SPRINT – 3

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

In [1]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
plt.style.use('fivethirtyeight')
plt.style.use('dark_background')
import seaborn as sns
color = sns.color_palette()
import plotly.express          as ex
import plotly.graph_objs       as go
import plotly.offline          as pyo
import scipy.stats             as stats
import pymc3                   as pm
import theano.tensor           as tt
from matplotlib.colors import ListedColormap
from scipy.stats import norm, boxcox
from sklearn.metrics import confusion_matrix, classification_report, accuracy_score
from collections import Counter
from scipy import stats
from tqdm import tqdm_notebook

from sklearn import metrics
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import mean_squared_error, mean_absolute_error, confusion_matrix, r2_score, accuracy_score
from sklearn.model_selection import (GridSearchCV, KFold, train_test_split, cross_val_score)

from imblearn.over_sampling import SMOTE
from collections import Counter

from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn.ensemble import RandomForestClassifier, ExtraTreesClassifier
from sklearn import svm
from xgboost.sklearn import XGBClassifier
from sklearn.tree import DecisionTreeClassifier
# from catboost import CatBoostClassifier
```

Importing The Dataset

In [2]:

```
path = "water_potability.csv"
df = pd.read_csv(path)
```

Initial Analysis

In [3]:
```
df.shape
```

Out[3]:
```
(3276, 10)
```

In [4]:
```
df.info()
```

```
RangeIndex: 3276 entries, 0 to 3275
Data columns (total 10 columns):
 #   Column           Non-Null Count  Dtype  
---  ------           --------------  -----  
 0   ph               2785 non-null   float64
 1   Hardness         3276 non-null   float64
 2   Solids           3276 non-null   float64
 3   Chloramines      3276 non-null   float64
 4   Sulfate          2495 non-null   float64
 5   Conductivity     3276 non-null   float64
 6   Organic_carbon   3276 non-null   float64
 7   Trihalomethanes  3114 non-null   float64
 8   Turbidity        3276 non-null   float64
 9   Potability       3276 non-null   int64  
dtypes: float64(9), int64(1)
memory usage: 256.1 KB
```

Except Target feature, other features are float and continueous value. we can convert the Portability into Categoring feature

In [5]:
```
df.nunique()
```

Out[5]:
```
ph                 2785
Hardness           3276
Solids             3276
Chloramines        3276
Sulfate            2495
Conductivity       3276
Organic_carbon     3276
Trihalomethanes    3114
Turbidity          3276
Potability            2
dtype: int64
```

Statistical Analysis

In [7]:
```
df.describe().T.style.background_gradient(subset=['mean','std','50%','count'], cmap='PuBu')
```

Out[7]:

	count	mean	std	min	25%	50%	75%	max
ph	2785.000000	7.080795	1.594320	0.000000	6.093092	7.036752	8.062066	14.000000
Hardness	3276.000000	196.369496	32.879761	47.432000	176.850538	196.967627	216.667456	323.124000
Solids	3276.000000	22014.092526	8768.570828	320.942611	15666.690297	20927.833607	27332.762127	61227.196008
Chloramines	3276.000000	7.122277	1.583085	0.352000	6.127421	7.130299	8.114887	13.127000
Sulfate	2495.000000	333.775777	41.416840	129.000000	307.699498	333.073546	359.950170	481.030642
Conductivity	3276.000000	426.205111	80.824064	181.483754	365.734414	421.884968	481.792304	753.342620
Organic_carbon	3276.000000	14.284970	3.308162	2.200000	12.065801	14.218338	16.557652	28.300000
Trihalomethanes	3114.000000	66.396293	16.175008	0.738000	55.844536	66.622485	77.337473	124.000000
Turbidity	3276.000000	3.966786	0.780382	1.450000	3.439711	3.955028	4.500320	6.739000

From the above table, we can see that the count of each feature are not same. so there must me some null values. Feature Solids has the high mean and standard deviation comparted to other feature. so the distribution must be high. However, the above description is for overall population. lets try the same for 2 samples based on Portability feature

In [8]:
```
#Portability is 1 - means good for Human
df[df['Potability']==1].describe().T.style.background_gradient(subset=['mean','std','50%','count'], cmap='PuBu')
```

Out[8]:

	count	mean	std	min	25%	50%	75%	max
ph	1101.000000	7.073783	1.448048	0.227499	6.179312	7.036752	7.933068	13.175402
Hardness	1278.000000	195.800744	35.547041	47.432000	174.330531	196.632907	218.003420	323.124000
Solids	1278.000000	22383.991018	9101.010208	728.750830	15668.985035	21199.386614	27973.236446	56488.672413
Chloramines	1278.000000	7.169338	1.702988	0.352000	6.094134	7.215163	8.199261	13.127000
Sulfate	985.000000	332.566990	47.692818	129.000000	300.763772	331.838167	365.941346	481.030642
Conductivity	1278.000000	425.383800	82.048446	201.619737	360.939023	420.712729	484.155911	695.369528
Organic carbon	1278.000000	14.160893	3.263907	2.200000	12.033897	14.162809	16.356245	23.604298

In [9]:

```
# Portability is 0 - means not good for Human
df[df['Potability']==0].describe().T.style.background_gradient(subset=['mean','std','50%','count'], cmap='RdBu')
```

Out[9]:

	count	mean	std	min	25%	50%	75%	max
ph	1684.000000	7.085378	1.683499	0.000000	6.037723	7.035456	8.155510	14.000000
Hardness	1998.000000	196.733292	31.057540	98.452931	177.823265	197.123423	216.120687	304.235912
Solids	1998.000000	21777.490788	8543.068788	320.942611	15663.057382	20809.618280	27006.249009	61227.196008
Chloramines	1998.000000	7.092175	1.501045	1.683993	6.155640	7.090334	8.066462	12.653362
Sulfate	1510.000000	334.564290	36.745549	203.444521	311.264006	333.389426	356.853897	460.107069
Conductivity	1998.000000	426.730454	80.047317	181.483754	368.498530	422.229331	480.677198	753.342620
Organic_carbon	1998.000000	14.364335	3.334554	4.371899	12.101057	14.293508	16.649485	28.300000
Trihalomethanes	1891.000000	66.303555	16.079320	0.738000	55.706530	66.542198	77.277704	120.030077
Turbidity	1998.000000	3.965800	0.780282	1.450000	3.444062	3.948076	4.496106	6.739000

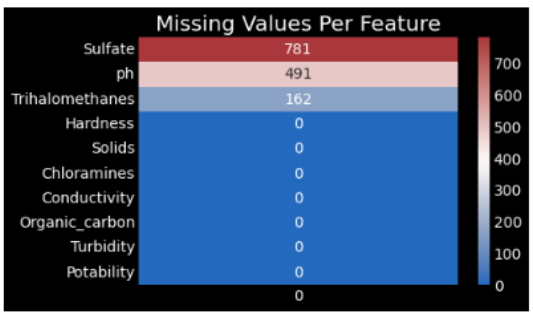
Mean and std of almost all features are similar for both samples. there are few differnces in Solids feature. Further analysis using hypothetical testing could help us to identify the significance.

Check for missing values

In [10]:

```
plt.title('Missing Values Per Feature')
nans = df.isna().sum().sort_values(ascending=False).to_frame()
sns.heatmap(nans,annot=True,fmt='d',cmap='vlag')
```

Out[10]:



In [11]:

```
df[df['Sulfate'].isnull()]
```

Out[11]:

	ph	Hardness	Solids	Chloramines	Sulfate	Conductivity	Organic_carbon	Trihalomethanes	Turbidity	Potability
1	3.716080	129.422921	18630.057858	6.635246	NaN	592.885359	15.180013	56.329076	4.500656	0
2	8.099124	224.236259	19909.541732	9.275884	NaN	418.606213	16.868637	66.420093	3.055934	0
11	7.974522	218.693300	18767.656682	8.110385	NaN	364.098230	14.525746	76.485911	4.011718	0
14	7.496232	205.344982	28388.004887	5.072558	NaN	444.645352	13.228311	70.300213	4.777382	0
16	7.051786	211.049406	30980.600787	10.094796	NaN	315.141267	20.397022	56.651604	4.268429	0
...	...	...	...	...	...	...	...	...	...	...
3266	8.372910	169.087052	14622.745494	7.547984	NaN	464.525552	11.083027	38.435151	4.906358	1
3272	7.808856	193.553212	17329.802160	8.061362	NaN	392.449580	19.903225	NaN	2.798243	1

1	3.716080	129.422921	18630.057858	6.635246	NaN	592.885359	15.180013	56.329076	4.500656	0
2	8.099124	224.236259	19909.541732	9.275884	NaN	418.606213	16.868637	66.420093	3.055934	0
11	7.974522	218.693300	18767.656682	8.110385	NaN	364.098230	14.525746	76.485911	4.011718	0
14	7.496232	205.344982	28388.004887	5.072558	NaN	444.645352	13.228311	70.300213	4.777382	0
16	7.051786	211.049406	30980.600787	10.094796	NaN	315.141267	20.397022	56.651604	4.268429	0
...	...	...	...	...	...	...	...	...	...	...
3266	8.372910	169.087052	14622.745494	7.547984	NaN	464.525552	11.083027	38.435151	4.906358	1
3272	7.808856	193.553212	17329.802160	8.061362	NaN	392.449580	19.903225	NaN	2.798243	1
3273	9.419510	175.762646	33155.578218	7.350233	NaN	432.044783	11.039070	69.845400	3.298875	1
3274	5.126763	230.603758	11983.869376	6.303357	NaN	402.883113	11.168946	77.488213	4.708658	1
3275	7.874671	195.102299	17404.177061	7.509306	NaN	327.459760	16.140368	78.698446	2.309149	1

781 rows × 10 columns

In [12]:

```
df[df['ph'].isnull()]
```

Out[12]:

	ph	Hardness	Solids	Chloramines	Sulfate	Conductivity	Organic_carbon	Trihalomethanes	Turbidity	Potability
0	NaN	204.890455	20791.318981	7.300212	368.516441	564.308654	10.379783	86.990970	2.963135	0
8	NaN	118.988579	14285.583854	7.804174	268.646941	389.375566	12.706049	53.928846	3.595017	0
13	NaN	150.174923	27331.361962	6.838223	299.415781	379.761835	19.370807	76.509996	4.413974	0
20	NaN	227.435048	22305.567414	10.333918	NaN	554.820086	16.331693	45.382815	4.133423	0
22	NaN	215.977859	17107.224226	5.607060	326.943978	436.256194	14.189062	59.855476	5.459251	0
...	...	...	...	...	...	...	...	...	...	...
3224	NaN	198.218700	31081.735264	7.419106	NaN	517.925946	11.711419	85.428785	3.345543	1
3229	NaN	203.204659	10643.186771	6.828936	NaN	384.597711	16.011328	72.911573	3.065910	1
3231	NaN	225.754109	28194.452646	5.892830	366.201583	418.272901	17.306832	103.912548	3.855895	1
3245	NaN	188.536608	24711.414927	7.129520	NaN	555.548534	16.959269	56.038702	4.331691	1
3260	NaN	134.736856	9000.025591	9.026293	NaN	428.213987	8.668672	74.773392	3.699558	1

491 rows × 10 columns

491 rows × 10 columns

In [13]:

```
df[df['Trihalomethanes'].isnull()]
```

Out[13]:

	ph	Hardness	Solids	Chloramines	Sulfate	Conductivity	Organic_carbon	Trihalomethanes	Turbidity	Potability
62	NaN	229.485694	35729.692709	8.810843	384.943779	296.397547	16.927092	NaN	3.855602	0
81	5.519126	168.728583	12531.601921	7.730723	NaN	443.570372	18.099078	NaN	3.758996	0
110	9.286155	222.661551	12311.268366	7.289866	332.239359	353.740100	14.171763	NaN	5.239982	0
118	7.397413	122.541040	8855.114121	6.888689	241.607532	489.851600	13.365906	NaN	3.149158	0
119	7.812804	196.583886	42550.841816	7.334648	NaN	442.545775	14.666917	NaN	6.204846	0
...	...	...	...	...	...	...	...	...	...	...
3174	6.698154	198.286268	34675.862845	6.263602	360.232834	430.935009	12.176678	NaN	3.758180	1
3185	6.110022	234.800957	16663.539074	5.984536	348.055211	437.892115	10.059523	NaN	2.817780	1
3219	6.417716	209.702425	31974.481631	7.263425	321.382124	289.450118	11.369071	NaN	4.210327	1
3259	9.271355	181.259617	16540.979048	7.022499	309.238865	487.692788	13.228441	NaN	4.333953	1
3272	7.808856	193.553212	17329.802160	8.061362	NaN	392.449580	19.903225	NaN	2.798243	1

162 rows × 10 columns

Since the missing values are on both classess (Potability 1 & 0), we can replace it with population mean. so, we will replace the Nan values bases on sample mean from both classes.

Imputing the missing values with the mean

In [14]:

```
##################################### Imputing 'ph' value #####################################

phMean_0 = df[df['Potability'] == 0]['ph'].mean(skipna=True)
df.loc[(df['Potability'] == 0) & (df['ph'].isna()), 'ph'] = phMean_0
phMean_1 = df[df['Potability'] == 1]['ph'].mean(skipna=True)
df.loc[(df['Potability'] == 1) & (df['ph'].isna()), 'ph'] = phMean_1

###################################### Imputing 'Sulfate' value ######################################

SulfateMean_0 = df[df['Potability'] == 0]['Sulfate'].mean(skipna=True)
df.loc[(df['Potability'] == 0) & (df['Sulfate'].isna()), 'Sulfate'] = SulfateMean_0
```

162 rows × 10 columns

Since the missing values are on both classess (Potability 1 & 0), we can replace it with population mean. so, we will replace the Nan values bases on sample mean from both classes.

Imputing the missing values with the mean

In [14]:
```
#################################### Imputing 'ph' value #####################################

phMean_0 = df[df['Potability'] == 0]['ph'].mean(skipna=True)
df.loc[(df['Potability'] == 0) & (df['ph'].isna()), 'ph'] = phMean_0
phMean_1 = df[df['Potability'] == 1]['ph'].mean(skipna=True)
df.loc[(df['Potability'] == 1) & (df['ph'].isna()), 'ph'] = phMean_1

##################################### Imputing 'Sulfate' value #####################################

SulfateMean_0 = df[df['Potability'] == 0]['Sulfate'].mean(skipna=True)
df.loc[(df['Potability'] == 0) & (df['Sulfate'].isna()), 'Sulfate'] = SulfateMean_0
SulfateMean_1 = df[df['Potability'] == 1]['Sulfate'].mean(skipna=True)
df.loc[(df['Potability'] == 1) & (df['Sulfate'].isna()), 'Sulfate'] = SulfateMean_1

################################ Imputing 'Trihalomethanes' value #####################################

TrihalomethanesMean_0 = df[df['Potability'] == 0]['Trihalomethanes'].mean(skipna=True)
df.loc[(df['Potability'] == 0) & (df['Trihalomethanes'].isna()), 'Trihalomethanes'] = TrihalomethanesMean_0
TrihalomethanesMean_1 = df[df['Potability'] == 1]['Trihalomethanes'].mean(skipna=True)
df.loc[(df['Potability'] == 1) & (df['Trihalomethanes'].isna()), 'Trihalomethanes'] = TrihalomethanesMean_1
```

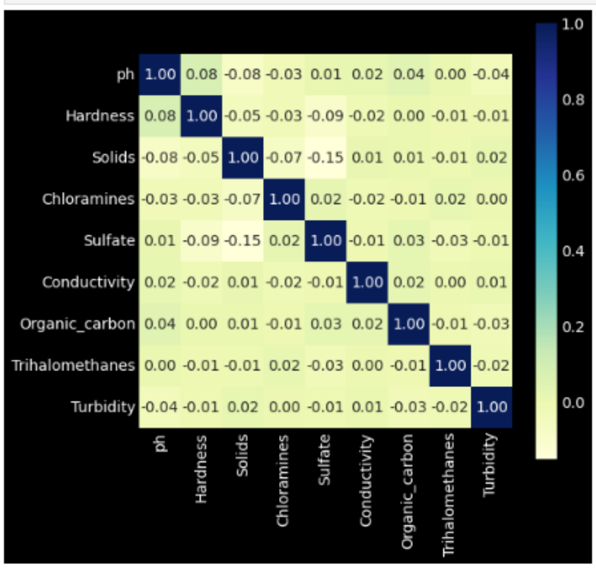
In [15]:
```
print('Checking to see any more missing data \n')
df.isna().sum()
```

```
Checking to see any more missing data
```

Out[15]:
```
ph                 0
Hardness           0
Solids             0
Chloramines        0
Sulfate            0
Conductivity       0
Organic_carbon     0
Trihalomethanes    0
Turbidity          0
Potability         0
```

Exploratory Data Analysis

In [16]:
```
Corrmat = df.corr()
plt.subplots(figsize=(7,7))
sns.heatmap(Corrmat, cmap="YlGnBu", square = True, annot=True, fmt='.2f')
plt.show()
```

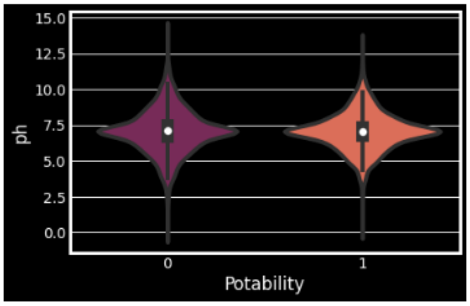


In [17]:
```
fig =  ex.pie (df, names = "Potability", hole = 0.4, template = "plotly_dark")
fig.show ()
```

In [18]:

```
sns.violinplot(x='Potability', y='ph', data=df, palette='rocket')
```

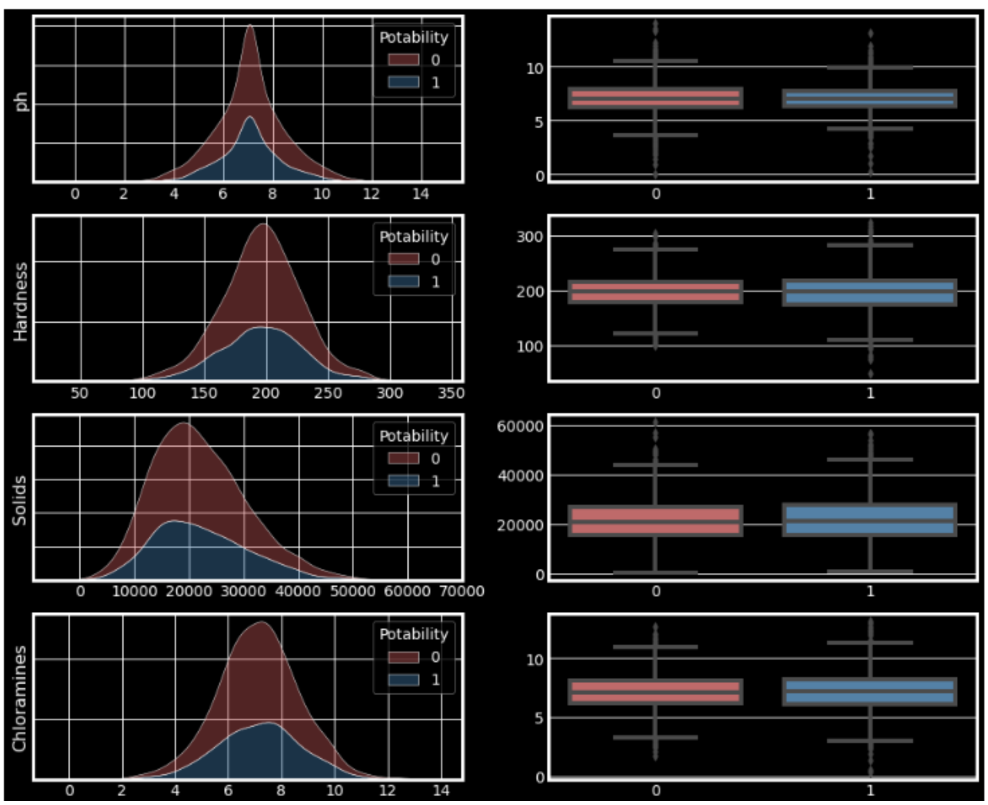
Out[18]:

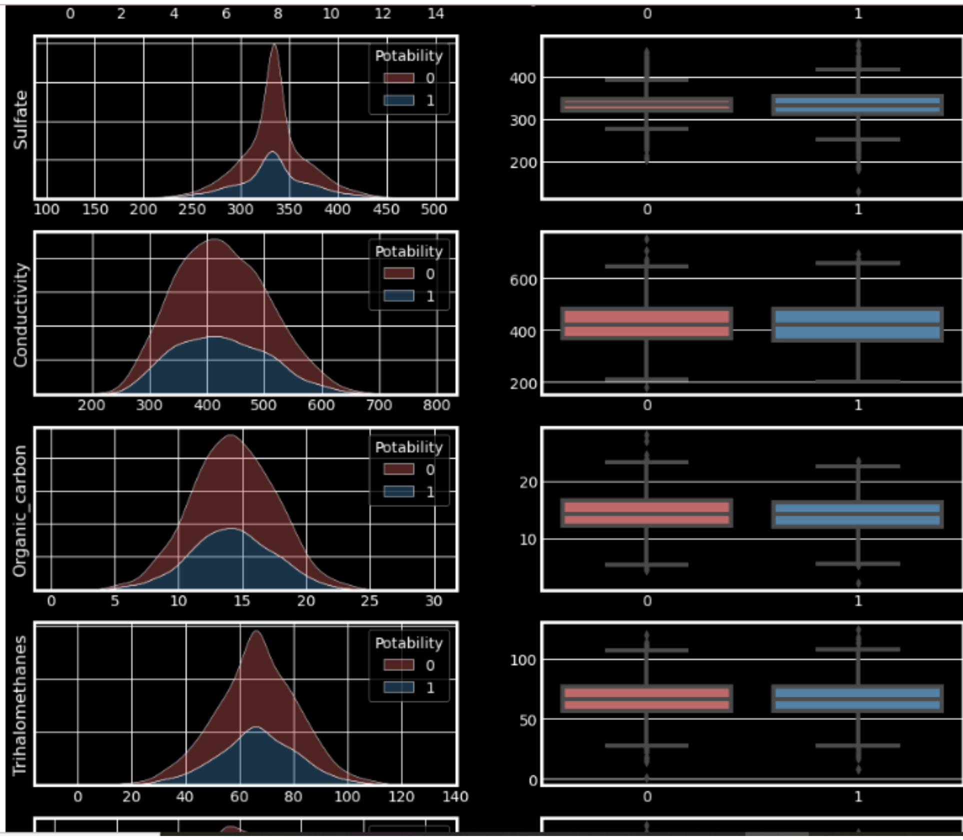


In [19]:

```
print('Boxplot and density distribution of different features by Potability\n')

fig, ax = plt.subplots(ncols=2, nrows=9, figsize=(14, 28))

features = list(df.columns.drop('Potability'))
i=0
for cols in features:
    sns.kdeplot(df[cols], fill=True, alpha=0.4, hue = df.Potability,
                palette=('indianred', 'steelblue'), multiple='stack', ax=ax[i,0])

    sns.boxplot(data= df, y=cols, x='Potability', ax=ax[i, 1],
               palette=('indianred', 'steelblue'))
    ax[i,0].set_xlabel(' ')
    ax[i,1].set_xlabel(' ')
    ax[i,1].set_ylabel(' ')
    ax[i,1].xaxis.set_tick_params(labelsize=14)
    ax[i,0].tick_params(left=False, labelleft=False)
    ax[i,0].set_ylabel(cols, fontsize=16)
    i=i+1

plt.show()
```

```
Boxplot and density distribution of different features by Potability
```





SMOTE

In [20]:

```
###################### Preparing the Data for Modelling ######################

X = df.drop('Potability', axis = 1).copy()
y = df['Potability'].copy()

############################## Train-Test split ##############################
X_train, X_test, y_train, y_test = train_test_split(X,y,test_size=0.25)

########################### Synthetic OverSampling ###########################
print('Balancing the data by SMOTE - Oversampling of Minority level\n')
smt = SMOTE()
counter = Counter(y_train)
print('Before SMOTE', counter)
X_train, y_train = smt.fit_resample(X_train, y_train)
counter = Counter(y_train)
print('\nAfter SMOTE', counter)

################################# Scaling #################################
ssc = StandardScaler()

X_train = ssc.fit_transform(X_train)
X_test = ssc.transform(X_test)

modelAccuracy = list()
```

```
Balancing the data by SMOTE - Oversampling of Minority level

Before SMOTE Counter({0: 1492, 1: 965})

After SMOTE Counter({0: 1492, 1: 1492})
```

Modelling and Prediction

In [21]:

```
model = [LogisticRegression(), DecisionTreeClassifier(), GaussianNB(), RandomForestClassifier(),
        svm.LinearSVC(), XGBClassifier()]
trainAccuracy = list()
testAccuracy = list()
kfold = KFold(n_splits=10, random_state=7, shuffle=True)
```

```
    y_pred = mdl.predict(X_test)
    testResult = metrics.accuracy_score(y_test, y_pred)
    testAccuracy.append(testResult)
```

```
/home/sid/Documents/archive (1)/water_qualtiy/lib/python3.8/site-packages/sklearn/svm/_base.py:1206: ConvergenceWarning:

Liblinear failed to converge, increase the number of iterations.

/home/sid/Documents/archive (1)/water_qualtiy/lib/python3.8/site-packages/sklearn/svm/_base.py:1206: ConvergenceWarning:

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Liblinear failed to converge, increase the number of iterations.

/home/sid/Documents/archive (1)/water_qualtiy/lib/python3.8/site-packages/xgboost/sklearn.py:1224: UserWarning:
```