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]: df.head(10)**Unnamed: Tartaric** Sodium Grape Citric Alcohol Residual.sugar Free.sulfur.dioxide Bound.sulfur.dioxide **Acid Density** Acid chloride Density

Out[4]: 0 1 7.4 0.70 0.00 1.9 0.076 11.0 34.0 1 2 7.8 0.88 0.00 2.6 0.098 25.0 3 2 7.8 0.76 0.04 2.3 0.092 15.0

3 4 11.2 0.28 0.56

7.4

7.4

#Import all the necessary libraries

import pandas as pd

4

5

5

1.9 0.076 1.9

1.8

0.075

17.0 11.0 13.0

67.0 54.0 60.0 0.9978 34.0 40.0

0.9978 3.51 0.9968 3.20 0.9970 3.26 0.9980 3.16 3.51

PH

3.51

3.30

3.39

3.36

3.35

- 1.0

- 0.8

0.6

Alcohol

Density

0.411500 0.664277 -0.979104

-0.379133 0.558274 1.288643

-0.379133 0.558274

Potassium

Levels

1.288643

chloride

-0.579207

0.128950

-0.048089

-0.461180

-0.579207 -0.960246

Alcohol

Content

-0.960246

-0.584777

-0.584777

-0.584777

Levels

0.56 0.68 0.65 0.58 0.56

chloride

Potassium Alcohol

9.8 9.8 9.4 9.4 9.4 10.0

Content

9.4

9.8

6 7 0.06 7.9 0.60 1.6 0.069 15.0 7.3 8 0.65 0.00 1.2 0.065 15.0 8 9 7.8 0.58 0.02 2.0 0.073 9.0

9 10 7.5 0.50 0.36 6.1

0.70

0.66

0.00

0.00

df.drop('Unnamed: 0',axis=1,inplace=True)

0.071

0.075 17.0

59.0 21.0 18.0 102.0 0.9978

0.9978 0.9964 0.9946 0.9968

0.46 0.47 0.57 0.80

0.56

9.5 10.5

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

Now, that we have dropped the 'ID' column, let us check the shape and the various data types

0 1599 non-null Tartaric Acid float64 Grape Density 1599 non-null float64 Citric Acid 1599 non-null float64 Residual.sugar 1599 non-null float64 Sodium chloride 1599 non-null float64 Free.sulfur.dioxide 1599 non-null Bound.sulfur.dioxide 1599 non-null float64 Alcohol Density 1599 non-null float64 8 PH Levels 1599 non-null float64 Potassium chloride 1599 non-null float64 10 Alcohol Content 1599 non-null float64 dtypes: float64(11) memory usage: 137.5 KB We see that all are numeric variables. 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() Tartaric Acid -

0.14

- 0.4 1 Sodium chloride 0.094 0.061 - 0.2 1 -0.15-0.011 -0.061 Free.sulfur.dioxide 0.047 0.67 1 -0.110.076 0.2 Bound.sulfur.dioxide - 0.0 1 0.67 0.022 -0.022 0.071 Alcohol Density - -0.2 -0.34 -0.68-0.54-0.086 -0.27 0.07 -0.066 PH Levels -0.4 -0.2 0.18 -0.260.0055 0.052 Potassium chloride 0.31 0.043 0.094 -0.062 -0.2 0.11 0.042 -0.22 -0.069 -0.21-0.5 Alcohol Content -**Tartaric Acid** Levels Alcohol Content Sodium chloride Alcohol Density Potassium chloride Residual.sugar Grape Density Free.sulfur.dioxide Bound.sulfur.dioxide We see that there is some degree of correlation amongst the variables given in the dataframe. Now, we will scale the data. # All variables are on same scale, hence we can omit scaling. In [8]: # But to standardize the process we will do it here

chloride **0** -0.528360 0.961877 -1.391472 -0.453218 -0.243707 -0.466193 -0.298547 1.967442 -1.391472 0.043416 0.223875 0.872638

-0.298547 1.297065 -1.186070 -0.169427 0.096353 -0.083669 0.107592

-1.384443 -0.453218 -0.264960 1.484154 -0.453218 -0.243707

0.961877 -1.391472

erform the Principal Component Analysis, let us build the

Sodium

Free.sulfur.dioxide Bound.sulfur.dioxide

-0.466193

pca transformed = pca.fit transform(data scaled)

0.88203886, -1.17139423, 0.41102067, -0.04353101, 0.40147313], [-1.45612897,0.31174559, 1.12423941, 0.19371564, 0.49187676, -0.50640956], 0.62796456, 0.63977007, [-2.27051793,0.97979111, 0.06773549,

-0.03615752, 0.02357485, 0.39535301, -0.43851962, 0.24292133, -0.11323207], [-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, -0.09261383,0.42879287, 0.3224145 , -0.33887135, 0.05769735, 0.27978615,

> [-0.22961737, 0.07895978, -0.07941826, -0.37279256, 0.66619476, -0.04353782, -0.03457712, -0.17449976, -0.00378775, 0.55087236,

> [-0.08261366, 0.21873452, -0.05857268, 0.73214429, 0.2465009]-0.15915198, -0.22246456, 0.15707671, 0.26752977, 0.22596222,

> [0.10147858, 0.41144893, 0.06959338, 0.04915555, 0.30433857, -0.01400021, 0.13630755, -0.3911523, -0.52211645, -0.38126343,

Using the given dataset, Find out eigenvalues? #Check the eigen values

#Note: This is always returned in descending order

As per given Scree Plot, how many principal components are preferred? plt.plot(pca.explained variance) plt.grid()

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 Eigen Values

1.0 Factors Using the given dataset, What are explained variances

#Check the explained variance for each PC #Note: Explained variance = (eigen value of each PC)/(sum of eigen values of all PCs) pca.explained_variance_ratio_ Out[17]: array([0.28173931, 0.1750827, 0.1409585, 0.11029387, 0.08720837, 0.05996439])

END

Grape Density -

Residual.sugar

from scipy.stats import zscore data_scaled=df.apply(zscore) data scaled.head() **Tartaric** Grape Citric Residual.sugar Acid Density Acid

1.654856 -0.528360

PCA	
Before we go ahead and p)(

covariance matrix. #Apply PCA taking all features from sklearn.decomposition import PCA pca = PCA(n components=6, random state=123)

pca_transformed Out[11]: array([[-1.61952988,

0.45095009, -1.77445415, 0.04374031, 0.06701448, -0.91392069], [-0.79916993, 1.85655306, -0.91169017, 0.54806597, -0.01839156,[-0.74847909,

-0.38618096],

0.47167322],

-0.12218109],

0.35068141],

0.36164504]])

pca.explained_variance_

0.66002104])

a=pca.explained_variance_

-0.86040762], [-0.42697475, -0.53669021, 1.6289552, -0.39171595,-0.4961536411)

Using given dataset, Find out the eigenvector of the 5th component #Extract eigen vectors pca.components_ Out[12]: array([[0.48931422, -0.23858436, 0.46363166, 0.14610715, 0.21224658,

Out[13]: array([3.10107182, 1.92711489, 1.55151379, 1.21399175, 0.95989238,

In [14]:

3.0

2.5

2.0

1.5

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