PROJECT DEVELOPMENT PHASE - SPRIT II

Date	14 October 2022
Team ID	PNT2022TMID54173
Project Title	Water Quality Analysis and Prediction using Machine Learning
Team Leader	Roshini R
Team Member	Sona E Preethi S Subhashree M
Maximum Marks	8 Marks

```
# pip install matplotlib

# pip install seaborn


# 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



# read csv file using pandas

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

   Unnamed: 0 STATION CODE \
0           1   1399
```

```
1            2   1475
2            3   3181
3            4   3182
4            5   1400

                                             LOCATIONS STATE Temp D.O.
(mg/l) \
0 ZUARI AT D/S OF PT. WHERE KUMBARJRIA CANAL JOI...     GOA 29.8
5.7
1                               ZUARI AT PANCHAWADI   GOA 29.5
6.3
2                        RIVER ZUARI AT BORIM BRIDGE GOA 29.7
5.8
3                        RIVER ZUARI AT MARCAIM JETTY GOA 29.5
5.8
4                        MANDOVI AT NEGHBOURHOOD OF PANAJI, GOA  GOA
                           30
5.5

    PH CONDUCTIVITY (µmhos/cm) B.O.D. (mg/l) \
0  7.2      189   2
1  6.9      179   1.7
2  6.9      64    3.8
3  7.3      83    1.9
4  7.4      81    1.5

  NITRATENAN N+ NITRITENANN (mg/l) FECAL COLIFORM (MPN/100ml) \
0                            0.2    4953
1                            0.1    3243
2                            0.5    5382
3                            0.4    3428
4                            0.1    2853

  TOTAL COLIFORM (MPN/100ml)Mean year
0                          8391 2014
1                          5330 2014
2                          8443 2014
3                          5500 2014
4                          4049 2014
```

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

```
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 (MPN/100ml)Mean']
df[df[l]=="NAN"]
```

```
     STATION CODE LOCATIONS STATE Temp D.O. (mg/l) PH \
0              NaN      NaN   NaN NaN    NaN NaN
```

```
1              NaN     NaN   NaN NaN    NaN NaN
2              NaN     NaN   NaN NaN    NaN NaN
3              NaN     NaN   NaN NaN    NaN NaN
4              NaN     NaN   NaN NaN    NaN NaN .. ...   ...   ... ...
                  ... ..
890            NaN        NaN    NaN   NaN           NaN NaN
891            NaN        NaN    NaN   NaN           NaN NaN
892            NaN        NaN    NaN   NaN           NaN NaN
893            NaN        NaN    NaN   NaN           NaN NaN
894            NaN        NaN    NaN   NaN           NaN NaN
     CONDUCTIVITY (µmhos/cm) B.O.D. (mg/l) NITRATENAN N+ NITRITENANN
(mg/l) \
0                        NaN     NaN
NaN
1                        NaN     NaN
NaN
2                        NaN     NaN
NaN
3                        NaN     NaN
NaN
4                        NaN     NaN
NaN
..                        ...           ...
...
890                      NaN     NaN
NaN
891                      NaN     NaN
NaN
892                      NaN     NaN
NaN
893                      NaN     NaN
NaN
894                      NaN     NaN
NaN
    FECAL COLIFORM (MPN/100ml) TOTAL COLIFORM (MPN/100ml)Mean   year
0                          NaN                          NaN    NaN
1                          NaN                          NaN    NaN
2                          NaN                          NaN    NaN
3                          NaN                          NaN    NaN
4                          NaN                          NaN    NaN
..                         ...                          ...    ...
890                        NaN                          NaN    NaN
891                        NaN                          NaN    NaN
892                        NaN                          NaN    NaN
893                        NaN                          NaN    NaN
894                        NaN                          NaN    NaN
[895 rows x 12 columns] # 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)

# convert all data type into float

for i in l:

df[i]=df[i].astype('float')

df.describe()
```

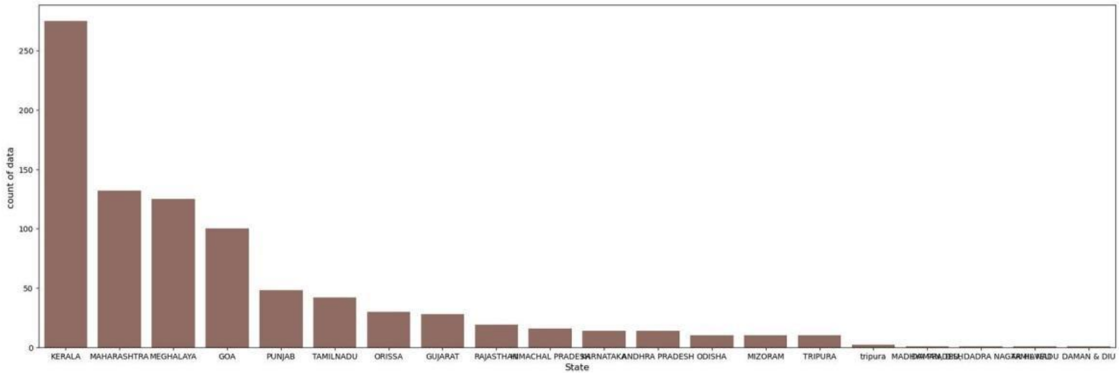
```
       STATION CODE        Temp D.O. (mg/l)           PH \

count    879.000000 879.000000 879.000000 879.000000

mean   2194.318544    26.093743     6.310728    7.232628

std     807.389674     3.261618     1.300479    0.606125

min      17.000000    16.000000     0.200000    2.600000

25%    1548.000000    24.450000     5.900000    6.950000

50%    2290.000000    27.000000     6.700000    7.200000

75%    2708.000000    28.400000     7.100000    7.600000

max    3473.000000    33.000000     9.900000    8.400000

       CONDUCTIVITY (µmhos/cm) B.O.D. (mg/l) \
count               879.000000     879.000000

mean               1650.803185       4.924061

std                4927.777303      12.770214

min                  27.000000       0.100000

25%                  75.000000       1.200000

50%                 159.000000       1.800000

75%                 505.500000       3.300000

max               37227.000000     185.800000

       NITRATENAN N+ NITRITENANN (mg/l) FECAL COLIFORM (MPN/100ml)   \
count                        879.000000                8.790000e+02

mean                           1.644994                6.869346e+05

std                            2.896984                1.209315e+07

min                            0.000000                2.000000e+00

25%                            0.280000                2.550000e+01
```

```
50%                        0.590000                 1.990000e+02

75%                        1.775000                 9.965000e+02

max                       20.300000                 2.725216e+08
```

```
       TOTAL COLIFORM (MPN/100ml)Mean          year
count                      8.790000e+02   879.000000

mean                        1.110502e+06 2012.559727

std                        2.069025e+07     1.102190

min                         4.000000e+00 2010.000000

25%                         9.000000e+01 2012.000000

50%                         5.000000e+02 2013.000000

75%                         2.425000e+03 2014.000000

max                         5.110909e+08 2014.000000
```

```
# 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()
```

