PROJECT DEVELOPMENT PHASE

SPRINT-1

TEAM ID	PNT2022TMID37730
PROJECT TITLE	Efficient Water Quality Analysis And Prediction Using machine Learning
MAXIMUM MARKS	8 Marks

```
# pip install matplotlib
```

In [427…

```
# pip install seaborn
```

In [428…

```
# import all needed libraries

import pandas as pd
import numpy as np
import os
import matplotlib.pyplot as plt
import seaborn as sns

from sklearn.model_selection import train_test_split

from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import OneHotEncoder
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import MinMaxScaler


from sklearn.ensemble import RandomForestRegressor
from sklearn.tree import DecisionTreeRegressor
from sklearn.linear_model import LogisticRegression
from sklearn.linear_model import LinearRegression

from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score,r2_score
from sklearn.metrics import confusion_matrix, classification_report
```

In [429…

```
# read csv file using pandas

df=pd.read_csv('Book0.1.csv')
df.head()
```

Out[429…

	Unnamed: 0	STATION CODE	LOCATIONS	STATE	Temp	D.O. (mg/l)	PH	CONDUCTIVITY (µmhos/cm)	B.O.D. (mg/l)	NITRATENAN N+ NITRITENANN (mg/l)	FECAL COLIFORM (MPN/100ml)	TOTAL COLIFORM (MPN/100ml)Mean	year
0	1	1399	ZUARI AT D/S OF PT. WHERE KUMBARJRIA CANAL JOI...	GOA	29.8	5.7	7.2	189	2	0.2	4953	8391	2014
1	2	1475	ZUARI AT PANCHAWADI	GOA	29.5	6.3	6.9	179	1.7	0.1	3243	5330	2014
2	3	3181	RIVER ZUARI AT BORIM	GOA	29.7	5.8	6.9	64	3.8	0.5	5382	8443	2014

```
df.head()
```

Out[429…

	Unnamed: 0	STATION CODE	LOCATIONS	STATE	Temp	D.O. (mg/l)	PH	CONDUCTIVITY (µmhos/cm)	B.O.D. (mg/l)	NITRATENAN N+ NITRITENANN (mg/l)	FECAL COLIFORM (MPN/100ml)	TOTAL COLIFORM (MPN/100ml)Mean	year
0	1	1399	ZUARI AT D/S OF PT. WHERE KUMBARJRIA CANAL JOI...	GOA	29.8	5.7	7.2	189	2	0.2	4953	8391	2014
1	2	1475	ZUARI AT PANCHAWADI	GOA	29.5	6.3	6.9	179	1.7	0.1	3243	5330	2014
2	3	3181	RIVER ZUARI AT BORIM BRIDGE	GOA	29.7	5.8	6.9	64	3.8	0.5	5382	8443	2014
3	4	3182	RIVER ZUARI AT MARCAIM JETTY	GOA	29.5	5.8	7.3	83	1.9	0.4	3428	5500	2014
4	5	1400	MANDOVI AT NEGHBOURHOOD OF PANAJI, GOA	GOA	30	5.5	7.4	81	1.5	0.1	2853	4049	2014

In [430…

```
# no need this because it give value error of continuous value error
df.drop(['Unnamed: 0'],inplace=True,axis=1)
```

In [431…

```
l=['Temp','D.O. (mg/l)','PH','CONDUCTIVITY (µmhos/cm)','B.O.D. (mg/l)','NITRATENAN N+ NITRITENANN (mg/l)','FECAL COLIFORM (MPN/100ml)','TOTAL COLIFORM
df[df[l]=="NAN"]
```

Out[431…

	STATION CODE	LOCATIONS	STATE	Temp	D.O. (mg/l)	PH	CONDUCTIVITY (µmhos/cm)	B.O.D. (mg/l)	NITRATENAN N+ NITRITENANN (mg/l)	FECAL COLIFORM (MPN/100ml)	TOTAL COLIFORM (MPN/100ml)Mean	year
0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
...	...	...	...	...	...	...	...	...	...	...	...	...
890	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
891	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN

In [432…

```
# drop the all nan and empty data

for i in l:
    df.drop(df.index[df[i]=="NAN"],inplace=True,axis=0)
    df.drop(df.index[df[i]==" "],inplace=True,axis=0)
```

In [433…

```
# convert all data type into float

for i in l:
    df[i]=df[i].astype('float')
```

In [434…

```
df.describe()
```

Out[434…

	STATION CODE	Temp	D.O. (mg/l)	PH	CONDUCTIVITY (µmhos/cm)	B.O.D. (mg/l)	NITRATENAN N+ NITRITENANN (mg/l)	FECAL COLIFORM (MPN/100ml)	TOTAL COLIFORM (MPN/100ml)Mean	year
count	879.000000	879.000000	879.000000	879.000000	879.000000	879.000000	879.000000	8.790000e+02	8.790000e+02	879.000000
mean	2194.318544	26.093743	6.310728	7.232628	1650.803185	4.924061	1.644994	6.869346e+05	1.110502e+06	2012.559727
std	807.389674	3.261618	1.300479	0.606125	4927.777303	12.770214	2.896984	1.209315e+07	2.069025e+07	1.102190
min	17.000000	16.000000	0.200000	2.600000	27.000000	0.100000	0.000000	2.000000e+00	4.000000e+00	2010.000000
25%	1548.000000	24.450000	5.900000	6.950000	75.000000	1.200000	0.280000	2.550000e+01	9.000000e+01	2012.000000
50%	2290.000000	27.000000	6.700000	7.200000	159.000000	1.800000	0.590000	1.990000e+02	5.000000e+02	2013.000000
75%	2708.000000	28.400000	7.100000	7.600000	505.500000	3.300000	1.775000	9.965000e+02	2.425000e+03	2014.000000
max	3473.000000	33.000000	9.900000	8.400000	37227.000000	185.800000	20.300000	2.725216e+08	5.110909e+08	2014.000000

In [ ]:

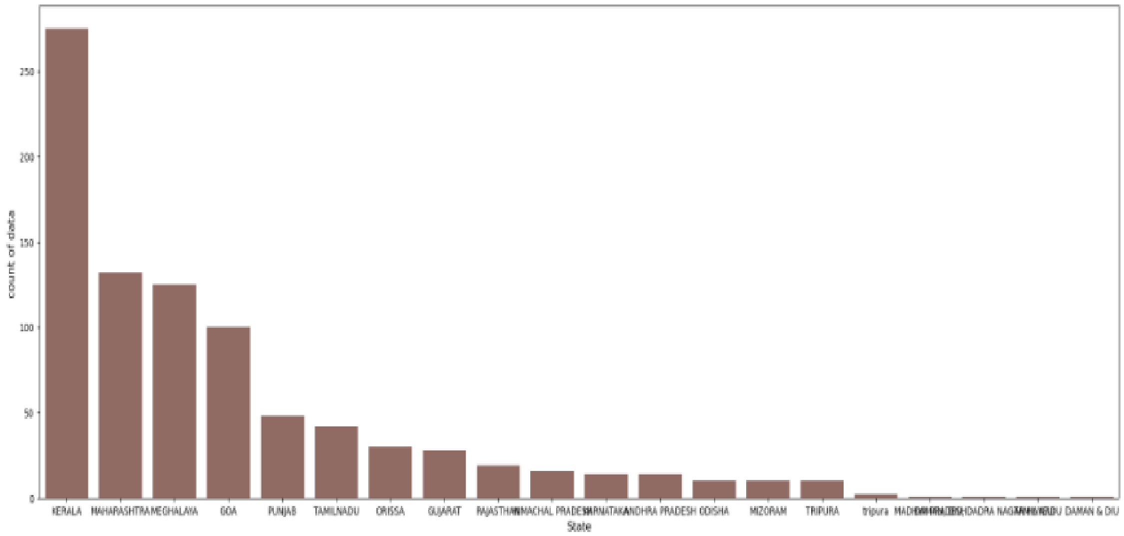
In [435…

```
# viewing the column of state

color=sns.color_palette()

int_level = df['STATE'].value_counts()

plt.figure(figsize=(25,8))
sns.barplot(int_level.index,int_level.values,alpha=0.9,color=color[5])
plt.ylabel('count of data ',fontsize=12)
```

