# 2.a. Write an R script to find subset of dataset by using subset (), aggregate().

### > subset(iris,iris\$Sepal.Length==5.0) Sepal.Length Sepal.Width Petal.Length Petal.Width Species 5 3.6 1.4 0.2 setosa 8 5 3.4 1.5 0.2 setosa 5 26 3.0 1.6 0.2 setosa 27 5 3.4 1.6 0.4 setosa 36 5 3.2 1.2 0.2 setosa 5 41 3.5 1.3 0.3 setosa 5 44 3.5 1.6 0.6 setosa 50 5 3.3 1.4 0.2 setosa 2.0 61 5 3.5 1.0 versicolor 94 5 2.3 3.3 1.0 versicolor

# > aggregate(. ~ Species,data = iris, mean)

	Species	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
1	setosa	5.006	3.428	1.462	0.246
2	versicolor	5.936	2.770	4.260	1.326
3	virainica	6.588	2.974	5.552	2.026

### b. Plot the correlation plot on dataset and visualize giving an overview of relationships

```
x<-matrix(rnorm(2),nrow=5,ncol=4)
y<-matrix(rnorm(15),nrow=5,ncol=3)
iris<- read.csv(file.choose(),header = T)
image(X<-seq(dim(x)[2]),
    Y<-seq(dim(y)[2]),
    z=cor(x,y),
    xlab="xcolumn",
    ylab="y column")
#install.packages("qtlcharts")
library("qtlcharts")
data(iris)
iris$species<-NULL
iplotCorr(iris,reorder=TRUE)</pre>
```

# **OUTPUT:**

