Rworksheet_Rabago#4b

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1.

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


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


print(matrix_result)
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    2    0    0    0
## [3,]    0    0    3    0    0
## [4,]    0    0    0    4    0
## [5,]    0    0    0    0    5
```

2.

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

for (i in vectorB){
  cat(rep("*",i), "\n")
}
```

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

3

```
fibonacci_sequence <- function(start) {
  a <- 0
  b <- 1
  fib_sequence <- c()

  repeat {
    fib <- a + b
    a <- b
    b <- fib
```

```
    if (fib > 500) {
      break
    }


    if (fib >= start) {
      fib_sequence <- c(fib_sequence, fib)
    }
  }

  return(fib_sequence)
}


start_input <- 8
if (start_input <= 0) {
  cat("Please enter a number greater than 0.\n")
} else {

  result <- fibonacci_sequence(start_input)
  cat("Fibonacci sequence starting from", start_input, "up to 500:\n")
  print(result)
}
```

```
## Fibonacci sequence starting from 8 up to 500:
## [1]   8  13  21  34  55  89 144 233 377
```

4.a.

```
datas <- read.csv("/cloud/project/Worksheet4/Household Data.csv")
```

4.b.

```
male <- subset(datas, Gender == "M")
male
```

```
##    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(datas, Gender == "F")
female
```

```
##    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
```

```
numbermale <- nrow(male)
numberfemale <- nrow(female)
cat("Number of observations for Male:", numbermale, "\n")
```

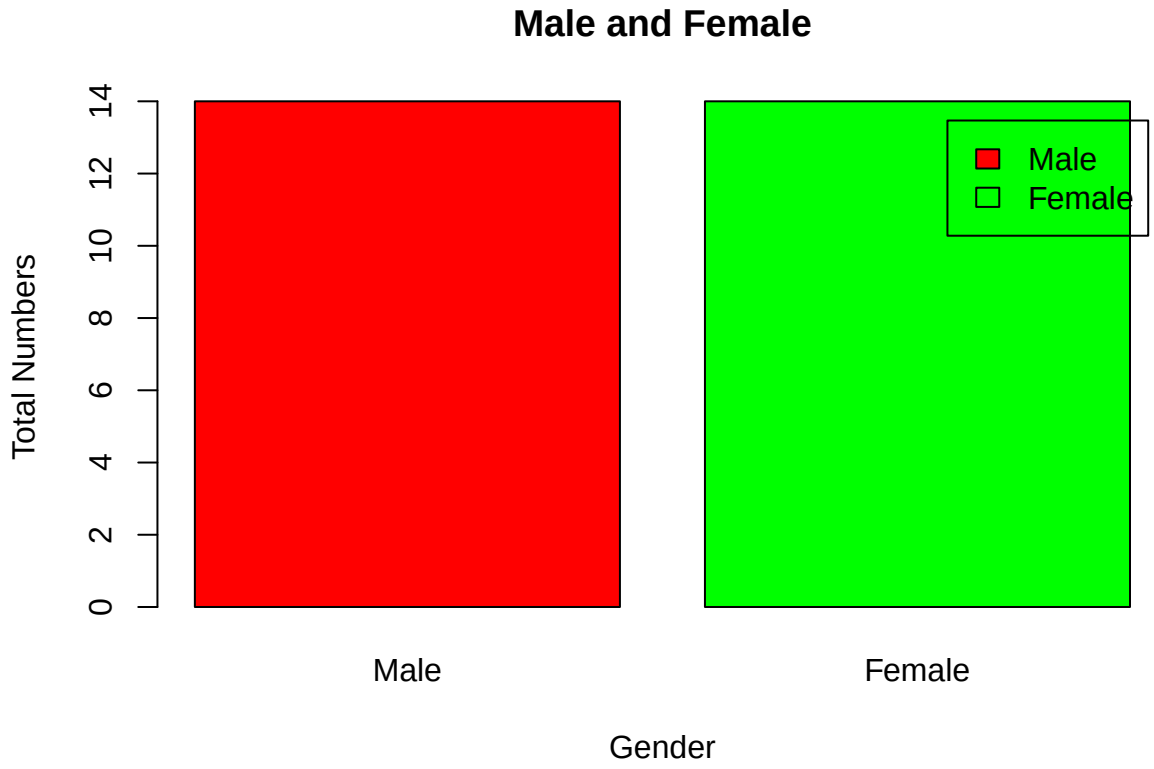
```
## Number of observations for Male: 14
```

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

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

4.c.

```
Plotting <- c(numbermale,numberfemale)
names(Plotting) <- c("Male", "Female")
barplot(Plotting, main = "Male and Female", xlab = "Gender", ylab = "Total Numbers", col = c("red", "gr
```



5

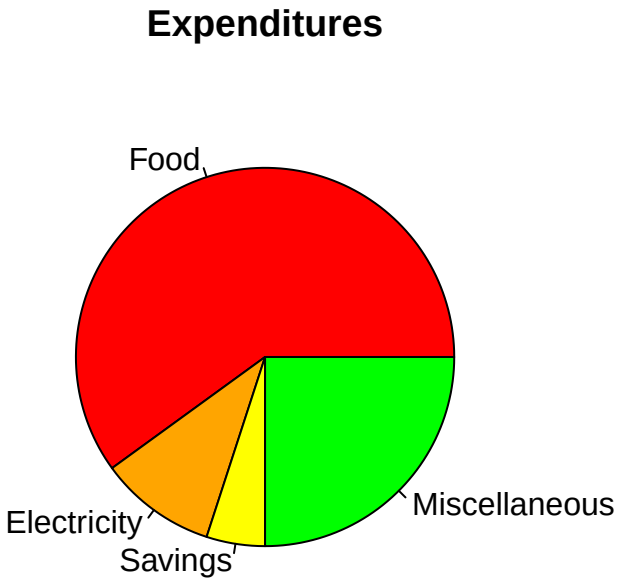
```
bills <- c("Food", "Electricity", "Savings", "Miscellaneous")
```

```r
values <- c(60, 10, 5, 25)

Bills <- matrix(values, nrow = 1, ncol = length(bills), dimnames = list(NULL, bills))
Bills
```

```
##      Food Electricity Savings Miscellaneous
## [1,]   60          10       5            25
```

```r
Plotters <- pie(values, labels = c("Food", "Electricity", "Savings", "Miscellaneous"),col = c("red", "o
```



6.a.

```r
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 ...
```

6.b.

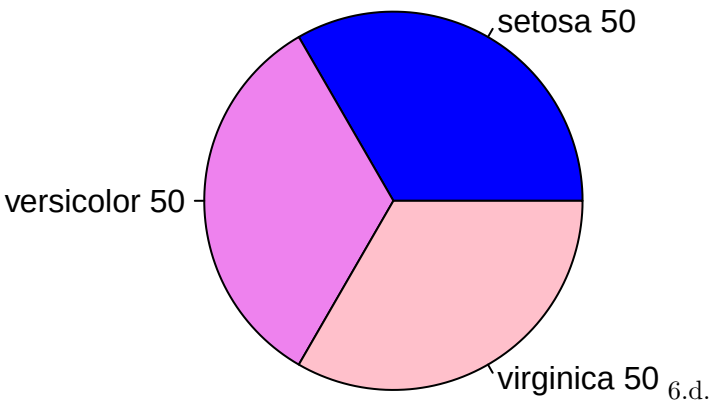
```r
meanvalues <- colMeans(iris[, 1:4])
meanvalues
```

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

6.c.

```r
species_count <- table(iris$Species)

pie(species_count,
    main = "Species Distribution",
    col = c("blue", "violet", "pink"),
    labels = paste(names(species_count),species_count))
```



6.d.

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

last6_setosa <- tail(setosa)
last6_versicolor <- tail(versicolor)
last6_virginica <- tail(virginica)

cat("Last six rows of Setosa:\n")
```

```
## Last six rows of Setosa:
```

```
print(last6_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
```

```
cat("\nLast six rows of Versicolor:\n")
```

```
##
## Last six rows of Versicolor:
```

```
print(last6_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
```

```
cat("\nLast six rows of Virginica:\n")
```

```
##
## Last six rows of Virginica:
```

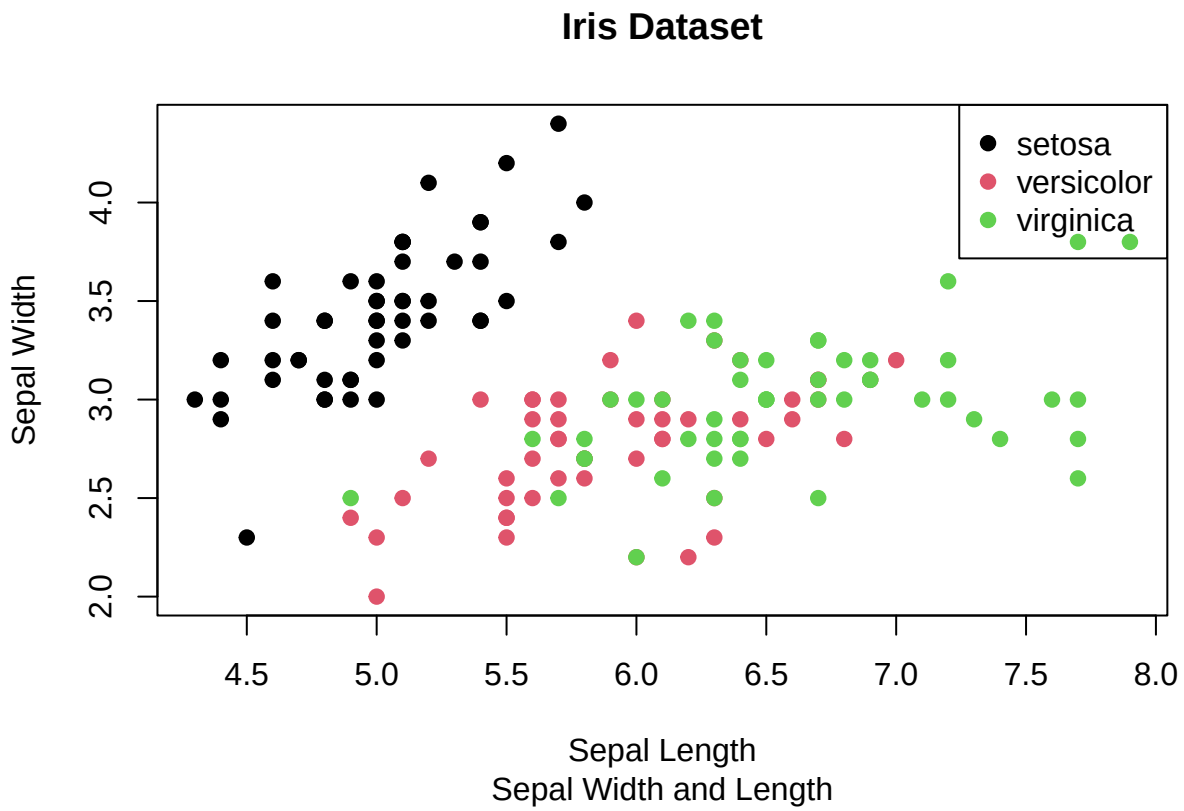
```
print(last6_virginica)
```

```
##     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
```

6.e.

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


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



6.f.

-The scatterplot shows the relationship between sepal width and length for different iris flower species. Versicolor and Virginica overlap a lot and have similar sepal sizes. However, Setosa is easy to identify because it has smaller sepal sizes than the other two species.

7.a.

```
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
```

7.b.

```
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
```

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


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

```r
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
```

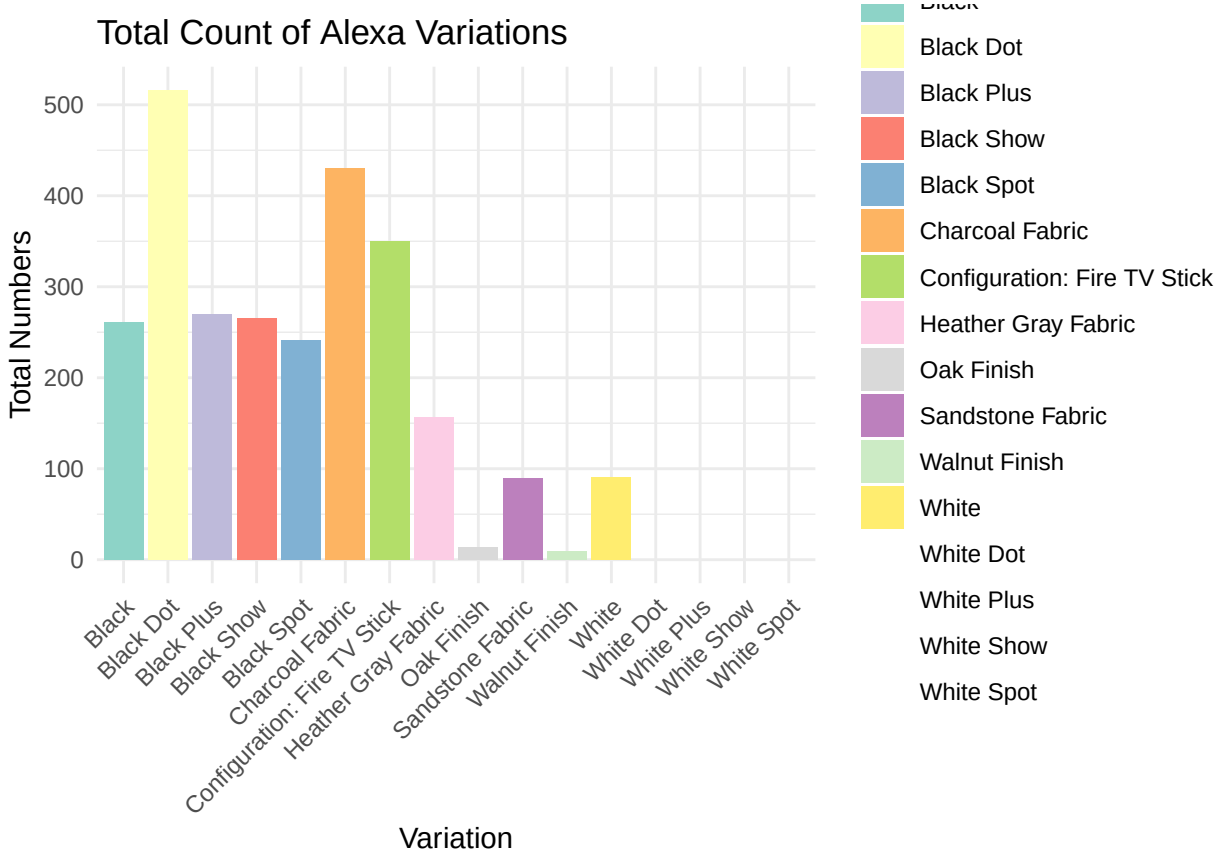
7.c.

```r
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
```



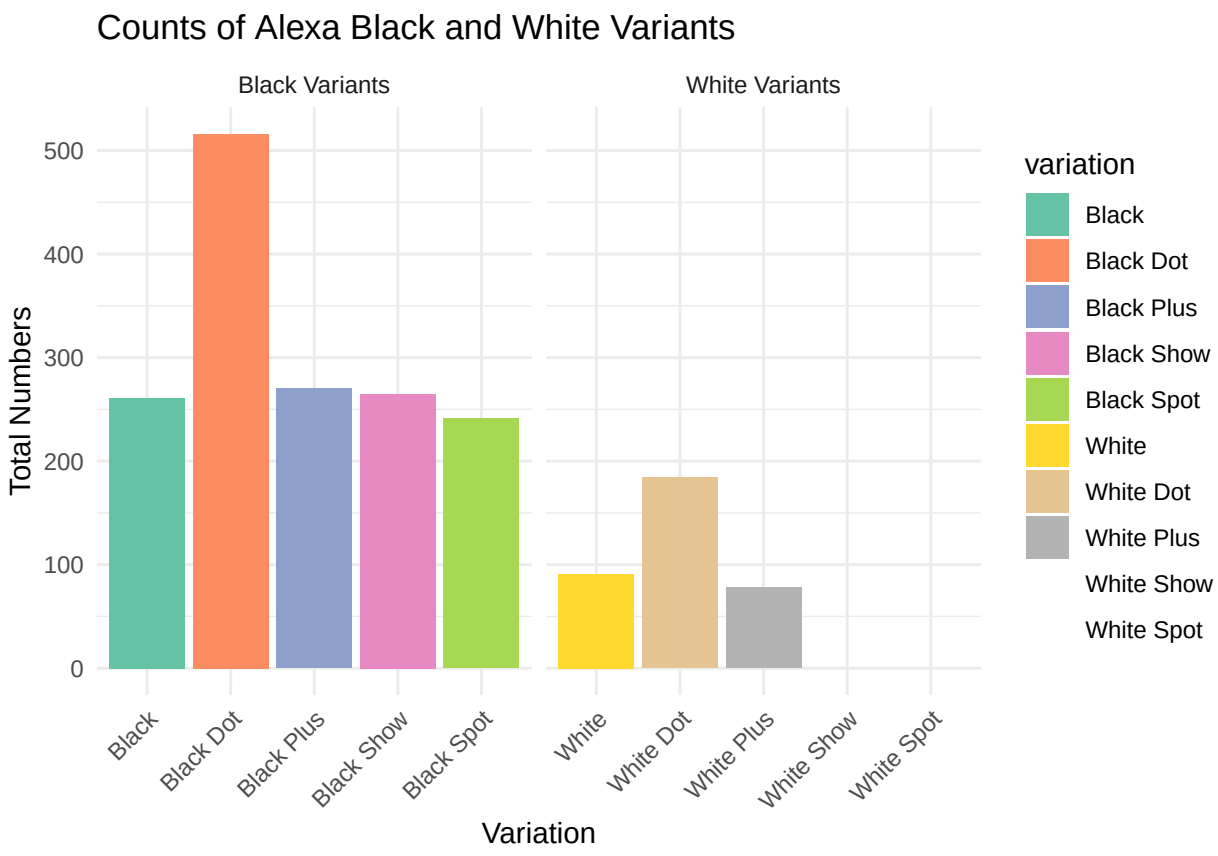
7.d.

```
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
500
400
300
200
100
0
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