RWorksheet_Aposaga#4b

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#1

```r
vectorA <- c(1,2,3,4,5)
patmat <- matrix(0, nrow = 5, ncol = 5)

for (i in 1:5) {
  for (j in 1:5) {
    patmat[i, j] <- vectorA[(j + i - 2) %% 5 + 1]
  }
}
cat("Pattern Matrix:\n")
```

```
## Pattern Matrix:
```

```r
print(patmat)
```

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

```r
zero_matrix <- matrix(0, nrow = 5, ncol = 5)
cat("\nZero Matrix:\n")
```

```
##
## Zero Matrix:
```

```r
print(zero_matrix)
```

```
##      [,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

```r
n <- 4


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

```
## *
## **
## ***
## ****
```

#3

```r
first <- as.integer(readline(prompt = "Enter starting number for fibonacci sequence(up to 500): "))
```

```
## Enter starting number for fibonacci sequence(up to 500):
```

```r
fibonacci <- c(0,1)

repeat {
  next_fib <- sum(tail(fibonacci, 2))
  if (next_fib > 500) {
    break
  }
  fibonacci <- c(fibonacci, next_fib)
}

result <- fibonacci[fibonacci >= first]
cat("Fibonacci sequence from", first, "up to 500:", result, "\n")
```

```
## Fibonacci sequence from NA up to 500: NA NA NA NA NA NA NA NA NA NA NA NA NA NA NA
```

#4a

```r
SHG <- read.csv("SHG.csv", header = TRUE, sep = ",")
SHG[1:6,]
```

```
##   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
```

#4b

```
male_sub <- subset(SHG, Gender == "M")
female_sub <- subset(SHG, Gender == "F")

num_male <- nrow(male_sub)
num_female <- nrow(female_sub)

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

```
## Number of Male observations: 14
```

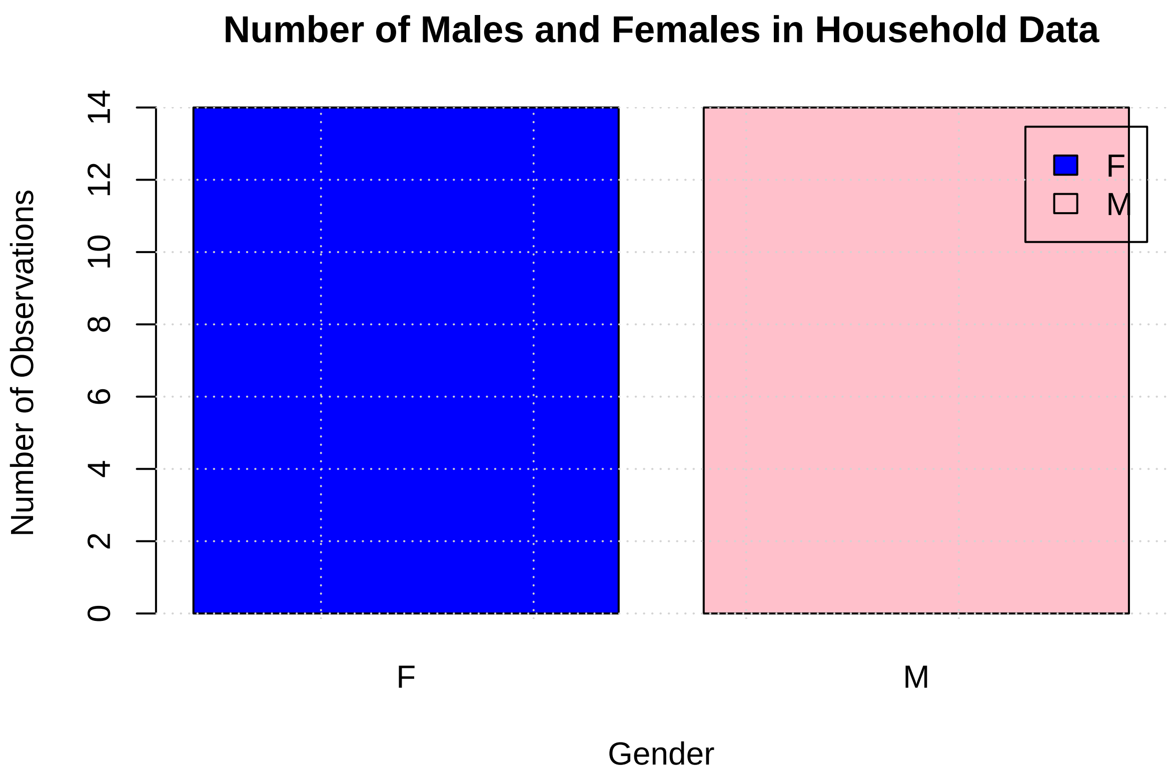
```
cat("Number of Female observations:", num_female, "\n")
```

```
## Number of Female observations: 14
```

#4c

```
gender_count <- table(SHG$Gender)
bar_colors <- c("blue", "pink")  # Colors for male and female
barplot(gender_count,
        main = "Number of Males and Females in Household Data",
        xlab = "Gender",
        ylab = "Number of Observations",
        col = bar_colors,
        legend = rownames(gender_count),
        beside = TRUE)

# Add grid lines
grid(nx = NULL, ny = NULL)
```



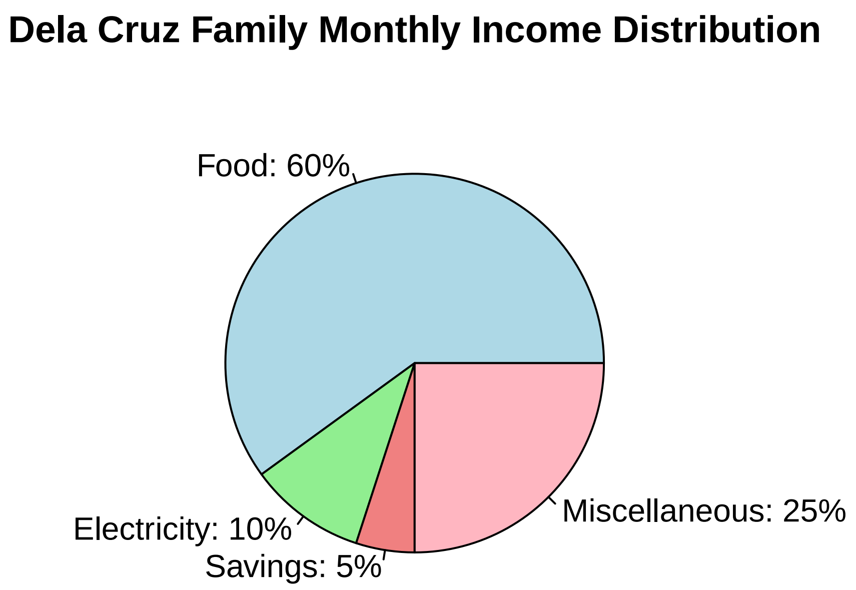
#5

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

percent_labels <- paste0(names(spending), ": ", round(spending / sum(spending) * 100, 1), "%")


colors <- c("lightblue", "lightgreen", "lightcoral", "lightpink")

pie(spending,
    labels = percent_labels,
    col = colors,
    main = "Dela Cruz Family Monthly Income Distribution"
)
```



