# Machine Learning and Data Mining II LABWORK 2: Clustering

# **Groupwork:**

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# I. AHC

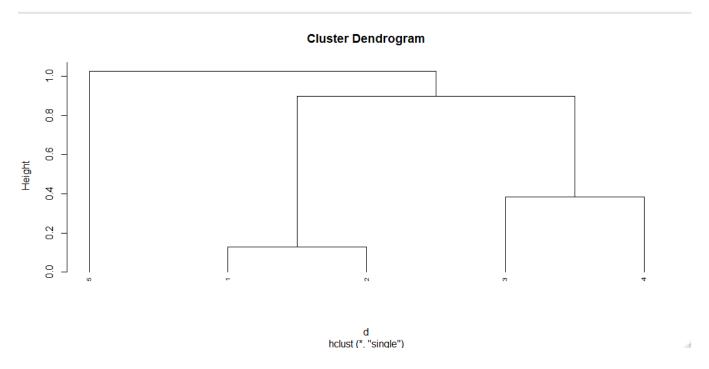
Given the data  $X = \{1, 2, 9, 12, 20\}$  in 1-D space.

- 1. Apply the AHC clustering using Single Linkage / Complete Linkage for the X dataset.
  - Using R studio

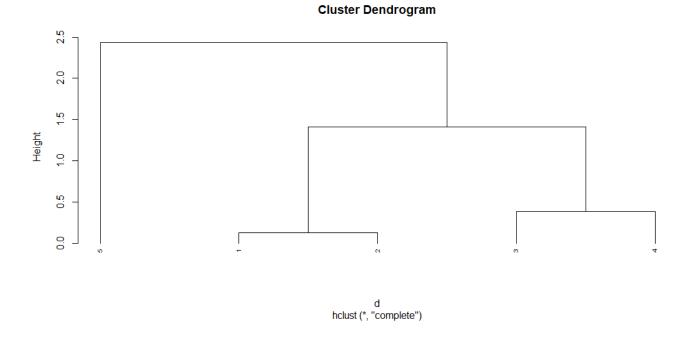
```
> X <- c(1,2,9,12,20)
> X <- na.omit(X)
> X <- scale(X)
> d <- dist(X, method ="euclidean")
> hc1 <- hclust(d, method = "single")
> hc2 <- hclust(d, method = "complete")
> plot(hc1, cex = 0.6, hang = -1)
> |
```

^	<b>V1</b>
1	-1.00115255
2	-0.87279966
3	0.02567058
4	0.41072925
5	1.43755238

- 2. Draw the clustering result using available functions (dendrogram() in Matlab or hclust() in R, etc.).
  - Single Linkage



## - Complete Linkage



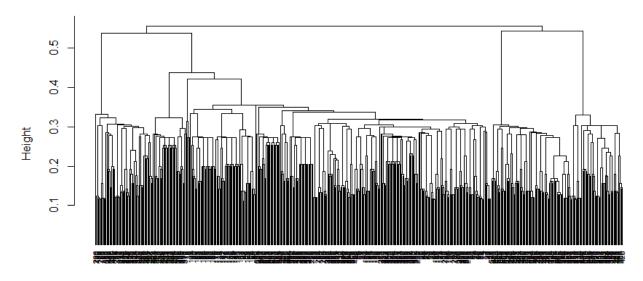
- 3. Apply on 2 more datasets from UCI. Make a study of data features. Observe the dendrogram and comment on results.
  - Dataset from UCI:
     Synchronous Machine Data Set:
     <a href="http://archive.ics.uci.edu/ml/datasets/Synchronous+Machine+Data+Set">http://archive.ics.uci.edu/ml/datasets/Synchronous+Machine+Data+Set</a>
     Energy efficiency Data Set:
     <a href="http://archive.ics.uci.edu/ml/datasets/Energy+efficiency">http://archive.ics.uci.edu/ml/datasets/Energy+efficiency</a>
  - For Synchronous Machine Dataset:

Since we have already made a data analysis for the Synchronous dataset in the previous labwork, so now we will just make a summary for it.

```
> View(synchronous.machine)
> syn <- synchronous.machine
> summary(syn)
                                           dIf
                                                          Ιf
     Ιy
Min. :3.0 Min. :0.6500 Min. :0.0000 Min. :0.0370
                                                     Min. :1.217
1st Qu.:1.369
                                                     Median :1.525
Mean :4.5 Mean :0.8253 Mean :0.1747 Mean :0.3507
                                                     Mean :1.531
                                                     3rd Qu.:1.666
3rd Qu.:5.3 3rd Qu.:0.9200 3rd Qu.:0.2600 3rd Qu.:0.4860
Max. :6.0 Max. :1.0000 Max. :0.3500 Max. :0.7690
                                                     Max. :1.949
> cor(syn)
                   PF
                                     dIf
          ΙV
                              e
  1.00000000 -0.04157389 0.04157389 0.4249449 0.4249449
PF -0.04157389 1.00000000 -1.00000000 -0.8610135 -0.8610135
e 0.04157389 -1.00000000 1.00000000 0.8610135 0.8610135
dIf 0.42494491 -0.86101347 0.86101347 1.0000000 1.0000000
If 0.42494491 -0.86101347 0.86101347 1.0000000 1.0000000
>
```

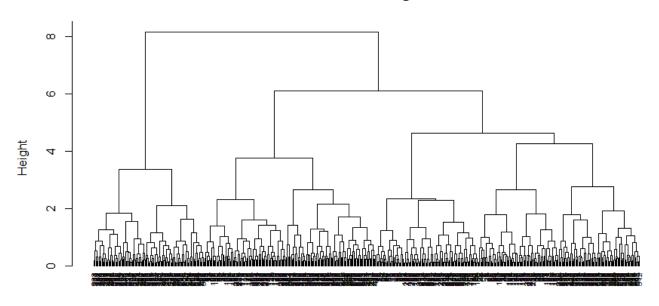
```
> syn <- na.omit(syn)
> syn <- scale(syn)
> d <- dist(syn, method ="euclidean")
> hc1 <- hclust(d, method = "single")
> hc2 <- hclust(d, method = "complete")
> plot(hc1, cex = 0.6, hang = -1)
> |
```

## **Cluster Dendrogram**



d hclust (\*, "single")

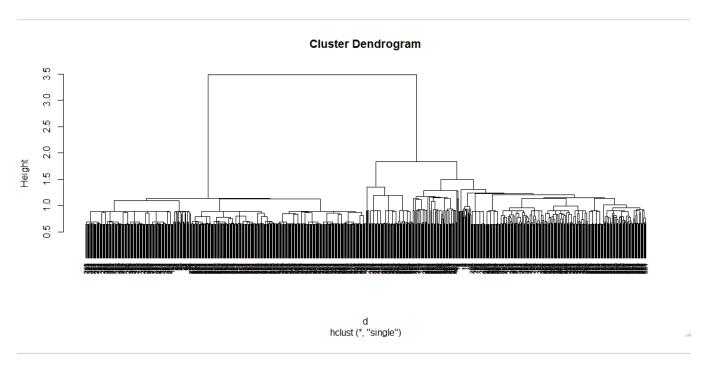
# **Cluster Dendrogram**

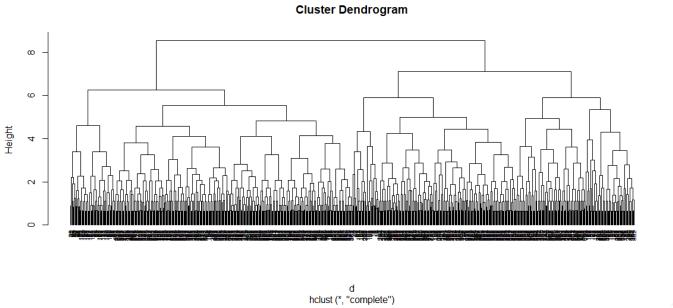


d hclust (\*, "complete")

- For Energy efficiency Dataset:

6.343391e-01 -6.729989e-01 0.4271170 -8.625466e-01 0.8957852 0.014289598 2.075050e-01 0.05052512 0.975861739 1.00000000





- 4. Conclude on the advantages and drawbacks of AHC.
  - Advantage:

- AHC outputs a hierarchy → easier to decide on the number of clusters (by looking at the dendrogram).
- Easy to implement, doesn't require any input.
- Drawbacks:
- For a n-element dataset, AHC must calculate the distance from one element to (n-1) remaining elements so the AHC has the complexity of O(n^2) → time complexity: not suitable for large databases.
- Initial seeds have a strong impact on the final results.
- The order of the data has an impact on the final results.
- Very sensitive to noise/outliers.

