RWorksheet_Calambro#4b

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#1

```
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:
```

```
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
```

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

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

```
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

```
n <- 4


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

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

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

#3

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

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

```
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

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

```
##   Shoe.size.1 Height.1 Gender.1 Shoe.size.2 Height.2 Gender.2
## 1         6.5     66.0        F        13.0       77        M
## 2         9.0     68.0        F        11.5       72        M
## 3         8.5     64.5        F         8.5       59        F
## 4         8.5     65.0        F         5.0       62        F
## 5        10.5     70.0        M        10.0       72        M
## 6         7.0     64.0        F         6.5       66        F
```

#4b

```
male_sub <- subset(SHG, Gender.1 == "M")
female_sub <- subset(SHG, Gender.1 == "F")

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

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

```
## Number of Male observations: 5
```

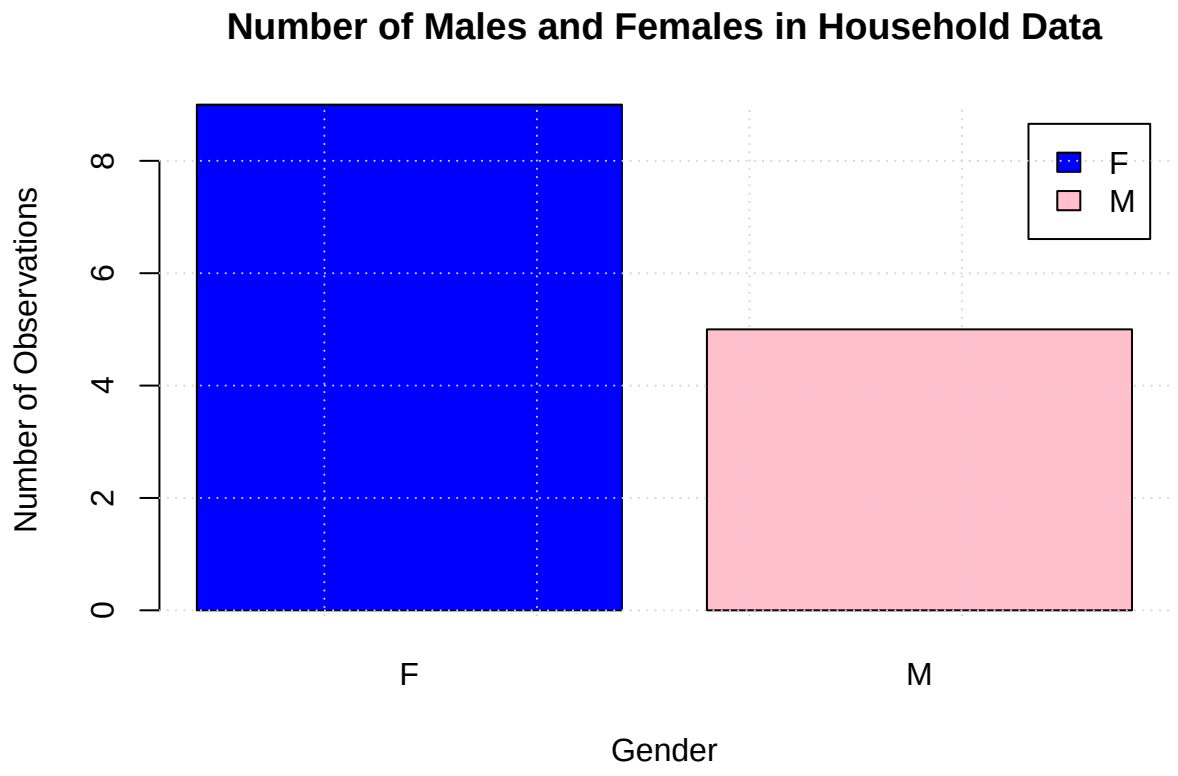
```
cat("Number of Female observations:", num_female, "\n")
```

```
## Number of Female observations: 9
```

#4c

```r
gender_count <- table(SHG$Gender.1)
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

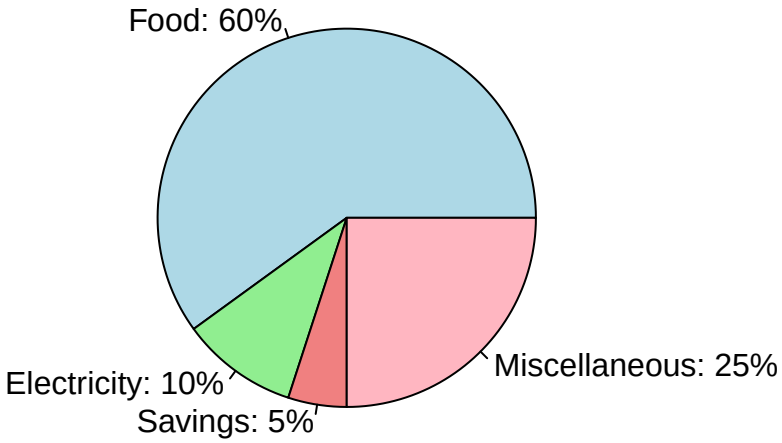
```r
spending <- c(Food = 60, Electricity = 10, Savings = 5, Miscellaneous = 25)

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"
)
```

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 ...
```

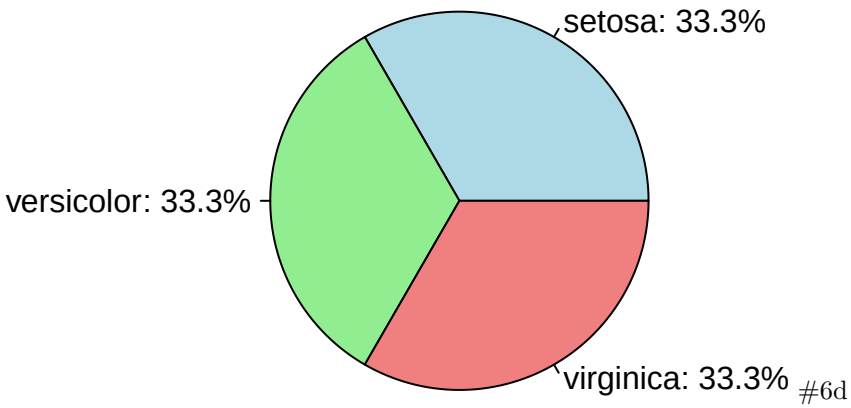
#6b

```
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
```

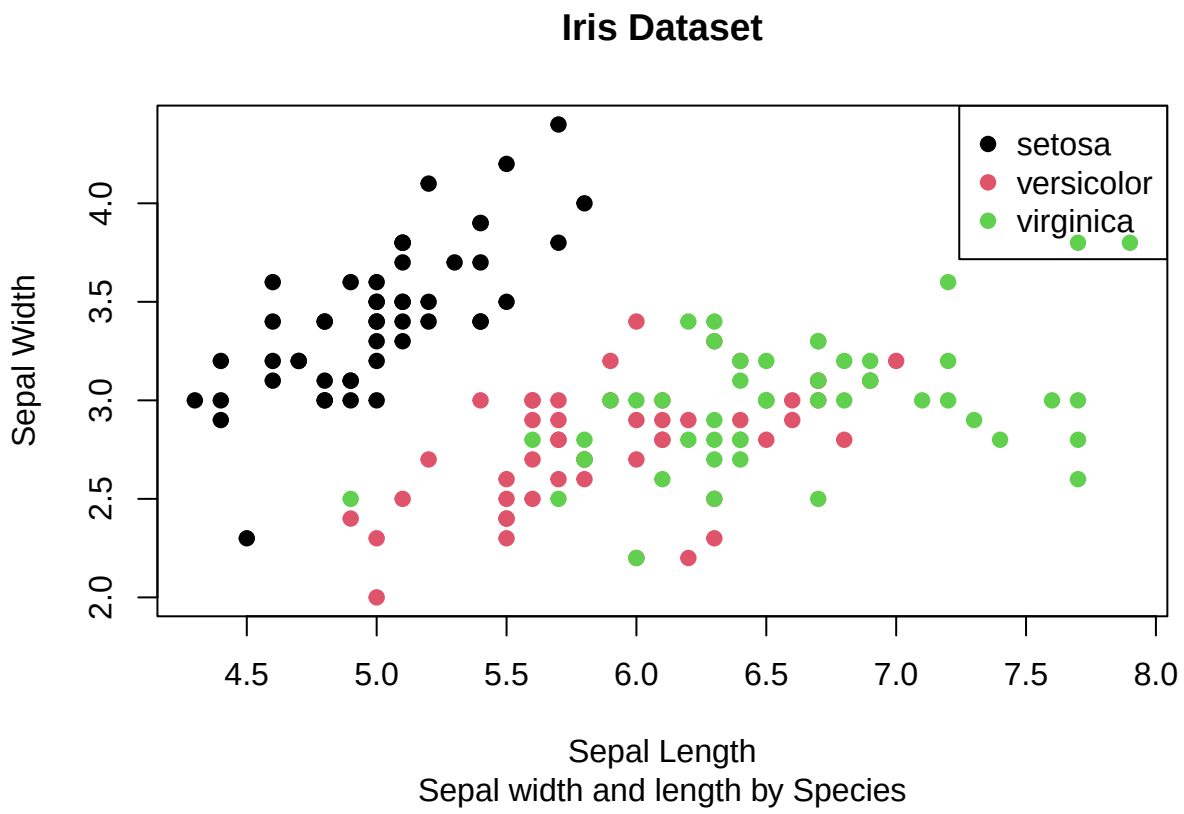
```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 145          6.7         3.3          5.7         2.5 virginica
## 146          6.7         3.0          5.2         2.3 virginica
## 147          6.3         2.5          5.0         1.9 virginica
## 148          6.5         3.0          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)
```

```r
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
```

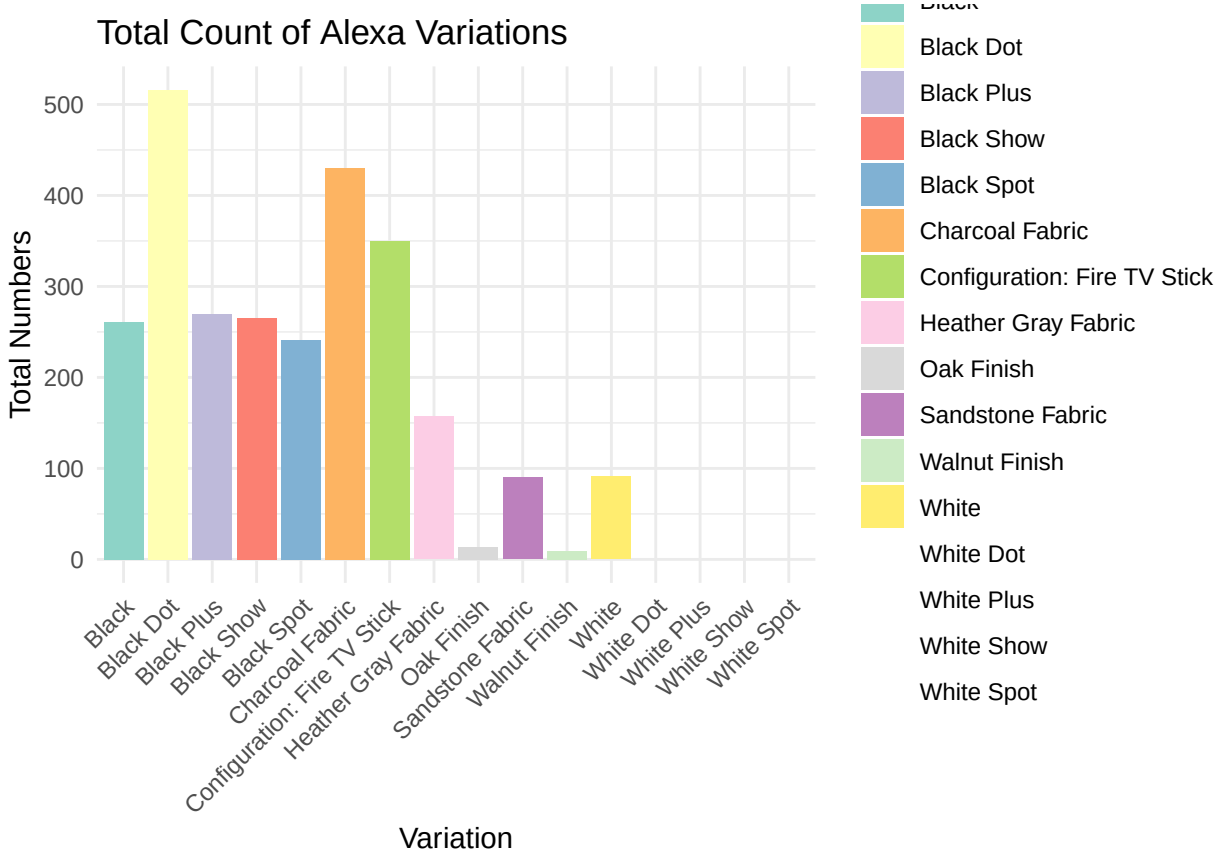
#7c

```
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
```