Worksheet-5 in R

Drake Francis M. Jaculina

2022-11-23

```
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

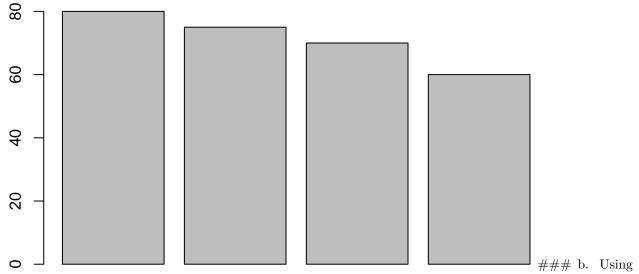
library(tinytex)
```

1. The table shows the enrollment of BS in Computer Science, SY 2010-2011.

```
## 1 1st 80
## 2 2nd 75
## 3 3rd 70
## 4 4th 60
```

a. Plot the data using a bar graph. Write the codes and copy the result.

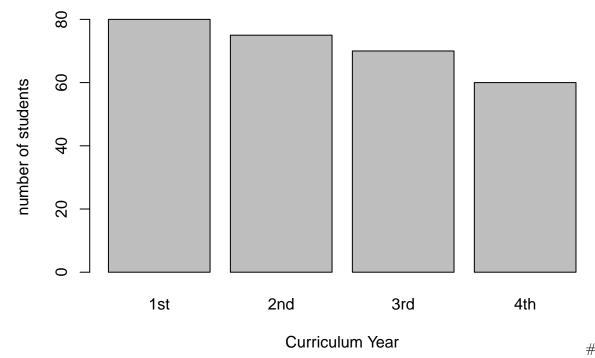
```
Enrollment2 <- c(80, 75, 70, 60)
barplot(Enrollment2)</pre>
```



the same table, label the barchart with Title = "Enrollment of BS Computer Science horizontal axis = "Curriculum Year" and vertical axis = "number of students"

```
course_list <- c("1st","2nd","3rd","4th")
bscs2 <- barplot(Enrollment2,
    main = "Enrollment of BS Computer Science",
    xlab = "Curriculum Year",
    ylab = "number of students",
    names.arg = course_list)</pre>
```

Enrollment of BS Computer Science



The monthly income of De Jesus family was spent on the following: 60% on Food, 10% on electricity, 5% for savings, and 25% for other miscellaneous expenses.

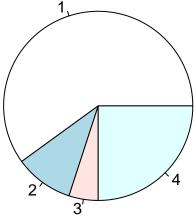
a. Create a table for the above scenario. Write the codes and its result.

```
expenses <- c("Food", "Electricity", "Savings", "Other Miscellaneous Expense")
percentage <- c(60, 10, 5, 25)
expensee2 <- data.frame(expenses,percentage)
table1 <- table(expensee2)
table1</pre>
```

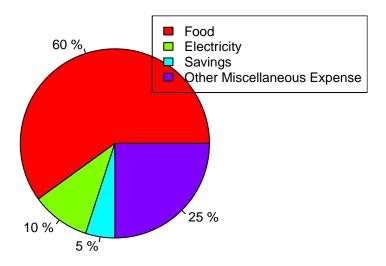
```
## expenses 5 10 25 60 ## Electricity 0 1 0 0 0 1 0 0 ## Other Miscellaneous Expense 0 0 0 1 0 0 ## Savings 1 0 0 0
```

b. Plot the data using a pie chart. Add labels, colors and legend. Write the codes and its result.

```
percentage_expenses <- c(60,10,5,25)
pie(percentage_expenses)</pre>
```



De Jesus family Monthly Expenses



3. Open the mtcars dataset.

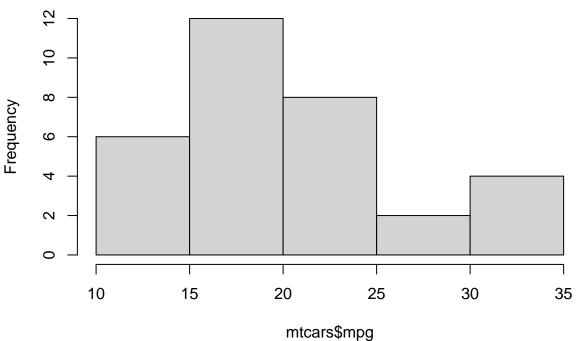
```
data("mtcars")
data_mpg <- mtcars$mpg
data_mpg

## [1] 21.0 21.0 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 17.8 16.4 17.3 15.2 10.4
## [16] 10.4 14.7 32.4 30.4 33.9 21.5 15.5 15.2 13.3 19.2 27.3 26.0 30.4 15.8 19.7
## [31] 15.0 21.4</pre>
```

a. Create a simple histogram specifically for mpg (miles per gallon) variable. Use \$ to select the mpg only. Write the codes and its result.