## II. K-means:

Select two datasets from UCI:

- 1.Iris Dataset: http://archive.ics.uci.edu/ml/datasets/Iris
- 2.Wine Data Set: <a href="http://archive.ics.uci.edu/ml/datasets/Wine">http://archive.ics.uci.edu/ml/datasets/Wine</a>
- 1. Run experiments with k-means. Explain the experimental protocol.

For Iris Dataset:

- Model kmeans re:

```
> # 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 ...
 $ Species
> # 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)
K-means clustering with 3 clusters of sizes 50, 62, 38
cluster means:
 Sepal.Length Sepal.Width Petal.Length Petal.Width
     5.006000 3.428000 1.462000 0.246000
     5.901613
               2.748387
                          4.393548
                                     1.433871
              3.073684
                          5.742105
     6.850000
                                    2.071053
Clustering vector:
Within cluster sum of squares by cluster:
[1] 15.15100 39.82097 23.87947
 (between_SS / total_SS = 88.4 %)
Available components:
                             "totss" "withinss"
[1] "cluster"
[8] "iter"
                "centers"
                                                      "tot.withinss" "betweenss"
                "ifault"
```

The 3 clusters are made which are of 50, 62, and 38 sizes respectively. Within the cluster, the sum of squares is 88.4%.

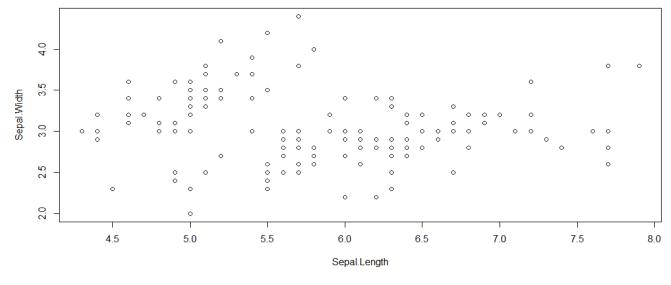
Cluster identification and confusion matrix:

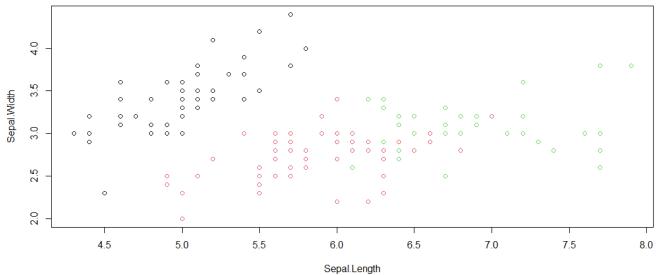
50 Setosa are so appropriately categorized as Setosa. 48 of the 62 Versicolor are appropriately categorized as Versicolor, and 14 are categorized as virginica. 19 of the 36 virginica have been reliably identified as virginica, while two have been identified as Versicolor.

### - K-means with 3 clusters plot:

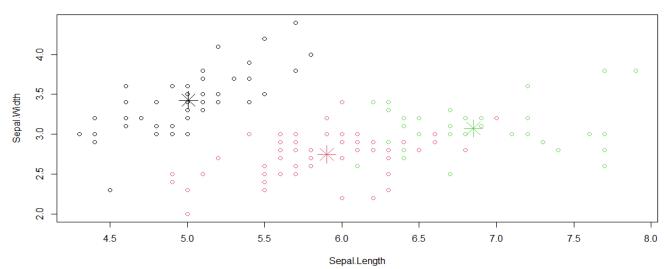
```
# Model Evaluation and visualization
plot(iris_1[c("Sepal.Length", "Sepal.Width")])
plot(iris_1[c("Sepal.Length", "Sepal.Width")],
        col = kmeans.re$cluster)
plot(iris_1[c("Sepal.Length", "Sepal.Width")],
        col = kmeans.re$cluster,
        main = "K-means with 3 clusters")

## Plotting cluster centers
kmeans.re$centers
kmeans.re$centers[, c("Sepal.Length", "Sepal.Width")]
```



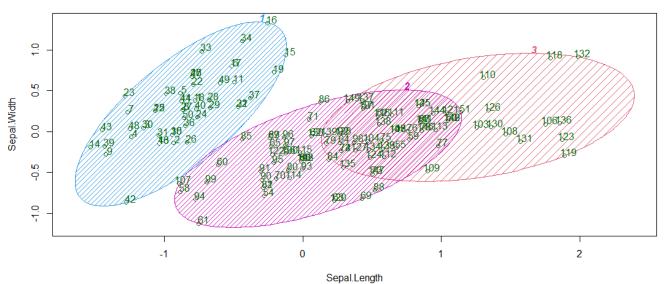


#### K-means with 3 clusters



#### - Plot of clusters:

#### Cluster iris



These two components explain 100 % of the point variability.

