```
> # Loading package
> library(clusterR)
> library(cluster)
> # Loading data
> data(iris)
> 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 0.4 0.3 0.2 0.2 0.1 ...
$ Species : Factor w/ 3 levels "setosa", "versicolor",..: 1 1 1 1 1 1 1 1 1 ...
> # Removing initial label of
> # Species from original dataset
> iris_1 <- iris[, -5]
> # Fitting K-Means clustering Model
> # to training dataset
 > # to training dataset

> set. seed(240) # Setting seed

> kmeans.re <- kmeans(iris_1, centers = 3, nstart = 20)

> kmeans.re
 > 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
3 6.850000 3.073684 5.742105 2.071053
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"
[9] "ifault"
> # Cluster identification for
                                     "centers" "totss"
                                                                                                           "withinss" "tot.withinss" "betweenss" "size"
                                                                                                                                                                                                                                                           "iter"
 # Confusion Matrix
 > cm <- table(iris$Species, kmeans.re$cluster)
    1 2 3
setosa 50 0 0
versicolor 0 48 2
virginica 0 14 36
# Model Evaluation and visualization
plot(iris_1[c("Sepal.Length", "Sepal.Width")],
col = kmeans.resColuster,
main = "K-means with 3 clusters")
## Ploting cluster centers
kmeans.resCenters

      Kmeans.re$centers

      Sepal.Length Sepal.Width Petal.Length Petal.Width

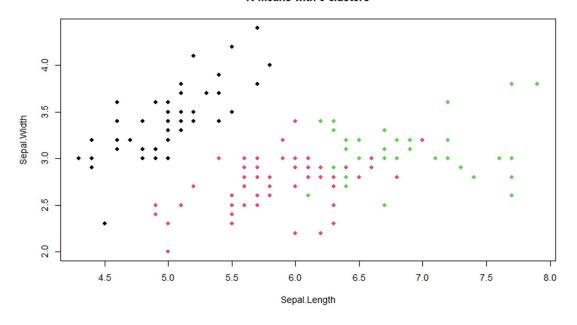
      5.006000
      3.428000
      1.462000
      0.246000

      5.901613
      2.748387
      4.393548
      1.433871

      6.850000
      3.073684
      5.742105
      2.071053

    b.850000 3.073684 5.742105 2.071053
kmeans.re$centers[, c("Sepal.Length", "Sepal.Width")]
Sepal.Length Sepal.Width
5.006000 3.428000
5.901613 2.748387
6.850000 3.073684
## Vigualizing clusters
 > ## Visualizing clusters
> y_kmeans <- kmeans.re$cluster
> 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')
```

K-means with 3 clusters



Cluster iris

