#importing library

library(ggplot2)

#importing the data

data(iris)

head(iris)

nrow(iris)

#copying the data into other variable

i1<-iris

#removing the species column

i1$Species=NULL

#applying the kmeans function as we know there are three types of species in the data set

res<-kmeans(i1,3)

res

res$size

res$cluster

head(iris)

#plotting the graph of the original data set with respect to cluster

pl<-ggplot(data=iris,aes(x=Sepal.Length,y=Sepal.Width))+geom\_point(aes(col=res$cluster))

pl

#plotting a table between the real species and the cluster

table(iris$Species,res$cluster)