RWorksheet_cabia#4b

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1.

```r
vector1 <- c(1, 2, 3, 4, 5)

zero_matrix <- matrix(0, nrow = 5, ncol = 5)

matrixr <- zero_matrix

for (i in 1:5) {
  for (j in 1:5) {
    matrixr[i, j] <- abs(vector1[i] - vector1[j])
  }
}

print(matrixr)
```

```
##      [,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
```

```r
# 2.
n <- 5

for (i in 1:n) {
  row_output <- paste(rep("*", i), collapse = " ")
  cat(row_output, "\n")
}
```

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

3.

```r
start <- as.numeric(readline(prompt = "Enter a starting number for Fibonacci sequence: "))

a <- 0
```

```r
b <- 1

cat("Fibonacci sequence starting from", start, "up to 500:\n")

repeat {
  fib <- a + b

  if (fib > 500) {
    break
  }

  if (fib >= start) {
    cat(fib, "\n")
  }

  a <- b
  b <- fib
}
```

4.

```r
# a.
library(readxl)
shoe_size <- read_excel("shoe_size.xlsx")
head(shoe_size)

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

male_subset <- subset(shoe_size, Gender == "M")
female_subset <- subset(shoe_size, Gender == "F")

num_male <- nrow(male_subset)
num_female <- nrow(female_subset)

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

## Number of observations in Male: 14

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

## Number of observations in Female: 14
# c.

gender_counts <- table(shoe_size$Gender)
```
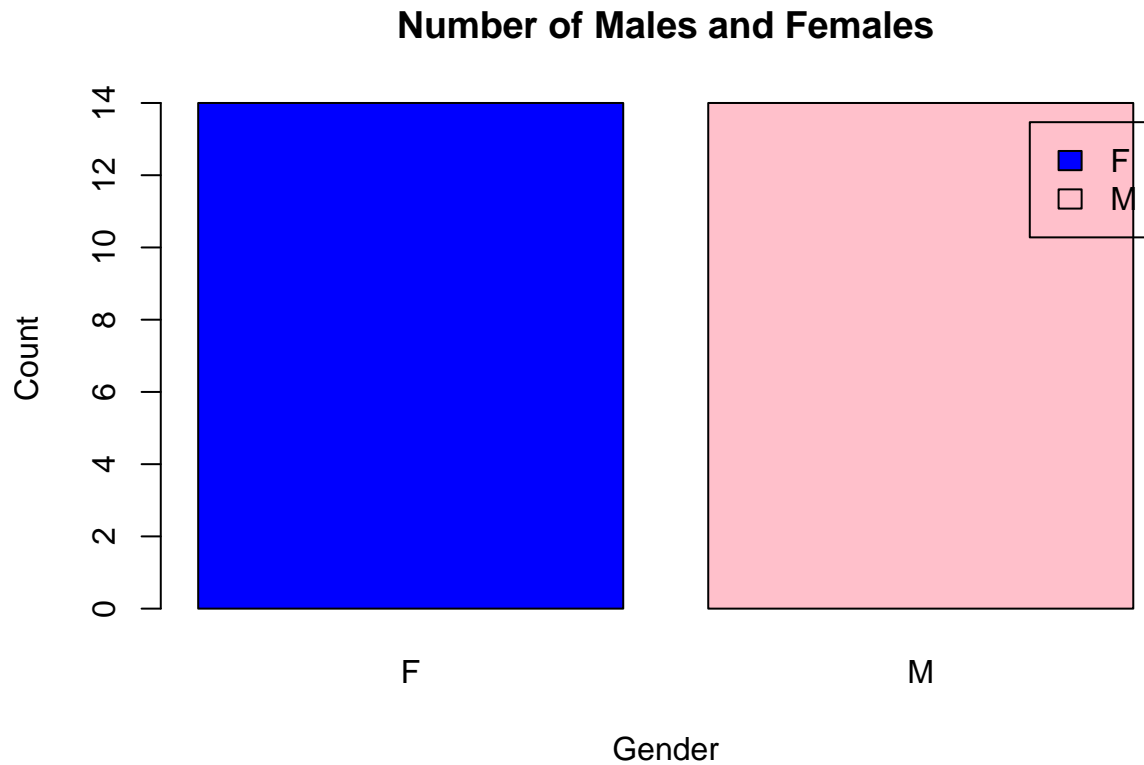
```r
barplot(gender_counts,
        main = "Number of Males and Females",
        xlab = "Gender",
        ylab = "Count",
        col = c("blue", "pink"),
        legend = rownames(gender_counts),
        beside = TRUE)
```
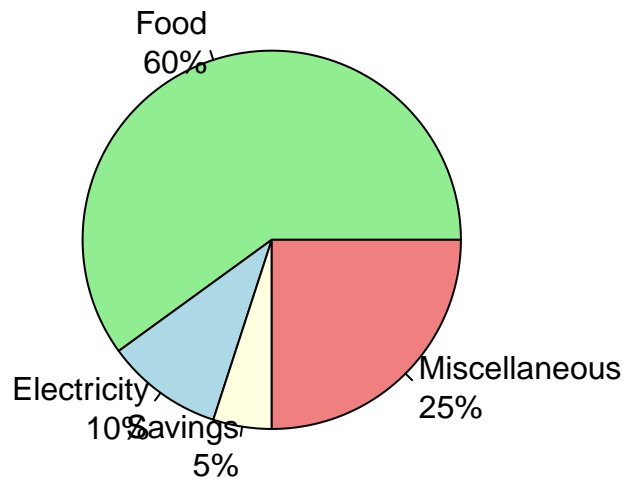
Number of Males and Females

