52. Clustering in ML

Unsupervised learning is divided into:

1. **Clustering** - divide the data into different clusters, classify/categorize the data
2. **Association** - Arrangement of data

List of some popular unsupervised learning algorithm:

- K-means clustering
- Hierarchal clustering
- DBSCAN Clustering
- Apriori Algorithm / F Growth
- Principle Component Analysis

```
In [ ]:
```

53. K-Means Clustering

- K-Means Clustering is an unsupervised learning algorithm, which groups the unlabelled dataset into different clusters.
- K defines the number of pre-defined clusters that need to be created in the process.

K-Means algo:

- First decide the centriod, center in the dataset
- take two data point, and draw a line b/w them
- pass another line from middle of the line
- take neighbouring data points from the decided central data point

How K-Means work:

1. Take random sample point
2. Create groups
3. Search nearest point
4. Calculate mean (Move points)

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Elbow Method:

- The Elbow method is one of the most popular ways to find the optimal number of clusters
- This method uses the concept of WCSS value. WCSS stands forWithin-Cluster Sum of Squares, which defines the total variations within a cluster.
- The formuls of **WCSS** is:

$$\text{WCSS} = \sum_{i=1}^{K} \sum_{x \in C_i} \|x - \mu_i\|^2$$

where:

- (K) = Number of clusters
- (C_i) = (i)-th cluster
- (x) = A data point in cluster (C_i)
- (\mu_i) = Centroid of cluster (C_i)
- (| x - \mu_i |) = Euclidean distance between data point (x) and centroid (\mu_i)

How does WCSS is calculated:

- Caclulate the distance from decided central data point and its neighbouring data points (x - u)
- Take square of the distance
- Sum of the distances from central point and all neighbouring data points

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K-Means ++: To have best clustering in the data. It takes 2 decided points away from each other.

In [ ]:

54. K-Means Clustering (Practical)

In [1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```
dataset = pd.read_csv(r'Data/iris_raw.csv')
dataset.head(3)
```

Out[2]:

	sepal_length	sepal_width	petal_length	petal_width
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2

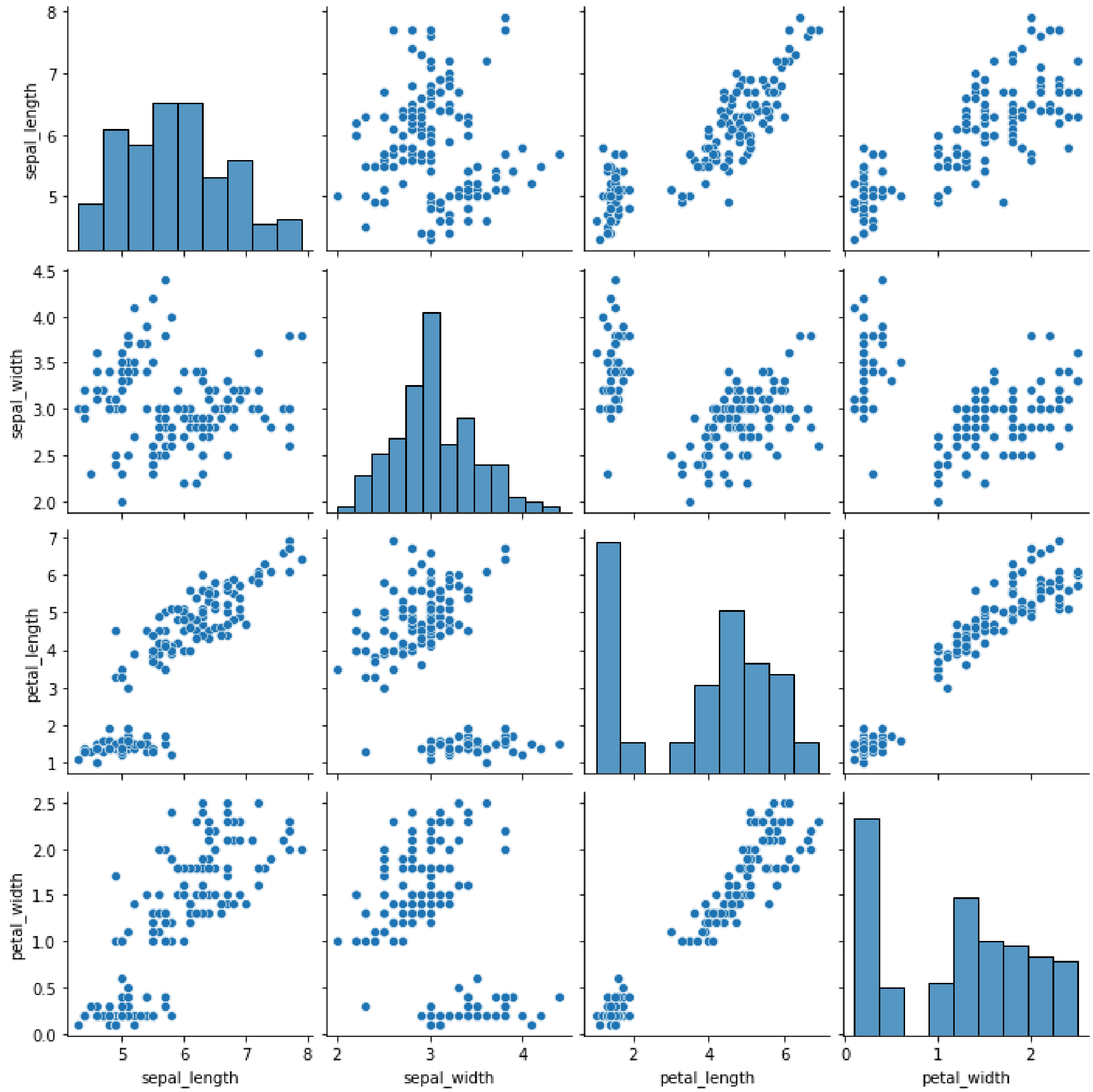
54.1 Making Clusters of Data

- Use K-mean clustering when **your data is linearly separable**

Check the data if it is linearly separable

In [3]:
```
sns.pairplot(data=dataset)
plt.show()
```

```
C:\Users\rashi\AppData\Local\Programs\Python\Python39\lib\site-packages\seaborn\axis
grid.py:123: UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```



- In supervised learning, the data is split into training and testing data
- In unsupervised learning, data is not split into training and testing data b/c the data is unlabelled