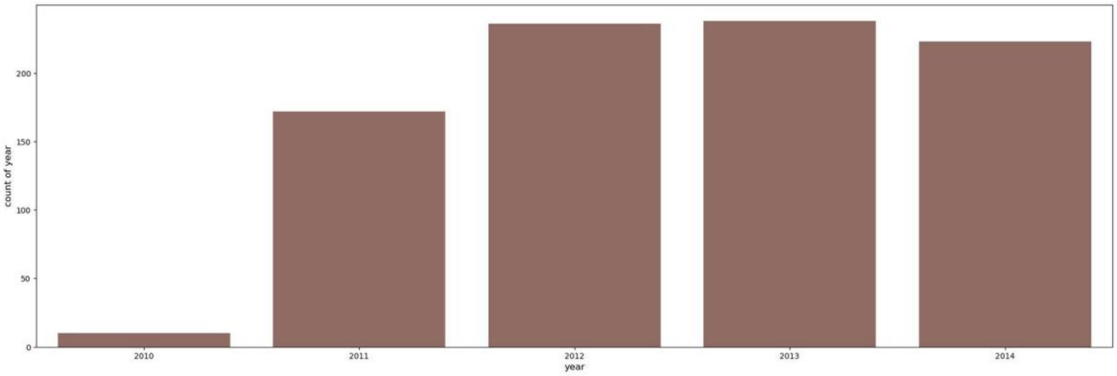
```
C:\ProgramData\Anaconda3\lib\site-packages\seaborn\_decorators.py:36:
FutureWarning: Pass the following variables as keyword args: x, y.
From version 0.12, the only valid positional argument will be `data`,
and passing other arguments without an explicit keyword will result in
an error or misinterpretation.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



```
# viewing the column data of year
```

```
color=sns.color_palette() int_level =

df['year'].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 year',fontsize=12) plt.xlabel('year',fontsize=12)
plt.show()
```

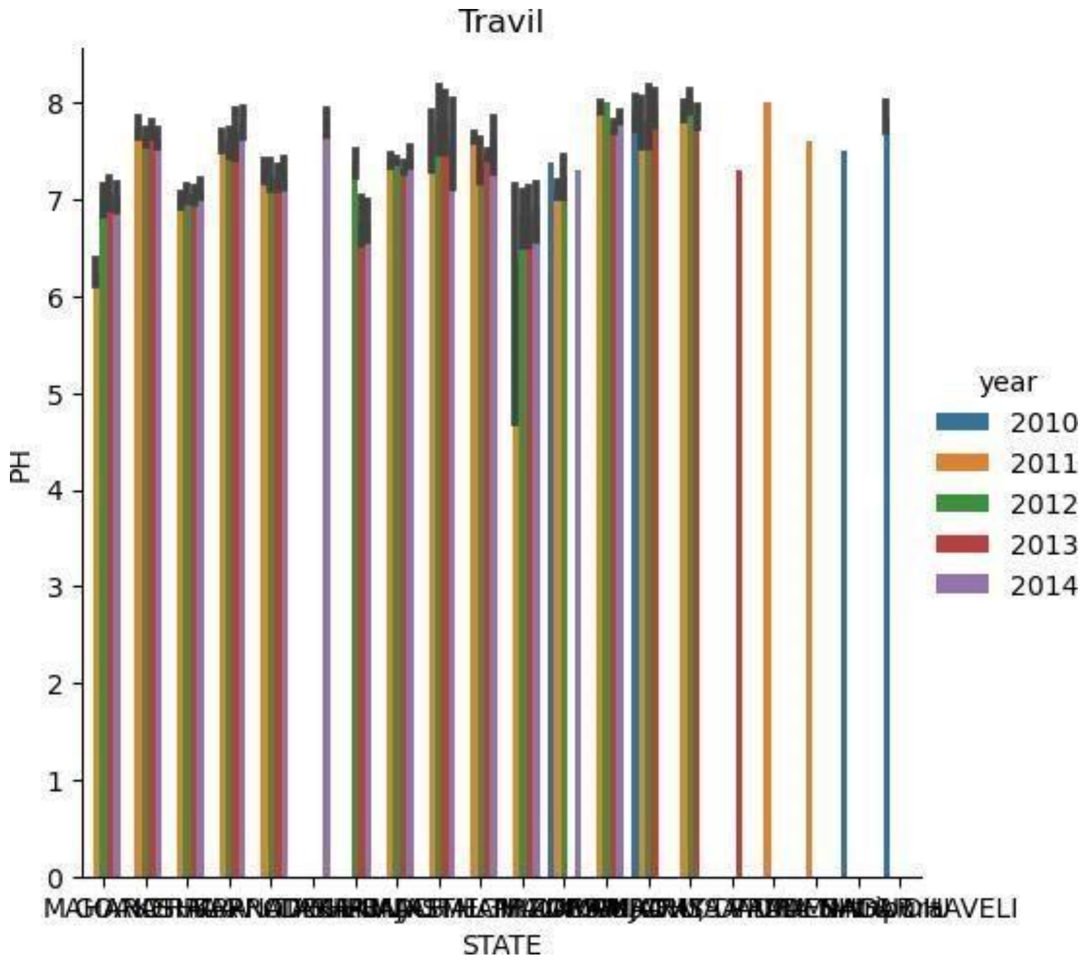
```
C:\ProgramData\Anaconda3\lib\site-packages\seaborn\_decorators.py:36:
FutureWarning: Pass the following variables as keyword args: x, y.
From version 0.12, the only valid positional argument will be `data`,
and passing other arguments without an explicit keyword will result in
an error or misinterpretation.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



