• The data set contains 3 calsses of 50 instances each, Where each class refers to a type of iris plant. · Predict the optimum number of clusters and represent it visually Attribute Information: 1. Sepal Length in cm 2. Sepal Width in cm 3. Petal Length in cm 4. Petal Width in cm 5. Species: (Iris-setosa, Iris-versicolor, Iris-virginica) Import necessary libraries In [18]: **import** pandas **as** pd import numpy as np import seaborn as sns import matplotlib.pyplot as plt from sklearn.cluster import KMeans import warnings warnings.filterwarnings('ignore') Load & Explore data data=pd.read_csv('D:/Projects/GRIP/Iris.csv') In [2]: data.head() Id SepalLengthCm SepalWidthCm PetalLengthCm PetalWidthCm Out[2]: **Species** 0 1 5.1 3.5 1.4 0.2 Iris-setosa **1** 2 4.9 3.0 1.4 0.2 Iris-setosa **2** 3 3.2 4.7 1.3 0.2 Iris-setosa **3** 4 4.6 3.1 1.5 0.2 Iris-setosa **4** 5 5.0 3.6 1.4 0.2 Iris-setosa # To show basic info about datatype data.info() shape = data.shape print(f'\n Number of Rows = {shape[0]}\n Number of columns = {shape[1]} ') <class 'pandas.core.frame.DataFrame'> RangeIndex: 150 entries, 0 to 149 Data columns (total 6 columns): Column Non-Null Count Dtype # ------ - ------0 Id 150 non-null int64 SepalLengthCm 150 non-null float64 1 SepalWidthCm 150 non-null float64 PetalLengthCm 150 non-null float64 3 PetalWidthCm 150 non-null float64 5 Species 150 non-null object dtypes: float64(4), int64(1), object(1) memory usage: 7.2+ KB Number of Rows = 150Number of columns = 6In [4]: # To display stats about the data data.describe() Id SepalLengthCm SepalWidthCm PetalLengthCm PetalWidthCm Out[4]: 150.000000 150.000000 150.000000 count 150.000000 150.000000 mean 75.500000 5.843333 3.054000 3.758667 1.198667 43.445368 0.433594 0.763161 0.828066 1.764420 std min 1.000000 4.300000 2.000000 1.000000 0.100000 **25**% 38.250000 5.100000 2.800000 1.600000 0.300000 **50**% 75.500000 5.800000 3.000000 4.350000 1.300000 **75%** 112.750000 1.800000 6.400000 3.300000 5.100000 max 150.000000 7.900000 4.400000 6.900000 2.500000 In [5]: # To display no. of samples on each class data['Species'].value_counts() Iris-setosa Out[5]: Iris-versicolor 50 Iris-virginica 50 Name: Species, dtype: int64 # Check for null values data.isnull().sum() Id 0 Out[6]: SepalLengthCm 0 SepalWidthCm 0 PetalLengthCm 0 PetalWidthCm 0 0 Species dtype: int64 In [7]: # drop ID and Species columns iris = data.drop(['Id', 'Species'], axis=1) iris.head() SepalLengthCm SepalWidthCm PetalLengthCm PetalWidthCm Out[7]: 0 5.1 3.5 1.4 0.2 4.9 1 3.0 1.4 0.2 2 3.2 1.3 0.2 3 1.5 4.6 3.1 0.2 4 5.0 3.6 1.4 0.2 Find the optimum number of clusters for K Means In [8]: x = iris.iloc[:, :].values# WCSS means >> Within cluster sum of squares wcss = []**for** i **in** range(1, 21): kmean = KMeans(n_clusters = i, init = 'k-means++', $max_iter = 200$, $n_init = 15$, $random_state = 0$) kmean.fit(x)wcss.append(kmean.inertia_) In [9]: # Plotting the results onto a line graph, # `allowing us to observe 'The elbow' plt.plot(range(1, 21), wcss, color = "blue") plt.title('The elbow method') plt.xlabel('Number of clusters') plt.ylabel('WCSS') plt.annotate('ELBOW', xytext=(5, 200), xy=(3, 100), arrowprops={'facecolor':'green'}) plt.grid() plt.show() The elbow method 700 600 500 400 300 ELBOW 200 100 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0 Number of clusters • You can clearly see why it is called 'The elbow method' from the above graph, the optimum clusters is where the elbow occurs. • This is when the within cluster sum of squares (WCSS) doesn't decrease significantly with every iteration. • From this we choose the number of clusters as 3 Clusters In [10]: # Applying kmeans to the dataset kmean = KMeans(n_clusters = 3, init = 'k-means++', $max_iter = 200$, $n_init = 15$, $random_state = 0$) $y = kmean.fit_predict(x)$ In [11]: fig, ax = plt.subplots(1, 2, figsize=(12, 4)) # Visualising the clusters - On the first two columns (sepal length, sepal width) ax[0].scatter(x[y == 0, 0], x[y == 0, 1],s=50, c='blue', label='Iris-setosa') ax[0].scatter(x[y == 1, 0], x[y == 1, 1],s=50, c='green', label='Iris-versicolour') ax[0].scatter(x[y == 2, 0], x[y == 2, 1],s=50, c='red', label='Iris-virginica') ax[0].scatter(kmean.cluster_centers_[:, 0], kmean.cluster_centers_[:, 1], s=80, c='black', label='Centroids') ax[0].set_xlabel('sepal_length') ax[0].set_ylabel('sepal_width') ax[0].set_title('Sepal Length and Width') ax[0].grid() ax[0].legend() # Visualising the clusters - On the second two columns (petal length, petal width) ax[1].scatter(x[y == 0, 2], x[y == 0, 3],s=50, c='blue', label='Iris-setosa') ax[1].scatter(x[y == 1, 2], x[y == 1, 3],s=50, c='green', label='Iris-versicolour') ax[1].scatter(x[y == 2, 2], x[y == 2, 3],s=50, c='red', label='Iris-virginica') ax[1].scatter(kmean.cluster_centers_[:, 2], kmean.cluster_centers_[:, 3], s=80, c='black', label='Centroids') ax[1].set_xlabel('petal_length') ax[1].set_ylabel('petal_width') ax[1].set_title('Petal Length and Width') ax[1].grid() ax[1].legend() plt.show() Sepal Length and Width Petal Length and Width 4.5 Iris-setosa Iris-setosa Iris-versicolour Iris-versicolour 4.0 Iris-virginica Iris-virginica 2.0 Centroids | | Centroids sepal_width .c o petal_width 2.5 2.0 6.5 7.0 7.5 4.5 5.0 5.5 6.0 8.0 sepal_length petal length The Original data In [12]: colors = ['green', 'blue', 'red'] species = ['Iris-setosa', 'Iris-versicolor', 'Iris-virginica'] In [13]: fig, (ax1, ax2) = plt.subplots(1,2, figsize=(15,6))for i in range(3): x_sepal = data[data['Species']==species[i]] ax1.scatter(x_sepal['SepalLengthCm'], x_sepal['SepalWidthCm'], c = colors[i], label = species[i]) ax1.set_xlabel('sepal_length') ax1.set_ylabel('sepal_width') ax1.legend() for i in range(3): x_petal = data[data['Species']==species[i]] ax2.scatter(x_petal['PetalLengthCm'], x_petal['PetalWidthCm'], c = colors[i], label = species[i]) ax2.set_xlabel('petal_length') ax2.set_ylabel('petal_width') ax2.legend() plt.show() 4.5 Iris-setosa Iris-setosa 2.5 Iris-versicolor Iris-versicolor Iris-virginica Iris-virginica 4.0 2.0 3.5 sepal_width petal_width 2.5 0.5 2.0 6.5 7.0 7.5 8.0 4.5 5.0 5.5 6.0 sepal_length petal_length In [15]: fig, (ax1, ax2) = plt.subplots(1,2, figsize=(15,6))for i in range(3): x = data[data['Species']==species[i]] ax1.scatter(x['SepalLengthCm'], x['PetalLengthCm'], c = colors[i], label = species[i]) ax1.set_xlabel('Petal_length') ax1.set_ylabel('petal_length') ax1.legend() for i in range(3): x = data[data['Species']==species[i]] ax2.scatter(x['SepalWidthCm'], x['PetalWidthCm'], c = colors[i], label = species[i]) ax2.set_xlabel('petal_width') ax2.set_ylabel('petal_width') ax2.legend() plt.show() Iris-setosa 2.5 Iris-versicolor Iris-virginica 2.0 petal_width petal_length Iris-setosa Iris-versicolor Iris-virginica 1.0 2 0.5 7.0 3.5 5.0 2.0 2.5 6.0 4.0 4.5 Petal_length petal_width **Coorelation Matrix** In [16]: data.corr() Out[16]: Id SepalLengthCm SepalWidthCm PetalLengthCm PetalWidthCm ld 1.000000 0.716676 -0.397729 0.882747 0.899759 SepalLengthCm 0.716676 1.000000 0.871754 0.817954 -0.109369 -0.109369 1.000000 -0.420516 -0.356544 SepalWidthCm -0.397729 PetalLengthCm 0.882747 0.871754 0.962757 -0.420516 1.000000 PetalWidthCm 0.899759 0.817954 -0.356544 0.962757 1.000000 corr = data.corr() In [19]: fig, ax = plt.subplots(figsize=(10,6)) sns.heatmap(corr, annot=True, ax=ax, cmap ='coolwarm') plt.show() 1.0 ld --0.4 0.88 0.9 - 0.8 - 0.6 SepalLengthCm -0.87 0.82 - 0.4 SepalWidthCm --0.4 1 -0.42 -0.36 - 0.2 PetalLengthCm -0.88 0.87 -0.42 1 0.96 - 0.0 -0.20.82 -0.36 0.96 PetalWidthCm -0.9 1 ld SepalLengthCm SepalWidthCm PetalLengthCm PetalWidthCm

Project Info