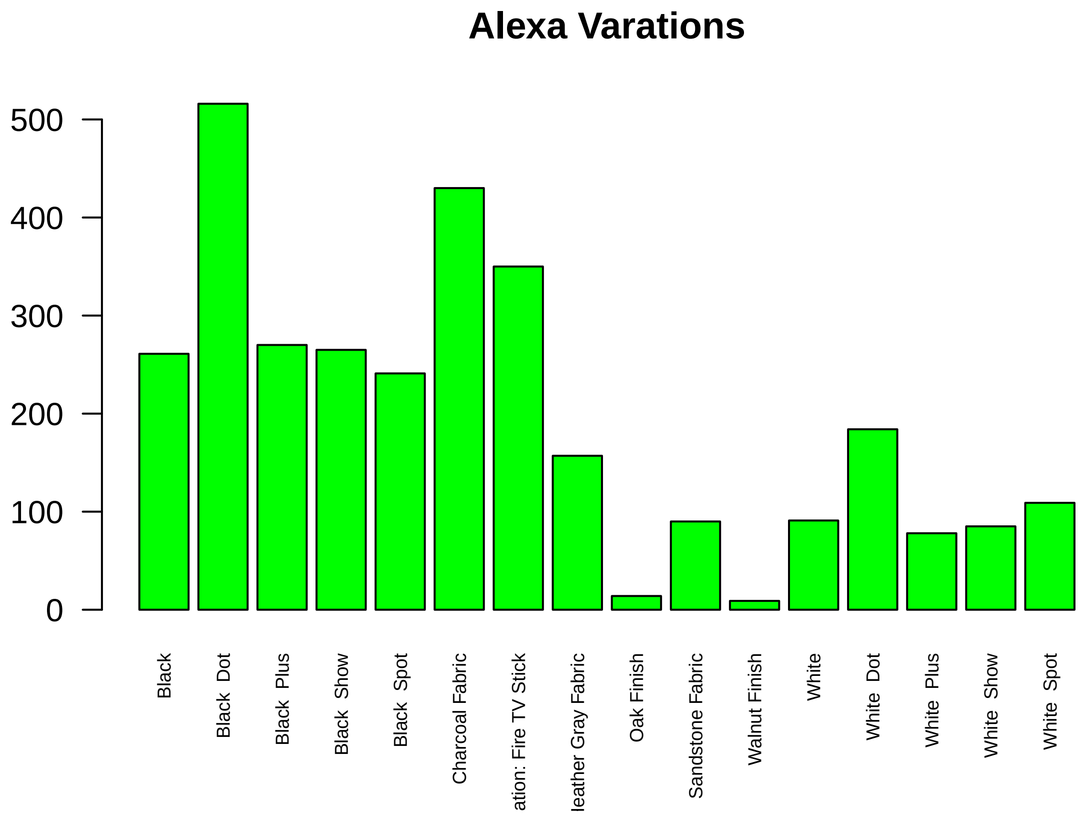
```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
save(alexa_file, file = "variations.RData")
load("variations.RData")
alexaVaration <- alexa_file%>%count(alexa_file$variation)
alexaVaration
```

```
## # 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
```

c. From the variations.RData, create a barplot(). Complete the details of the chart which include the title, color, labels of each bar

```
barplot(
height = alexaVaration$n,
names.arg = alexaVaration$`alexa_file$variation`,
col = "green",
main = "Alexa Varations",
las = 2,
cex.names = 0.58
)
```



d. Create a barplot() for the black and white variations. Plot it in 1 frame, side by side. Complete the details of the chart

```
par(mfrow = c(1, 2))
```

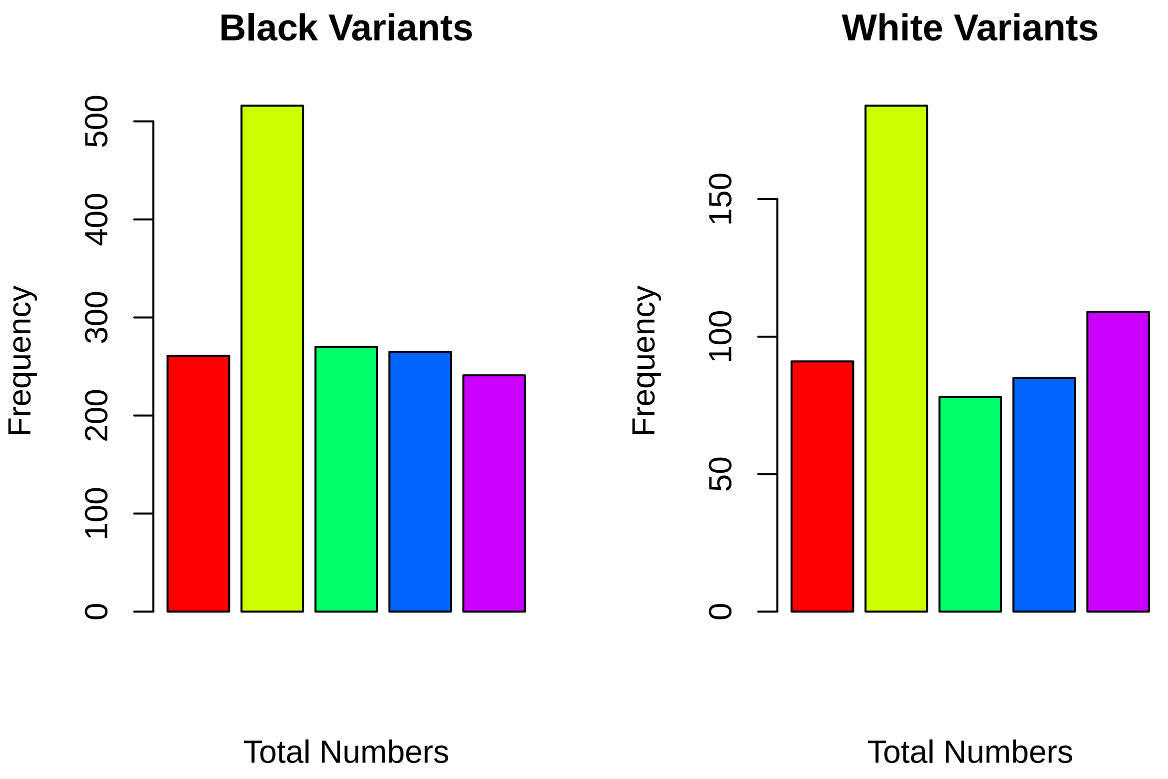
```
black_variants <- alexaVaration[1:5,]
white_variants <- alexaVaration[12:16,]

barplot(
  height = black_variants$n,
  names.arg = black_variants$variation,
  main = "Black Variants",
  col = rainbow(5),
  xlab = 'Total Numbers',
  ylab = 'Frequency',
  cex.names = 0.35
)
```

```
## Warning: Unknown or uninitialised column: `variation`.
```

```
barplot(
  height = white_variants$n,
  names.arg = white_variants$variation,
  main = "White Variants",
  col = rainbow(5),
  xlab = 'Total Numbers',
  ylab = 'Frequency',
  cex.names = 0.35
)
```

```
## Warning: Unknown or uninitialised column: `variation`.
```


Black Variants
Frequency
Total Numbers
White Variants
Frequency
Total Numbers