

RWorksheet_Sabarillo#4b

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1.

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

matrix_5x5 <- matrix(0, nrow = 5, ncol = 5)
for (i in 1:5) {
  for (j in 1:5) {
    matrix_5x5[i, j] <- abs(i - j)
  }
}

print(matrix_5x5)
```

```
##      [,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) {
  cat(rep(" ", 1 * i - 0), "\n")
}
```

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

3.

```
first <- as.integer(readline(prompt="Enter the first number of the Fibonacci sequence: "))

## Enter the first number of the Fibonacci sequence:

second <- as.integer(readline(prompt="Enter the second number of the Fibonacci sequence: "))

## Enter the second number of the Fibonacci sequence:

#for knitting purposes
if (is.null(first) || is.na(first)) first <- 1
if (is.null(second) || is.na(second)) second <- 1

fibonacci <- c(first, second)
```

```

prev <- first
current <- second
repeat {
  next_val <- prev + current
  if (next_val > 500) break
  fibonacci <- c(fibonacci, next_val)
  prev <- current
  current <- next_val
}
print(fibonacci)

```

```
## [1] 1 1 2 3 5 8 13 21 34 55 89 144 233 377
```

4.

```

#4.a
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

```

```

#4.b
males <- subset(shoe_data, Gender == "M")
females <- subset(shoe_data, Gender == "F")

```

```

num_males <- nrow(males)
num_females <- nrow(females)

```

```
cat("Number of males:", num_males, "\n")
```

```
## Number of males: 14
```

```
cat("Number of females:", num_females, "\n")
```

```
## Number of females: 14
```

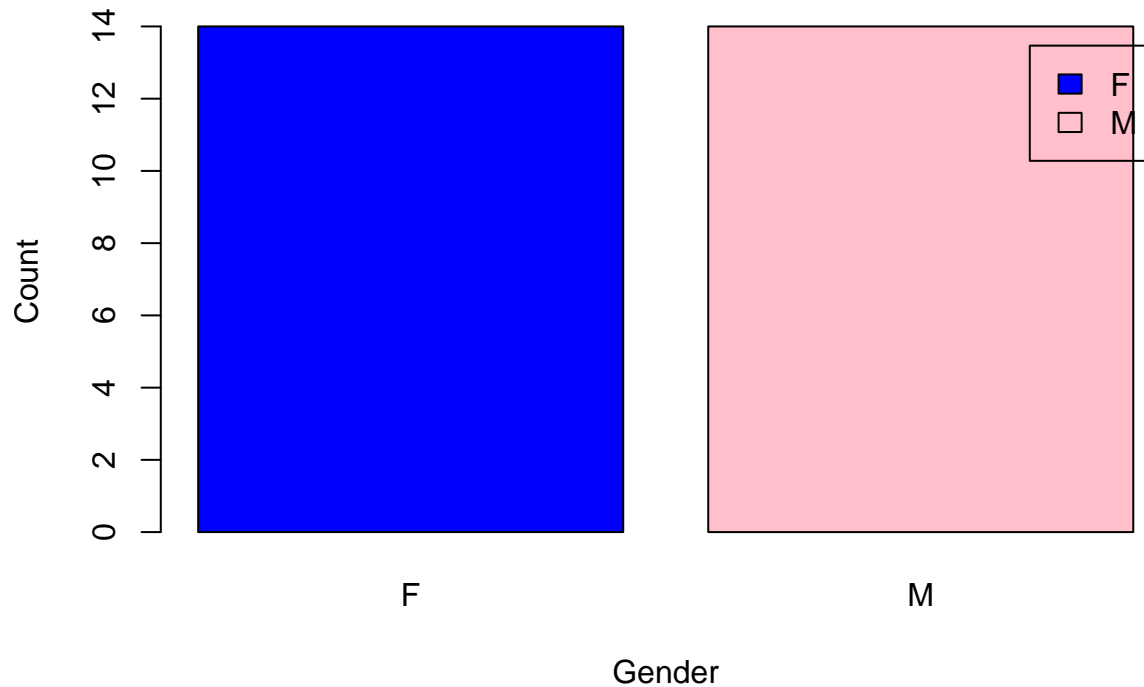
```

#4.c
gender_counts <- table(shoe_data$Gender)