hist(mtcars\$mpg)

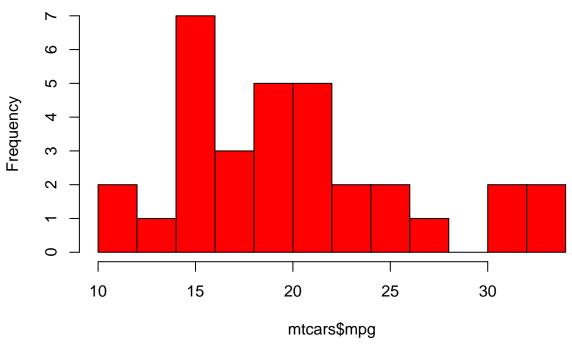
Histogram of mtcars\$mpg



Colored histogram with different number of bins. #### hist(mtcars\$mpg, breaks=12, col="red") ####
Note: breaks= controls the number of bins

hist(mtcars\$mpg, breaks=12, col="red")

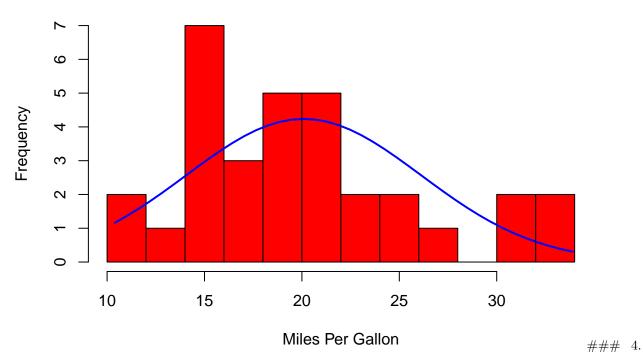
Histogram of mtcars\$mpg



c. Add a Normal Curve

###

Histogram with Normal Curve



Open the iris dataset. Create a subset for each species.

a. Write the codes and its result.

```
data("iris")
data_setosa <- subset(iris, Species == "setosa")
data_setosa</pre>
```

##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	1	5.1	3.5	1.4	0.2	setosa
##	2	4.9	3.0	1.4	0.2	setosa
##	3	4.7	3.2	1.3	0.2	setosa
##	4	4.6	3.1	1.5	0.2	setosa
##	5	5.0	3.6	1.4	0.2	setosa
##	6	5.4	3.9	1.7	0.4	setosa
##	7	4.6	3.4	1.4	0.3	setosa
##	8	5.0	3.4	1.5	0.2	setosa
##	9	4.4	2.9	1.4	0.2	setosa
##	10	4.9	3.1	1.5	0.1	setosa
##	11	5.4	3.7	1.5	0.2	setosa
##	12	4.8	3.4	1.6	0.2	setosa
##	13	4.8	3.0	1.4	0.1	setosa

##	14	4.3	3.0	1.1	0.1	setosa
##	15	5.8	4.0	1.2	0.2	setosa
##	16	5.7	4.4	1.5	0.4	setosa
##	17	5.4	3.9	1.3	0.4	setosa
##	18	5.1	3.5	1.4	0.3	setosa
##	19	5.7	3.8	1.7	0.3	setosa
##	20	5.1	3.8	1.5	0.3	setosa
##	21	5.4	3.4	1.7	0.2	setosa
##	22	5.1	3.7	1.5	0.4	setosa
##	23	4.6	3.6	1.0	0.2	setosa
##	24	5.1	3.3	1.7	0.5	setosa
##	25	4.8	3.4	1.9	0.2	setosa
##	26	5.0	3.0	1.6	0.2	setosa
##	27	5.0	3.4	1.6	0.4	setosa
##	28	5.2	3.5	1.5	0.2	setosa
##	29	5.2	3.4	1.4	0.2	setosa
##	30	4.7	3.2	1.6	0.2	setosa
##	31	4.8	3.1	1.6	0.2	setosa
##	32	5.4	3.4	1.5	0.4	setosa
	33	5.2	4.1	1.5	0.1	setosa
##	34	5.5	4.2	1.4	0.2	setosa
##	35	4.9	3.1	1.5	0.2	setosa
##	36	5.0	3.2	1.2	0.2	setosa
	37	5.5	3.5	1.3	0.2	setosa
##	38	4.9	3.6	1.4	0.1	setosa
##	39	4.4	3.0	1.3	0.2	setosa
##	40	5.1	3.4	1.5	0.2	setosa
##	41	5.0	3.5	1.3	0.3	setosa
##	42	4.5	2.3	1.3	0.3	setosa
##	43	4.4	3.2	1.3	0.2	setosa
##	44	5.0	3.5	1.6	0.6	setosa
##	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

data_versicolor <- subset(iris, Species == "versicolor")
data_versicolor</pre>

##		Sepal.Length	Sepal.Width	Petal.Length	${\tt Petal.Width}$	Species
##	51	7.0	3.2	4.7	1.4	versicolor
##	52	6.4	3.2	4.5	1.5	versicolor
##	53	6.9	3.1	4.9	1.5	versicolor
##	54	5.5	2.3	4.0	1.3	versicolor
##	55	6.5	2.8	4.6	1.5	versicolor
##	56	5.7	2.8	4.5	1.3	versicolor
##	57	6.3	3.3	4.7	1.6	versicolor
##	58	4.9	2.4	3.3	1.0	versicolor
##	59	6.6	2.9	4.6	1.3	versicolor
##	60	5.2	2.7	3.9	1.4	versicolor
##	61	5.0	2.0	3.5	1.0	versicolor
##	62	5.9	3.0	4.2	1.5	versicolor
##	63	6.0	2.2	4.0	1.0	versicolor

##	64	6.1	2.9	4.7	1.4 versicolor
##	65	5.6	2.9	3.6	1.3 versicolor
##	66	6.7	3.1	4.4	1.4 versicolor
##	67	5.6	3.0	4.5	1.5 versicolor
##	68	5.8	2.7	4.1	1.0 versicolor
##	69	6.2	2.2	4.5	1.5 versicolor
##	70	5.6	2.5	3.9	1.1 versicolor
##	71	5.9	3.2	4.8	1.8 versicolor
##	72	6.1	2.8	4.0	1.3 versicolor
##	73	6.3	2.5	4.9	1.5 versicolor
##	74	6.1	2.8	4.7	1.2 versicolor
##	75	6.4	2.9	4.3	1.3 versicolor
##	76	6.6	3.0	4.4	1.4 versicolor
##	77	6.8	2.8	4.8	1.4 versicolor
##	78	6.7	3.0	5.0	1.7 versicolor
##	79	6.0	2.9	4.5	1.5 versicolor
##	80	5.7	2.6	3.5	1.0 versicolor
##	81	5.5	2.4	3.8	1.1 versicolor
##	82	5.5	2.4	3.7	1.0 versicolor
##	83	5.8	2.7	3.9	1.2 versicolor
##	84	6.0	2.7	5.1	1.6 versicolor
##	85	5.4	3.0	4.5	1.5 versicolor
##	86	6.0	3.4	4.5	1.6 versicolor
##	87	6.7	3.1	4.7	1.5 versicolor
##	88	6.3	2.3	4.4	1.3 versicolor
##	89	5.6	3.0	4.1	1.3 versicolor
##	90	5.5	2.5	4.0	1.3 versicolor
##	91	5.5	2.6	4.4	1.2 versicolor
##	92	6.1	3.0	4.6	1.4 versicolor
##	93	5.8	2.6	4.0	1.2 versicolor
##	94	5.0	2.3	3.3	1.0 versicolor
##	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

data_virginica <- subset(iris, Species == "virginica")
data_virginica</pre>

##		Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
##	101	6.3	3.3	6.0	2.5	virginica
##	102	5.8	2.7	5.1	1.9	virginica
##	103	7.1	3.0	5.9	2.1	virginica
##	104	6.3	2.9	5.6	1.8	virginica
##	105	6.5	3.0	5.8	2.2	virginica
##	106	7.6	3.0	6.6	2.1	virginica
##	107	4.9	2.5	4.5	1.7	virginica
##	108	7.3	2.9	6.3	1.8	virginica
##	109	6.7	2.5	5.8	1.8	virginica
##	110	7.2	3.6	6.1	2.5	virginica
##	111	6.5	3.2	5.1	2.0	virginica
##	112	6.4	2.7	5.3	1.9	virginica
##	113	6.8	3.0	5.5	2.1	virginica

##	114	5.7	2.5	5.0	2 0 mirainica
##	115	5.8	2.8	5.1	2.0 virginica
##	116	6.4	3.2	5.3	2.4 virginica
##	117	6.5	3.0	5.5	2.3 virginica
##	118	7.7	3.8	6.7	1.8 virginica
##					2.2 virginica
	119	7.7	2.6	6.9	2.3 virginica
##	120 121	6.0	2.2	5.0	1.5 virginica
##		6.9	3.2	5.7	2.3 virginica
##	122	5.6	2.8	4.9	2.0 virginica
##	123	7.7	2.8	6.7	2.0 virginica
##	124	6.3	2.7	4.9	1.8 virginica
##	125	6.7	3.3	5.7	2.1 virginica
##	126	7.2	3.2	6.0	1.8 virginica
##	127	6.2	2.8	4.8	1.8 virginica
##	128	6.1	3.0	4.9	1.8 virginica
##	129	6.4	2.8	5.6	2.1 virginica
##	130	7.2	3.0	5.8	1.6 virginica
##	131	7.4	2.8	6.1	1.9 virginica
##	132	7.9	3.8	6.4	2.0 virginica
##	133	6.4	2.8	5.6	2.2 virginica
##	134	6.3	2.8	5.1	1.5 virginica
##	135	6.1	2.6	5.6	1.4 virginica
##	136	7.7	3.0	6.1	2.3 virginica
##	137	6.3	3.4	5.6	2.4 virginica
##	138	6.4	3.1	5.5	1.8 virginica
##	139	6.0	3.0	4.8	1.8 virginica
##	140	6.9	3.1	5.4	2.1 virginica
##	141	6.7	3.1	5.6	2.4 virginica
##	142	6.9	3.1	5.1	2.3 virginica
##	143	5.8	2.7	5.1	1.9 virginica
##	144	6.8	3.2	5.9	2.3 virginica
##	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

b. Get the mean for every characteristics of each species using colMeans().

```
Write the codes and its result. Example: setosa <- colMeans(setosa[sapply(setosaDF,is.numeric)])
```

```
setosa <- colMeans(data_setosa[sapply(data_setosa,is.numeric)])
setosa</pre>
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 5.006 3.428 1.462 0.246
versicolor <- colMeans(data_versicolor[sapply(data_versicolor,is.numeric)])
versicolor</pre>
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 5.936 2.770 4.260 1.326
virginica <- colMeans(data_virginica[sapply(data_virginica,is.numeric)])
virginica</pre>
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width ## 6.588 2.974 5.552 2.026
```

c. Combine all species by using rbind()

The table should be look like this:

```
rbind_species <- rbind(setosa, versicolor, virginica)
rbind_species</pre>
```

```
##
              Sepal.Length Sepal.Width Petal.Length Petal.Width
## setosa
                      5.006
                                   3.428
                                                 1.462
## versicolor
                      5.936
                                   2.770
                                                 4.260
                                                              1.326
## virginica
                      6.588
                                   2.974
                                                 5.552
                                                              2.026
```

d. From the data in 4-c: Create the barplot(). Write the codes and its result. The barplot should be like this.

```
barplot(rbind_species, beside = TRUE,
    main = "Iris Data",
    xlab = "Characteristics",
    ylab = "Mean Scores",
    col = c("red", "green", "blue"))
```

Iris Data

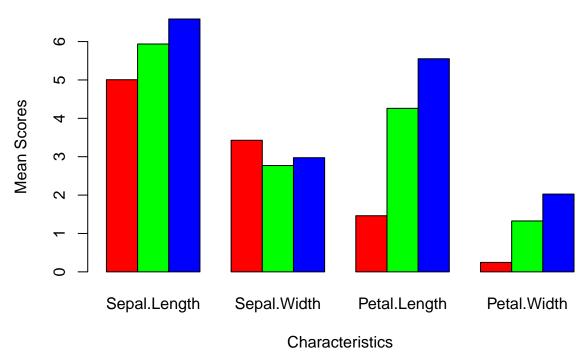


Figure 1: Iris Data using Barplot