Rworksheet_Rabago#4b

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1.

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


for (i in 1:5) {
  matrix_result[i, i] <- abs(vectorA[i])
}


print(matrix_result)
```

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

2.

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

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

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

3

```
# Function to generate Fibonacci sequence
fibonacci_sequence <- function(start) {
  a <- 0
  b <- 1
  fib_sequence <- c()

  repeat {
    fib <- a + b
    a <- b
    b <- fib
    # Break if the Fibonacci number exceeds 500
    if (fib > 500) {
      break
    }

    # Add the Fibonacci number to the sequence if it is greater than or equal to the starting number
    if (fib >= start) {
      fib_sequence <- c(fib_sequence, fib)
    }
  }

  return(fib_sequence)
}

# Set a starting number for the Fibonacci sequence
start_input <- 8  # Example starting value; you can change this as needed

# Check if the starting number is valid
if (start_input <= 0) {
  cat("Please enter a number greater than 0.\n")
} else {
  # Get and print Fibonacci sequence starting from the defined input
  result <- fibonacci_sequence(start_input)
  cat("Fibonacci sequence starting from", start_input, "up to 500:\n")
  print(result)
}
```

```
## Fibonacci sequence starting from 8 up to 500:
## [1]   8  13  21  34  55  89 144 233 377
```

4.a.

```
datas <- read.csv("/cloud/project/Worksheet4/Household Data.csv")
```

4.b.

```
male <- subset(datas, Gender == "M")
male
```

```
##    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
```

```r
female <- subset(datas, Gender == "F")
female
```

```
##    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
## 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
```

```r
numbermale <- nrow(male)
numberfemale <- nrow(female)
cat("Number of observations for Male:", numbermale, "\n")
```

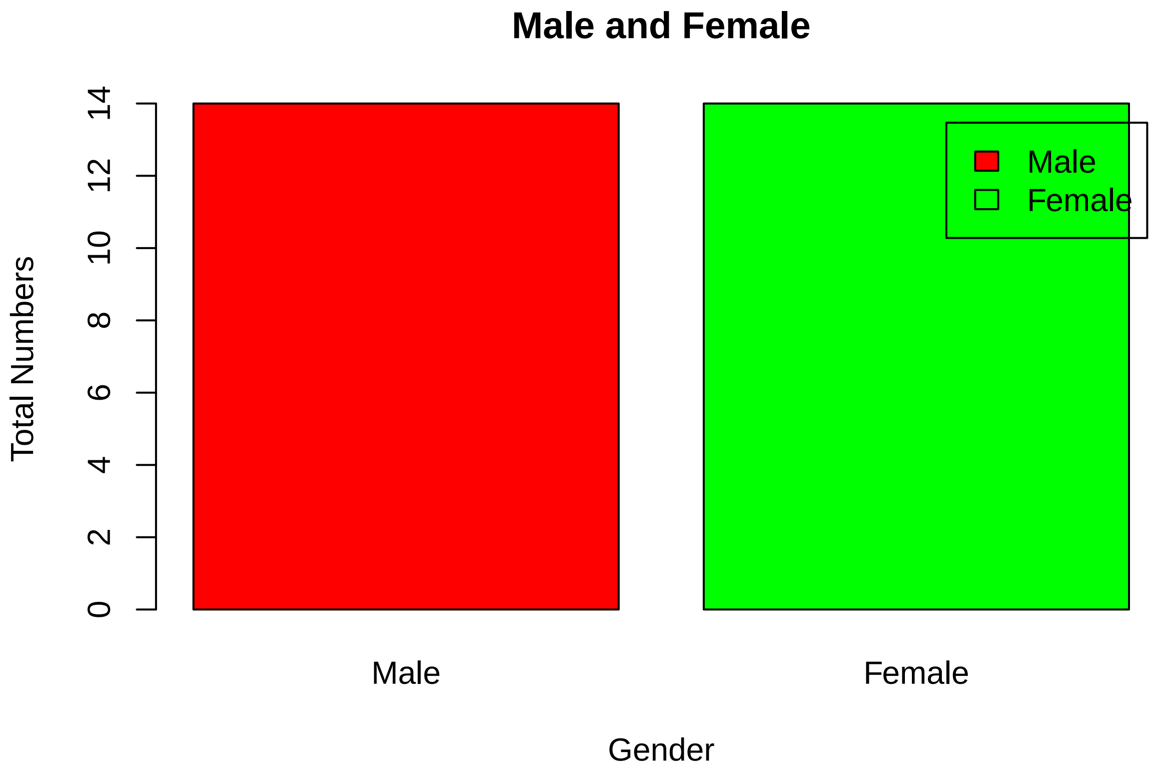
```
## Number of observations for Male: 14
```

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

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

4.c.

```r
Plotting <- c(numbermale,numberfemale)
names(Plotting) <- c("Male", "Female")
barplot(Plotting, main = "Male and Female", xlab = "Gender", ylab = "Total Numbers", col = c("red", "gr
```



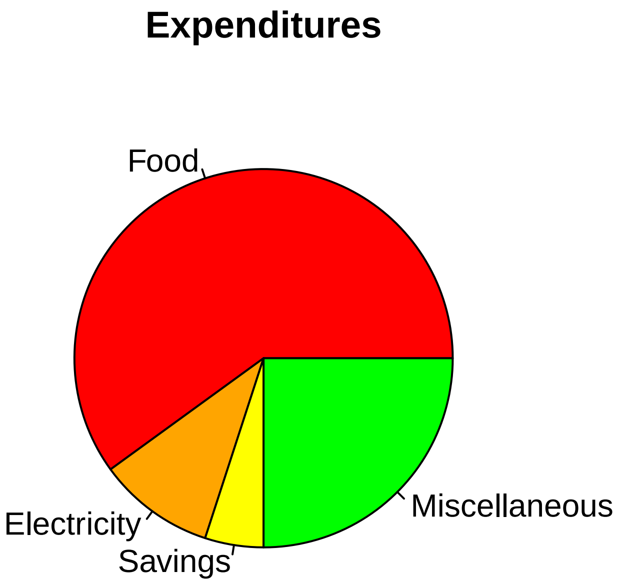
5

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

Bills <- matrix(values, nrow = 1, ncol = length(bills), dimnames = list(NULL, bills))
Bills
```

```
##      Food Electricity Savings Miscellaneous
## [1,]   60          10       5            25
```

```
Plotters <- pie(values, labels = c("Food", "Electricity", "Savings", "Miscellaneous"),col = c("red", "o
```



6.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 ...
```

6.b.

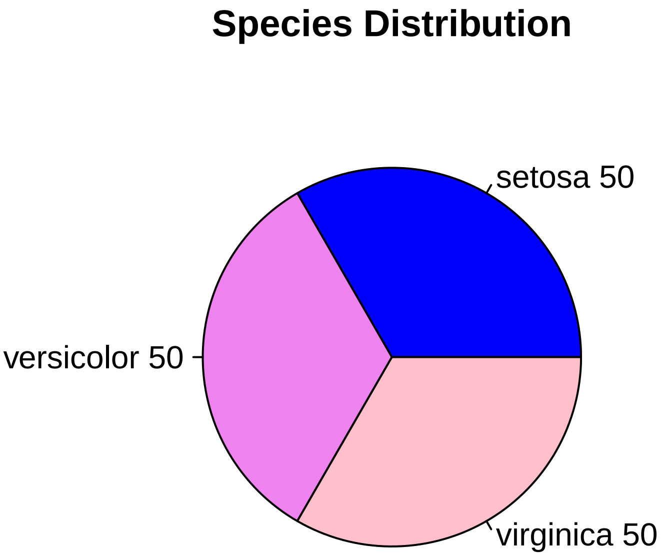
```
meanvalues <- colMeans(iris[, 1:4])
meanvalues
```

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

6.c.

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

pie(species_count,
    main = "Species Distribution",
    col = c("blue", "violet", "pink"),
    labels = paste(names(species_count),species_count))
```



6.d.

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

last6_setosa <- tail(setosa)
last6_versicolor <- tail(versicolor)
last6_virginica <- tail(virginica)

cat("Last six rows of Setosa:\n")
```

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

```r
print(last6_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
```

```r
cat("\nLast six rows of Versicolor:\n")
```

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

```r
print(last6_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
```

```r
cat("\nLast six rows of Virginica:\n")
```

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

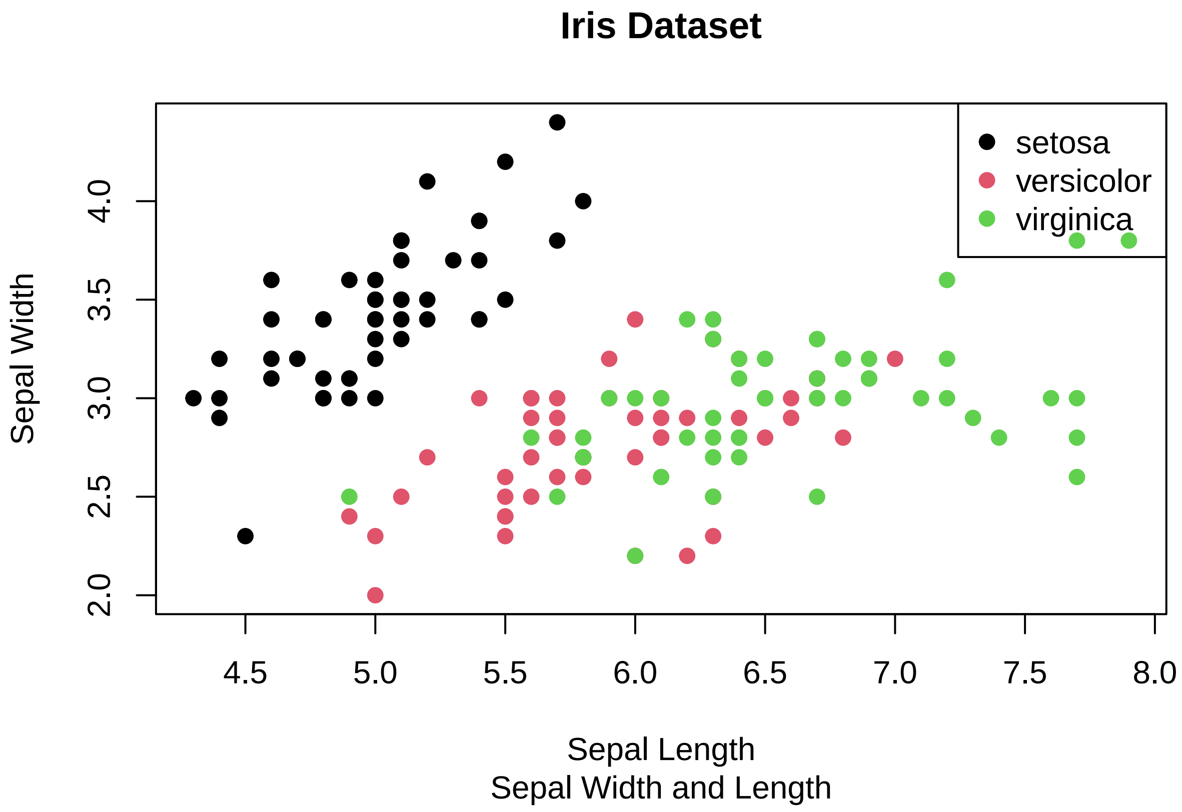
```r
print(last6_virginica)
```

```
##     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
```

6.e.

```r
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)
```



6.f.

#The scatterplot shows the relationship between sepal width and length for different iris flower species. Versicolor and Virginica overlap a lot and have similar sepal sizes. However, Setosa is easy to identify because it has smaller sepal sizes than the other two species.