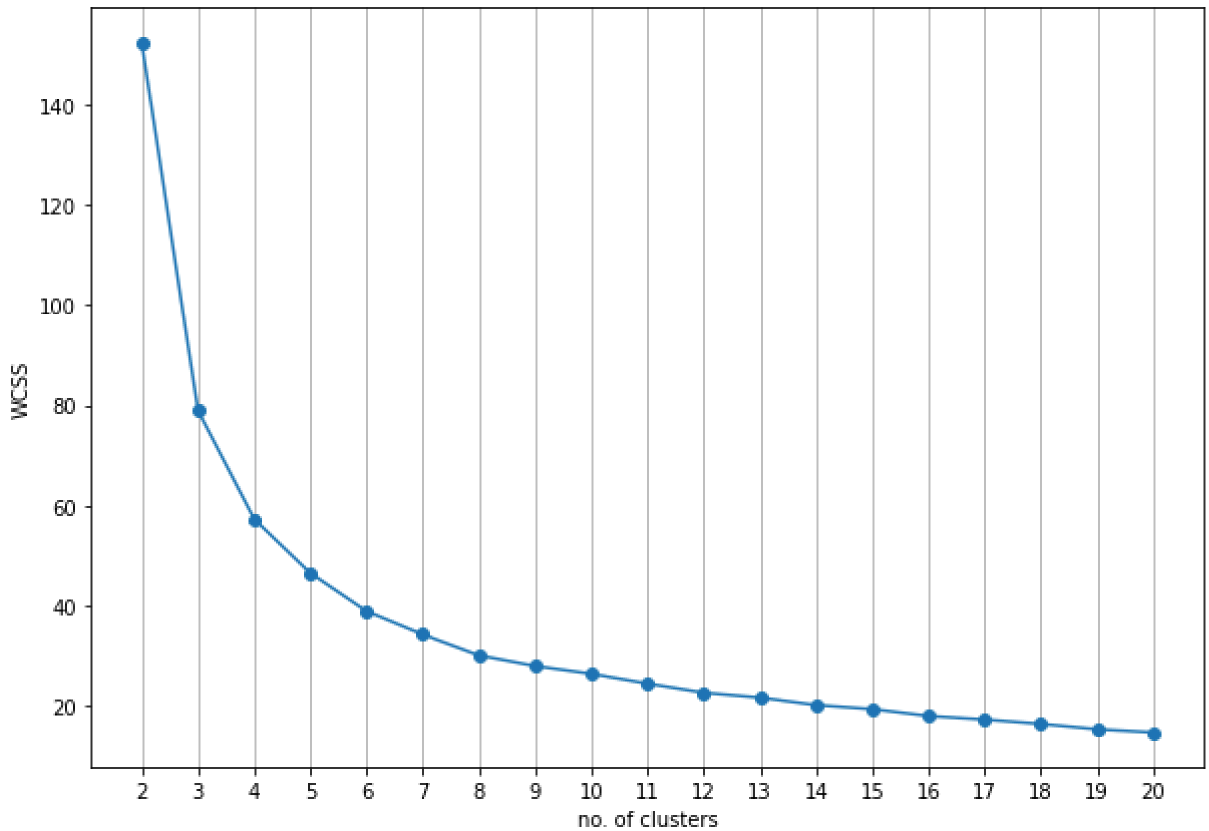
54.1.1 Find Number of clusters

In [7]:
```
from sklearn.cluster import KMeans
```

In [14]:
```
# Use a loop to find best number of clusters from 2 to 20
wcss = []

for i in range(2,21):
    km = KMeans(n_clusters=i, init='k-means++')
    km.fit(dataset)
    wcss.append(km.inertia_) # it assings value of wcss {Elbow graph}
```

In [29]:
```
plt.figure(figsize=(10,7))
plt.plot([i for i in range(2,21)], wcss, marker='o')
plt.xlabel('no. of clusters')
plt.xticks([i for i in range(2,21)])
plt.ylabel('WCSS')
plt.grid(axis='x')
plt.show()
```



Elbow point = 3

It means that will have 3 number of clusters

In [ ]:

In [30]:
```
kmn = KMeans(n_clusters=3)
kmn.fit_predict(dataset)
```

Out[30]:
```
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, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 2, 2, 2, 2, 1, 2, 2, 2,
       2, 2, 2, 1, 1, 2, 2, 2, 2, 1, 2, 1, 2, 1, 2, 2, 1, 1, 2, 2, 2, 2,
       2, 1, 2, 2, 2, 2, 1, 2, 2, 2, 1, 2, 2, 2, 1, 2, 2, 1])
```

In [32]:
```
dataset['Predict'] = kmn.fit_predict(dataset)
```

In [33]:
```
dataset
```

Out[33]:

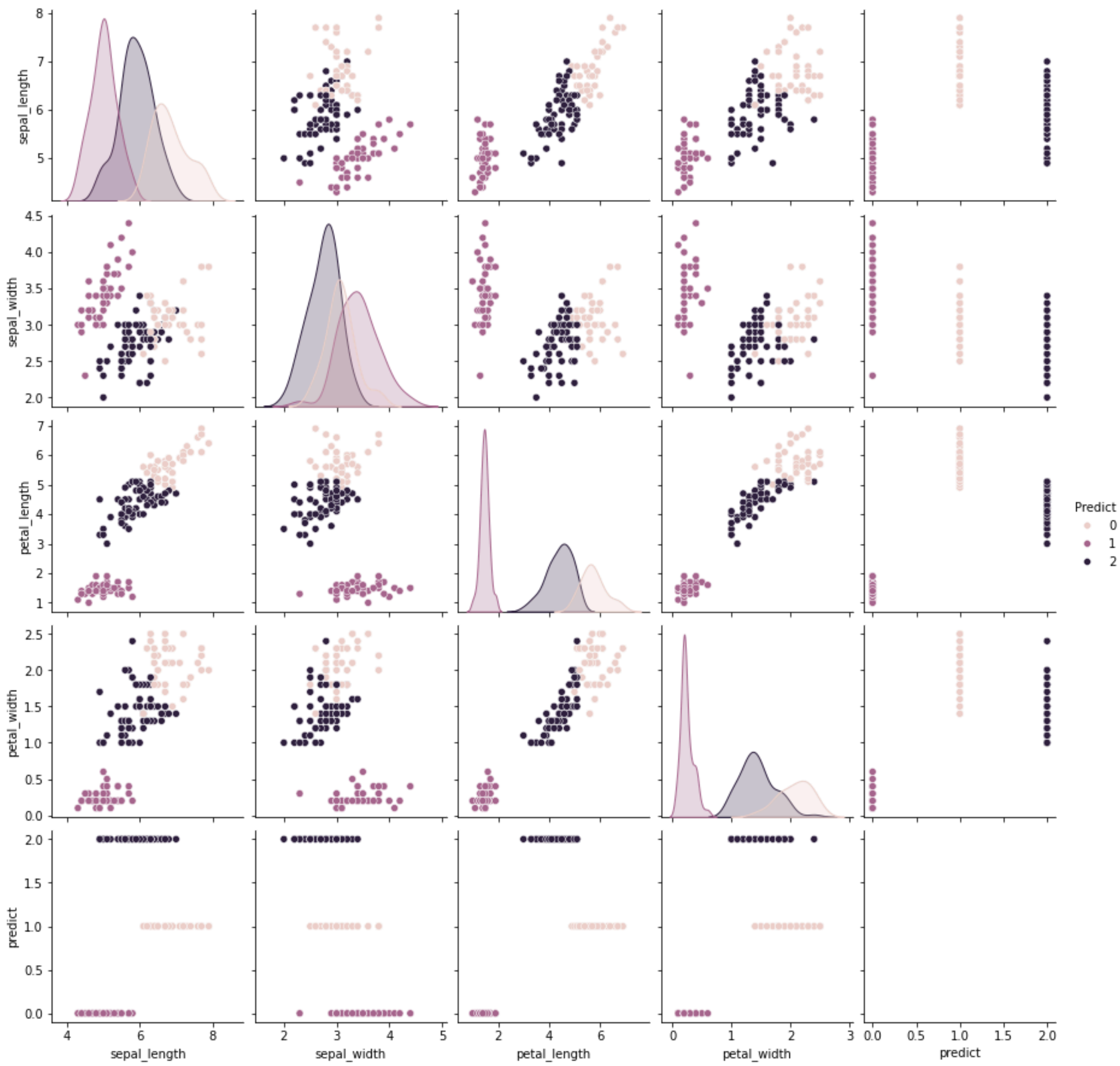
	sepal_length	sepal_width	petal_length	petal_width	predict	Predict
0	5.1	3.5	1.4	0.2	0	1
1	4.9	3.0	1.4	0.2	0	1
2	4.7	3.2	1.3	0.2	0	1
3	4.6	3.1	1.5	0.2	0	1
4	5.0	3.6	1.4	0.2	0	1
...	...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	1	0
146	6.3	2.5	5.0	1.9	2	2
147	6.5	3.0	5.2	2.0	1	0
148	6.2	3.4	5.4	2.3	1	0
149	5.9	3.0	5.1	1.8	2	2

