Practical No. 04

AIM - Practical of Clustering.

Source Code -

```
"k-means clustering "
data("iris")
names(iris)
new_data<-subset(iris,select = c(-Species))</pre>
new data
cl <- kmeans(new data,3)</pre>
cl
data <- new_data</pre>
wss <- sapply(1:15, function(k){kmeans(data, k )$tot.withinss})</pre>
plot(1:15, wss, type="b", pch=19, frame=FALSE, xlab="Number of clusters K",
     ylab="Total within-clusters sum of squares")
install.packages("cluster")
library(cluster)
clusplot(new data, cl$cluster, color=TRUE, shade=TRUE, labels=2, lines=0)
cl$cluster
cl$centers
"agglomerative clustering"
clusters <- hclust(dist(iris[, 3:4]))</pre>
plot(clusters)
clusterCut <- cutree(clusters, 3)</pre>
table(clusterCut, iris$Species)
install.packages("ggplot2")
library("ggplot2")
ggplot(iris, aes(Petal.Length, Petal.Width, color = Species)) +
  geom point(alpha = 0.4, size = 3.5) + geom point(col = clusterCut) +
  scale_color_manual(values = c('black', 'red', 'green'))
clusters <- hclust(dist(iris[, 3:4]), method='average')</pre>
clusterCut1 <- cutree(clusters, 3)</pre>
table(clusterCut1, iris$Species)
plot(clusters)
ggplot(iris, aes(Petal.Length, Petal.Width, color=Species)) +
  geom point(alpha = 0.4, size = 3.5) + geom point(col=clusterCut1) +
  scale_color_manual(values = c('black', 'red', 'green'))
```

OUTPUT -

```
> "k-means clustering "
[1] "k-means clustering"
> data("iris")
> names(iris)
[1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width"
                                                                                           "Species"
> new_data<-subset(iris,select = c(-Species))</pre>
> new_data
    Sepal.Length Sepal.Width Petal.Length Petal.Width
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87 88	6.7 6.3	3.1 2.3	4.7	1.5 121	6.9	3.2	5.7	2.3
89	5.6	3.0	4.4 4.1	1.3 122 1.3 123	5.6	2.8	4.9	2.0
90	5.5	2.5	4.0		7.7	2.8	6.7	2.0
91	5.5	2.6	4.4	127	6.3	2.7	4.9	1.8
92	6.1	3.0	4.4	123	6.7	3.3	5.7	2.1
93	5.8	2.6	4.0	4 2 120	7.2	3.2	6.0	1.8
94	5.0	2.3	3.3	1 0 12/	6.2	2.8	4.8	1.8
95	5.6	2.7	4.2	1.3 128	6.1	3.0	4.9	1.8
96	5.7	3.0	4.2	1.2 129	6.4	2.8	5.6	2.1
97	5.7	2.9	4.2	1.3 130	7.2	3.0	5.8	1.6
98	6.2	2.9	4.3	1.3 131	7.4	2.8	6.1	1.9
99	5.1	2.5	3.0	1.1 132	7.9	3.8	6.4	2.0
100	5.7	2.8	4.1	1.3 133	6.4	2.8	5.6	2.2
101	6.3	3.3	6.0	2.5 134	6.3	2.8	5.1	1.5
102	5.8	2.7	5.1	1.9 135	6.1	2.6	5.6	1.4
103	7.1	3.0	5.9	2.1 136	7.7	3.0	6.1	2.3
104	6.3	2.9	5.6	1.8 137	6.3	3.4	5.6	2.4
105	6.5	3.0	5.8	2.2 138	6.4	3.1	5.5	1.8
106	7.6	3.0	6.6	2.1 139	6.0	3.0	4.8	1.8
107	4.9	2.5	4.5	1.7 140	6.9	3.1	5.4	2.1
108	7.3	2.9	6.3	1.8 141	6.7	3.1	5.6	2.4
109	6.7	2.5	5.8	1.8 142	6.9	3.1	5.1	2.3
110	7.2	3.6	6.1	2.5 1/12	5.8	2.7	5.1	1.9
111	6.5	3.2	5.1	2.0	6.8	3.2	5.9	2.3
112	6.4	2.7	5.3	1.9	6.7		5.7	
113	6.8	3.0	5.5	2.1 145		3.3		2.5
114	5.7	2.5	5.0	2.0 146	6.7	3.0	5.2	2.3
115	5.8	2.8	5.1	2.4 147	6.3	2.5	5.0	1.9
116	6.4	3.2	5.3	2.3 148	6.5	3.0	5.2	2.0
117	6.5	3.0	5.5	1.8 149	6.2	3.4	5.4	2.3
118	7.7	3.8	6.7	2.2 150	5.9	3.0	5.1	1.8
119	7.7	2.6	6.9	2.3				
120	6.0	2.2	5.0	1.5				

> cl <- kmeans(new_data,3)</pre>

> c1

K-means clustering with 3 clusters of sizes 21, 96, 33

Cluster means:

Sepal.Length Sepal.Width Petal.Length Petal.Width 1 4.738095 2.904762 1.790476 0.3523810 2 6.314583 2.895833 4.973958 1.7031250 3 5.175758 3.624242 1.472727 0.2727273

Clustering vector:

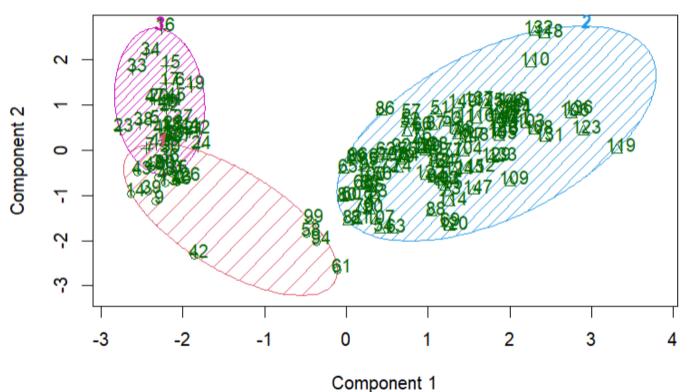
2 2

2 2 2 2 2

15 16 23 24 25 42 43 44 45 - 3 - 1 64 65 84 85 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 2 2 141 142 143 144 145 146 147 148 149 150

