

RWorksheet_Bernasol#4b

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#1. Using the for loop Function

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

for(i in 1:5){
  for(j in 1:5){
    matrixA[i, j] <-ifelse(j>=i, vectorA[abs(j-i)+1],0)
  }
}

matrixA
```

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

#2. using for() function.

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

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

#3. Get an input from the user

```
A <- as.integer(readline(prompt = "Enter starting position: "))
```

```
## Enter starting position:
```

```
fib1 <- 0
fib2 <- 1
count <- 1
fib_sequence <- c()

repeat {
```

```

z <- fib1 + fib2

if (!is.na(A) && count >= A && z <= 500) {
  fib_sequence <- c(fib_sequence, z)
}

fib1 <- fib2
fib2 <- z
count <- count + 1

if (z > 500) break
}

print(fib_sequence)

## NULL

#4 A. Display first 6 rows
library(readr)

shoe_Sizes <- read_csv("/cloud/project/Worksheet 4/Worksheet 4B/Shoe-Sizes.csv")

## Rows: 28 Columns: 3
## -- Column specification -----
## Delimiter: ","
## chr (1): Gender
## dbl (2): Shoe size, Height
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
head(shoe_Sizes)

## # 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

#4 B. Creating subset for gender (female and male)

male <- subset(shoe_Sizes, Gender == "M")
female <- subset(shoe_Sizes, Gender == "F")
num_males <- nrow(male)
num_females <- nrow(female)

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

## Number of Male observations: 14

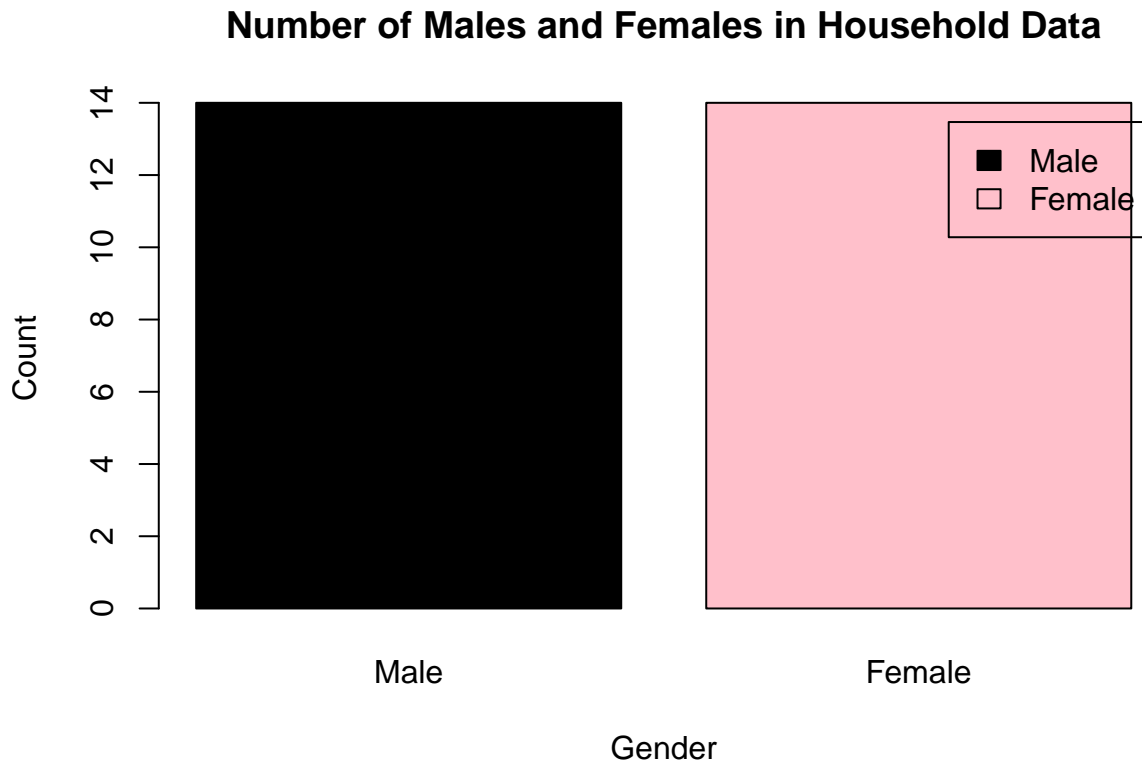
cat("Number of Female observations:", num_females, "\n")

## Number of Female observations: 14

```

#4 C. Create a graph for the number of males and females for Household Data

```
gender_counts <- c(num_males, num_females)
names(gender_counts) <- c("Male", "Female")
barplot(gender_counts,
        main = "Number of Males and Females in Household Data", xlab = "Gender", ylab = "Count", col = c("black", "pink"))
```



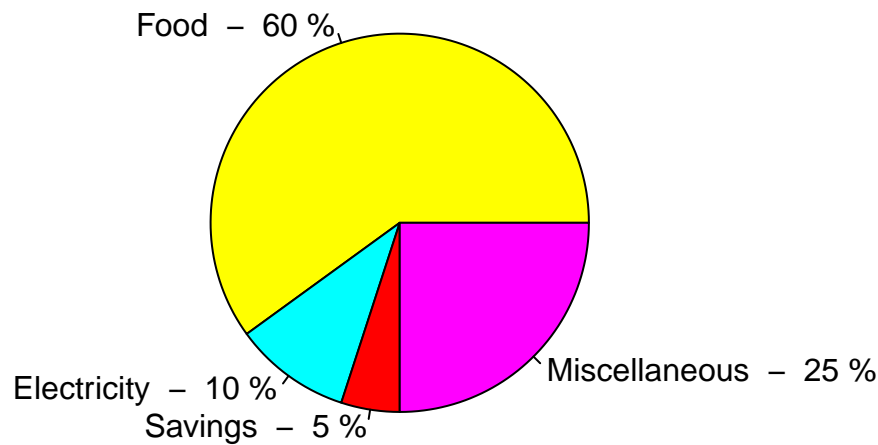
5a.

Monthly income of Dela Cruz family

#5 A. Monthly income of Dela Cruz family

```
expenses <- c(Food = 60, Electricity = 10, Savings = 5, Miscellaneous = 25)
colors <- c("yellow", "cyan", "red", "magenta")
pie(expenses, labels = paste(names(expenses), " - ", round((expenses / sum(expenses)) * 100, 1), "%"), col = colors)
```

Dela Cruz Family Monthly Income Distribution



#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.

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

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

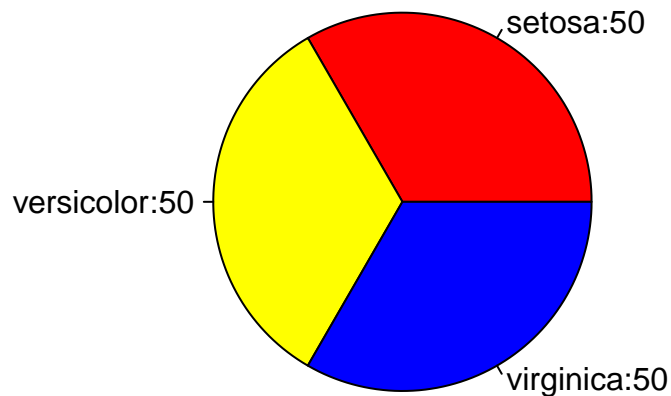
#6 C.

```
species_count <- table(iris$Species)
species_labels <- paste(names(species_count), species_count, sep = ":")

color <- c("red", "yellow", "blue")

pie(species_count, labels= species_labels, col= color, main="Species Distribution in Iris DataSet")
```

Species Distribution in Iris DataSet



#6 D.

```
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
```

#6 E.

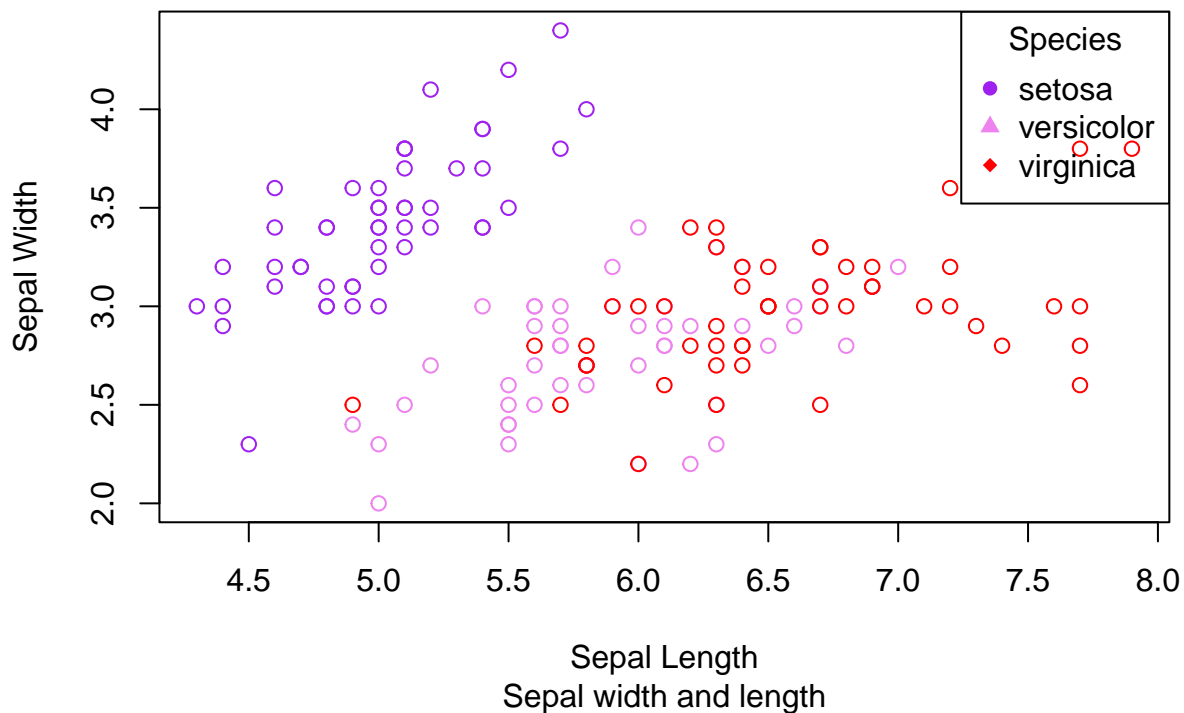
```
iris$Species <-as.factor(iris$Species)
```

```
Species_color <- c("setosa"="purple", "versicolor"="violet", "virginica"="red")
species_pch <- c("setosa"= 16, "versicolor"= 17, "virginica"= 18)

plot(iris$Sepal.Length, iris$Sepal.Width, col= Species_color[iris$Species],
     xlab = "Sepal Length",
     ylab= "Sepal Width", main ="Iris Dataset", sub= "Sepal width and length")

legend ("topright", legend=levels(iris$Species), col= Species_color, pch = species_pch, title = "Species")
```

Iris Dataset



#6 F. Interpret the result.

```
# Interpretation of the Scatterplot Result
# The scatterplot shows the relationship between Sepal.Length and Sepal.Width for the three species.
# Setosa points (in orange) tend to have shorter sepal lengths and widths.
# Versicolor points (in pink) are more spread out and overlap slightly with virginica.
# Virginica points (in yellow) have larger sepal lengths and widths, distinguishing them from setosa and versicolor.
```

#7. Import the alexa-file.xlsx

```
library(readxl)
data <- read_excel("/cloud/project/Worksheet 4/Worksheet 4B/alexa-file.xlsx")

data$variation <- gsub("Black Dot", "Black Dot", data$variation)
data$variation <- gsub("White Plus", "White Plus", data$variation)

head(data$variation)
```

```
## [1] "Black Dot" "Black Dot" "Black Dot" "Black Dot" "Black Dot"
```

```
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
```

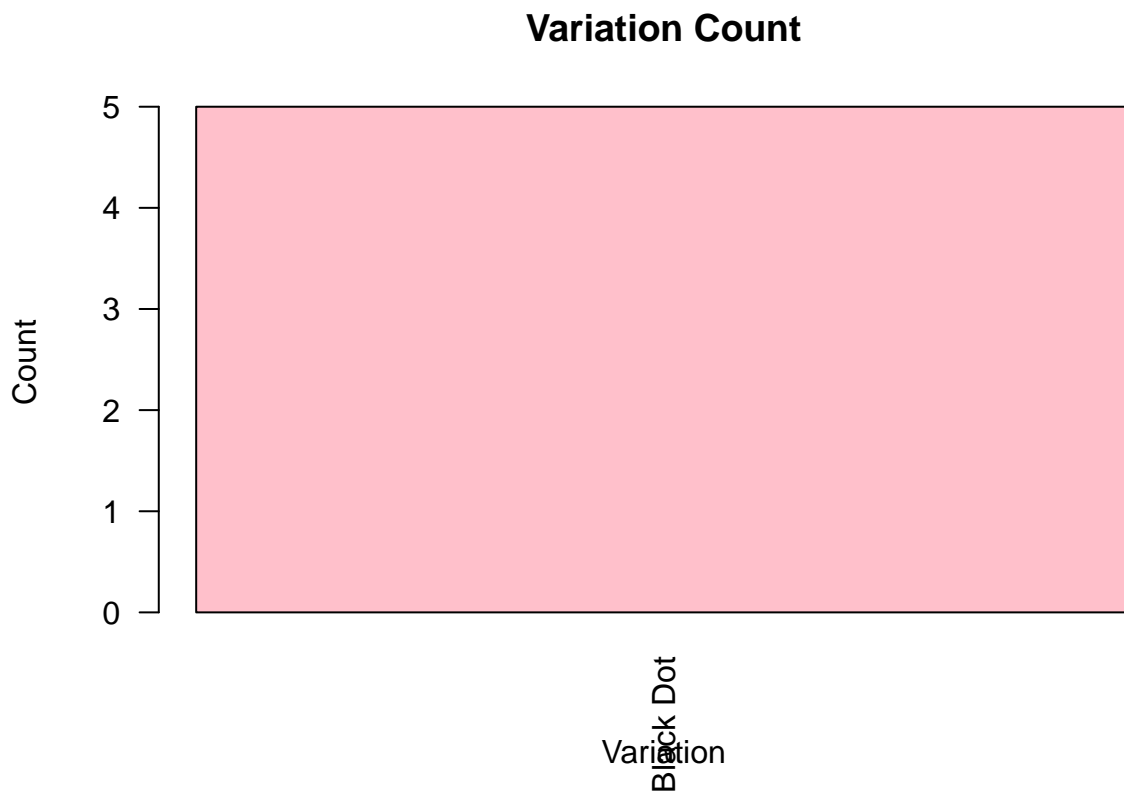
```
variation_count <- data %>%  
  count(variation)  
save(variation_count, file = "variations.RData")  
print(variation_count)
```

```
## # A tibble: 1 x 2  
##   variation      n  
##   <chr>    <int>  
## 1 Black Dot      5
```

```
#7 B.
```

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

```
barplot(variation_count$n, names.arg = variation_count$variation, col = "pink",  
        main = "Variation Count", xlab = "Variation", ylab = "Count", las = 2)
```



```

library(dplyr)

variation_count <- data %>%
  count(variation)

save(variation_count, file = "variations.RData")
print(variation_count)

## # A tibble: 1 x 2
##   variation      n
##   <chr>      <int>
## 1 Black Dot      5

black_variations <- variation_count[grepl("Black", variation_count$variation), ]
white_variations <- variation_count[grepl("White", variation_count$variation), ]

barplot(cbind(black_variations$n, white_variations$n),
        beside = TRUE,
        names.arg = c(black_variations$variation, white_variations$variation),
        main = "Black vs. White Alexa Variations",
        ylab = "Number of Variations",
        col = c("black", "white"),
        legend.text = c("Black", "White"),
        args.legend = list(x = "topright"))

```

Black vs. White Alexa Variations

