

Untitled

2023-11-11

```
#num1
vectorA <- c(1, 2, 3, 4, 5)
matrixA <- matrix(0, nrow=5, ncol=5)
```

```
# Fill the matrix
for(i in 1:5) {
  for(j in 1:5) {
    if(j <= (6 - i)) {
      matrixA[i,j] <- j - 1
    }
  }
}
```

```
# Display the matrix
print(matrixA)
```

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

```
#num2
matrixA <- matrix(0,nrow=5, ncol=5)
```

```
# Fill the matrix with asterisks
for(i in 1:5) {
  for(j in 1:5) {
    if(j <= i) {
      matrixA[i, j] <- "*"
    }
  }
}
```

```
for (i in 1:5) {
  for (j in 1:i) {
    cat("*")
  }
  cat("\n")
}
```

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

```
## *****
input_number <- as.numeric(readline("Enter a number to start the Fibonacci sequence: "))

## Enter a number to start the Fibonacci sequence:
assume_number <- 0
a <- 0
b <- 1

repeat {

  if (a > 500) {
    break
  }

  if (a >= assume_number) {
    cat(a, " ")
  }

  temp <- a + b
  a <- b
  b <- temp
}

## 0 1 1 2 3 5 8 13 21 34 55 89 144 233 377

cat("\n")

shoenga <- read.csv("Shoe_sizes.csv")
shoenga
```

```
##      Shoe.Size Height Gender
## 1          6.5   66.0      F
## 2          9.5   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
## 7          9.5   70.0      F
## 8          9.0   71.0      F
## 9         13.0   72.0      M
## 10         7.5   64.0      F
## 11         10.5   74.5      M
## 12          8.5   67.0      F
## 13         12.0   71.0      M
## 14         10.5   71.0      M
## 15         13.0   77.0      M
## 16         11.5   72.0      M
## 17          8.5   59.0      F
## 18          5.0   62.0      F
## 19         10.0   72.0      M
## 20          6.5   66.0      F
## 21          7.5   64.0      F
## 22          8.5   67.0      M
## 23         10.5   73.0      M
```

```
## 24      8.5  69.0    F
## 25     10.5  72.0    M
## 26     11.0  70.0    M
## 27      9.0  69.0    M
## 28     13.0  70.0    M
```

```
shoenganga <- shoenga[c(1:6),]
shoenganga
```

```
##   Shoe.Size Height Gender
## 1      6.5   66.0      F
## 2      9.5   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
```

```
female_data <- subset(shoenga, Gender == "F")
female_data
```

```
##   Shoe.Size Height Gender
## 1      6.5   66.0      F
## 2      9.5   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
```

```
male_data <- subset(shoenga, Gender == "M")
male_data
```

```
##   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
```

```
nrow(female_data)
```