```
Within cluster sum of squares by cluster:
[1] 17.669524 118.651875
                              6.432121
 (between_SS / total_SS = 79.0 \%)
Available components:
[1] "cluster"
                     "centers"
                                                      "withinss"
                                                                      "tot.withinss"
                                     "totss"
[6] "betweenss"
                     "size"
                                     "iter"
                                                      "ifault"
> data <- new_data
> wss <- sapply(1:15, function(k){kmeans(data, k)$tot.withinss})</pre>
> WSS
 [1] 681.37060 152.34795
                            78.85144
                                       57.22847
                                                  69.24240 47.61943
                                                                        39.98885
      32.96739 28.17230 26.26447
                                       25.65746 23.93863 22.48749
 [8]
[15]
      20.19866
> plot(1:15, wss, type="b", pch=19, frame=FALSE,
        xlab="Number of clusters K",
       ylab="Total within-clusters sum of squares")
     700
Total within-clusters sum of squares
     500
     300
      100
                  2
                                                8
                                                          10
                                                                    12
                            4
                                      6
                                                                              14
                                      Number of clusters K
```

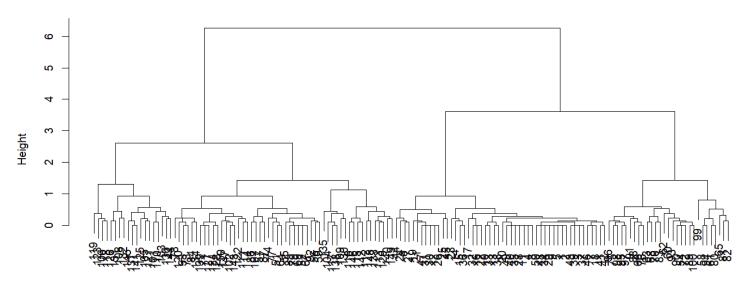
CLUSPLOT(new_data)



These two components explain 95.81 % of the point variability.