#### For Wine dataset:

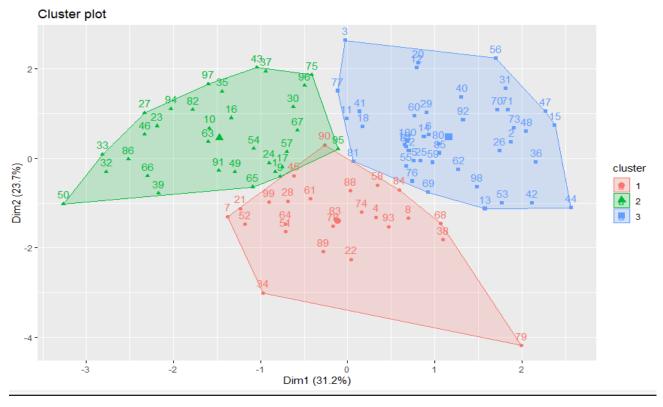
# - Model kmeans\_re:

```
> # standardize continuous variables
> data <- wine %>% select(-1, -14) %>% scale()
> # create clusters with k-means

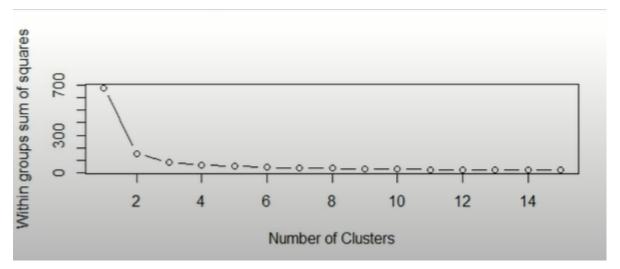
> kmeans(data, centers = 3, iter.max = 100, nstart = 100)

K-means clustering with 3 clusters of sizes 62, 64, 51
Cluster means:
      14.23
                           2.43
                                                 127
                                                           2.8
                                                                      3.06
  0.7987121 \ -0.3638891 \ 0.3546289 \ -0.5644599 \ 0.51157963 \ 0.9610990 \ 1.01856614 \ -0.589199261 \ 0.628154853 \ 0.1719609
  1.04
                 3.92
1 0.5150541 0.7837745
 0.4227232 0.2664770
3 -1.1566204 -1.2872265
within cluster sum of squares by cluster:
[1] 372.2401 512.5285 319.0040
(between_SS / total_SS = 43.0 %)
Available components:
[1] "cluster"
[8] "iter"
                                                           "tot.withinss" "betweenss"
                 "centers"
                               "totss"
                                             "withinss"
                                                                                       "size"
                 "ifault"
```

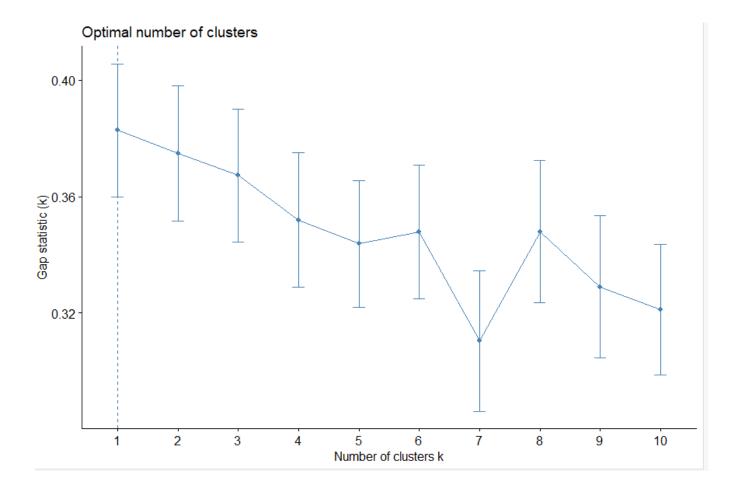
## - Plot of clusters:



# 2. Explain the centroid initialization of the k-means used in the first question.



We base on the elbow method to choose k = 3 for the Iris Dataset



And silhouette method to choose k = 3 for Wine Dataset

## 3. Analyze and compare the results with different values of k.

#### For Iris dataset: k = 2

```
> # Fitting K-Means clustering Model to training dataset
> set.seed(240) # Setting seed
> kmeans.re <- kmeans(iris_1, centers = 2, nstart = 20)
> kmeans.re
K-means clustering with 2 clusters of sizes 53, 97
Cluster means:
  Sepal.Length Sepal.width Petal.Length Petal.width 5.005660 3.369811 1.560377 0.290566
      6.301031
                 2.886598
                              4.958763
within cluster sum of squares by cluster:
[1] 28.55208 123.79588
 (between_SS / total_SS = 77.6 \%)
Available components:
[1] "cluster"
[9] "ifault"
                  "centers"
                                 "totss"
                                               "withinss"
                                                              "tot.withinss" "betweenss"
                                                                                           "size"
                                                                                                          "iter"
```

#### For Wine dataset: k = 4

```
> # create clusters with k-means
> kmeans(data, centers = 4, iter.max = 100, nstart = 177)
K-means clustering with 4 clusters of sizes 41, 57, 50, 29
Cluster means:
                        1.71
                                       2.43
                                                     15.6
                                                                                                  3.06
                                                                                                                  . 28
                                                                                                                              2.29
1 -0.77233064 -0.4174020 -1.0048046 -0.3903739 -0.47336765 0.2393353 0.2678889 -0.6055783 0.2822938 -0.7787523 2 0.8919484 -0.3157252 0.4629576 -0.5293868 0.61826550 0.9426657 1.0193255 -0.5562158 0.6554689 0.2075293
3 0.1858631 0.8990441 0.2160888 0.5434689 -0.0668264 -0.9817944 -1.2180815 0.7066309 -0.7533079 0.9507904 -0.9817122 -0.3393926 0.1380678 0.6554114 -0.43070439 -0.4984474 -0.2821009 0.7310850 -0.3886337 -0.9458576
                          3.92
          1.04
   0.3963681 0.50032327
   0.5039521 0.78214923
  -1.1817618 -1.28420092
4 0.4866113 -0.03054188
Clustering vector:
within cluster sum of squares by cluster:
[1] 290.3908 326.5426 307.6225 184.4747
 (between_SS / total_SS = 47.5 \%)
Available components:
[1] "cluster"
[8] "iter"
                         "centers"
                                            "totss"
                                                                "withinss"
                                                                                   "tot.withinss" "betweenss"
                        "ifault"
```

4. Calculate the clustering quality (any criteria in slides).

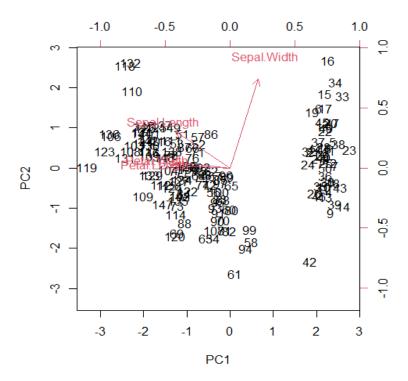
```
confusionMatrix(cm)
Confusion Matrix and Statistics
             setosa versicolor virginica
  setosa
                  20
                              0
                                         0
  versicolor
                                         0
                  0
                             20
  virginica
                   0
                              0
                                        20
Overall Statistics
               Accuracy: 1
95% CI: (0.9404, 1)
    No Information Rate: 0.3333
    P-Value [Acc > NIR] : < 2.2e-16
                   Kappa: 1
Mcnemar's Test P-Value : NA
Statistics by Class:
                      Class: setosa Class: versicolor Class: virginica
Sensitivity
                             1.0000
                                                1.0000
                                                                  1.0000
Specificity
                             1.0000
                                                1.0000
                                                                  1.0000
Pos Pred Value
                             1.0000
                                                1.0000
                                                                  1.0000
Neg Pred Value
                             1.0000
                                                                  1.0000
                                                1.0000
Prevalence
                             0.3333
                                                0.3333
                                                                  0.3333
                             0.3333
                                                0.3333
                                                                  0.3333
Detection Rate
Detection Prevalence
                             0.3333
                                                0.3333
                                                                  0.3333
Balanced Accuracy
                             1.0000
                                                1.0000
                                                                  1.0000
```

The model's accuracy was 100% and its p-value was less than 1.

This suggests that the model is good.

## 5. Use PCA or SVD to visualize the data distribution in 2D/3D.

## - PCA for Iris dataset:



## - PCA for Wine dataset:

