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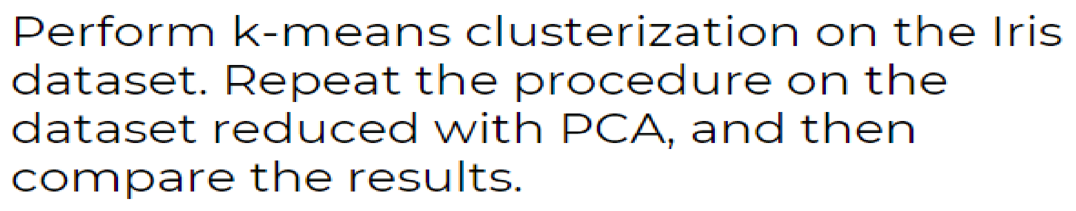
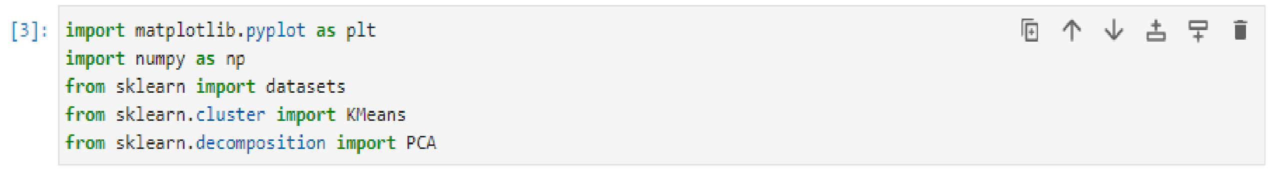
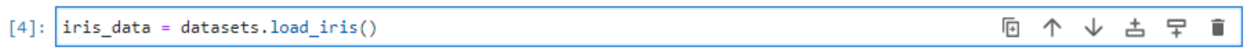
Assignment 3.3


Perform k-means clusterization on the Iris dataset. Repeat the procedure on the dataset reduced with PCA, and then compare the results.

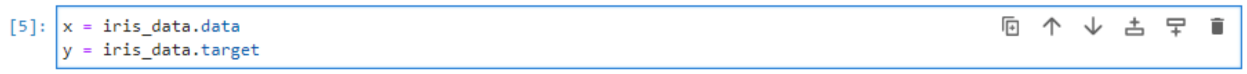
In the beginning we import the required libraries


```
[3]: import matplotlib.pyplot as plt
     import numpy as np
     from sklearn import datasets
     from sklearn.cluster import KMeans
     from sklearn.decomposition import PCA
```

And store the Iris dataset to variable 'Iris_data'


```
[4]: iris_data = datasets.load_iris()
```

Assign the dataset Features to variable 'x' and target value to variable 'y'


```
[5]: x = iris_data.data
     y = iris_data.target
```

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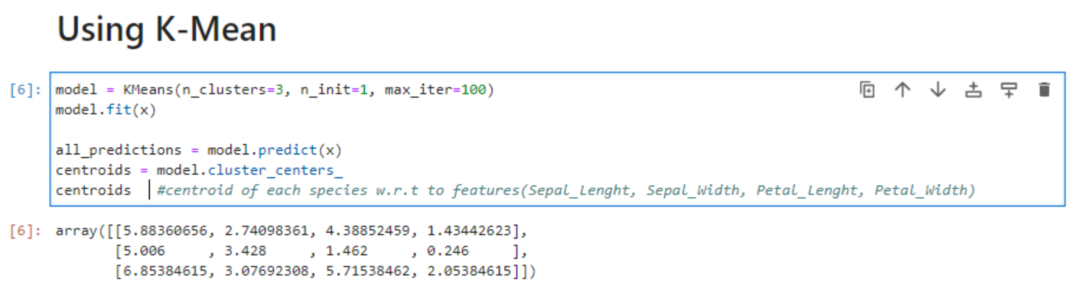
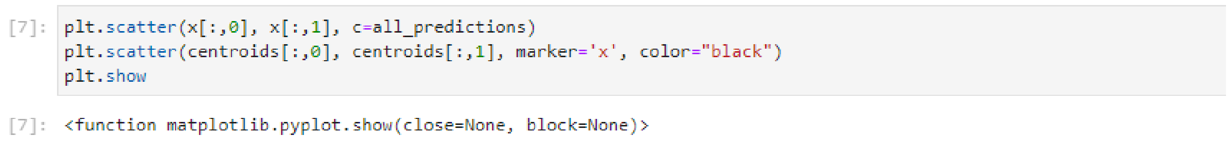
Then we create K-Mean clustering model and setting cluster value to 3 because in Iris datasets, there are 3 different species of Iris flower, in which we want to cluster data point into it
n_init = 1 mean that the algorithm will be only run at once with single random initialization of centroids
max_iter = 100 indicates that the algorithm will perform 100 iteration
then fit our model to the 'x' datasets using fit() method
Predict the cluster assignment for each data point
Storing result in 'all predictions' variable
And find centroid, by using cluster_centers_ attribute



