RWorksheet_lauron_4b.Rmd

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```
#1

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

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

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

# output
#print(matrixA)
#[,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

for (i in 1:5) {
  for (j in 1:i) {
    cat('"*"')
  }
  cat("\n")
}
```

```
## "*"
## "*""*"
## "*""*""*"
## "*""*""*""*"
## "*""*""*""*""*"
```

```
#output
#"*"
#"*""*"
#"*""*""*"
#"*""*""*""*"
#"*""*""*""*""*"
```

```
#3 fibonacci

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

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

```
if (is.na(start)) {
  cat("Invalid input! Please enter a numeric value.\n")
} else {
  # Initialize first two Fibonacci numbers
  a <- 0
  b <- 1

  cat("Fibonacci sequence starting from", start, "up to 500:\n")

  repeat {
    # Only print numbers >= start
    if (a >= start) {
      cat(a, " ")
    }

    # Stop if the next number will be greater than 500
    if (a > 500) {
      break
    }

    # Generate next Fibonacci number
    temp <- a + b
    a <- b
    b <- temp
  }

  cat("\nDone!\n")
}
```

```
## Invalid input! Please enter a numeric value.
```

```
#4

#a For CSV and display first 6 rows
shoe_data <- read.csv("shoe_data.csv")

head(shoe_data)
```

```
##   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
```

```
#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 Subset for males and females
male_subset <- shoe_data[shoe_data$Gender == "M", ]
female_subset <- shoe_data[shoe_data$Gender == "F", ]
male_subset
```

```
##    Shoe_size Height Gender
## 5       10.5   70.0      M
## 9       13.0   72.0      M
## 11      10.5   74.5      M
## 13      12.0   71.0      M
## 14      10.5   71.0      M
## 15      13.0   77.0      M
## 16      11.5   72.0      M
## 19      10.0   72.0      M
## 22       8.5   67.0      M
## 23      10.5   73.0      M
## 25      10.5   72.0      M
## 26      11.0   70.0      M
## 27       9.0   69.0      M
## 28      13.0   70.0      M
```

```
female_subset
```

```
##    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
## 6        7.0   64.0      F
## 7        9.5   70.0      F
## 8        9.0   71.0      F
## 10       7.5   64.0      F
## 12       8.5   67.0      F
## 17       8.5   59.0      F
## 18       5.0   62.0      F
## 20       6.5   66.0      F
## 21       7.5   64.0      F
## 24       8.5   69.0      F
```

```
# Count observations in each
nrow(male_subset)
```

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

```
nrow(female_subset)
```

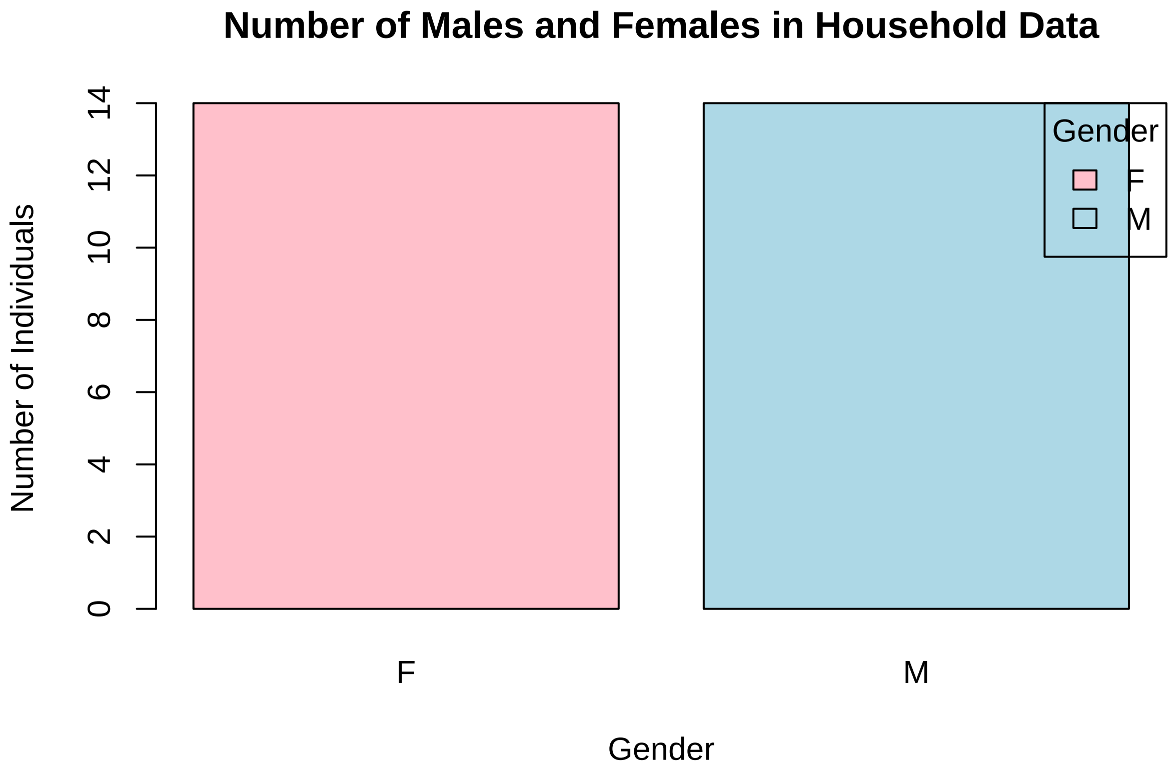
```
## [1] 14
```

```
#output
#nrow(male_data)
#[1] 14
# nrow(female_data)
```

