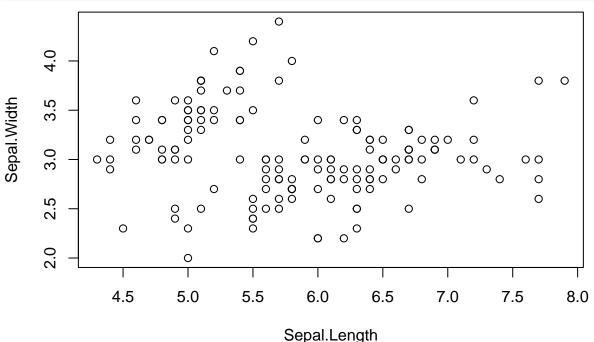
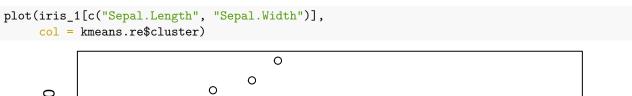
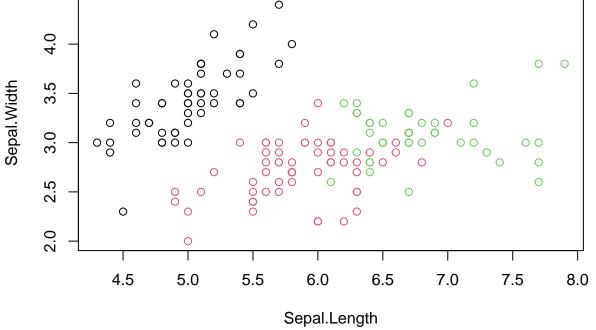
R Notebook

```
# Loading data
data(iris)
# Structure
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 1 ...
# Installing Packages
install.packages("ClusterR")
## Installing package into '/home/6b/R/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
install.packages("cluster")
## Installing package into '/home/6b/R/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
# Loading package
library(ClusterR)
library(cluster)
# Removing initial label of
# Species from original dataset
iris_1 <- iris[, -5]</pre>
# Fitting K-Means clustering Model
# to training dataset
set.seed(240) # Setting seed
kmeans.re <- kmeans(iris_1, centers = 3, nstart = 20)</pre>
kmeans.re
## K-means clustering with 3 clusters of sizes 50, 62, 38
##
## Cluster means:
    Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1
       5.006000
                  3.428000
                           1.462000
                                         0.246000
## 2
        5.901613
                  2.748387
                              4.393548
                                         1.433871
        6.850000
                  3.073684
## 3
                              5.742105
                                         2.071053
##
## Clustering vector:
```

```
[149] 3 2
##
## Within cluster sum of squares by cluster:
## [1] 15.15100 39.82097 23.87947
  (between_SS / total_SS = 88.4 %)
##
##
## Available components:
##
## [1] "cluster"
            "centers"
                    "totss"
                             "withinss"
                                     "tot.withinss"
            "size"
                    "iter"
                             "ifault"
## [6] "betweenss"
# Cluster identification for
# each observation
kmeans.re$cluster
##
  ## [149] 3 2
# Confusion Matrix
cm <- table(iris$Species, kmeans.re$cluster)</pre>
cm
##
##
##
        50
           0
  setosa
##
  versicolor
        0 48
##
  virginica
         0 14 36
# Model Evaluation and visualization
plot(iris_1[c("Sepal.Length", "Sepal.Width")])
                     0
```

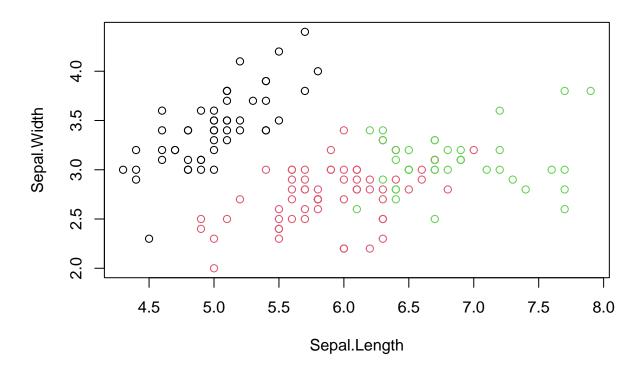






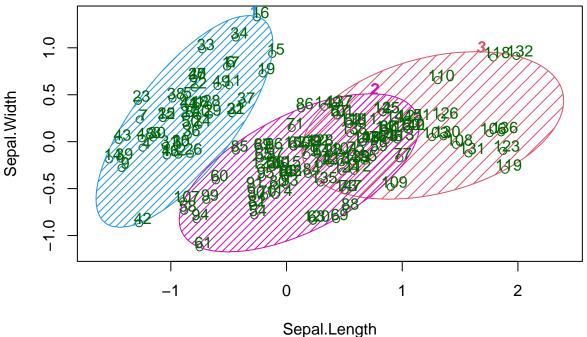
```
plot(iris_1[c("Sepal.Length", "Sepal.Width")],
    col = kmeans.re$cluster,
    main = "K-means with 3 clusters")
```

K-means with 3 clusters



```
## Plotiing cluster centers
kmeans.re$centers
     Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1
         5.006000
                     3.428000
                                   1.462000
                                               0.246000
## 2
         5.901613
                     2.748387
                                   4.393548
                                               1.433871
                                   5.742105
         6.850000
                     3.073684
## 3
                                               2.071053
kmeans.re$centers[, c("Sepal.Length", "Sepal.Width")]
##
     Sepal.Length Sepal.Width
## 1
         5.006000
                     3.428000
## 2
         5.901613
                     2.748387
## 3
         6.850000
                     3.073684
## Visualizing clusters
y_kmeans <- kmeans.re$cluster</pre>
clusplot(iris_1[, c("Sepal.Length", "Sepal.Width")],
         y_kmeans,
         lines = 0,
         shade = TRUE,
         color = TRUE,
         labels = 2,
         plotchar = FALSE,
         span = TRUE,
         main = paste("Cluster iris"),
         xlab = 'Sepal.Length',
         ylab = 'Sepal.Width')
```

Cluster iris



Code contributed by Manja