RWorksheet_Francisco#4b

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```
#1
vectorA <- c(1,2,3,4,5)
for(i in vectorA){
  print(vectorA)
}
```

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

```
abs(vectorA)
```

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

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

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

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

```
#3
fibonacci_sequence <- function(start){
a <- 0
b <- 1

repeat {
  fib <- a+b
  a <- b
  b <- fib
  if (fib >= 500) {
      break
    }
  if (fib >= start) {
      print(fib)
    }
  }
```

```
}
sequencing <- as.numeric(readline(prompt="Enter a Number:"))
```

```
## Enter a Number:
```

```
if (!is.na(sequencing)<1) {
  print("Please enter a higher number")
} else {
  cat("Fibonacci sequence starting from", sequencing, "up to 500:\n")
  fibonacci_sequence(sequencing)
}
```

```
## [1] "Please enter a higher number"
```

```
#4a
datas <- read.csv("/cloud/project/worksheet#4/Household Data.csv")

#4b
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
```

```
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
```

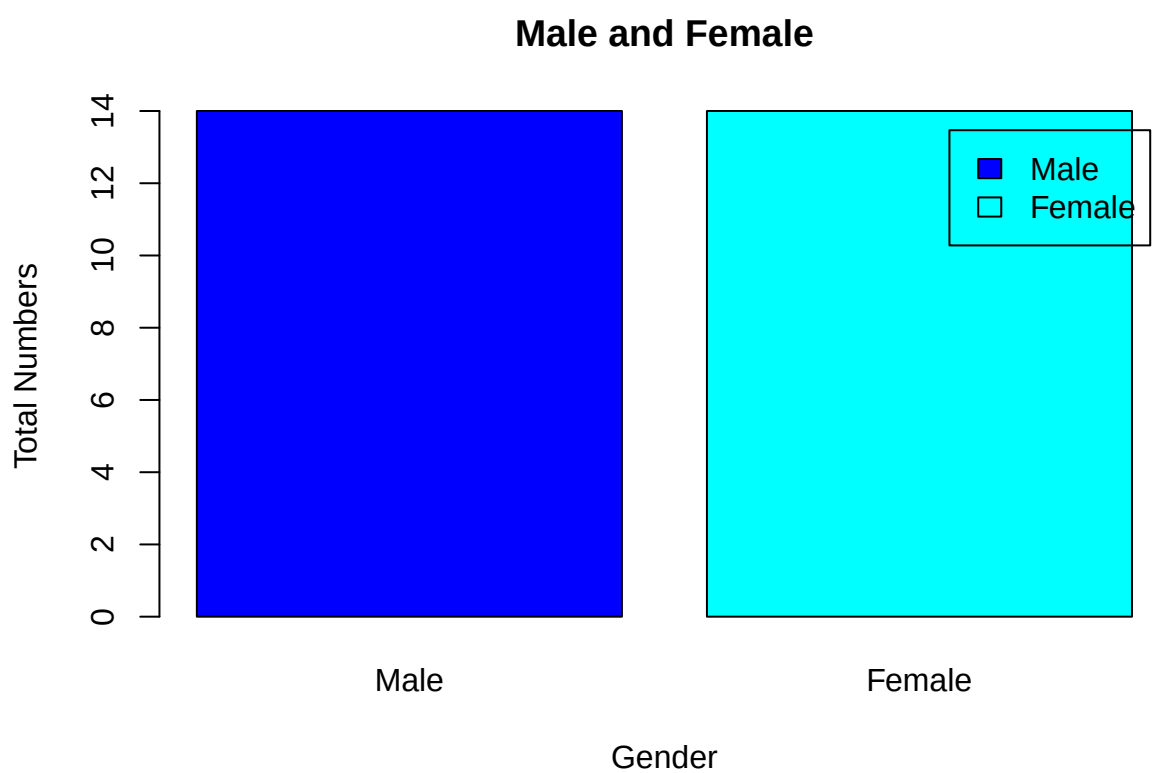
```r
num_male <- nrow(male)
num_female <- nrow(female)
cat("Number of observations for Male:", num_male, "\n")
```

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

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

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

```r
#4c
Plotting <- c(num_male,num_female)
names(Plotting) <- c("Male", "Female")
barplot(Plotting, main = "Male and Female", xlab = "Gender", ylab = "Total Numbers", col = c("blue", "cy
```

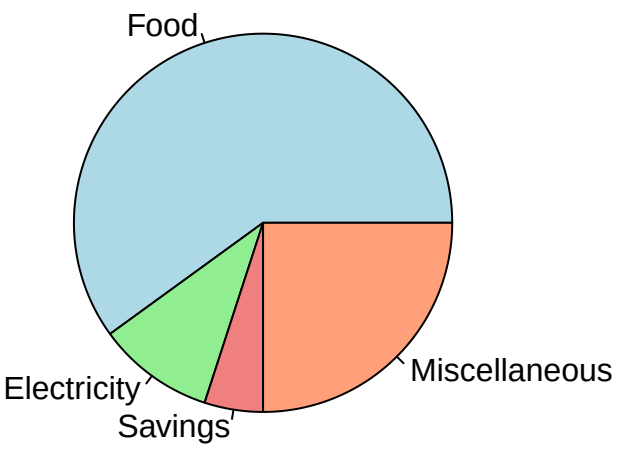



```r
#5
bills <- c("Food", "Electricity", "Savings", "Miscellaneous")
values <- c(60, 10, 5, 25)

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

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

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



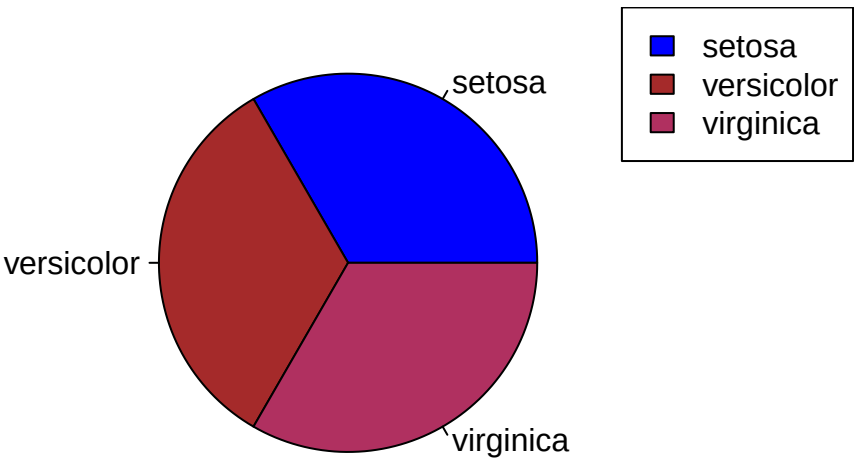

```
#6
data(iris)
str(iris)
```

```
## '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 ...
```

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

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

```
#6c
species <- table(iris$Species)
colors <- c("blue", "brown","maroon")
Pie <- pie(species, main = "Species Distribution", col = colors ,labels = names(species))
legend("topright", legend = names(species), fill = colors)
```




```
#6d
setosa <- subset(iris, Species == "setosa")
versicolor <- subset(iris, Species == "versicolor")
virginica <- subset(iris, Species == "virginica")
s<-tail(setosa)
v<- tail(versicolor)
v2<- tail(virginica)
s
```

```
##    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
```

```
v
```

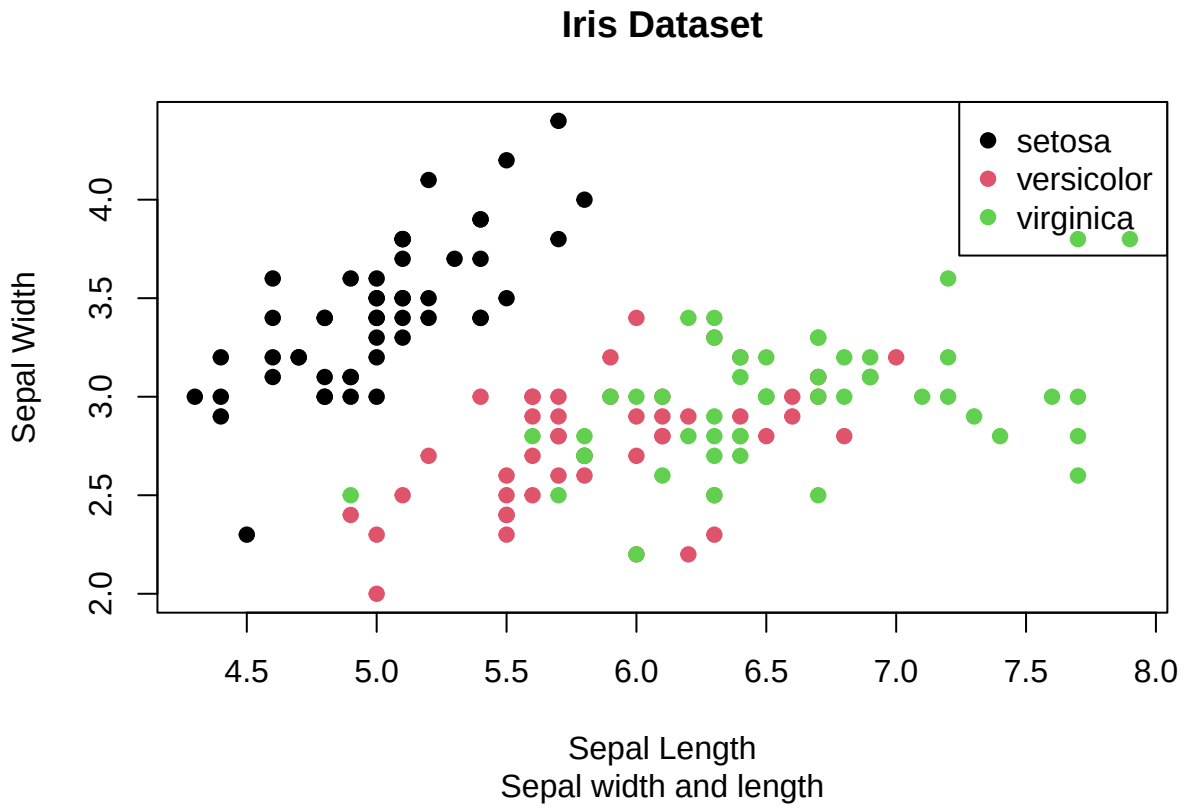
```
##     Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
## 95           5.6         2.7          4.2         1.3 versicolor
## 96           5.7         3.0          4.2         1.2 versicolor
## 97           5.7         2.9          4.2         1.3 versicolor
## 98           6.2         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
```

```
v2
```

```
##     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
```

```
#6e
plot(iris$Sepal.Length, iris$Sepal.Width, main = "Iris Dataset", sub = "Sepal width and length", xlab =
```

```r
legend("topright", legend = levels(iris$Species), pch = 19, col = 1:3)
```




```r
#6f
#The scatterplot shows the relation of sepal width and length for various species of iris flowers. Vers
```

```r
#7
library(readxl)
```