

RWorksheet_Layson#4b

Gilmar Layson

2024-10-28

#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

  while (b < 500) {
    fib <- a + b
```

```

a <- b
b <- fib
if (fib >= start) {
  print(fib)
}
}
}

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

```

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

```

if (is.na(sequencing) || 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"
```

```
#4.a.
```

```
HOUSE <- read.csv("C:\\Users\\User\\OneDrive\\Desktop\\Rworksheet\\Worksheet_4\\HOUSE.csv", header
```

```
#b.
```

```

male <- subset(HOUSE, 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(HOUSE, 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
```

```
nmale <- nrow(male)
nfemale <- nrow(female)
cat("Number of observations for Male:", nmale, "\n")
```

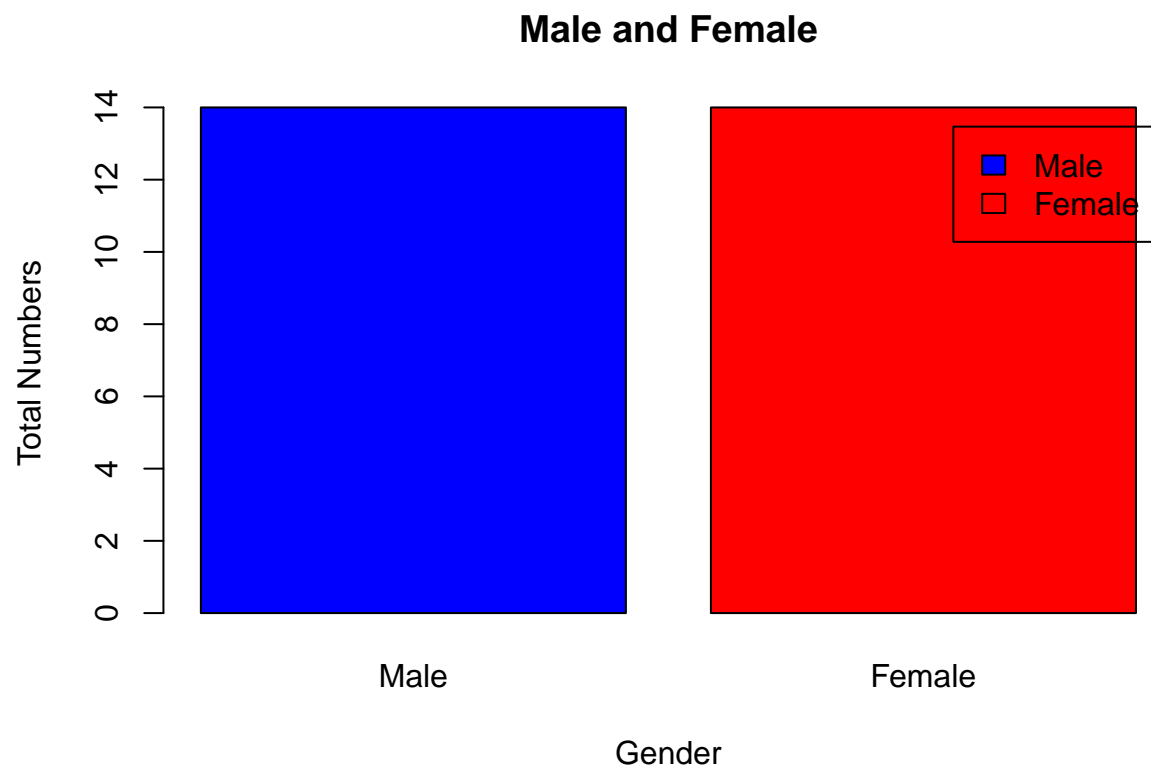
```
## Number of observations for Male: 14
```

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

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

```
#c.
```

```
Plotting <- c(nmale,nfemale)
names(Plotting) <- c("Male", "Female")
barplot(Plotting, main = "Male and Female", xlab = "Gender", ylab = "Total Numbers", col = c("blue", "red"))
```



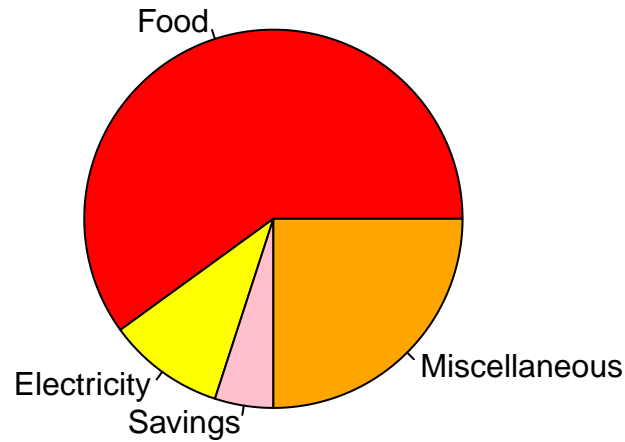
#5.

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

bill_data <- data.frame(bills, values)

pie(bill_data$values, labels = bill_data$bills,
    col = c("red", "yellow", "pink", "orange"),
    main = "Expenditures")
```

Expenditures



#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.

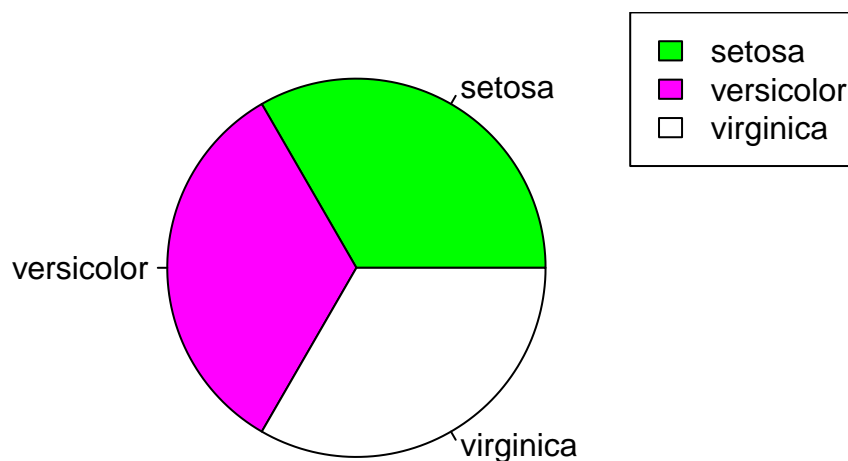
```
mean_values <- colMeans(iris[, c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")])
mean_values
```

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

#c.

```
species <- table(iris$Species)
colors <- c("green", "magenta", "white")
Pie <- pie(species, main = "Species Distribution", col = colors, labels = names(species))
legend("topright", legend = names(species), fill = colors)
```

Species Distribution



#d.

```
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
```

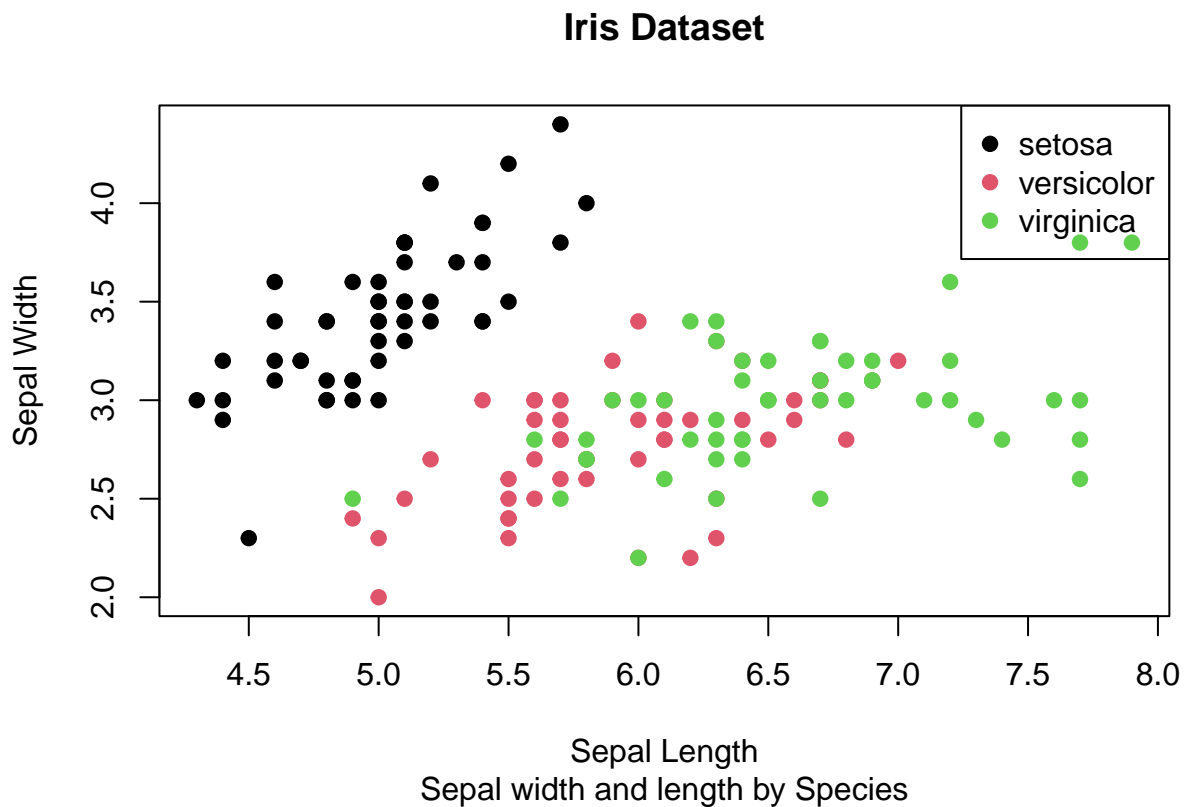
```
v2
```

```
##      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
```

```
#e.
```

```
plot(iris$Sepal.Length, iris$Sepal.Width,
     col = iris$Species,
     pch = 19,
     xlab = "Sepal Length",
     ylab = "Sepal Width",
     main = "Iris Dataset",
     sub = "Sepal width and length by Species"
)

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



```
#f.
```

```
#The relationship between sepal length and width for several iris flower species is displayed in a scat
```

```
#7.
```

```
library(readxl)
```