

# RWorksheet\_LLANERA#4b

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2024-12-16

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

```
vectorA <- c(1, 2, 3, 4, 5)
```

```
matrix <- matrix(0, nrow = 5, ncol = 5)
```

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

```
for (i in 1:5) {  
  for (j in 1:i) {  
    cat("*")  
  }  
  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_number <- readline(prompt = "Enter the starting number: ")
```

```
## Enter the starting number:
```

```
start_number <- as.numeric(start_number)
```

```

fib_1 <- 0
fib_2 <- 1

print(fib_1)

## [1] 0
repeat {

  fib_next <- fib_1 + fib_2

  print(fib_next)

  fib_1 <- fib_2
  fib_2 <- fib_next

  if (fib_next > 500) {
    break
  }
}

```

```

## [1] 1
## [1] 2
## [1] 3
## [1] 5
## [1] 8
## [1] 13
## [1] 21
## [1] 34
## [1] 55
## [1] 89
## [1] 144
## [1] 233
## [1] 377
## [1] 610

```

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

```

shoes <- read.csv("shoes_data.csv")
shoes

```

```

##      Gender Shoe_Size Height
## 1      F      6.5    66.0
## 2      F      9.0    68.0
## 3      F      8.5    64.5
## 4      F      8.5    65.0
## 5      M     10.5    70.0
## 6      F      7.0    64.0
## 7      F      9.5    70.0
## 8      F      9.0    71.0

```

```
## 9      M      13.0  72.0
## 10     F       7.5  64.0
## 11     M     10.5  74.5
## 12     F       8.5  67.0
## 13     M     12.0  71.0
## 14     M     10.5  71.0
## 15     M     13.0  77.0
## 16     M     11.5  72.0
## 17     F       8.5  59.0
## 18     F       5.0  62.0
## 19     M     10.0  72.0
## 20     F       6.5  66.0
## 21     F       7.5  64.0
## 22     M       8.5  67.0
## 23     M     10.5  73.0
## 24     F       8.5  69.0
## 25     M     10.5  72.0
## 26     M     11.0  70.0
## 27     M       9.0  69.0
## 28     M     13.0  70.0
```

- 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.

```
femalesubset <- subset(shoes, Gender == "F")
malesubset <- subset(shoes, Gender == "M")
femalecount <- nrow(femalesubset)
malecount <- nrow(malesubset)
cat("Female:", femalecount, "\n")
```

```
## Female: 14
```

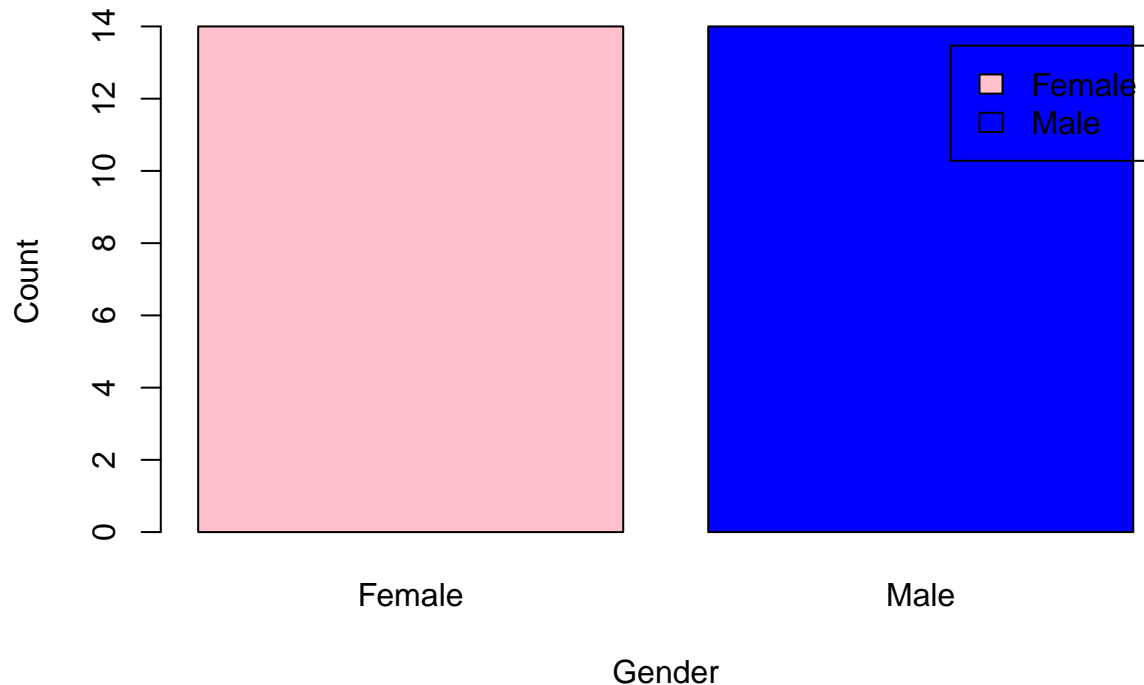
```
cat("Male:", malecount, "\n")
```

```
## Male: 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.

```
gendercounts <- table(shoes$Gender)
barplot(gendercounts,
  main = "Number of Males and Females in Household Data",
  xlab = "Gender",
  ylab = "Count",
  col = c("pink", "blue"),
  legend = c("Female", "Male"),
  names.arg = c("Female", "Male"))
```

## Number of Males and Females in Household Data

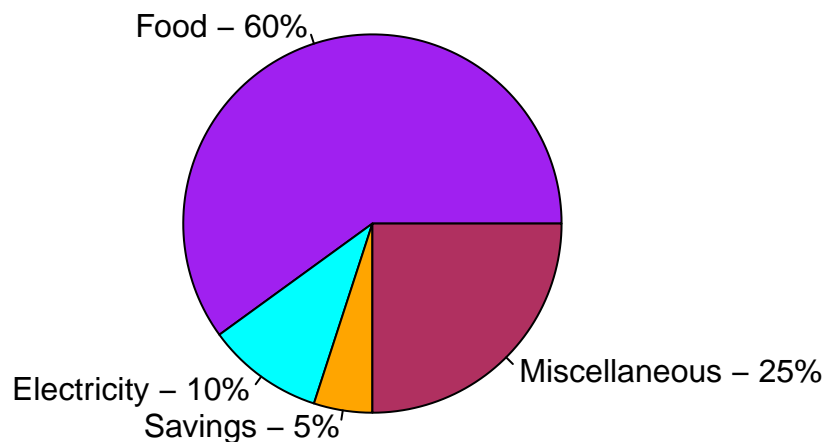


5. The monthly income of Dela Cruz family was spent on the following:

- 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)
percent_labels <- paste0(names(expenses), " - ", round(expenses / sum(expenses) * 100), "%")
pie(expenses,
    labels = percent_labels,
    col = c("purple", "cyan", "orange", "maroon"),
    main = "Dela Cruz Family Monthly Expenses")
```

## Dela Cruz Family Monthly Expenses



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?

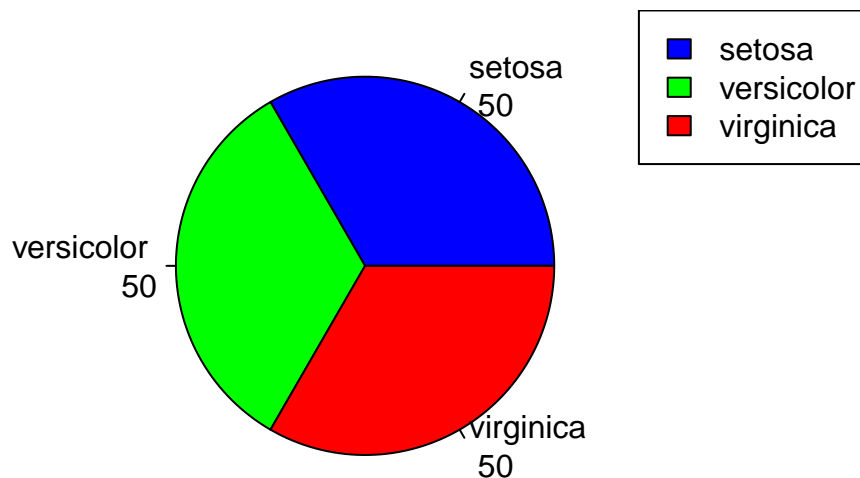
```
colMeans(iris[, 1:4])

## 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)
pie(species_counts,
    main = "Species Distribution in Iris Dataset",
    col = c("blue", "green", "red"),
    labels = paste(names(species_counts), "\n", species_counts))
legend("topright",
    legend = names(species_counts),
    fill = c("blue", "green", "red"))
```

## Species Distribution in Iris Dataset



- 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
```

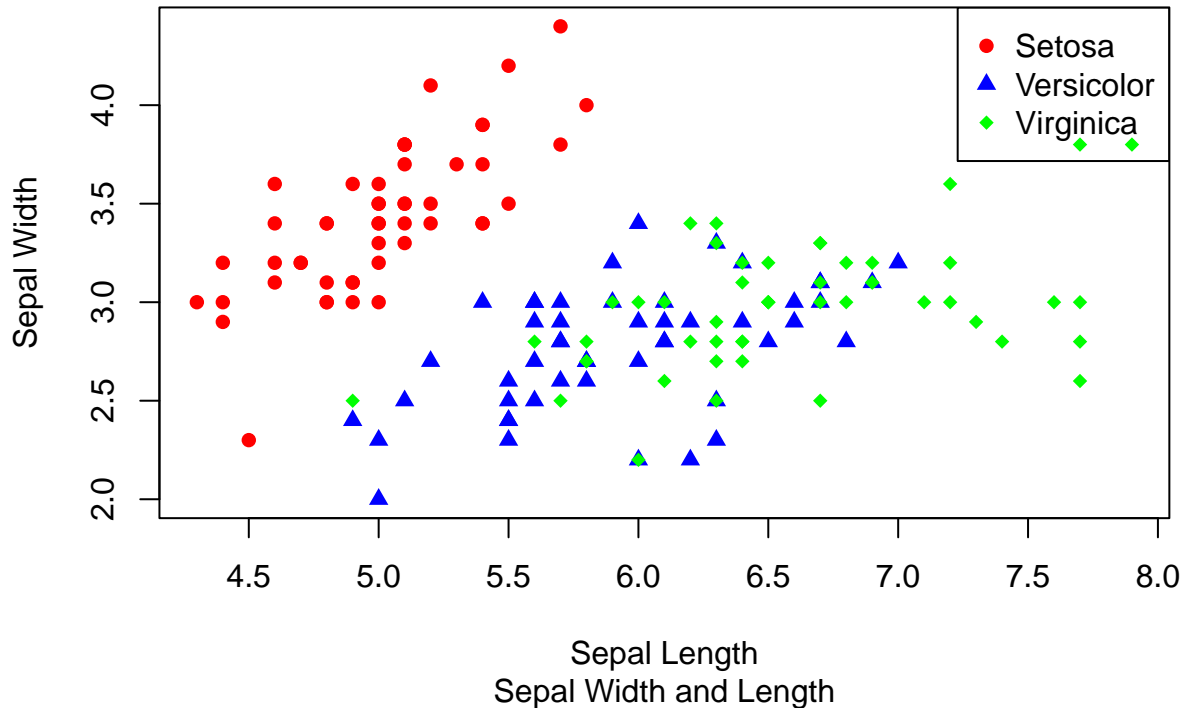
```
tail(virginica)
```

```
##      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.

```
colors <- c("setosa" = "red", "versicolor" = "blue", "virginica" = "green")
symbols <- c("setosa" = 16, "versicolor" = 17, "virginica" = 18)
plot(iris$Sepal.Length, iris$Sepal.Width,
     col = colors[iris$Species],
     pch = symbols[iris$Species],
     main = "Iris Dataset",
     sub = "Sepal Width and Length",
     xlab = "Sepal Length",
     ylab = "Sepal Width")
legend("topright", legend = c("Setosa", "Versicolor", "Virginica"),
     col = c("red", "blue", "green"),
     pch = c(16, 17, 18))
```

## Iris Dataset



f. Interpret the result. The data structure supported both basic analysis and detailed modeling, with mean values offering a quick look at iris flower traits. Visualizations like the pie chart and scatterplot illustrated species distribution and trait correlations, enabling focused, species-specific analysis.

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_data <- read_excel("alexa_file.xlsx")
unique(alexa_data$variation)

## [1] "Charcoal Fabric"          "Walnut Finish"
## [3] "Heather Gray Fabric"     "Sandstone Fabric"
## [5] "Oak Finish"              "Black"
## [7] "White"                   "Black Spot"
## [9] "White Spot"              "Black Show"
## [11] "White Show"              "Black Plus"
## [13] "White Plus"              "Configuration: Fire TV Stick"
## [15] "Black Dot"               "White Dot"

alexa_data$variation <- gsub("Black Dot", "BlackDot", alexa_data$variation)
alexa_data$variation <- gsub("Black Plus", "BlackPlus", alexa_data$variation)
alexa_data$variation <- gsub("Black Show", "BlackShow", alexa_data$variation)
alexa_data$variation <- gsub("Black Spot", "BlackSpot", alexa_data$variation)
alexa_data$variation <- gsub("White Dot", "WhiteDot", alexa_data$variation)
alexa_data$variation <- gsub("White Plus", "WhitePlus", alexa_data$variation)
alexa_data$variation <- gsub("White Show", "WhiteShow", alexa_data$variation)
alexa_data$variation <- gsub("White Spot", "WhiteSpot", alexa_data$variation)
```

```
unique(alexa_data$variation)
```

```
## [1] "Charcoal Fabric"      "Walnut Finish"
## [3] "Heather Gray Fabric"  "Sandstone Fabric"
## [5] "Oak Finish"           "Black"
## [7] "White"                "Black Spot"
## [9] "White Spot"           "Black Show"
## [11] "White Show"           "Black Plus"
## [13] "White Plus"           "Configuration: Fire TV Stick"
## [15] "Black Dot"            "White Dot"
```

- 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?

```
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)
print(variation_counts)
```

```
## # A tibble: 16 x 2
##   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
```

```
save(variation_counts, 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.

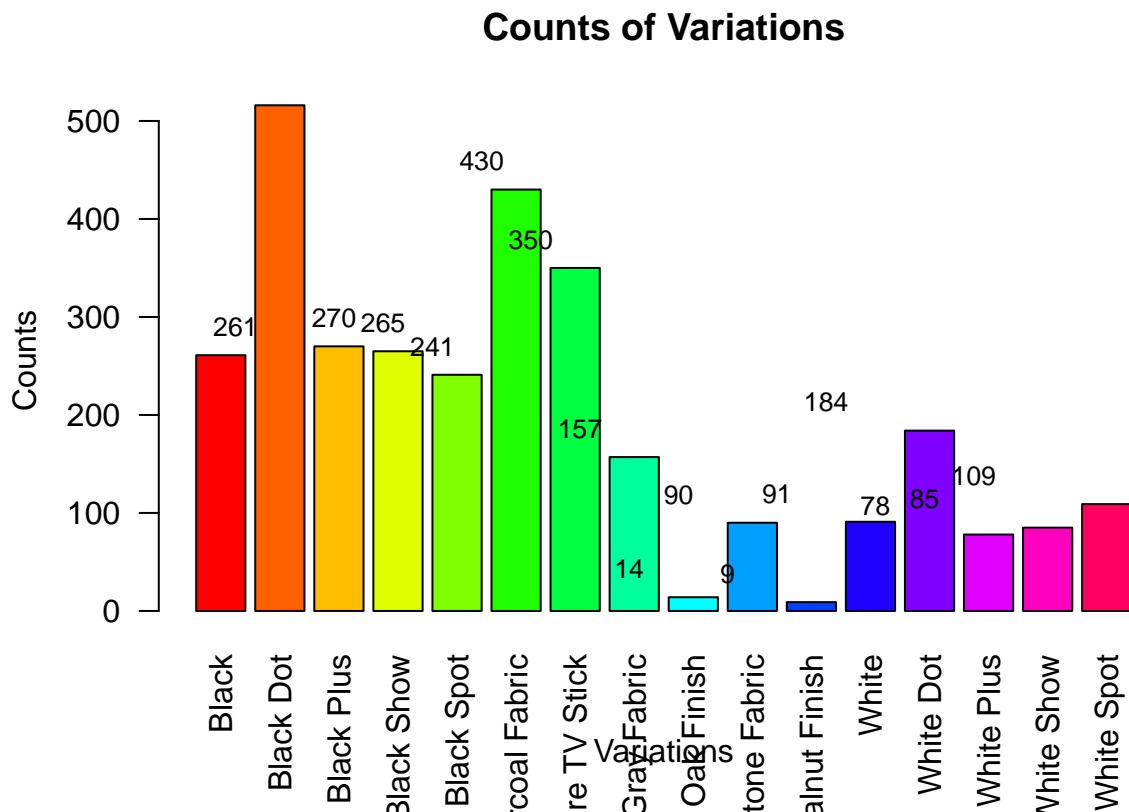
```
library(dplyr)
load("variations.RData")
```



```

variation_counts$variation <- gsub(" +", " ", variation_counts$variation)
variation_counts$variation <- trimws(variation_counts$variation)
bar_data <- variation_counts$n
bar_names <- variation_counts$variation
barplot(
  bar_data,
  main = "Counts of Variations",
  col = rainbow(length(bar_data)),
  names.arg = bar_names,
  xlab = "Variations",
  ylab = "Counts",
  las = 2,
  border = "black"
)
text(x = seq_along(bar_data), y = bar_data, labels = bar_data, pos = 3, cex = 0.8, col = "black")

```



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

```

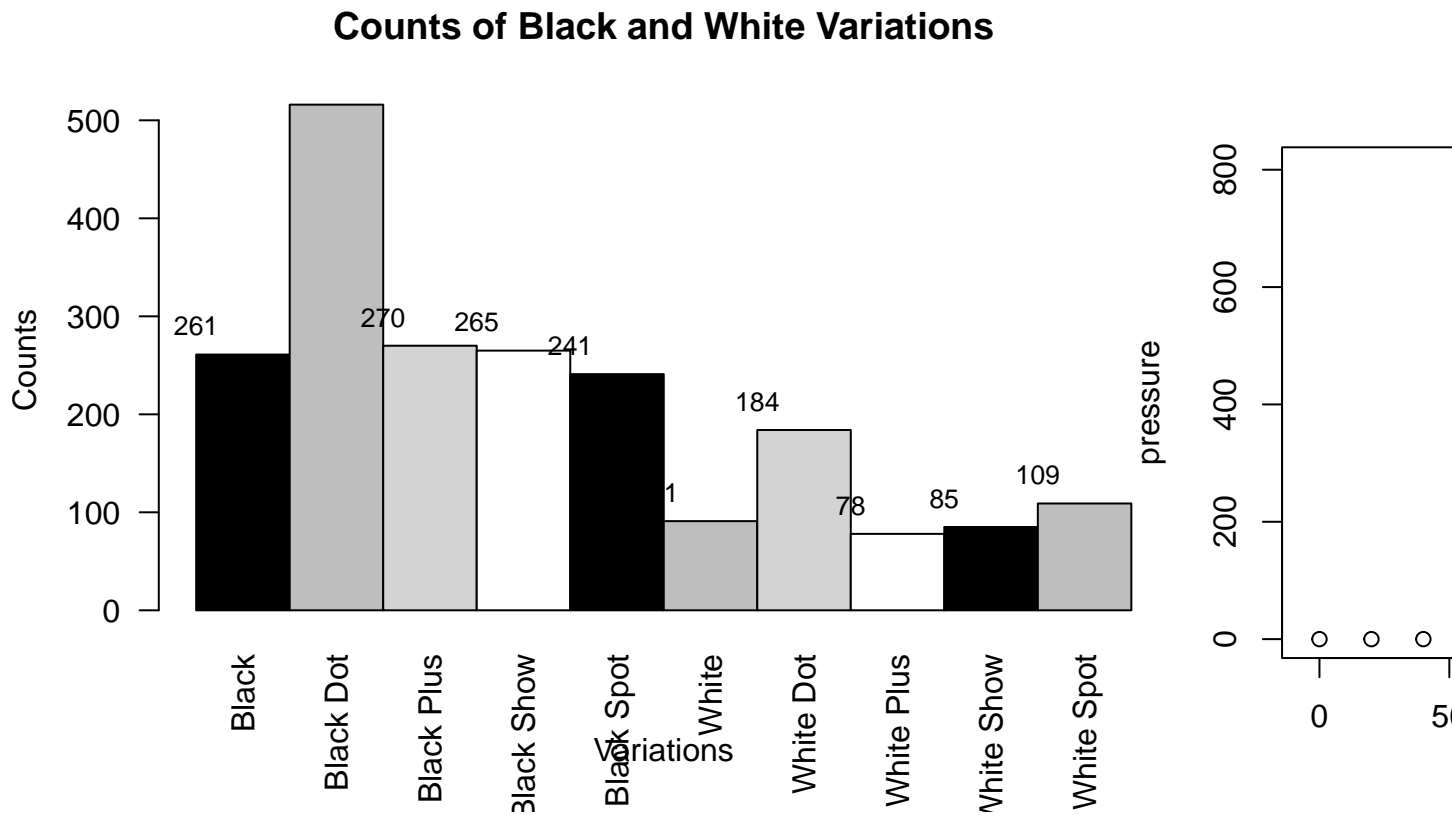
library(ggplot2)
library(dplyr)
load("variations.RData")
variation_counts$variation <- gsub(" +", " ", variation_counts$variation)
variation_counts$variation <- trimws(variation_counts$variation)
bw_variations <- variation_counts %>%
  filter(grepl("Black|White", variation))
bar_data <- as.matrix(bw_variations$n)
bar_names <- bw_variations$variation

```

```

barplot(
  bar_data,
  beside = TRUE,
  main = "Counts of Black and White Variations",
  col = c("black", "gray", "lightgray", "white"),
  names.arg = bar_names,
  xlab = "Variations",
  ylab = "Counts",
  las = 2,
  border = "black"
)
text(x = seq_along(bar_data), y = bar_data, labels = bar_data, pos = 3, cex = 0.8, col = "black")

```



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.