

RWorksheet_camasa#4b

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1. Using the for loop, create an R script that will display a 5x5 matrix as shown in Figure 1. It must contain vectorA = [1,2,3,4,5] and a 5 x 5 zero matrix.

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

zmat <- matrix(0, nrow = 5, ncol = 5)
rmat <- zmat

for (i in 1:5) {
  for (j in 1:5) {
    rmat[i, j] <- abs(vectorA[i] - zmat[i, j])
  }
}
print(rmat)
```

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

2. Print the string “*” using for() function.

```
a <- 5

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

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

3. Get an input from the user to print the Fibonacci sequence starting from the 1st input up to 500. Use repeat and break statements.

```
start <- as.numeric(readline(prompt = "Enter a number: "))

x <- 0
y <- 1

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

repeat {
  fib_seq <- x + y

  if (fib_seq > 500) {
    break
  }

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

  x <- y
  y <- fib_seq
}
```

4. Import the dataset as shown in Figure 1 you have created previously.

a. What is the R script for importing an excel or a csv file? Display the first 6 rows of the dataset?

```
data <- read.csv("shoe_sizes.csv")

head(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
```

b. Create a subset for gender(female and male). How many observations are there in Male? How about in Female?

```
fdata <- subset(data, Gender == "F")
mdata <- subset(data, Gender == "M")
```

```
num_female <- nrow(fdata)
num_male <- nrow(mdata)

num_female
```

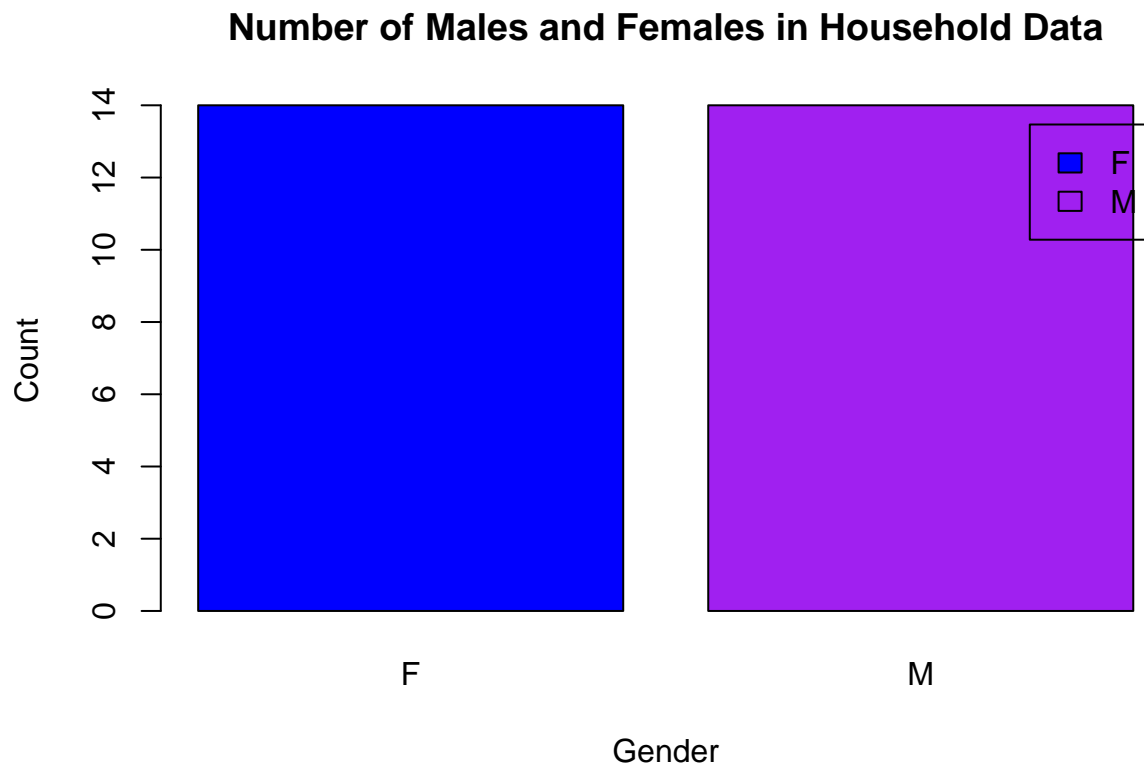
```
## [1] 14
```

```
num_male
```

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

C.

```
genderCount <- table(data$Gender)
barplot(genderCount,
  main = "Number of Males and Females in Household Data",
  col = c("blue", "purple"),
  legend = rownames(genderCount),
  ylab = "Count",
  xlab = "Gender",
  beside = TRUE)
```

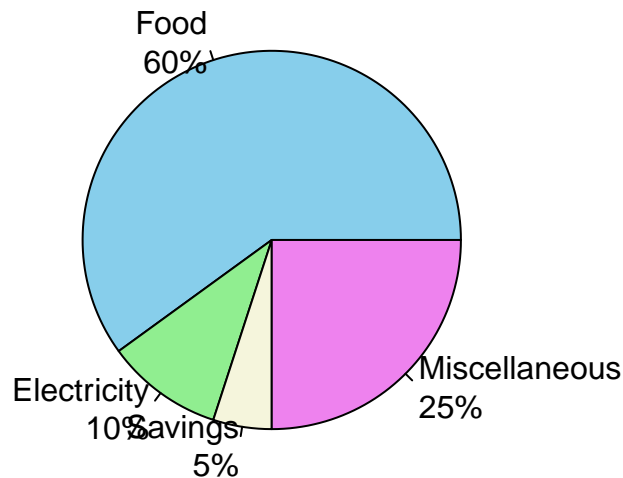


5.

```
exp <- c(60, 10, 5, 25)
labels <- c("Food", "Electricity", "Savings", "Miscellaneous")
colors <- c("skyblue", "lightgreen", "beige", "violet")
```

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

Monthly Income Distribution of Dela Cruz Family



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 ...
```

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

print(meanValues)
```

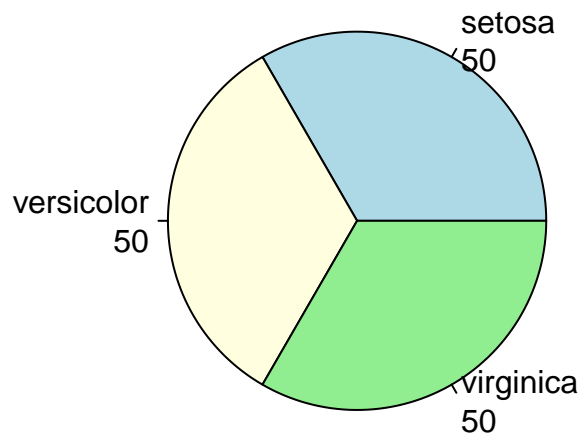
```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
##      5.843333      3.057333      3.758000      1.199333
```

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

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

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

Species Distribution in Iris Dataset



```
# d.
setosaSubset <- iris[iris$Species == "setosa", ]
versicolorSubset <- iris[iris$Species == "versicolor", ]
virginicaSubset <- iris[iris$Species == "virginica", ]
```

```
setosaLastSix <- tail(setosaSubset, 6)
versicolorLastSix <- tail(versicolorSubset, 6)
virginicaLastSix <- tail(virginicaSubset, 6)
```

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

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

```
print(setosaLastSix)
```

```
##      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
```

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

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

```
print(versicolorLastSix)
```

```
##      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
```

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

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

```
print(virginicaLastSix)
```

```
##      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
```

```
# 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