In [435…

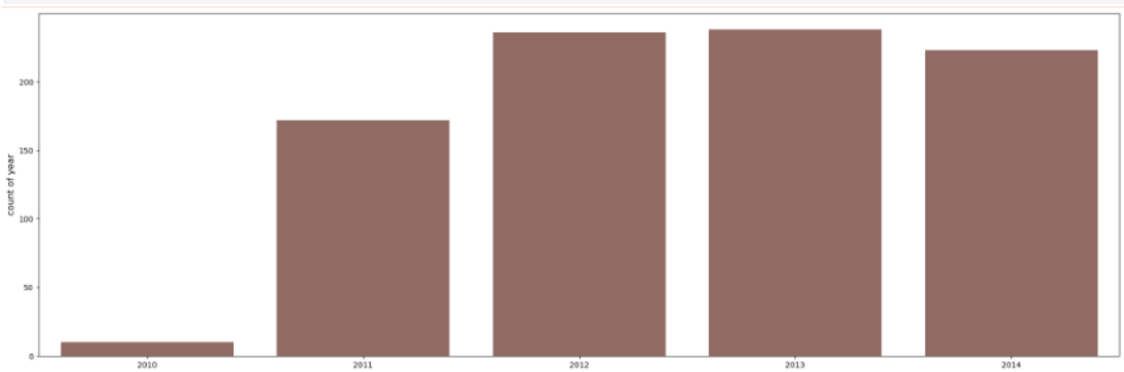
```python
# viewing the column of state

color=sns.color_palette()

int_level = df['STATE'].value_counts()

plt.figure(figsize=(25,8))
sns.barplot(int_level.index,int_level.values,alpha=0.9,color=color[5])
plt.ylabel('count of data ',fontsize=12)
plt.xlabel('State',fontsize=12)
plt.show()
```

```
C:\ProgramData\Anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```



In [436…

```python
# viewing the column data of year

color=sns.color_palette()

int_level = df['year'].value_counts()
```



In [ ]:

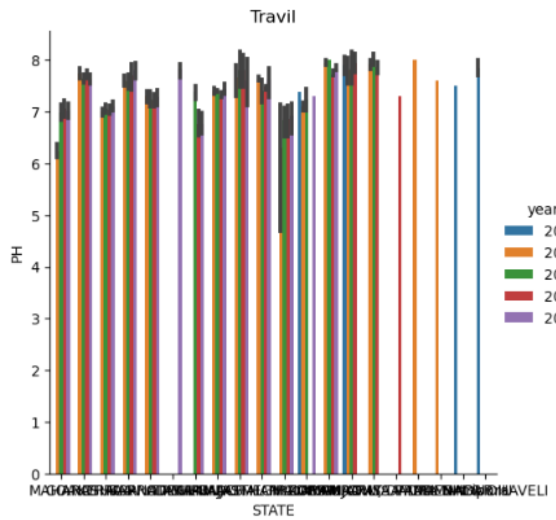
In [437…

```python
# State and year comparision with ph rate

plt.figure(figsize=(20,20))
g=sns.catplot(data=df,kind="bar",x="STATE",y="PH",hue="year")
plt.title("Travil")
```

In [437…

```
# State and year comparision with ph rate

plt.figure(figsize=(20,20))
g=sns.catplot(data=df,kind="bar",x="STATE",y="PH",hue="year")
plt.title("Travil")
```

Out[437… Text(0.5, 1.0, 'Travil')



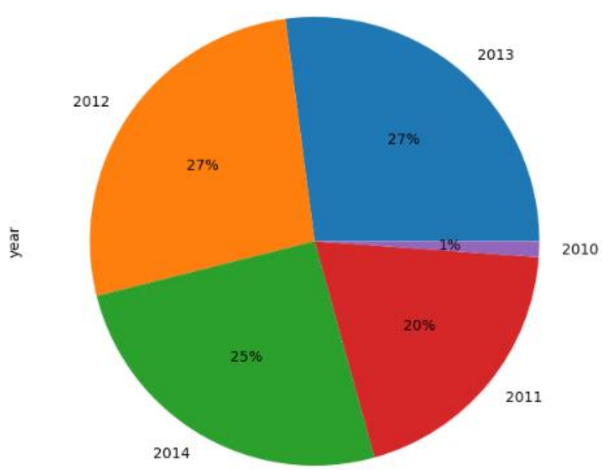
In [438…

```
df['year'].value_counts().plot(kind='pie',figsize=(7,7),autopct='%1.0f%%')
```

In [438…

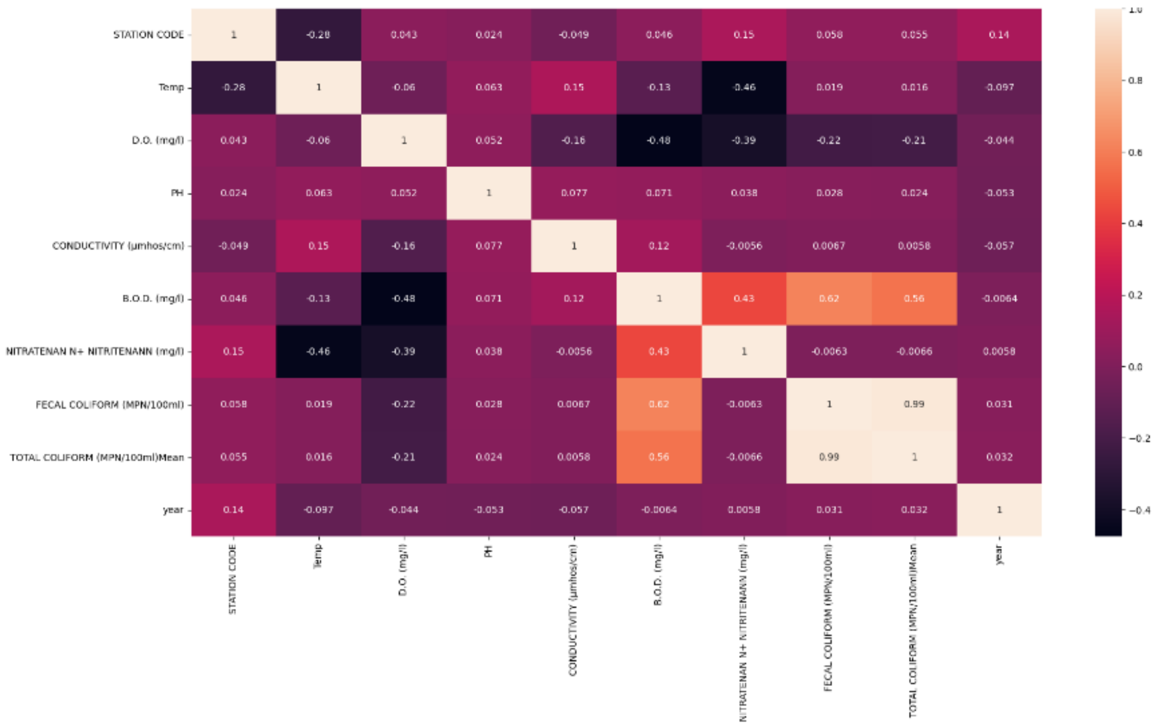

```
df['year'].value_counts().plot(kind='pie',figsize=(7,7),autopct='%1.0f%%')
```


Out[438…



In [439…

```
plt.figure(figsize=(20,10))
sns.heatmap(df.corr(),annot=True)
plt.show()
```



In [440…

```
# Create column for the pure water range and split with undrikingable water

df['PH Range']=pd.cut(x=df['PH'],bins=[0,6.49,7.5,14],labels=['0-6.49','6.5-7.5','7.5-14'])
df['Water Qu']=df['PH Range'].map({'6.5-7.5':1,'7.5-14':0,'0-6.49':0})

df.drop(df.index[df['PH Range']=="NaN"],inplace=True,axis=0)
```

In [441…

```
df.describe()
```

Out[441…

	STATION CODE	Temp	D.O. (mg/l)	PH	CONDUCTIVITY (µmhos/cm)	B.O.D. (mg/l)	NITRATENAN N+ NITRITENANN (mg/l)	FECAL COLIFORM (MPN/100ml)	TOTAL COLIFORM (MPN/100ml)Mean	year	Water Qu
count	879.000000	879.000000	879.000000	879.000000	879.000000	879.000000	879.000000	8.790000e+02	8.790000e+02	879.000000	879.000000
mean	2194.318544	26.093743	6.310728	7.232628	1650.803185	4.924061	1.644994	6.869346e+05	1.110502e+06	2012.559727	0.673493
std	807.389674	3.261618	1.300479	0.606125	4927.777303	12.770214	2.896984	1.209315e+07	2.069025e+07	1.102190	0.469202
min	17.000000	16.000000	0.200000	2.600000	27.000000	0.100000	0.000000	2.000000e+00	4.000000e+00	2010.000000	0.000000
25%	1548.000000	24.450000	5.900000	6.950000	75.000000	1.200000	0.280000	2.550000e+01	9.000000e+01	2012.000000	0.000000
50%	2290.000000	27.000000	6.700000	7.200000	159.000000	1.800000	0.590000	1.990000e+02	5.000000e+02	2013.000000	1.000000
75%	2708.000000	28.400000	7.100000	7.600000	505.500000	3.300000	1.775000	9.965000e+02	2.425000e+03	2014.000000	1.000000
max	3473.000000	33.000000	9.900000	8.400000	37227.000000	185.800000	20.300000	2.725216e+08	5.110909e+08	2014.000000	1.000000

In [ ]:

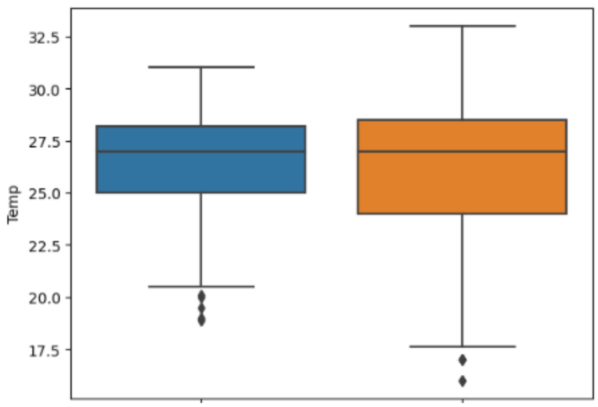
In [ ]:

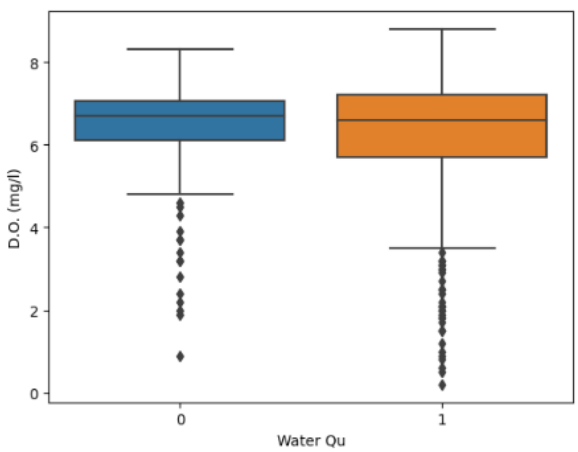
In [442…

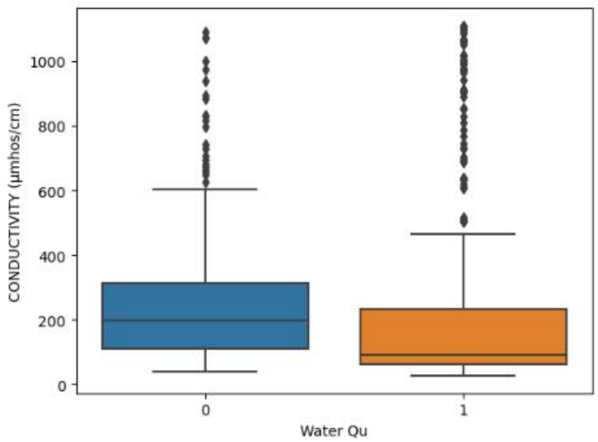
```
# Box plot for comparing the ph with other column and finding the outliers


col_pruning=['Temp','D.O. (mg/l)','CONDUCTIVITY (µmhos/cm)','B.O.D. (mg/l)','NITRATENAN N+ NITRITENANN (mg/l)','FECAL COLIFORM (MPN/100ml)']

for col in col_pruning:
    print("\n\n")
    coldesc=df[col].describe()
    col_IQR=coldesc[6]-coldesc[4]
    col_Lower=coldesc[4]-(1.5*col_IQR)
```

In [442…

```python
# Box plot for comparing the ph with other column and finding the outliers


col_pruning=['Temp','D.O. (mg/l)','CONDUCTIVITY (µmhos/cm)','B.O.D. (mg/l)','NITRATENAN N+ NITRITENANN (mg/l)','FECAL COLIFORM (MPN/100ml)']

for col in col_pruning:
    print("\n\n")
    coldesc=df[col].describe()
    col_IQR=coldesc[6]-coldesc[4]
    col_Lower=coldesc[4]-(1.5*col_IQR)

    col_Higher=coldesc[6]+(1.5*col_IQR)

#     print(col_Lower,col_Higher)
#     df.drop(df.index[(df[col]col_Higher)],inplace=True,axis=0)
    df.drop(df.index[(df[col]>col_Higher)],inplace=True,axis=0)
    sns.boxplot(x='Water Qu',y=df[col],data=df)
    plt.show()


    print(df[col].describe())
```








```
count      745.000000
mean       222.344966
std        243.275990
min         27.000000
25%         69.000000
50%        120.000000
75%        274.000000
max       1110.000000
Name: CONDUCTIVITY (µmhos/cm), dtype: float64
```

Water Qu

```
count      486.000000
mean       284.436214
std        383.079776
min          2.000000
25%         22.000000
50%        131.500000
75%        380.750000
max       1850.000000
Name: FECAL COLIFORM (MPN/100ml), dtype: float64
```

In [ ]:

In [443…
```
df.drop(['year'],inplace=True,axis=1)
```

In [444…
```
df.drop(['STATION CODE','LOCATIONS','STATE','PH Range','Water Qu'],inplace=True,axis=1)
```

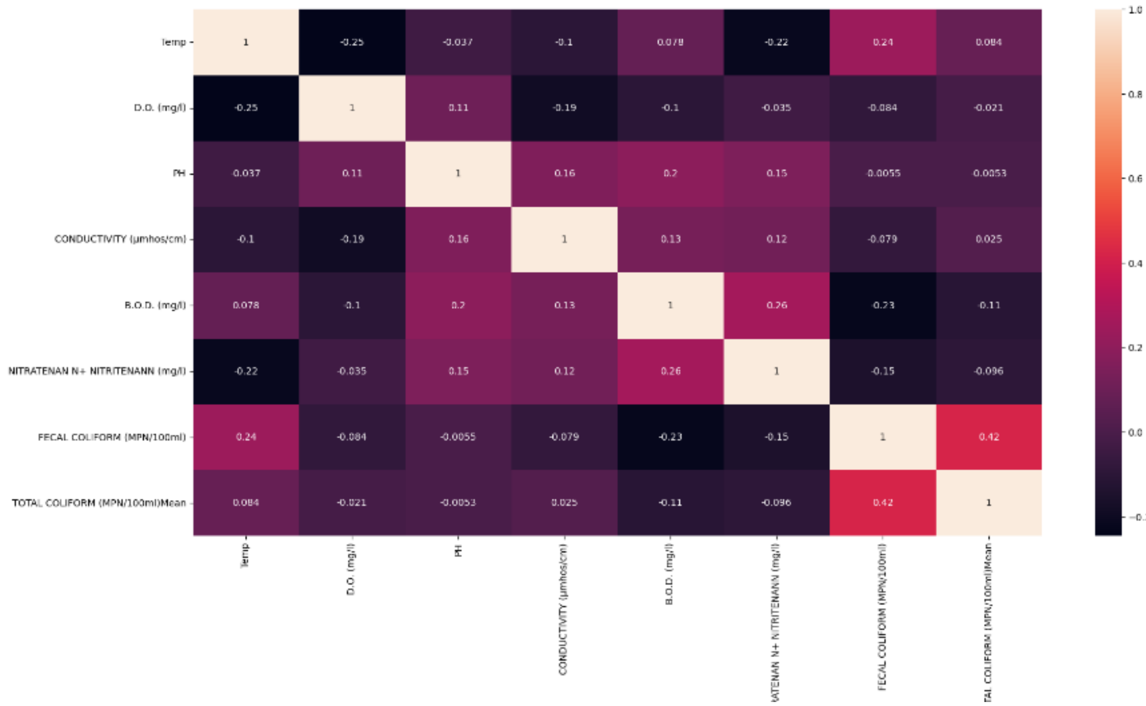
In [ ]:

In [445…
```
# transforming your data so that it fits within a specific scale

mm=MinMaxScaler()
df[l]=mm.fit_transform(df[l])
df.describe()
```

Out[445…

	Temp	D.O. (mg/l)	PH	CONDUCTIVITY (µmhos/cm)	B.O.D. (mg/l)	NITRATENAN N+ NITRITENANN (mg/l)	FECAL COLIFORM (MPN/100ml)	TOTAL COLIFORM (MPN/100ml)Mean
count	486.000000	486.000000	486.000000	486.000000	486.000000	486.000000	486.000000	486.000000
mean	0.600061	0.724280	0.813046	0.147103	0.307922	0.254203	0.152833	0.013122
std	0.157548	0.118957	0.101386	0.177769	0.204720	0.214196	0.207294	0.047275
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	0.534091	0.695122	0.754386	0.038853	0.150000	0.095238	0.010823	0.001265
50%	0.629870	0.743902	0.807018	0.077706	0.233333	0.190476	0.070076	0.005544
75%	0.701299	0.792683	0.877193	0.184089	0.450000	0.351190	0.204951	0.014127
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000

```
# heat map for finding the corrlation between columns

plt.figure(figsize=(20,10))
sns.heatmap(df.corr(),annot=True)
plt.show()
```



Split the Data

In [449…

```
#  train and test date spliting

x_train, x_test, y_train, y_test= train_test_split(x, y, test_size= 0.25, random_state=42)
```

In [450…

