Lab 8: Unsupervised Learning – Clustering

1. Implementation and analysis of Clustering algorithms like:

    1. K-Means
    2. Hierarchical Clustering - Agglomerative

Theory:

K-Means Clustering:

K-Means Clustering is an Unsupervised Learning algorithm, which groups the unlabeled dataset into different clusters. Here K defines the number of pre-defined clusters that need to be created in the process, as if K=2, there will be two clusters, and for K=3, there will be three clusters, and so on. It is an iterative algorithm that divides the unlabeled dataset into k different clusters in such a way that each dataset belongs to only one group that has similar Properties. It allows us to cluster the data into different groups and a convenient way to discover the categories of groups in the unlabeled dataset on its own without the need for any training. It is a centroid-based algorithm, where each cluster is associated with a centroid. The main aim of this algorithm is to minimize the sum of distances between the data point and their corresponding clusters. The algorithm takes the unlabeled dataset as input, divides the dataset into k-number of clusters, and repeats the process until it does not find the best clusters. The value of k should be predetermined in this algorithm.

Working of K-Means algorithm:

Step-1: Select the number K to decide the number of clusters.

Step-2: Select random K points or centroids. (It can be other from the input dataset).

Step-3: Assign each data point to their closest centroid, which will form the predefined K clusters.

Step-4: Calculate the variance and place a new centroid of each cluster.

Step-5: Repeat the third steps, which mean reassign each datapoint to the new closest centroid of each cluster.

Step-6: If any reassignment occurs, then go to step-4 else go to FINISH**.**

Step-7: The model is ready.

Hierarchical Clustering-Agglomerative:

In agglomerative clustering,Initially consider every data point as an individual Cluster and at every step, merge the nearest pairs of the cluster. (It is a bottom-up method). At first, every dataset is considered as an individual entity or cluster. At every iteration, the clusters merge with different clusters until one cluster is formed. we develop the hierarchy of clusters in the form of a tree, and this tree-shaped structure is known as the dendrogram.

Hierarchical Clustering-Agglomerative Algorithm:

1. Calculate the similarity of one cluster with all the other clusters (calculate proximity matrix)
2. Consider every data point as an individual cluster
3. Merge the clusters which are highly similar or close to each other.
4. Recalculate the proximity matrix for each cluster
5. Repeat Steps 3 and 4 until only a single cluster remains.

Program:

1. Implementation of K-Means Clustering:

Source

Console | Terminal | Background Jobs

R 4.2.2 · D:/akashadms/

```
R version 4.2.2 (2022-10-31 ucrt) -- "Innocent and Trusting"
Copyright (C) 2022 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

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'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> setwd("D:/akashadms")
> getwd()
[1] "D:/akashadms"
> iris<-read.csv('D:/akashadms/iris.csv')
> library(ggplot2)
> ggplot(iris, aes(petal.length, petal.width, color = variety)) + geom_point()
>
```