barplot(gender_counts,
  main = "Number of Males and Females",
  xlab = "Gender",
  ylab = "Count",
  col = c("blue", "pink"),
  legend = names(gender_counts))

```

Number of Males and Females



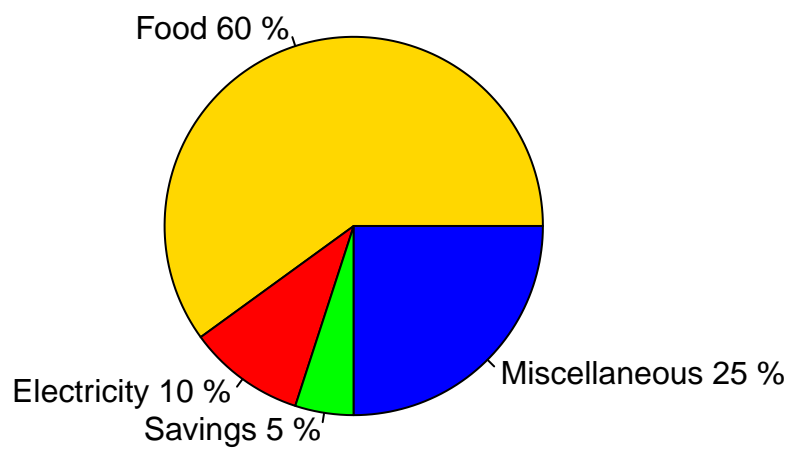
5.

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

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

pie(expenses,
    labels = paste(labels, percentages, "%"), main = "Monthly Expenses of Dela Cruz Family",
    col = c("gold", "red", "green", "blue")
)
```

Monthly Expenses of Dela Cruz Family



6.

```

data(iris)

#6a.
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 description: The iris dataset is a data frame with 150 observations and 5 variables.
# The variables are:
# - Sepal.Length: numeric, representing the sepal length in centimeters
# - Sepal.Width: numeric, representing the sepal width in centimeters
# - Petal.Length: numeric, representing the petal length in centimeters
# - Petal.Width: numeric, representing the petal width in centimeters
# - Species: Factor with 3 levels "setosa", "versicolor", and "virginica"

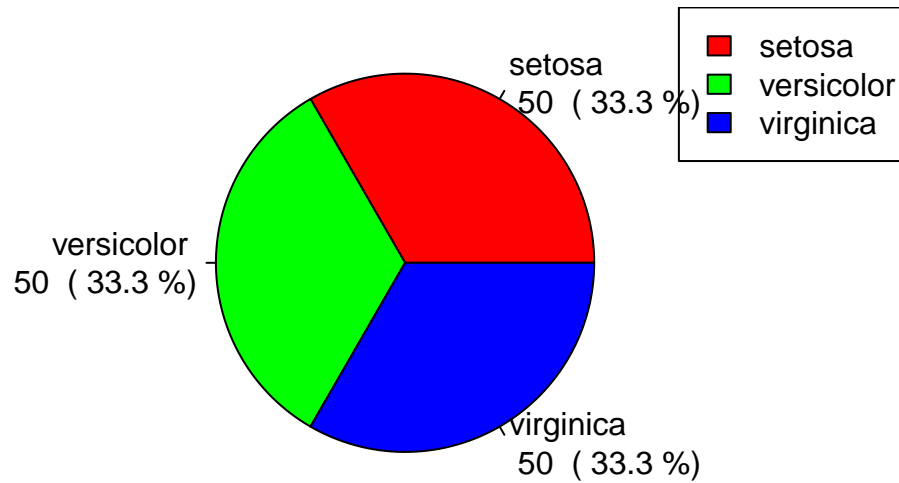
#6b.
mean_measurements <- c(
  mean(iris$Sepal.Length),
  mean(iris$Sepal.Width),
  mean(iris$Petal.Length),
  mean(iris$Petal.Width)
)
names(mean_measurements) <- c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")
print(mean_measurements)

## 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,
  main = "Iris Species Distribution",
  col = c("red", "green", "blue"),
  labels = paste(names(species_counts), "\n", species_counts, " (", round(species_counts / sum(species_counts), 1), "%)"
)
legend("topright", legend = names(species_counts), fill = c("red", "green", "blue"))

```

Iris Species Distribution



#6d.

```
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
```

#6e.