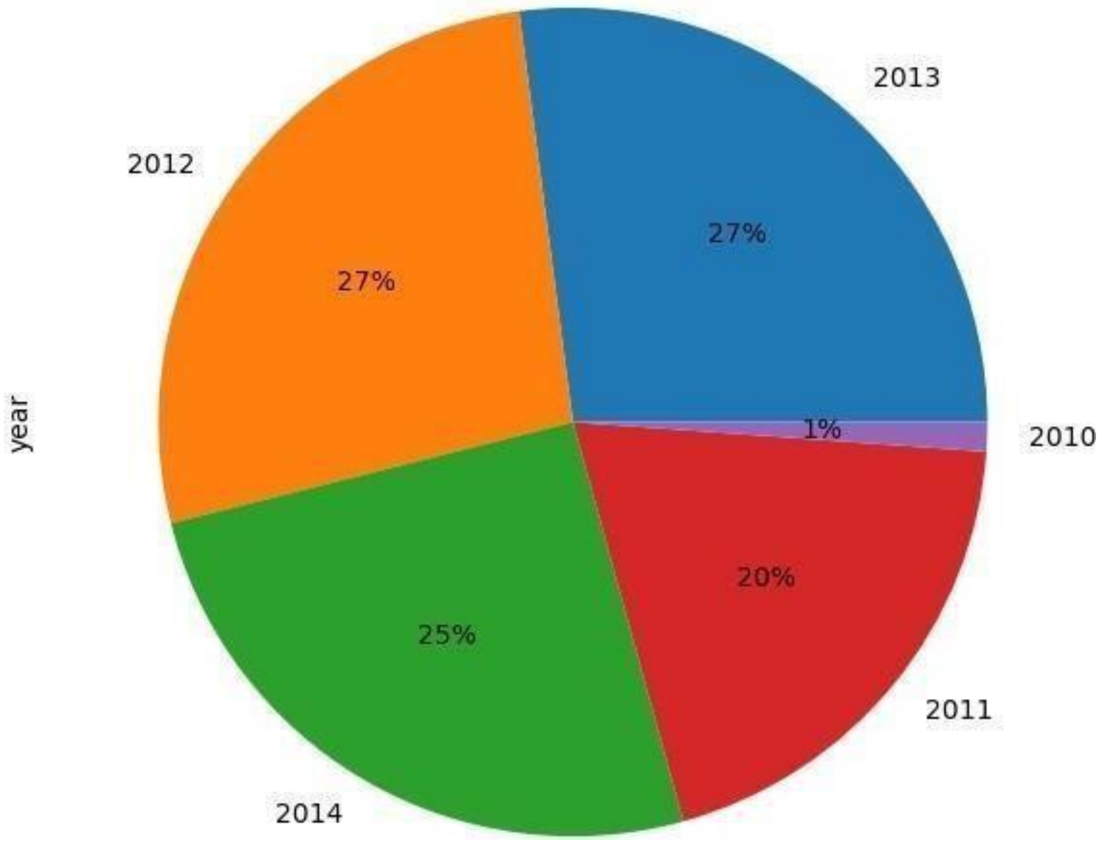
```
# State and year comparision with ph rate

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

```
Text(0.5, 1.0, 'Travil')
```

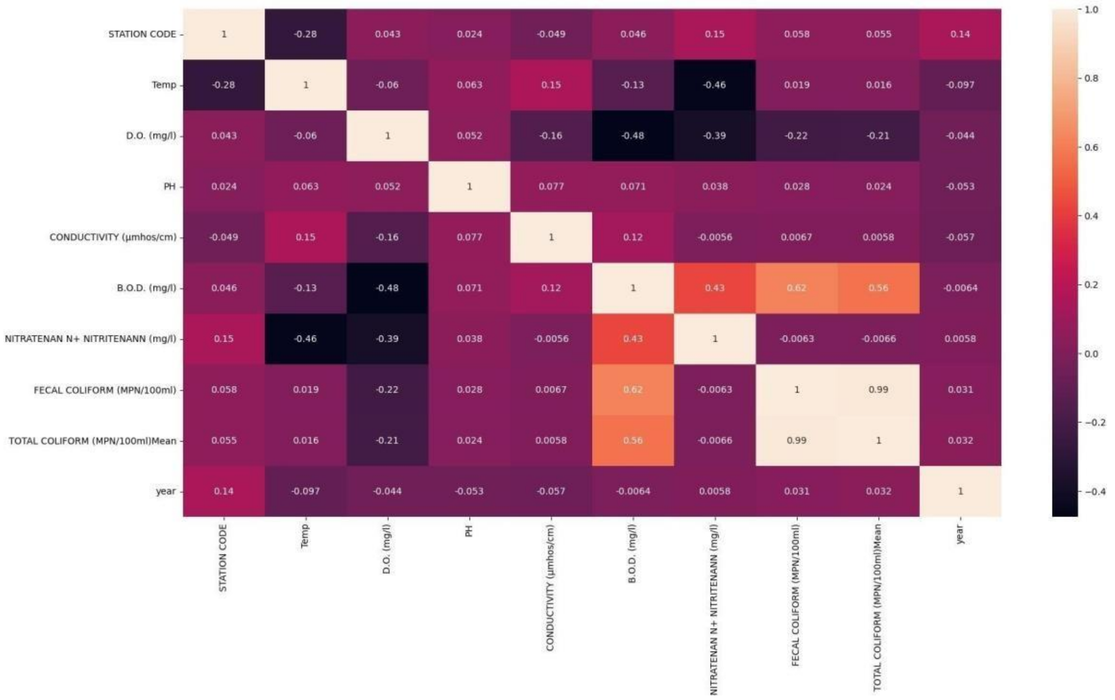
```
<Figure size 2000x2000 with 0 Axes>
```



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



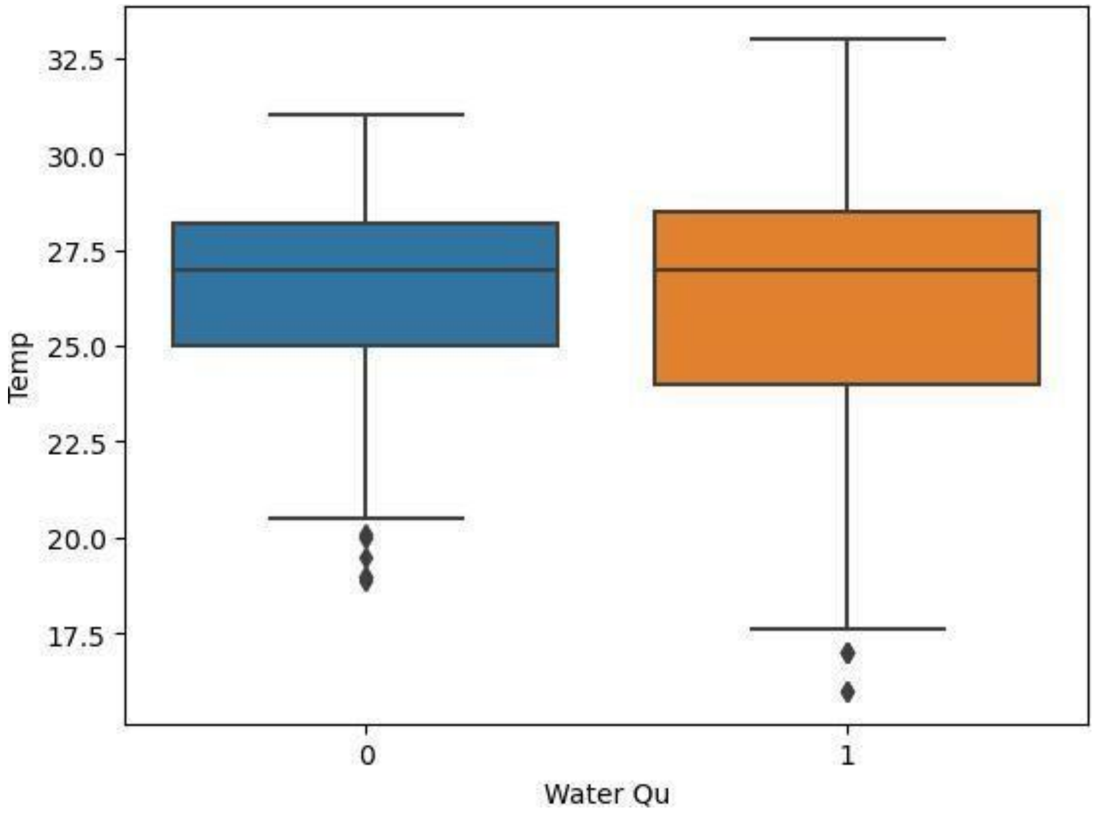
```
plt.figure(figsize=(20,10))
sns.heatmap(df.corr(),annot=True)
plt.show()
```



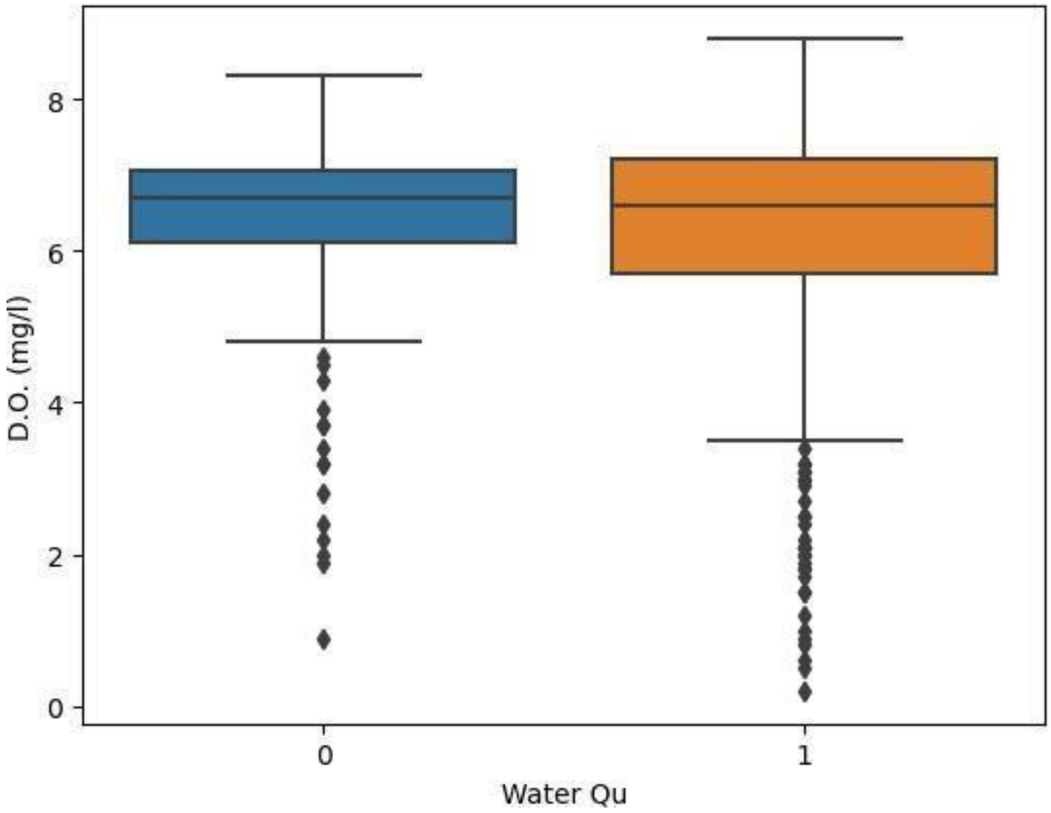
```
# Create column for the pure water range and split with undrikingable water

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)   df.describe()
       STATION CODE         Temp  D.O. (mg/l)          PH  \
count    879.000000  879.000000   879.000000  879.000000
mean    2194.318544    26.093743     6.310728    7.232628
std      807.389674     3.261618     1.300479    0.606125
min       17.000000    16.000000     0.200000    2.600000
25%     1548.000000    24.450000     5.900000    6.950000
50%     2290.000000    27.000000     6.700000    7.200000
75%     2708.000000    28.400000     7.100000    7.600000
max     3473.000000    33.000000     9.900000    8.400000

       CONDUCTIVITY (µmhos/cm)  B.O.D. (mg/l)  \
count               879.000000     879.000000
mean               1650.803185       4.924061
std                4927.777303      12.770214
min                  27.000000       0.100000
```

```
25%                    75.000000       1.200000

50%   159.000000   1.800000   75%   505.500000
3.300000 max 37227.000000 185.800000

          NITRATENAN N+ NITRITENANN (mg/l) FECAL COLIFORM (MPN/100ml) \
count                           879.000000                8.790000e+02
mean                              1.644994                6.869346e+05
std                               2.896984                1.209315e+07
min                               0.000000                2.000000e+00
25%                               0.280000                2.550000e+01
50%                               0.590000                1.990000e+02
75%                               1.775000                9.965000e+02
max
                                 20.300000                2.725216e+08

       TOTAL COLIFORM (MPN/100ml)Mean          year    Water Qu
count
                           8.790000e+02    879.000000  879.000000
mean                       1.110502e+06   2012.559727    0.673493
std                        2.069025e+07      1.102190    0.469202
min                        4.000000e+00   2010.000000    0.000000
25%                        9.000000e+01   2012.000000    0.000000
50%                        5.000000e+02   2013.000000    1.000000
75%                        2.425000e+03   2014.000000    1.000000
max
                           5.110909e+08   2014.000000    1.000000
```

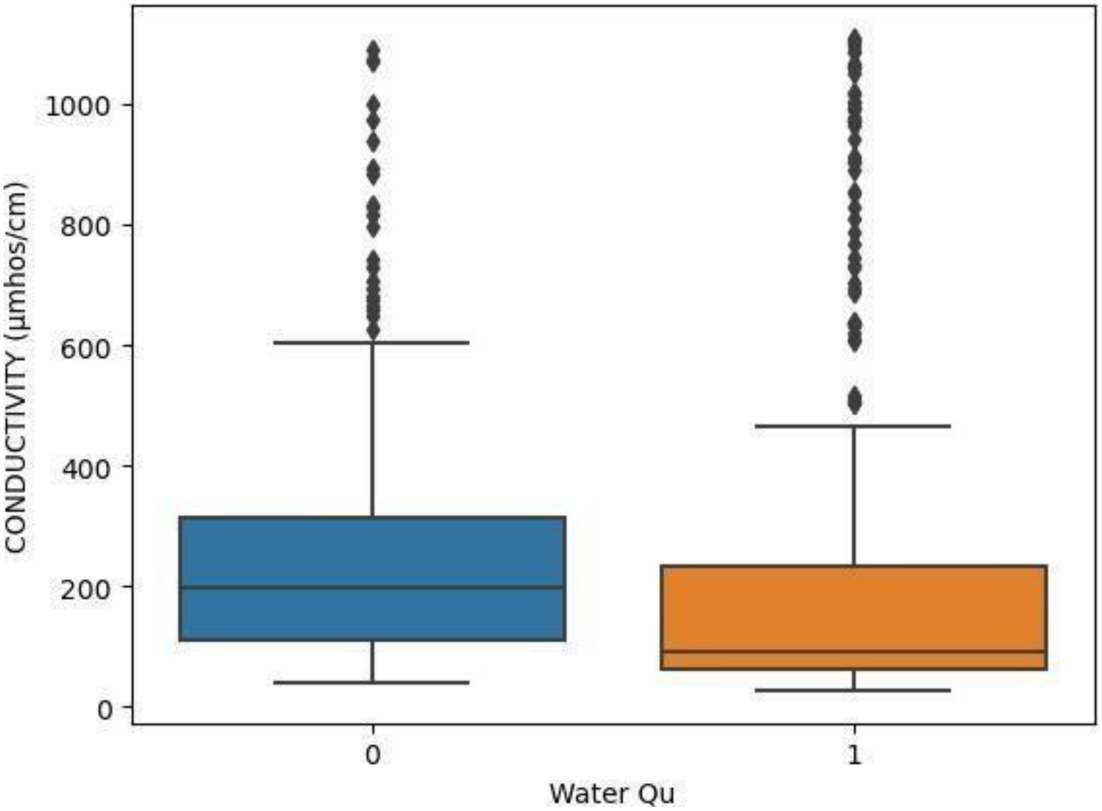
```
# Box plot for comparing the ph with other column and finding the
outliers


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_Lower)  +
(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    879.000000
mean      26.093743
std        3.261618
min       16.000000
25%       24.450000
50%       27.000000
75%       28.400000
max       33.000000
Name: Temp, dtype: float64
```



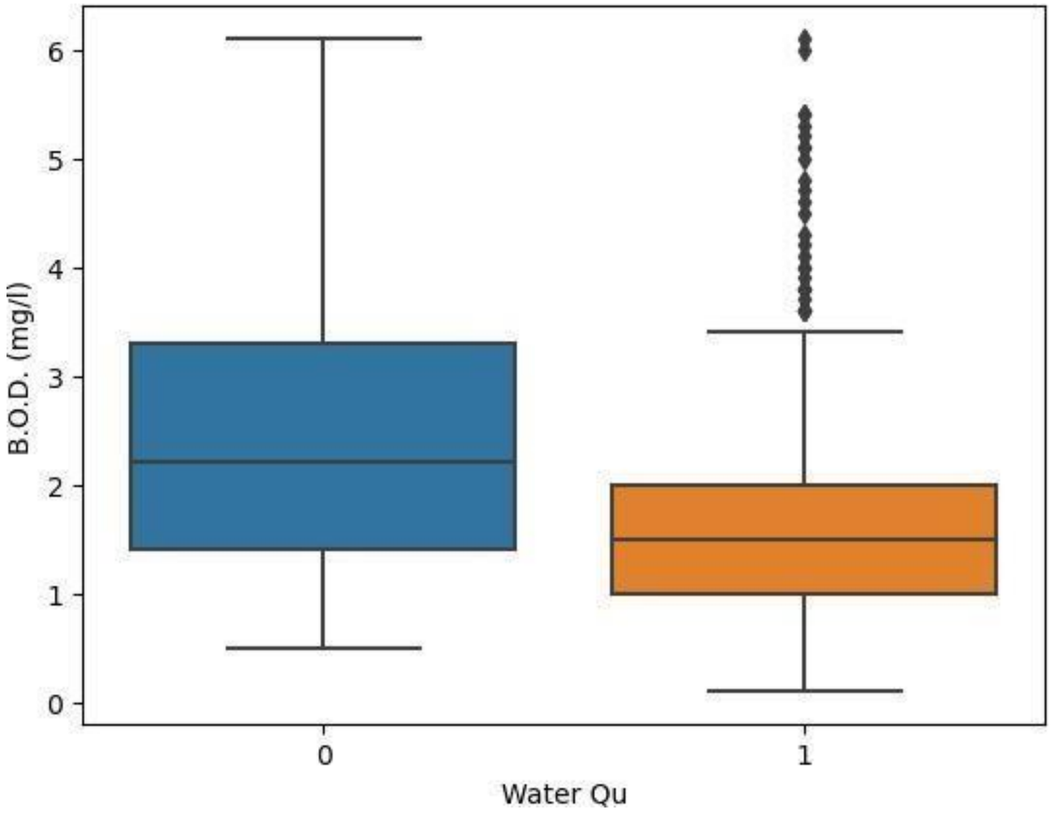
```
count 878.000000  mean
      6.306640 std
      1.295557 min
      0.200000
25%
50%
75%
max
Name:
        5.900000
        6.700000
        7.100000
        8.800000
    D.O. (mg/l), dtype: float64
```



```
25%
50%
75%
max
Name:
```

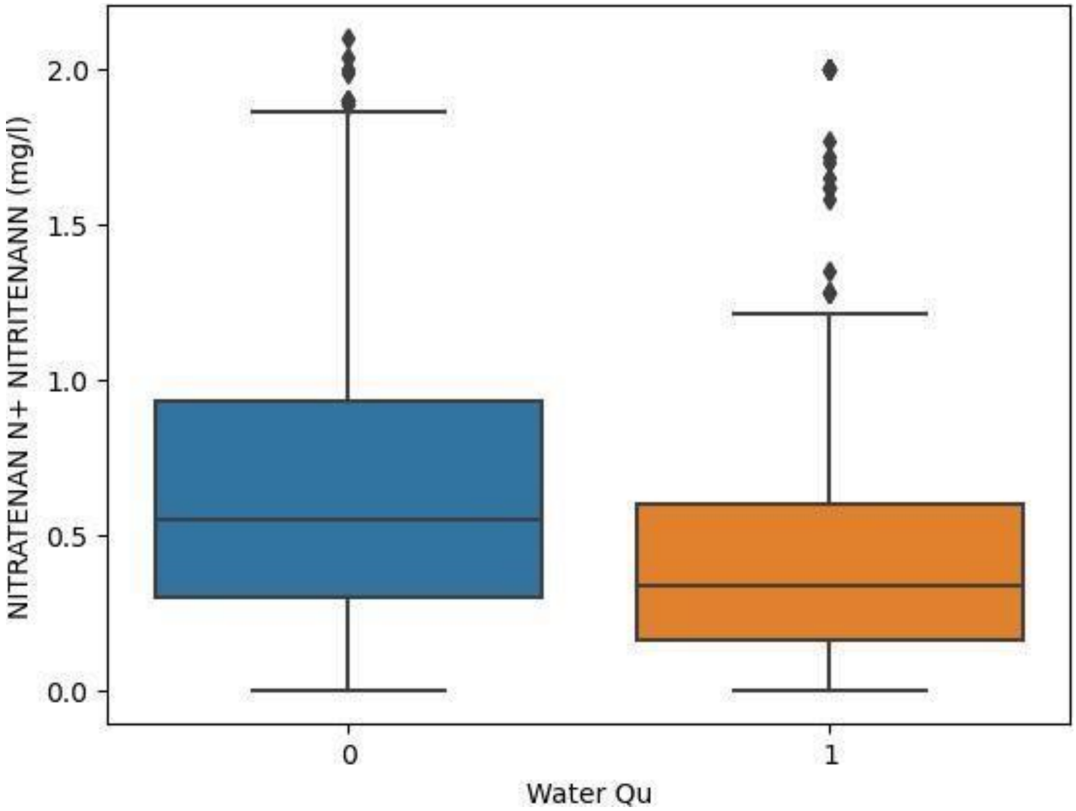
```
count     745.000000
mean  222.344966  std
243.275990       min
27.000000
           69.000000
          120.000000
          274.000000
         1110.000000
      CONDUCTIVITY (µmhos/cm), dtype: float64
```

```
25%
50%
75%
max
Name:
```



```
count 675.000000  mean
      1.939630 std
      1.140444 min
      0.100000
25%
50%
75%
max
Name:
```

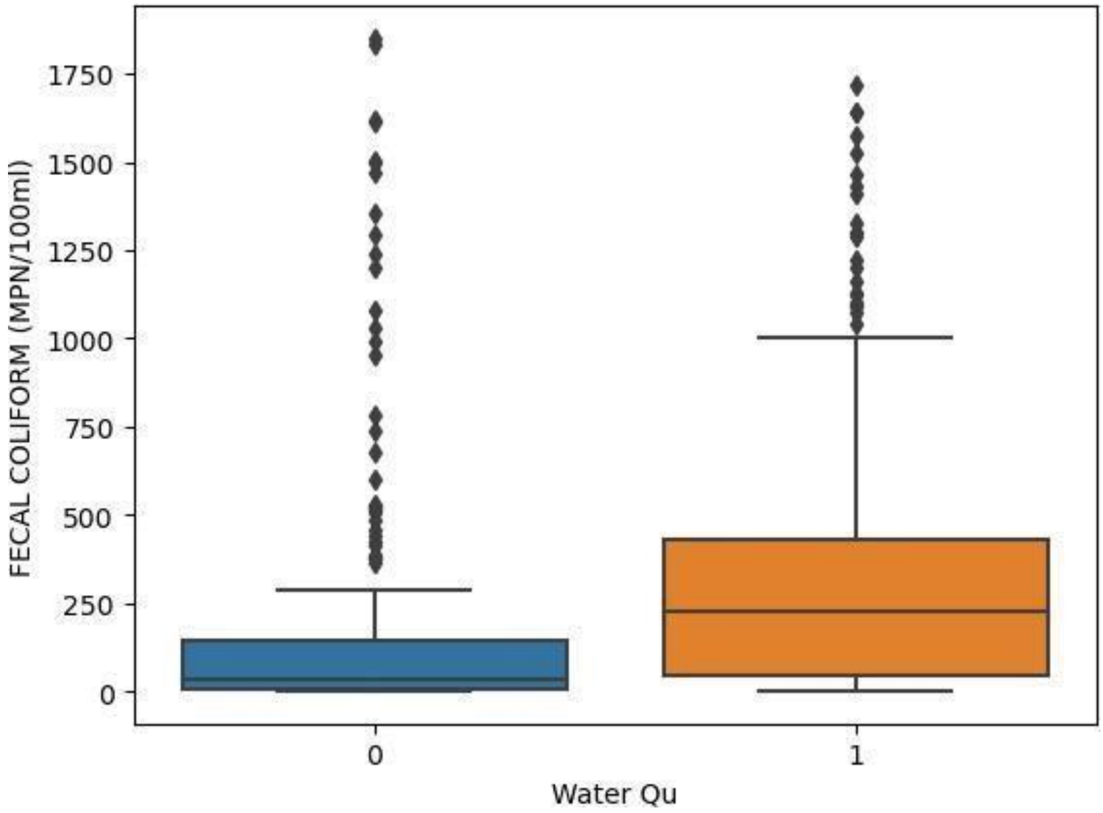
```
          1.100000
          1.600000
          2.500000
          6.100000
   B.O.D. (mg/l), dtype: float64
```



```
25%
50%
75%
max
Name:
```

```
count 571.000000  mean
      0.523135 std
      0.451816 min
      0.000000
            0.200000
            0.400000
            0.720000
            2.100000
       NITRATENAN N+ NITRITENANN (mg/l), dtype: float64
```

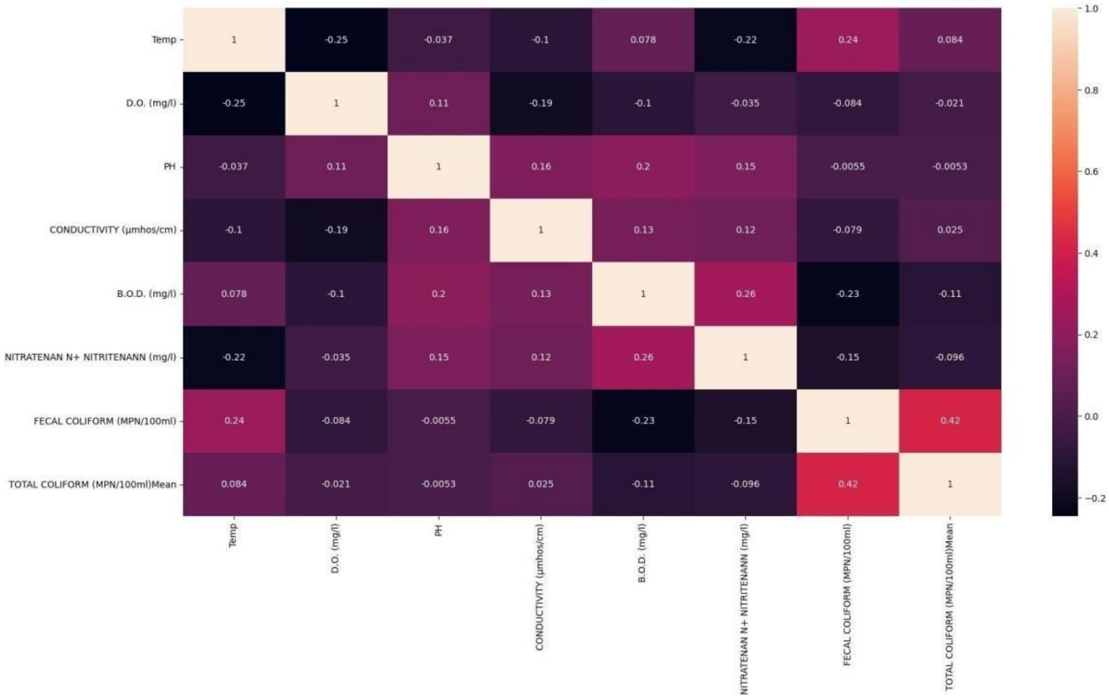
```
25%
50%
75%
max
Name:
```



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

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



# transforming your data so that it fits within a specific scale

mm=MinMaxScaler()
df[l]=mm.fit_transform(df[l])
df.describe()
             Temp D.O. (mg/l)           PH CONDUCTIVITY (µmhos/cm)   \

count  486.000000 486.000000 486.000000                   486.000000
```

```
mean     0.600061     0.724280    0.813046                  0.147103

std      0.157548     0.118957    0.101386                  0.177769

min      0.000000     0.000000    0.000000                  0.000000

25%      0.534091     0.695122    0.754386                  0.038853

50%      0.629870     0.743902    0.807018                  0.077706

75%      0.701299     0.792683    0.877193                  0.184089

max      1.000000     1.000000    1.000000                  1.000000

       B.O.D. (mg/l) NITRATENAN N+ NITRITENANN (mg/l)    \
count     486.000000                         486.000000

mean        0.307922                           0.254203

std         0.204720                           0.214196

min         0.000000                           0.000000

25%         0.150000                           0.095238

50%         0.233333                           0.190476

75%         0.450000                           0.351190

max         1.000000                           1.000000

       FECAL COLIFORM (MPN/100ml)   TOTAL COLIFORM (MPN/100ml)Mean
count                  486.000000                       486.000000

mean                     0.152833                         0.013122

std                      0.207294                         0.047275

min                      0.000000                         0.000000

25%                      0.010823                         0.001265

50%                      0.070076                         0.005544

75%                      0.204951                         0.014127

max                      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()
```



```
df

         Temp D.O. (mg/l)          PH CONDUCTIVITY (µmhos/cm) B.O.D.
(mg/l) \

14   0.740260    0.817073 0.771930     0.203515
0.233333
15   0.746753    0.817073 0.771930     0.148936
0.150000
26   0.811688      0.719512 0.859649                   0.358927
0.316667
28   0.487013    0.731707 0.912281     0.062905
0.800000
29   0.779221    0.768293 0.929825     0.066605
0.816667
..        ...           ...        ...                      ...
...
882  0.370130    0.756098 0.789474     0.239593
0.200000
883  0.714286    0.695122 0.947368     0.126735
0.550000
884  0.707792    0.731707 0.929825     0.156337
0.716667
893  0.675325    0.682927 0.894737     0.137835
0.566667
894  0.740260    0.695122 0.947368     0.158187
```

```
0.683333
      NITRATENAN N+ NITRITENANN (mg/l) FECAL COLIFORM (MPN/100ml)  \
14                             0.095238 0.591450
15                             0.047619 0.694805
26                             0.047619                   0.466450
28                             0.095238 0.007576
29                             0.190476 0.007035
..                                  ...                        ...
882   0.052381   0.003247 883     0.142857   0.204545
884                            0.380952                   0.228896
893                            0.095238 0.286797
894                            0.142857 0.282468

     TOTAL COLIFORM (MPN/100ml)Mean
14                           0.036895
15                           0.045859
26                           0.023110
28                           0.000482
29                           0.000452
..                                ...
882                          0.000377
883                          0.007894
884                          0.009702
893                          0.008858
894                          0.010274

[486 rows x 8 columns]
```

```
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
(MPN/100ml)Mean'] split=l.copy() y=df['PH']
split.remove('PH') x=df[split]
```