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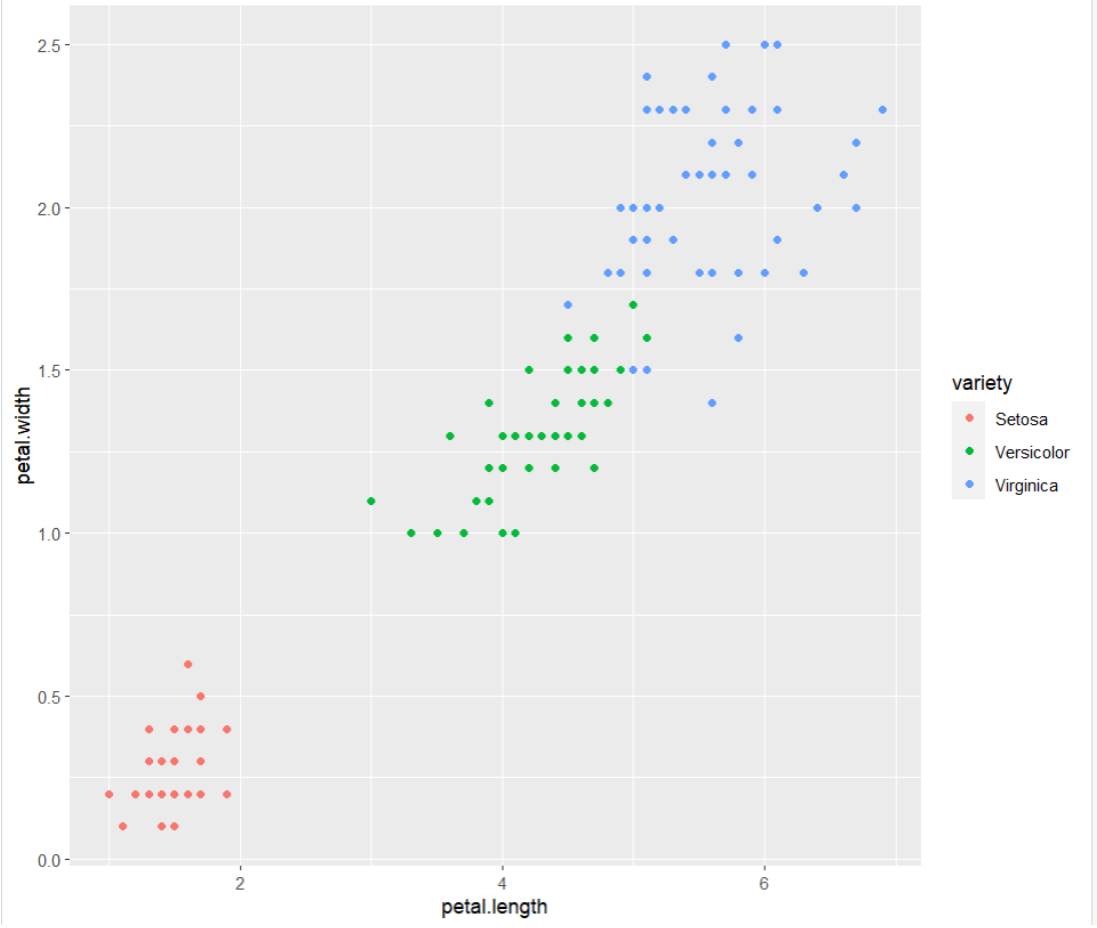



```
> iris <- iris[sample(nrow(iris), ), ]
> set.seed(20)
```

```
> irisCluster <- kmeans(iris[, 3:4], 3, nstart = 20)
> irisCluster
K-means clustering with 3 clusters of sizes 48, 50, 52

Cluster means:
  petal.length petal.width
1     5.595833    2.037500
2     1.462000    0.246000
3     4.269231    1.342308

Clustering vector:
 24 124   8  16  33  15 142  31  18  59 105  98  46  74  97  56  53  29  47  80  55
  2   1   2   2   2   2   1   2   2   3   1   3   2   3   3   3   3   2   2   3   3
 72 126  99  81  78  52 132  90  62 109  34 135  32  22  73  61  21  13  51 125 100
  3   1   3   3   1   3   1   3   3   1   2   1   2   2   3   3   2   2   3   1   3
 26 150   6  11  28  43 111 128 145 122 148  19  91 138   2  35 141  14 123  12  30
  2   1   2   2   2   2   1   1   1   1   2   3   1   2   2   1   2   1   2   2
 40 144 107   3 114 119 118  37 106 133 149  25 136 143  69  48   7  85 113 131  41
  2   1   3   2   1   1   1   2   1   1   1   2   1   1   3   2   2   3   1   1   2
 58  44   4  57  96 102  42  36  27 147 112 101 139 110   9 108  50 117  95  70  79
  3   2   2   3   3   1   2   2   2   1   1   1   3   1   2   1   2   1   3   3   3
137  68  82  84 121  38 140  92  54  10 129  94  76  89 134 120 104  39  23  20   5
  1   3   3   1   1   2   1   3   3   2   1   3   3   3   1   3   1   2   2   2   2
 49 130  63  83  88 116  87  77  86 127  17  66 115  67  60 146  64  93   1  45 103
  2   1   3   3   3   1   3   3   3   3   2   3   1   3   3   1   3   3   2   2   1
 75  71  65
  3   3   3

Within cluster sum of squares by cluster:
[1] 16.29167  2.02200 13.05769
 (between_SS / total_SS =  94.3 %)

Available components:

[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
[6] "betweenss"    "size"         "iter"         "ifault"
```

```
> table(irisCluster$cluster, iris$variety)

    Setosa Versicolor Virginica
  1      0          2        46
  2     50          0         0
  3      0         48         4
```

```
> irisCluster$iter # total iteration
[1] 2
```