```
> cl$cluster
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101 102 103 104 105
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126 127 128 129 130 131 132 133 134 135 136 137 138
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> cl$centers
  Sepal.Length Sepal.Width Petal.Length Petal.Width
                    2.904762
                                   1.790476
                                                0.3523810
       4.738095
2
                    2.895833
                                   4.973958
                                                1.7031250
       6.314583
       5.175758
                    3.624242
                                   1.472727
                                                0.2727273
> "agglomarative clustering "
[1] "agglomarative clustering "
> clusters <- hclust(dist(iris[, 3:4]))</pre>
> plot(clusters)
```

Cluster Dendrogram



```
> clusterCut <- cutree(clusters, 3)</pre>
                                                      dist(iris[, 3:4])
  table(clusterCut, iris$Species)
                                                    hclust (*, "complete")
clusterCut setosa versicolor virginica
                 50
                               0
          1
          2
                  0
                                          50
                              21
          3
                  0
                              29
                                           0
> install.packages("ggplot2")
```

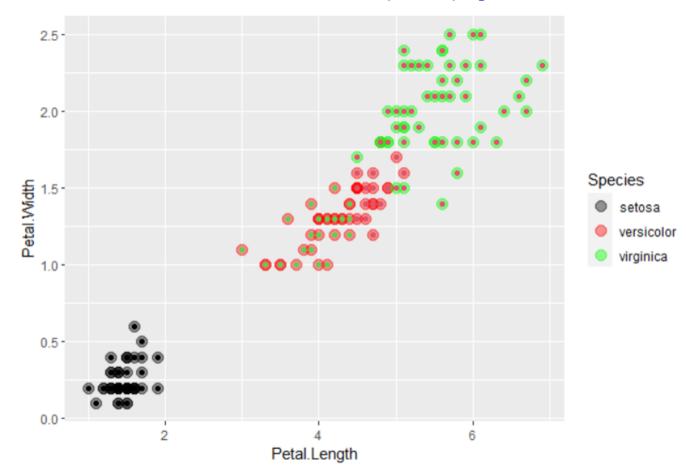
```
package 'ggplot2' successfully unpacked and MD5 sums checked
```

The downloaded binary packages are in

C:\Users\Kunal\AppData\Local\Temp\RtmpmKwA7v\downloaded_packages > library("ggplot2")

Need help? Try Stackoverflow: https://stackoverflow.com/tags/ggplot2

- > ggplot(iris, aes(Petal.Length, Petal.Width, color = Species)) +
- geom_point(alpha = 0.4, size = 3.5) + geom_point(col = clusterCut) +
 scale_color_manual(values = c('black', 'red', 'green'))



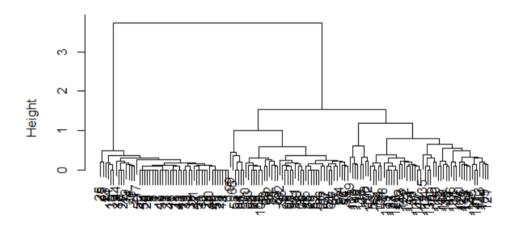
- > clusters <- hclust(dist(iris[, 3:4]), method='average')</pre>
- > clusterCut1 <- cutree(clusters, 3)</pre>
- > table(clusterCut1, iris\$Species)

clusterCut1 setosa versicolor virginica

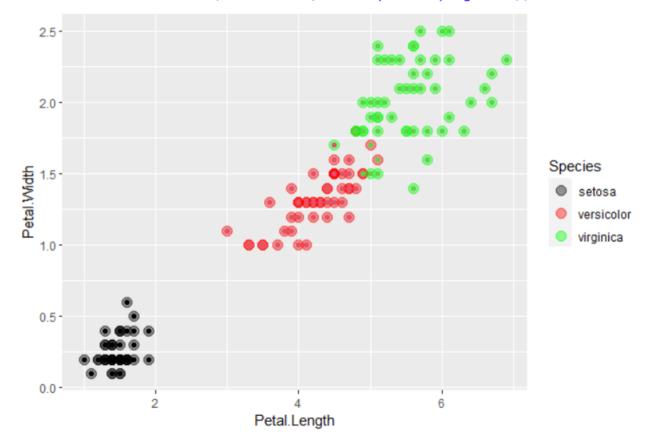
1	50	0	0
2	0	45	1
3	0	5	49

> plot(clusters)

Cluster Dendrogram



dist(iris[, 3:4]) hclust (*, "average")



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