150 rows × 6 columns

In [39]:

```
sns.pairplot(data=dataset, hue='Predict')
plt.savefig(r"Generated_images/raw-iris-clustering-predict.jpg")
plt.show()
```

```
C:\Users\rashi\AppData\Local\Programs\Python\Python39\lib\site-packages\seaborn\axis
grid.py:123: UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```



54.2 Making raw data with original data

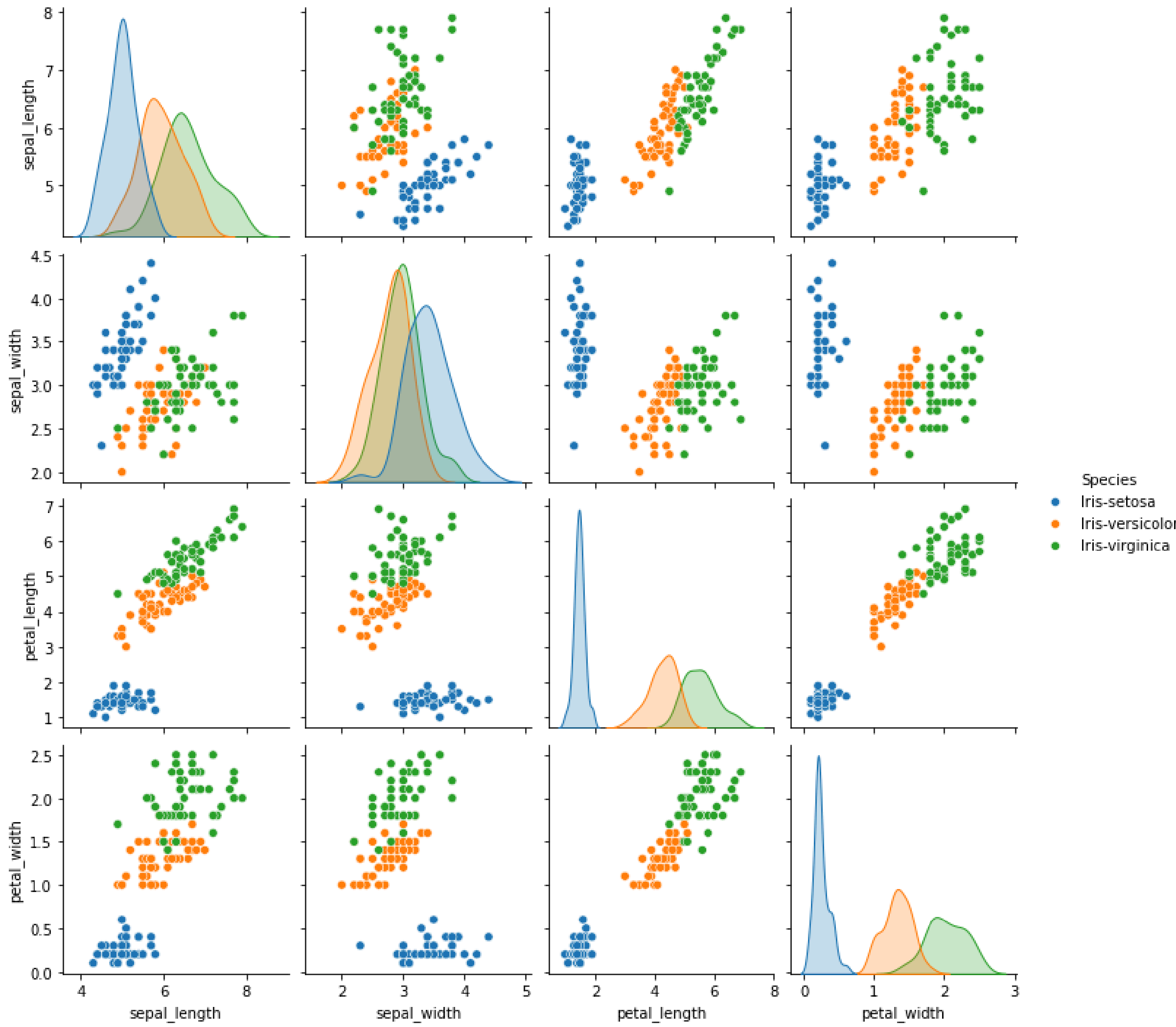
In [35]:
```
org_dataset = pd.read_csv(r'Data/iris.csv')
org_dataset.head(3)
```

Out[35]:

	sepal_length	sepal_width	petal_length	petal_width	Species
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa

In [40]:
```
sns.pairplot(data=org_dataset, hue='Species')
plt.savefig(r"Generated_images/raw-iris-clustering-original-data.jpg")
plt.show()
```

```
C:\Users\rashi\AppData\Local\Programs\Python\Python39\lib\site-packages\seaborn\axis
grid.py:123: UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```




```
In [ ]:
```

55. Hierarchical Clustering

It is applied for linearly separable data

- It is used to group the unlabelled datasets into a cluster and aslo known as hierarchical cluster analysis or HCA.
- In the algorithm, we develop the hierarchy of clusters in the form of a tree, and this tree-shaped structure is known as the **dendrogam**.

Dendrogram

- It is a tree like structure that is mainly used to store each step as a memory that the HC algorithm performs.
- The dendrogram plot, the Y-axis shows the **Euclidean distances** b/w the data points, and the x-axis shows all the data points of the given dataset.

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Hierarchical clustering technique has two approaches:

1. **Agglomerate:** Agglomerative is a bottom-up approach, in which the algorithm starts with taking all data points as single clusters and merging them until one cluster is left. This is popular algorithem and **bottom-up approach**.
2. **Divisive:** Divisive algorithm is the reverse of the agglomerative algorithm as it is **top-down approach**.

Agglomerate Clustering:

No description has been provided for this image

Divisive Clustering:

No description has been provided for this image

Measure for the distance between two clusters

- The closest distance b/w the two clusters is crucial for the hierarchical clustering.
- There are various ways to calculate the distance b/w two clusters, and these ways decided the rule for clustering. These measures are called **Linkage methods:**

- **Single Linkage** - We take minimum distance b/w two clusters
- **Complete Linkage** - We take maximum distance b/w two clusters
- **Average Linkage** - We take average distance b/w two clusters
- **Centroid Linkage** - We take central point and then calculate distance b/w two clusters

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No description has been provided for this image

No description has been provided for this image

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To desing best number of clusters

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In [ ]:

56. Agglomerate Hierarchical (Practical)

In [1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [3]:
```
dataset = pd.read_csv(r'Data/iris_raw.csv')
dataset.head(3)
```

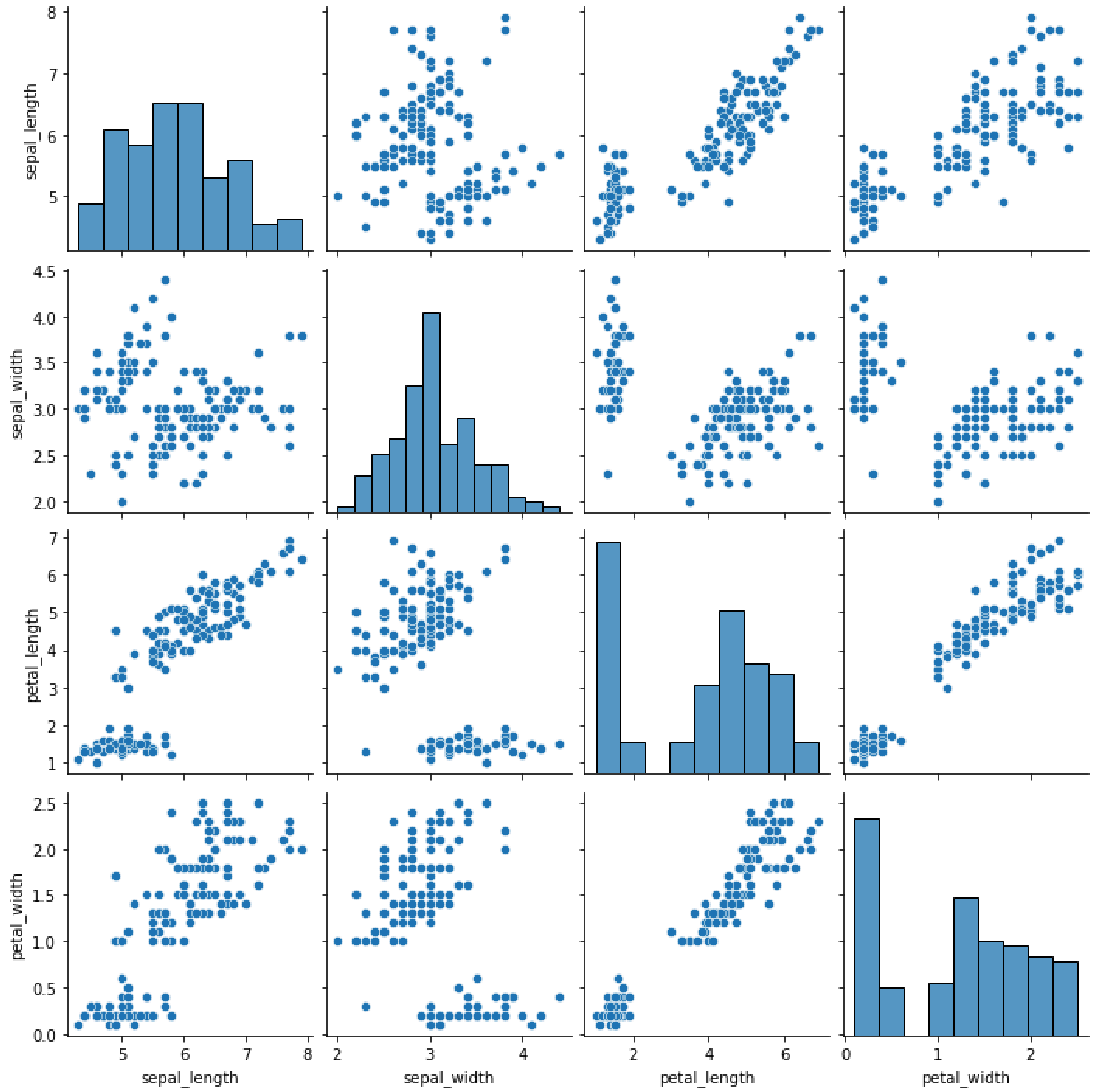
Out[3]:

	sepal_length	sepal_width	petal_length	petal_width
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2

As agglomerate clustering works on **linearly separable data**, so we will see if our data is linear or not through graph

In [4]:
```
sns.pairplot(data=dataset)
plt.show()
```

```
C:\Users\rashi\AppData\Local\Programs\Python\Python39\lib\site-packages\seaborn\axis
grid.py:123: UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```



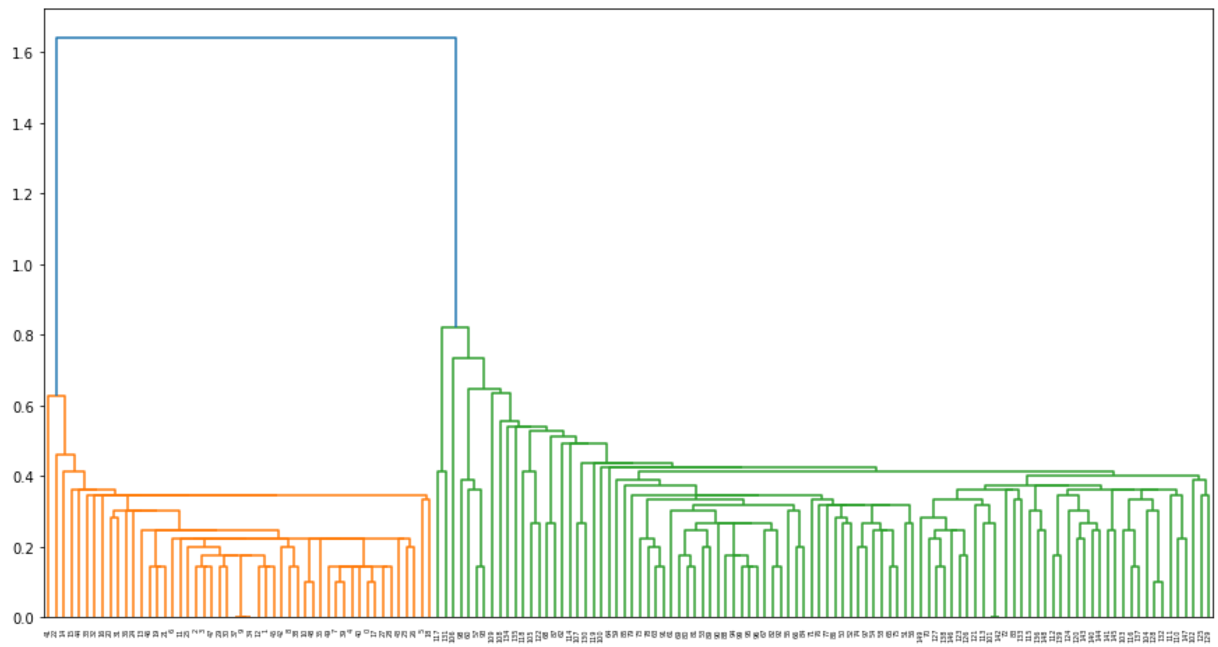
Make Dendrogram

SciPy Library is needed for making dendrogram

In [6]:
```
import scipy.cluster.hierarchy as sc
```

We will need **Linkage** fro making dendrogram

In [10]:
```
'''Z : ndarray
    The linkage matrix encoding the hierarchical clustering to
    render as a dendrogram. See the ``linkage`` function for more
    information on the format of ``Z``.'''
plt.figure(figsize=(15,8))
sc.dendrogram(sc.linkage(dataset, method='single', metric='euclidean'))
plt.savefig(r'Generated_images/dendrogram.jpg')
plt.show()
```



Dendrogram is showing two clusters only in the data

In [11]:
```
from sklearn.cluster import AgglomerativeClustering
```

In [13]:
```
ac = AgglomerativeClustering(n_clusters=2, linkage='single')
ac.fit_predict(dataset)
```

Out[13]:
```
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 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, 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, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0], dtype=int64)
```

In [14]:
```
dataset['Predict'] = ac.fit_predict(dataset)
```

In [15]:
```
dataset
```

Out[15]:

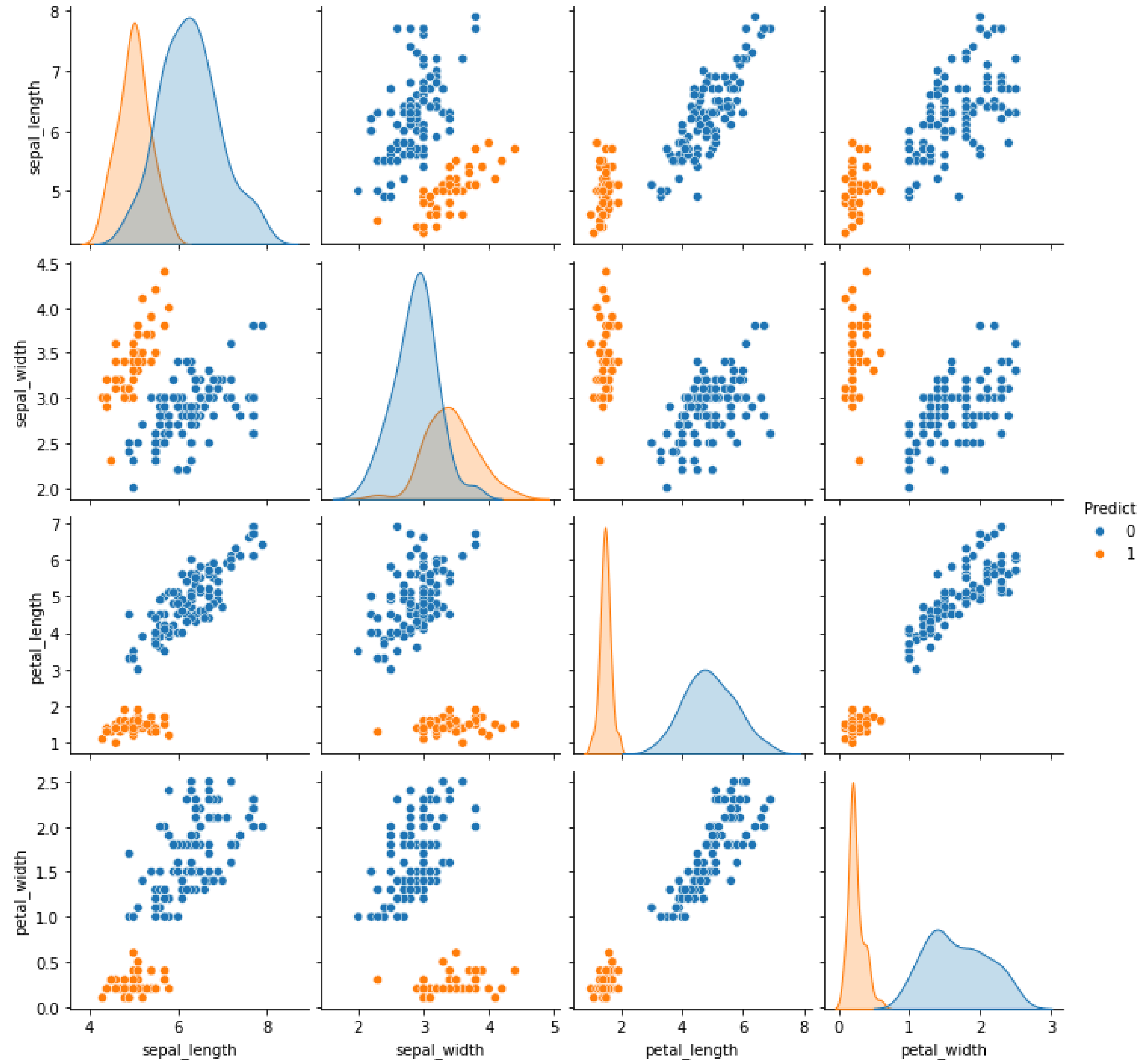
	sepal_length	sepal_width	petal_length	petal_width	Predict
0	5.1	3.5	1.4	0.2	1
1	4.9	3.0	1.4	0.2	1
2	4.7	3.2	1.3	0.2	1
3	4.6	3.1	1.5	0.2	1
4	5.0	3.6	1.4	0.2	1
...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	0
146	6.3	2.5	5.0	1.9	0
147	6.5	3.0	5.2	2.0	0
148	6.2	3.4	5.4	2.3	0
149	5.9	3.0	5.1	1.8	0

150 rows × 5 columns

In [16]:

```
sns.pairplot(data=dataset, hue='Predict')
plt.show()
```

```
C:\Users\rashi\AppData\Local\Programs\Python\Python39\lib\site-packages\seaborn\axis
grid.py:123: UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```



Prediction is also showing two clusters only in the data

In [ ]:

57. DBScan Clustering Algorithm

- Density-Based Spatial Clustering of Applications with Noise.
- The clusters found by DBScan can be any shape, which can deal with some special cases that other methods cannot.
- It is used for **non-linear separable data**
- DBScan Clustering also used in **detection of outlier in the data**

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Requirements for DBCLUSTRING

1. Minimum points (at least 4)
2. Espsilon (radius)
3. Core point (#points >= minpoints)
4. Boundary point (#points < minpoints)
5. Noise Point (outlier)

In [ ]:

```

```

58. DBScan Clustering Algorithm (Practical)

In [33]:
```
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.datasets import make_moons
import pandas as pd
```

In [34]:
```
x, y = make_moons(n_samples=250, noise=0.05)
```

In [35]:
```
# First column data
x[:,0]
```

```
Out[35]: array([ 1.82154686,  0.33039765,  1.11621412,  1.75338817,  0.79406254,
                 0.09592268,  0.77490969, -0.96252073,  0.78806259,  0.23980237,
                 1.89848596,  0.01310029,  0.07091097,  0.58314369, -0.96699757,
                 1.04928892,  0.57445541,  0.74501548, -1.00650714, -0.82152061,
                 0.86190156,  0.49126856,  1.8694458 ,  1.49802939,  0.6728559 ,
                 0.98720469,  0.45047353, -0.2865276 ,  0.42354262,  0.88007291,
                 0.36500296,  1.03385062,  0.3360013 , -0.01448323,  0.89163708,
                -0.49418874, -0.35425069,  0.50247661,  0.85778933, -0.64054093,
                 0.04832991,  2.01015645,  1.2204363 ,  1.88956628, -0.13252252,
                -0.49523227,  0.33669497,  0.76153465, -0.27186532,  1.28870288,
                 0.93076493,  1.90104103,  0.02543826,  0.44853317,  1.00448433,
                -0.25031522,  1.92847973,  0.42609288,  1.27725596, -0.87659926,
                 0.61413887,  0.22505794, -0.04512895,  0.69131929,  0.259285  ,
                 1.84036998,  0.47866329, -0.2844214 ,  1.31106194, -0.23293884,
                 1.31976039,  1.93209062,  0.01521537,  1.80101873, -0.0391596 ,
                -0.49585375,  1.58238117,  0.01637799,  0.72630669,  0.91538441,
                -0.02865494,  1.45737014,  0.64884606, -0.74483793,  1.06418573,
                 2.01778072, -0.37167832, -0.81173842, -0.91412945,  0.91606385,
                 0.6136725 , -0.43538794, -0.7255368 ,  0.96102712,  1.91454596,
                -0.89253863,  0.12816908,  0.1788169 ,  0.12848506, -0.63151123,
                -0.86587253,  0.71871253,  0.04011572, -0.98749825,  1.50781231,
                 0.87760821, -1.00423248,  1.44746249,  0.78287742, -0.44868368,
                 1.89144999,  0.80058548,  1.88844507, -0.42427662, -1.02605411,
                -0.06589804,  1.92603512, -0.80463147,  1.51462527,  0.09590861,
                 1.67803099, -0.70384095,  0.99436775, -0.10206081,  0.05106181,
                 1.62449215, -0.90402427,  1.42745557,  1.92430944,  0.29091015,
                 0.80306352,  1.4728536 ,  0.6063805 ,  1.07151034,  0.77765877,
                -0.79018459,  0.07756758, -0.6810462 ,  0.23387981, -0.9338624 ,
                 0.4196469 ,  1.0743206 , -1.07958865,  0.66710905, -0.98994215,
                 0.66449098,  0.49932715,  0.82120004,  0.48939705,  1.63825117,
                 1.86809186, -0.91683607,  1.96477994, -0.48955672,  0.56543806,
                 0.22563531, -0.93097574,  0.07804955,  0.68306482,  0.61259675,
                 2.0154066 ,  1.63111271,  0.99459508,  0.613061  ,  0.34693487,
                -0.65125101, -1.08710097,  0.05320543, -0.97583562,  0.14590846,
                 1.28499957, -0.01456049,  0.99183249,  1.95048888,  0.22331433,
                 0.09418366,  0.84157974,  0.15503721, -0.73386657,  1.05716677,
                 0.4758061 ,  1.20194107,  1.76139437,  0.99175489,  0.88443974,
                 1.77304674,  0.72292497,  0.02948542,  0.19793304,  0.77849153,
                 0.23332147, -0.07093789,  0.35773924, -0.80533347,  0.36514192,
                -0.00781175,  0.54951133,  1.74424235,  0.05659029, -0.85842631,
                 1.69412089,  0.08545157,  0.30568356,  1.72318384, -0.04890115,
                -0.07264175, -0.63270247,  0.15343203, -0.69145099,  0.94662445,
                 0.84613359,  0.22515933,  1.64017442,  0.95298684, -0.0749229 ,
                 0.32118047, -0.56206221, -1.06808907,  1.20337727,  0.03416578,
                -1.00746399,  0.94031733,  1.99598102, -0.19158745,  0.28515341,
                 1.30521283, -0.55735516,  1.36320489, -0.83877886,  1.08372752,
                 0.45287718,  0.8876371 ,  1.03408887,  0.23404788,  1.89919484,
                 0.80054814,  2.0020812 ,  1.0442318 ,  1.86594006,  1.72375506,
                -0.3131739 ,  0.13166397,  1.04628395,  1.88899169,  1.98677442,
                 2.03239475,  0.43570842,  1.04879911,  1.04383872, -0.80846152])
```

```
In [36]: df = {"data1":x[:,0], "data2":x[:,1], "output":y}
```

```
In [37]: dataset = pd.DataFrame(df)
```

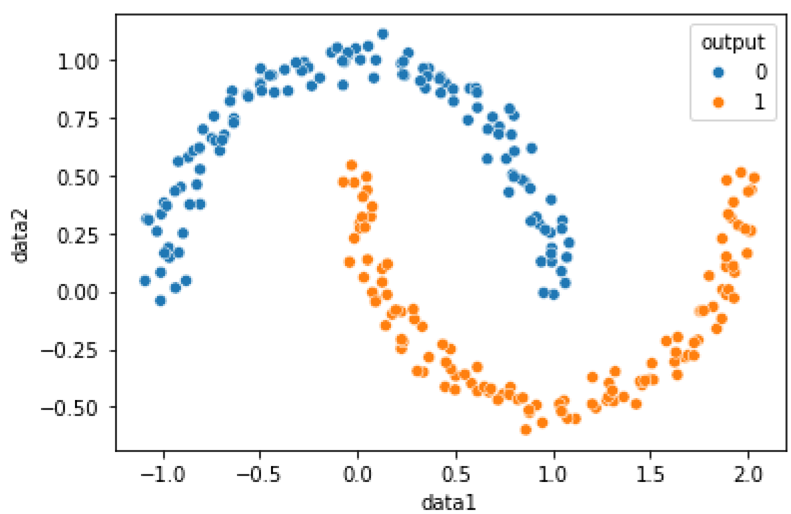
In [38]:
```
dataset
```

Out[38]:

	data1	data2	output
0	1.821547	-0.067198	1
1	0.330398	-0.152611	1
2	1.116214	-0.551311	1
3	1.753388	-0.086491	1
4	0.794063	0.502981	0
...	...	...	...
245	2.032395	0.488380	1
246	0.435708	-0.229602	1
247	1.048799	-0.520698	1
248	1.043839	-0.518346	1
249	-0.808462	0.618646	0

250 rows × 3 columns

In [39]:
```
sns.scatterplot(x='data1', y='data2', data=dataset, hue='output')
plt.show()
```



- The data is **non-linear**, so we will apply DBSCAN Clustering algorithm

In [40]:
```
dataset.head(3)
```

Out[40]:

	data1	data2	output
0	1.821547	-0.067198	1
1	0.330398	-0.152611	1
2	1.116214	-0.551311	1

- We cannot apply DBSCAN on 0 and 1 as this is present in output column, so will remove this column before applying this algo.

In [41]:
```
dataset.drop('output', axis=1, inplace=True)
```

In [42]:
```
dataset
```

Out[42]:

	data1	data2
0	1.821547	-0.067198
1	0.330398	-0.152611
2	1.116214	-0.551311
3	1.753388	-0.086491
4	0.794063	0.502981
...	...	...
245	2.032395	0.488380
246	0.435708	-0.229602
247	1.048799	-0.520698
248	1.043839	-0.518346
249	-0.808462	0.618646

250 rows × 2 columns

In [43]:
```
from sklearn.cluster import DBSCAN
```

In [44]:
```
db = DBSCAN(eps=0.2, min_samples=5)
db.fit_predict(dataset)
```

Out[44]:
```
array([0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 1, 1, 1, 0, 1, 1, 0, 1,
       0, 0, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 1, 1, 1, 0, 1, 1, 0, 0, 0, 0,
       1, 1, 1, 1, 1, 0, 1, 0, 0, 0, 1, 1, 0, 1, 0, 1, 0, 0, 1, 1, 1, 0,
       0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 1, 0, 1, 1,
       1, 0, 1, 1, 1, 1, 0, 1, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 0, 1,
       0, 1, 0, 1, 1, 1, 0, 1, 0, 0, 0, 1, 1, 1, 0, 0, 1, 0, 0, 0, 1, 0,
       1, 1, 0, 1, 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1,
       1, 0, 1, 0, 0, 1, 0, 0, 1, 0, 1, 1, 1, 0, 1, 0, 0, 0, 1, 0, 0, 0,
       1, 0, 1, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 1, 1, 0, 1, 1, 0, 1, 0, 0,
       1, 1, 0, 1, 0, 0, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 1, 1, 0, 0,
       1, 1, 0, 1, 0, 0, 1, 0, 1, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 0, 1, 1,
       1, 0, 0, 0, 0, 0, 0, 1], dtype=int64)
```

In [45]:
```python
dataset['Predict'] = db.fit_predict(dataset)
```

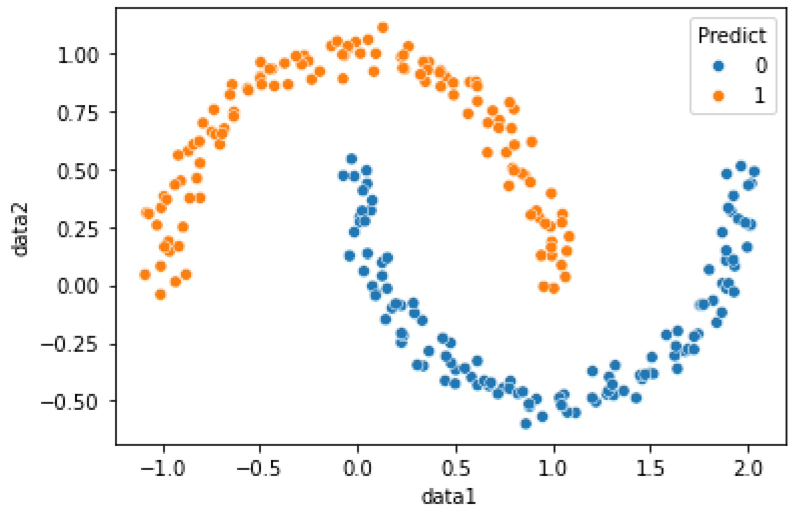
In [46]:
```python
dataset
```

Out[46]:

	data1	data2	Predict
0	1.821547	-0.067198	0
1	0.330398	-0.152611	0
2	1.116214	-0.551311	0
3	1.753388	-0.086491	0
4	0.794063	0.502981	1
...	...	...	...
245	2.032395	0.488380	0
246	0.435708	-0.229602	0
247	1.048799	-0.520698	0
248	1.043839	-0.518346	0
249	-0.808462	0.618646	1

250 rows × 3 columns

In [47]:
```python
sns.scatterplot(x='data1', y='data2', data=dataset, hue='Predict')
plt.show()
```



So predicted data resembles with actual output as shown in the graphs of predict and original data

In [ ]:

59. Silhouette Score

- It validates that cluster predicted from the data are right or wrong number of clusters
- Silhouette refers to a method of interpretation and validation of consistency within clusters of data.
- Silhouette Coefficient or Silhouette Score is a metric used to calculate the goodness of a clustering technique
- Its values ranges from -1 to 1

No description has been provided for this image

Silhouette Score Formula

The Silhouette score is calculated using the following formula:

$$s(i) = \frac{b(i) - a(i)}{\max(a(i), b(i))}$$

where:

- (s(i)) is the silhouette score for a data point (i).
- (a(i)) is the mean distance between (i) and all other data points in the same cluster.
- (b(i)) is the mean distance between (i) and all data points in the nearest neighboring cluster.

The Silhouette score ranges from -1 to 1, where:

- A score of 1 indicates that the data point is well clustered.
- A score of 0 indicates that the data point lies on the boundary between clusters.
- A score of -1 indicates that the data point is poorly clustered.

In [ ]:

60. Silhouette Score (Practical)

In [1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```
dataset = pd.read_csv(r'Data/iris_raw.csv')
dataset.head(3)
```

Out[2]:

	sepal_length	sepal_width	petal_length	petal_width
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2

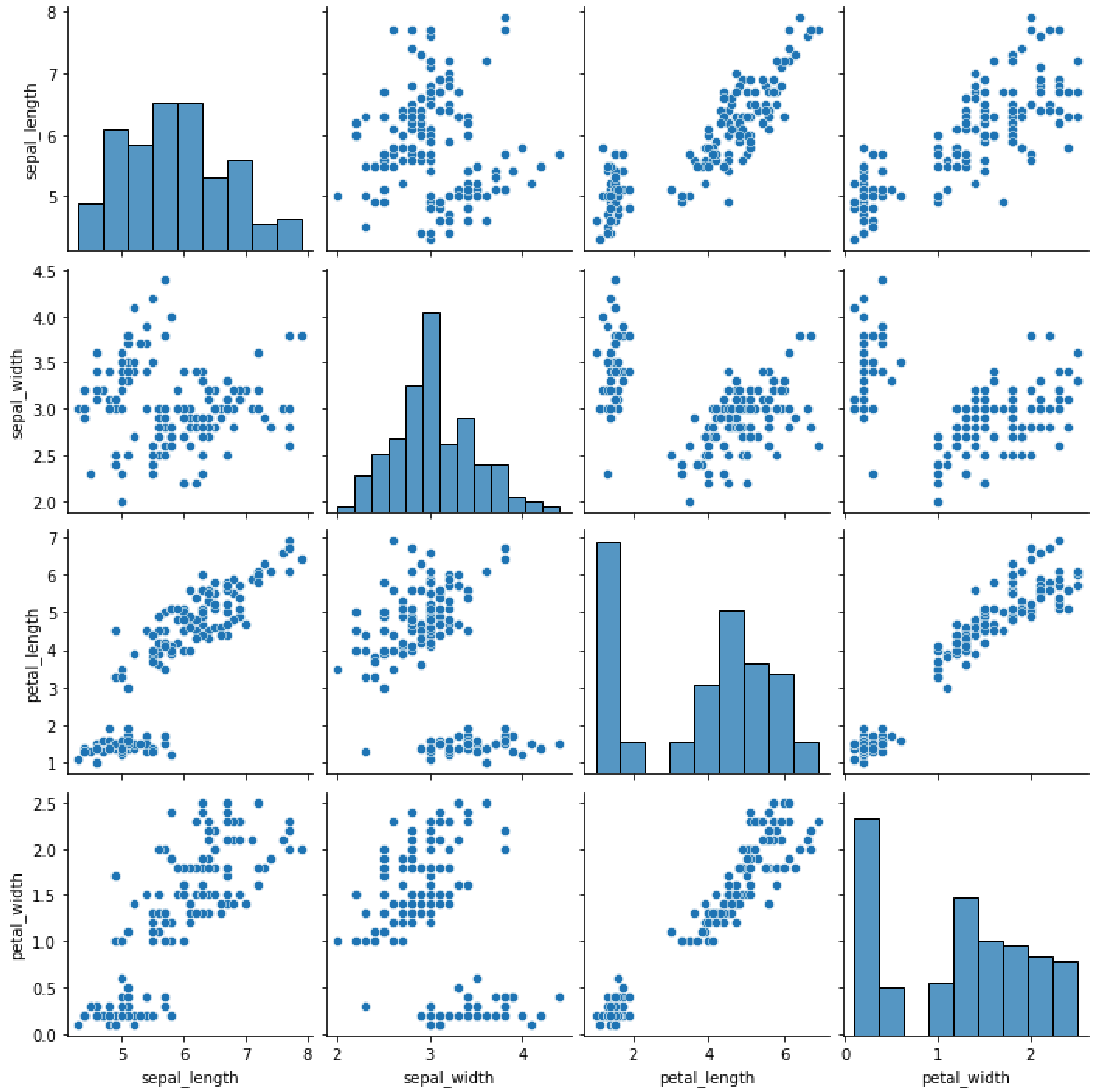
54.1 Making Clusters of Data

- Use K-mean clustering when **your data is linearly separable**

Check the data if it is linearly separable

In [3]:
```
sns.pairplot(data=dataset)
plt.show()
```

```
C:\Users\rashi\AppData\Local\Programs\Python\Python39\lib\site-packages\seaborn\axis
grid.py:123: UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```



- In supervised learning, the data is split into training and testing data
- In unsupervised learning, data is not split into training and testing data b/c the data is unlabelled

