# **Assesment Report CLO-2 Case Based**

**K-Means Algorithm** 



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### Statement

I do this assignment honestly and follow the rule of conduct of academic ethics in case I do not follow the rule I am ready to get a 0 (zero) mark for my assignment.

**Muhammad Rizky Aulia Gobel** 

SWIKY

## **Import library**

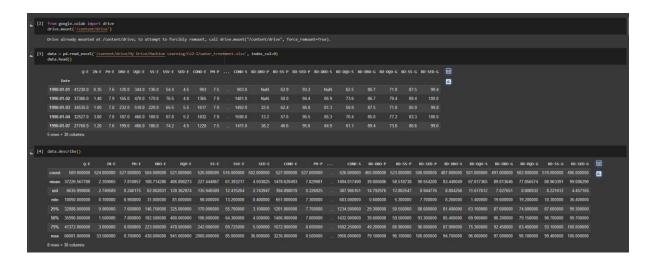
For this assignment, the author used several libraries as follows

```
Import library and file

import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import random
import seaborn as sns
import openpyxl
```

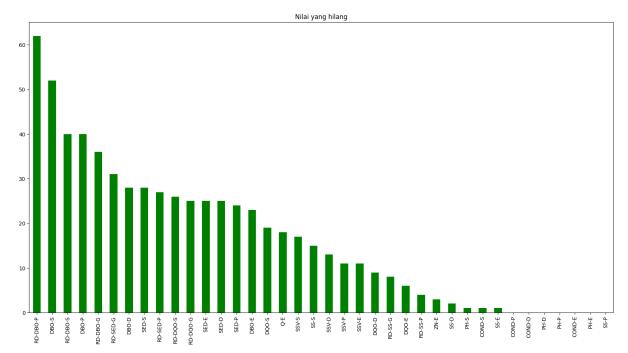
### **Overview the dataset**

To run an .xlsx file, the author uses Google Colab mount to mount to the author's drive. Then, the author creates a variable called data that is used to read the water-treatment file that has been converted to an .xlsx file previously. Then, the author runs data.head() which is used to display the first 5 rows.



# **Preprocessing**

The author then ran data.describe() to check the contents of the dataset as a whole. What surprised the author was that the values in the count series had different values. There were some with 526 data points, 527 data points, 509 data points, and so on.



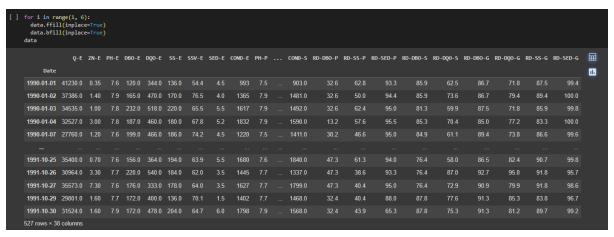
```
<class 'pandas.core.frame.DataFrame'>
DatetimeIndex: 527 entries, 1990-01-01 to 1991-10-30
Data columns (total 38 columns):
# Column Non-Null Count Dtype
                                               float64
                      524 non-null
       ZN-E
                                               float64
                      527 non-null
                                               float64
       DBO-E
                                               float64
       D00-E
                                               float64
       SSV-E
                                               float64
                      502 non-null
527 non-null
       SED-E
                                               float64
       PH-P
DBO-P
                      527 non-null
487 non-null
                                               float64
 12 SSV-P
13 SED-P
                      503 non-null
                                               float64
      PH-D
DBO-D
                                               float64
       DQO-D
                      518 non-null
                                               float64
                                               float64
                      514 non-null
502 non-null
      SSV-D
                                               float64
       SED-D
       COND-D
       PH-S
DBO-S
                      526 non-null
475 non-null
                                               float64
                      512 non-null
510 non-null
       SS-S
SSV-S
                                               float64
                                               float64
                     499 non-null
526 non-null
      COND-S
                                               float64
       RD-DBO-P 465 non-null
                                               float64
 30 RD-SS-P 523 non-null
31 RD-SED-P 500 non-null
                                               float64
 32 RD-DBO-5 487 non-null
33 RD-DBO-5 591 non-null
34 RD-DBO-6 491 non-null
35 RD-DQO-6 502 non-null
                                               float64
                                               float64
 36 RD-SS-G 519 non-null
37 RD-SED-G 496 non-null
                                               float64
dtypes: float64(34), int64(4)
memory usage: 160.6 KB
```

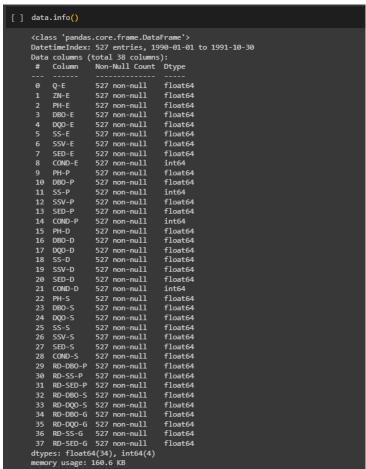
The author filled in the missing data using the bfill and ffill methods. The methods work as follows:

bfill fills in the missing data from top to bottom.

ffill fills in the missing data from bottom to top.

