The Sparks Foundation

Function: Data Science and Business Analytics

Task 2- Prediction Using Unsupervised ML

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In [1]:
```
# Import all the required libraries
import pandas as pd

import matplotlib.pyplot as plt
import seaborn as sns

import warnings
warnings.filterwarnings('ignore')

from sklearn.cluster import KMeans
```

In [2]:
```
# Load the dataset
data = pd.read_csv("Iris.csv")

# Print top 5 values of the dataset to get idea about the dataset
data.head()
```

Out[2]:

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	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	4.7	3.2	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

In [3]:
```
# Check if there is any null value in the Dataset
data.isnull().sum()

# We observe that there is no null value present
```

Out[3]:
```
Id               0
SepalLengthCm    0
SepalWidthCm     0
PetalLengthCm    0
PetalWidthCm     0
Species          0
dtype: int64
```

In [4]:
```
# Print the information of the dataset to get ingights of the dataset
data.info()
```

```
<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
 1   SepalLengthCm  150 non-null    float64
 2   SepalWidthCm   150 non-null    float64
 3   PetalLengthCm  150 non-null    float64
 4   PetalWidthCm   150 non-null    float64
 5   Species        150 non-null    object
```

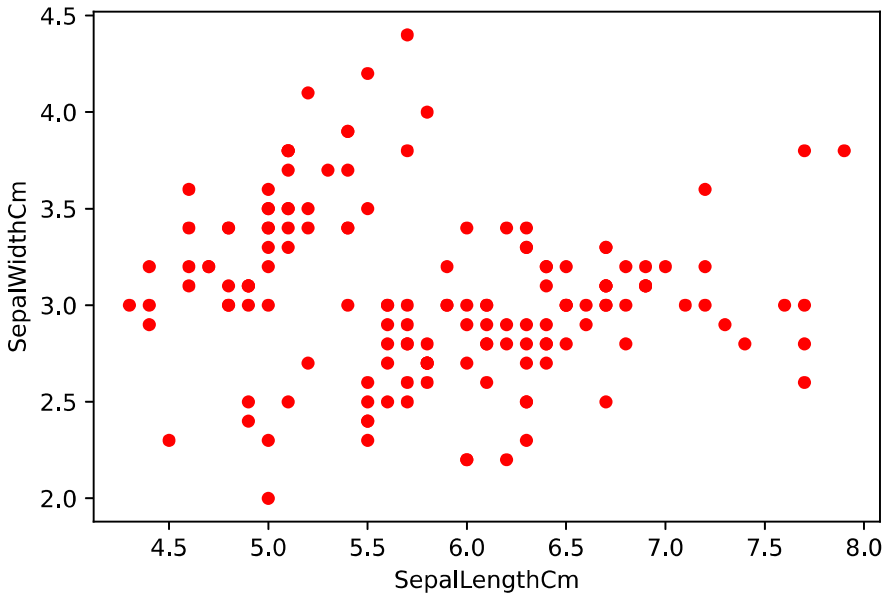
```
dtypes: float64(4), int64(1), object(1)
memory usage: 7.2+ KB
```

In [5]:
```
# Count of each species
data["Species"].value_counts()
```

Out[5]:
```
Iris-versicolor    50
Iris-setosa        50
Iris-virginica     50
Name: Species, dtype: int64
```

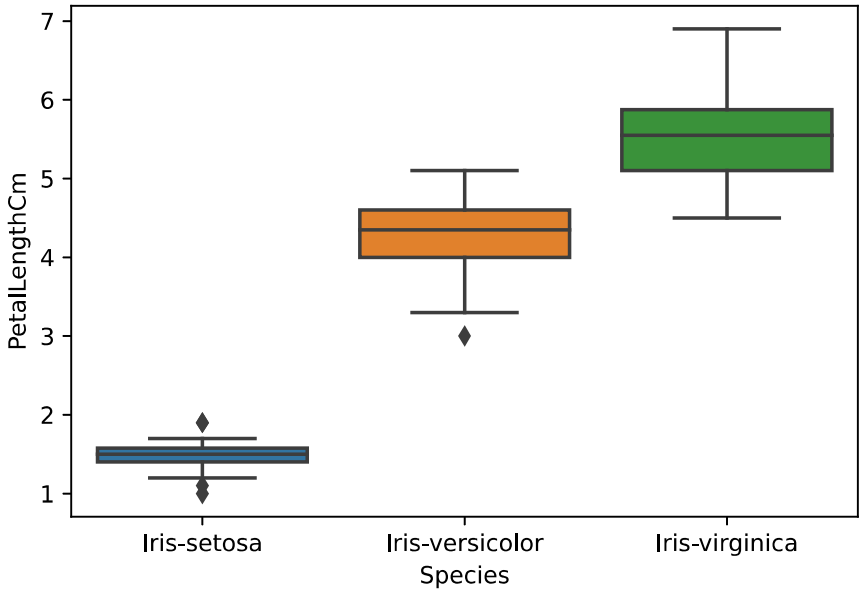
In [6]:
```
# Visualizing the data
data.plot(kind="scatter", x="SepalLengthCm", y="SepalWidthCm", color= "red")
```

Out[6]:
```
<AxesSubplot:xlabel='SepalLengthCm', ylabel='SepalWidthCm'>
```



In [7]:
```
#Box plot
sns.boxplot(x="Species", y="PetalLengthCm", data= data)
```

Out[7]:
```
<AxesSubplot:xlabel='Species', ylabel='PetalLengthCm'>
```



In [8]:
```
# Creating another dataframe which is a copy of data but does not contain ID
data1= data.iloc[:, 1:]
data1
```

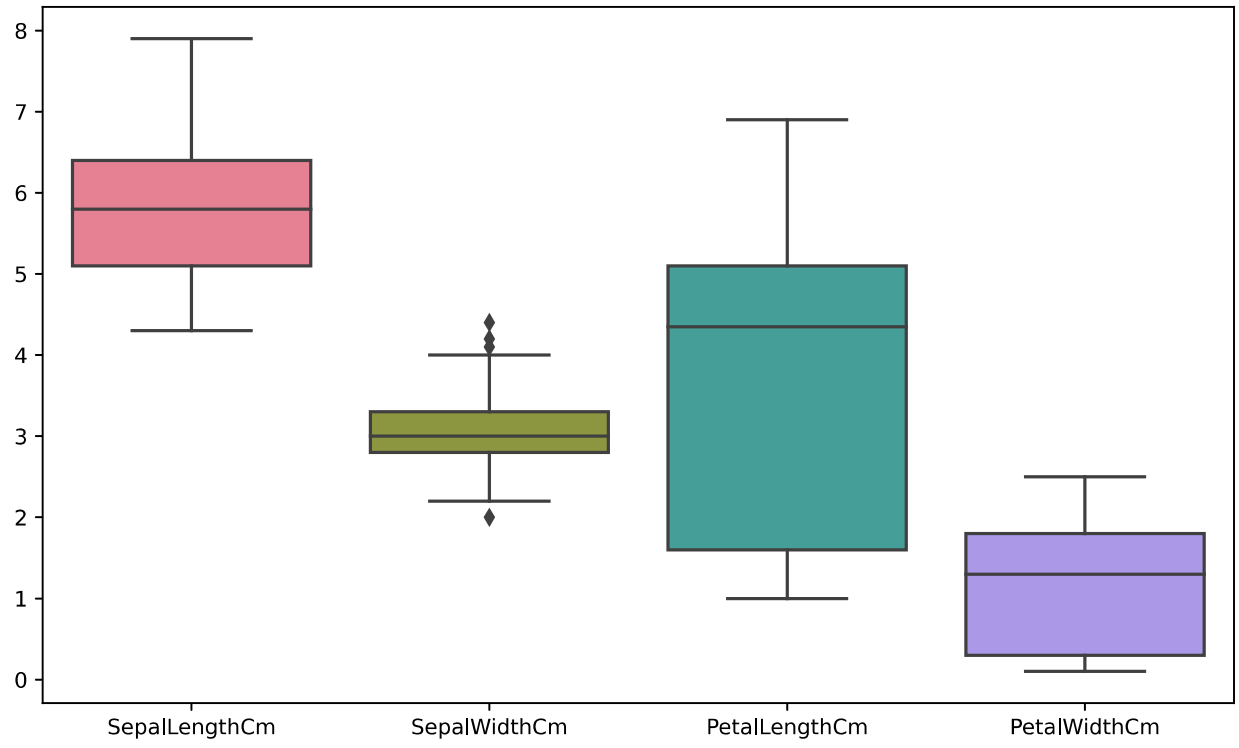
Out[8]:

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	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
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa
...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	Iris-virginica
146	6.3	2.5	5.0	1.9	Iris-virginica
147	6.5	3.0	5.2	2.0	Iris-virginica
148	6.2	3.4	5.4	2.3	Iris-virginica
149	5.9	3.0	5.1	1.8	Iris-virginica

150 rows × 5 columns

In [9]:

```
# Distribution of data using Boxplot
plt.figure(figsize=(10,6))
sns.boxplot(data=data1, palette= "husl")
plt.show()
```

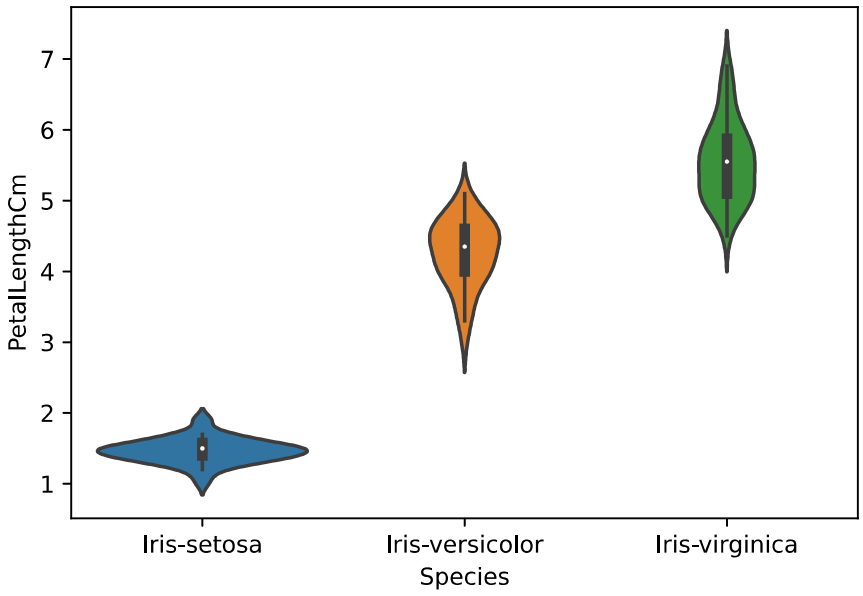


In [10]:

```
# Violinplot
sns.violinplot(x="Species", y="PetalLengthCm", data= data)
```

Out[10]:

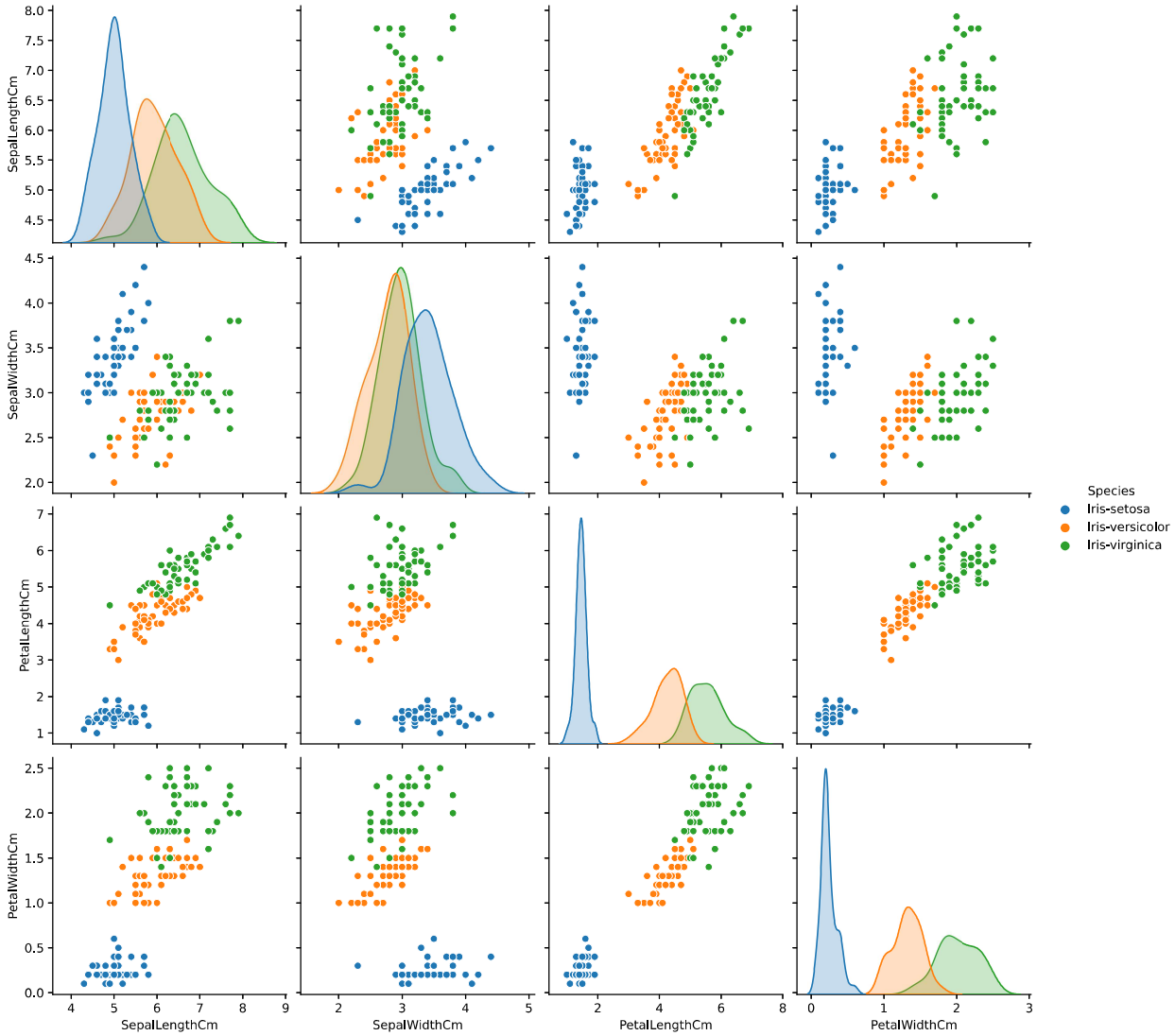
```
<AxesSubplot:xlabel='Species', ylabel='PetalLengthCm'>
```



In [11]:

```
# Bivariate relation between each pair of features
sns.pairplot(data1, hue="Species", size=3)
```

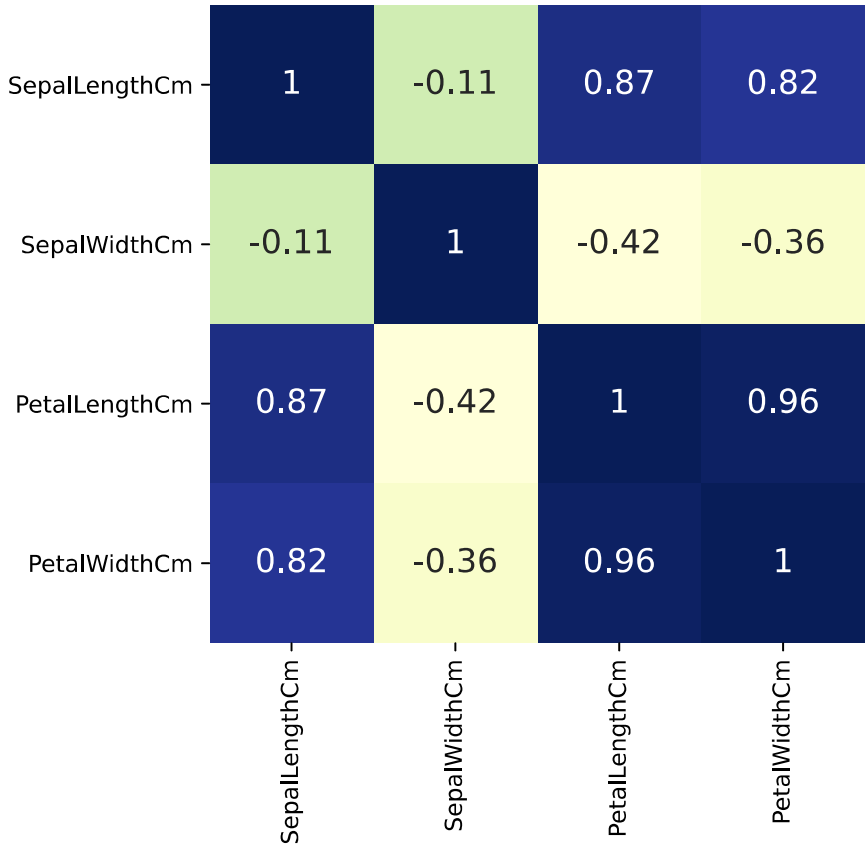
Out[11]: <seaborn.axisgrid.PairGrid at 0x1bb25637340>



In [12]:

```
# Correlation of data
plt.figure(figsize=(5,5))
sns.heatmap(data1.corr(), cmap='YlGnBu', annot=True,
```

```
            cbar=False, annot_kws={'size': 14})
plt.show()
```



In [13]:
```
# Let X be a data frame containing only independent attributes of data1
X = data1.iloc[:, [0,1,2,3]].values
```

In [14]:
```
# K Means Clustering
#Let k=7
kMeans7=KMeans(n_clusters=7)
y_kMeans7= kMeans7.fit_predict(X) #we don't need ID
print(y_kMeans7)
```

```
[0 5 5 5 0 0 5 5 5 5 0 5 5 5 0 0 0 0 0 0 0 5 0 5 5 0 0 0 5 5 0 0 0 5 5 0
 5 5 0 0 5 5 0 0 5 0 5 0 5 3 3 3 2 3 2 3 2 3 2 2 2 2 3 2 3 6 2 3 2 6 2 6 3
 3 3 3 3 3 2 2 2 2 6 2 3 3 3 2 2 2 3 2 2 2 2 2 3 2 2 1 6 4 1 1 4 2 4 1 4 1
 1 1 6 6 1 1 4 4 6 1 6 4 6 1 4 6 6 1 4 4 4 1 6 6 4 1 1 6 1 1 1 6 1 1 1 6 1
 1 6]
```

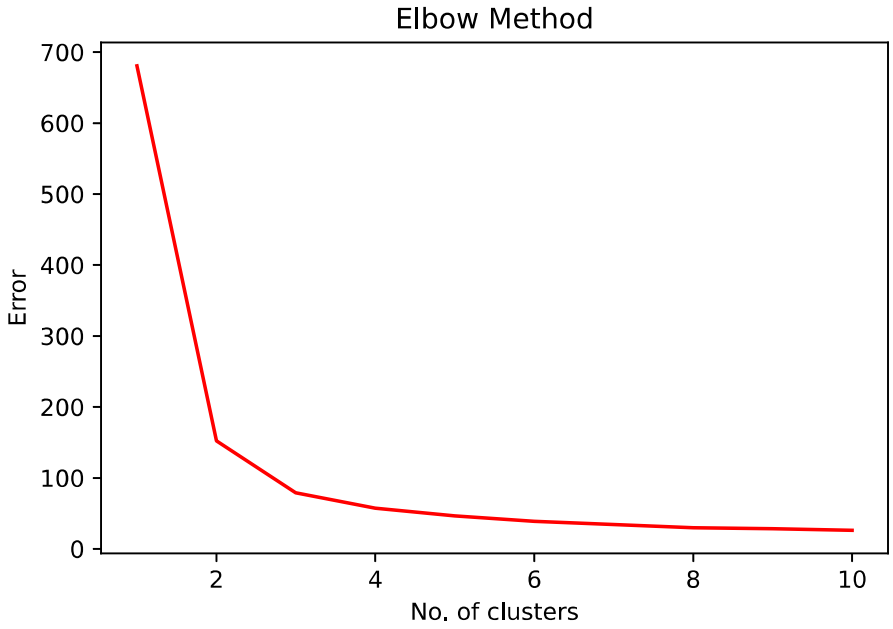
In [15]:
```
# Printing the cluster centres
kMeans7.cluster_centers_
```

Out[15]:
```
array([[5.26538462, 3.68076923, 1.50384615, 0.29230769],
       [6.56086957, 3.06956522, 5.52608696, 2.15217391],
       [5.52962963, 2.62222222, 3.94074074, 1.21851852],
       [6.43      , 2.94      , 4.59      , 1.435     ],
       [7.475     , 3.125     , 6.3       , 2.05      ],
       [4.725     , 3.13333333, 1.42083333, 0.19166667],
       [5.98333333, 2.75      , 4.98333333, 1.77222222]])
```

In [16]:
```
# ELBOW Method
Error =[]
for i in range(1, 11):
    kmeans = KMeans(n_clusters = i).fit(X)
    kmeans.fit(X)
    Error.append(kmeans.inertia_)

plt.plot(range(1, 11), Error, color= "red")
plt.title('Elbow Method')
plt.xlabel('No. of clusters')
```

```
plt.ylabel('Error')
plt.show()
```



Observation:

The shape of elbow is approximately formed at k=3.

Optimal value of k is 3.

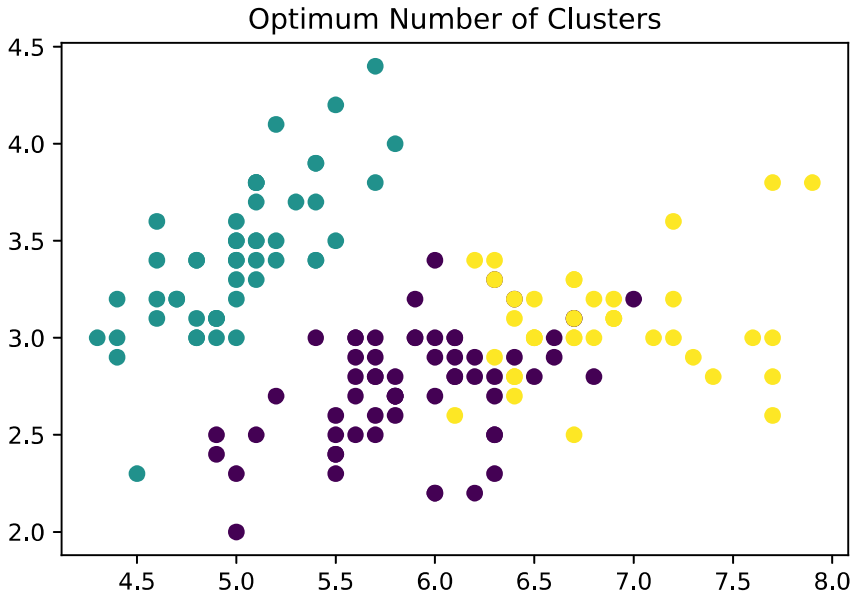
In [17]:
```
# Let's implement k-means using k=3.
kMeans3=KMeans(n_clusters=3)
y_kMeans3= kMeans3.fit_predict(X) # we don't need ID
print(y_kMeans3)
```

```
[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 2 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 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2 0 2 2 2 2 0 2 2 2 2
 2 2 0 0 2 2 2 2 0 2 0 2 0 2 2 0 0 2 2 2 2 2 0 2 2 2 2 0 2 2 2 0 2 2 2 0 2
 2 0]
```

In [18]:
```
# Printing the cluster centres
kMeans3.cluster_centers_
```

Out[18]:
```
array([[5.9016129 , 2.7483871 , 4.39354839, 1.43387097],
       [5.006     , 3.418     , 1.464     , 0.244     ],
       [6.85      , 3.07368421, 5.74210526, 2.07105263]])
```

In [19]:
```
# Visualizing the three clusters
plt.scatter(X[:,0], X[:,1], c= y_kMeans3)
plt.title('Optimum Number of Clusters')
plt.show()
```


Optimum Number of Clusters
4.5
4.0
3.5
3.0
2.5
2.0
4.5
5.0
5.5
6.0
6.5
7.0
7.5
8.0

THANK YOU ^_^