#6a

```
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 ...
```

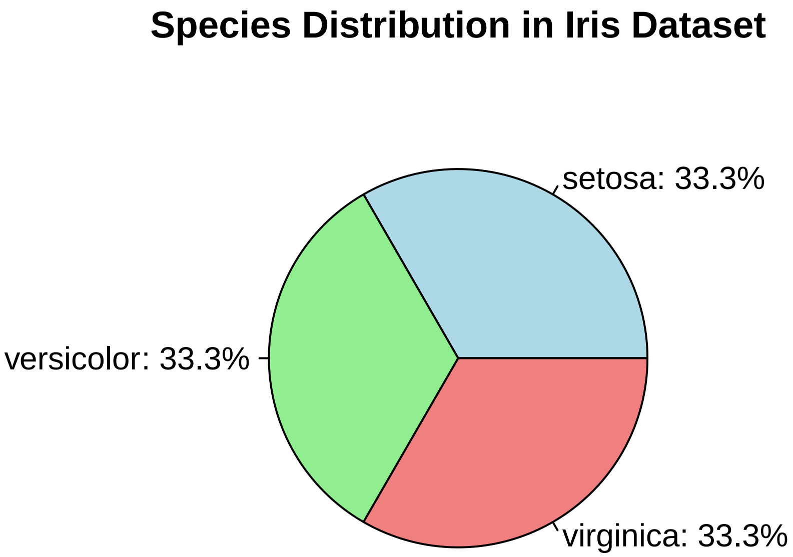
#6b

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

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

#6c

```
species_counts <- table(iris$Species)
pie(species_counts,
    labels = paste(names(species_counts), ": ", round(species_counts / sum(species_counts) * 100, 1), "
    col = c("lightblue", "lightgreen", "lightcoral"),
    main = "Species Distribution in Iris Dataset"
)
```



#6d

```
setosa_subset <- tail(subset(iris, Species == "setosa"), 6)
versicolor_subset <- tail(subset(iris, Species == "versicolor"), 6)
virginica_subset <- tail(subset(iris, Species == "virginica"), 6)

setosa_subset
```

```
##    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_subset
```

```
##     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
```

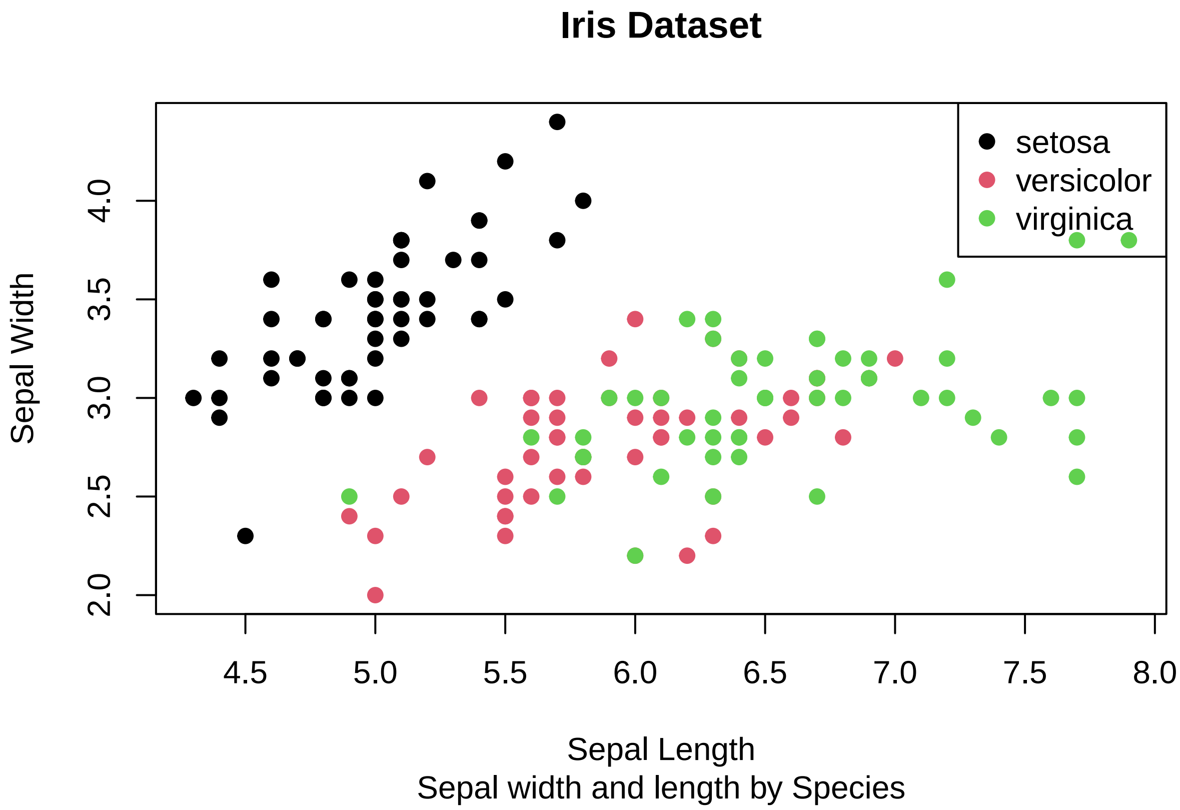
```
virginica_subset
```

```
##     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
```

#6e

```
plot(iris$Sepal.Length, iris$Sepal.Width,
     col = iris$Species,
     pch = 19,
     xlab = "Sepal Length",
     ylab = "Sepal Width",
     main = "Iris Dataset",
     sub = "Sepal width and length by Species"
)

legend("topright", legend = levels(iris$Species),
       col = 1:3, pch = 19)
```



#6f #For part f, after making the scatterplot, you can explain what you see by looking at how the points are #grouped for each species. Notice if certain species have bigger or smaller sepals (the lengths and widths of #the flower parts). See if each type of flower is grouped together or spread out differently, which might #tell you how their sepal sizes vary from one species to another.

#7a

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


alexa_data$variation <- gsub("Black\\s+Dot", "Black Dot", alexa_data$variation)
alexa_data$variation <- gsub("Black\\s+Plus", "Black Plus", alexa_data$variation)
alexa_data$variation <- gsub("Black\\s+Show", "Black Show", alexa_data$variation)
alexa_data$variation <- gsub("Black\\s+Spot", "Black Spot", alexa_data$variation)
alexa_data$variation <- gsub("White\\s+Dot", "White Dot", alexa_data$variation)
alexa_data$variation <- gsub("White\\s+Plus", "White Plus", alexa_data$variation)
alexa_data$variation <- gsub("White\\s+Show", "White Show", alexa_data$variation)
alexa_data$variation <- gsub("White\\s+Spot", "White Spot", alexa_data$variation)


table(alexa_data$variation)
```

```
##
##                         Black                    Black Dot
##                           261                          516
##                    Black Plus                   Black Show
##                            270                          265
##                     Black Spot              Charcoal Fabric
##                            241                          430
## Configuration: Fire TV Stick         Heather Gray Fabric
##                            350                          157
##                     Oak Finish             Sandstone Fabric
##                             14                           90
##                  Walnut Finish                        White
##                              9                           91
##                      White Dot                   White Plus
##                            184                           78
##                     White Show                   White Spot
##                             85                          109
```

#7b

```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_count <- alexa_data %>%
  count(variation, name = "Total")


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


print(variations_count)
```

```
## # A tibble: 16 x 2
##    variation                    Total
##    <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
```

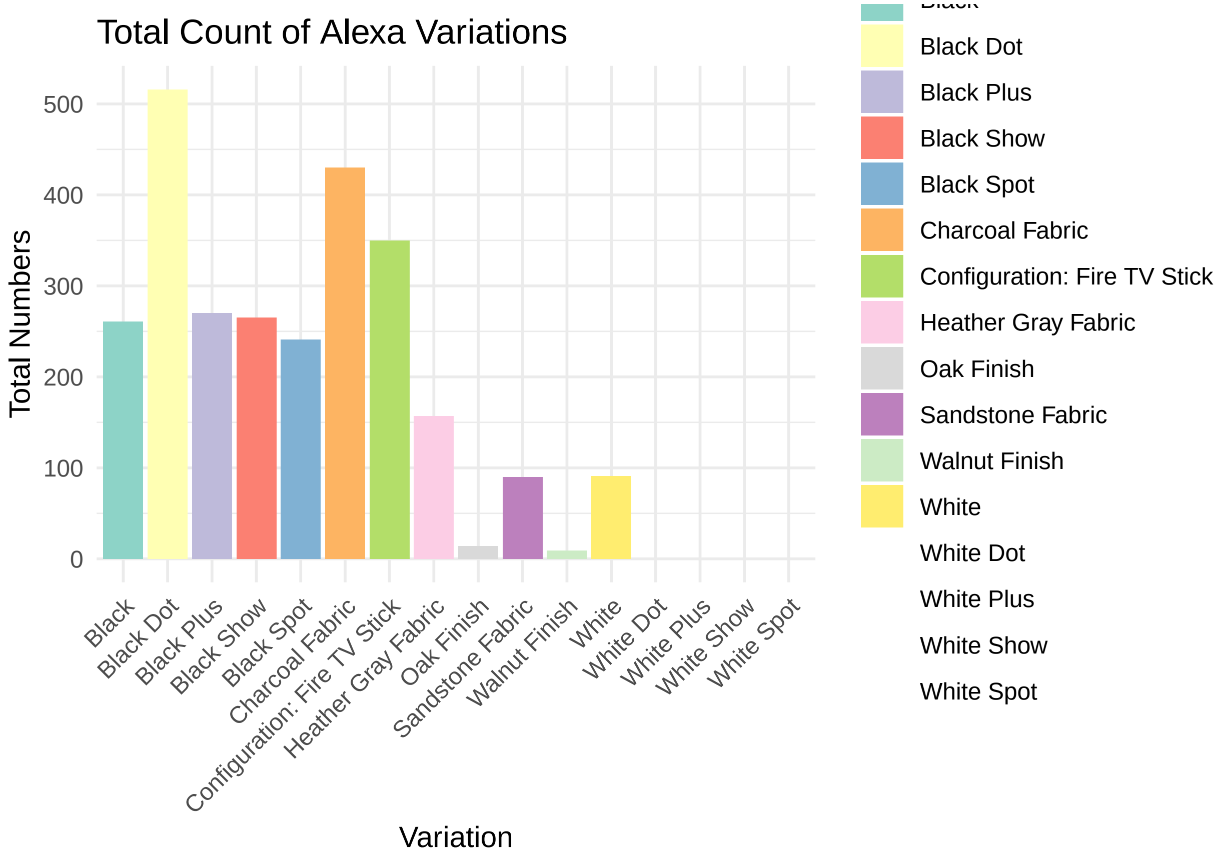
#7c

```
library(ggplot2)

load("variations.RData")


ggplot(variations_count, aes(x = variation, y = Total, fill = variation)) +
  geom_bar(stat = "identity") +
  ggtitle("Total Count of Alexa Variations") +
  xlab("Variation") +
  ylab("Total Numbers") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  scale_fill_brewer(palette = "Set3")
```

```
## Warning in RColorBrewer::brewer.pal(n, pal): n too large, allowed maximum for palette Set3 is 12
## Returning the palette you asked for with that many colors
```



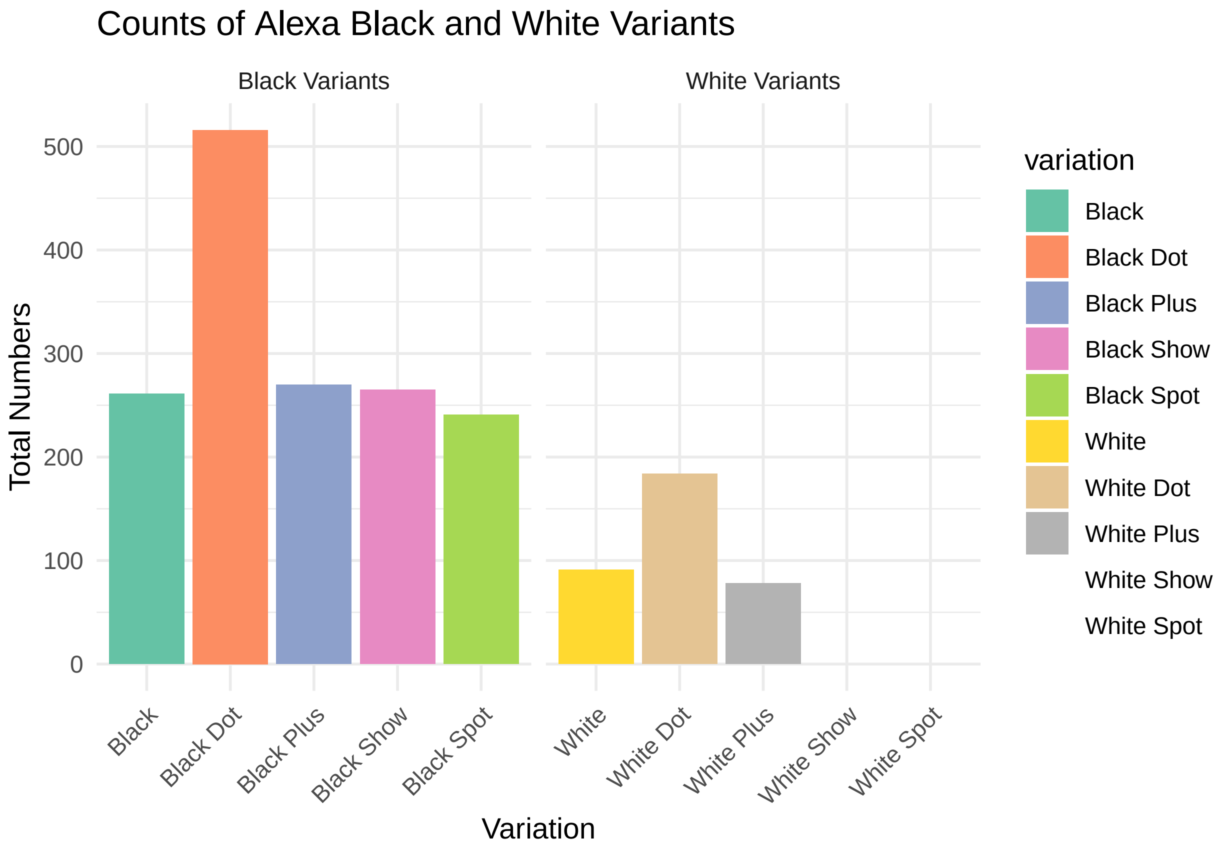
#7d

```r
variations_count$Category <- ifelse(grepl("Black", variations_count$variation), "Black Variants",
                                    ifelse(grepl("White", variations_count$variation), "White Variants"

black_white_variants <- variations_count %>% filter(!is.na(Category))


ggplot(black_white_variants, aes(x = variation, y = Total, fill = variation)) +
  geom_bar(stat = "identity") +
  facet_wrap(~ Category, scales = "free_x") +
  ggtitle("Counts of Alexa Black and White Variants") +
  xlab("Variation") +
  ylab("Total Numbers") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  scale_fill_brewer(palette = "Set2")
```

```
## Warning in RColorBrewer::brewer.pal(n, pal): n too large, allowed maximum for palette Set2 is 8
## Returning the palette you asked for with that many colors
```


Counts of Alexa Black and White Variants
Black Variants
White Variants
Total Numbers
Black
Black Dot
Black Plus
Black Show
Black Spot
White
White Dot
White Plus
White Show
White Spot
Variation
variation
Black
Black Dot
Black Plus
Black Show
Black Spot
White
White Dot
White Plus
White Show
White Spot