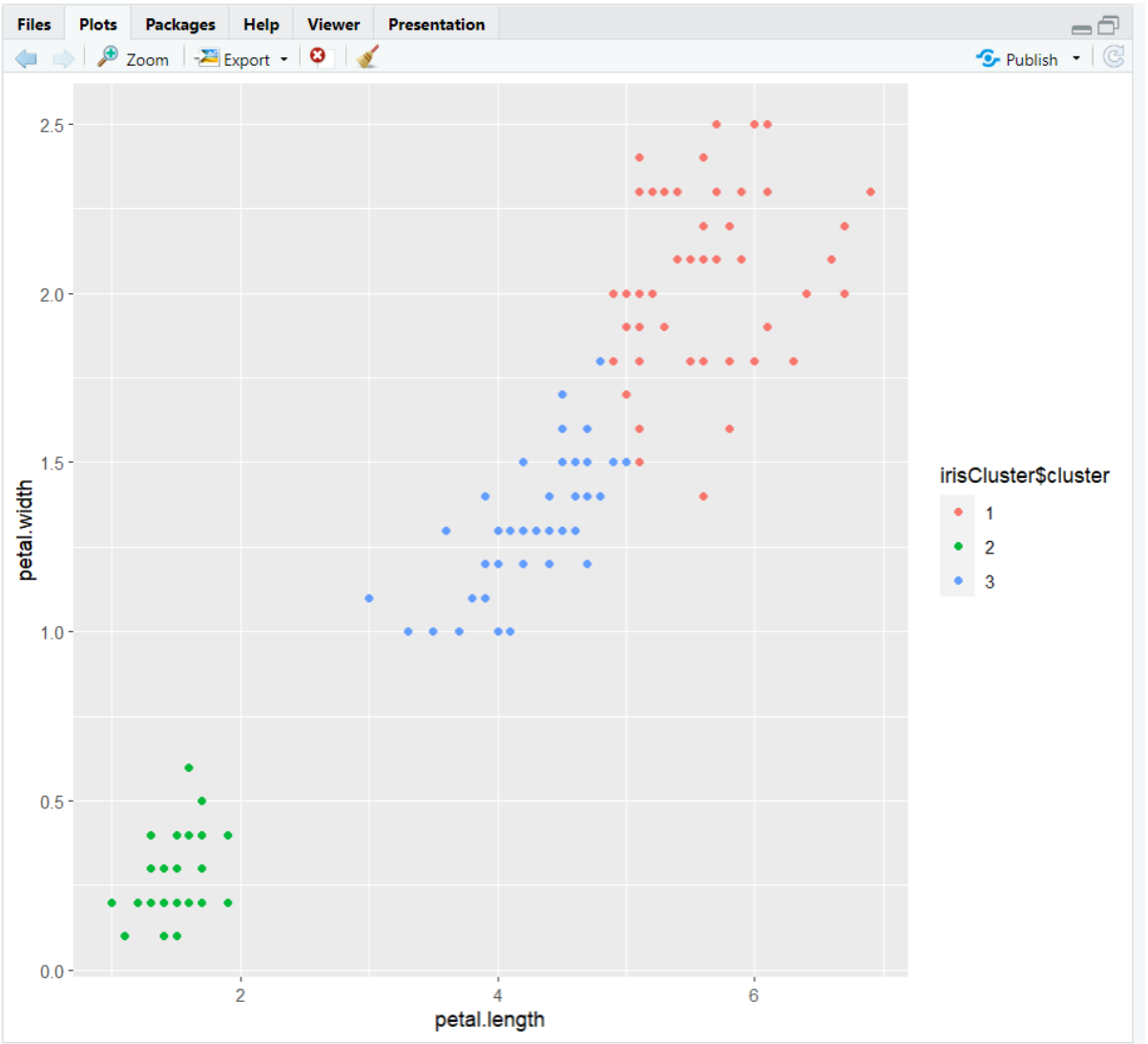
```
> irisCluster$centers # three centroid for three cluster
  petal.length petal.width
1     5.595833    2.037500
2     1.462000    0.246000
3     4.269231    1.342308
```

```
> irisCluster$size # no of record in each cluster
[1] 48 50 52
```

```
> irisCluster$ifault # fault or wrong interpreted record
[1] 0
```

```
> irisCluster$cluster # final cluster assign to each record
 24 124   8  16  33  15 142  31  18  59 105  98  46  74  97  56  53  29  47  80  55
  2   1   2   2   2   2   1   2   2   3   1   3   2   3   3   3   3   2   2   3   3
 72 126  99  81  78  52 132  90  62 109  34 135  32  22  73  61  21  13  51 125 100
  3   1   3   3   1   3   1   3   3   1   2   1   2   2   3   3   2   2   3   1   3
 26 150   6  11  28  43 111 128 145 122 148  19  91 138   2  35 141  14 123  12  30
  2   1   2   2   2   2   1   1   1   1   1   2   3   1   2   2   1   2   1   2   2
 40 144 107   3 114 119 118  37 106 133 149  25 136 143  69  48   7  85 113 131  41
  2   1   3   2   1   1   1   2   1   1   1   2   1   1   3   2   2   3   1   1   2
 58  44   4  57  96 102  42  36  27 147 112 101 139 110   9 108  50 117  95  70  79
  3   2   2   3   3   1   2   2   2   1   1   1   3   1   2   1   2   1   3   3   3
137  68  82  84 121  38 140  92  54  10 129  94  76  89 134 120 104  39  23  20   5
  1   3   3   1   1   2   1   3   3   2   1   3   3   3   1   3   1   2   2   2   2
 49 130  63  83  88 116  87  77  86 127  17  66 115  67  60 146  64  93   1  45 103
  2   1   3   3   3   1   3   3   3   3   2   3   1   3   3   1   3   3   2   2   1
 75  71  65
  3   3   3
```

```
> irisCluster$cluster<- as.factor(irisCluster$cluster)
> ggplot(iris, aes(petal.length, petal.width, color = irisCluster$cluster)) +geom_point()
```

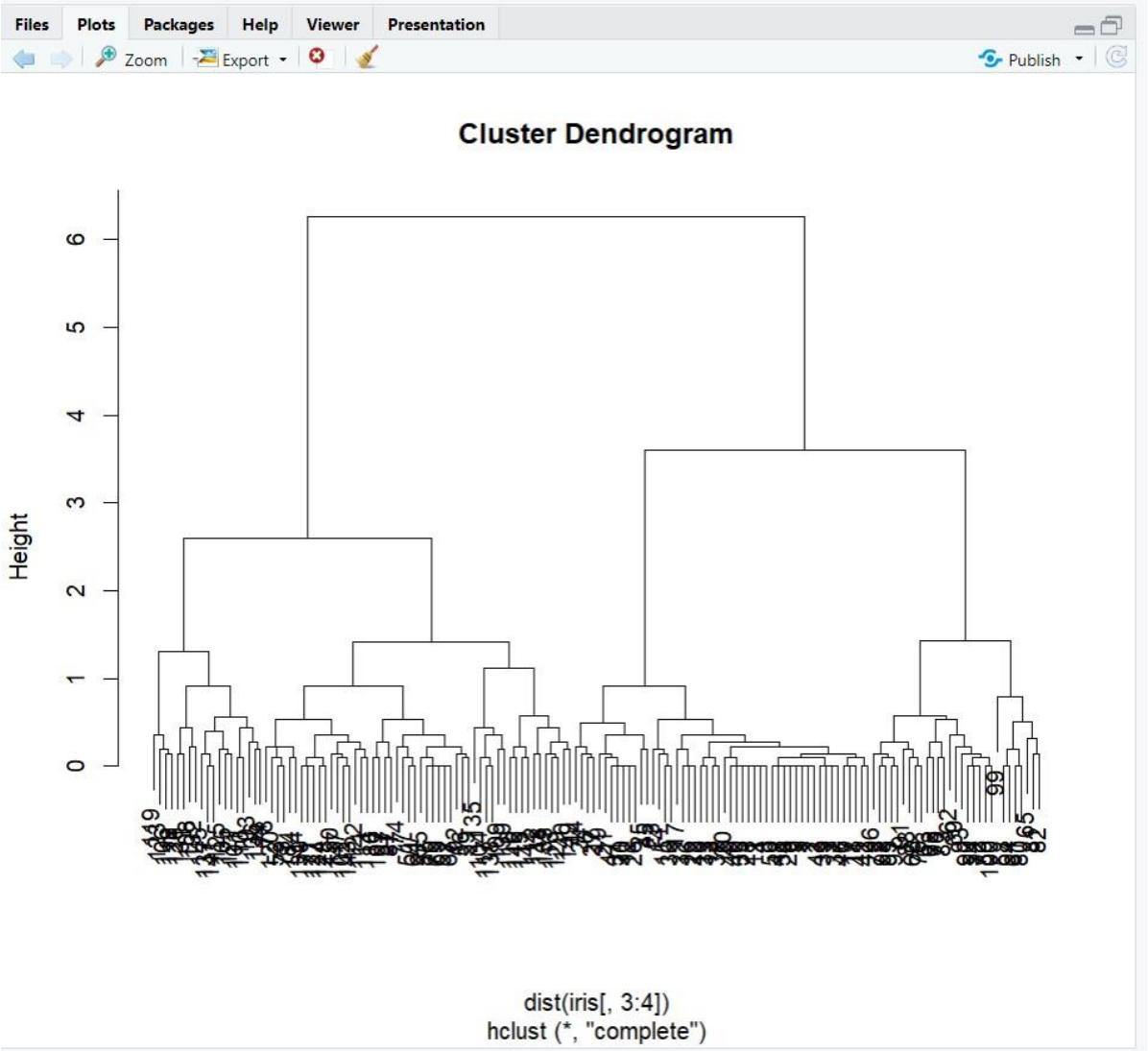


2.Implementation of Hierarchical Clustering-Agglomerative

```
> iris<-read.csv('D:/akashadms/iris.csv')
> head(iris)
  sepal.length sepal.width petal.length petal.width variety
1          5.1         3.5          1.4         0.2  Setosa
2          4.9         3.0          1.4         0.2  Setosa
3          4.7         3.2          1.3         0.2  Setosa
4          4.6         3.1          1.5         0.2  Setosa
5          5.0         3.6          1.4         0.2  Setosa
6          5.4         3.9          1.7         0.4  Setosa
```

```
> clusters <- hclust(dist(iris[, 3:4]), method="complete")
> clusters

Call:
hclust(d = dist(iris[, 3:4]), method = "complete")

Cluster method   : complete
Distance         : euclidean
Number of objects: 150
```

```
> plot(clusters)
```

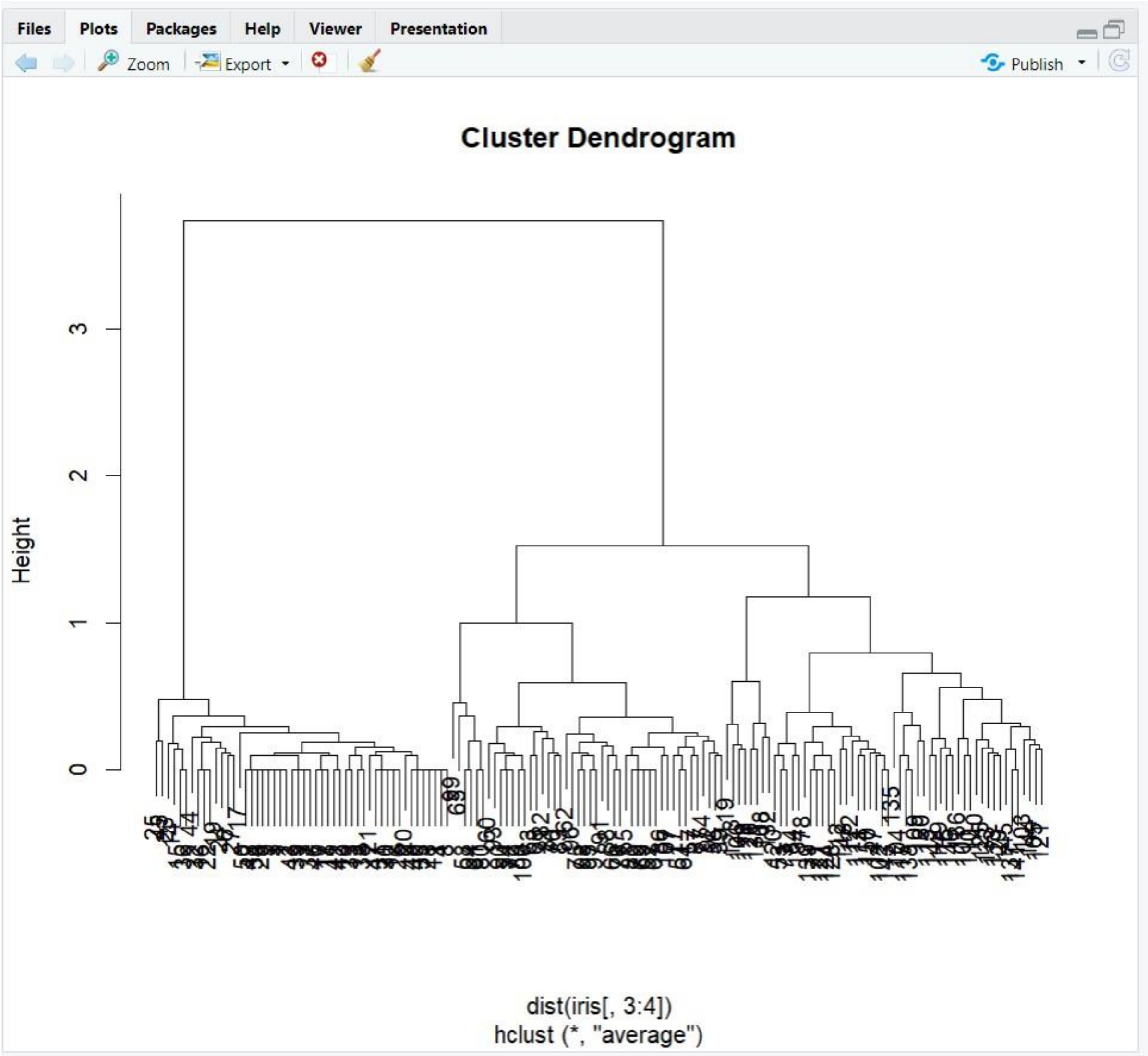


```
> clusterCut <- cutree(clusters, 3)
> clusterCut
  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [41] 1 1 1 1 1 1 1 1 1 1 2 2 2 3 2 2 2 3 2 3 3 3 3 2 3 3 2 3 2 3 2 3 2 2 3 3 2 2 2 3
 [81] 3 3 3 2 2 2 2 3 3 3 3 2 3 3 3 3 3 3 3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
[121] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
```

```
> table(clusterCut, iris$ variety)

clusterCut Setosa Versicolor Virginica
         1     50          0         0
         2      0         21        50
         3      0         29         0
```

```
> clusters <- hclust(dist(iris[, 3:4]), method = "average")
> clusters

Call:
hclust(d = dist(iris[, 3:4]), method = "average")

Cluster method   : average
Distance         : euclidean
Number of objects: 150
```

```
> plot(clusters)
```



```
> clusterCut <- cutree(clusters, 3)
> table(clusterCut, iris$variety)

clusterCut Setosa Versicolor Virginica
         1     50          0         0
         2      0         45         1
         3      0          5        49
```