RWorksheet_Gagante#4b.Rmd

Liza Claire Gagante

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Using Loop Function for() loop 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, 2, 3, 4, 5)
matrix_5x5 <- matrix( nrow = 5, ncol = 5)

for (i in 1:5) {
  for (j in 1:5) {
    matrix_5x5[i, j] <- abs(i - j)
  }
}

print(matrix_5x5)
```

```
##      [,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. 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.

```
# start <- as.integer(readline(prompt = "Enter the starting number: "))

#a <- start
#b <- 1
#cat(a, b, sep = " ")
```

```
#repeat {
 # next_term <- a + b
 # if (!is.na(next_term) && next_term > 500) {
 #   break
#  }
#  cat(next_term, " ")
 # a <- b
#  b <- next_term
  #}
#cat("\n")
```

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_sizes.csv")

head(data)
```

```
##   Show.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_data <- subset(data, Gender == "M")
female_data <- subset(data, Gender == "F")

num_males <- nrow(male_data)
num_females <- nrow(female_data)

num_males
```

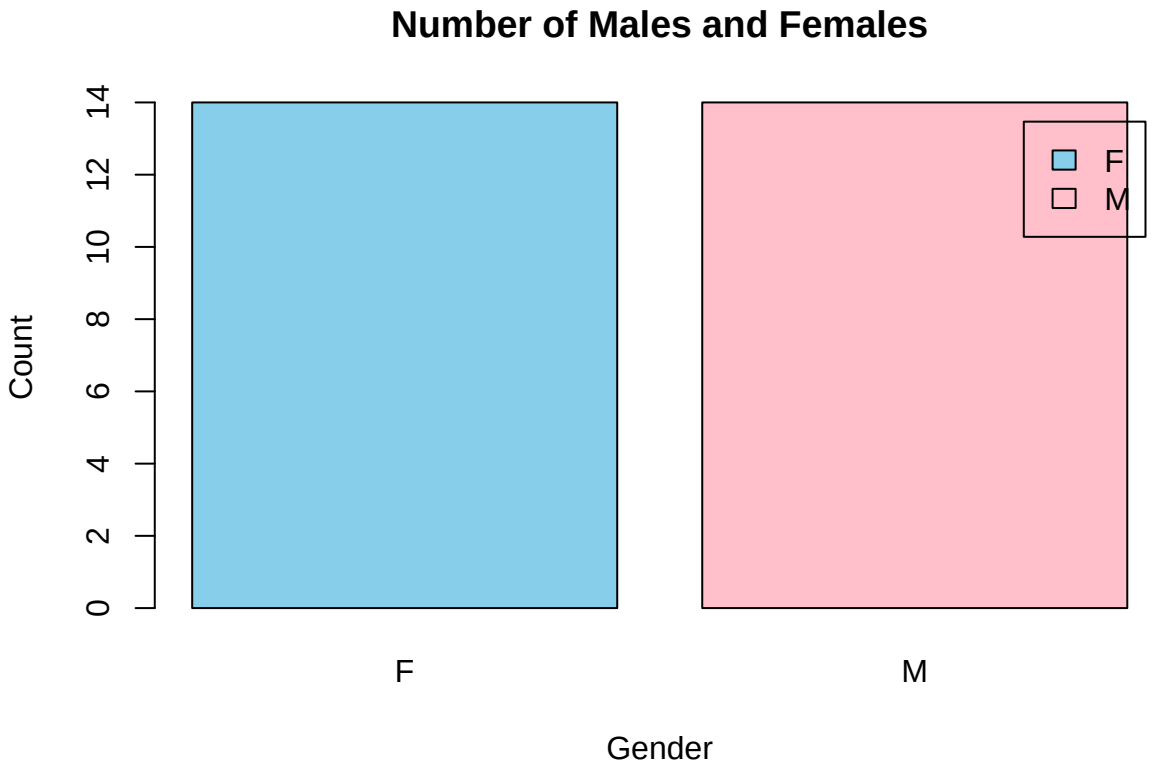
```
## [1] 14
```

```
num_females
```

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

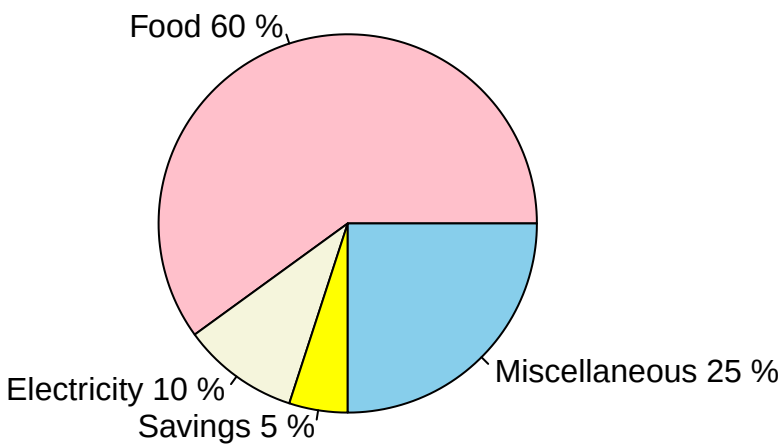
c. Create a graph for the number of males and females for Household Data. Use plot(), chart type = barplot. Make sure to place title, legends, and colors. Write the R scripts and its result.

```
gender_counts <- table(data$Gender)

barplot(gender_counts,
        main = "Number of Males and Females",
        xlab = "Gender",
        ylab = "Count",
        col = c("skyblue", "pink"),
        legend = rownames(gender_counts))
```



5. The monthly income of Dela Cruz family was spent on the following: Food Electricity Savings Miscellaneous 60 10 5 25 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.

```
expenses <- c(Food = 60, Electricity = 10, Savings = 5, Miscellaneous = 25)
percentages <- round(expenses / sum(expenses) * 100)
labels <- paste(names(expenses), percentages, "%")
colors <- c("pink", "beige", "yellow", "skyblue")
pie(expenses,
    labels = labels,
    col = colors,
    main = "Dela Cruz Family Monthly Expenses")
```



6. Use the iris dataset. data(iris) 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 ...
```

#The output shows the sepal length and width, petal width and length and also the species. #It will show that iris is a data frame with 150 observations and 5 variables: Sepal.Length: Numeric, lengths of sepals (in cm). Sepal.Width: Numeric, widths of sepals (in cm). Petal.Length: Numeric, lengths of petals (in cm). Petal.Width: Numeric, widths of petals (in cm). Species: Factor with 3 levels - setosa, versicolor, virginica. This gives us an idea of what data types are present in each column and how many levels the Species factor has.

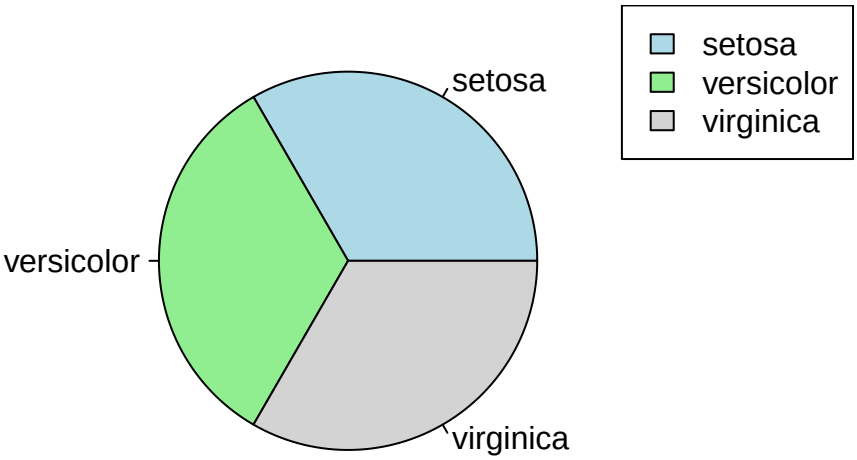
b. Create an R object that will contain the mean of the sepal.length, sepal.width,petal.length,and petal.width. What is the R script and its result?

```
means <- colMeans(subset(iris, select = -Species))
means
```

```
## 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.

```
species_counts <- table(iris$Species)

colors <- c("lightblue", "lightgreen", "lightgray")

pie(species_counts,
    main = "Species Distribution in Iris Dataset",
    col = colors,
    labels = names(species_counts))


legend("topright", legend = names(species_counts), fill = colors)
```



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

```
setosa <- subset(iris, Species == "setosa")
versicolor <- subset(iris, Species == "versicolor")
virginica <- subset(iris, Species == "virginica")


tail(setosa)
```

```
##    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
```

```
tail(versicolor)
```

```
##     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
```

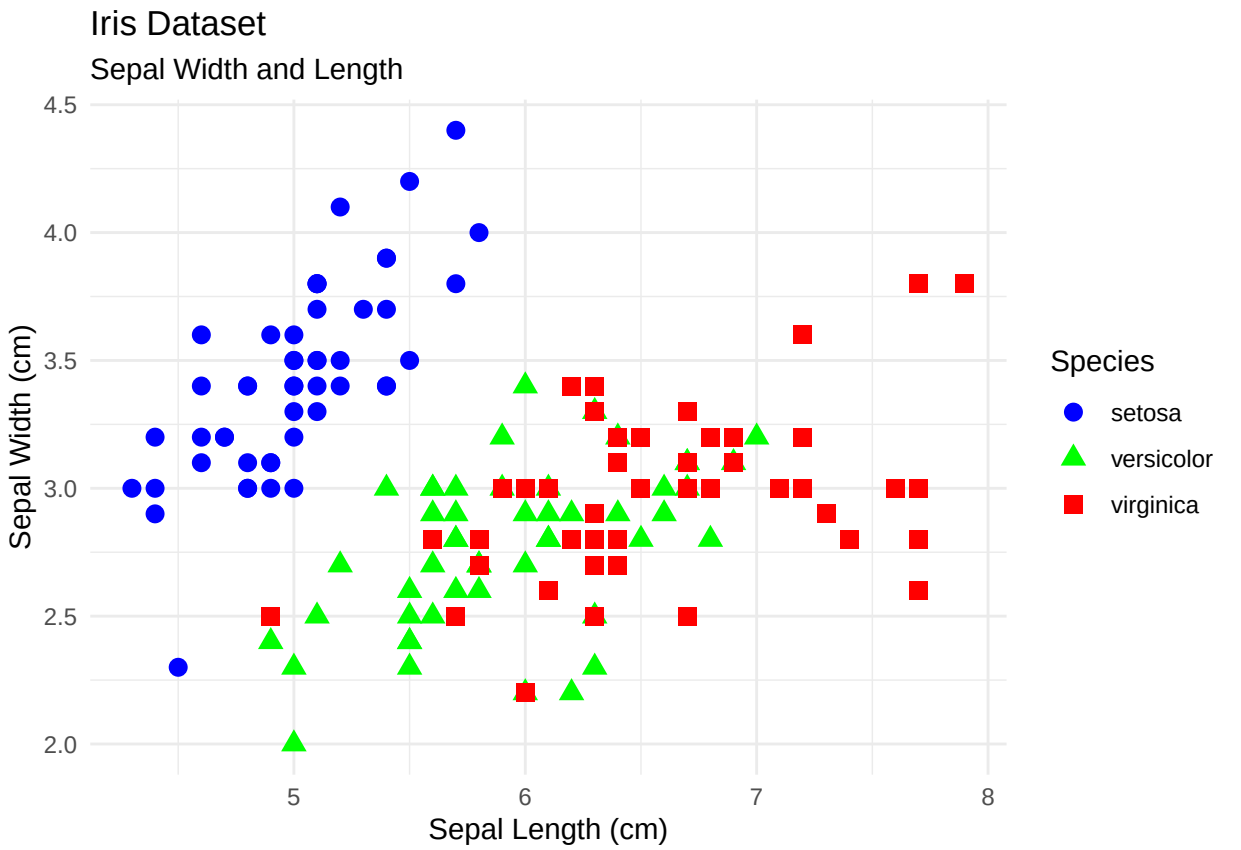
```
tail(virginica)
```

```
##     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,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. Hint: Need to convert to factors the species to store

categorical variables.

```
library(ggplot2)

ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width, color = Species, shape = Species)) +
  geom_point(size = 3) +
  labs(
    title = "Iris Dataset",
    subtitle = "Sepal Width and Length",
    x = "Sepal Length (cm)",
    y = "Sepal Width (cm)"
  ) +
  theme_minimal() +
  scale_color_manual(values = c("setosa" = "blue", "versicolor" = "green", "virginica" = "red"))
```



f. Interpret the result. #The scatter plot of Sepal.Length vs. Sepal.Width shows the relationship between these two measurements for each species:

#Setosa: Typically has smaller sepal lengths and widths, clustering separately from the other two species. #Versicolor and Virginica: Overlap more in their sepal dimensions, but Virginica generally has the largest sepal dimensions. #Overall Pattern: The species are distinguishable based on sepal size, with Setosa forming a distinct cluster. Versicolor and Virginica have some overlap, but Virginica tends to have larger sepal lengths and widths on average. This plot illustrates how sepal dimensions vary by species and how these features can help differentiate the species. 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. Hint: Need to convert to factors the species to store categorical variables.

f. Interpret the result.

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).

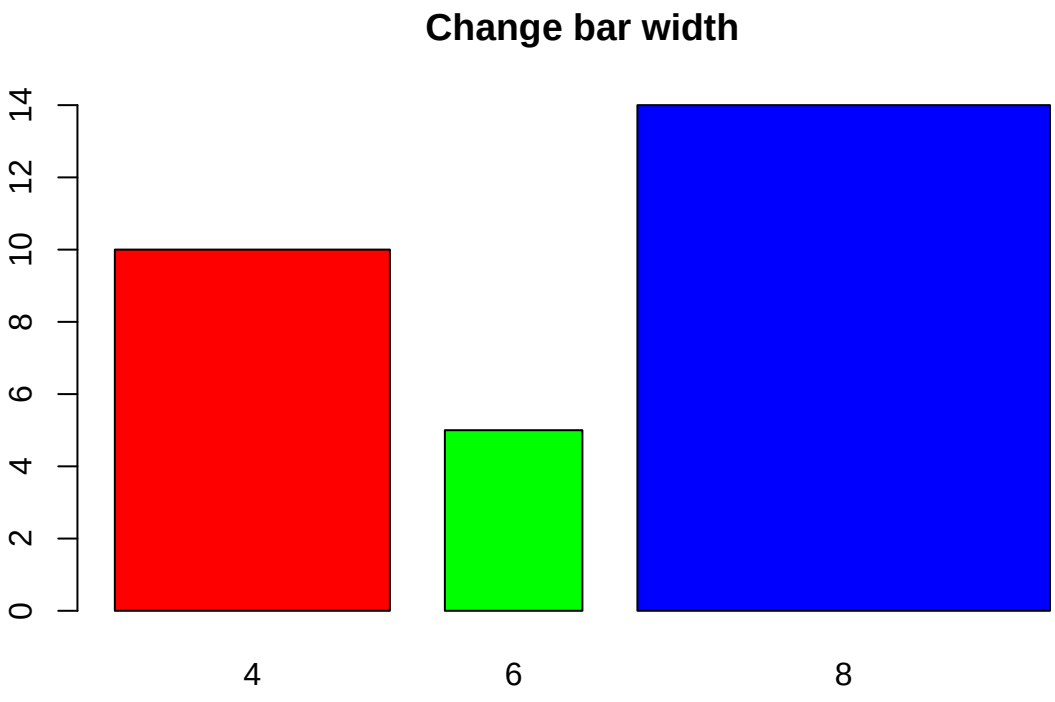
```
library(readxl)

alexa_data <- read_excel("alexa_file.xlsx")
```

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

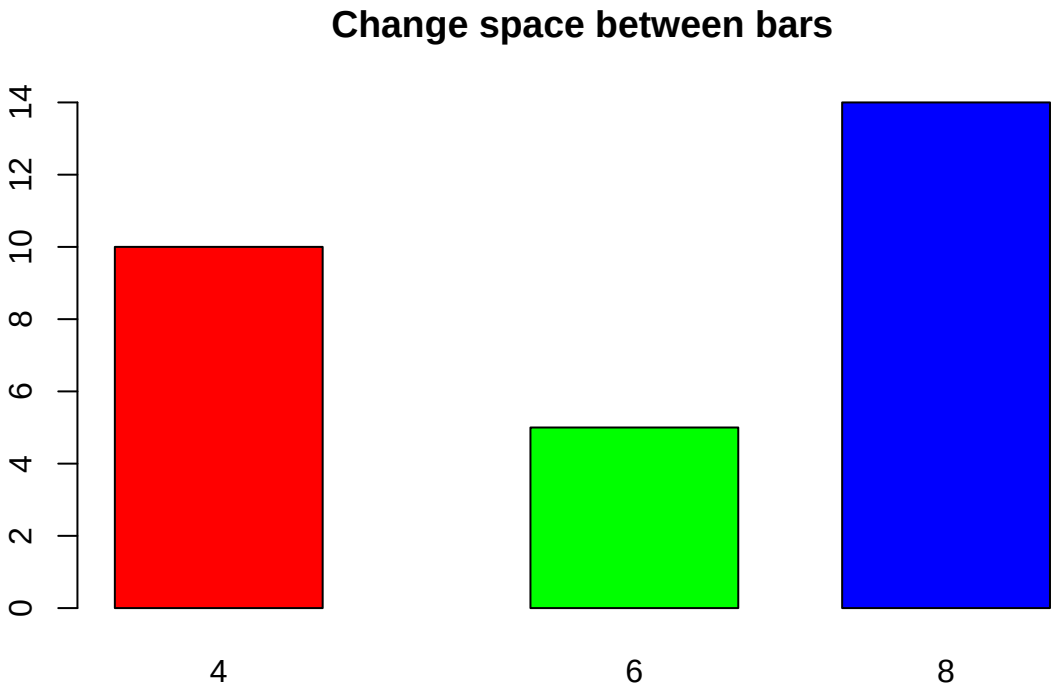
```
alexa_data$variation <- gsub("Black", "Dark", alexa_data$variation)
alexa_data$variation <- gsub("White", "Light", alexa_data$variation)
```

Write the R scripts and show an example of the output by getting a snippet. To embed an image into Rmd, use the function below:

```
library(knitr)

values <- c(10, 5, 14)
names <- c(4, 6, 8)
colors <- c("red", "green", "blue")

barplot(values, names.arg=names, col=colors, main="Change bar width", width=c(1, 0.5, 1.5))
```




```
barplot(values, names.arg=names, col=colors, main="Change space between bars", space=c(0.2, 1, 0.5))
```