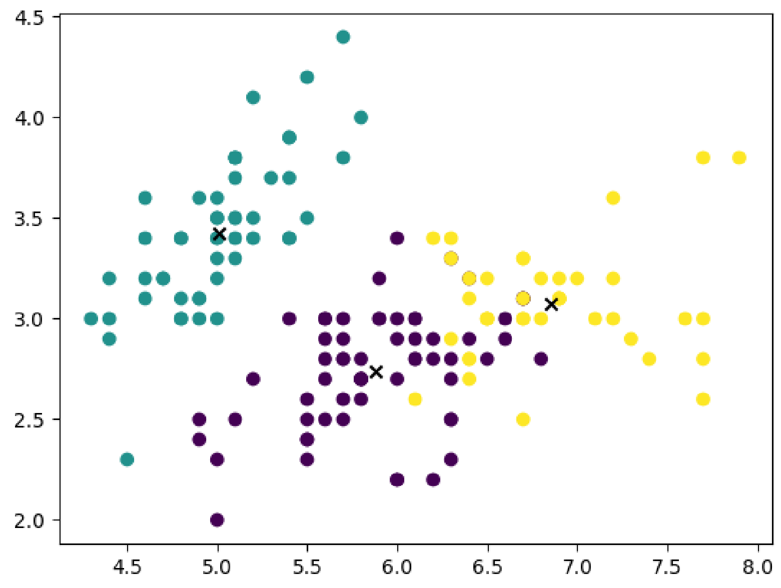
Using K-Mean

```
[6]: model = KMeans(n_clusters=3, n_init=1, max_iter=100)
     model.fit(x)

     all_predictions = model.predict(x)
     centroids = model.cluster_centers_
     centroids  #centroid of each species w.r.t to features(Sepal_Lenght, Sepal_Width, Petal_Lenght, Petal_Width)

[6]: array([[5.88360656, 2.74098361, 4.38852459, 1.43442623],
            [5.006     , 3.428     , 1.462     , 0.246     ],
            [6.85384615, 3.07692308, 5.71538462, 2.05384615]])
```

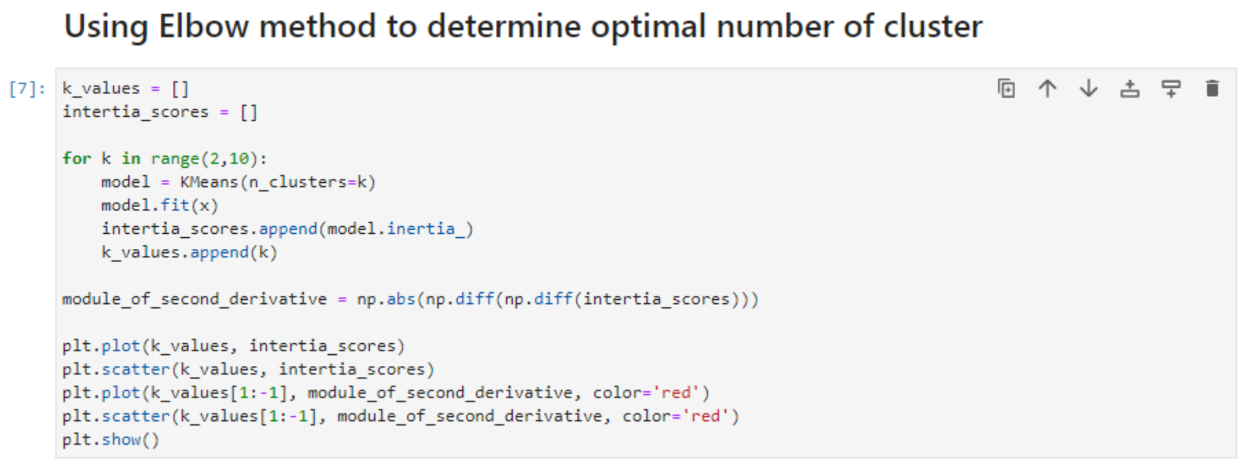
After that we visualize the cluster assignment and centroid using plt.scatter() and plt.show()



```
[7]: plt.scatter(x[:,0], x[:,1], c=all_predictions)
     plt.scatter(centroids[:,0], centroids[:,1], marker='x', color="black")
     plt.show

[7]: <function matplotlib.pyplot.show(close=None, block=None)>
```

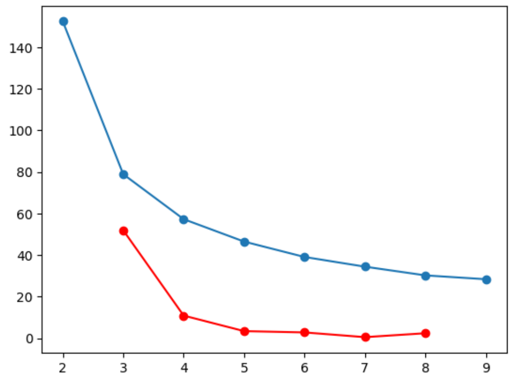


Then we Use elbow method for confirming that either we selected the optimal number of cluster or not



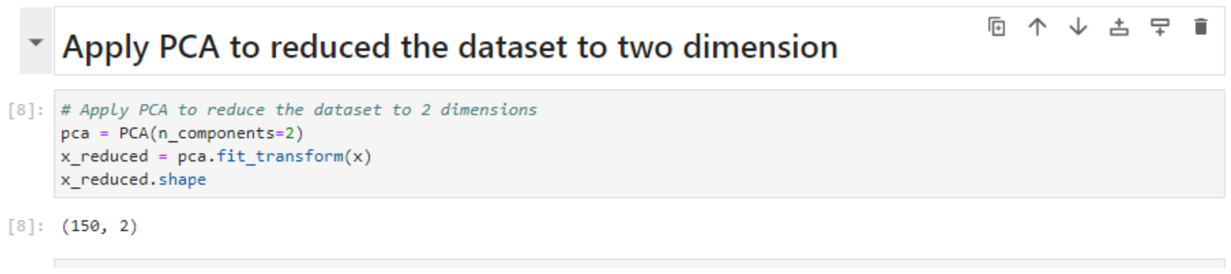
Using Elbow method to determine optimal number of cluster

```
[7]: k_values = []
     intertia_scores = []

     for k in range(2,10):
         model = KMeans(n_clusters=k)
         model.fit(x)
         intertia_scores.append(model.inertia_)
         k_values.append(k)

     module_of_second_derivative = np.abs(np.diff(np.diff(intertia_scores)))

     plt.plot(k_values, intertia_scores)
     plt.scatter(k_values, intertia_scores)
     plt.plot(k_values[1:-1], module_of_second_derivative, color='red')
     plt.scatter(k_values[1:-1], module_of_second_derivative, color='red')
     plt.show()
```



And from plot, we observer the sharp change appears at k= 3, so it means, we select optimal number of clusters

After that, we apply PCA (Principal component Analysis) to reduce the datasets to two dimension using 'PCA()' function



Apply PCA to reduced the dataset to two dimension

```
[8]: # Apply PCA to reduce the dataset to 2 dimensions
     pca = PCA(n_components=2)
     x_reduced = pca.fit_transform(x)
     x_reduced.shape

[8]: (150, 2)
```

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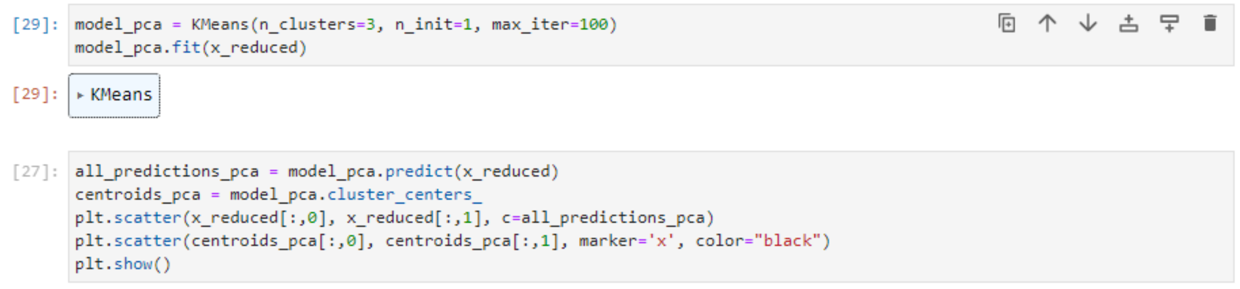
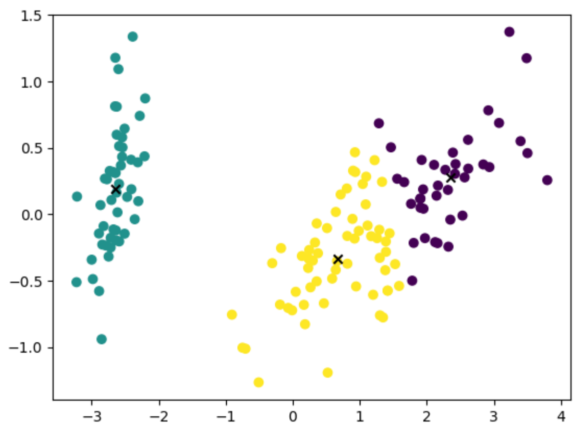
Similarly, apply K-mean on reduced datasets



```
[29]: model_pca = KMeans(n_clusters=3, n_init=1, max_iter=100)
      model_pca.fit(x_reduced)

[29]: ▸ KMeans

[27]: all_predictions_pca = model_pca.predict(x_reduced)
      centroids_pca = model_pca.cluster_centers_
      plt.scatter(x_reduced[:,0], x_reduced[:,1], c=all_predictions_pca)
      plt.scatter(centroids_pca[:,0], centroids_pca[:,1], marker='x', color="black")
      plt.show()
```



So, from both plots, we observe that first plot shows the clustering of Iris dataset based on all four features while the other plot shows the clustering on reduced dataset to two dimensions
Additionally, there is wide space between clusters in second plot, it means that we lost some information and on the other hand, clusters are very close it means almost all information is covered and some information is overlapped
Also, second plot show less overlapping of information as compared to first plot