RWorkseet_Trongoy#4b

George Eduard Trongoy

2024-10-30

.

```r
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 - vectorA[j])
  }
}

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.

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

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

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

3.

```r
start_num <- as.integer(readline(prompt="Enter the starting number for the Fibonacci sequence: "))
```

```
## Enter the starting number for the Fibonacci sequence:
```

```r
a <- 0
b <- 1
if (!is.na(start_num) < 0) {
```

```
1
cat("Please enter a non-negative starting number.\n")
} else {
repeat {
if (!is.na(start_num) && a >= start_num) {
cat(a, "\n")
}
temp <- a + b
a <- b
b <- temp
if (!is.na(start_num) && a > 500) {
break
}
}
}
```

```
## Please enter a non-negative starting number.
```

4. a.

```
library(readxl)
Shoesizes <-read_xlsx("customerdata.xlsx")
```

```
## New names:
## * `` -> `...1`
```

```
head(Shoesizes)
```

```
## # A tibble: 6 x 4
##   ...1  Shoe_Size Height Gender
##   <chr>     <dbl>  <dbl> <chr>
## 1 1           6.5   66   F
## 2 2           9     68   F
## 3 3           8.5   64.5 F
## 4 4           8.5   65   F
## 5 5          10.5   70   M
## 6 6           7     64   F
```

b.

```
male_data <- subset(Shoesizes, Gender == "M")
female_data <- subset(Shoesizes, Gender == "F")

num_males <- nrow(male_data)
num_females <- nrow(female_data)

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

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

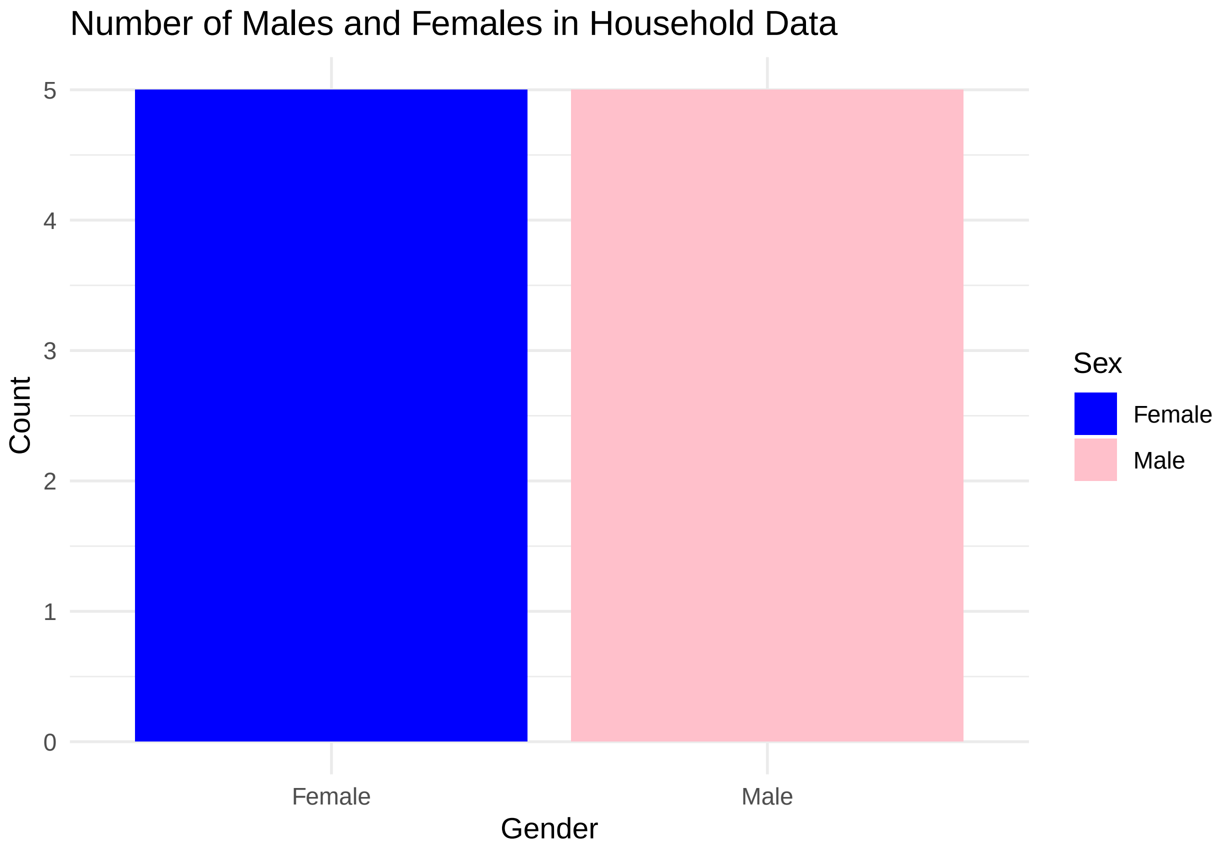
```
cat("Number of observations for Female: ", num_females, "\n")
```

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

c.

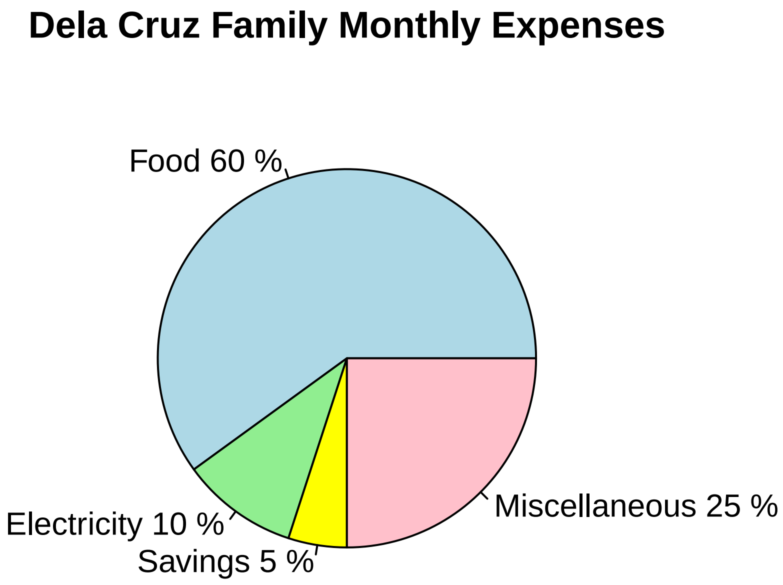
```
library(ggplot2)

HouseHoldData <-read.csv("Householddata.csv")
```

```r
ggplot(HouseHoldData, aes(x=Sex, fill=Sex)) +
  geom_bar() +
  ggtitle("Number of Males and Females in Household Data") +
  xlab("Gender") +
  ylab("Count") +
  scale_fill_manual(values = c("blue", "pink")) +
  theme_minimal()
```



5.

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

percentages <- round(100 * expenses / sum(expenses), 1)

labels <- paste(names(expenses), percentages, "%")

colors <- c("lightblue", "lightgreen", "yellow", "pink")

pie(expenses, labels = labels, col = colors, main = "Dela Cruz Family Monthly Expenses")
```



6.

```
data(iris)
```

a. The output shows number of variables and objects, and rows and columns

```
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.

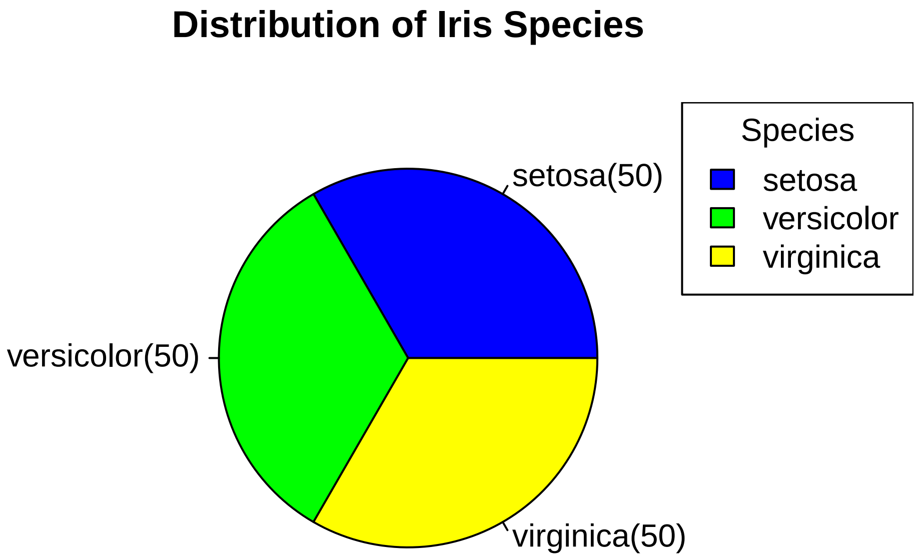
```
means <- colMeans(iris[, c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")])

means
```

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

c.

```
species_distribution <- table(iris$Species)

colors <- c("blue", "green", "yellow")
```

```
pie(species_distribution,
    main = "Distribution of Iris Species",
    col = colors,
    labels = paste(names(species_distribution), "(", species_distribution, ")", sep=""))

legend("topright", legend = names(species_distribution), fill = colors, title = "Species")
```



d.

```
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)
```

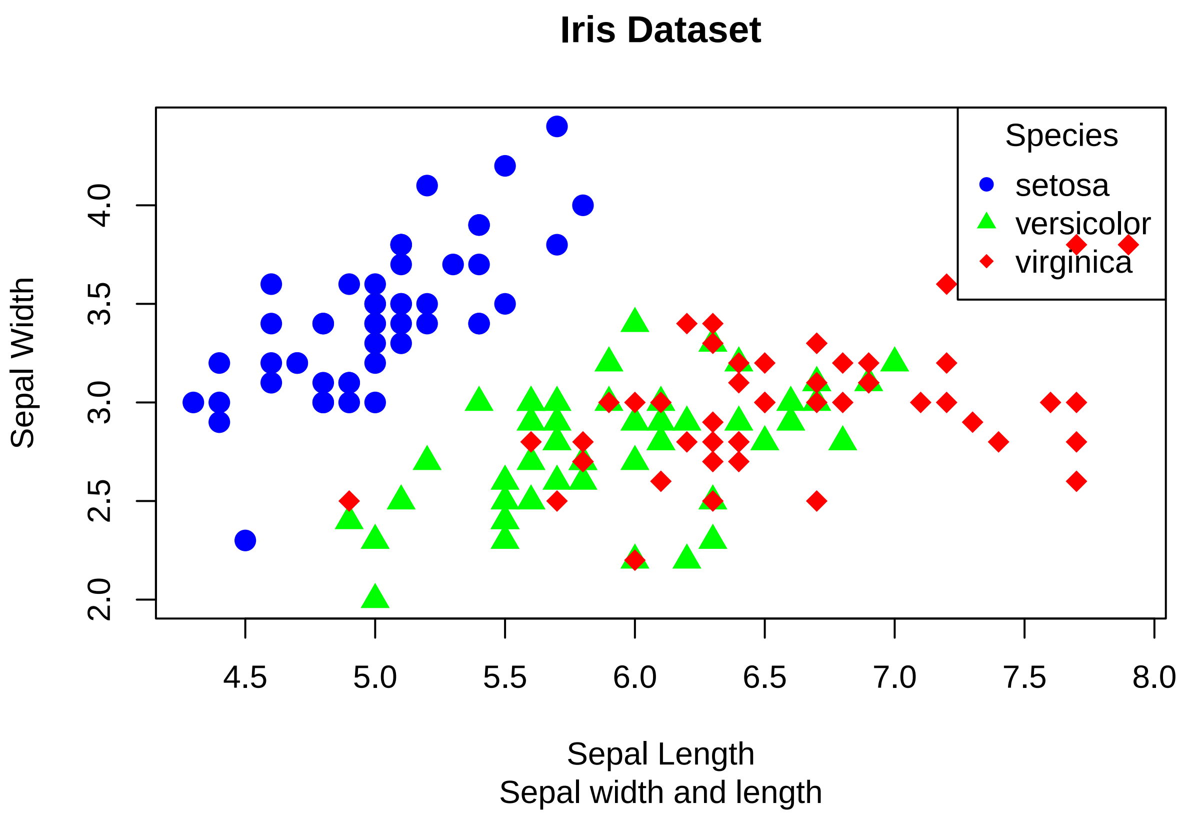
```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
## 95           5.6         2.7          4.2         1.3 versicolor
## 96           5.7         3.0          4.2         1.2 versicolor
## 97            5.7         2.9          4.2         1.3 versicolor
## 98            6.2   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

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

colors <- c("setosa" = "blue", "versicolor" = "green", "virginica" = "red")
symbols <- c("setosa" = 16, "versicolor" = 17, "virginica" = 18)

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",
     cex = 1.5)

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



f. The scatterplot shows clear separation between setosa and the other two species based on Sepal Length and Sepal Width. Setosa has distinctively shorter and wider sepals, forming a separate cluster. Versicolor and virginica overlap more, particularly in sepal width, but virginica tends to have longer sepals. Overall, there is a slight negative correlation, where longer sepals tend to be narrower, especially in virginica.

8.

a.

```
library(readxl)

alexa <- read_xlsx("alexa.xlsx")

alexa$variation <- gsub("Black  Show", "BlackShow", alexa$variation)

alexa$variation <- gsub("Black  Dot", "BlackDot", alexa$variation)

alexa$variation <- gsub("Black  Plus", "BlackPlus", alexa$variation)

alexa$variation <- gsub("Black  Spot", "BlackSpot", alexa$variation)

alexa$variation <- gsub("White  Show", "WhiteShow", alexa$variation)

alexa$variation <- gsub("White  Dot", "WhiteDot", alexa$variation)

alexa$variation <- gsub("White  Plus", "WhitePlus", alexa$variation)

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

b.

```
library(dplyr)
```

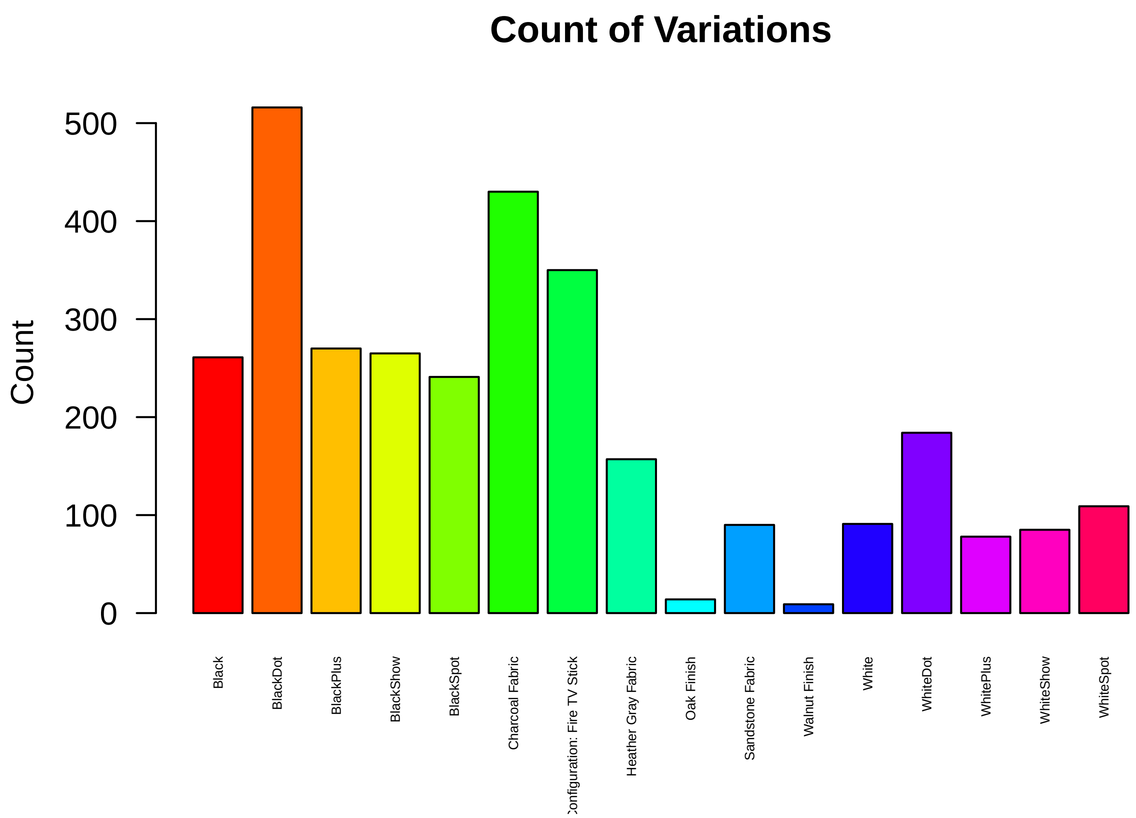
```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
variations.RData <- alexa %>%
  count (alexa$variation)

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

print(variations.RData)
```

```
## # A tibble: 16 x 2
##    `alexa$variation`                n
##    <chr>                        <int>
##  1 Black                          261
##  2 BlackDot                       516
##  3 BlackPlus                      270
##  4 BlackShow                      265
##  5 BlackSpot                      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 WhiteDot                       184
## 14 WhitePlus                       78
## 15 WhiteShow                       85
## 16 WhiteSpot                      109
```

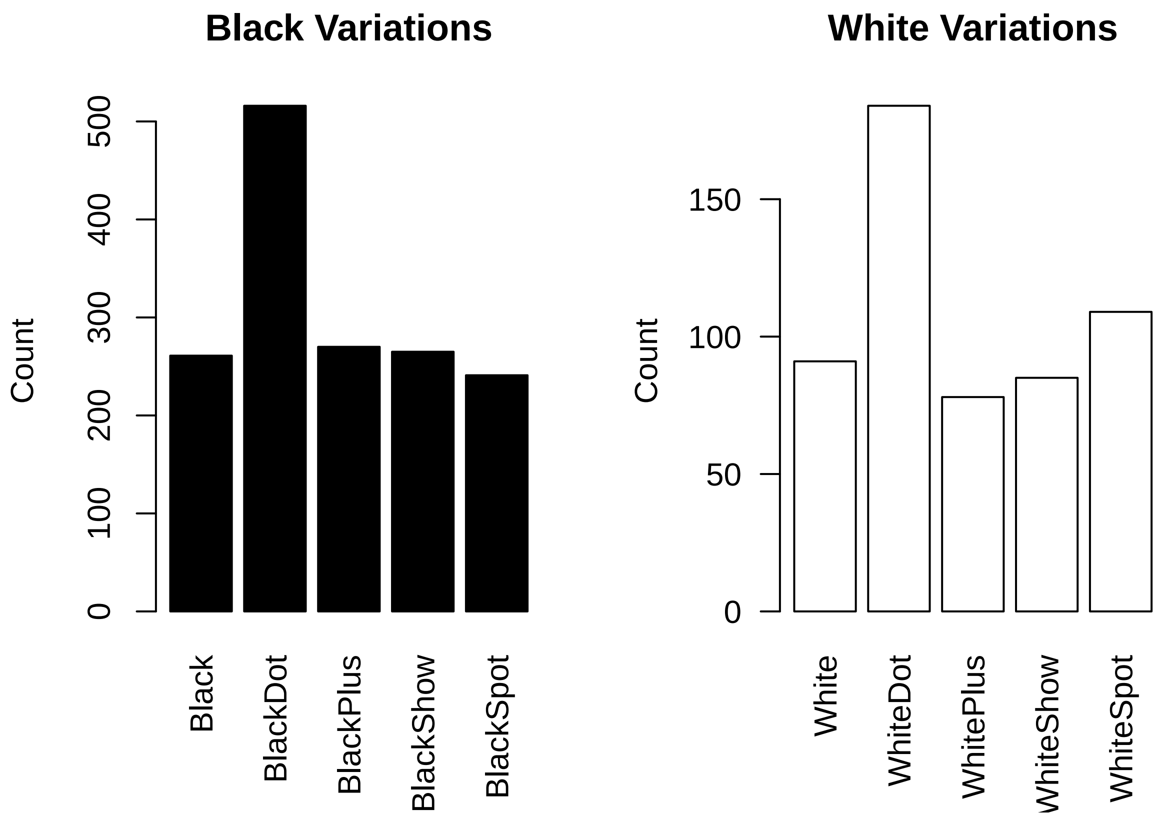
c.

```
barplot(
  variations.RData$n,
  names.arg = variations.RData$`alexa$variation`,
  cex.names = 0.4,
  main = "Count of Variations",
  ylab = "Count",
  col = rainbow(length(variations.RData$n)),
  border = "black",
  las = 2
)
```



d.

```
bv <- variations.RData %>%
  filter(grepl("^Black|^White", `alexa$variation`))

par(mfrow = c(1, 2))

barplot(
  bv$n[bv$`alexa$variation` %in% c("Black", "BlackPlus", "BlackShow", "BlackSpot", "BlackDot")],
  names.arg = bv$`alexa$variation`[bv$`alexa$variation` %in% c("Black", "BlackPlus", "BlackShow", "Blac
  las = 3,
  cex.names = 1,
  main = "Black Variations",
  ylab = "Count",
  col = "black",
  border = "black"
)

barplot(
  bv$n[bv$`alexa$variation` %in% c("White", "WhitePlus", "WhiteShow", "WhiteSpot", "WhiteDot")],
  names.arg = bv$`alexa$variation`[bv$`alexa$variation` %in% c("White", "WhitePlus", "WhiteShow", "Whit
  las = 2,
  cex.names = 1,
  main = "White Variations",
  ylab = "Count",
  col = "white",
  border = "black"
)
```


Black Variations
Count
0
100
200
300
400
500
Black
BlackDot
BlackPlus
BlackShow
BlackSpot
White Variations
Count
0
50
100
150
White
WhiteDot
WhitePlus
WhiteShow
WhiteSpot