Team ID	PNT2022TMID51603
Project Name	Efficient Water Quality Analysis and Prediction using Machine Learning

Handling Missing values 3

In [14]:
```
data['Temp'].fillna(data['Temp'].mean(),inplace=True)
data['D.O. (mg/l)'].fillna(data['D.O. (mg/l)'].mean(),inplace=True)
data['PH'].fillna(data['PH'].mean(),inplace=True)
data['CONDUCTIVITY (µmhos/cm)'].fillna(data['CONDUCTIVITY (µmhos/cm)'].mean(),inplace=True)
data['B.O.D. (mg/l)'].fillna(data['B.O.D. (mg/l)'].mean(),inplace=True)
data['NITRATENAN N+ NITRITENANN (mg/l)'].fillna(data['NITRATENAN N+ NITRITENANN (mg/l)'].mean(),inplace
data['TOTAL COLIFORM (MPN/100ml)Mean'].fillna(data['TOTAL COLIFORM (MPN/100ml)Mean'].mean(),inplace=Tru
```

In [15]:
```
data.drop(["FECAL COLIFORM (MPN/100ml)"],axis=1,inplace=True)
```

Renaming the Column Names

In [16]:
```
data=data.rename(columns = {'D.O. (mg/l)': 'do'})
data=data.rename(columns = {'CONDUCTIVITY (µmhos/cm)': 'co'})
data=data.rename(columns = {'B.O.D. (mg/l)': 'bod'})
data=data.rename(columns = {'NITRATENAN N+ NITRITENANN (mg/l)': 'na'})
data=data.rename(columns = {'TOTAL COLIFORM (MPN/100ml)Mean': 'tc'})
data=data.rename(columns = {'STATION CODE': 'station'})
data=data.rename(columns = {'LOCATIONS': 'location'})
data=data.rename(columns = {'STATE': 'state'})
data=data.rename(columns = {'PH': 'ph'})
```