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
```

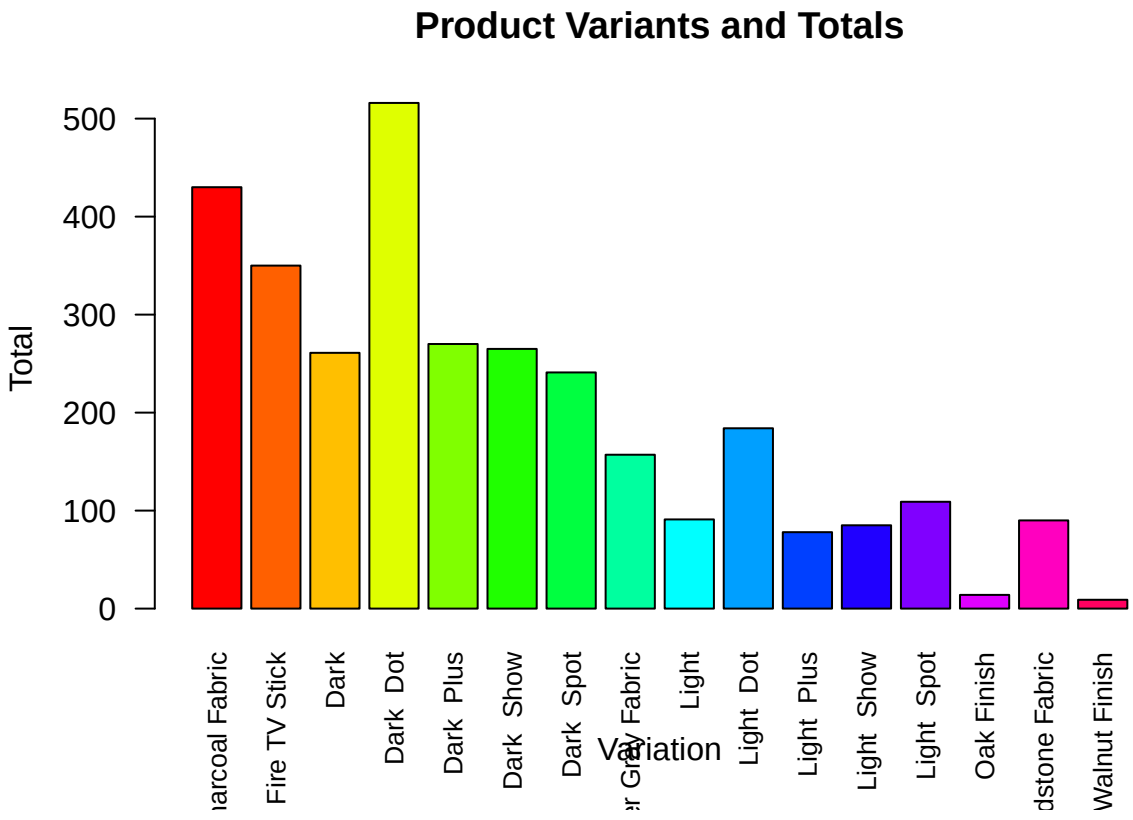
```
variation_counts <- alexa_data %>%
  count(variation)

save(variation_counts, file = "variations.RData")

print(variation_counts)
```

```
## # A tibble: 16 x 2
##    variation                        n
##    <chr>                        <int>
##  1 Charcoal Fabric                430
##  2 Configuration: Fire TV Stick   350
##  3 Dark                           261
##  4 Dark  Dot                      516
##  5 Dark  Plus                     270
##  6 Dark  Show                     265
##  7 Dark  Spot                     241
##  8 Heather Gray Fabric            157
```

```
##  9 Light                          91
## 10 Light  Dot                    184
## 11 Light  Plus                    78
## 12 Light  Show                    85
## 13 Light  Spot                   109
## 14 Oak Finish                     14
## 15 Sandstone Fabric               90
## 16 Walnut Finish                   9
```

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