Split the Data

```
# 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)
```

```
x_train
```

```
        Temp D.O. (mg/l) CONDUCTIVITY (µmhos/cm) B.O.D. (mg/l)  \
795 0.577922      0.804878                 0.023127       0.083333
105 0.623377      0.560976                 0.025902       0.083333
```

```
355 0.785714       0.573171                         0.066605       0.450000

830  0.662338      0.682927                         0.015726       0.100000
775  0.500000      0.768293                         0.164662       0.350000
..        ...           ...                              ...            ...
226  0.642857      0.573171                         0.730805       0.450000
532  0.545455      0.731707                         0.037003       0.166667
661  0.415584      0.658537                         0.407956       0.216667
808  0.584416      0.817073                         0.024977       0.200000
220  0.629870      0.682927                         0.127660       0.333333

     NITRATENAN N+ NITRITENANN (mg/l)  FECAL COLIFORM (MPN/100ml)   \
795                          0.071429                   0.160173
105                          0.333333                   0.091450
355                          0.376190                   0.056277
830                          0.100000                   0.385823
775                          0.442857                   0.000000
..                                ...                        ...
226                          0.476190                    0.003788
532                          0.252381                   0.147727
661                          0.204762                   0.001623
808                          0.195238                   0.223485
220                          0.000000                   0.151515

     TOTAL COLIFORM (MPN/100ml)Mean
795                        0.010290
105                        0.004655
355                        0.007819
830                        0.024496
775                        0.000768
..                              ...
226                        0.000286
532                        0.010033
661                        0.000181
808                        0.013694
220                        0.005062

[364 rows x 7 columns]
```

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

LinearRegression

```
# 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)
```

```
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  else0)
ypred_pd['WQ']=ypred_pd['WQ'].map(lambda x:1 if x>0.7 else 0)
ypred_pd.head()
```

```
   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
```

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

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

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

```
0.9344262295081968
```

Decision Tree

```
# Fit the desiontree regression clf_gini =

DecisionTreeRegressor(random_state = 0)

clf_gini.fit(x_train, y_train) y_pred =

clf_gini.predict(x_test)

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>0.7  else0)
ypred_pd['WQ']=ypred_pd['WQ'].map(lambda x:1 if x>0.7 else 0)
ypred_pd.head()
```

```
   WQ    WQ_Pred predicted
0    1 0.947368   1
1    1 0.947368   1
2    1 0.736842   1
3    1 0.789474   1
4    1 0.719298   1
```

```
print('Model accuracy score with criterion gini index: {0:0.4f}'.
format(accuracy_score(ypred_pd['WQ'],ypred_pd['predicted'])))
```

```
Model accuracy score with criterion gini index: 0.9180
```

Random Forest

```
# Fit the random forest regression

forest_model = RandomForestRegressor(random_state=1)
forest_model.fit(x_train, y_train) melb_preds =
forest_model.predict(x_test)

# print(mean_absolute_error(val_y, melb_preds))

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>0.7 else0)
ypred_pd['WQ']=ypred_pd['WQ'].map(lambda x:1 if x>0.7 else 0)
ypred_pd.head()
```

```
   WQ   WQ_Pred predicted
0   1 0.947368   1
1   1 0.947368   1
2   1 0.736842   1
3   1 0.789474   1
4   1 0.719298   1
```

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

```
0.9180327868852459
```

Linear regression has the highest accuracy score = 0.93442

Pickle

```
# Load the model into pickle for serializing and deserializing a
Python object structure

import pickle

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(
array([0.74676269])
```

```
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( ar

ray([0.73684211])
```

```
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( ar ray([0.74894737])
```