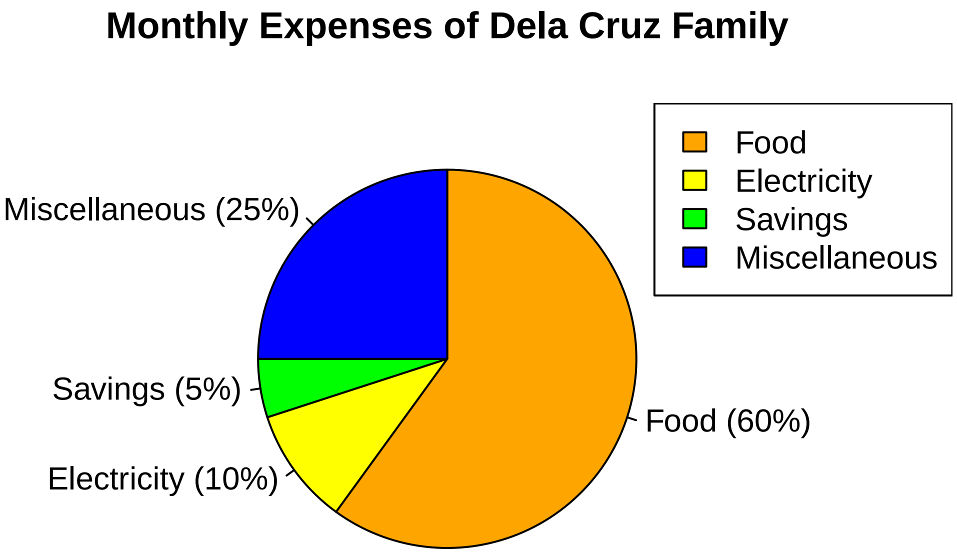
```
#[1] 14


gender_count <- table(shoe_data$Gender)

# Display counts
gender_count
```

```
##
##  F  M
## 14 14
```

```
#c Create a bar plot
barplot(gender_count,
        main = "Number of Males and Females in Household Data",
        xlab = "Gender",
        ylab = "Number of Individuals",
        col = c("pink", "lightblue"),
        legend.text = TRUE,
        args.legend = list(x = "topright", title = "Gender"))
```



```
# 5
expenses <- c(Food = 60, Electricity = 10, Savings = 5, Miscellaneous = 25)

labels <- paste0(names(expenses),
                 " (", round(100 * expenses / sum(expenses), 1), "%)")

# Create pie chart
pie(expenses,
    main = "Monthly Expenses of Dela Cruz Family",
    col = c("orange", "yellow", "green", "blue"),
    labels = labels,
    clockwise = TRUE)

legend("topright", legend = names(expenses), fill = c("orange", "yellow", "green", "blue"))
```



```
#6 iris dataset
data(iris)

#a Check structure
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 ...
```

```
#output
#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 sepal width, the the petal length and petal
#width, and the species.

#b mean of the sepal.length,sepal.width,petal.length,and petal.width.
iris_mean <- colMeans(iris[, 1:4])
iris_mean
```