The results are then displayed as follows:

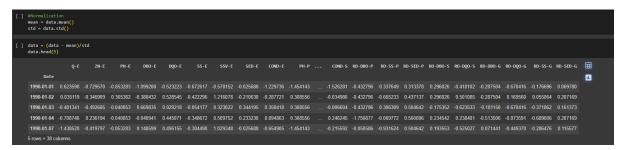




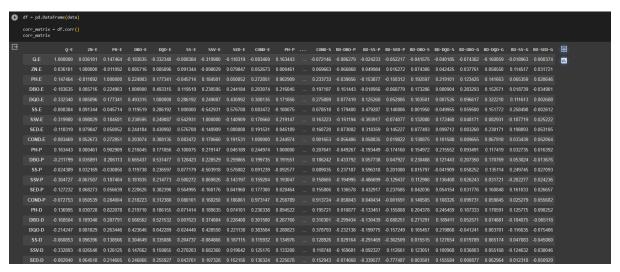
If you look at the first page, the rows 1990-01-01 and 1990-01-02 have NaN values. The NaN values are located in RD-DBO-P and RD-DBO-S, and on 1990-01-02, they are located in RD-DBO-P. After running bfill and ffill, the values are immediately filled in with the values below them. For example, the value of RD-DBO-S on row 1990-01-01 is filled in with the same value as RD-DBO-S on row 1990-01-02. In addition, with data.info(), the non-null values are

the same from Q-E to RD-SED-G, indicating that there are no more missing values and the dataset is ready to be used.

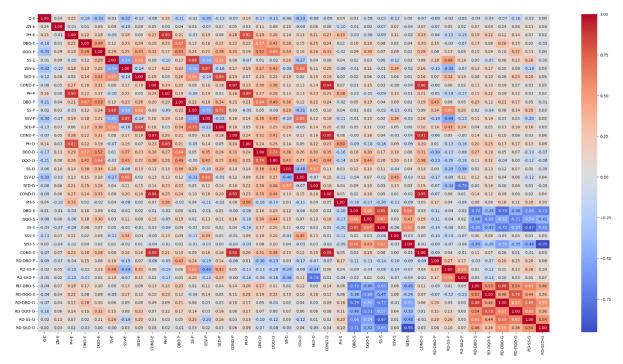
Now author can perform normalization, normalization will standardize the data so that it has a mean of 0 and a standard deviation of 1. This is important for many machine learning algorithms, as they often assume that the data is normally distributed, the method that is used is Z-Score, here's the code:



After that, author will create the correlation matrix, correlation matrix is a table that summarizes the correlation between every pair of variables in a dataset. It is used to identify relationships between variables and can be used to inform feature selection and model building.

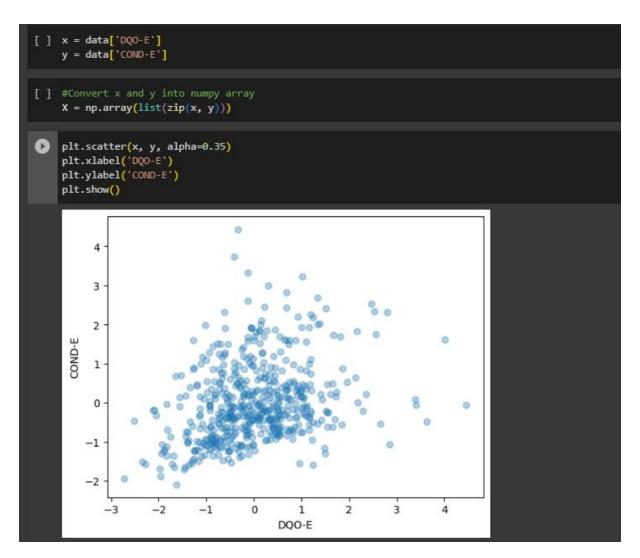


And here's the heatmap:



# Algorithm(K-Means)

Before performing k-means clustering, author will choose 2 column from the dataset, the column that author pick is DQO-E and COND-E, and then DQO-E and COND-E will be converted into numPy array, then visualized with scatterplot



Then onto the K-Means, here's the code that author create:

```
def kmeans(X, k, max_iters=100):
    centroids = X[np.random.choice(range(len(X)), k, replace=False)]

for _ in range(max_iters):
    distances = np.sqrt(((X - centroids[:, np.newaxis])**2).sum(axis=2))
    labels = np.argmin(distances, axis=0)
    new_centroids = np.array([X[labels == i].mean(axis=0) for i in range(k)])

if np.all(centroids == new_centroids):
    break
    centroids = new_centroids
return labels, centroids
```

def kmeans(X, k, max\_iters=100) = function, X is the data points to cluster and represented numPy array, k is clusters to identify, and max\_iters= is the maximum number to run the clustering algorithm

centroids = X[np.random.choice(range(len(X)), k, replace=False)] = initial centroid selection

```
for _ in range(max_iters):
    distances = np.sqrt(((X - centroids[:, np.newaxis])**2).sum(axis=2))
    labels = np.argmin(distances, axis=0)
    new_centroids = np.array([X[labels == i].mean(axis=0) for i in range(k)])

if np.all(centroids == new_centroids):
    break
    centroids = new_centroids

= The clustering algorithm, it iterates until convergence or the maximum number of iterations is reached, each iteration involves the following steps:

1.Calculate distances;

2.Assign data points;

3.Recompute centroids, and

4.Check for convergence
then ended with
return labels, centroids
```

### **Elbow method**

Elbow method is a method used in clustering to determine the optimum number of clusters in dataset, It is a heuristic method, doesn't guarantee that the optimum number will be found but it's relatively simple and effective method to quickly get the idea of the optimal numbers of clusters.

```
[ ] #Calculates the within-cluster sum of squares
    def calculate_wcss(X, labels, centroids):
        for i, centroid in enumerate(centroids):
            cluster_points = X[labels == i]
            distance = np.sum((cluster_points - centroid)**2)
            wcss += distance
        return wcss
[ ] wcss_values = []
    k_values = range(1, 11)
    for k in k_values:
        labels, centroids = kmeans(X, k)
        wcss = calculate_wcss(X, labels, centroids)
        wcss_values.append(wcss)
    plt.plot(k_values, wcss_values, 'bo-')
    plt.xlabel('Number of clusters')
    plt.ylabel('WCSS')
    plt.title('Elbow Method')
    plt.show()
                                       Elbow Method
        1000
         800
         600
         400
         200
                       2
                                                 6
                                                                           10
                                      Number of clusters
```

def calculate\_wcss(X, labels, centroids) = Define the function to calculate wcss, takes 3 arguments, X = data points to cluster, labels = an array of labels indicating the cluster assignment for each data point, and centroids = the final centroids representating centers of the cluster

```
for i, centroid in enumerate(centroids):
    cluster_points = X[labels == i]
    distance = np.sum((cluster_points - centroid)**2)
    wcss += distance
```

return wcss

= Calculation within wcss, a measure of how tightly the data points within each cluster are grouped together

wcss\_values = [] = Create empty list

k\_values = range(1, 11) = define range of k values to test

for k in k values:

labels, centroids = kmeans(X, k) = run the k-means function to obtain the cluster labels and centroids to the current k value

wcss = calculate\_wcss(X, labels, centroids) = calculate the wcss for the resulting clusters using the calculate wcss() function

wcss\_values.append(wcss) = append the calculated wcss to the wcss\_values list

= Calculating WCSS for Different k Values

Author decide that third cluster is the optimum, because it's resembles human-elbow, and for the silhouette method, here's the code:

#### Silhouette method

Silhouette method is a method used in cluster analysis to assess the quality of clustering algorithms. It measures how well each data point is assigned to its cluster based on two parameters that is:

- -Cohesion
- -Separation

```
[ ] #Calculates the Silhouette Coefficient for a given clustering result
    def calculate_silhouette(X, labels):
        n = len(X)
        silhouette_values = np.zeros(n)
        for i in range(n):
             a = np.mean(np.sqrt(np.sum((X - X[i])**2, axis=1))[labels == labels[i]])
             b_values = []
             for j in range(k):
                 if j != labels[i]:
                     b = np.mean(np.sqrt(np.sum((X - X[i])**2, axis=1))[labels == j])
                     b_values.append(b)
             b = np.min(b_values) if len(b_values) > 0 else np.inf
             silhouette_value = (b - a) / max(a, b)
             silhouette_values[i] = silhouette_value
        return np.mean(silhouette_values)
    silhouette_values = []
    k_values = range(2, 11)
    for k in k_values:
        labels, centroids = kmeans(X, k)
        silhouette = calculate_silhouette(X, labels)
        silhouette_values.append(silhouette)
[ ] plt.figure(figsize=(8, 4))
    plt.plot(k_values, silhouette_values, marker='o')
    plt.xlabel('Number of Clusters (k)')
plt.ylabel('Silhouette Score')
    plt.title('Silhouette scores for different number of clusters')
    plt.xticks(k_values)
    plt.show()
```

def calculate\_silhouette(X, labels) = define the function for calculating silhouette
silhouette\_values = initialize empty list
for i in range(n):

```
a = np.mean(np.sqrt(np.sum((X - X[i])**2, axis=1))[labels == labels[i]])
```

= Calculate the cohesion by averaging the distances between current data point and other data points in the same cluster

```
b_values = []
for j in range(k):
    if j != labels[i]:
        b = np.mean(np.sqrt(np.sum((X - X[i])**2, axis=1))[labels == j])
        b_values.append(b)
```

b = np.min(b values) if len(b values) > 0 else np.inf

= Calculate the separation by finding the minimum average distance between current data point and data points in all other clusters

silhouette\_value = (b - a) / max(a, b)

silhouette\_values[i] = silhouette\_value

= calculate the silhouette coefficient using the formula, then store the result silhouette values[i]

silhouette values = [] = Create empty list

k\_values = range(2, 11) = define range of k values to test

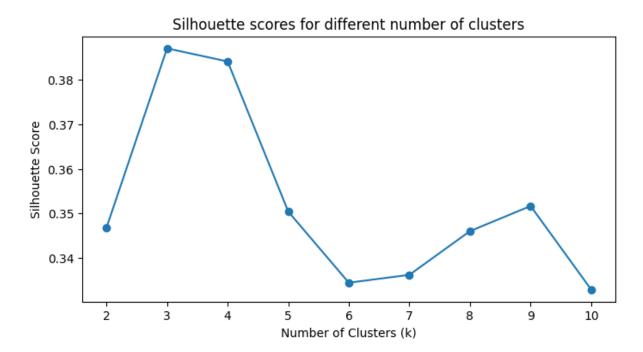
for k in k\_values:

labels, centroids = kmeans(X, k) = run the k-means to obtain cluster labels for the current value(k)

silhouette = calculate\_silhouette(X, labels) = calculate average silhouette coefficient for the resulting clusters using the calculate\_silhouette function

silhouette\_values.append(silhouette) = append the calculated average silhouette coefficient to the silhouette\_value s

= Evaluating Silhouette for Different Cluster Numbers



Because author is curious what's the score, then author create this code

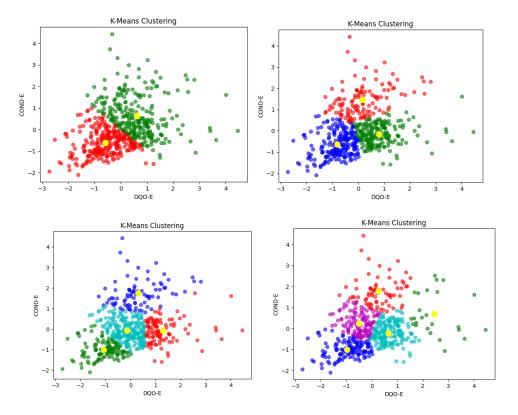
```
[ ] for i, k in enumerate(k_values):
    labels, centroids = kmeans(X, k)
    silhouette = calculate_silhouette(X, labels)
    print("Silhouette score for cluster =", k, "is", "{:.5f}".format(silhouette))

Silhouette score for cluster = 2 is 0.34679
Silhouette score for cluster = 3 is 0.38657
Silhouette score for cluster = 4 is 0.36955
Silhouette score for cluster = 5 is 0.36856
Silhouette score for cluster = 6 is 0.32595
Silhouette score for cluster = 7 is 0.33605
Silhouette score for cluster = 8 is 0.33328
Silhouette score for cluster = 9 is 0.34167
Silhouette score for cluster = 10 is 0.35039
```

With this, we know that third cluster is the most optimum cluster for silhouette method Author conclude that elbow method and silhouette method has the same cluster which is 3.

### **Evaluate the results**

Author create a test from second cluster to fifth cluster, and here's the result:



From left up -> right up -> bottom left -> bottom right : second cluster -> third cluster -> forth cluster -> fifth cluster.

Author conclude that the second cluster is the closest to 0.

During working for this assignment, troubles that author have met:

- -Some of the column won't work really well with elbows method as they sometime spiked or drop randomly
- -Creating kmeans without sklearn
- -Choosing what pre-processing that suitable for this case

## **LINKS**

Video Presentation: <a href="https://www.youtube.com/watch?v=PbY9aTiKtZU">https://www.youtube.com/watch?v=PbY9aTiKtZU</a>

**GDrive:**<a href="https://drive.google.com/drive/folders/1lOa5vJnLr0by2lKfXpB">https://drive.google.com/drive/folders/1lOa5vJnLr0by2lKfXpB</a> e6st4GBlU6Ph?usp= sharing