Work sheet 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

```
# Define the vector
vectorA <- 1:5
matrix_result <- matrix(0, nrow = 5, ncol = 5)

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

print(matrix_result)
```

```
##      [,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 2.

```
for (i in 1:5) {
  for (j in 1:i) {
    cat('"*"\t')
  }
  cat("\n\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.

```
fib_sequence <- function() {
  start <- as.integer(readline(prompt = "Enter starting number: "))
```

```
  if (start <= 0) {
    print("Please enter a positive number")
    return()
  }

  a <- 0
  b <- 1
  count <- 0
  result <- c()

  repeat {
    if (count >= start) {
      if (b > 500) {
        break
      }
      result <- c(result, b)
    }

    temp <- a + b
    a <- b
    b <- temp
    count <- count + 1
  }
  print(result)
}
```

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

```
library(readxl)

# Import the Excel file
data <- read_excel("import_march.xlsx")

head(data)
```

```
## # A tibble: 6 x 4
##   Students `Strategy 1` `Strategy 2` `Strategy 3`
##   <chr>           <dbl>        <dbl>        <dbl>
## 1 Male                8           10            8
## 2 <NA>                4            8            6
## 3 <NA>                0            6            4
## 4 Female             14            4           15
## 5 <NA>               10            2           12
## 6 <NA>                6            0            9
```

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, Students == "Male")
female_data <- subset(data, Students == "Female")

male_count <- nrow(male_data)
female_count <- nrow(female_data)
```

```r
cat("Number of Male observations:", male_count, "\n")
```

```
## Number of Male observations: 1
```

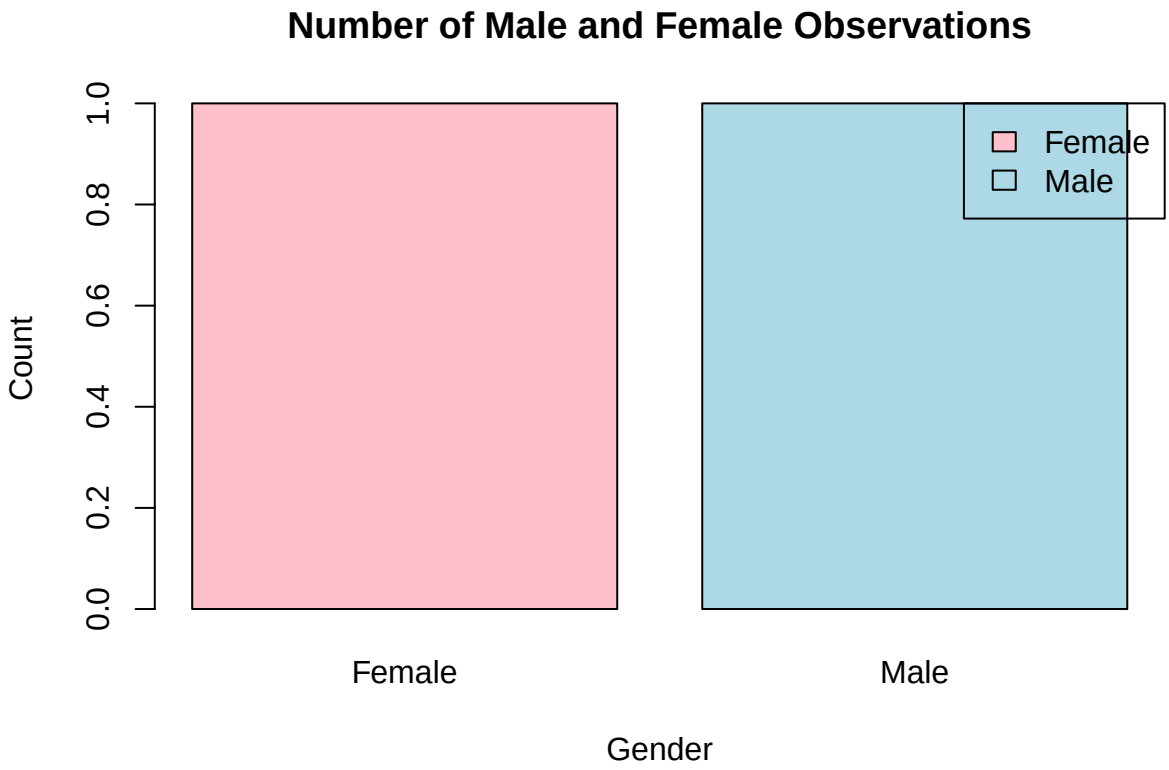
```r
cat("Number of Female observations:", female_count, "\n\n")
```

```
## Number of Female observations: 1
```

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
gender_counts <- table(data$Students)

barplot(
  gender_counts,
  main = "Number of Male and Female Observations",
  xlab = "Gender",
  ylab = "Count",
  col = c("pink", "lightblue"),
  legend.text = TRUE,
  args.legend = list(x = "topright", legend = c("Female", "Male"))
)
```



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

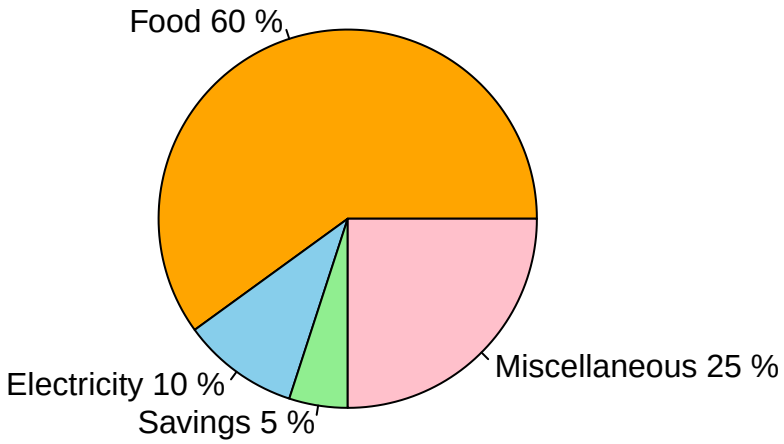
a. Create a piechart that will include labels in percentage.Add some colors and title of the chart. Write the R scripts and show its output.

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

percent <- round(expenses / sum(expenses) * 100)
```

```
labels <- paste(categories, percent, "%")

pie(expenses,
    labels = labels,
    col = c("orange", "skyblue", "lightgreen", "pink"),
    main = "Monthly Income Distribution of Dela Cruz Family")
```



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 ...
```

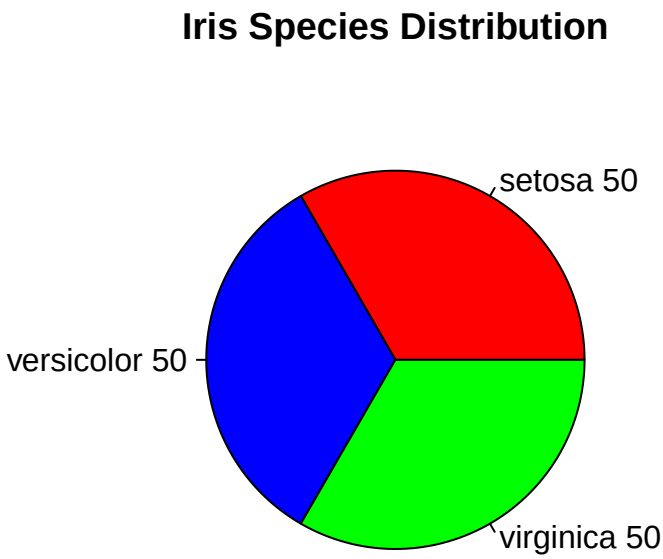
b. Create an R object that will contain the mean of the sepal.length,sepal.width,petal.length,and petal.width. What is the R script and its result?

```
iris_means <- data.frame(
  Sepal.Length = mean(iris$Sepal.Length),
  Sepal.Width = mean(iris$Sepal.Width),
  Petal.Length = mean(iris$Petal.Length),
  Petal.Width = mean(iris$Petal.Width)
)
print(iris_means)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1     5.843333    3.057333        3.758    1.199333
```

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

```r
species_counts <- table(iris$Species)
pie(species_counts,
    main = "Iris Species Distribution",
    col = c("red", "blue", "green"),
    labels = paste(names(species_counts), species_counts))
```



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

```r
setosa <- iris[iris$Species == "setosa", ]
versicolor <- iris[iris$Species == "versicolor", ]
virginica <- iris[iris$Species == "virginica", ]

print("Last 6 rows of Setosa:")
```

```
## [1] "Last 6 rows of Setosa:"
```

```r
print(tail(setosa, 6))
```

```
##    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
```

```r
print("Last 6 rows of Versicolor:")
```

```
## [1] "Last 6 rows of Versicolor:"
```

```r
print(tail(versicolor, 6))
```

```
##     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
```

```
print("Last 6 rows of Virginica:")
```

```
## [1] "Last 6 rows of Virginica:"
```

```
print(tail(virginica, 6))
```

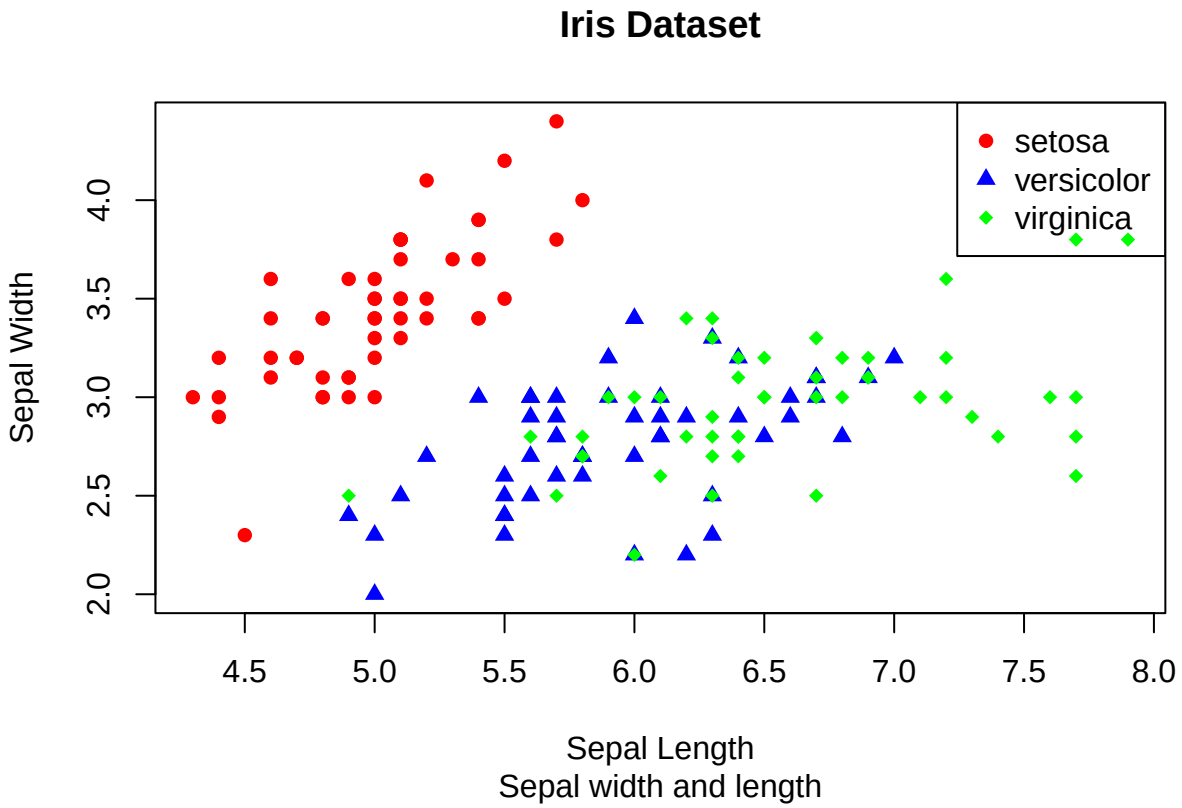
```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 145          6.7         3.3          5.7         2.5 virginica
## 146          6.7         3.0          5.2         2.3 virginica
## 147          6.3         2.5          5.0         1.9 virginica
## 148          6.5         3.0          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
```

```
iris$Species <- as.factor(iris$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.

```
plot(iris$Sepal.Length, iris$Sepal.Width,
     main = "Iris Dataset",
     sub = "Sepal width and length",
     xlab = "Sepal Length",
     ylab = "Sepal Width",
     pch = c(16, 17, 18)[as.numeric(iris$Species)],
     col = c("red", "blue", "green")[as.numeric(iris$Species)])

legend("topright",
       legend = levels(iris$Species),
       pch = c(16, 17, 18),
       col = c("red", "blue", "green"))
```



f. Interpret the result.

```
"The scatterplot shows that the three kinds of Iris flowers have different sepal sizes. The red dots (S
```

```
## [1] "The scatterplot shows that the three kinds of Iris flowers have different sepal sizes. The red
```

7. Import the alexa-file.xlsx. Check on the variations. Notice that there are ex-tra whitespaces among black variants (Black Dot, Black Plus, Black Show, BlackSpot). 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)
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
```

```
alexa <- read_xlsx("alexa-file.xlsx")

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

```
alexa$variation <- gsub("White  Plus", "White Plus", alexa$variation)
alexa$variation <- gsub("White  Show", "White Show", alexa$variation)
alexa$variation <- gsub("White  Spot", "White Spot", alexa$variation)

head(alexa, 10)
```

```
## # A tibble: 8 x 5
##   rating date       variation  verified_reviews                        feedback
##    <dbl> <chr>      <chr>      <chr>                                      <dbl>
## 1      5 2018-07-30 Black Dot  It works great!!                               1
## 2      5 2018-07-30 Black Plus PHENOMENAL                                     1
## 3      4 2018-07-30 Black Show I used it to control my smart devices.         1
## 4      3 2018-07-30 Black Spot Very convenient                                1
## 5      5 2018-07-31 White Dot  I love it!                                     1
## 6      4 2018-07-31 White Plus Nice sound quality                             1
## 7      5 2018-07-31 White Show Great screen!                                  1
## 8      4 2018-07-31 White Spot Easy to use                                    1
```

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?

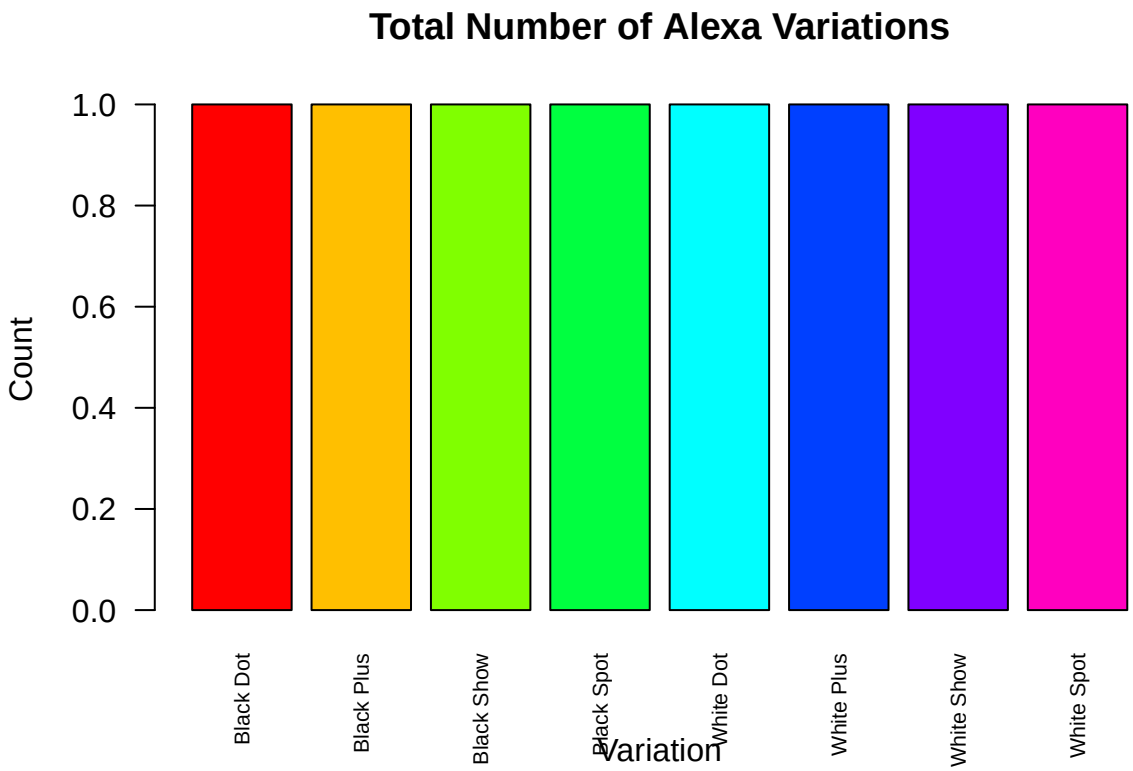
```
variations <- alexa %>% count(variation)
print(variations)
```

```
## # A tibble: 8 x 2
##   variation      n
##   <chr>      <int>
## 1 Black Dot      1
## 2 Black Plus     1
## 3 Black Show     1
## 4 Black Spot     1
## 5 White Dot      1
## 6 White Plus     1
## 7 White Show     1
## 8 White Spot     1
```

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

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

```
barplot(variations$n,
        names.arg = variations$variation,
        main = "Total Number of Alexa Variations",
        xlab = "Variation",
        ylab = "Count",
        col = rainbow(nrow(variations)),
        las = 2,
        cex.names = 0.7)
```



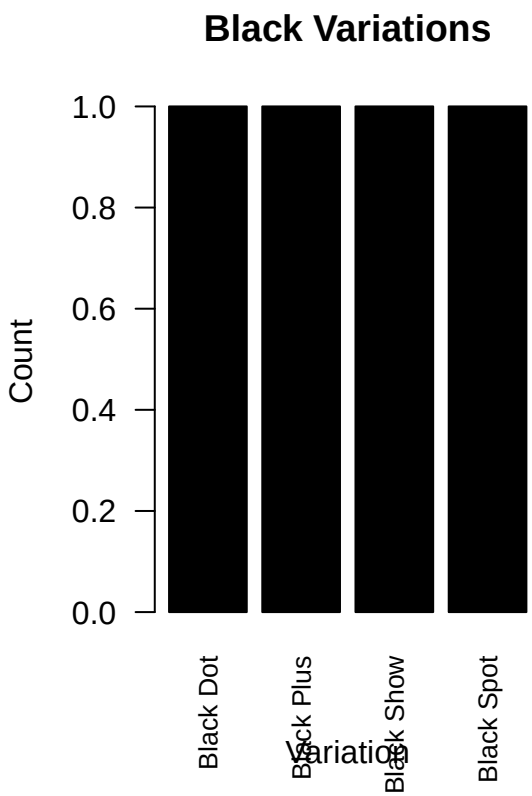
d. Create a barplot() for the black and white variations. Plot it in 1 frame, side b y side. Complete the details of the chart.

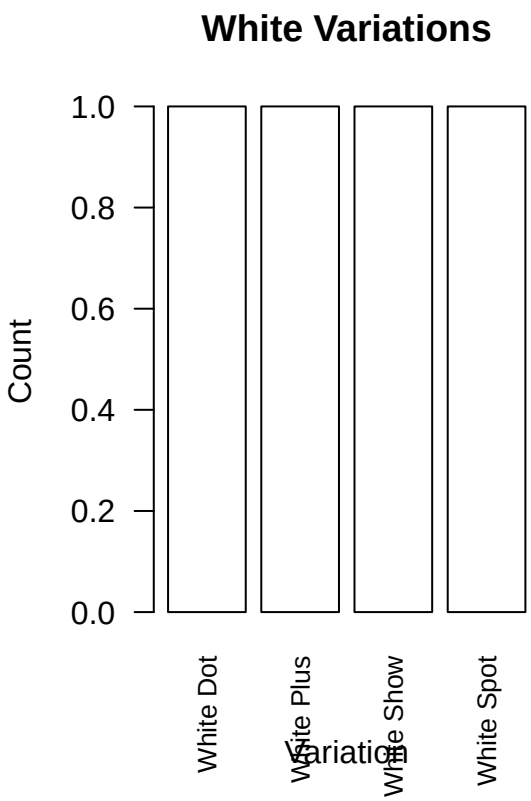
```
black_vars <- variations[grepl("Black", variations$variation), ]
white_vars <- variations[grepl("White", variations$variation), ]

par(mfrow = c(1, 2))

barplot(black_vars$n,
        names.arg = black_vars$variation,
        main = "Black Variations",
        xlab = "Variation",
        ylab = "Count",
        col = "black",
        las = 2,
        cex.names = 0.8)

barplot(white_vars$n,
        names.arg = white_vars$variation,
        main = "White Variations",
        xlab = "Variation",
        ylab = "Count",
        col = "white",
        las = 2,
        cex.names = 0.8)
```






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