5.

```r
expenses <- c(60, 10, 5, 25)
labels <- c("Food", "Electricity", "Savings", "Miscellaneous")
colors <- c("lightgreen", "lightblue", "lightyellow", "lightcoral")

pie(expenses,
    labels = paste(labels, "\n", round((expenses / sum(expenses)) * 100, 1), "%", sep = ""),
    col = colors,
    main = "Monthly Income Distribution of Dela Cruz Family")
```

Monthly Income Distribution of Dela Cruz Family

6.

```r
# a.
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 ...
```

```r
# b.
mean_values <- colMeans(iris[, 1:4])

print(mean_values)
```
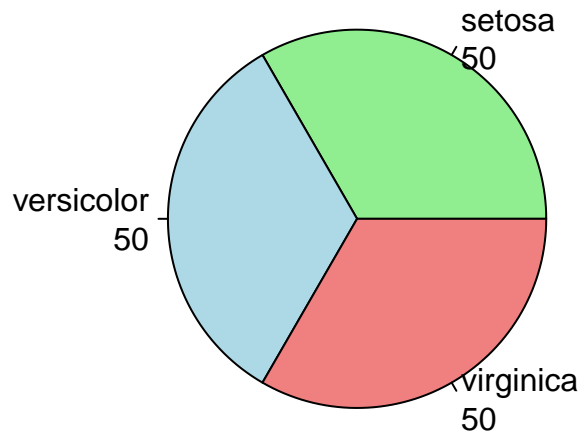
```
## Sepal.Length  Sepal.Width Petal.Length  Petal.Width
##     5.843333     3.057333     3.758000     1.199333
```

```r
# c.
species_counts <- table(iris$Species)

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

pie(species_counts,
    labels = paste(names(species_counts), "\n", species_counts, sep = ""),
    col = colors,
    main = "Species Distribution in Iris Dataset")
```

Species Distribution in Iris Dataset

setosa
50

versicolor
50

virginica
50

```r
# d.
setosa_subset <- iris[iris$Species == "setosa", ]
versicolor_subset <- iris[iris$Species == "versicolor", ]
virginica_subset <- iris[iris$Species == "virginica", ]

setosa_last_six <- tail(setosa_subset, 6)
versicolor_last_six <- tail(versicolor_subset, 6)
virginica_last_six <- tail(virginica_subset, 6)

print("Last six rows of Setosa:")
```

```
## [1] "Last six rows of Setosa:"
```

```r
print(setosa_last_six)
```

```
##    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
```

```r
print("Last six rows of Versicolor:")
```

```
## [1] "Last six rows of Versicolor:"
```

```r
print(versicolor_last_six)
```

```
##     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
```

```r
print("Last six rows of Virginica:")
```

```
## [1] "Last six rows of Virginica:"
```
```
print(virginica_last_six)
```
```
##     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
```
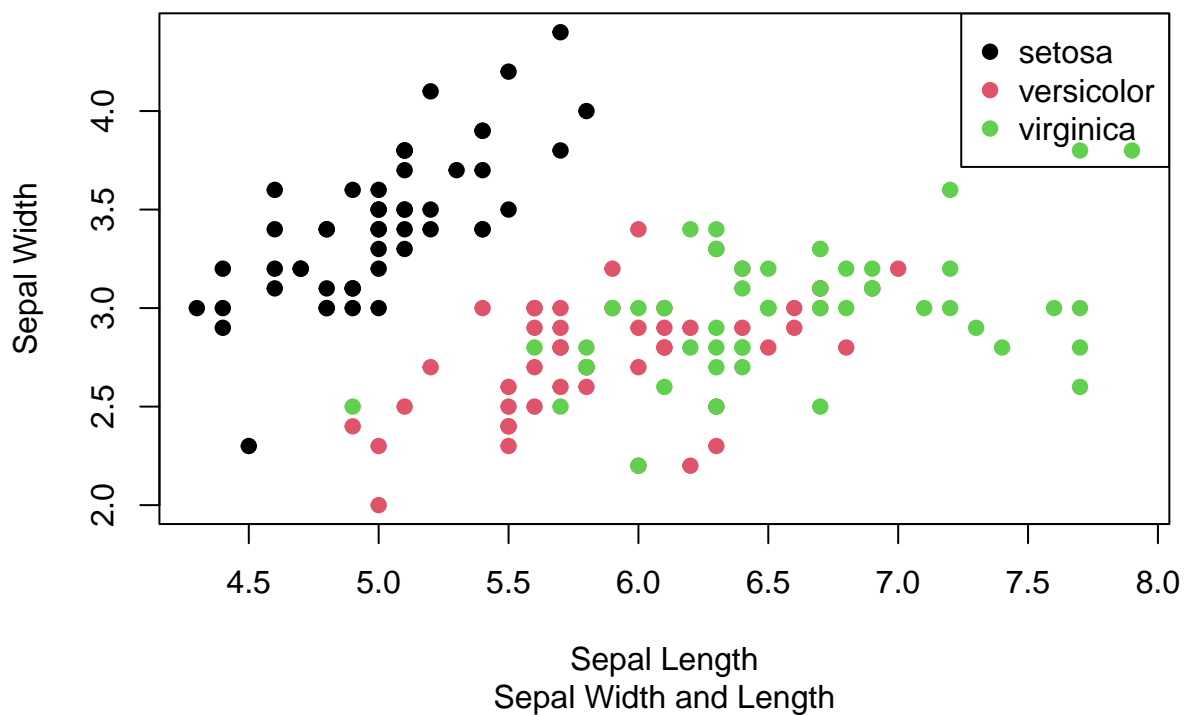```r
e.
iris$Species <- as.factor(iris$Species)

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)
```



**Iris Dataset**

```r
# 4.
# Pie Chart. The pie chart visually represents the distribution of species, making it easy to see which

#Scatterplot, The scatterplot illustrates the relationship between sepal length and width, revealing ho
```