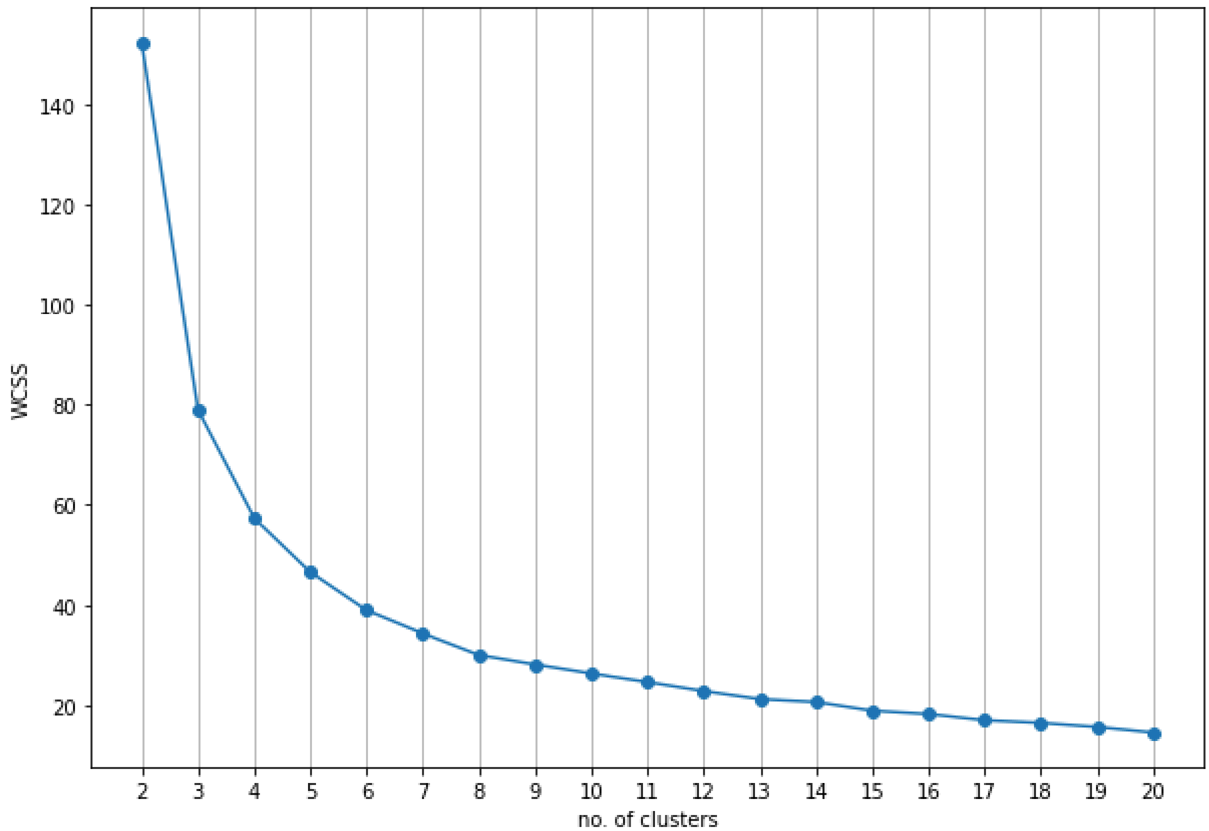
54.1.1 Find Number of clusters

In [4]:
```
from sklearn.cluster import KMeans
```

In [5]:
```
# Use a loop to find best number of clusters from 2 to 20
wcss = []

for i in range(2,21):
    km = KMeans(n_clusters=i, init='k-means++')
    km.fit(dataset)
    wcss.append(km.inertia_) # it assings value of wcss {Elbow graph}
```

In [6]:
```
plt.figure(figsize=(10,7))
plt.plot([i for i in range(2,21)], wcss, marker='o')
plt.xlabel('no. of clusters')
plt.xticks([i for i in range(2,21)])
plt.ylabel('WCSS')
plt.grid(axis='x')
plt.show()
```



Elbow point = 3

It means that will have 3 number of clusters

In [7]:
```
kmn = KMeans(n_clusters=3)
kmn.fit_predict(dataset)
```

Out[7]:
```
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 2, 2, 0, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 0, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 0, 2, 0, 0, 0, 0, 2, 0, 0, 0,
       0, 0, 0, 2, 2, 0, 0, 0, 0, 2, 0, 2, 0, 2, 0, 0, 2, 2, 0, 0, 0, 0,
       0, 2, 0, 0, 0, 0, 2, 0, 0, 0, 2, 0, 0, 0, 2, 0, 0, 2])
```

In [8]:
```
dataset['Predict'] = kmn.fit_predict(dataset)
```

In [9]:
```
dataset
```

Out[9]:

	sepal_length	sepal_width	petal_length	petal_width	Predict
0	5.1	3.5	1.4	0.2	0
1	4.9	3.0	1.4	0.2	0
2	4.7	3.2	1.3	0.2	0
3	4.6	3.1	1.5	0.2	0
4	5.0	3.6	1.4	0.2	0
...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	2
146	6.3	2.5	5.0	1.9	1
147	6.5	3.0	5.2	2.0	2
148	6.2	3.4	5.4	2.3	2
149	5.9	3.0	5.1	1.8	1

150 rows × 5 columns

54.2 Apply Silhouette Score to validate above results

In [17]:
```
from sklearn.metrics import silhouette_score
```

In [18]:
```
kmn.labels_
```

Out[18]:
```
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, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 2, 2, 2, 2, 1, 2, 2, 2,
       2, 2, 2, 1, 1, 2, 2, 2, 2, 1, 2, 1, 2, 1, 2, 2, 1, 1, 2, 2, 2, 2,
       2, 1, 2, 2, 2, 2, 1, 2, 2, 2, 1, 2, 2, 2, 1, 2, 2, 1])
```

In [19]:
```
silhouette_score(dataset, labels=kmn.labels_)
```

Out[19]:
```
0.6126634972047179
```

We are not sure about the results. So will apply loop to determine which silhouette_score is best and determine what is acutal number of clusters.

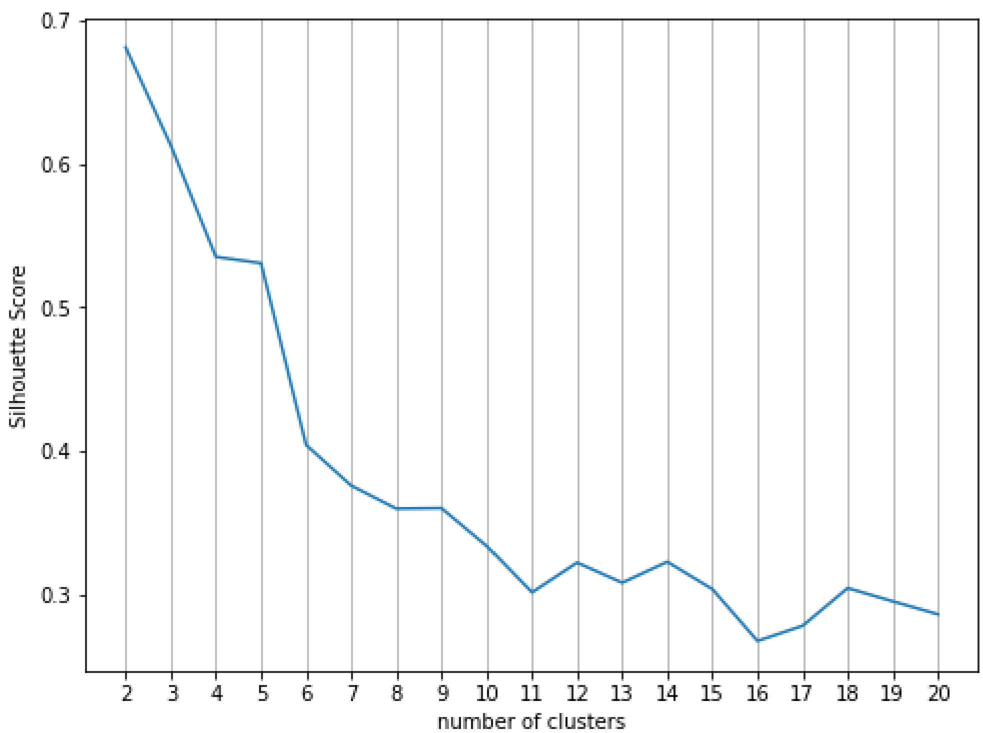
In [29]:
```
ss = []
n_clusters= [j for j in range(2,21)]

for i in range(2,21):
    kmn1 = KMeans(n_clusters=i)
```

```
    kmn1.fit(dataset)
    ss.append(silhouette_score(dataset, labels=kmn1.labels_))
```

- We are going to make graph b/w ss vs #clusters

In [39]:
```
plt.figure(figsize=(8,6))
plt.plot(n_clusters, ss)
plt.xlabel('number of clusters')
plt.ylabel('Silhouette Score')
plt.xticks(n_clusters)
plt.grid(axis='x')
plt.show()
```



Best Silhouette Score = 2

In [ ]: