EXPERIMENT NO. 1 A (Group A)

- **Aim:** To use PCA Algorithm for dimensionality reduction. You have a dataset that includes measurements for different variables on wine (alcohol, ash, magnesium, and so on). Apply PCA algorithm & transform this data so that most variations in the measurements of the variables are captured by a small number of principal components so that it is easier to distinguish between red and white wine by inspecting these principal components

- **Outcome: At end of this experiment, student will be able understand the scheduler, and how its behaviour influences the performance of the system**

- **Hardware Requirement:**

▪ 6 GB free disk space.
▪ 2 GB RAM.
▪ 2 GB of RAM, plus additional RAM for virtual machines.
▪ 6 GB disk space for the host, plus the required disk space for the virtual machine(s).
▪ Virtualization is available with the KVM hypervisor
▪ Intel 64 and AMD64 architectures

- **Software Requirement:**

Jupyter Nootbook/Ubuntu

- **Theory:**

Principal Component Analysis (PCA)

PCA is an unsupervised machine learning algorithm. PCA is mainly used for dimensionality reduction in a dataset consisting of many variables that are highly correlated or lightly correlated with each other while retaining the variation present in the dataset up to a maximum extent.
It is also a great tool for exploratory data analysis for making predictive models.
PCA performs a linear transformation on the data so that most of the variance or information in your high-dimensional dataset is captured by the first few principal components. The first principal component will capture the most variance, followed by the second principal component, and so on.
Each principal component is a linear combination of the original variables. Because all the principal components are orthogonal to each other, there is no redundant information. So, the total variance in the data is defined as the sum of the variances of the individual component. So decide the total number of principal components according to cumulative variance ‘‘explained’’ by them.

Implementation:

```
import pandas as pd
from sklearn.decomposition import PCA
```

```
from sklearn.preprocessing import StandardScaler
import matplotlib.pyplot as plt

df = pd.read_csv("C:/Users/HP/Dropbox/PC/Downloads/Wine.csv")

df.keys()

print(df['DESCR'])

df.head(5)
```

```
   Alcohol  Malic_Acid   Ash  Ash_Alcanity  Magnesium  Total_Phenols  \
0    14.23        1.71  2.43          15.6        127           2.80
1    13.20        1.78  2.14          11.2        100           2.65
2    13.16        2.36  2.67          18.6        101           2.80
3    14.37        1.95  2.50          16.8        113           3.85
4    13.24        2.59  2.87          21.0        118           2.80

   Flavanoids  Nonflavanoid_Phenols  Proanthocyanins  Color_Intensity   Hue  \
0        3.06                  0.28             2.29             5.64  1.04
1        2.76                  0.26             1.28             4.38  1.05
2        3.24                  0.30             2.81             5.68  1.03
3        3.49                  0.24             2.18             7.80  0.86
4        2.69                  0.39             1.82             4.32  1.04

   OD280  Proline  Customer_Segment
0   3.92     1065                 1
1   3.40     1050                 1
2   3.17     1185                 1
3   3.45     1480                 1
4   2.93      735                 1
```

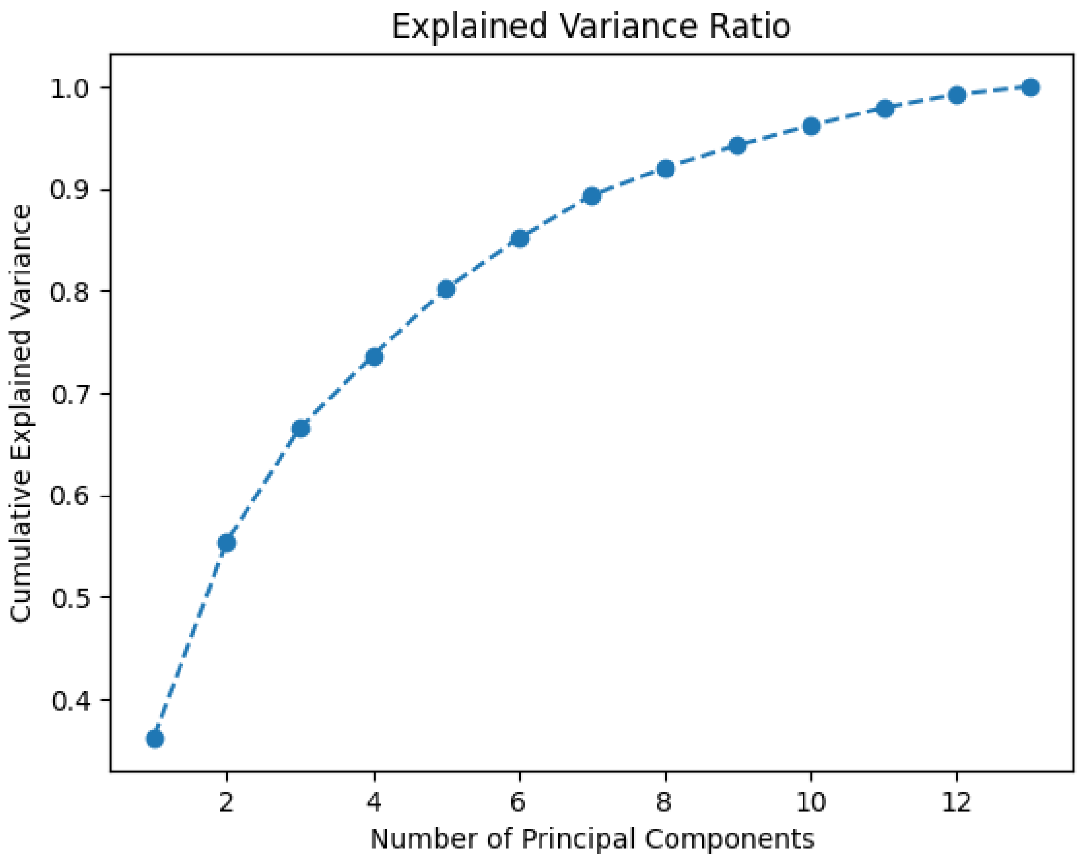
```
df.Customer_Segment.unique()
```

```
array([1, 2, 3], dtype=int64)
```

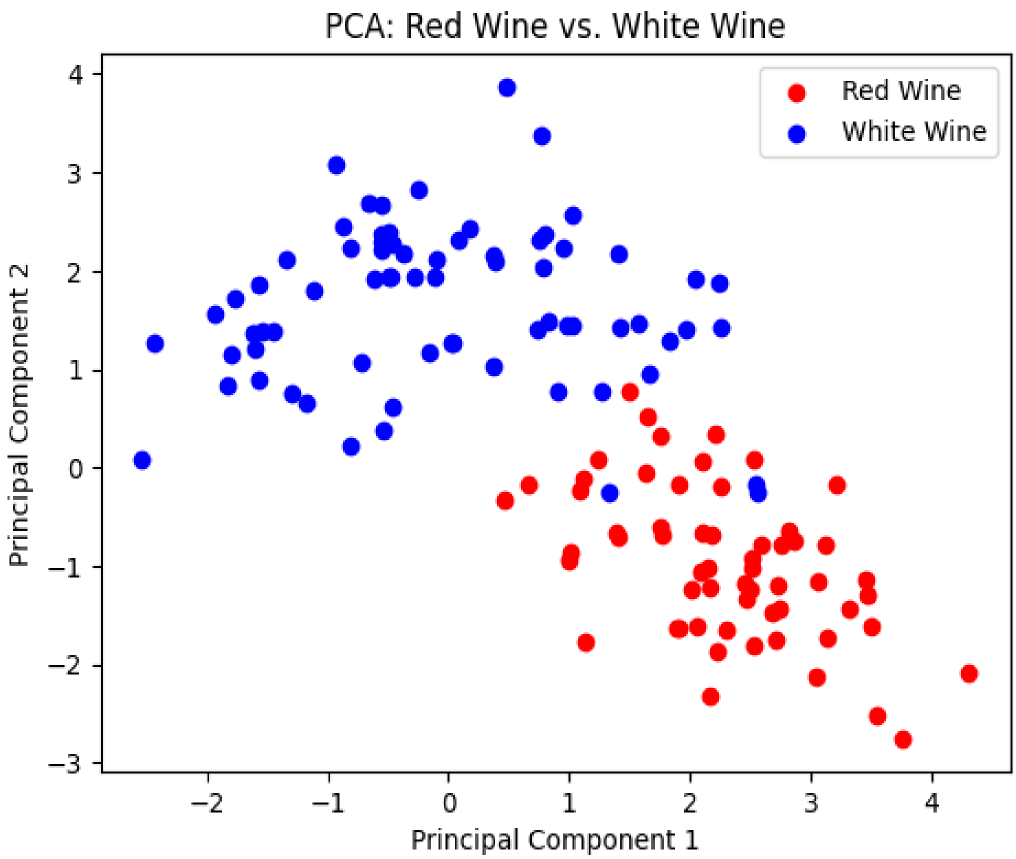
```
print(df.isnull().sum())      #checking is null
```

```
Alcohol                 0
Malic_Acid              0
Ash                     0
Ash_Alcanity            0
Magnesium               0
Total_Phenols           0
Flavanoids              0
Nonflavanoid_Phenols    0
Proanthocyanins         0
Color_Intensity         0
Hue                     0
OD280                   0
```

```
Proline              0
Customer_Segment     0
dtype: int64

X = df.drop('Customer_Segment', axis=1)  # Features
y = df['Customer_Segment']  # Target variable

for col in X.columns:
   sc = StandardScaler()                          #Standardize features by removing the mean and scaling to unit variance.z = (x - u) / s  mean=0, Stddeviation=1
   X[col] = sc.fit_transform(X[[col]])                   #Fit to data, then transform it.Compute the mean and std to be used for later scaling.

X.head(5)

    Alcohol  Malic_Acid       Ash  Ash_Alcanity  Magnesium  Total_Phenols  \
0  1.518613   -0.562250  0.232053     -1.169593   1.913905       0.808997
1  0.246290   -0.499413 -0.827996     -2.490847   0.018145       0.568648
2  0.196879    0.021231  1.109334     -0.268738   0.088358       0.808997
3  1.691550   -0.346811  0.487926     -0.809251   0.930918       2.491446
4  0.295700    0.227694  1.840403      0.451946   1.281985       0.808997

   Flavanoids  Nonflavanoid_Phenols  Proanthocyanins  Color_Intensity  \
0    1.034819             -0.659563         1.224884         0.251717
1    0.733629             -0.820719        -0.544721        -0.293321
2    1.215533             -0.498407         2.135968         0.269020
3    1.466525             -0.981875         1.032155         1.186068
4    0.663351              0.226796         0.401404        -0.319276

        Hue     OD280   Proline
0  0.362177  1.847920  1.013009
1  0.406051  1.113449  0.965242
2  0.318304  0.788587  1.395148
3 -0.427544  1.184071  2.334574
4  0.362177  0.449601 -0.037874

pca = PCA()
X_pca = pca.fit_transform(X)

explained_variance_ratio = pca.explained_variance_ratio_

plt.plot(range(1, len(explained_variance_ratio) + 1), explained_variance_ratio.cumsum(), marker='o', linestyle='--')
plt.xlabel('Number of Principal Components')
plt.ylabel('Cumulative Explained Variance')
plt.title('Explained Variance Ratio')
plt.show()
```




```
n_components = 12  # Choose the desired number of principal components you want to reduce a dimention to
pca = PCA(n_components=n_components)
X_pca = pca.fit_transform(X)

X_pca.shape

X.shape

red_indices = y[y == 1].index
white_indices = y[y == 2].index

plt.scatter(X_pca[red_indices, 0], X_pca[red_indices, 1], c='red', label='Red Wine')
plt.scatter(X_pca[white_indices, 0], X_pca[white_indices, 1], c='blue', label='White Wine')
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.legend()
plt.title('PCA: Red Wine vs. White Wine')
plt.show()
```



#Conclusion: Here we have reduce the dimention now we can able to apply any algorithm like classification, Regression etc.