CAPAIAN PEMBELAJARAN PRAKTIKUM

1. Menjelaskan konsep dari pembelajaran mesin kemudian di terapkan pada permasalahan – (C2)
2. Mengimplementasikan algoritma dan/atau metode di pembelajaran mesin untuk mendapatkan pemecahan maslaah dan model yang sesuai – (C3)
3. Menghasilkan suatu model terbaik dari permasalahan dan terus melakukan jika terdapat perkembangan di bidang rekayasa cerdas – (C6)

MINGGU 9

Algoritma Partisi

DESKRIPSI TEMA

Mahasiswa mempelajari pembelajaran tidak terbimbing dengan algoritma partisi yaitu algoritma K Means, K Medois, dan K Modes serta menerapkannya dengan Bahasa Pemrograman Python

CAPAIAN PEMBELAJARAN MINGGUAN (SUB CPMK)

Mahasiswa dapat menerapkan algoritma partisi sehingga bisa menghassilkan model terbaik

PERALATAN YANG DIGUNAKAN

Anaconda Python 3

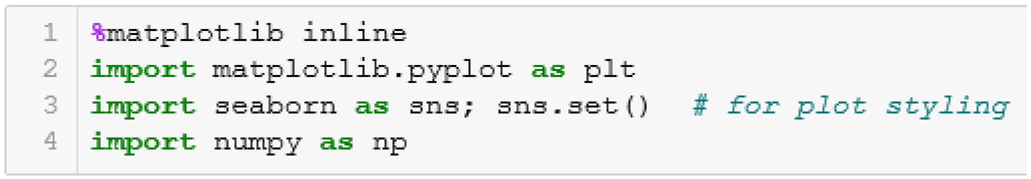
Laptop atau Personal Computer

LANGKAH-LANGKAH PRAKTIKUM

<u>K-Means Clustering</u>

Many clustering algorithms are available in Scikit-Learn and elsewhere, but perhaps the simplest to understand is an algorithm known as k means clustering, which is implemented in sklearn.cluster.KMeans.

1. We begin with standard imports :



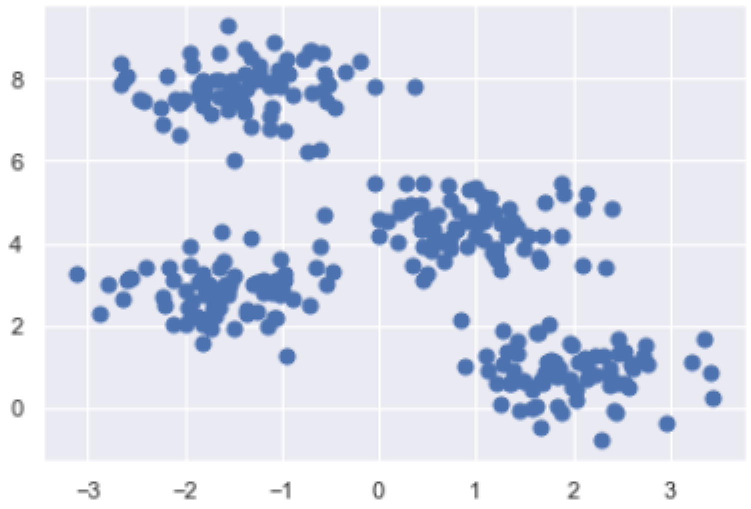
```
%matplotlib inline
import matplotlib.pyplot as plt
import seaborn as sns; sns.set()   # for plot styling
import numpy as np
```

The k-means algorithm searches for a pre-determined number of cluster within an unlabeled multidimensional dataset. It accomplished this using a simple conception of what the optional clustering looks like :

- The "cluster center" is the arithmetic mean of all the points belonging to the cluster
- Each point is closer to its own cluster center than to other cluster center

2. First, lets generate a two-dimensional dataset containing four distinct blobs. To emphasize that this is an unsupervised algorithm, we will leave the labels out the visualization :

```python
from sklearn.datasets.samples_generator import make_blobs
X, y_true = make_blobs(n_samples=300, centers=4,
                       cluster_std=0.60, random_state=0)
plt.scatter(X[:, 0], X[:, 1], s=50);
```

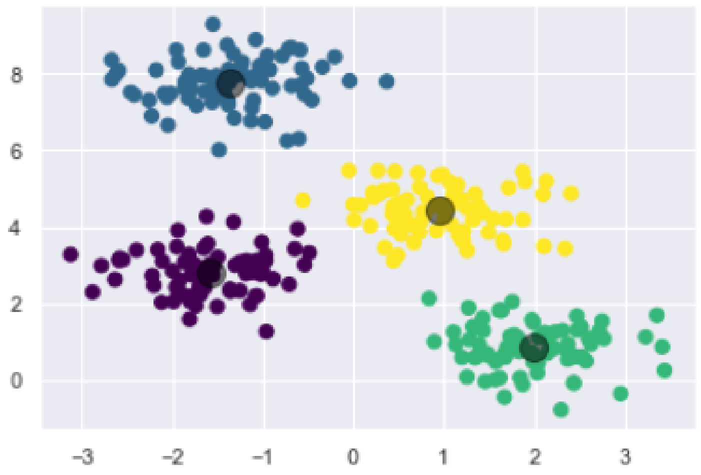


3. By eye, it is relatively easy to pick out the four clusters. The k-means algorithm does this automatically and in Scikit-Learn uses the typical estimator API :

```python
from sklearn.cluster import KMeans
kmeans = KMeans(n_clusters=4)
kmeans.fit(X)
y_kmeans = kmeans.predict(X)
```

4. Lets visualize the result by plotting the data colored by these labels. We will also plot the cluster centers as determined by the k-means estimator :

```python
plt.scatter(X[:, 0], X[:, 1], c=y_kmeans, s=50, cmap='viridis')

centers = kmeans.cluster_centers_
plt.scatter(centers[:, 0], centers[:, 1], c='black', s=200, alpha=0.5);
```



The good news is that the k means algorithm assigns the points to clusters very similarity to how we might assign them by eye. After all, the number of possible combinations of cluster assignments is exponential in the number of data points – an exhaustive search would be very costly. Fortunately for us, such an exhaustive search is not necessary: instead, the typical approach to *k*-means involves an intuitive iterative approach known as *expectation–maximization*.

k-Means Algorithm : Expectation-Maximization

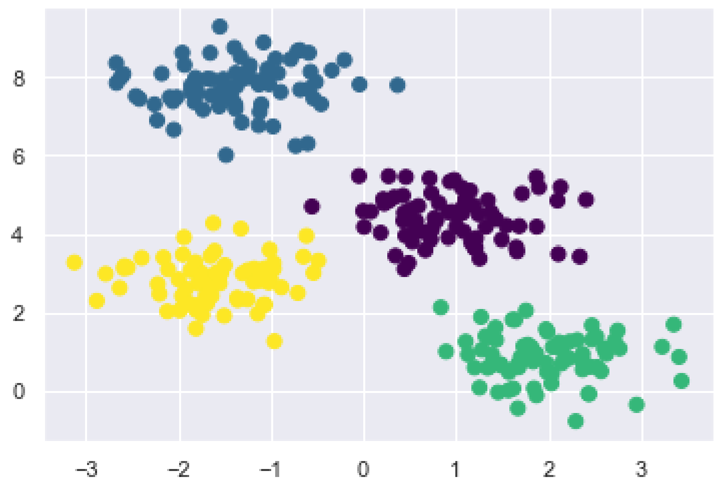
Expectation–maximization (E–M) is a powerful algorithm that comes up in a variety of contexts within data science. *k*-means is a particularly simple and easy-to-understand application of the algorithm, and we will walk through it briefly here. In short, the expectation–maximization approach here consists of the following procedure :

- Guess some cluster centers
- Repeat until converged :
    - E-Step : assign points to the nearest cluster center
    - M-Step : set the cluster centers to the mean

Here the "E-step" or "Expectation step" is so-named because it involves updating our expectation of which cluster each point belongs to. The "M-step" or "Maximization step" is so-named because it involves maximizing some fitness function that defines the location of the cluster centers—in this case, that maximization is accomplished by taking a simple mean of the data in each cluster.

5. The *k*-Means algorithm is simple enough that we can write it in a few lines of code. The following is a very basic implementation:

```python
from sklearn.metrics import pairwise_distances_argmin

def find_clusters(X, n_clusters, rseed=2):
    # 1. Randomly choose clusters
    rng = np.random.RandomState(rseed)
    i = rng.permutation(X.shape[0])[:n_clusters]
    centers = X[i]

    while True:
        # a. Assign labels based on closest center
        labels = pairwise_distances_argmin(X, centers)

        # b. Find new centers from means of points
        new_centers = np.array([X[labels == i].mean(0)
                                for i in range(n_clusters)])

        # c. Check for convergence
        if np.all(centers == new_centers):
            break
        centers = new_centers

    return centers, labels

centers, labels = find_clusters(X, 4)
plt.scatter(X[:, 0], X[:, 1], c=labels,
            s=50, cmap='viridis');
```



Most well-tested implementations will do a bit more than this under the hood, but the preceding function gives the gist of the expectation–maximization approach.

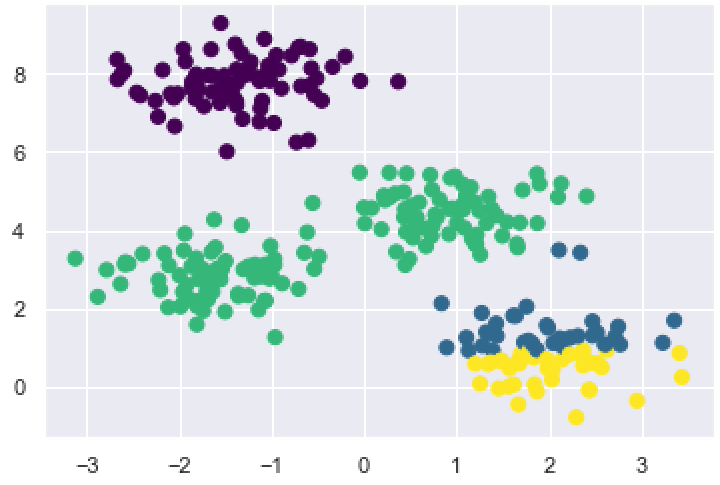
Caveats of Expectation-Maximization

There are a few issues to be aware of when using the expectation-maximization algorithm.

The globally optimal result may not be achieved

6. First, although the E–M procedure is guaranteed to improve the result in each step, there is no assurance that it will lead to the *global* best solution. For example, if we use a different random seed in our simple procedure, the particular starting guesses lead to poor results :

```python
centers, labels = find_clusters(X, 4, rseed=0)
plt.scatter(X[:, 0], X[:, 1], c=labels,
            s=50, cmap='viridis');
```

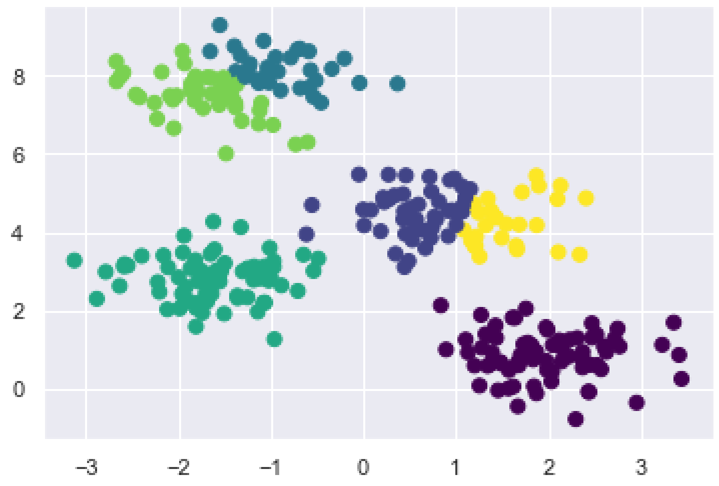


Here the E–M approach has converged, but has not converged to a globally optimal configuration. For this reason, it is common for the algorithm to be run for multiple starting guesses, as indeed Scikit-Learn does by default (set by the n_init parameter, which defaults to 10).

The number of clusters must be selected beforehand

7. Another common challenge with *k*-means is that you must tell it how many clusters you expect: it cannot learn the number of clusters from the data. For example, if we ask the algorithm to identify six clusters, it will happily proceed and find the best six clusters:

```python
labels = KMeans(6, random_state=0).fit_predict(X)
plt.scatter(X[:, 0], X[:, 1], c=labels,
            s=50, cmap='viridis');
```



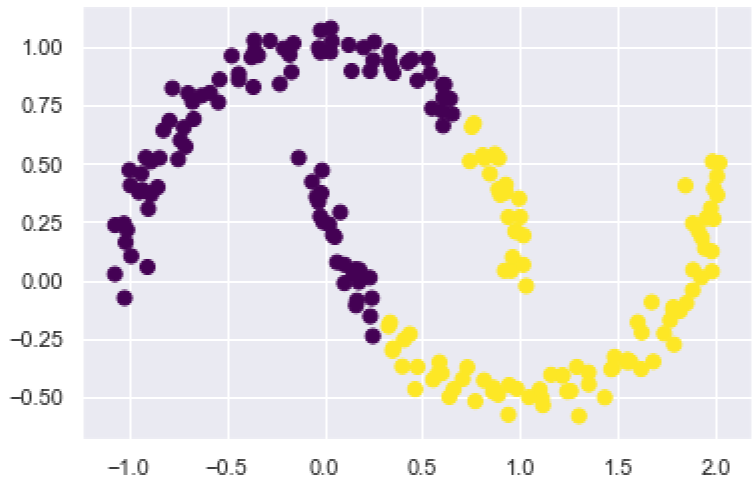
k-Means is Limited to Linear Cluster Boundaries

The fundamental model assumptions of k-means (points will be closer to their own cluster center than to others) means that the algorithm will often be ineffective if the clusters have complicated geometries.

8. In particular, the boundaries between k-means cluster will always be linear, which means that it will fail for more complicated boundaries. Consider the following data, along with the cluster labels found by the typical k-means approach ;

```python
from sklearn.datasets import make_moons
X, y = make_moons(200, noise=.05, random_state=0)
```

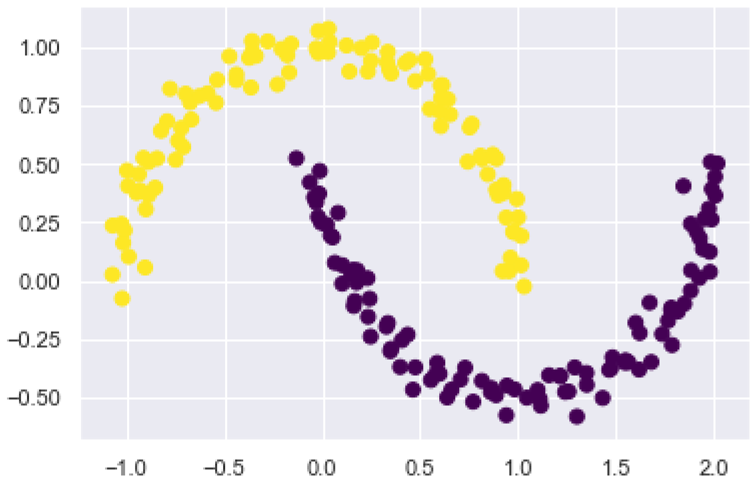
```python
labels = KMeans(2, random_state=0).fit_predict(X)
plt.scatter(X[:, 0], X[:, 1], c=labels,
            s=50, cmap='viridis');
```



Where we used a kernel transformation to project the data into a higher dimension where a linear separation is possible. We might imagine using the same trick to allow *k*-means to discover non-linear boundaries.

9. One version of this kernelized *k*-means is implemented in Scikit-Learn within the SpectralClustering estimator. It uses the graph of nearest neighbors to compute a higher-dimensional representation of the data, and then assigns labels using a *k*-means algorithm:

```python
from sklearn.cluster import SpectralClustering
model = SpectralClustering(n_clusters=2, affinity='nearest_neighbors',
                           assign_labels='kmeans')
labels = model.fit_predict(X)
plt.scatter(X[:, 0], X[:, 1], c=labels,
            s=50, cmap='viridis');
```



We see that with this kernel transform approach, the kernelized *k*-means is able to find the more complicated nonlinear boundaries between clusters.

Example : k-means on digits

10. We will start by loading the digits and then finding the KMeans clusters. Recall that the digits consist of 1,797 samples with 64 features, where each of the 64 features is the brightness of one pixel in an 8×8 image:

```
from sklearn.datasets import load_digits
digits = load_digits()
digits.data.shape
```

```
(1797, 64)
```

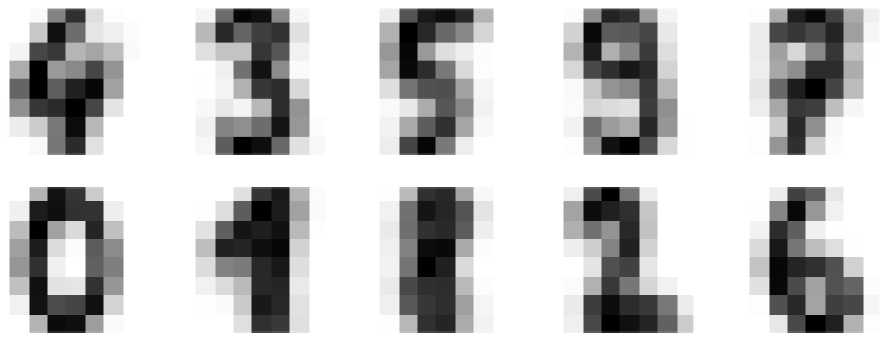
11. The clustering can be performed as we did before:

```
kmeans = KMeans(n_clusters=10, random_state=0)
clusters = kmeans.fit_predict(digits.data)
kmeans.cluster_centers_.shape
```

```
(10, 64)
```

12. The result is 10 clusters in 64 dimensions. Notice that the cluster centers themselves are 64-dimensional points, and can themselves be interpreted as the "typical" digit within the cluster. Let's see what these cluster centers look like:

```python
fig, ax = plt.subplots(2, 5, figsize=(8, 3))
centers = kmeans.cluster_centers_.reshape(10, 8, 8)
for axi, center in zip(ax.flat, centers):
    axi.set(xticks=[], yticks=[])
    axi.imshow(center, interpolation='nearest', cmap=plt.cm.binary)
```



We see that *even without the labels*, KMeans is able to find clusters whose centers are recognizable digits, with perhaps the exception of 1 and 8.