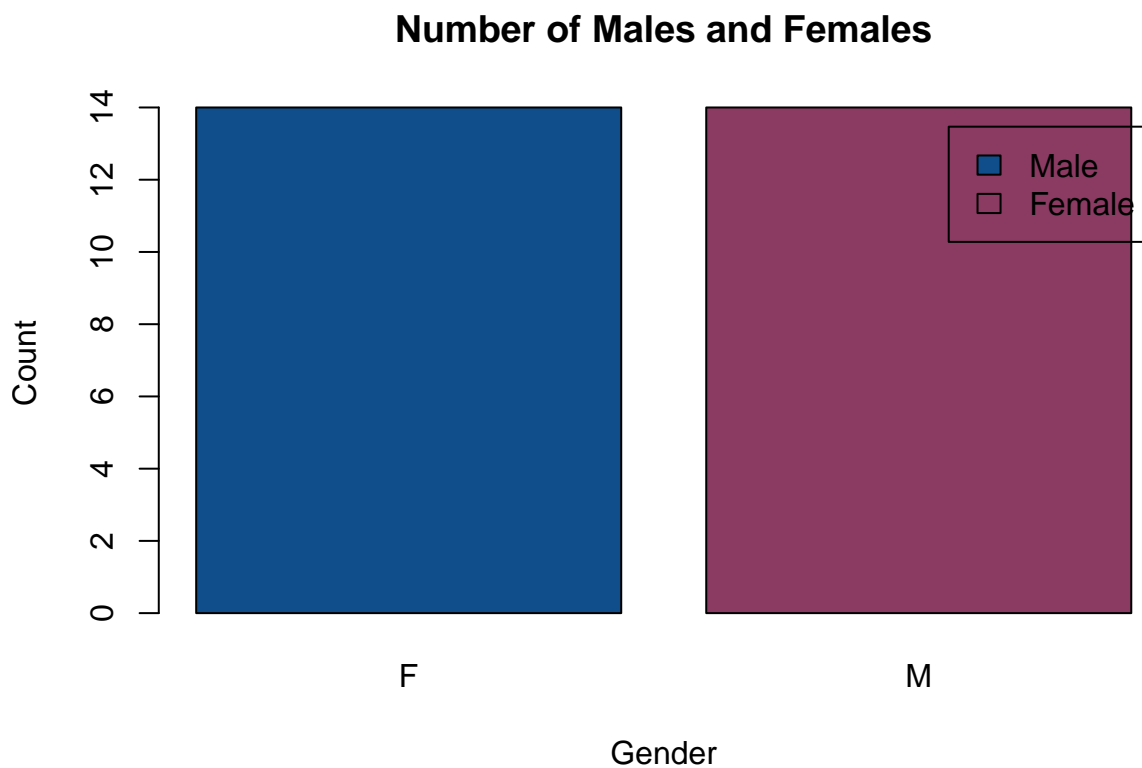
```
## [1] 14
```

```
nrow(male_data)
```

```
## [1] 14
```

```
#They have both 14 observations
```

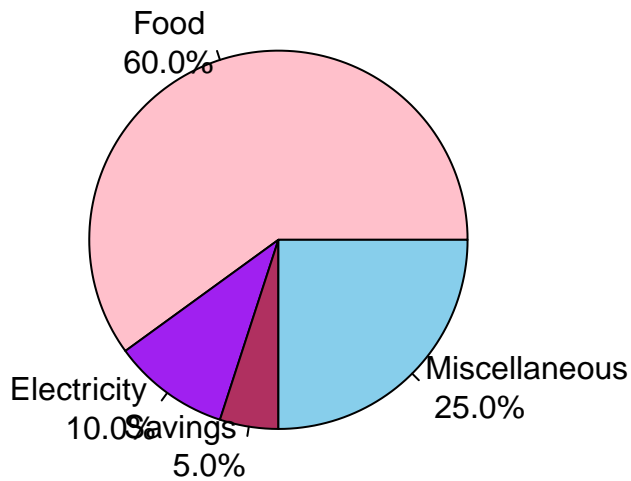
```
GraphMF<- table(shoenga$Gender)
barplot(GraphMF,
  main = "Number of Males and Females",
  xlab = "Gender",
  ylab = "Count",
  col = c("dodgerblue4", "hotpink4"),
  legend.text = c("Male", "Female"),
  beside = TRUE
)
```



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

```
pie(Expenses,
  labels = paste(names(Expenses), "\n", sprintf("%.1f%%", prop.table(Expenses) * 100)),
  col = c("pink", "purple", "maroon", "skyblue"),
  main = "Monthly Expenses of the Dela Cruz Family"
)
```

Monthly Expenses of the Dela Cruz Family



```
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 ...

#The iris dataset has 150 observations and 5 variables.
#These variables are the Sepal.Length, Sepal.Width, Petal.Length, Petal.Width, and Species.

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

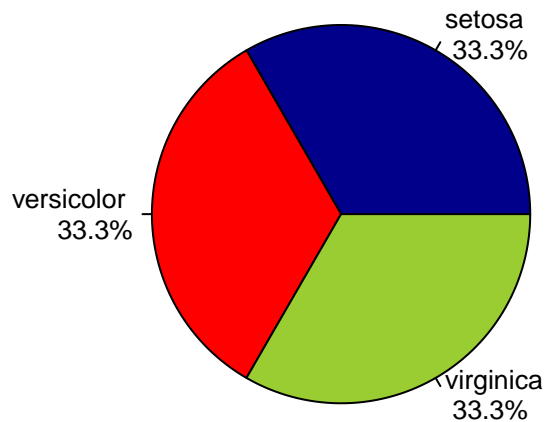
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 5.843333 3.057333 3.758000 1.199333

Spec <- table(iris$Species)

clors <- c("darkblue", "red", "yellowgreen")

pie(Spec,
    labels = paste(names(Spec), "\n", sprintf("%.1f%%", prop.table(Spec) * 100)),
    col = clors,
    main = "Species Distribution",
    cex.main = 1.5,
    cex = 0.8
)
```

Species Distribution



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

```
# Display the last six rows of each species
cat("Last six rows of Setosa:")
```

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

```
print(tail(SetosaSub))
```

```
##      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("Last six rows of Versicolor:")
```

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

```
print(tail(VersiSub))
```

```
##      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("Last six rows of Virginica:")
```

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

```
print(tail(VirgiSub))
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
```

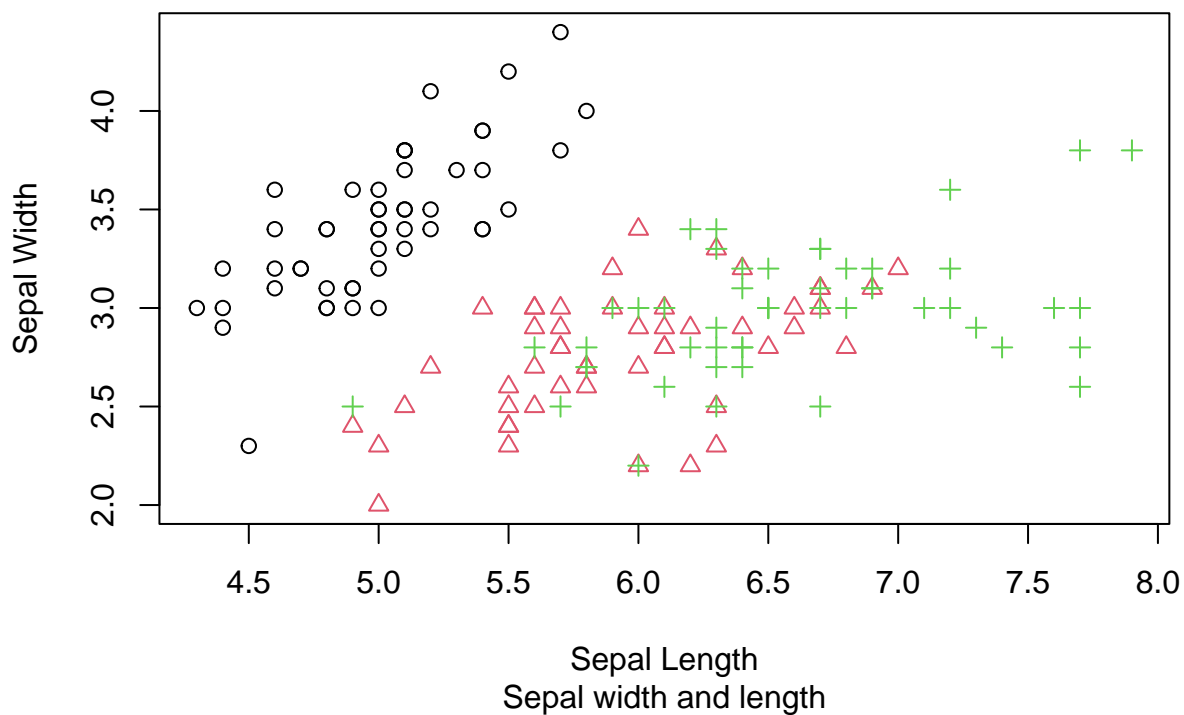
```
## 145      6.7      3.3      5.7      2.5 virginica
## 146      6.7      3.0      5.2      2.3 virginica
## 147      6.3      2.5      5.0      1.9 virginica
## 148      6.5      3.0      5.2      2.0 virginica
## 149      6.2      3.4      5.4      2.3 virginica
## 150      5.9      3.0      5.1      1.8 virginica
```

```
data(iris)

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

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

Iris Dataset



#The scatterplot shows similarities between the sepal width and length ranging from 5.5 to 7.0

```
#library(readr)
#alexa_file <- read_xlsx("alexa_file.xlsx")
#alexa_file <- load("alexa_file.xlsx")
#alexa_file
```