#Import all the necessary libraries import pandas as pd import numpy as np import os import seaborn as sns import matplotlib.pyplot as plt Let us now load the data and check the first 10 rows of the dataframe. df = pd.read csv("Redwine+Quality.csv") In [4]:

Free.sulfur.dioxide Bound.sulfur.dioxide

PH

Levels

Potassium Alcohol

Content

chloride

Alcohol

Sodium

chloride

**Acid Density** Density 0.9978 0 1 7.4 0.70 0.00 1.9 0.076 11.0 34.0 3.51 0.56 9.4 1 2 7.8 0.88 0.00 2.6 0.098 25.0 67.0 0.9968 3.20 0.68 9.8 3 2 7.8 0.76 0.04 2.3 0.092 15.0 54.0 0.9970 3.26 0.65 9.8 0.9980 0.58 3 4 11.2 0.28 0.56 1.9 0.075 17.0 60.0 3.16 9.8 4 5 0.076 0.9978 0.56 7.4 0.70 0.00 1.9 11.0 34.0 3.51 9.4 5 0.56 7.4 0.66 0.00 1.8 0.075 13.0 40.0 0.9978 3.51 9.4 6 7 0.06 0.9964 7.9 0.60 1.6 0.069 15.0 59.0 3.30 0.46 9.4 7.3 8 0.65 0.00 1.2 0.065 15.0 21.0 0.9946 3.39 0.47 10.0 8 9 0.57 7.8 0.58 0.02 2.0 0.073 9.0 18.0 0.9968 3.36 9.5 9 10 7.5 0.50 0.36 6.1 0.071 17.0 102.0 0.9978 3.35 0.80 10.5 df.drop('Unnamed: 0',axis=1,inplace=True) Now, that we have dropped the 'ID' column, let us check the shape and the various data types of the variables of the dataframe.

In [6]: df.info() <class 'pandas.core.frame.DataFrame'> RangeIndex: 1599 entries, 0 to 1598

Data columns (total 11 columns): Non-Null Count Dtype # Column 0 1599 non-null Tartaric Acid float64

Let us check the correlation between these variables. plt.figure(figsize=(12,6)) sns.heatmap(df.corr(),cmap='plasma',fmt='.2g',annot=True,mask=np.triu(df.corr(),+1)) plt.show() - 1.0 Tartaric Acid -- 0.8 Grape Density -0.6 0.14 Residual.sugar - 0.4 1 Sodium chloride 0.094 0.061 - 0.2 1 -0.15-0.011 -0.061 Free.sulfur.dioxide 0.076 0.047 0.67 1 -0.110.2 Bound.sulfur.dioxide - 0.0 1 0.67 0.022 -0.022 0.071 Alcohol Density - -0.2 -0.54 -0.34 -0.68-0.086 -0.27 0.07 -0.066 PH Levels -0.4 -0.2 Potassium chloride 0.18 -0.260.0055 0.052 0.31 0.043 0.094 Alcohol Content --0.062 -0.2 0.11 0.042 -0.22 -0.069 -0.21-0.5 **Tartaric Acid** Sodium chloride Levels Alcohol Content Alcohol Density Potassium chloride Residual.sugar Free.sulfur.dioxide Grape Density Bound.sulfur.dioxide

data\_scaled=df.apply(zscore) data scaled.head()

Residual.sugar

-0.453218

0.043416

-0.169427

Sodium

chloride

-0.243707

0.223875

0.096353

We see that there is some degree of correlation amongst the variables given in the dataframe.

# All variables are on same scale, hence we can omit scaling.

# But to standardize the process we will do it here

Citric

Acid

**Tartaric** Grape Acid Density

**0** -0.528360

-0.298547

-0.298547

Now, we will scale the data.

from scipy.stats import zscore

0.961877 -1.391472

1.967442 -1.391472

1.297065 -1.186070

#Apply PCA taking all features

#Extract eigen vectors

-0.11323207],

-0.38618096],

a=pca.explained\_variance\_

plt.grid()

2.5

Eigen Value

In [14]:

plt.plot(pca.explained variance )

pca.components\_

from sklearn.decomposition import PCA

pca = PCA(n components=6, random state=123) pca transformed = pca.fit transform(data scaled)

In [8]:

df.head(10)

Out[4]:

**Unnamed: Tartaric** 

Grape Density

Residual.sugar

Sodium chloride

Alcohol Density

Potassium chloride

We see that all are numeric variables.

PH Levels

dtypes: float64(11) memory usage: 137.5 KB

10 Alcohol Content

8

Free.sulfur.dioxide 1599 non-null Bound.sulfur.dioxide 1599 non-null

Citric Acid

Grape

Citric

Acid

Residual.sugar

1599 non-null

1.654856 -1.384443 -0.453218 -0.264960 0.107592 0.411500 0.664277 -0.979104 -0.461180 -0.584777 1.484154 -0.528360 0.961877 -1.391472 -0.453218 -0.243707 -0.466193 -0.379133 0.558274 1.288643 -0.579207 -0.960246 **PCA** Before we go ahead and perform the Principal Component Analysis, let us build the covariance matrix.

Free.sulfur.dioxide Bound.sulfur.dioxide

-0.466193

0.872638

-0.083669

Alcohol

Density

-0.379133 0.558274

**Potassium** 

Levels

1.288643

chloride

-0.579207

0.128950

-0.048089

Alcohol

Content

-0.960246

-0.584777

-0.584777

### pca\_transformed Out[11]: array([[-1.61952988,

### -0.91392069], [-0.79916993, 1.85655306, -0.91169017, 0.54806597, -0.01839156,

0.45095009, -1.77445415, 0.04374031, 0.06701448,

0.88203886, -1.17139423, [-0.74847909,0.41102067, -0.04353101, 0.40147313], [-1.45612897,0.31174559, 1.12423941, 0.49187676, 0.19371564, -0.50640956], 0.62796456, 0.63977007, [-2.27051793,0.97979111, 0.06773549, -0.86040762], [-0.42697475, -0.53669021, 1.6289552, -0.39171595,-0.4961536411)

#### 0.42879287, 0.3224145 , -0.33887135, 0.05769735, 0.27978615, 0.47167322], [-0.22961737, 0.07895978, -0.07941826, -0.37279256, 0.66619476,

Out[12]: array([[ 0.48931422, -0.23858436, 0.46363166, 0.14610715, 0.21224658,

Using given dataset, Find out the eigenvector of the 5th component

-0.03615752, 0.02357485, 0.39535301, -0.43851962, 0.24292133,

[-0.11050274, 0.27493048, -0.15179136, 0.27208024, 0.14805156,0.51356681, 0.56948696, 0.23357549, 0.00671079, -0.03755392,

[-0.12330157, -0.44996253, 0.23824707, 0.10128338, -0.09261383,

-0.04353782, -0.03457712, -0.17449976, -0.00378775, 0.55087236, -0.12218109], [-0.08261366, 0.21873452, -0.05857268, 0.73214429, 0.2465009]-0.15915198, -0.22246456, 0.15707671, 0.26752977, 0.22596222, 0.35068141], [ 0.10147858, 0.41144893, 0.06959338, 0.04915555, 0.30433857, -0.01400021, 0.13630755, -0.3911523, -0.52211645, -0.38126343, 0.36164504]]) Using the given dataset, Find out eigenvalues? #Check the eigen values #Note: This is always returned in descending order pca.explained\_variance\_ Out[13]: array([3.10107182, 1.92711489, 1.55151379, 1.21399175, 0.95989238, 0.66002104])

## 3.0

As per given Scree Plot, how many principal components are preferred?

2.0 1.5 1.0 Plot of eigen values with the number of factors or Principal Components plt.plot(range(0,6),a) plt.grid() plt.ylabel('Eigen Values') plt.xlabel('Factors') plt.hlines(y=1,xmin=0,xmax=6,linestyles='dashed'); 3.0

## 2.5

1.0 Factors

#Note: Explained variance = (eigen value of each PC)/(sum of eigen values of all PCs)

Out[17]: array([0.28173931, 0.1750827, 0.1409585, 0.11029387, 0.08720837, 0.05996439])

Using the given dataset, What are explained variances

#Check the explained variance for each PC

pca.explained\_variance\_ratio\_

# **END**