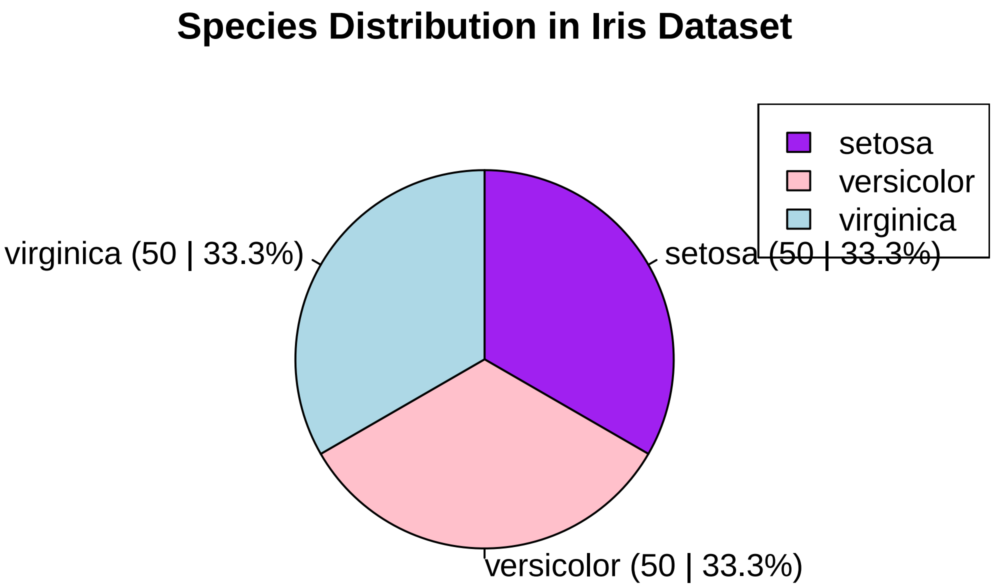
```
## Sepal.Length  Sepal.Width Petal.Length  Petal.Width
##     5.843333     3.057333     3.758000     1.199333
```

```
#output
#Sepal.Length  Sepal.Width Petal.Length  Petal.Width
```

```
#    5.843333     3.057333     3.758000     1.199333

#c Count species
species_distribution <- table(iris$Species)
species_distribution
```

```
##
##     setosa versicolor  virginica
##         50         50         50
```

```
labels <- paste0(names(species_distribution),
                 " (", species_distribution, " | ",
                 round(100 * species_distribution / sum(species_distribution), 1), "%)")

# Create pie chart
pie(species_distribution,
    main = "Species Distribution in Iris Dataset",
    col = c("purple", "pink", "lightblue"),
    labels = labels,
    clockwise = TRUE)

legend("topright", legend = names(species_distribution), fill = c("purple", "pink", "lightblue"))
```



```
#d Subset each species
setosa <- subset(iris, Species == "setosa")
versicolor <- subset(iris, Species == "versicolor")
virginica <- subset(iris, Species == "virginica")

#last 6 rows of each
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)
```

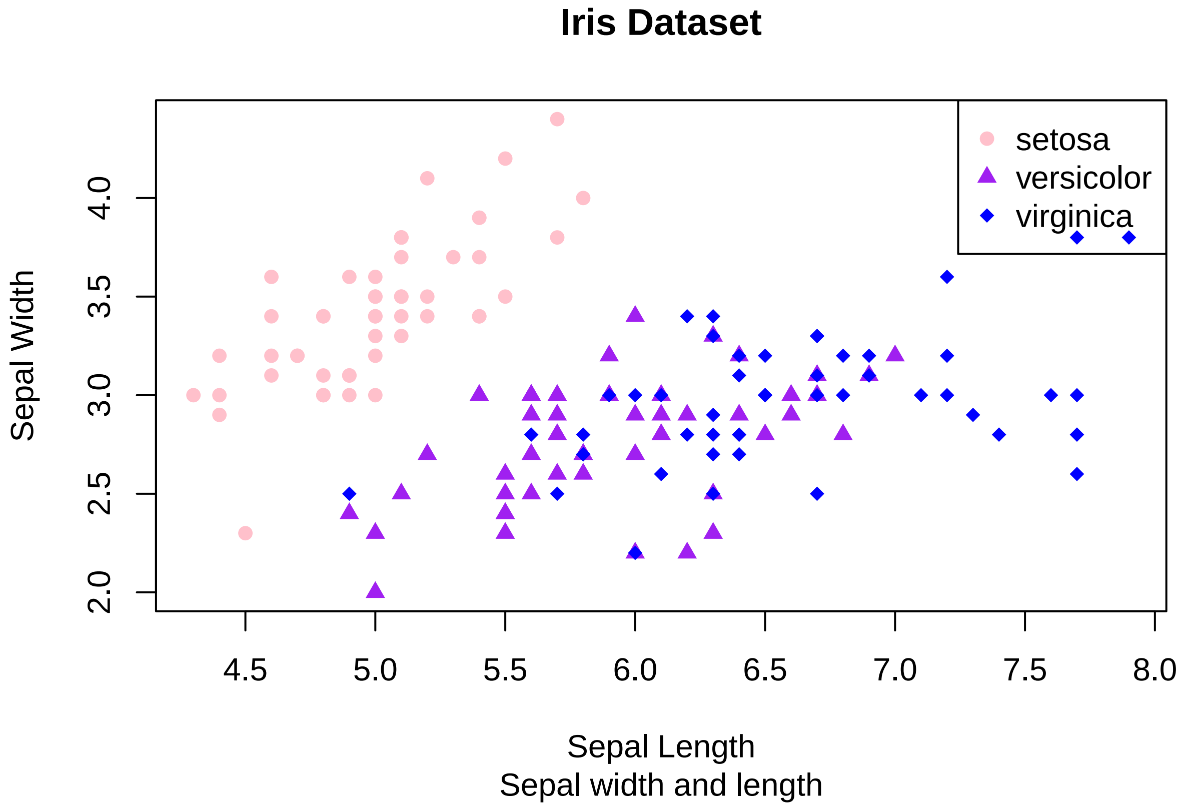
```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
## 95           5.6         2.7          4.2         1.3 versicolor
## 96           5.7         3.0          4.2         1.2 versicolor
## 97           5.7         2.9          4.2         1.3 versicolor
## 98           6.2     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

```
#output
#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 scatter_plot

data(iris)

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

```
colors <- c("setosa" = "pink", "versicolor" = "purple", "virginica" = "blue")
symbols <- c("setosa" = 16, "versicolor" = 17, "virginica" = 18)

# Create scatterplot
plot(iris$Sepal.Length, iris$Sepal.Width,
     col = colors[iris$Species],
     pch = symbols[iris$Species],
     xlab = "Sepal Length",
     ylab = "Sepal Width",
     main = "Iris Dataset",
     sub = "Sepal width and length")

legend("topright",
       legend = levels(iris$Species),
       col = colors,
       pch = symbols)
```



```
#f. Interpret the result.
#Setosa species has wider sepal but shorter in length, the versicolor is in between or in average in  s
#The clear separation among clusters suggests that Sepal.Length and Sepal.Width can help distinguish sp




#7 import alexa.xlsx

library(readxl)
alexa <- read_excel("alexa-file.xlsx")
```

```r
# Show first rows
head(alexa)
```

```
## # A tibble: 6 x 5
##   rating date                variation   verified_reviews               feedback
##    <dbl> <dttm>              <chr>       <chr>                             <dbl>
## 1      5 2018-07-30 00:00:00 Black Dot   It works great!!                      1
## 2      5 2018-07-30 00:00:00 Black  Dot  PHENOMENAL                            1
## 3      4 2018-07-30 00:00:00 Black Dot   I used it to control my smart~        1
## 4      5 2018-07-30 00:00:00 White  Plus Excellent device                      1
## 5      3 2018-07-30 00:00:00 White Show  Very convenient                       1
## 6      4 2018-07-29 00:00:00 White Dot   Great quality!                        1
```

```r
alexa$variation <- gsub("\\s+", " ", alexa$variation)
alexa$variation <- trimws(alexa$variation)

#a Rename the variants
alexa$variation <- gsub("Black Dot", "Black - Dot", alexa$variation)
alexa$variation <- gsub("White Dot", "White - Dot", alexa$variation)
alexa$variation
```

```
##  [1] "Black - Dot" "Black - Dot" "Black - Dot" "White Plus"  "White Show"
##  [6] "White - Dot" "Black Spot"  "Black Plus"  "White Plus"  "White Spot"
```

```r
#output
#[1] "Black - Dot" "Black - Dot" "Black - Dot" "White Plus"  "White Show"  "White - Dot"
#[7] "Black Spot"  "Black Plus"  "White Plus"  "White Spot"


# Count each variation
install.packages("dplyr")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.5'
## (as 'lib' is unspecified)
```

```r
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
```

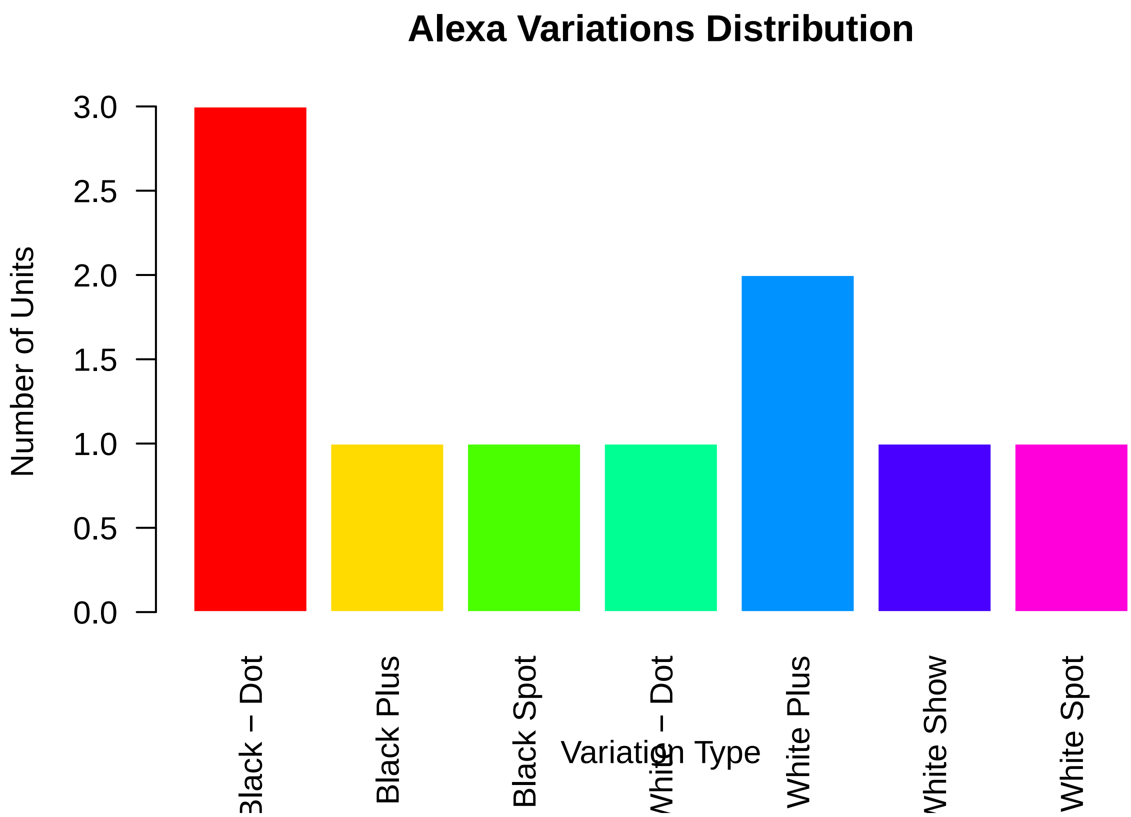
```r
variations <- alexa %>%
  count(variation)

# Display result
print(variations)
```