```
x_train
```

Out[450…

	Temp	D.O. (mg/l)	CONDUCTIVITY (µmhos/cm)	B.O.D. (mg/l)	NITRATENAN N+ NITRITENANN (mg/l)	FECAL COLIFORM (MPN/100ml)	TOTAL COLIFORM (MPN/100ml)Mean
795	0.577922	0.804878	0.023127	0.083333	0.071429	0.160173	0.010290
105	0.623377	0.560976	0.025902	0.083333	0.333333	0.091450	0.004655
355	0.785714	0.573171	0.066605	0.450000	0.376190	0.056277	0.007819
830	0.662338	0.682927	0.015726	0.100000	0.100000	0.385823	0.024496
775	0.500000	0.768293	0.164662	0.350000	0.442857	0.000000	0.000768
...	...	...	...	...	...	...	...
226	0.642857	0.573171	0.730805	0.450000	0.476190	0.003788	0.000286
532	0.545455	0.731707	0.037003	0.166667	0.252381	0.147727	0.010033
661	0.415584	0.658537	0.407956	0.216667	0.204762	0.001623	0.000181
808	0.584416	0.817073	0.024977	0.200000	0.195238	0.223485	0.013694
220	0.629870	0.682927	0.127660	0.333333	0.000000	0.151515	0.005062

364 rows × 7 columns

In [451…

```
# print(list(x_train.iloc[1]))
```

LinearRegression

In [452…
```
# fit the Linear regression model

regressor= LinearRegression()
regressor.fit(x_train, y_train)
y_pred= regressor.predict(x_test)
# x_pred= regressor.predict(x_train)
```

In [453…
```
ypred_pd=pd.DataFrame({'WQ':y_test.values,'WQ_Pred':y_pred})
ypred_pd['predicted']=ypred_pd['WQ_Pred'].map(lambda x:1 if x>0.5 else 0)
ypred_pd['WQ']=ypred_pd['WQ'].map(lambda x:1 if x>0.7 else 0)
ypred_pd.head()
```

Out[453…

	WQ	WQ_Pred	predicted
0	1	0.795986	1
1	1	0.845279	1
2	1	0.789093	1
3	1	0.802417	1
4	1	0.861372	1

In [454…
```
confusion=confusion_matrix(ypred_pd['WQ'],ypred_pd['predicted'])
print(confusion)
```

```
[[  0   8]
 [  0 114]]
```

In [455…
```
print(accuracy_score(ypred_pd['WQ'],ypred_pd['predicted']))
```

```
0.9344262295081968
```

Pickle

In [462…
```
# Load the model into pickle for serializing and deserializing a Python object structure
```

In [463…
```
import pickle
```

In [464…
```
with open('model_pkl', 'wb') as files:
    pickle.dump(regressor, files)
with open('model_pkl' , 'rb') as f:
    lr = pickle.load(f)
lr.predict([list(x_train.iloc[1])])
```

```
C:\ProgramData\Anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but LinearRegression was fitted with feature names
  warnings.warn(
```

Out[464…
```
array([0.74676269])
```

In [ ]:

In [465…
```
with open('model_pkl', 'wb') as files:
    pickle.dump(clf_gini, files)
with open('model_pkl' , 'rb') as f:
    lr = pickle.load(f)
lr.predict([list(x_train.iloc[1])])
```

```
C:\ProgramData\Anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeRegressor was fitted with feature names
  warnings.warn(
```

Out[465…
```
array([0.73684211])
```

In [ ]:

In [466…
```
with open('model_pkl', 'wb') as files:
    pickle.dump(forest_model, files)
with open('model_pkl' , 'rb') as f:
```

In [ ]:

In [465…

```
with open('model_pkl', 'wb') as files:
    pickle.dump(clf_gini, files)
with open('model_pkl' , 'rb') as f:
    lr = pickle.load(f)
lr.predict([list(x_train.iloc[1])])
```

```
C:\ProgramData\Anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeRegressor was fitted
with feature names
  warnings.warn(
```

Out[465…

```
array([0.73684211])
```

In [ ]:

In [466…

```
with open('model_pkl', 'wb') as files:
    pickle.dump(forest_model, files)
with open('model_pkl' , 'rb') as f:
    lr = pickle.load(f)
lr.predict([list(x_train.iloc[1])])
```

```
C:\ProgramData\Anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but RandomForestRegressor was fitted
with feature names
  warnings.warn(
```

Out[466…

```
array([0.74894737])
```

In [ ]: