DATA COLLECTION

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

In [2]: # To Import Dataset
sd=pd.read_csv(r"c:\Users\user\Downloads\11_winequality-red.csv")
sd

Out[2]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alcol
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
1594	6.2	0.600	80.0	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	1
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	1
1596	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	1
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	1
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	1

1599 rows × 12 columns

```
In [3]: # to display top 10 rows
sd.head(10)
```

Out[3]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pН	sulphates	alcohol
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4
5	7.4	0.66	0.00	1.8	0.075	13.0	40.0	0.9978	3.51	0.56	9.4
6	7.9	0.60	0.06	1.6	0.069	15.0	59.0	0.9964	3.30	0.46	9.4
7	7.3	0.65	0.00	1.2	0.065	15.0	21.0	0.9946	3.39	0.47	10.0
8	7.8	0.58	0.02	2.0	0.073	9.0	18.0	0.9968	3.36	0.57	9.5
9	7.5	0.50	0.36	6.1	0.071	17.0	102.0	0.9978	3.35	0.80	10.5
4.6											

DATA CLEANING AND PRE_PROCESSING

In [4]: sd.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1599 entries, 0 to 1598
Data columns (total 12 columns):

	(
#	Column	Non-Null Count	Dtype
0	fixed acidity	1599 non-null	float64
1	volatile acidity	1599 non-null	float64
2	citric acid	1599 non-null	float64
3	residual sugar	1599 non-null	float64
4	chlorides	1599 non-null	float64
5	free sulfur dioxide	1599 non-null	float64
6	total sulfur dioxide	1599 non-null	float64
7	density	1599 non-null	float64
8	рН	1599 non-null	float64
9	sulphates	1599 non-null	float64
10	alcohol	1599 non-null	float64
11	quality	1599 non-null	int64

dtypes: float64(11), int64(1)

memory usage: 150.0 KB

```
In [5]: # to display summary of statistics
sd.describe()
```

Out[5]:

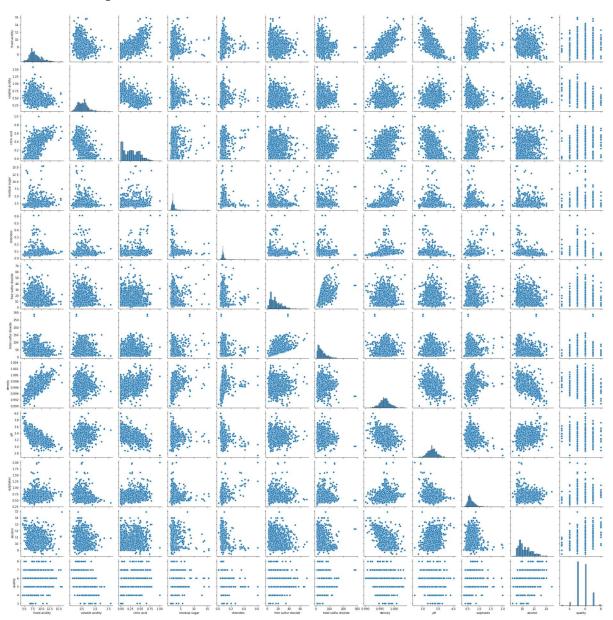
	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfu dioxid
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.00000
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.46779
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.89532
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.00000
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.00000
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.00000
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.00000
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.00000

```
In [6]: #to display colums heading
sd.columns
```

EDA and visualization

In [7]: sns.pairplot(sd)

Out[7]: <seaborn.axisgrid.PairGrid at 0x17589b8c6a0>

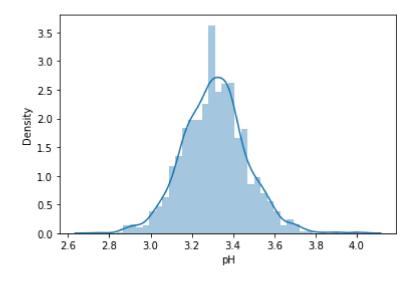


In [8]: sns.distplot(sd['pH'])

C:\ProgramData\Anaconda3\lib\site-packages\seaborn\distributions.py:2557: Fut ureWarning: `distplot` is a deprecated function and will be removed in a futu re version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for hi stograms).

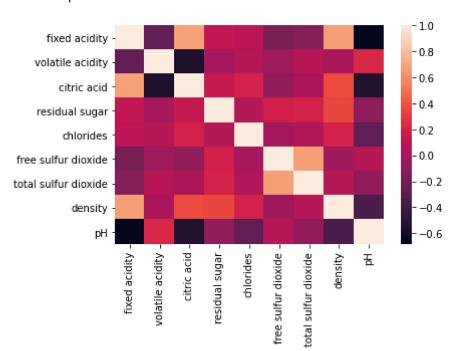
warnings.warn(msg, FutureWarning)

Out[8]: <AxesSubplot:xlabel='pH', ylabel='Density'>



In [11]: | sns.heatmap(sd1.corr())

Out[11]: <AxesSubplot:>



TO TRAIN THE MODEL _MODEL BUILDING

we are goint train Liner Regression model; we need to split out the data into two varibles x and y where x is independent on x (output) and y is dependent on x(output) adress coloumn as it is not required our model

```
In [12]: x= sd1[['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar',
                  chlorides', 'free sulfur dioxide', 'total sulfur dioxide', 'density']]
         y=sd1['pH']
In [13]: # To split my dataset into training data and test data
          from sklearn .model_selection import train_test_split
          x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.3)
In [16]: from sklearn.linear_model import LinearRegression
          lr=LinearRegression()
          lr.fit(x train,y train)
Out[16]: LinearRegression()
In [17]: print(lr.intercept )
          -24.2319398828055
         coeff= pd.DataFrame(lr.coef_,x.columns,columns=['Co-efficient'])
In [18]:
          coeff
Out[18]:
                           Co-efficient
                fixed acidity
                             -0.080467
              volatile acidity
                             0.030126
                 citric acid
                             0.029432
              residual sugar
                            -0.005546
                  chlorides
                            -0.707034
```

free sulfur dioxide

total sulfur dioxide

density

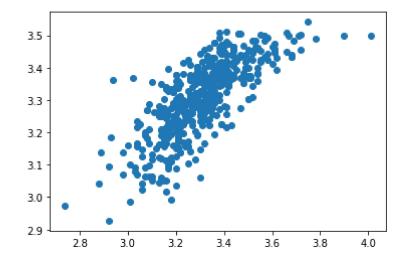
0.002009

-0.001239

28.382052

```
In [19]: prediction = lr.predict(x_test)
plt.scatter(y_test,prediction)
```

Out[19]: <matplotlib.collections.PathCollection at 0x17597229850>



```
In [20]: print(lr.score(x_test,y_test))
```

0.5773760251066155

```
In [ ]:
```