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

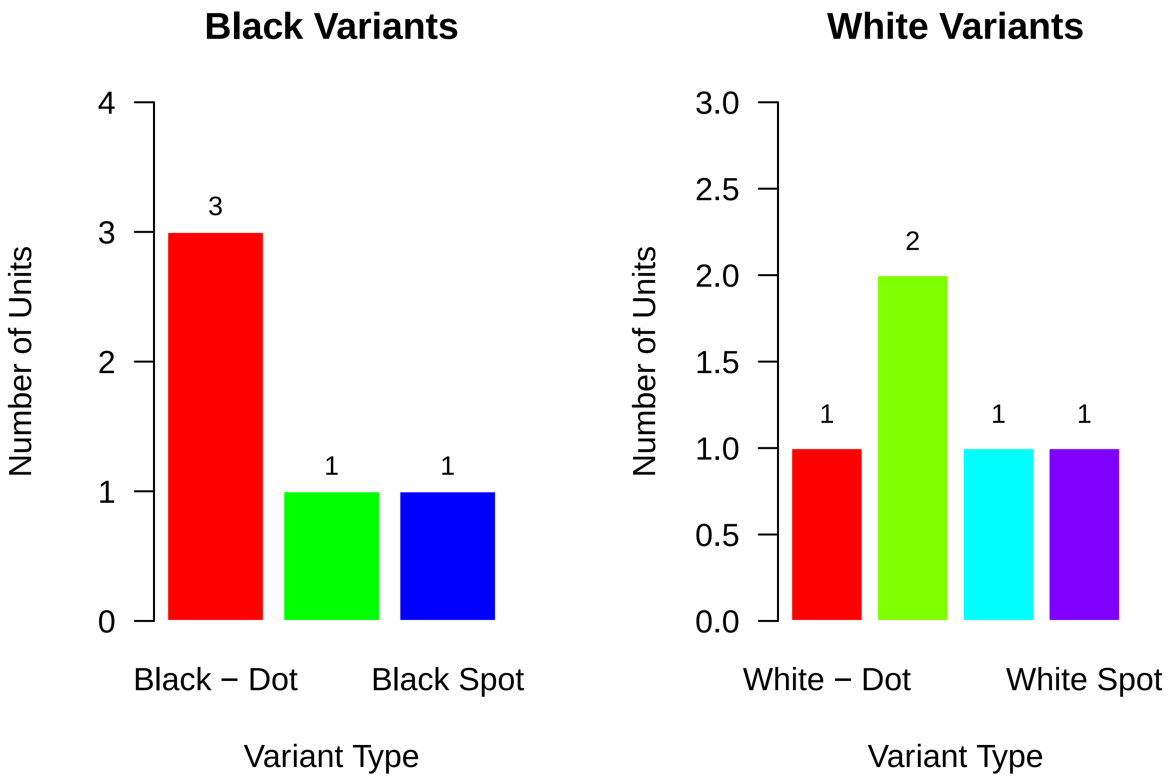
```r
# Save the object to an RData file
save(variations, file = "variations.RData")

# Load the saved data (example)
load("variations.RData")
variations
```

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

```r
#output
#variation       n
#  <chr>       <int>
#1 Black - Dot     3
#2 Black Plus      1
#3 Black Spot      1
#4 White - Dot     1
#5 White Plus      2
#6 White Show      1
#7 White Spot      1

#C
barplot(variations$n,
        names.arg = variations$variation,
        main = "Alexa Variations Distribution",
        xlab = "Variation Type",
        ylab = "Number of Units",
        col = rainbow(nrow(variations)),
        las = 2,
        border = "white")
```



```
#d

load("variations.RData")

# Separate Black and White variants
black <- variations[grep("Black", variations$variation), ]
white <- variations[grep("White", variations$variation), ]

par(mfrow = c(1, 2), mar = c(5, 5, 4, 2))

#black
bar_black <- barplot(black$n,
                     names.arg = black$variation,
                     main = "Black Variants",
                     xlab = "Variant Type",
                     ylab = "Number of Units",
                     col = rainbow(nrow(black)),
                     ylim = c(0, max(black$n) + 1),
                     border = "white",
                     las = 1)

text(x = bar_black, y = black$n + 0.2, labels = black$n, cex = 0.8, col = "black")
#white
bar_white <- barplot(white$n,
                     names.arg = white$variation,
                     main = "White Variants",
                     xlab = "Variant Type",
                     ylab = "Number of Units",
                     col = rainbow(nrow(white)),
                     ylim = c(0, max(white$n) + 1),
                     border = "white",
                     las = 1)

text(x = bar_white, y = white$n + 0.2, labels = white$n, cex = 0.8, col = "black")
```



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