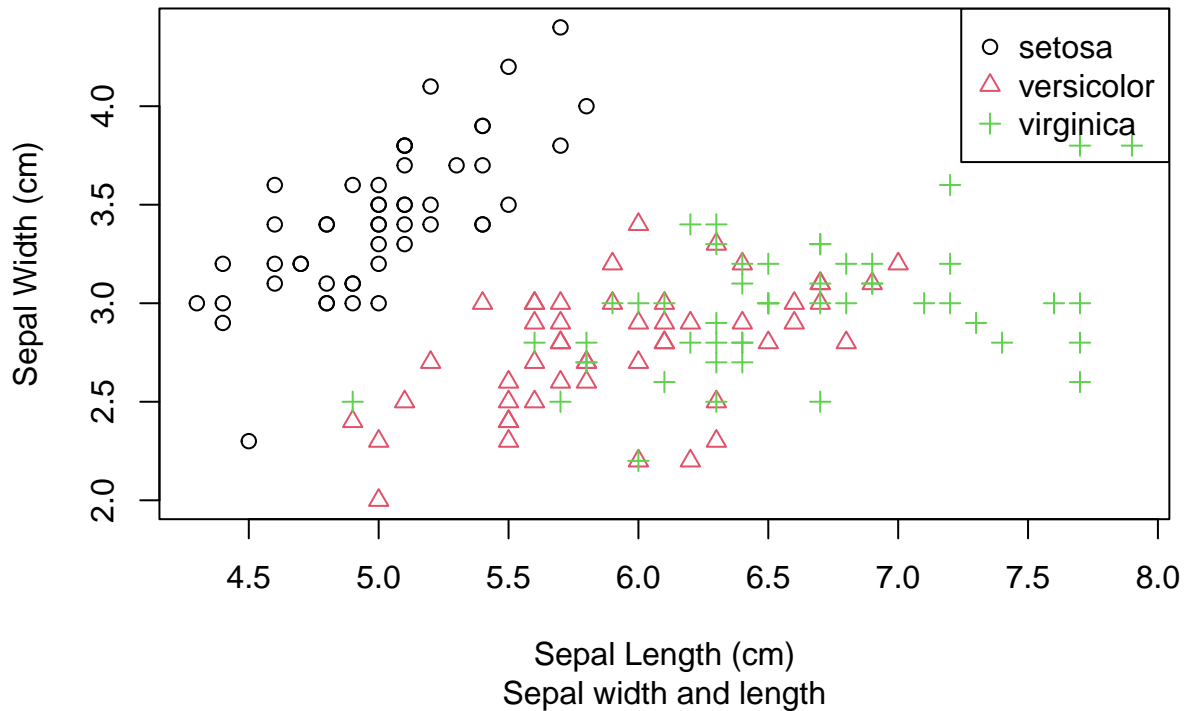
```
plot(iris$Sepal.Length, iris$Sepal.Width,
     main = "Iris Dataset",
     sub = "Sepal width and length",
```

```

xlab = "Sepal Length (cm)",
ylab = "Sepal Width (cm)",
pch = as.numeric(iris$Species), col = as.numeric(iris$Species)
)
legend("topright", legend = levels(iris$Species), pch = 1:3, col = 1:3)

```

Iris Dataset



#6f. -The scatterplot shows a relationship between sepal length and width, with different species clustering in different areas of the plot. Setosa tends to have smaller sepal length and larger sepal width, while virginica has larger sepal length and smaller sepal width. There is some overlap between versicolor and the other two species.

```
library(readxl)
```

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

#7a.

```
unique(alexa_data$variation)
```

```
## [1] "Charcoal Fabric"      "Walnut Finish"
## [3] "Heather Gray Fabric" "Sandstone Fabric"
## [5] "Oak Finish"          "Black"
## [7] "White"               "Black Spot"
## [9] "White Spot"          "Black Show"
## [11] "White Show"          "Black Plus"
## [13] "White Plus"          "Configuration: Fire TV Stick"
## [15] "Black Dot"           "White Dot"
```

```

alexa_data$variation <- gsub("Black Dot", "Black Dot", alexa_data$variation)
alexa_data$variation <- gsub("Black Plus", "Black Plus", alexa_data$variation)
alexa_data$variation <- gsub("Black Show", "Black Show", alexa_data$variation)
alexa_data$variation <- gsub("Black Spot", "Black Spot", alexa_data$variation)

alexa_data$variation <- gsub("White Dot", "White Dot", alexa_data$variation)
alexa_data$variation <- gsub("White Plus", "White Plus", alexa_data$variation)
alexa_data$variation <- gsub("White Show", "White Show", alexa_data$variation)
alexa_data$variation <- gsub("White Spot", "White Spot", alexa_data$variation)
unique(alexa_data$variation)

```

```

## [1] "Charcoal Fabric"      "Walnut Finish"
## [3] "Heather Gray Fabric"  "Sandstone Fabric"
## [5] "Oak Finish"           "Black"
## [7] "White"                "Black Spot"
## [9] "White Spot"           "Black Show"
## [11] "White Show"           "Black Plus"
## [13] "White Plus"           "Configuration: Fire TV Stick"
## [15] "Black Dot"            "White Dot"

```

```
head(alexa_data)
```

```

## # A tibble: 6 x 5
##   rating date          variation      verified_reviews      feedback
##   <dbl> <dtm>          <chr>          <chr>          <dbl>
## 1     5 2018-07-31 00:00:00 Charcoal Fabric Love my Echo!          1
## 2     5 2018-07-31 00:00:00 Charcoal Fabric Loved it!              1
## 3     4 2018-07-31 00:00:00 Walnut Finish  Sometimes while playi~ 1
## 4     5 2018-07-31 00:00:00 Charcoal Fabric I have had a lot of f~ 1
## 5     5 2018-07-31 00:00:00 Charcoal Fabric Music                1
## 6     5 2018-07-31 00:00:00 Heather Gray Fabric I received the echo a~ 1

```

```
#7b.
```

```
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

```

```

variation_counts <- alexa_data %>% count(variation)
print(variation_counts)

```

```

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

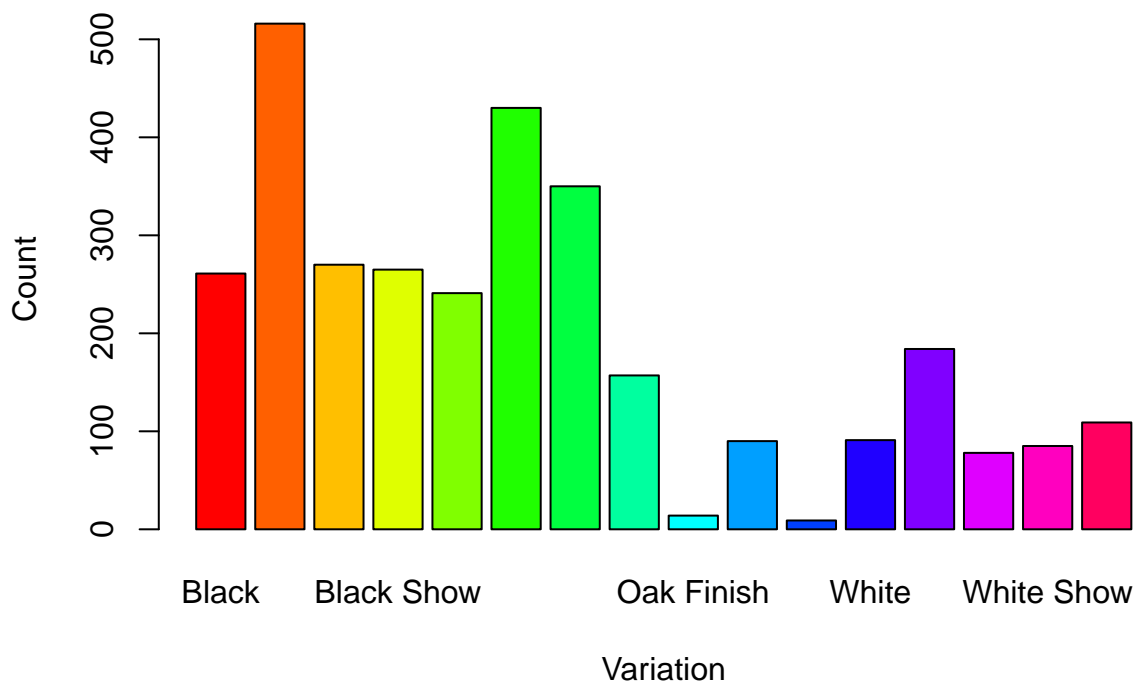
```
save(variation_counts, file = "variations.RData")
```

```
#7c.
```

```
load("variations.RData")
```

```
barplot(variation_counts$n,
        names.arg = variation_counts$variation,
        main = "Alexa Variations",
        xlab = "Variation",
        ylab = "Count",
        col = rainbow(nrow(variation_counts))
)
```

Alexa Variations



```
#7d.
```

```
black_variants <- variation_counts[grepl("Black", variation_counts$variation), ]
white_variants <- variation_counts[grepl("White", variation_counts$variation), ]
```

```
par(mfrow = c(1, 2))
```



```

barplot(black_variants$n,
        names.arg = black_variants$variation,
        main = "Black Variants",
        xlab = "Variation",
        ylab = "Count",
        col = rainbow(nrow(black_variants))
)

barplot(white_variants$n,
        names.arg = white_variants$variation,
        main = "White Variants",
        xlab = "Variation",
        ylab = "Count",
        col = rainbow(nrow(white_variants))
)

```