13. Because *k*-means knows nothing about the identity of the cluster, the 0–9 labels may be permuted. We can fix this by matching each learned cluster label with the true labels found in them:

```python
from scipy.stats import mode

labels = np.zeros_like(clusters)
for i in range(10):
    mask = (clusters == i)
    labels[mask] = mode(digits.target[mask])[0]
```

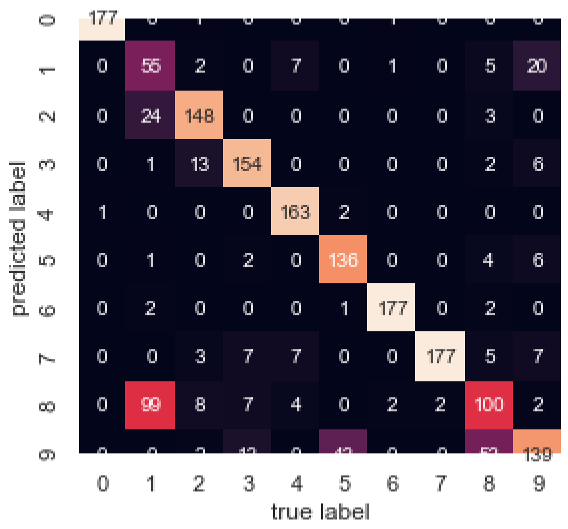
14. Now we can check how accurate our unsupervised clustering was in finding similar digits within the data:

```python
from sklearn.metrics import accuracy_score
accuracy_score(digits.target, labels)
```

```
0.7935447968836951
```

15. With just a simple *k*-means algorithm, we discovered the correct grouping for 80% of the input digits! Let's check the confusion matrix for this:

```python
from sklearn.metrics import confusion_matrix
mat = confusion_matrix(digits.target, labels)
sns.heatmap(mat.T, square=True, annot=True, fmt='d', cbar=False,
            xticklabels=digits.target_names,
            yticklabels=digits.target_names)
plt.xlabel('true label')
plt.ylabel('predicted label');
```



As we might expect from the cluster centers we visualized before, the main point of confusion is between the eights and ones. But this still shows that using *k*-means, we can essentially build a digit classifier *without reference to any known labels*!

Example : k-means for color compression

One interesting application of clustering is in color compression within images. For example, imagine you have an image with millions of colors. In most images, a large number of the colors will be unused, and many of the pixels in the image will have similar or even identical colors.

16. The image shown in the following figure, which is from scikit-learn datasets module (note : this requires the "pillow" package to be installed) :

```python
from sklearn.datasets import load_sample_image
china = load_sample_image("china.jpg")
ax = plt.axes(xticks=[], yticks=[])
ax.imshow(china);
```

17. The image itself is stored in a three-dimensional array of size (height, width, RGB), containing red/blue/green contributions as integers from 0 to 255:

```
china.shape
```

```
(427, 640, 3)
```

18. One way we can view this set of pixels is as a cloud of points in a three-dimensional color space. We will reshape the data to [n_samples x n_features], and rescale the colors so that they lie between 0 and 1:

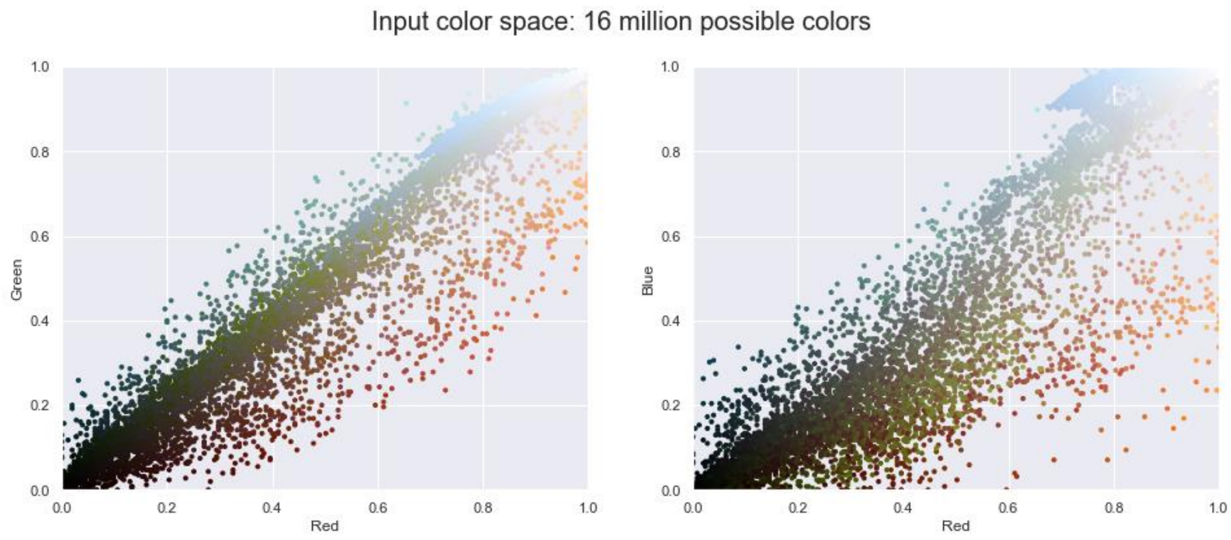
```
data = china / 255.0 # use 0...1 scale
data = data.reshape(427 * 640, 3)
data.shape
```

```
(273280, 3)
```

19. We can visualize these pixels in this color space, using a subset of 10,000 pixels for efficiency:

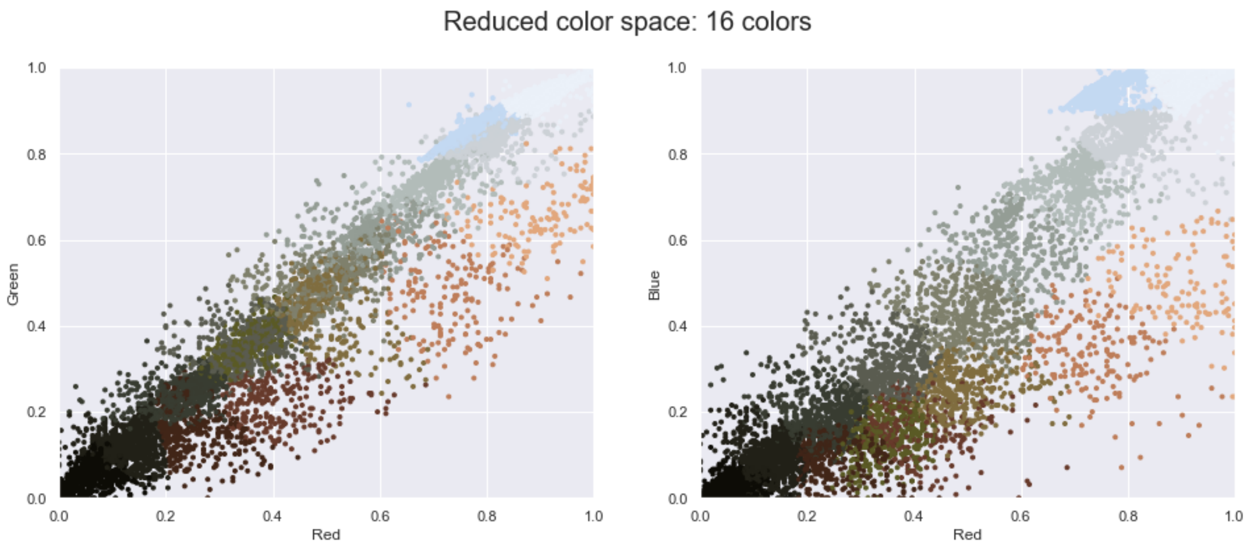
```python
def plot_pixels(data, title, colors=None, N=10000):
    if colors is None:
        colors = data

    # choose a random subset
    rng = np.random.RandomState(0)
    i = rng.permutation(data.shape[0])[:N]
    colors = colors[i]
    R, G, B = data[i].T

    fig, ax = plt.subplots(1, 2, figsize=(16, 6))
    ax[0].scatter(R, G, color=colors, marker='.')
    ax[0].set(xlabel='Red', ylabel='Green', xlim=(0, 1), ylim=(0, 1))

    ax[1].scatter(R, B, color=colors, marker='.')
    ax[1].set(xlabel='Red', ylabel='Blue', xlim=(0, 1), ylim=(0, 1))

    fig.suptitle(title, size=20);
```

```python
plot_pixels(data, title='Input color space: 16 million possible colors')
```



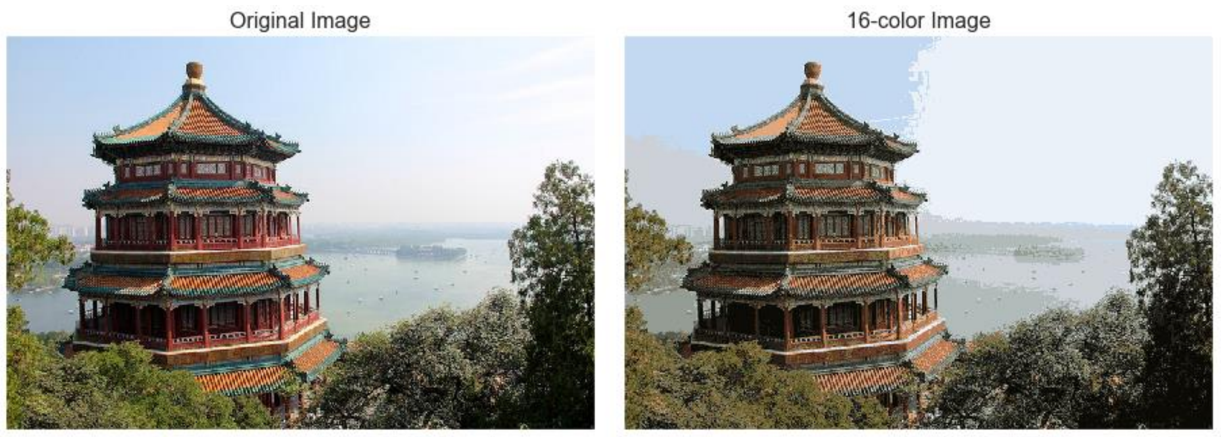
20. Now let's reduce these 16 million colors to just 16 colors, using a *k*-means clustering across the pixel space. Because we are dealing with a very large dataset, we will use the mini batch *k*-means, which operates on subsets of the data to compute the result much more quickly than the standard *k*-means algorithm:

```python
import warnings; warnings.simplefilter('ignore')  # Fix NumPy issues.

from sklearn.cluster import MiniBatchKMeans
kmeans = MiniBatchKMeans(16)
kmeans.fit(data)
new_colors = kmeans.cluster_centers_[kmeans.predict(data)]

plot_pixels(data, colors=new_colors,
            title="Reduced color space: 16 colors")
```



21. The result is a re-coloring of the original pixels, where each pixel is assigned the color of its closest cluster center. Plotting these new colors in the image space rather than the pixel space shows us the effect of this:

```python
china_recolored = new_colors.reshape(china.shape)

fig, ax = plt.subplots(1, 2, figsize=(16, 6),
                       subplot_kw=dict(xticks=[], yticks=[]))
fig.subplots_adjust(wspace=0.05)
ax[0].imshow(china)
ax[0].set_title('Original Image', size=16)
ax[1].imshow(china_recolored)
ax[1].set_title('16-color Image', size=16);
```

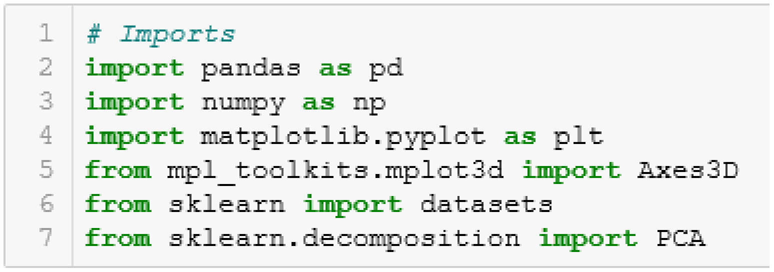


Some detail is certainly lost in the rightmost panel, but the overall image is still easily recognizable. This image on the right achieves a compression factor of around 1 million! While this is an interesting application of *k*-means, there are certainly better way to compress information in images. But the example shows the power of thinking outside of the box with unsupervised methods like *k*-means.

k-Medoids Algorithm

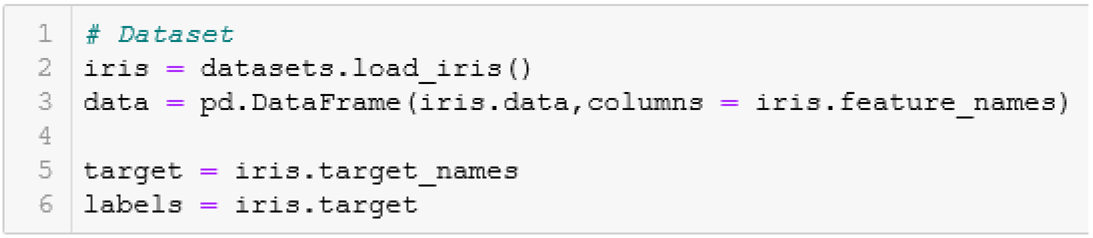
both k-means and k-medoids are partitional, which involves breaking the dataset into groups. K-medoids attempts to minimize the sum of dissimilarities between objects labeled to be in a cluster and one of the objects designed as the representative of that cluster. These of representatives are called medoids.

22. For the beginning, we import the important libraries :



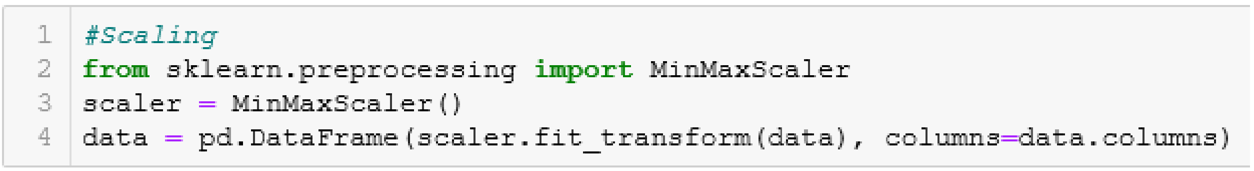
```
# Imports
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D
from sklearn import datasets
from sklearn.decomposition import PCA
```

23. We load the dataset. We will use a copy of iris data set from sklearn library.



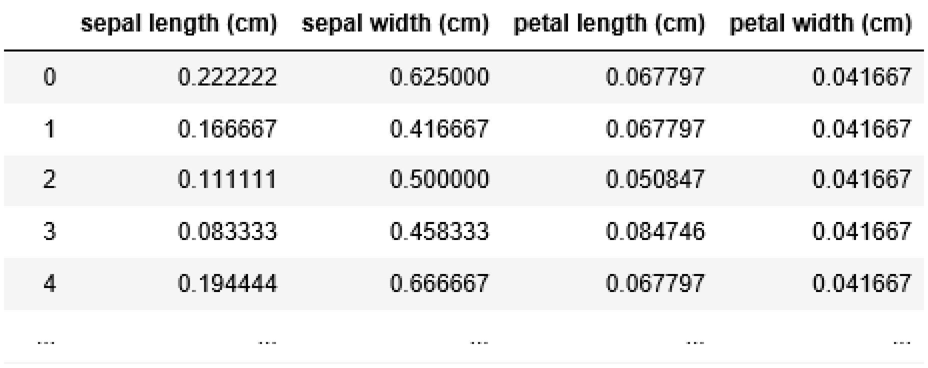
```
# Dataset
iris = datasets.load_iris()
data = pd.DataFrame(iris.data,columns = iris.feature_names)

target = iris.target_names
labels = iris.target
```

24. We scaling the data for these types of problem when data is on different scales across the columns. Since there is no missing data, let’s proceed with the scaling. We are utilized the MinMaxScaler class from the same sklearn library



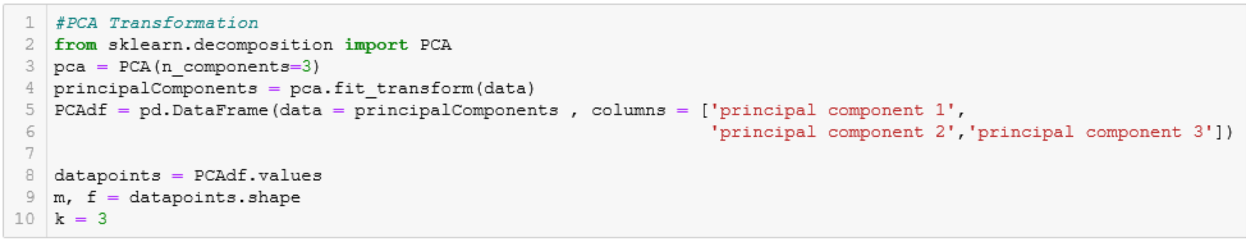
```python
#Scaling
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()
data = pd.DataFrame(scaler.fit_transform(data), columns=data.columns)
```

The output of data scaling :



	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
0	0.222222	0.625000	0.067797	0.041667
1	0.166667	0.416667	0.067797	0.041667
2	0.111111	0.500000	0.050847	0.041667
3	0.083333	0.458333	0.084746	0.041667
4	0.194444	0.666667	0.067797	0.041667
...	...	...	...	...

25. There are 4 features which might not be ideal for visualization and fitting of the clustering model since some of them might be highly correlated. Therefore, we will employ the Principal Component Analysis (PCA) to transform 4-dimensional data into 3-dimensional data while keeping the significance of those predictors with the PCA class from sklearn.



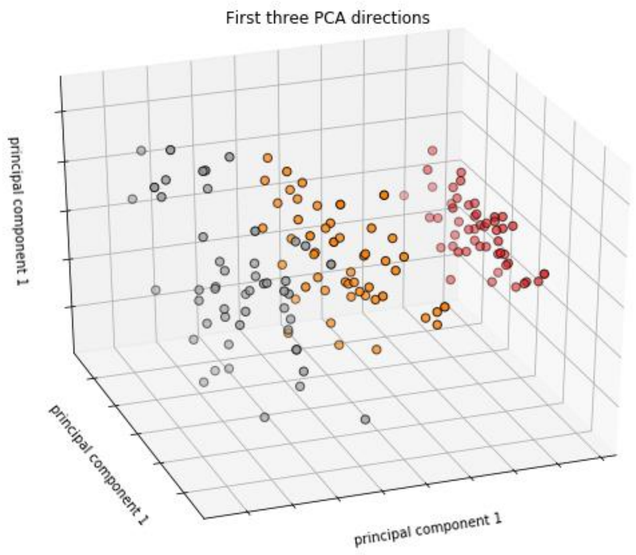
```python
#PCA Transformation
from sklearn.decomposition import PCA
pca = PCA(n_components=3)
principalComponents = pca.fit_transform(data)
PCAdf = pd.DataFrame(data = principalComponents , columns = ['principal component 1',
                                                             'principal component 2','principal component 3'])

datapoints = PCAdf.values
m, f = datapoints.shape
k = 3
```

The output :

```
array([[-6.30702931e-01,  1.07577910e-01, -1.87190977e-02],
       [-6.22904943e-01, -1.04259833e-01, -4.91420253e-02],
       [-6.69520395e-01, -5.14170597e-02,  1.96441728e-02],
       [-6.54152759e-01, -1.02884871e-01,  2.32185515e-02],
       [-6.48788056e-01,  1.33487576e-01,  1.51155243e-02],
       [-5.35272778e-01,  2.89615724e-01,  2.54378874e-02],
       [-6.56537790e-01,  1.07244911e-02,  9.18347789e-02],
       [-6.25780499e-01,  5.71335411e-02, -1.40277647e-02],
       [-6.75643504e-01, -2.00703283e-01,  3.59520802e-02],
       [-6.45644619e-01, -6.72080097e-02, -6.17055833e-02],
       [-5.97408238e-01,  2.17151953e-01, -5.12740810e-02],
       [-6.38943190e-01,  3.25988375e-02,  2.44981902e-02],
       [-6.61612593e-01, -1.15605495e-01, -5.47803418e-02],
       [-7.51967943e-01, -1.71313322e-01,  4.76777938e-02],
       [-6.00371589e-01,  3.80240692e-01, -8.51695344e-02],
       [-5.52157227e-01,  5.15255982e-01,  3.82732690e-02],
       [-5.77053593e-01,  2.93709492e-01,  2.99057044e-02],
       [-6.03799228e-01,  1.07167941e-01,  6.74067339e-03],
       [-5.20483461e-01,  2.87627289e-01, -7.34994148e-02],
```

26. Visualize on a 3-D plane :

```python
#Visualization
fig = plt.figure(1, figsize=(8, 6))
ax = Axes3D(fig, elev=-150, azim=110)
X_reduced = datapoints
ax.scatter(X_reduced[:, 0], X_reduced[:, 1], X_reduced[:, 2], c=labels,
           cmap=plt.cm.Set1, edgecolor='k', s=40)
ax.set_title("First three PCA directions")
ax.set_xlabel("principal component 1")
ax.w_xaxis.set_ticklabels([])
ax.set_ylabel("principal component 1")
ax.w_yaxis.set_ticklabels([])
ax.set_zlabel("principal component 1")
ax.w_zaxis.set_ticklabels([])
plt.show()
```



Medoid Initialization

27. To start the algorithm, we need an initial guess. Lets randomly choose k observation from the data. In this case, k = 3 representing 3 different types of iris. Next we will create function, init_medoids(X,k), so that it randomly selects k of the given observations to serve as medoids. It should return a NumPy array of size (k x d), where d is the number of columns of X.

```
def init_medoids(X, k):
    from numpy.random import choice
    from numpy.random import seed

    seed(1)
    samples = choice(len(X), size=k, replace=False)
    return X[samples, :]

medoids_initial = init_medoids(datapoints, 3)
```

After initializing 3 random medoid from the data points, we have :

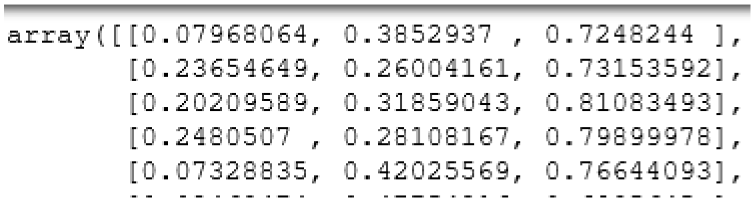
```
array([[-0.60037159,  0.38024069, -0.08516953],
       [-0.15863457, -0.28913985,  0.0524159 ],
       [ 0.21396272,  0.059963  , -0.11409813]])
```

Computing the Distances

28. Implementing a function that computes a distance matrix (S = s_ij) such that s_ij = d^p_ij is the Minkowski distance of order p point x_i to medoid. It should return a NumPy matrix S with shape (m,k).

```
def compute_d_p(X, medoids, p):
    m = len(X)
    medoids_shape = medoids.shape
    # If a 1-D array is provided,
    # it will be reshaped to a single row 2-D array
    if len(medoids_shape) == 1:
        medoids = medoids.reshape((1,len(medoids)))
    k = len(medoids)

    S = np.empty((m, k))

    for i in range(m):
        d_i = np.linalg.norm(X[i, :] - medoids, ord=p, axis=1)
        S[i, :] = d_i**p

    return S

S = compute_d_p(datapoints, medoids_initial, 2)
```

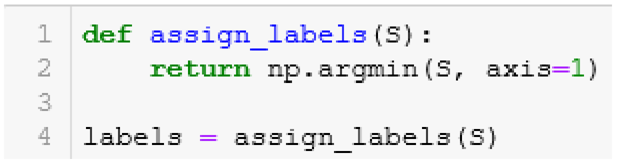
Based on that, the first 5 elements of the matrix S are :



```
array([[0.07968064, 0.3852937 , 0.7248244 ],
       [0.23654649, 0.26004161, 0.73153592],
       [0.20209589, 0.31859043, 0.81083493],
       [0.2480507 , 0.28108167, 0.79899978],
       [0.07328835, 0.42025569, 0.76644093],
```

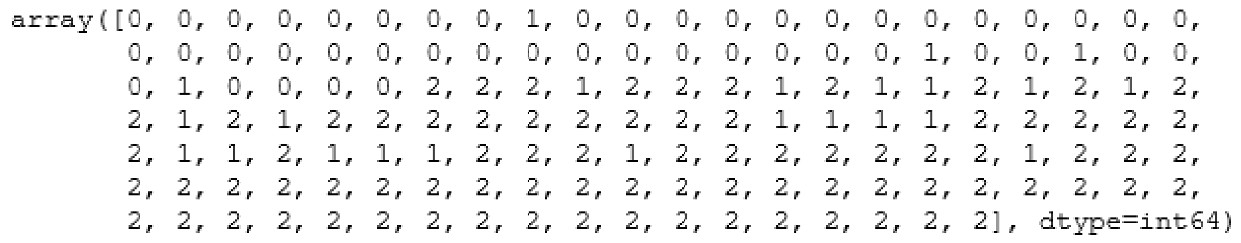
Cluster Assignment

29. Now we build a function that acts on the distance matrix S to assign a "Cluster Label" of 0, 1 and 2 to each point using the minimum distance to find the "most similar" medoid.



```python
def assign_labels(S):
    return np.argmin(S, axis=1)

labels = assign_labels(S)
```

We then get the labels for the data points of the first iteration :



```
array([0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0,
       0, 1, 0, 0, 0, 0, 2, 2, 2, 1, 2, 2, 2, 1, 2, 1, 1, 2, 1, 2, 1, 2,
       2, 1, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 1, 1, 1, 2, 2, 2, 2, 2,
       2, 1, 1, 2, 1, 1, 1, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 1, 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, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2], dtype=int64)
```

Swap Test

30. In this step, for each medoid j and each data point i associated to j swap and i and compute the total cost of the configuration as Step 29. Select the medoid j with the lowest cost of the configuration. That is, for each cluster, search if any of the points in the cluster decreases the average dissimilarity coefficient. Select the point that decreases this coefficient the most as the new medoid for this cluster.

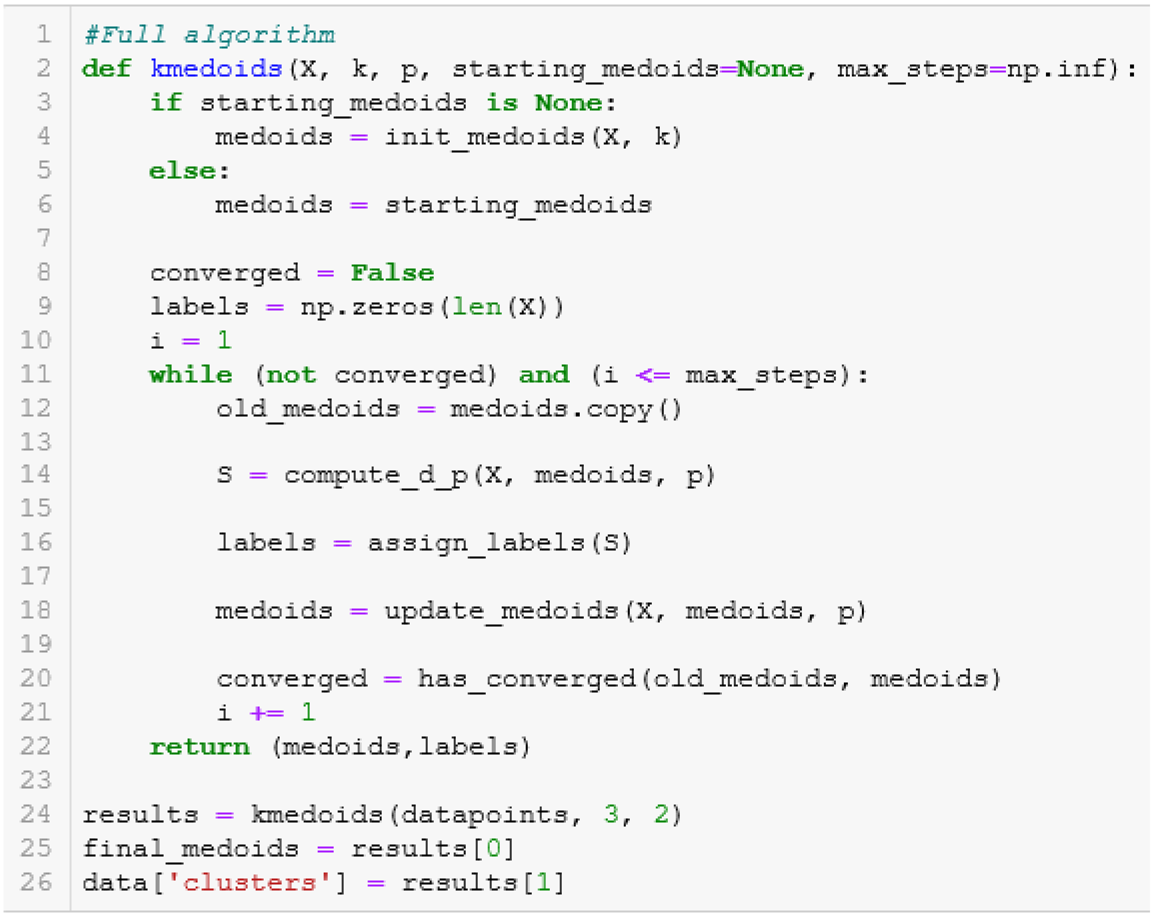
```python
def update_medoids(X, medoids, p):

    S = compute_d_p(datapoints, medoids, p)
    labels = assign_labels(S)

    out_medoids = medoids

    for i in set(labels):

        avg_dissimilarity = np.sum(compute_d_p(datapoints, medoids[i], p))

        cluster_points = datapoints[labels == i]

        for datap in cluster_points:
            new_medoid = datap
            new_dissimilarity= np.sum(compute_d_p(datapoints, datap, p))

            if new_dissimilarity < avg_dissimilarity :
                avg_dissimilarity = new_dissimilarity

                out_medoids[i] = datap

    return out_medoids
```

31. We also need a function that checks whether the medoid have “moved”, given two instances of the medoid values. This is the function to check whether the medoids no longer moves and the iteration should be stopped.

```python
def has_converged(old_medoids, medoids):
    return set([tuple(x) for x in old_medoids]) == set([tuple(x) for x in medoids])
```

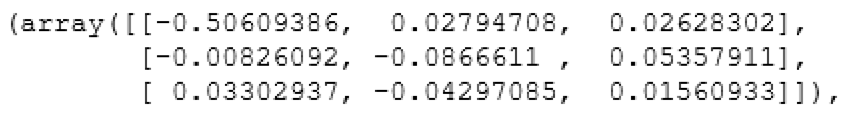
Putting all Together

32. When we combined all the function above, we essentially combine the steps of a k-medois algorithm :



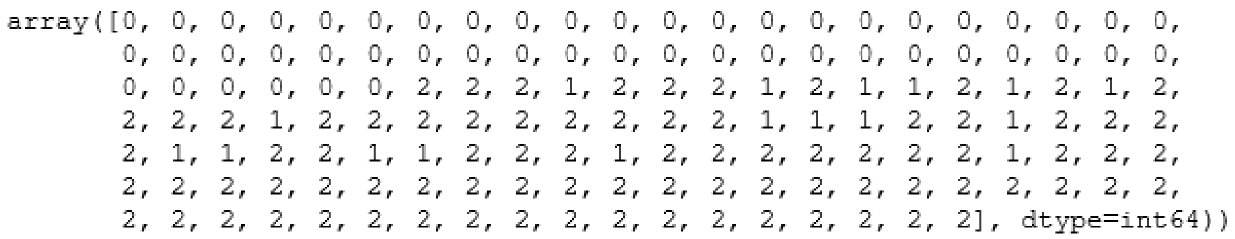
```python
#Full algorithm
def kmedoids(X, k, p, starting_medoids=None, max_steps=np.inf):
    if starting_medoids is None:
        medoids = init_medoids(X, k)
    else:
        medoids = starting_medoids

    converged = False
    labels = np.zeros(len(X))
    i = 1
    while (not converged) and (i <= max_steps):
        old_medoids = medoids.copy()

        S = compute_d_p(X, medoids, p)

        labels = assign_labels(S)

        medoids = update_medoids(X, medoids, p)

        converged = has_converged(old_medoids, medoids)
        i += 1
    return (medoids,labels)

results = kmedoids(datapoints, 3, 2)
final_medoids = results[0]
data['clusters'] = results[1]
```

By running the function over the data points that we have, the final medoids are found to be :



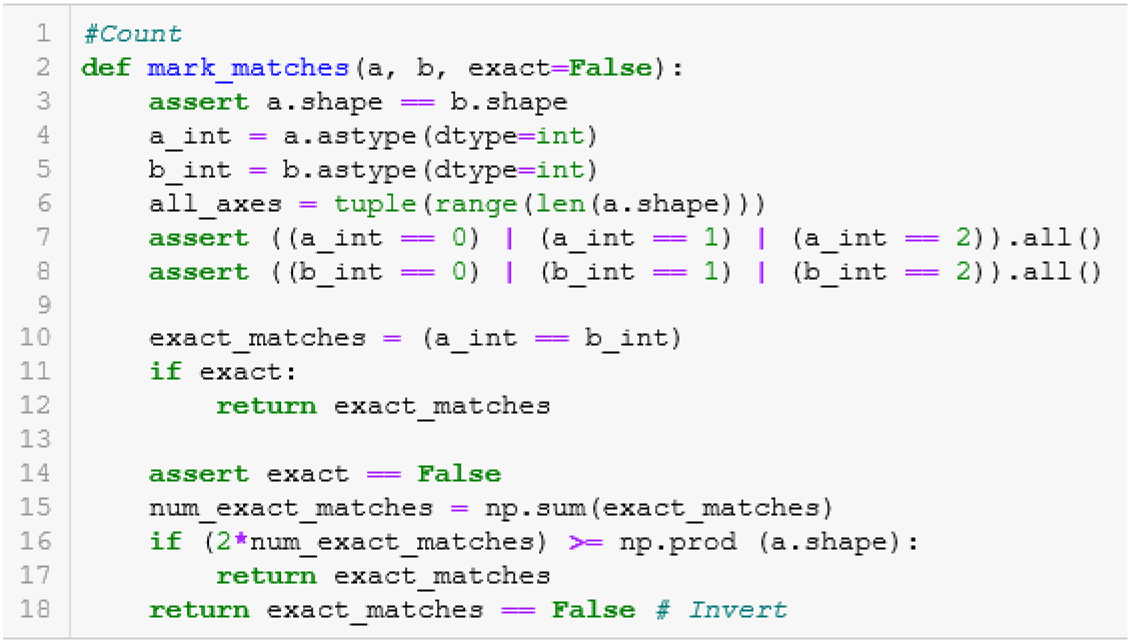
```
(array([[-0.50609386,  0.02794708,  0.02628302],
        [-0.00826092, -0.0866611 ,  0.05357911],
        [ 0.03302937, -0.04297085,  0.01560933]]),
```

And the cluster labels of each data points are :

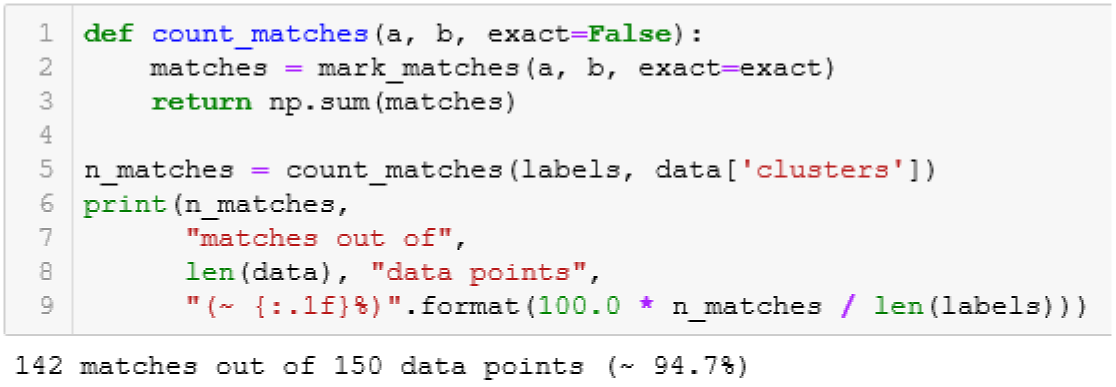


```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 2, 2, 2, 1, 2, 2, 2, 1, 2, 1, 1, 2, 1, 2, 1, 2,
       2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 1, 1, 2, 2, 1, 2, 2, 2,
       2, 1, 1, 2, 2, 1, 1, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 1, 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, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2], dtype=int64))
```

33. By considering “inexact” matches, the k-medoids above labels correctly 94.7% of the data points. This is just for demonstration purpose of how the algorithm works and this number does not mean much as we did not split the data into training and testing set.



```python
#Count
def mark_matches(a, b, exact=False):
    assert a.shape == b.shape
    a_int = a.astype(dtype=int)
    b_int = b.astype(dtype=int)
    all_axes = tuple(range(len(a.shape)))
    assert ((a_int == 0) | (a_int == 1) | (a_int == 2)).all()
    assert ((b_int == 0) | (b_int == 1) | (b_int == 2)).all()

    exact_matches = (a_int == b_int)
    if exact:
        return exact_matches

    assert exact == False
    num_exact_matches = np.sum(exact_matches)
    if (2*num_exact_matches) >= np.prod (a.shape):
        return exact_matches
    return exact_matches == False # Invert
```



```python
def count_matches(a, b, exact=False):
    matches = mark_matches(a, b, exact=exact)
    return np.sum(matches)

n_matches = count_matches(labels, data['clusters'])
print(n_matches,
      "matches out of",
      len(data), "data points",
      "(~ {:.1f}%)".format(100.0 * n_matches / len(labels)))
```

```
142 matches out of 150 data points (~ 94.7%)
```

k-Modes Algorithm : Unsupervised Learning for Categorical Data

Introduced in 1998 by ZHehue Huang, k-modes provides a much needed alternative to k-means when the data at hand are **categorical rather than numeric**. Categorical here means that we can make a finite list all possible categories as column headings and then for each row, indicate whether the category indicated is observed.

For example, we use data categorical from UCI Machine Learning, Bank Marketing (UCI Repository: https://archive.ics.uci.edu/ml/datasets/bank+marketing).

34. Import the important libraries :

```python
# supress warnings
import warnings
warnings.filterwarnings('ignore')

# Importing all required packages
import numpy as np
import pandas as pd

# Data viz lib
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
from matplotlib.pyplot import xticks
```

35. Reading the data and understanding the data and shown the data

```python
bank = pd.read_csv('bankmarketing.csv')
```

```python
bank.head()
```

```
   age        job  marital   education  default housing loan    contact month day_of_week ... campaign pdays previous    poutcome emp.var.rate
0   56  housemaid  married    basic.4y       no      no   no  telephone   may         mon ...        1   999        0 nonexistent          1.1
1   57   services  married high.school  unknown      no   no  telephone   may         mon ...        1   999        0 nonexistent          1.1
2   37   services  married high.school       no     yes   no  telephone   may         mon ...        1   999        0 nonexistent          1.1
3   40     admin.  married    basic.6y       no      no   no  telephone   may         mon ...        1   999        0 nonexistent          1.1
4   56   services  married high.school       no      no  yes  telephone   may         mon ...        1   999        0 nonexistent          1.1

5 rows × 21 columns
```

Show the data columns and importing the categorical columns :

```python
bank.columns
```

```
Index(['age', 'job', 'marital', 'education', 'default', 'housing', 'loan',
       'contact', 'month', 'day_of_week', 'duration', 'campaign', 'pdays',
       'previous', 'poutcome', 'emp.var.rate', 'cons.price.idx',
       'cons.conf.idx', 'euribor3m', 'nr.employed', 'y'],
      dtype='object')
```

```python
# Importing Categorical Columns
bank_cust = bank[['age','job', 'marital', 'education', 'default', 'housing', 'loan',
                  'contact','month','day_of_week','poutcome']]
```

Show the data after importing :

```
bank_cust.head()
```

	age	job	marital	education	default	housing	loan	contact	month	day_of_week	poutcome
0	56	housemaid	married	basic.4y	no	no	no	telephone	may	mon	nonexistent
1	57	services	married	high.school	unknown	no	no	telephone	may	mon	nonexistent
2	37	services	married	high.school	no	yes	no	telephone	may	mon	nonexistent
3	40	admin.	married	basic.6y	no	no	no	telephone	may	mon	nonexistent
4	56	services	married	high.school	no	no	yes	telephone	may	mon	nonexistent

We need converting age into categorical value :

```
# Converting age into categorical variable.
bank_cust['age_bin'] = pd.cut(bank_cust['age'], [0, 20, 30, 40, 50, 60, 70, 80, 90, 100],
                              labels=['0-20', '20-30', '30-40', '40-50','50-60','60-70',
                                      '70-80', '80-90','90-100'])
bank_cust  = bank_cust.drop('age',axis = 1)
```

Take a look the data after converting :

```
bank_cust.head()
```

	job	marital	education	default	housing	loan	contact	month	day_of_week	poutcome	age_bin
0	housemaid	married	basic.4y	no	no	no	telephone	may	mon	nonexistent	50-60
1	services	married	high.school	unknown	no	no	telephone	may	mon	nonexistent	50-60
2	services	married	high.school	no	yes	no	telephone	may	mon	nonexistent	30-40
3	admin.	married	basic.6y	no	no	no	telephone	may	mon	nonexistent	30-40
4	services	married	high.school	no	no	yes	telephone	may	mon	nonexistent	50-60

36. Data inspection; we need to know the data shape, describe and information from data :

```
bank_cust.shape
```

```
(41188, 11)
```

```
bank_cust.describe()
```

	job	marital	education	default	housing	loan	contact	month	day_of_week	poutcome	age_bin
count	41188	41188	41188	41188	41188	41188	41188	41188	41188	41188	41188
unique	12	4	8	3	3	3	2	10	5	3	9
top	admin.	married	university.degree	no	yes	no	cellular	may	thu	nonexistent	30-40
freq	10422	24928	12168	32588	21576	33950	26144	13769	8623	35563	16385

```
bank_cust.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 41188 entries, 0 to 41187
Data columns (total 11 columns):
job            41188 non-null object
marital        41188 non-null object
education      41188 non-null object
default        41188 non-null object
housing        41188 non-null object
loan           41188 non-null object
contact        41188 non-null object
month          41188 non-null object
day_of_week    41188 non-null object
poutcome       41188 non-null object
age_bin        41188 non-null category
dtypes: category(1), object(10)
memory usage: 3.2+ MB
```

37. Data cleaning : first, we need to checking null values in the data. After that, we need to encoding the data. In this case, we use LabelEncoder.

```
# Checking Null values
bank_cust.isnull().sum()*100/bank_cust.shape[0]

```

```
job            0.0
marital        0.0
education      0.0
default        0.0
housing        0.0
loan           0.0
contact        0.0
month          0.0
day_of_week    0.0
poutcome       0.0
age_bin        0.0
dtype: float64
```

There are no NULL values in the dataset, hence it is clean.

```
# First we will keep a copy of data
bank_cust_copy = bank_cust.copy()
```

Data preprocessing with LabelEncoder :

```
from sklearn import preprocessing
le = preprocessing.LabelEncoder()
bank_cust = bank_cust.apply(le.fit_transform)
bank_cust.head()
```

	job	marital	education	default	housing	loan	contact	month	day_of_week	poutcome	age_bin
0	3	1	0	0	0	0	1	6	1	1	4
1	7	1	3	1	0	0	1	6	1	1	4
2	7	1	3	0	2	0	1	6	1	1	2
3	0	1	1	0	0	0	1	6	1	1	2
4	7	1	3	0	0	2	1	6	1	1	4

38. Installing the kmodes to building the model

```
!pip install kmodes
```

```
Requirement already satisfied:
Requirement already satisfied:
Requirement already satisfied:
2)
Requirement already satisfied:
Requirement already satisfied:
```

```
pip install --upgrade kmodes
```

```
Requirement already up-to-date: km
Requirement already satisfied, ski
es) (0.13.2)
Requirement already satisfied, ski
des) (1.4.1)
Requirement already satisfied, ski
rom kmodes) (0.21.2)
Requirement already satisfied, ski
des) (1.16.4)
```

39. Importing the important libraries :

```
# Importing Libraries
from kmodes.kmodes import KModes
```

40. Using k-modes with “Cao” Initialization :

```
km_cao = KModes(n_clusters=2, init = "Cao", n_init = 1, verbose=1)
fitClusters_cao = km_cao.fit_predict(bank_cust)
```

```
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 5322, cost: 192203.0
Run 1, iteration: 2/100, moves: 1160, cost: 192203.0
```

```
# Predicted Clusters
fitClusters_cao
```

```
array([1, 1, 0, ..., 0, 1, 0], dtype=uint16)
```

```
clusterCentroidsDf = pd.DataFrame(km_cao.cluster_centroids_)
clusterCentroidsDf.columns = bank_cust.columns
```

```
# Mode of the clusters
clusterCentroidsDf
```

	job	marital	education	default	housing	loan	contact	month	day_of_week	poutcome	age_bin
0	0	1	6	0	2	0	0	6	2	1	2
1	1	1	3	0	0	0	1	6	0	1	3

41. Using k-modes with “Huang” initialization :

```
km_huang = KModes(n_clusters=2, init = "Huang", n_init = 1, verbose=1)
fitClusters_huang = km_huang.fit_predict(bank_cust)
```

```
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 8091, cost: 199291.0
Run 1, iteration: 2/100, moves: 5859, cost: 199291.0
```

```
# Predicted clusters
fitClusters_huang
```

```
array([1, 0, 0, ..., 0, 0, 0], dtype=uint16)
```

42. Choosing K by comparing Cost against each K

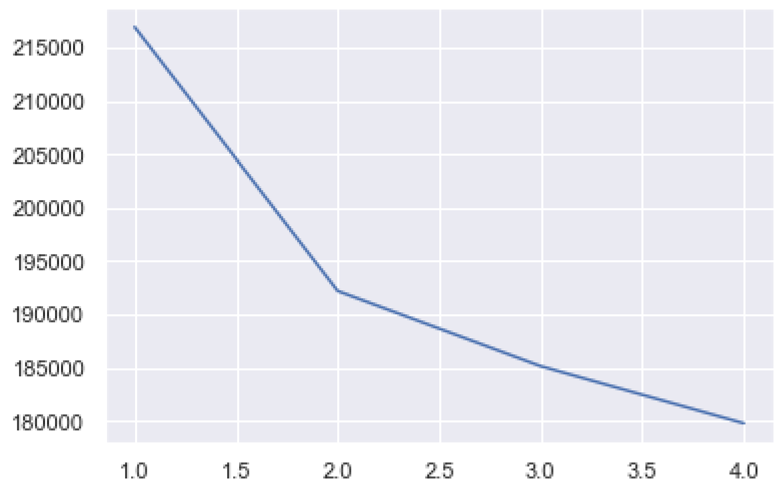
```python
cost = []
for num_clusters in list(range(1,5)):
    kmode = KModes(n_clusters=num_clusters, init = "Cao", n_init = 1, verbose=1)
    kmode.fit_predict(bank_cust)
    cost.append(kmode.cost_)
```

```
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 0, cost: 216952.0
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 5322, cost: 192203.0
Run 1, iteration: 2/100, moves: 1160, cost: 192203.0
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 4993, cost: 185138.0
Run 1, iteration: 2/100, moves: 1368, cost: 185138.0
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 6186, cost: 179774.0
Run 1, iteration: 2/100, moves: 1395, cost: 179774.0
```

Plotting the data frame :

```python
y = np.array([i for i in range(1,5,1)])
plt.plot(y,cost)
```

```
[<matplotlib.lines.Line2D at 0x201f39c4be0>]
```



```
## Choosing K=2
km_cao = KModes(n_clusters=2, init = "Cao", n_init = 1, verbose=1)
fitClusters_cao = km_cao.fit_predict(bank_cust)
```

```
Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 5322, cost: 192203.0
Run 1, iteration: 2/100, moves: 1160, cost: 192203.0
```

The result after fit the cluster :

```
fitClusters_cao
```

```
array([1, 1, 0, ..., 0, 1, 0], dtype=uint16)
```

43. Combining the predicted clusters with the original data frame :

```
bank_cust = bank_cust_copy.reset_index()
```

```
clustersDf = pd.DataFrame(fitClusters_cao)
clustersDf.columns = ['cluster_predicted']
combinedDf = pd.concat([bank_cust, clustersDf], axis = 1).reset_index()
combinedDf = combinedDf.drop(['index', 'level_0'], axis = 1)


```

Take a look the data after combining :

```
combinedDf.head()
```

	job	marital	education	default	housing	loan	contact	month	day_of_week	poutcome	age_bin	cluster_predicted
0	housemaid	married	basic.4y	no	no	no	telephone	may	mon	nonexistent	50-60	1
1	services	married	high.school	unknown	no	no	telephone	may	mon	nonexistent	50-60	1
2	services	married	high.school	no	yes	no	telephone	may	mon	nonexistent	30-40	0
3	admin.	married	basic.6y	no	no	no	telephone	may	mon	nonexistent	30-40	0
4	services	married	high.school	no	no	yes	telephone	may	mon	nonexistent	50-60	1

44. Cluster identification :

```
cluster_0 = combinedDf[combinedDf['cluster_predicted'] == 0]
cluster_1 = combinedDf[combinedDf['cluster_predicted'] == 1]
```

Display cluster info :

```python
cluster_0.info()
```

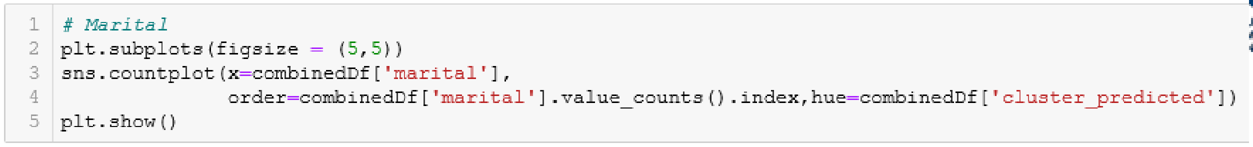
```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 28293 entries, 2 to 41187
Data columns (total 12 columns):
job                  28293 non-null object
marital              28293 non-null object
education            28293 non-null object
default              28293 non-null object
housing              28293 non-null object
loan                 28293 non-null object
contact              28293 non-null object
month                28293 non-null object
day_of_week          28293 non-null object
poutcome             28293 non-null object
age_bin              28293 non-null category
cluster_predicted    28293 non-null uint16
dtypes: category(1), object(10), uint16(1)
memory usage: 2.5+ MB
```

```python
cluster_1.info()
```

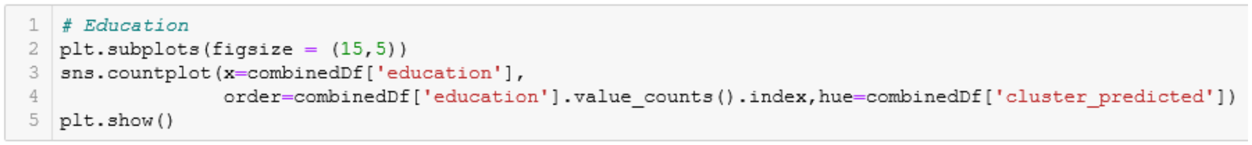
```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 12895 entries, 0 to 41186
Data columns (total 12 columns):
job                  12895 non-null object
marital              12895 non-null object
education            12895 non-null object
default              12895 non-null object
housing              12895 non-null object
loan                 12895 non-null object
contact              12895 non-null object
month                12895 non-null object
day_of_week          12895 non-null object
poutcome             12895 non-null object
age_bin              12895 non-null category
cluster_predicted    12895 non-null uint16
dtypes: category(1), object(10), uint16(1)
memory usage: 1.1+ MB
```

Plotting the result based on attributes :

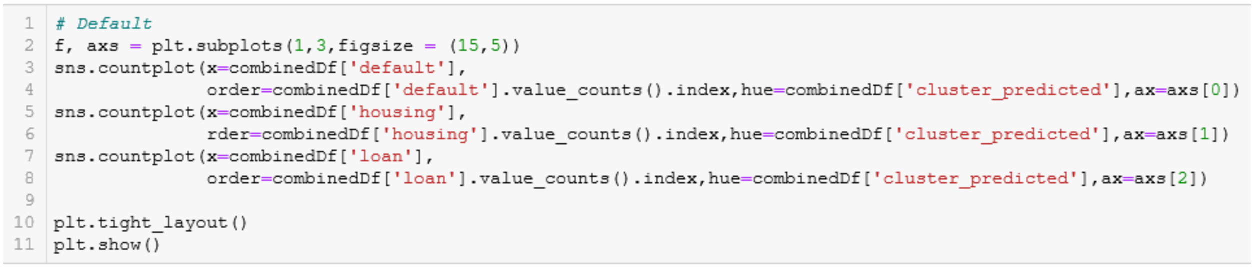
```python
# Job
plt.subplots(figsize = (15,5))
sns.countplot(x=combinedDf['job'],
              order=combinedDf['job'].value_counts().index,hue=combinedDf['cluster_predicted'])
plt.show()
```



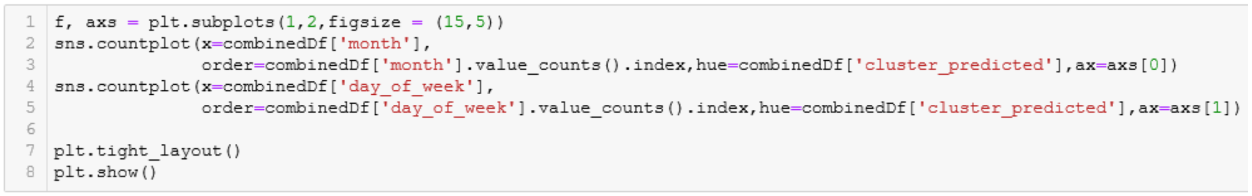
```python
# Marital
plt.subplots(figsize = (5,5))
sns.countplot(x=combinedDf['marital'],
              order=combinedDf['marital'].value_counts().index,hue=combinedDf['cluster_predicted'])
plt.show()
```



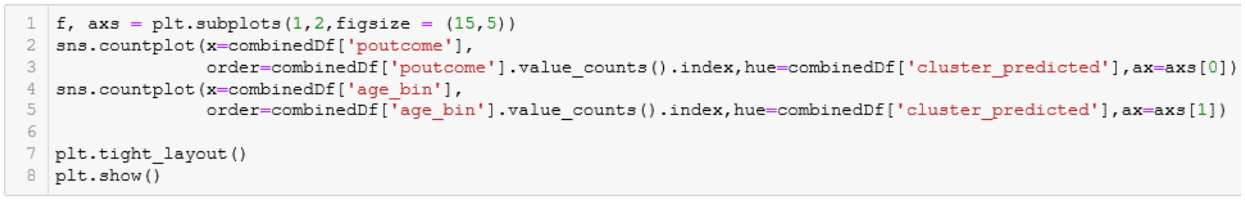
```python
# Education
plt.subplots(figsize = (15,5))
sns.countplot(x=combinedDf['education'],
              order=combinedDf['education'].value_counts().index,hue=combinedDf['cluster_predicted'])
plt.show()
```



```python
# Default
f, axs = plt.subplots(1,3,figsize = (15,5))
sns.countplot(x=combinedDf['default'],
              order=combinedDf['default'].value_counts().index,hue=combinedDf['cluster_predicted'],ax=axs[0])
sns.countplot(x=combinedDf['housing'],
              rder=combinedDf['housing'].value_counts().index,hue=combinedDf['cluster_predicted'],ax=axs[1])
sns.countplot(x=combinedDf['loan'],
              order=combinedDf['loan'].value_counts().index,hue=combinedDf['cluster_predicted'],ax=axs[2])

plt.tight_layout()
plt.show()
```



```python
f, axs = plt.subplots(1,2,figsize = (15,5))
sns.countplot(x=combinedDf['month'],
              order=combinedDf['month'].value_counts().index,hue=combinedDf['cluster_predicted'],ax=axs[0])
sns.countplot(x=combinedDf['day_of_week'],
              order=combinedDf['day_of_week'].value_counts().index,hue=combinedDf['cluster_predicted'],ax=axs[1])

plt.tight_layout()
plt.show()
```



```python
f, axs = plt.subplots(1,2,figsize = (15,5))
sns.countplot(x=combinedDf['poutcome'],
              order=combinedDf['poutcome'].value_counts().index,hue=combinedDf['cluster_predicted'],ax=axs[0])
sns.countplot(x=combinedDf['age_bin'],
              order=combinedDf['age_bin'].value_counts().index,hue=combinedDf['cluster_predicted'],ax=axs[1])

plt.tight_layout()
plt.show()
```

Above visualization can help in identification of clusters.

Referensi :

Raschka S, Mirjailili. 2017. Phython Machine Leraning 2nd edition. Packt Publishing