

RWorksheet 4b

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

matrixB <- matrix(0, nrow = 5, ncol = 5)
print(matrixB)

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

for(i in 1:5){
  for(j in 1:5){
    matrixB[i,j] <- abs(vectorB[i] - vectorB[j])
  }
}
print(matrixB)
```

```
##      [,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
```

```
#2.
for(i in 1:5) {
  for(j in 1:i) {
    cat("*")
  }
  cat("\n")
}
```

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

```
#3.
print("Enter a positive integer to start the Fibonacci sequence: ")
```

```
## [1] "Enter a positive integer to start the Fibonacci sequence: "
```

```

start <- as.integer(readline(prompt = ""))

#repeat {
#  print(start)
#  if(start > 500) break
#  next <- start + tail(fib, n=1)
#  start <- next
#}

#4.
#a.
shoe <- read.csv("shoe data.csv")
shoes <- shoe[c(1:6),]
shoes

##   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

#b.
MaleSub<- subset(shoes, Gender == "Male")
FemSub<- subset(shoes, Gender == "Female")

print("Male Subset:")

## [1] "Male Subset:"
print(MaleSub)

## [1] Shoe.Size Height      Gender
## <0 rows> (or 0-length row.names)
print("Female Subset:")

## [1] "Female Subset:"
print(FemSub)

## [1] Shoe.Size Height      Gender
## <0 rows> (or 0-length row.names)
nrow(MaleSub)

## [1] 0
nrow(FemSub)

## [1] 0

#c
GraphMF<- table(shoes$Gender)
barplot(GraphMF,
  main = "Number of Males and Females",
  xlab = "Gender",
  ylab = "Count",
  col = c("red", "blue"),

```

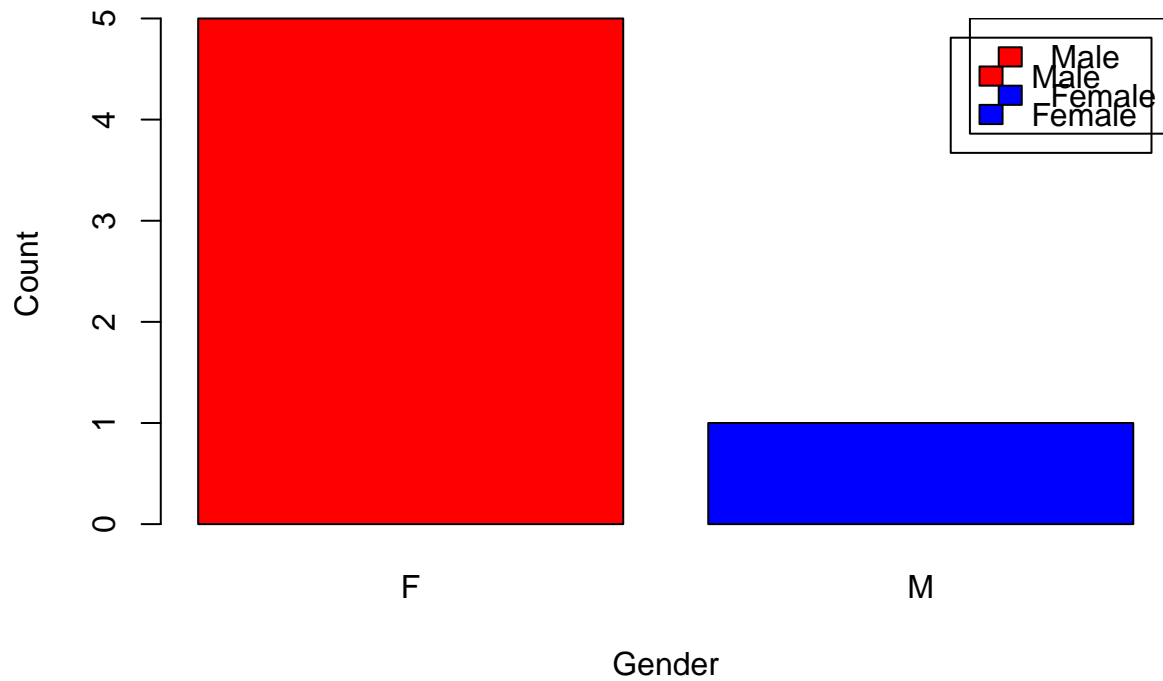
```

    legend.text = c("Male", "Female"),
    beside = TRUE
)

legend("topright", legend = c("Male", "Female"), fill = c("red", "blue"))

```

Number of Males and Females



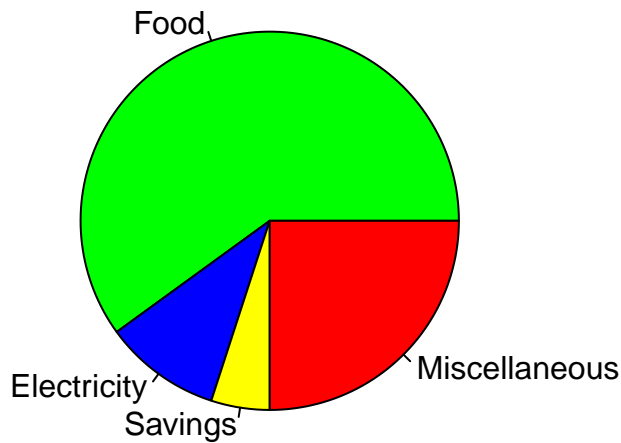
```

#5.
expenses <- c(60, 10, 5, 25)
labels <- c("Food", "Electricity", "Savings", "Miscellaneous")

pie(expenses, labels = labels, col = c("green","blue","yellow","red"),
    main = "Monthly Expenses of Dela Cruz Family")

```

Monthly Expenses 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.

```
mean_iris <- c(mean(iris$Sepal.Length),
```

```
               mean(iris$Sepal.Width),
```

```
               mean(iris$Petal.Length),
```

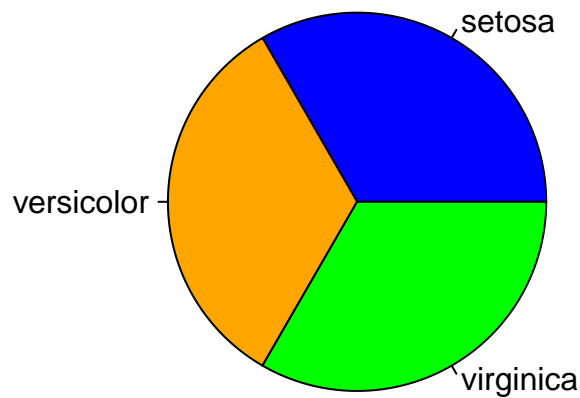
```
               mean(iris$Petal.Width))
```

#c.

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

```
pie(species, labels = names(species), col = c("blue","orange","green"), main = "Species Distribution in
```

Species Distribution in Iris Data



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

```
tail(setosa, n=6)
```

##	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, n=6)
```

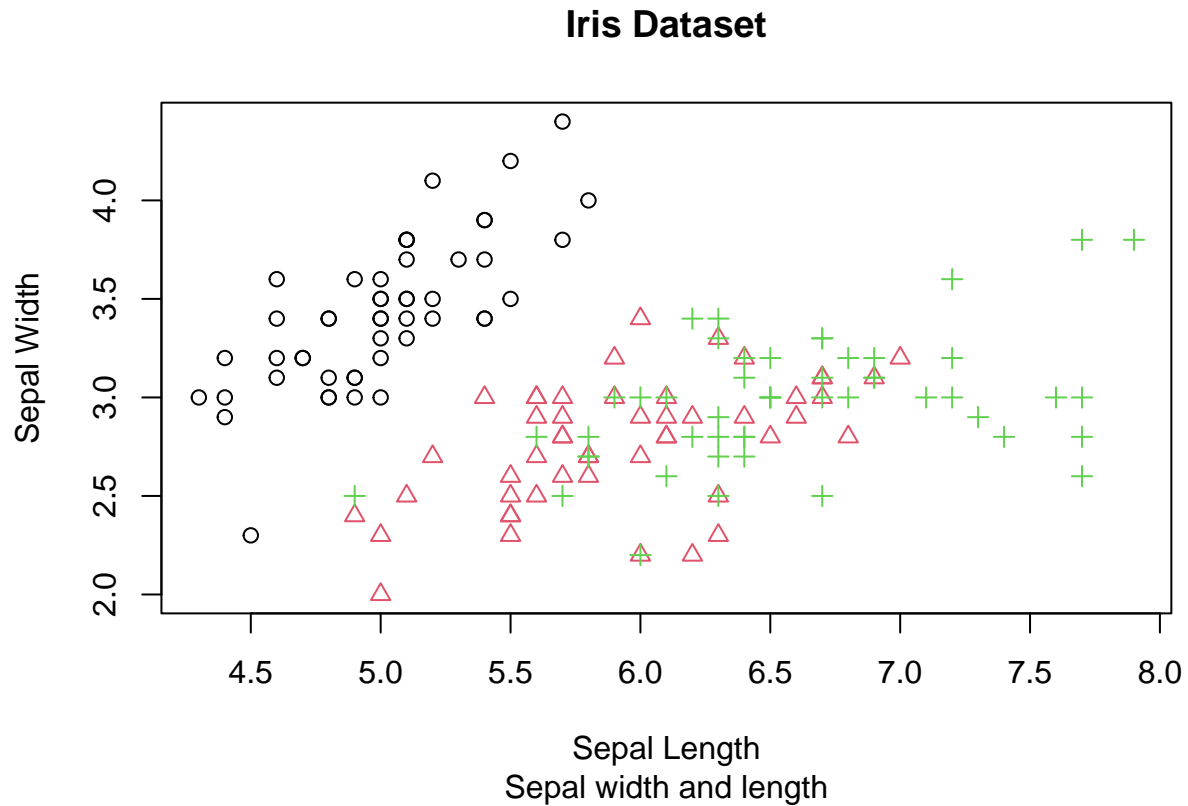
##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 95	5.6	2.7	4.2	1.3	versicolor
## 96	5.7	3.0	4.2	1.2	versicolor
## 97	5.7	2.9	4.2	1.3	versicolor
## 98	6.2	2.9	4.3	1.3	versicolor
## 99	5.1	2.5	3.0	1.1	versicolor
## 100	5.7	2.8	4.1	1.3	versicolor

```
tail(virginica, n=6)
```

##	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.  
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")
```



#f.
#The scatterplot shows similarities between the sepal width and length. It ranges from 5.5 to 7.0.
 #7.