```
barplot(
  variation_counts$n,
  names.arg = variation_counts$variation,
  col = rainbow(length(variation_counts$variation)),
  main = "Product Variants and Totals",
  xlab = "Variation",
  ylab = "Total",
   las = 2,
   cex.names = 0.8
)
```



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

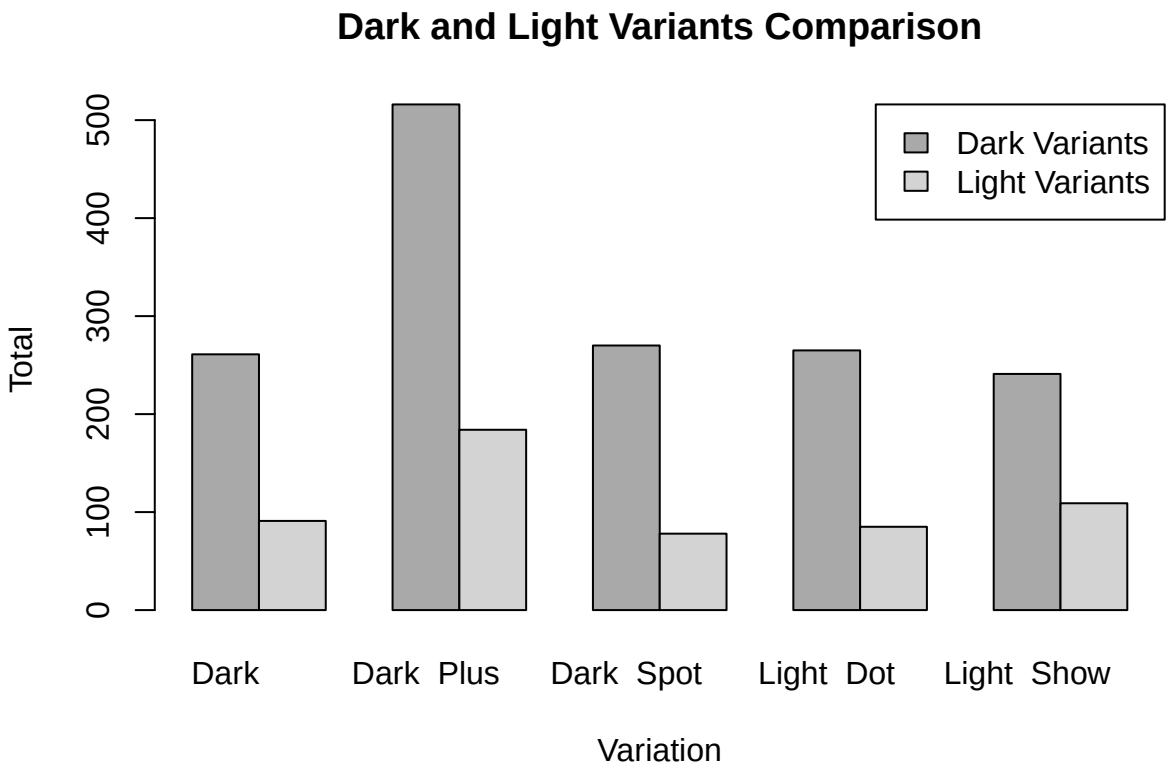
```
dark_variants <- subset(variation_counts, grepl("Dark", variation))
light_variants <- subset(variation_counts, grepl("Light", variation))

dark_variants
```

```
## # A tibble: 5 x 2
##   variation      n
##   <chr>      <int>
## 1 Dark         261
## 2 Dark  Dot    516
## 3 Dark  Plus   270
## 4 Dark  Show   265
## 5 Dark  Spot   241
```

```
light_variants
```

```
## # A tibble: 5 x 2
##   variation       n
##   <chr>       <int>
## 1 Light          91
## 2 Light  Dot    184
## 3 Light  Plus    78
## 4 Light  Show    85
## 5 Light  Spot   109
```

```
if (nrow(dark_variants) > 0 & nrow(light_variants) > 0) {
  max_length <- max(nrow(dark_variants), nrow(light_variants))
  dark_data <- c(dark_variants$n, rep(NA, max_length - nrow(dark_variants)))
  light_data <- c(light_variants$n, rep(NA, max_length - nrow(light_variants)))

    bar_data <- rbind(dark_data, light_data)
  colnames(bar_data) <- c(dark_variants$variation, light_variants$variation)[1:max_length]

   barplot(bar_data,
          beside = TRUE,
          col = c("darkgray", "lightgray"),
          main = "Dark and Light Variants Comparison",
          xlab = "Variation",
          ylab = "Total",
          names.arg = c(dark_variants$variation, light_variants$variation),
          legend.text = c("Dark Variants", "Light Variants"),
          args.legend = list(x = "topright"))
} else {
  print("No data found for Dark or Light variants.")
}
```


Dark and Light Variants Comparison
Total
0
100
200
300
400
500
Dark Variants
Light Variants
Dark
Dark Plus
Dark Spot
Light Dot
Light Show
Variation