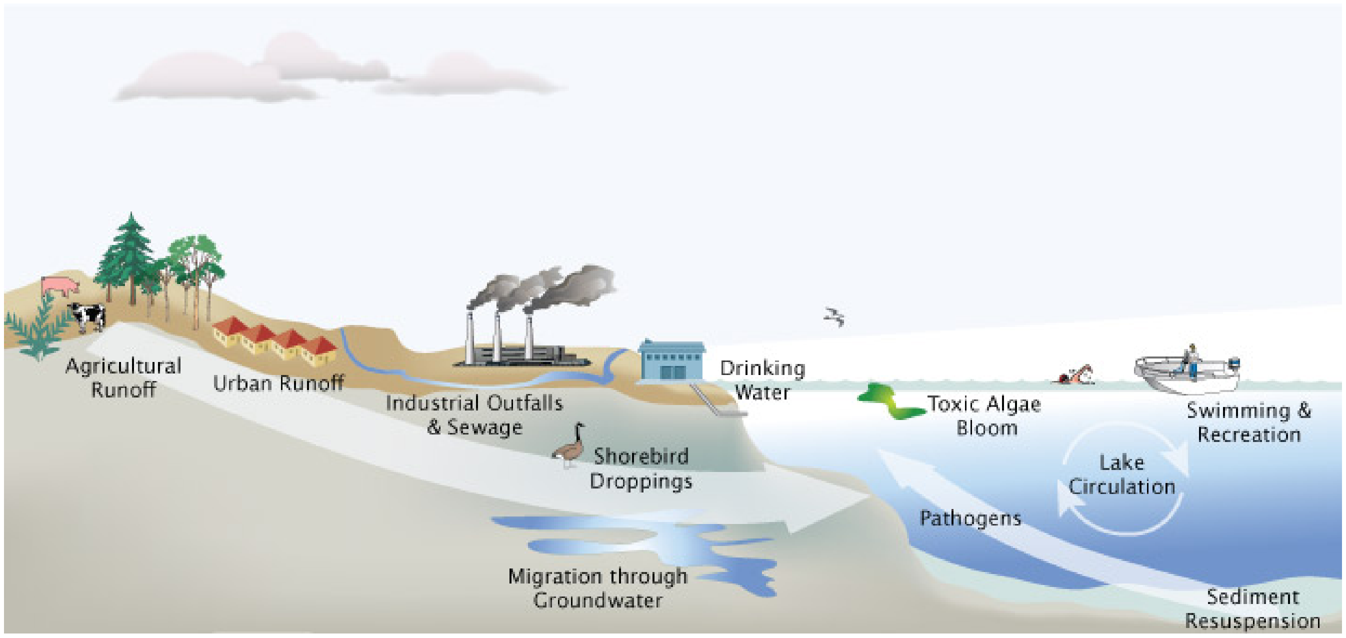


In [1]:
```
# This Python 3 environment comes with many helpful analytics libraries installed
# It is defined by the kaggle/python Docker image: https://github.com/kaggle/docker-pyth
# For example, here's several helpful packages to load
import seaborn as sns
import plotly.express as px
import matplotlib.pyplot as plt
import plotly.graph_objects as go
from tqdm import tqdm_notebook
import plotly.figure_factory as ff

import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)

import warnings
warnings.filterwarnings('ignore')

plt.style.use('fivethirtyeight')
%matplotlib inline
# Input data files are available in the read-only "../input/" directory
# For example, running this (by clicking run or pressing Shift+Enter) will list all file

import os
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))

# You can write up to 20GB to the current directory (/kaggle/working/) that gets preserv
# You can also write temporary files to /kaggle/temp/, but they won't be saved outside o
```

In [2]:
```
data=pd.read_csv('../input/water-potability/water_potability.csv')
data.head()
```

Out[2]:

	ph	Hardness	Solids	Chloramines	Sulfate	Conductivity	Organic_carbon	Trihalomethanes
0	NaN	204.890455	20791.318981	7.300212	368.516441	564.308654	10.379783	86.990970
1	3.716080	129.422921	18630.057858	6.635246	NaN	592.885359	15.180013	56.329076
2	8.099124	224.236259	19909.541732	9.275884	NaN	418.606213	16.868637	66.420093
3	8.316766	214.373394	22018.417441	8.059332	356.886136	363.266516	18.436524	100.341674
4	9.092223	181.101509	17978.986339	6.546600	310.135738	398.410813	11.558279	31.997993

EDA

- ph-> pH of water
- Hardness-> Capacity of water to precipitate soap in mg/L
- Solids-> Total dissolved solids in ppm
- Chloramines-> Amount of Chloramines in ppm
- Sulfate-> Amount of Sulfates dissolved in mg/L
- Conductivity-> Electrical conductivity of water in μS/cm
- Organic_carbon-> Amount of organic carbon in ppm
- Trihalomethanes-> Amount of Trihalomethanes in μg/L
- Turbidity-> Measure of light emiting property of water in NTU (Nephelometric Turbidity Units)
- Potability-> Indicates if water is safe for human consumption

In [3]:

```
data.describe()
```

Out[3]:

	ph	Hardness	Solids	Chloramines	Sulfate	Conductivity	Organic_carbon	Trihal
count	2785.000000	3276.000000	3276.000000	3276.000000	2495.000000	3276.000000	3276.000000	3
mean	7.080795	196.369496	22014.092526	7.122277	333.775777	426.205111	14.284970	
std	1.594320	32.879761	8768.570828	1.583085	41.416840	80.824064	3.308162	
min	0.000000	47.432000	320.942611	0.352000	129.000000	181.483754	2.200000	
25%	6.093092	176.850538	15666.690297	6.127421	307.699498	365.734414	12.065801	
50%	7.036752	196.967627	20927.833607	7.130299	333.073546	421.884968	14.218338	
75%	8.062066	216.667456	27332.762127	8.114887	359.950170	481.792304	16.557652	
max	14.000000	323.124000	61227.196008	13.127000	481.030642	753.342620	28.300000	1

In [4]:

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
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
```

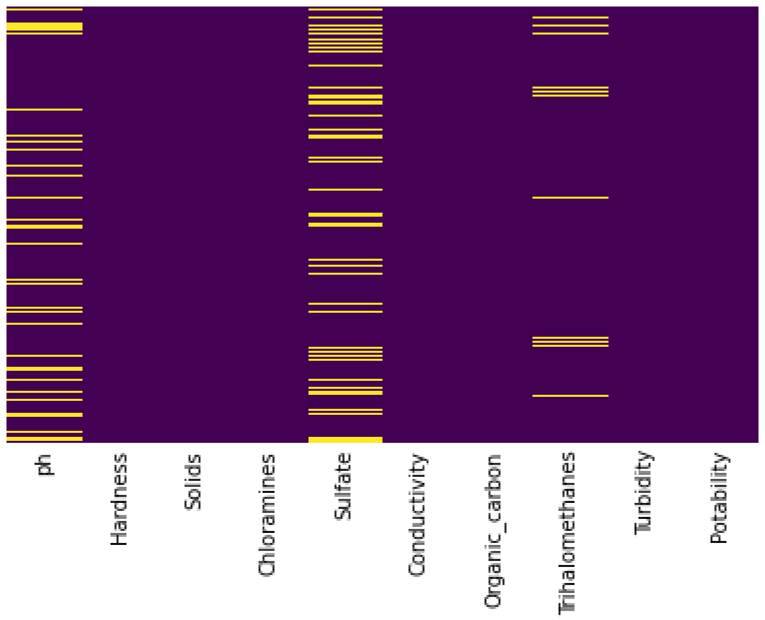
In [5]:
```
print('There are {} data points and {} features in the data'.format(data.shape[0],data.s
```

```
There are 3276 data points and 10 features in the data
```

Null Values

In [6]:
```
sns.heatmap(data.isnull(),yticklabels=False,cbar=False,cmap='viridis')
```

Out[6]:
```
<AxesSubplot:>
```



In [7]:
```
for i in data.columns:
    if data[i].isnull().sum()>0:
        print("There are {} null values in {} column".format(data[i].isnull().sum(),i))
```

```
There are 491 null values in ph column
There are 781 null values in Sulfate column
There are 162 null values in Trihalomethanes column
```

Handling Null Values

PH

```
In [8]: data['ph'].describe()
```

```
Out[8]: count    2785.000000
        mean        7.080795
        std         1.594320
        min         0.000000
        25%         6.093092
        50%         7.036752
        75%         8.062066
        max        14.000000
        Name: ph, dtype: float64
```

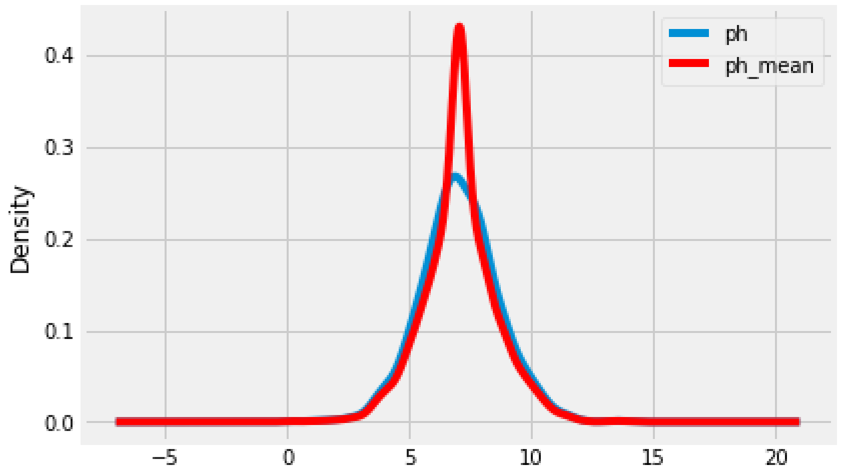
Filling the missing values by mean

```
In [9]: data['ph_mean']=data['ph'].fillna(data['ph'].mean())
```

```
In [10]: data['ph_mean'].isnull().sum()
```

```
Out[10]: 0
```

```
In [11]: fig = plt.figure()
         ax = fig.add_subplot(111)
         data['ph'].plot(kind='kde', ax=ax)
         data.ph_mean.plot(kind='kde', ax=ax, color='red')
         lines, labels = ax.get_legend_handles_labels()
         ax.legend(lines, labels, loc='best')
         plt.show()
```



The distribution is not uniform

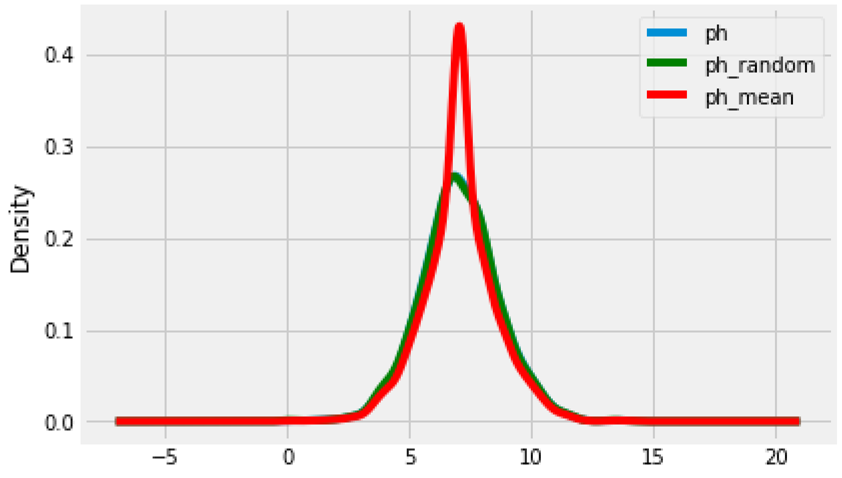
Filling the data with random values

```
In [12]: def impute_nan(df,variable):
             df[variable+"_random"]=df[variable]
             ##It will have the random sample to fill the na
             random_sample=df[variable].dropna().sample(df[variable].isnull().sum(),random_state=
             ##pandas need to have same index in order to merge the dataset
             random_sample.index=df[df[variable].isnull()].index
             df.loc[df[variable].isnull(),variable+'_random']=random_sample
```

```
In [13]: impute_nan(data,"ph")
```

```
In [14]: fig = plt.figure()
         ax = fig.add_subplot(111)
         data['ph'].plot(kind='kde', ax=ax)
```

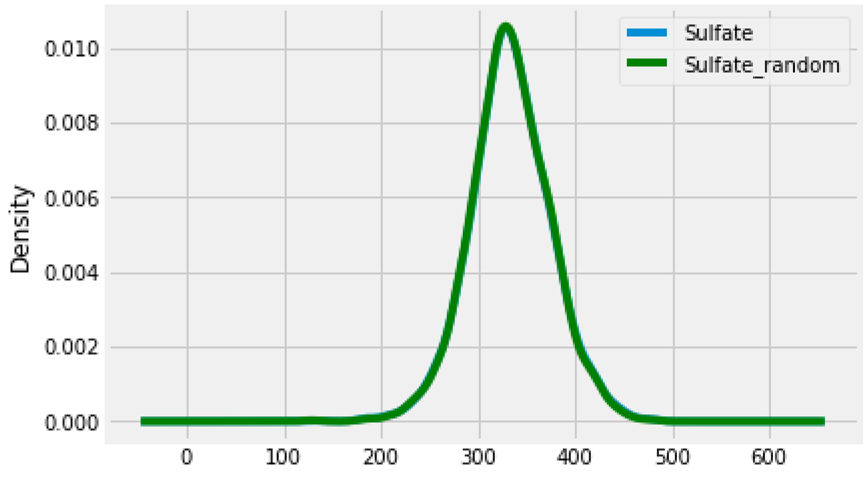
```
data.ph_random.plot(kind='kde', ax=ax, color='green')
data.ph_mean.plot(kind='kde', ax=ax, color='red')
lines, labels = ax.get_legend_handles_labels()
ax.legend(lines, labels, loc='best')
plt.show()
```



Uniform distribution with random initialization

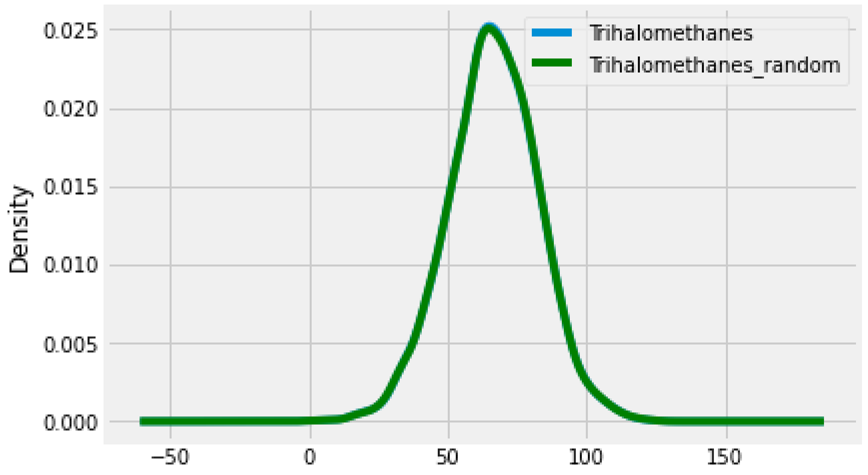
In [15]:
```
impute_nan(data,"Sulfate")
```

In [16]:
```
fig = plt.figure()
ax = fig.add_subplot(111)
data['Sulfate'].plot(kind='kde', ax=ax)
data["Sulfate_random"].plot(kind='kde', ax=ax, color='green')
#data.ph_mean.plot(kind='kde', ax=ax, color='red')
lines, labels = ax.get_legend_handles_labels()
ax.legend(lines, labels, loc='best')
plt.show()
```



In [17]:
```
impute_nan(data,"Trihalomethanes")
```

In [18]:
```
fig = plt.figure()
ax = fig.add_subplot(111)
data['Trihalomethanes'].plot(kind='kde', ax=ax)
data.Trihalomethanes_random.plot(kind='kde', ax=ax, color='green')
lines, labels = ax.get_legend_handles_labels()
ax.legend(lines, labels, loc='best')
plt.show()
```



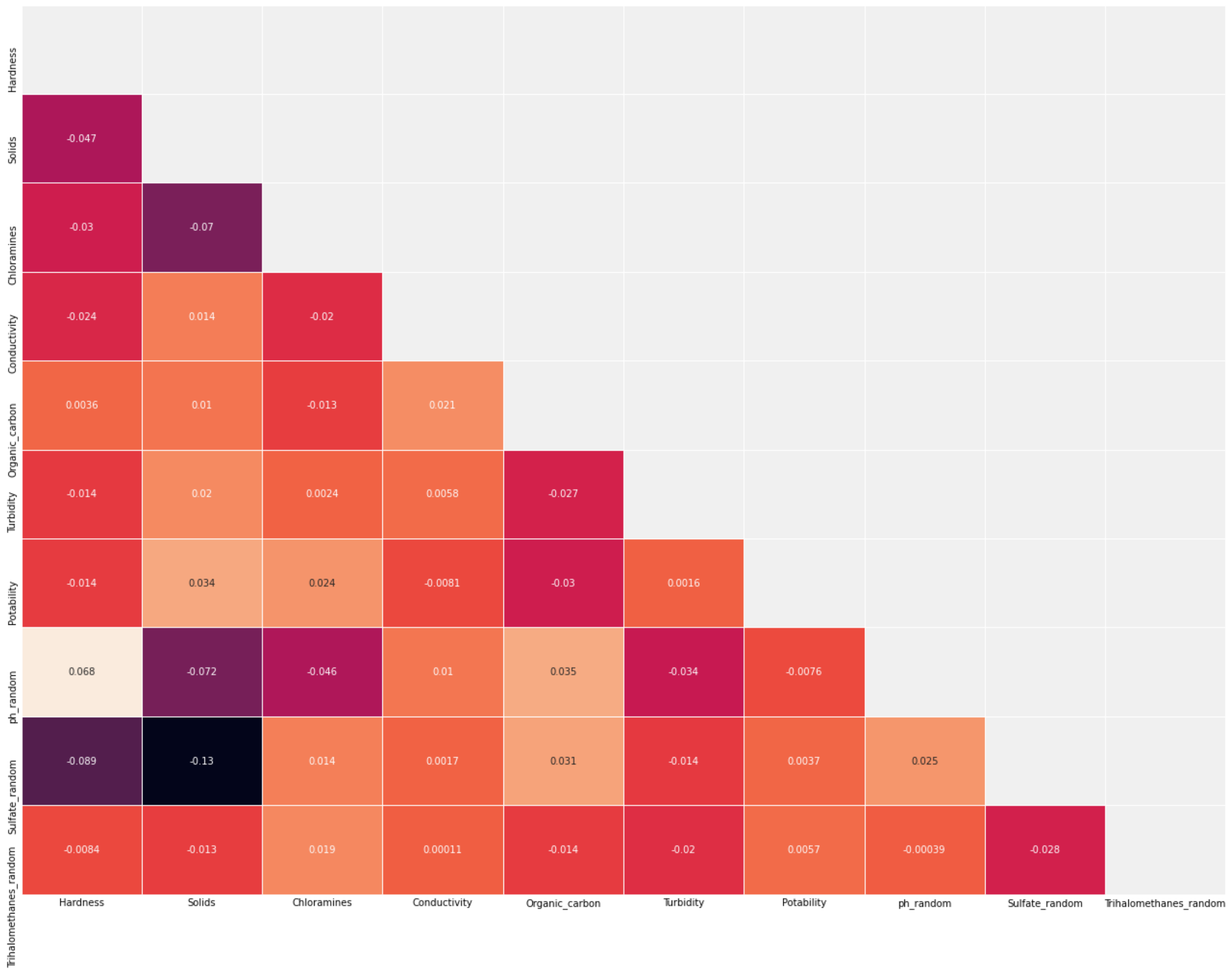
```
In [19]: data=data.drop(['ph','Sulfate','Trihalomethanes','ph_mean'],axis=1)
```

```
In [20]: data.isnull().sum()
```

```
Out[20]: Hardness                  0
         Solids                    0
         Chloramines               0
         Conductivity              0
         Organic_carbon            0
         Turbidity                 0
         Potability                0
         ph_random                 0
         Sulfate_random            0
         Trihalomethanes_random    0
         dtype: int64
```

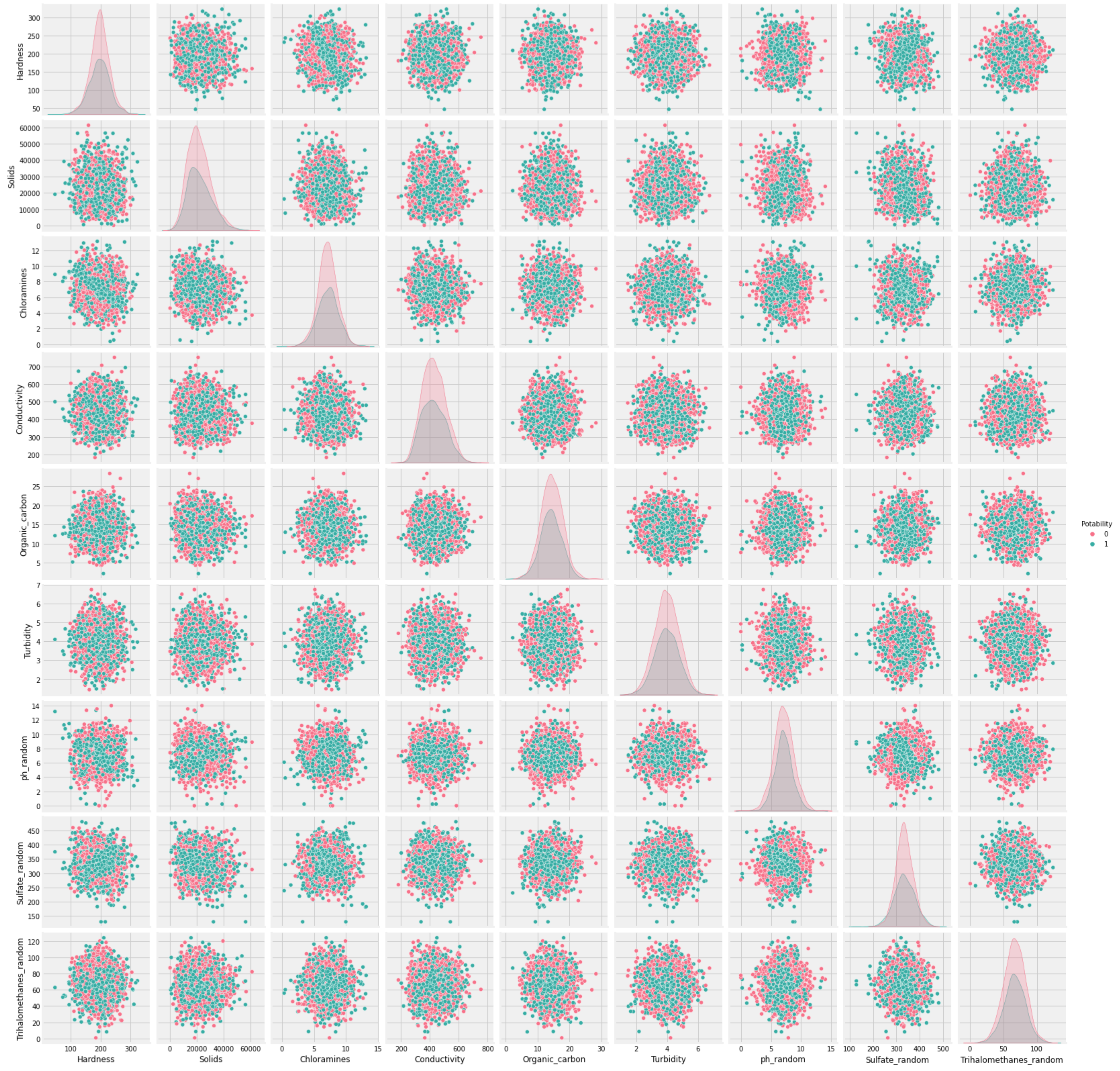
Check for Correlation

```
In [21]: plt.figure(figsize=(20, 17))
         matrix = np.triu(data.corr())
         sns.heatmap(data.corr(), annot=True,linewidth=.8, mask=matrix, cmap="rocket",cbar=False)
```



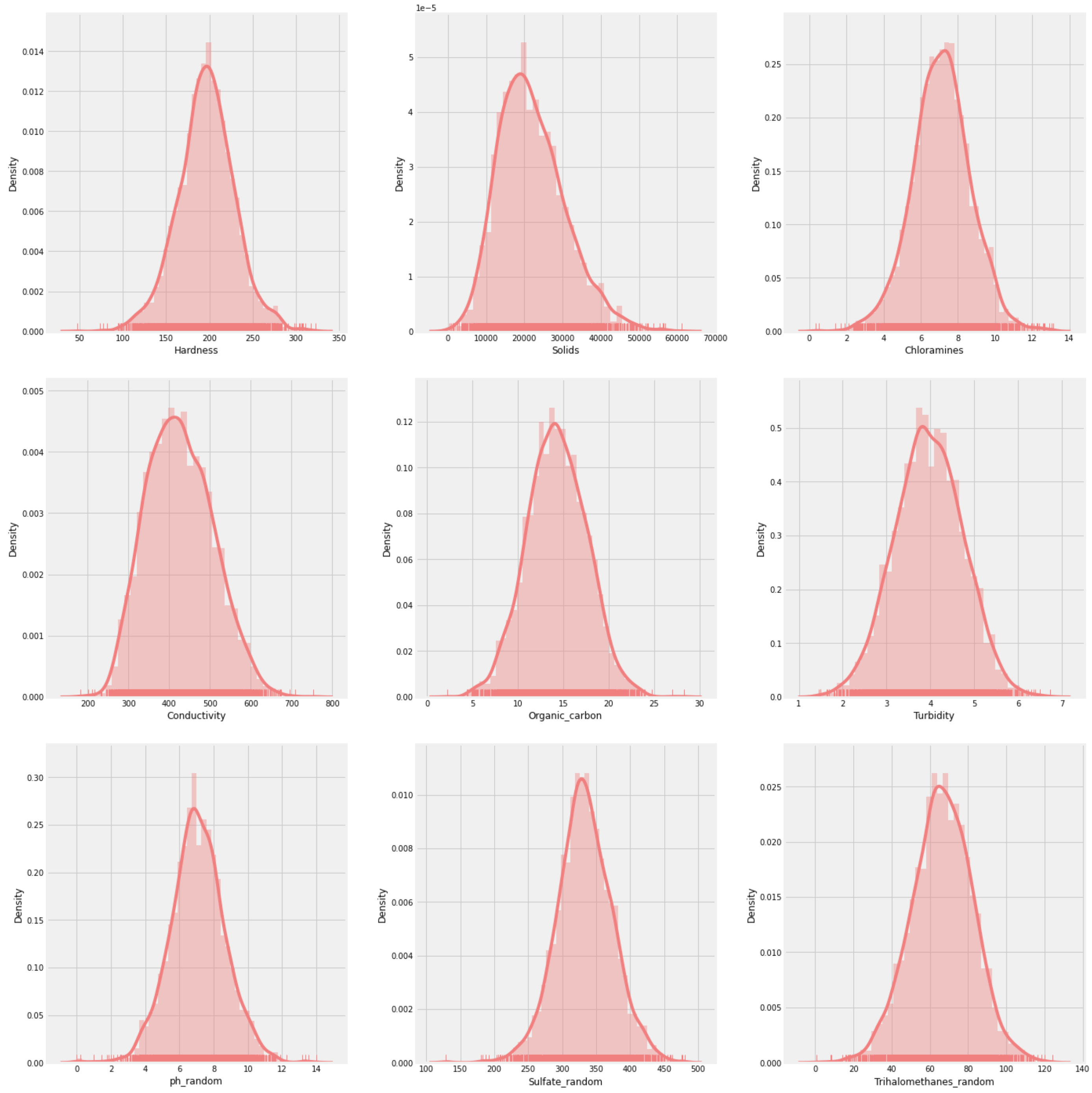
There are no correlated columns presebt in the data

In [22]:
```
sns.pairplot(data, hue="Potability", palette="husl");
```



```
In [23]: def distributionPlot(data):
             """
             Creates distribution plot.
             """
             fig = plt.figure(figsize=(20, 20))
             for i in tqdm_notebook(range(0, len(data.columns))):
                 fig.add_subplot(np.ceil(len(data.columns)/3), 3, i+1)
                 sns.distplot(
                     data.iloc[:, i], color="lightcoral", rug=True)
                 fig.tight_layout(pad=3.0)
         plot_data = data.drop(['Potability'], axis =1)
         distributionPlot(plot_data)
```

```
  0%|          | 0/9 [00:00<?, ?it/s]
```

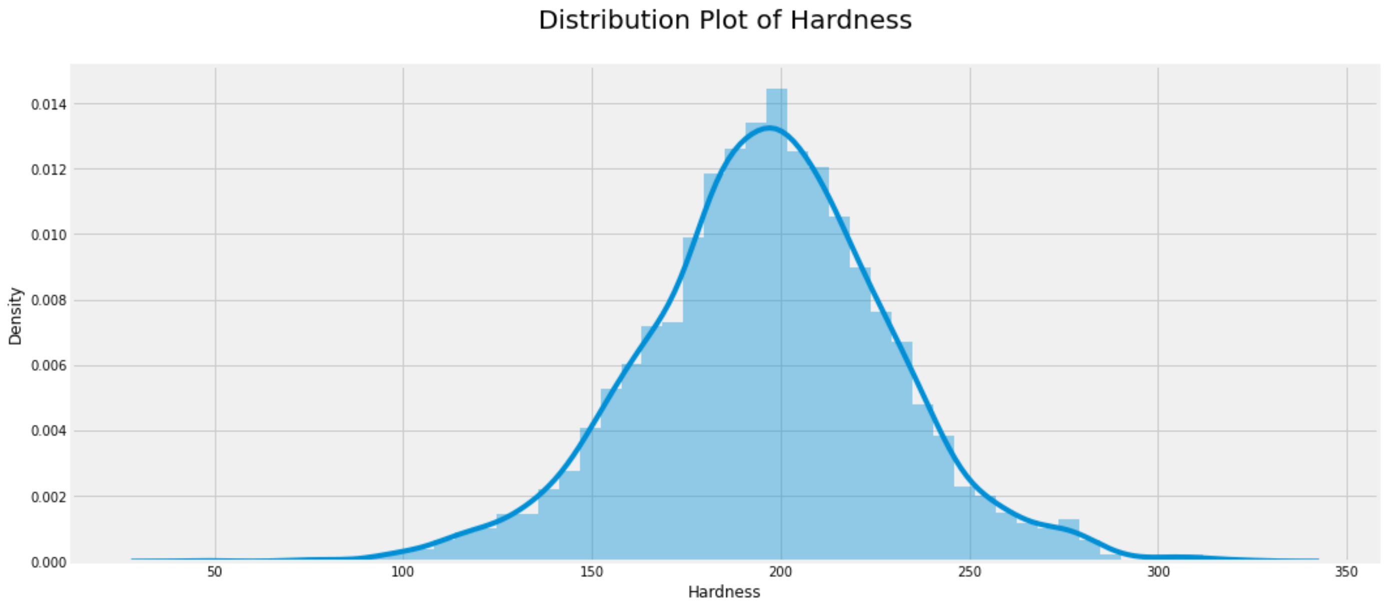


Hardness

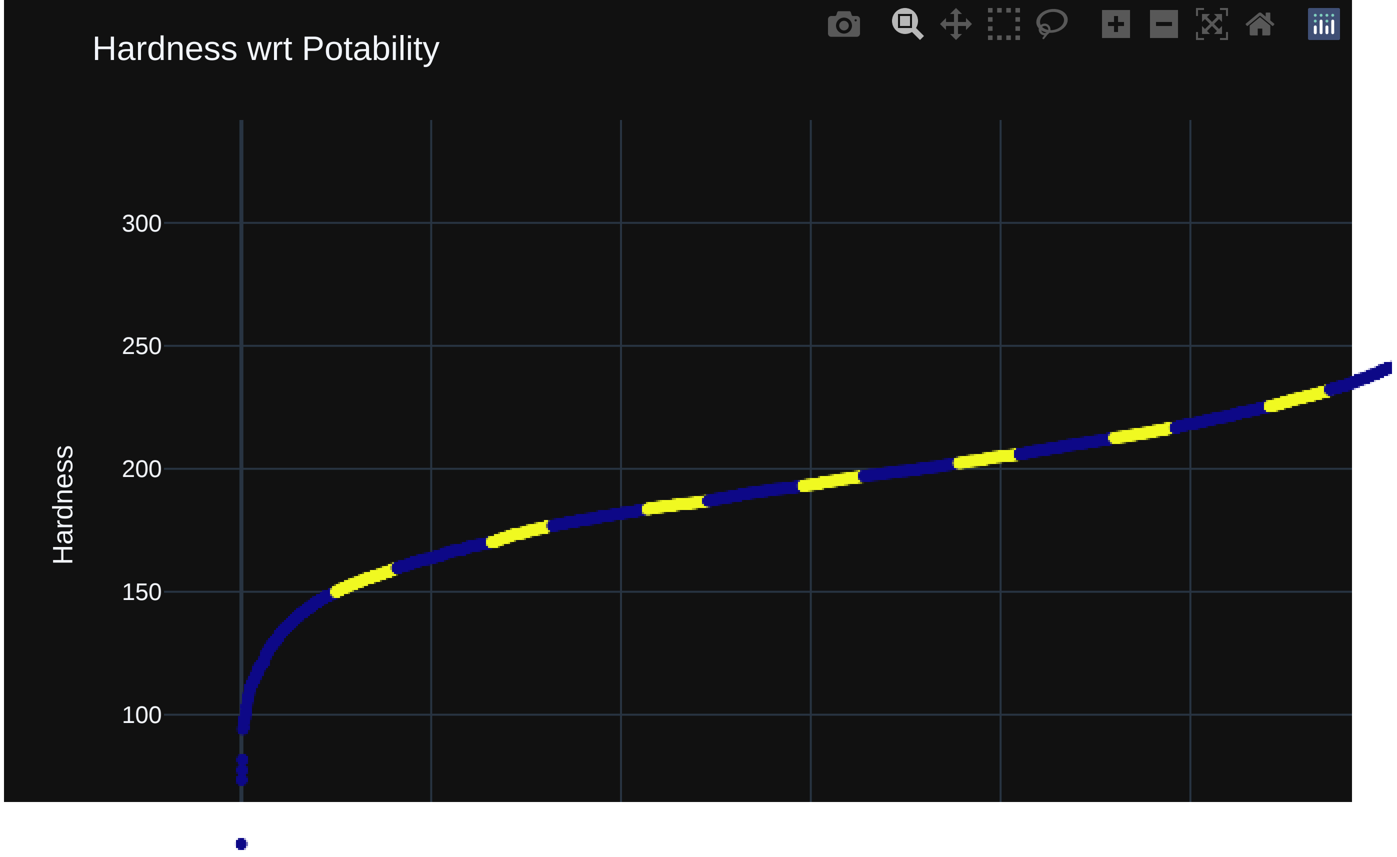
```
In [24]: data['Hardness'].describe()
```

```
Out[24]: count    3276.000000
         mean      196.369496
         std        32.879761
         min        47.432000
         25%       176.850538
         50%       196.967627
         75%       216.667456
         max       323.124000
         Name: Hardness, dtype: float64
```

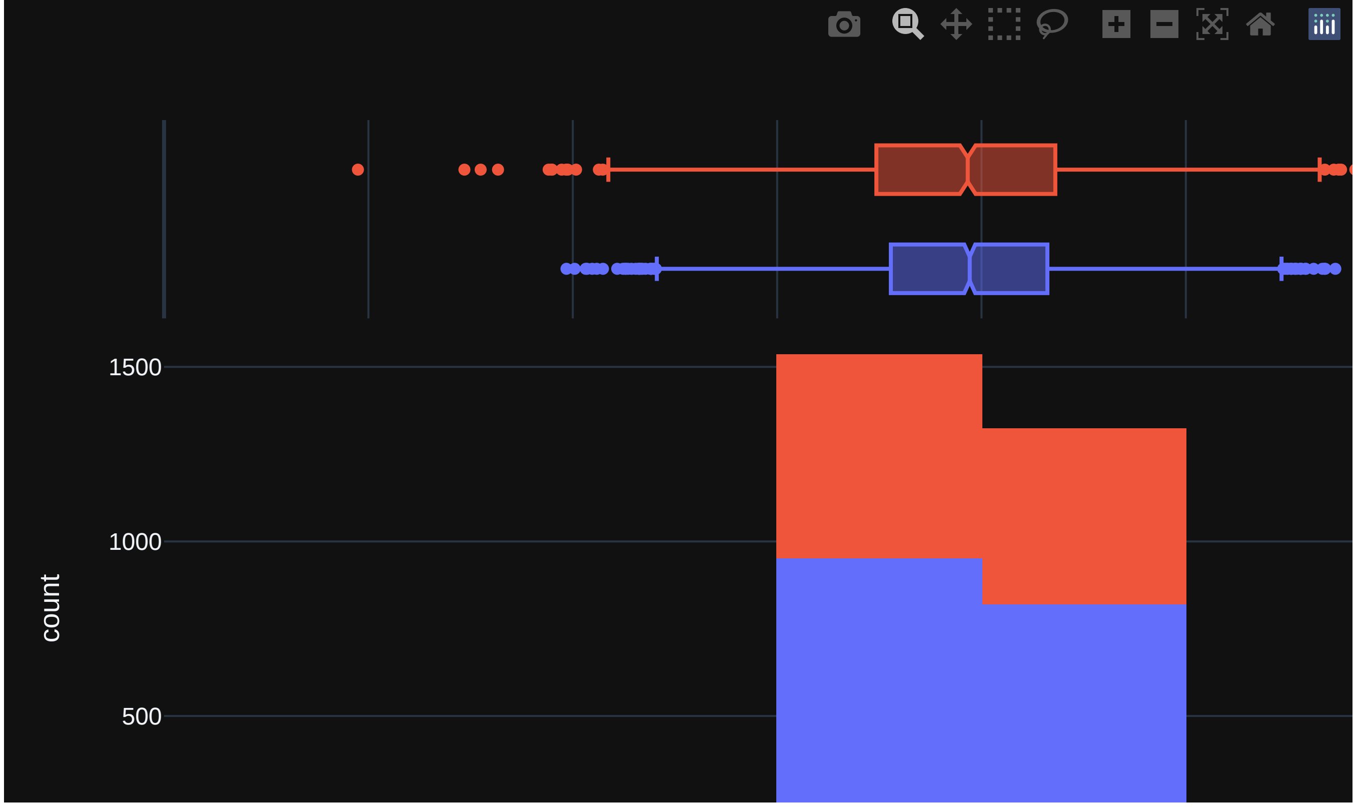
```
In [25]: plt.figure(figsize = (16, 7))
         sns.distplot(data['Hardness'])
         plt.title('Distribution Plot of Hardness\n', fontsize =  20)
         plt.show()
```



In [26]:
```
# basic scatter plot
fig = px.scatter(data,range(data['Hardness'].count()), sorted(data['Hardness']),
                 color=data['Potability'],
                 labels={
                     'x': "Count",
                     'y': "Hardness",
                     'color':'Potability'

                 }, template = 'plotly_dark')
fig.update_layout(title='Hardness wrt Potability')
fig.show()
```



```
In [27]: px.histogram(data_frame = data, x = 'Hardness', nbins = 10, color = 'Potability', margin
                    template = 'plotly_dark')
```

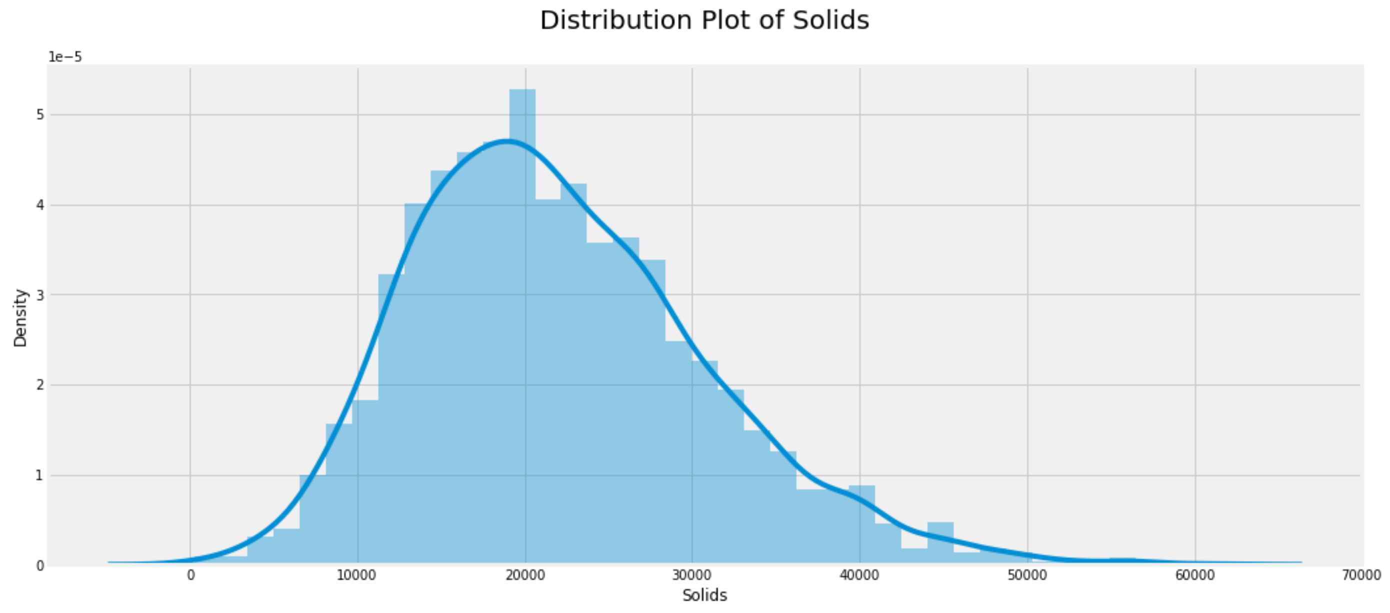


Solids

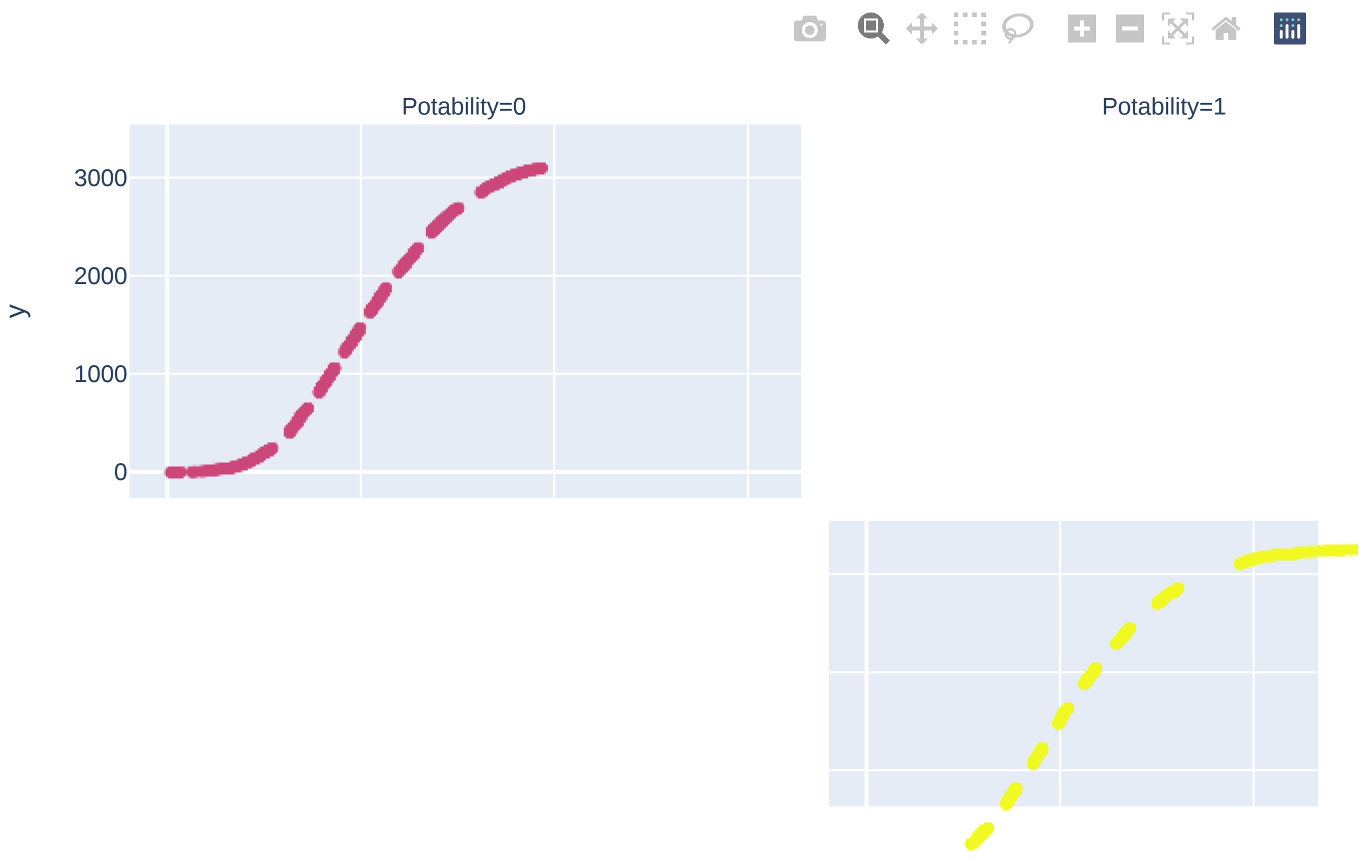
In [28]:
```
data['Solids'].describe()
```

Out[28]:
```
count     3276.000000
mean     22014.092526
std       8768.570828
min        320.942611
25%      15666.690297
50%      20927.833607
75%      27332.762127
max      61227.196008
Name: Solids, dtype: float64
```

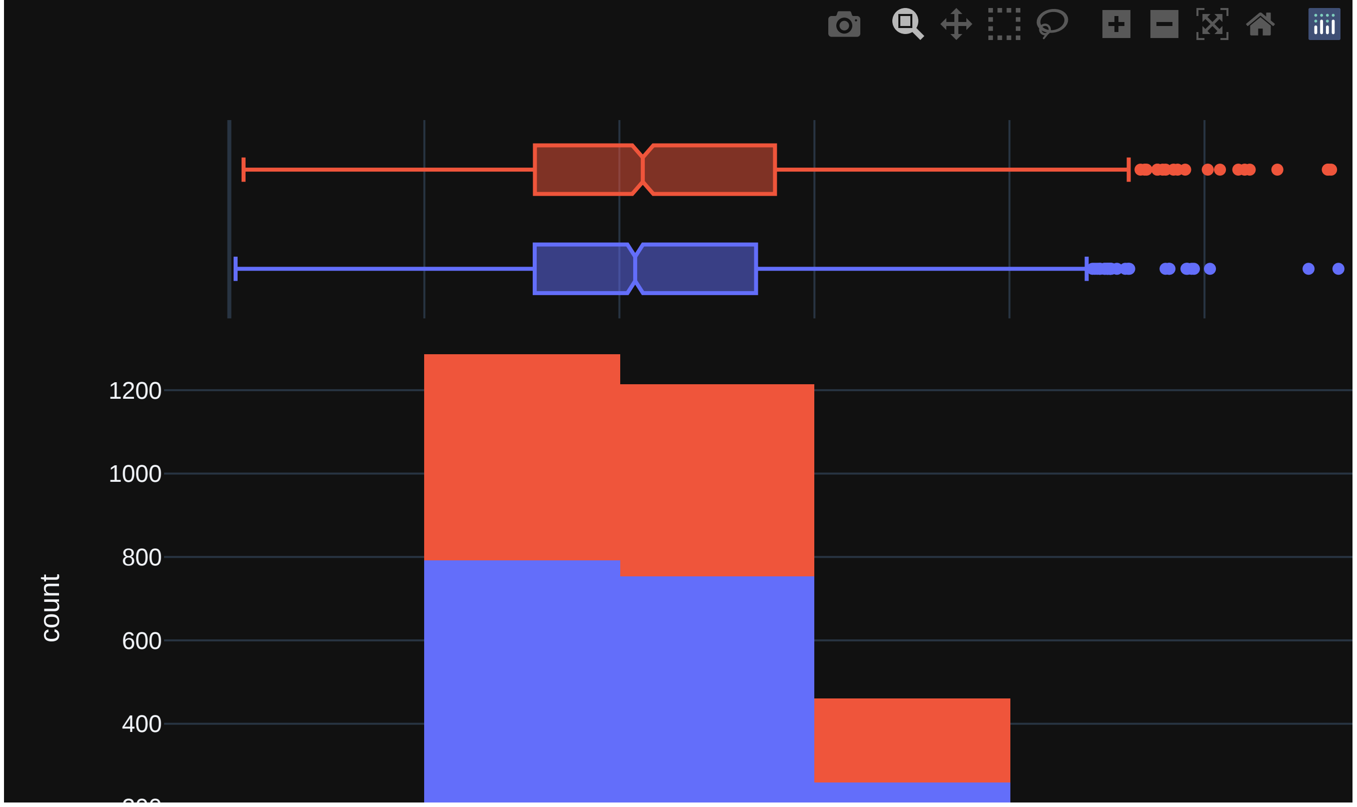
In [29]:
```
plt.figure(figsize = (16, 7))
sns.distplot(data['Solids'])
plt.title('Distribution Plot of Solids\n', fontsize =  20)
plt.show()
```



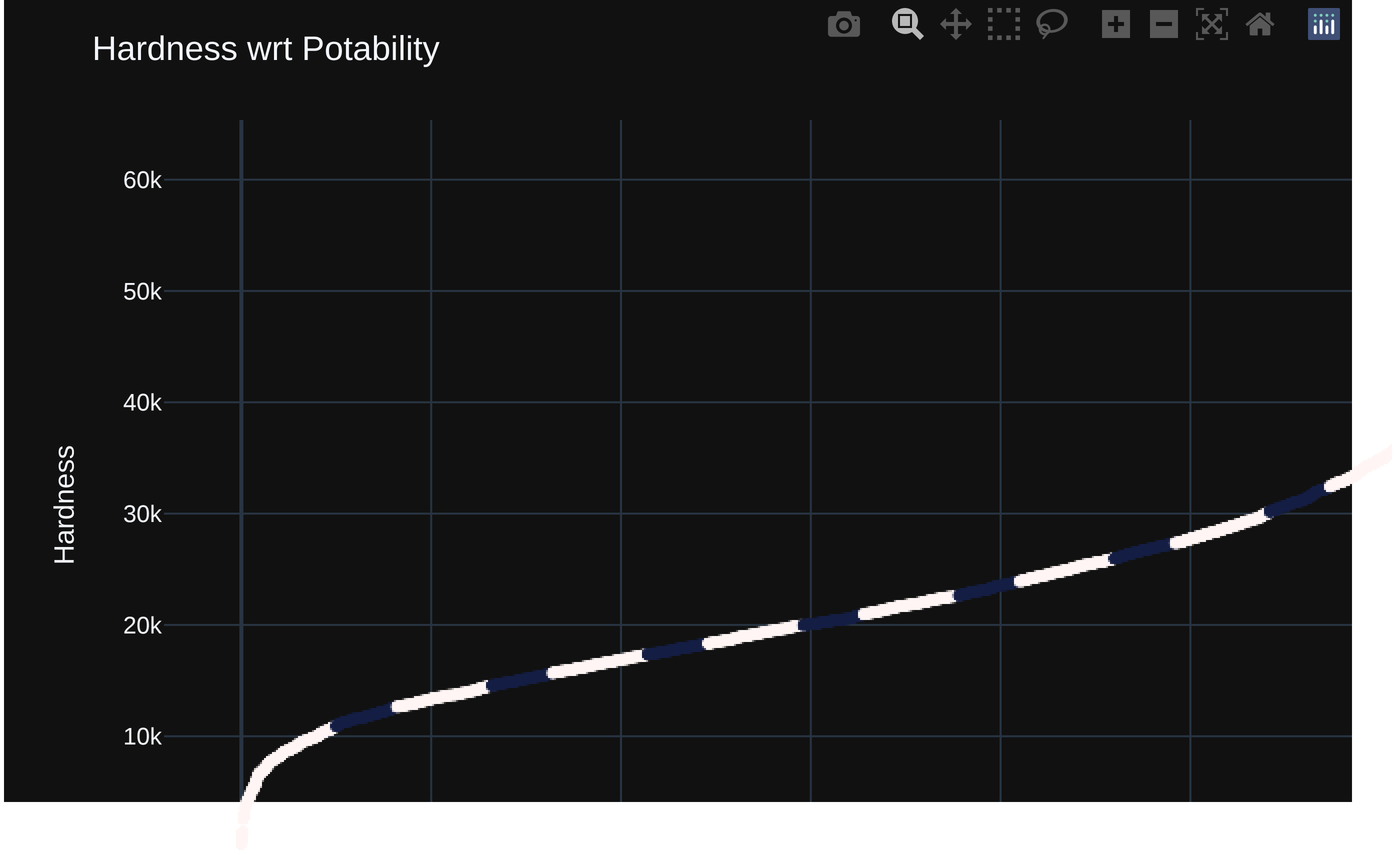
In [30]:
```
fig = px.scatter(data, sorted(data["Solids"]), range(data["Solids"].count()), color="Pot
                 facet_row="Potability")
fig.show()
```



In [31]:
```
px.histogram(data_frame = data, x = 'Solids', nbins = 10, color = 'Potability', marginal
             template = 'plotly_dark')
```



```
In [32]: # basic scatter plot
fig = px.scatter(data,range(data['Solids'].count()), sorted(data['Solids']),
                 color=data['Potability'],
                 labels={
                     'x': "Count",
                     'y': "Hardness",
                     'color':'Potability'

                 },
                 color_continuous_scale=px.colors.sequential.tempo,
                 template = 'plotly_dark')
fig.update_layout(title='Hardness wrt Potability')
fig.show()
```

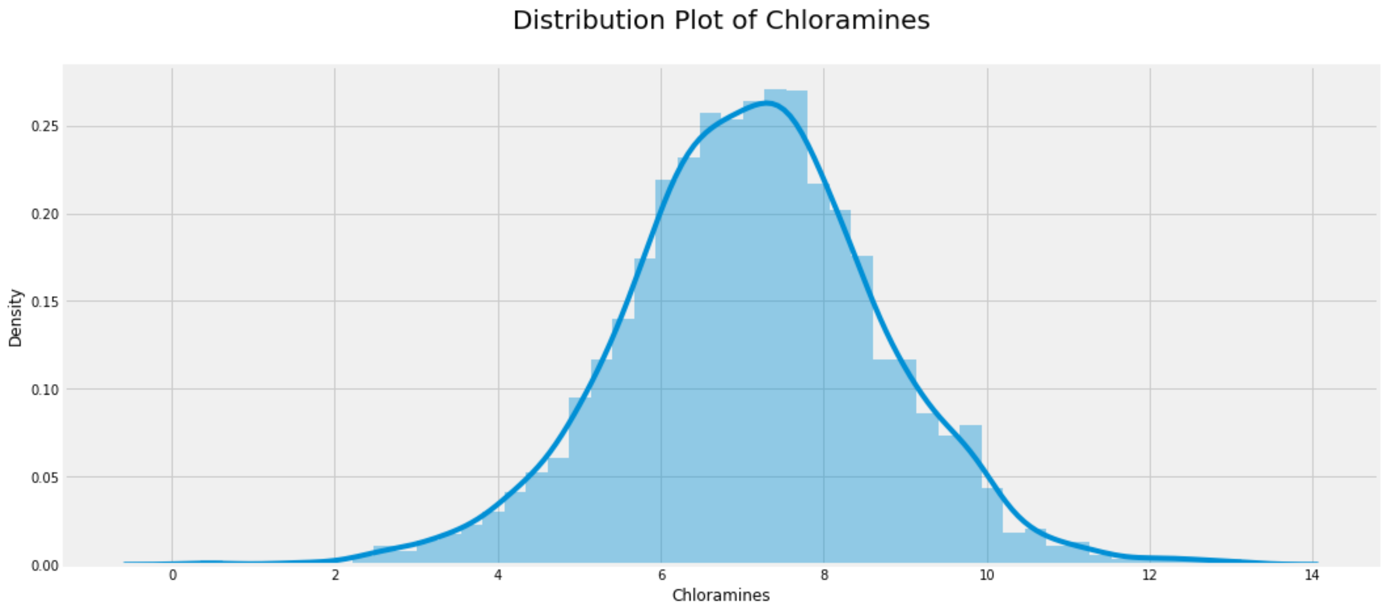


Chloramines

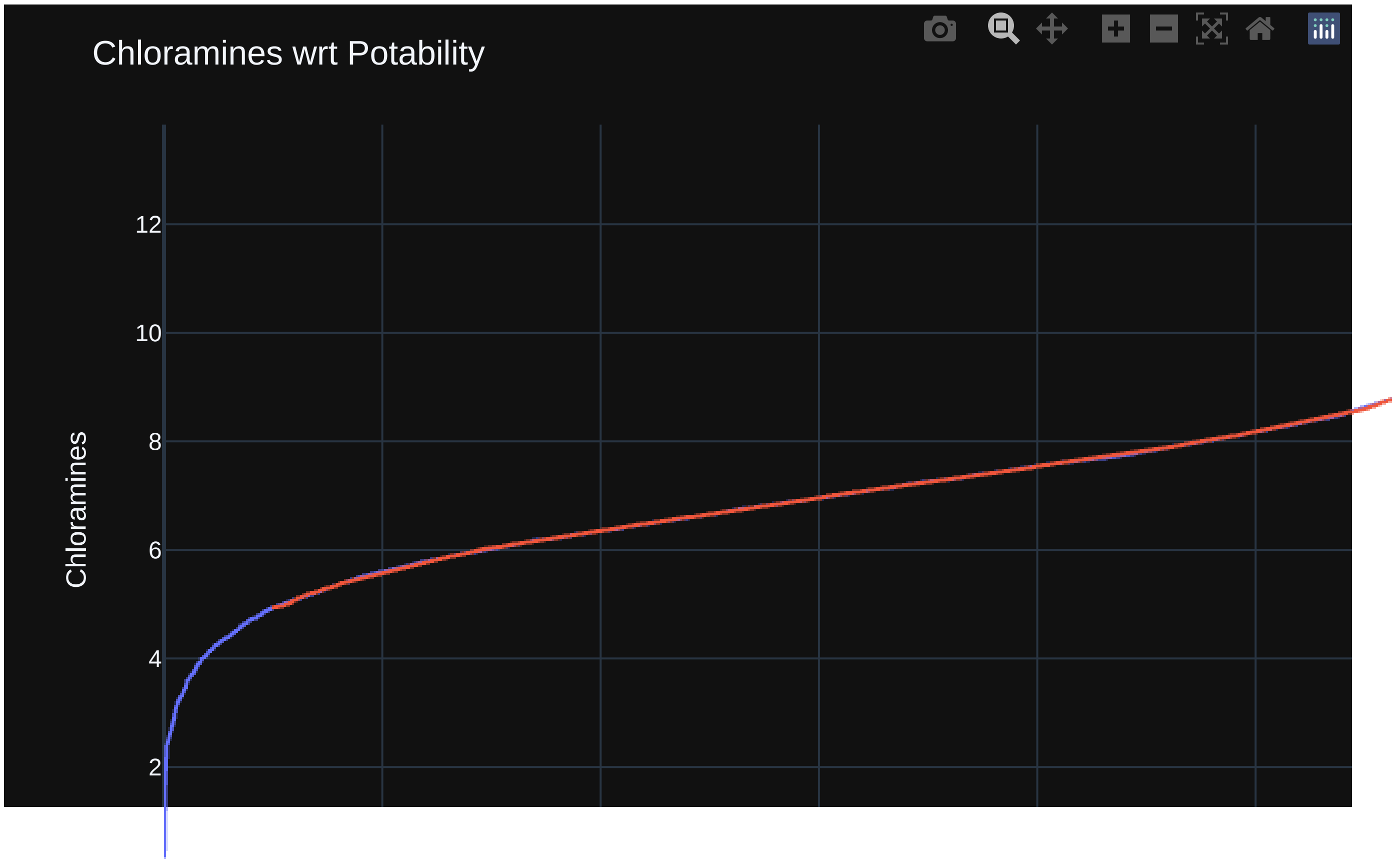
In [33]:
```
data['Chloramines'].describe()
```

Out[33]:
```
count    3276.000000
mean        7.122277
std         1.583085
min         0.352000
25%         6.127421
50%         7.130299
75%         8.114887
max        13.127000
Name: Chloramines, dtype: float64
```

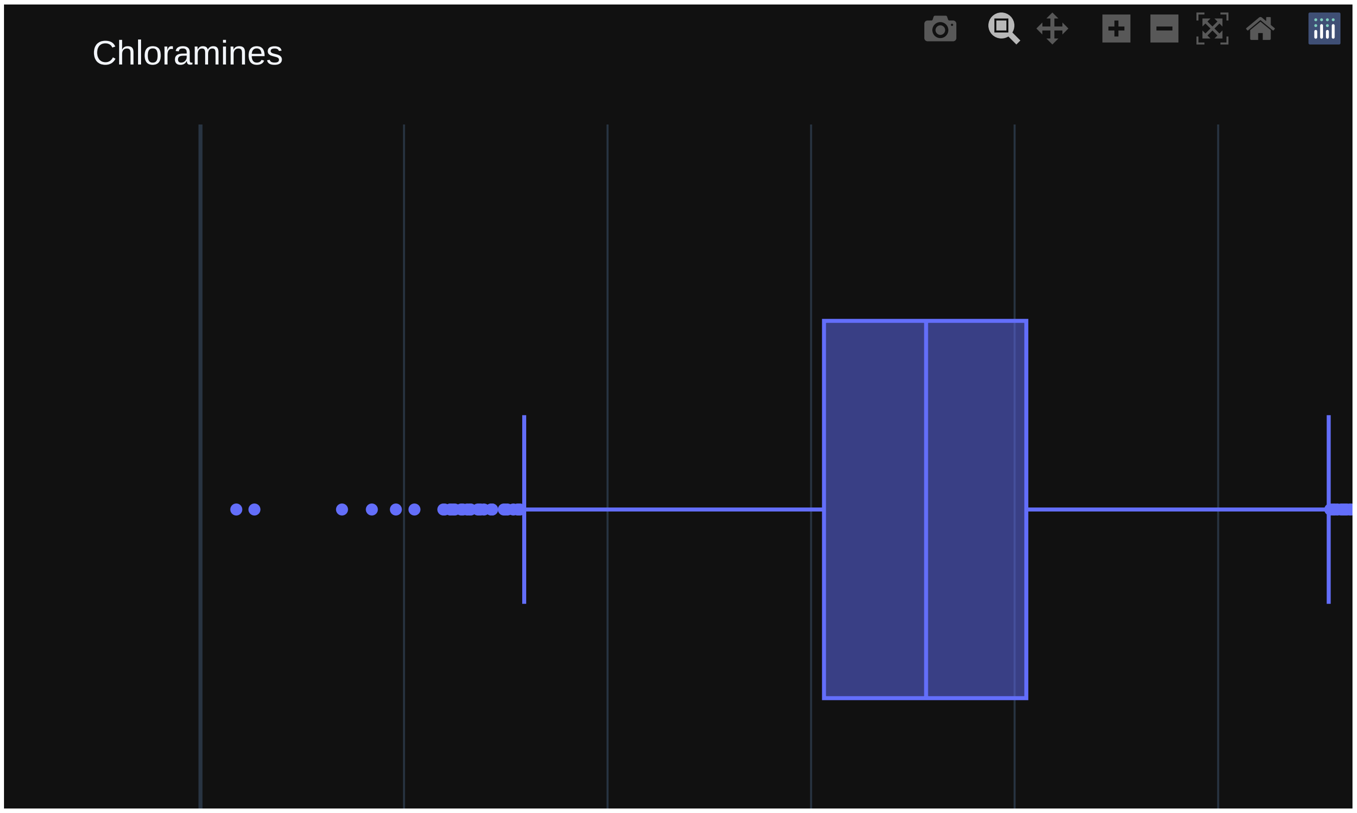
In [34]:
```
plt.figure(figsize = (16, 7))
sns.distplot(data['Chloramines'])
plt.title('Distribution Plot of Chloramines\n', fontsize =  20)
plt.show()
```



In [35]:
```
fig = px.line(x=range(data['Chloramines'].count()), y=sorted(data['Chloramines']),color=
                     'x': "Count",
                     'y': "Chloramines",
                     'color':'Potability'

                 }, template = 'plotly_dark')
fig.update_layout(title='Chloramines wrt Potability')
fig.show()
```



In [36]:
```
fig = px.box(x = 'Chloramines', data_frame = data, template = 'plotly_dark')
fig.update_layout(title='Chloramines')
fig.show()
```

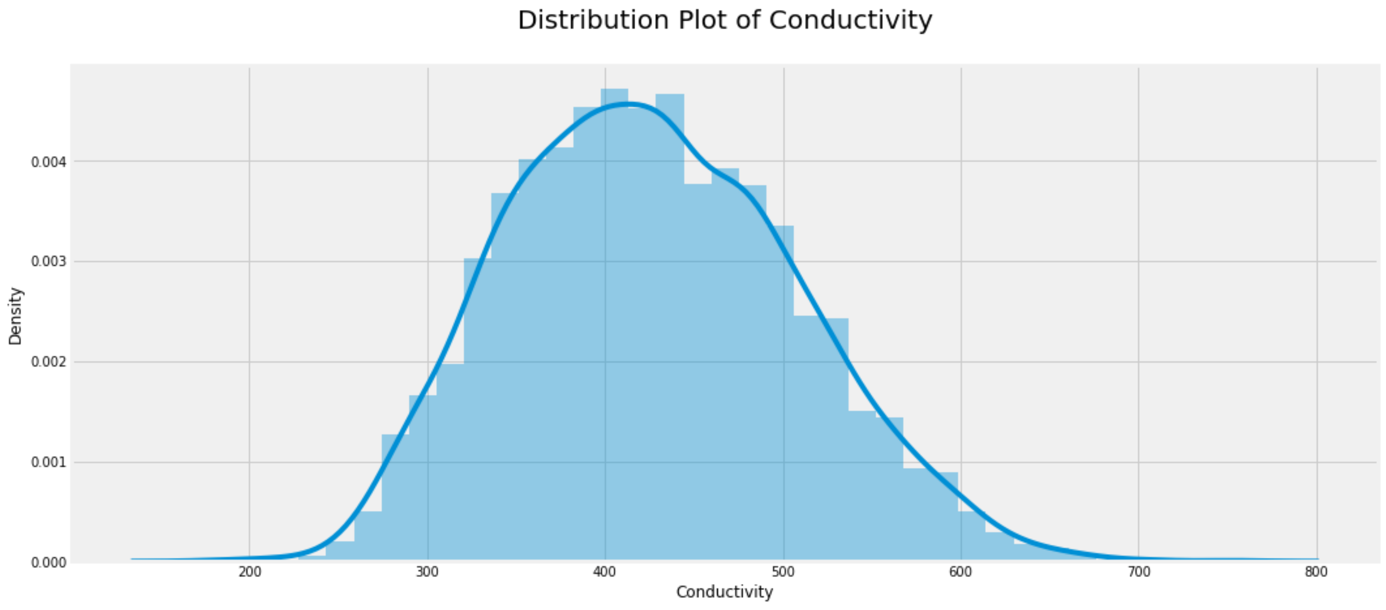


Conductivity

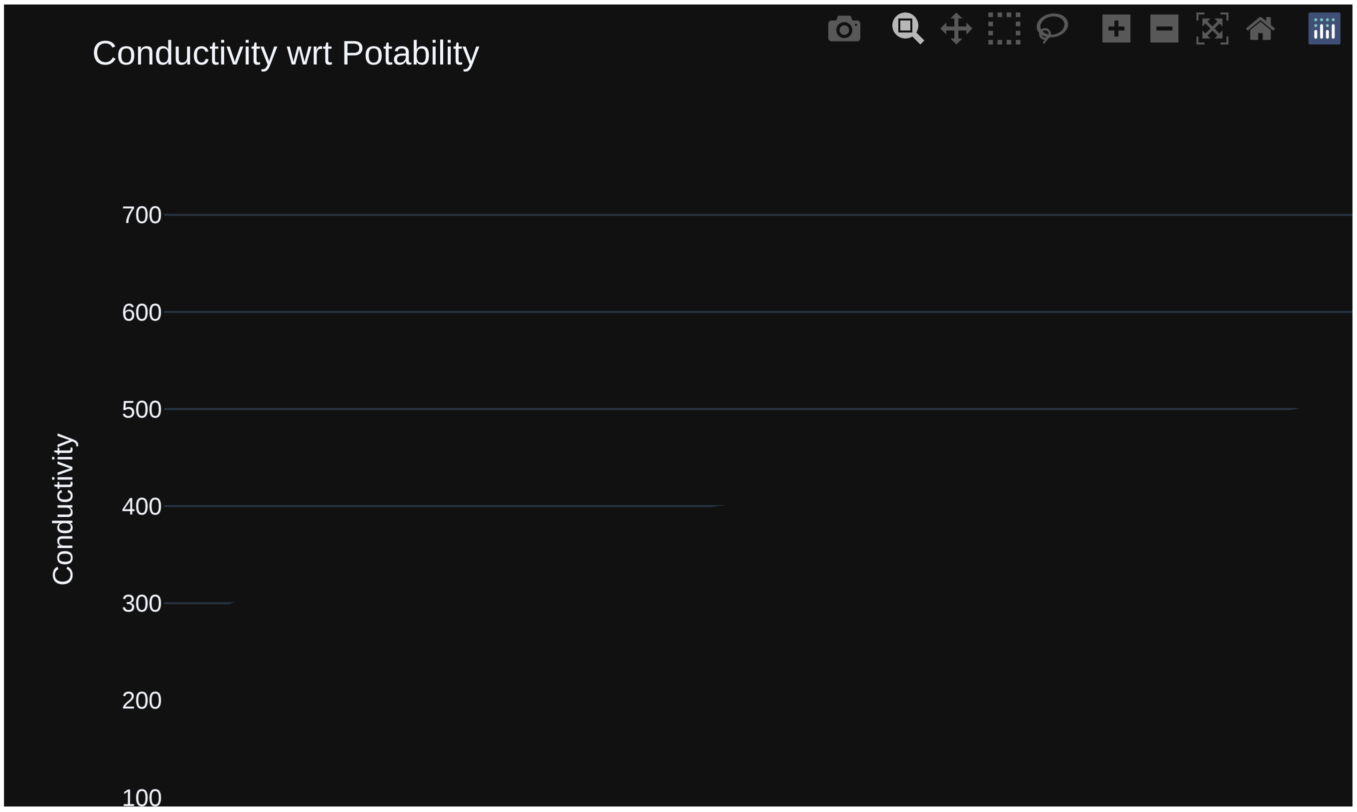
In [37]:
```
data["Conductivity"].describe()
```

Out[37]:
```
count    3276.000000
mean      426.205111
std        80.824064
min       181.483754
25%       365.734414
50%       421.884968
75%       481.792304
max       753.342620
Name: Conductivity, dtype: float64
```

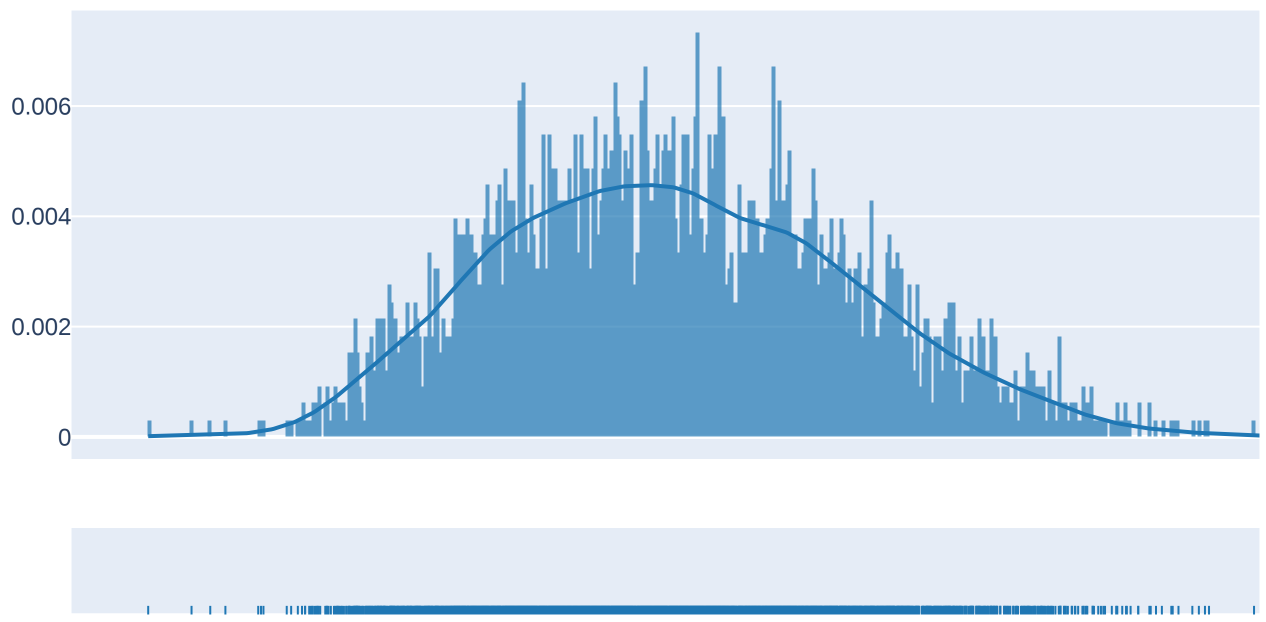
In [38]:
```
plt.figure(figsize = (16, 7))
sns.distplot(data['Conductivity'])
plt.title('Distribution Plot of Conductivity\n', fontsize =  20)
plt.show()
```



```
In [39]: fig = px.bar(data, x=range(data['Conductivity'].count()),
                      y=sorted(data['Conductivity']), labels={
                              'x': "Count",
                              'y': "Conductivity",
                              'color':'Potability'

                          },
                      color=data['Potability']
                      ,template = 'plotly_dark')
         fig.update_layout(title='Conductivity wrt Potability')
         fig.show()
```



In [40]:
```
group_labels = ['distplot'] # name of the dataset

fig = ff.create_distplot([data['Conductivity']], group_labels)
fig.show()
```

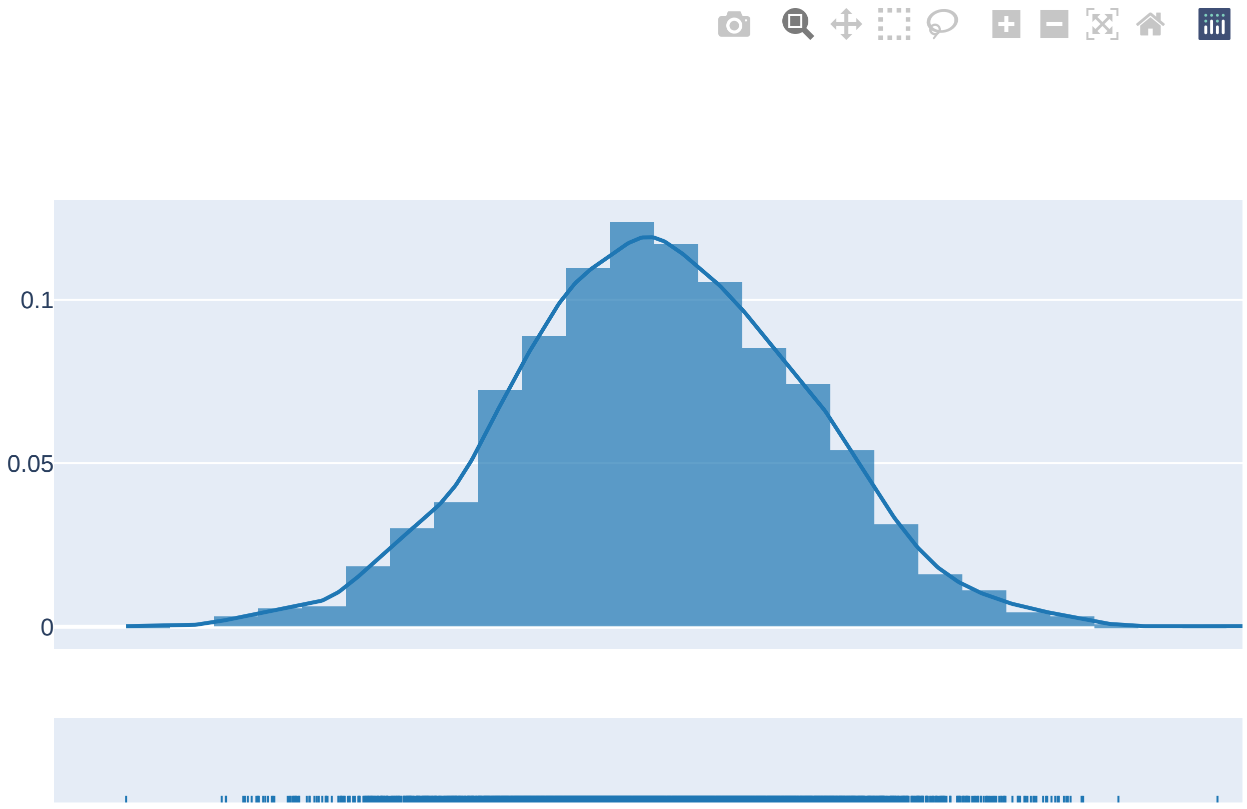


Organic_carbon

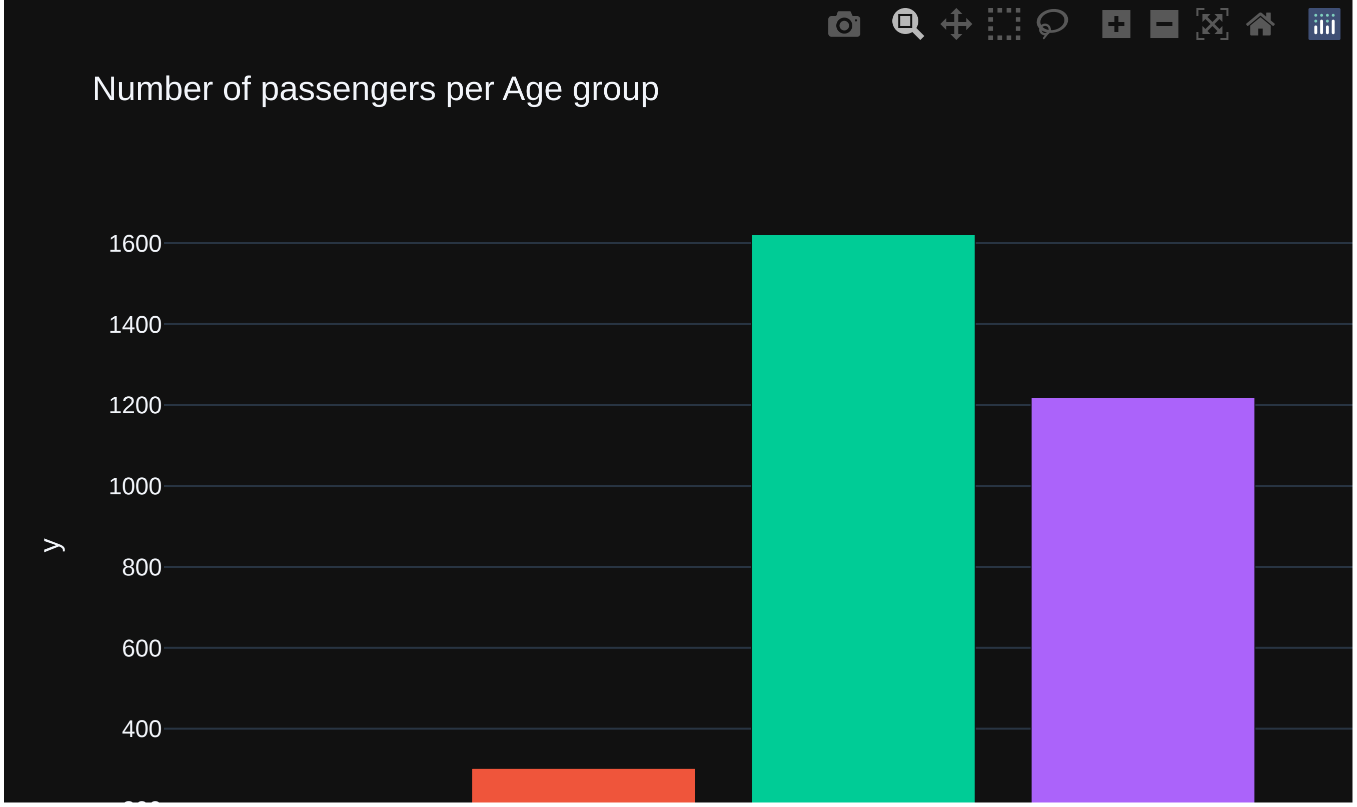
In [41]:
```
data['Organic_carbon'].describe()
```

Out[41]:
```
count    3276.000000
mean       14.284970
std         3.308162
min         2.200000
25%        12.065801
50%        14.218338
75%        16.557652
max        28.300000
Name: Organic_carbon, dtype: float64
```

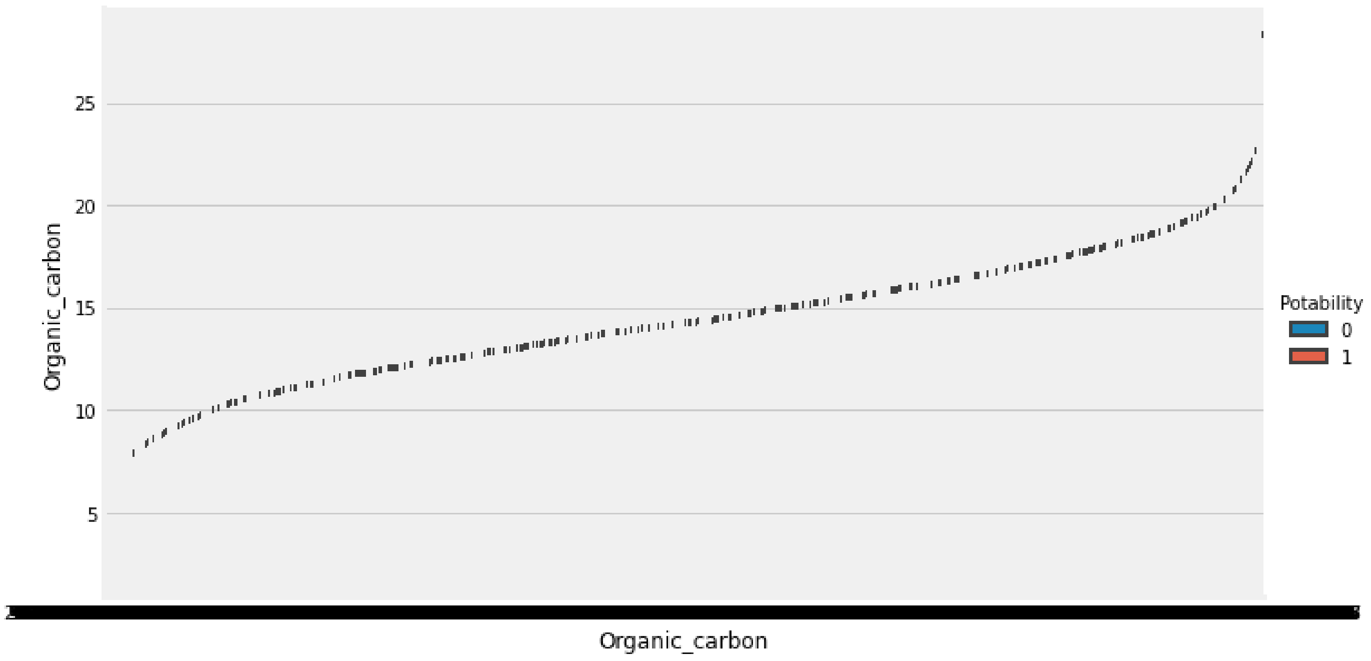
In [42]:
```
group_labels = ['Organic_carbon'] # name of the dataset

fig = ff.create_distplot([data['Organic_carbon']], group_labels)
fig.show()
```



```
In [43]: dt_5=data[data['Organic_carbon']<5]
         dt_5_10=data[(data['Organic_carbon']>5)&(data['Organic_carbon']<10)]
         dt_10_15=data[(data['Organic_carbon']>10)&(data['Organic_carbon']<15)]
         dt_15_20=data[(data['Organic_carbon']>15)&(data['Organic_carbon']<20)]
         dt_20_25=data[(data['Organic_carbon']>20)&(data['Organic_carbon']<25)]
         dt_25=data[(data['Organic_carbon']>25)]

         x_Age = ['5', '5-10', '10-15', '15-20', '25+']
         y_Age = [len(dt_5.values), len(dt_5_10.values), len(dt_10_15.values), len(dt_15_20.value
              len(dt_25.values)]

         px.bar(data_frame = data, x = x_Age, y = y_Age, color = x_Age, template = 'plotly_dark',
               title = 'Number of passengers per Age group')
```



In [44]:
```
sns.catplot(x = 'Organic_carbon', y = 'Organic_carbon', hue = 'Potability', data = data,
            height = 5, aspect = 2)
plt.show()
```

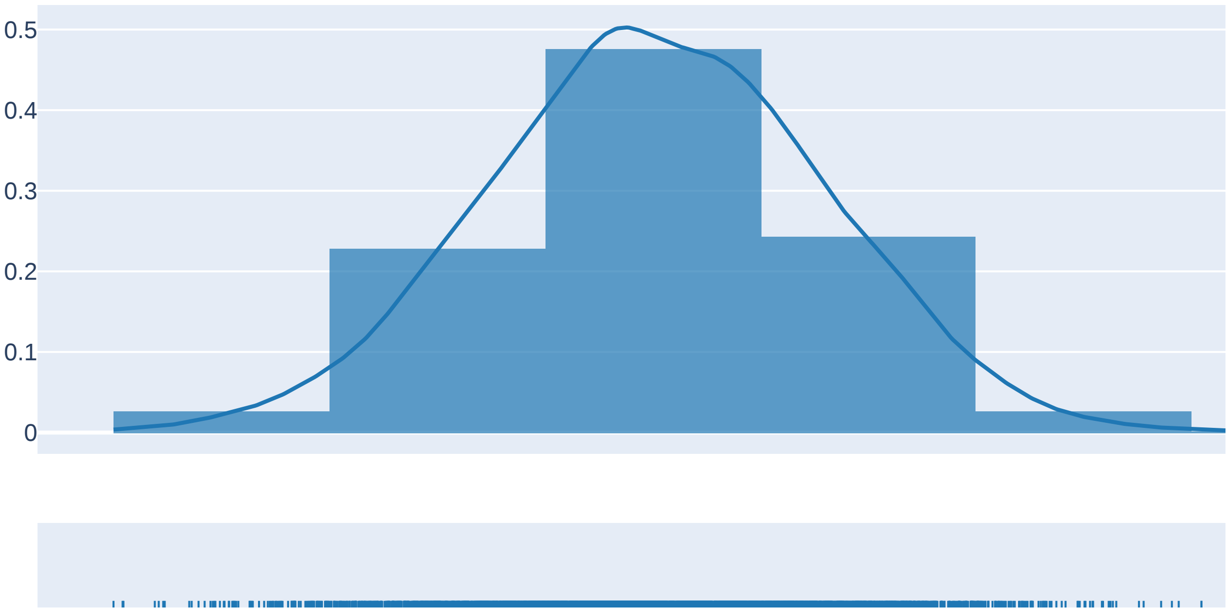


Turbidity

In [45]:
```
data['Turbidity'].describe()
```

Out[45]:
```
count    3276.000000
mean        3.966786
std         0.780382
min         1.450000
25%         3.439711
50%         3.955028
75%         4.500320
max         6.739000
Name: Turbidity, dtype: float64
```

In [46]:
```
group_labels = ['Turbidity'] # name of the dataset

fig = ff.create_distplot([data['Turbidity']], group_labels)
fig.show()
```

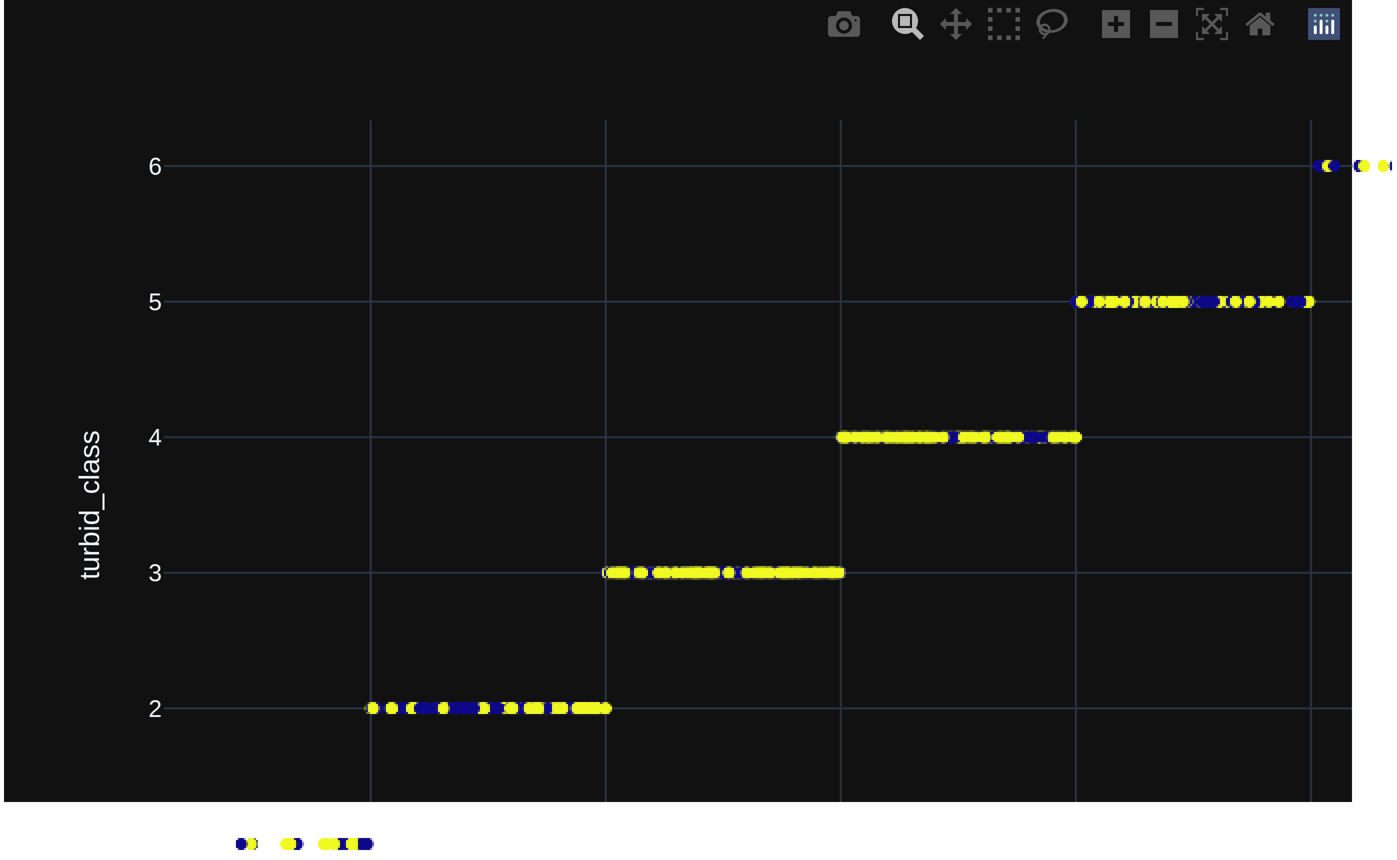


In [47]:
```
data['turbid_class']=data['Turbidity'].astype(int)
```

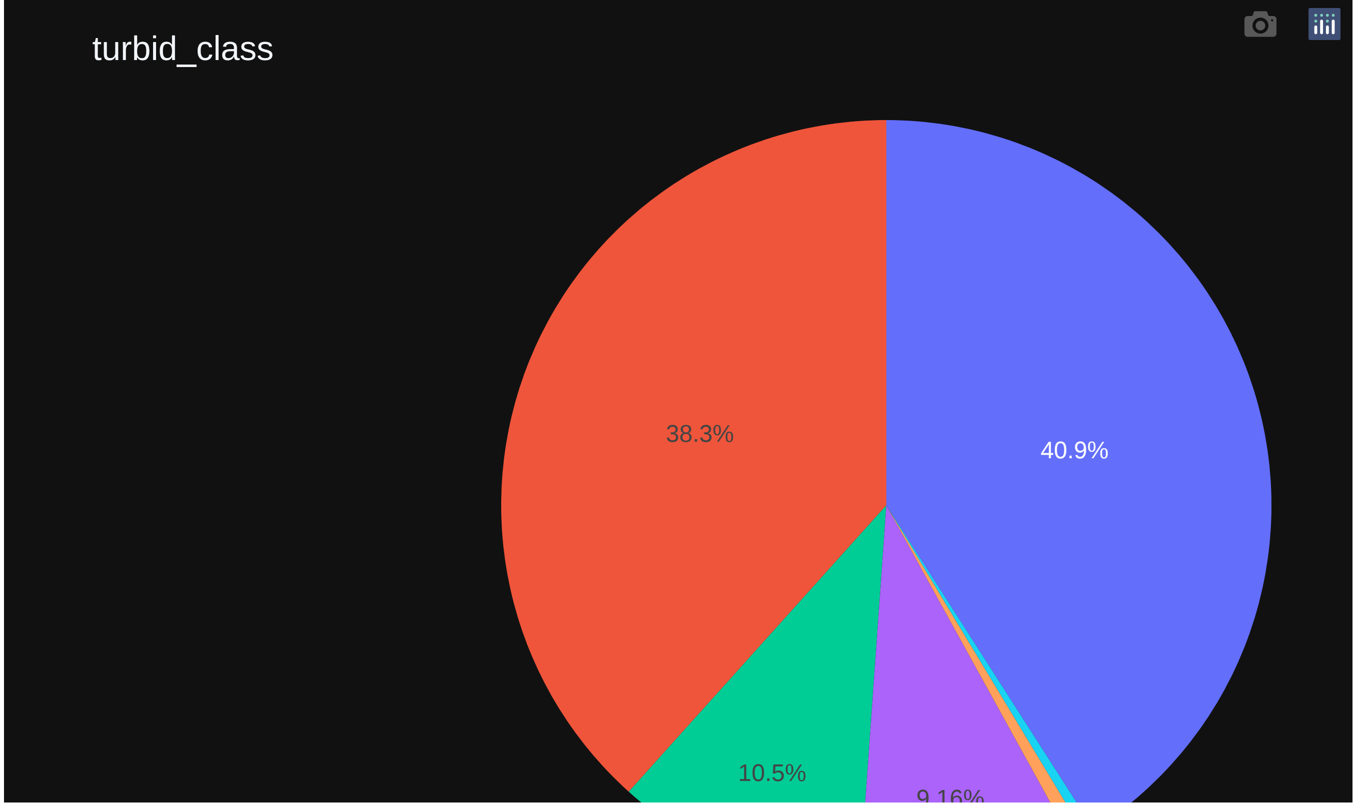
In [48]:
```
data['turbid_class'].unique()
```

Out[48]:
```
array([2, 4, 3, 5, 6, 1])
```

In [49]:
```
px.scatter(data_frame = data, x = 'Turbidity', y = 'turbid_class', color = 'Potability',
```



```
In [50]: fig = px.pie(data,
                      values=data['turbid_class'].value_counts(),
                      names=data['turbid_class'].value_counts().keys(),
                     )
         fig.update_layout(
             title='turbid_class',
             template = 'plotly_dark'
         )
         fig.show()
```



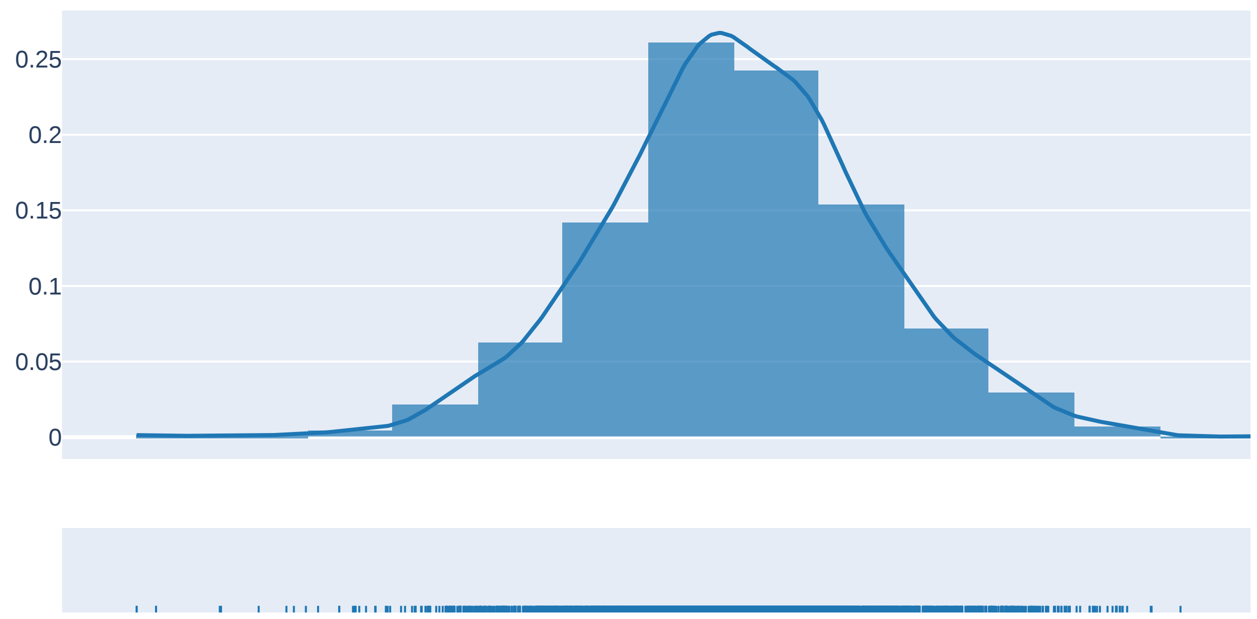
```
In [51]: data=data.drop(['turbid_class'],axis=1)
```

ph_random

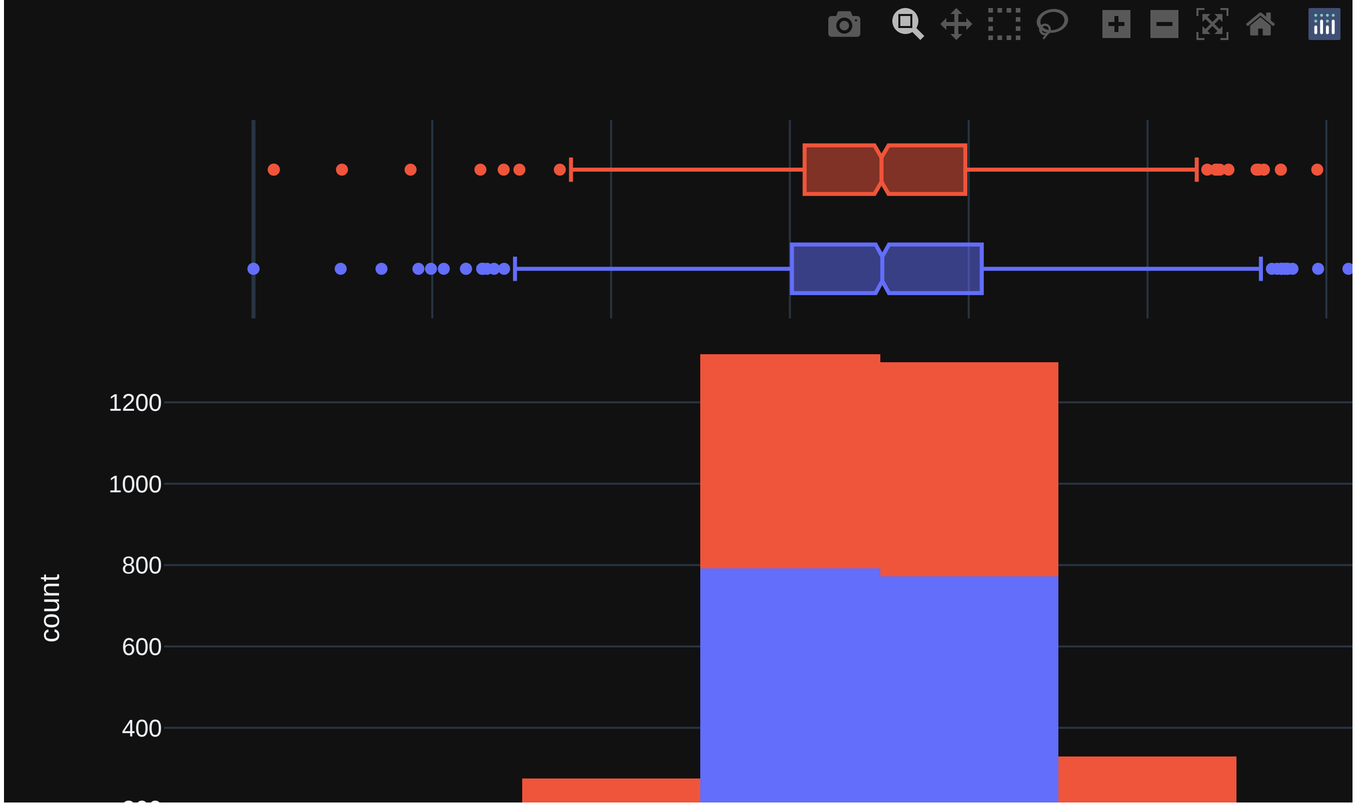
```
In [52]: data['ph_random'].describe()
```

```
Out[52]: count    3276.000000
         mean        7.071639
         std         1.607991
         min         0.000000
         25%         6.081460
         50%         7.029490
         75%         8.063147
         max        14.000000
         Name: ph_random, dtype: float64
```

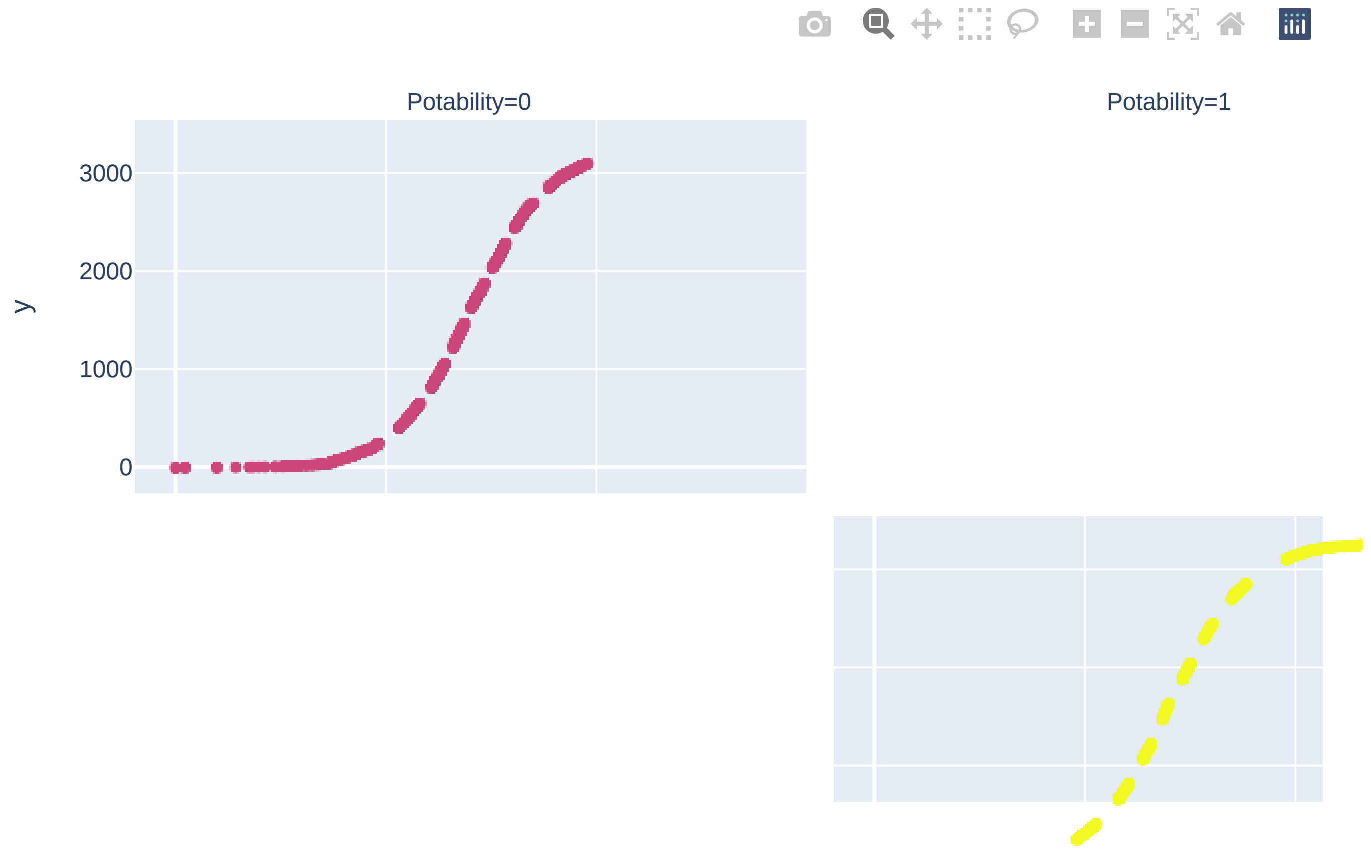
```
In [53]: group_labels = ['ph_random'] # name of the dataset

         fig = ff.create_distplot([data['ph_random']], group_labels)
         fig.show()
```



```
In [54]: px.histogram(data_frame = data, x = 'ph_random', nbins = 10, color = 'Potability', margi
                      template = 'plotly_dark')
```



```
In [55]: fig = px.scatter(data, sorted(data["ph_random"]), range(data["ph_random"].count()), colo
                          facet_row="Potability")
         fig.show()
```

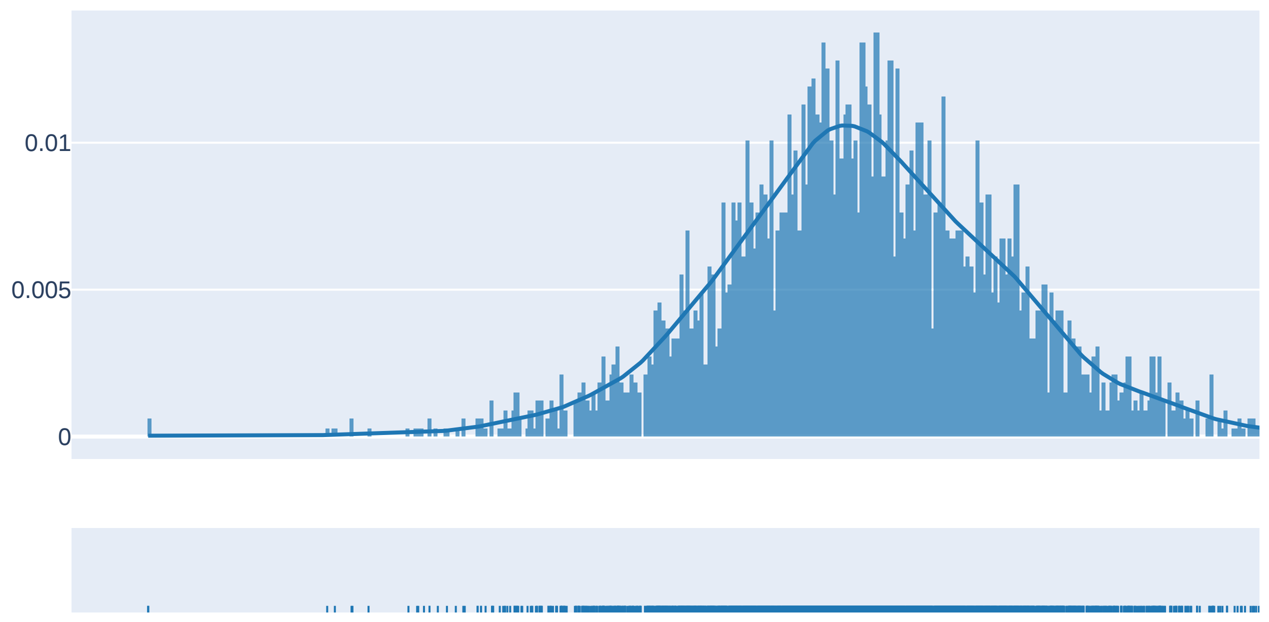


Sulfate_random

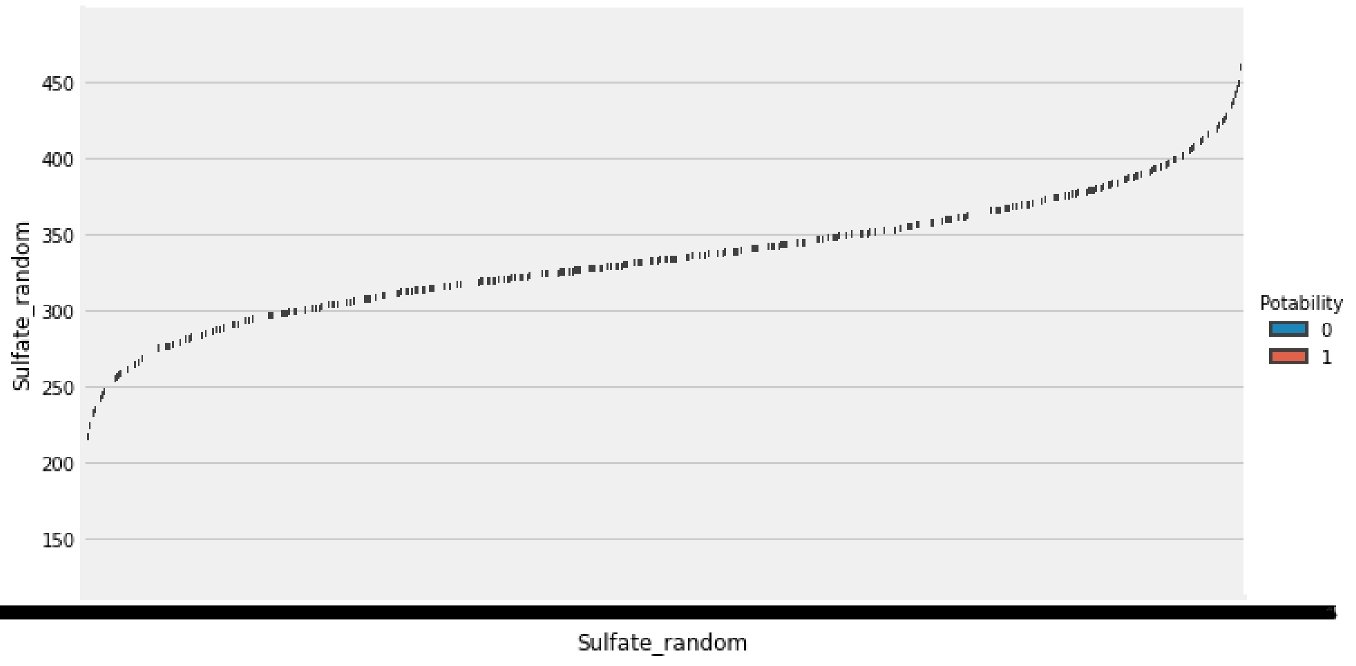
In [56]:
```
data['Sulfate_random'].describe()
```

Out[56]:
```
count    3276.000000
mean      333.430954
std        41.026947
min       129.000000
25%       307.523159
50%       332.879578
75%       359.710517
max       481.030642
Name: Sulfate_random, dtype: float64
```

In [57]:
```
group_labels = ['distplot'] # name of the dataset

fig = ff.create_distplot([data['Sulfate_random']], group_labels)
fig.show()
```



```
In [58]: sns.catplot(x = 'Sulfate_random', y = 'Sulfate_random', hue = 'Potability', data = data,
                     height = 5, aspect = 2)
         plt.show()
```

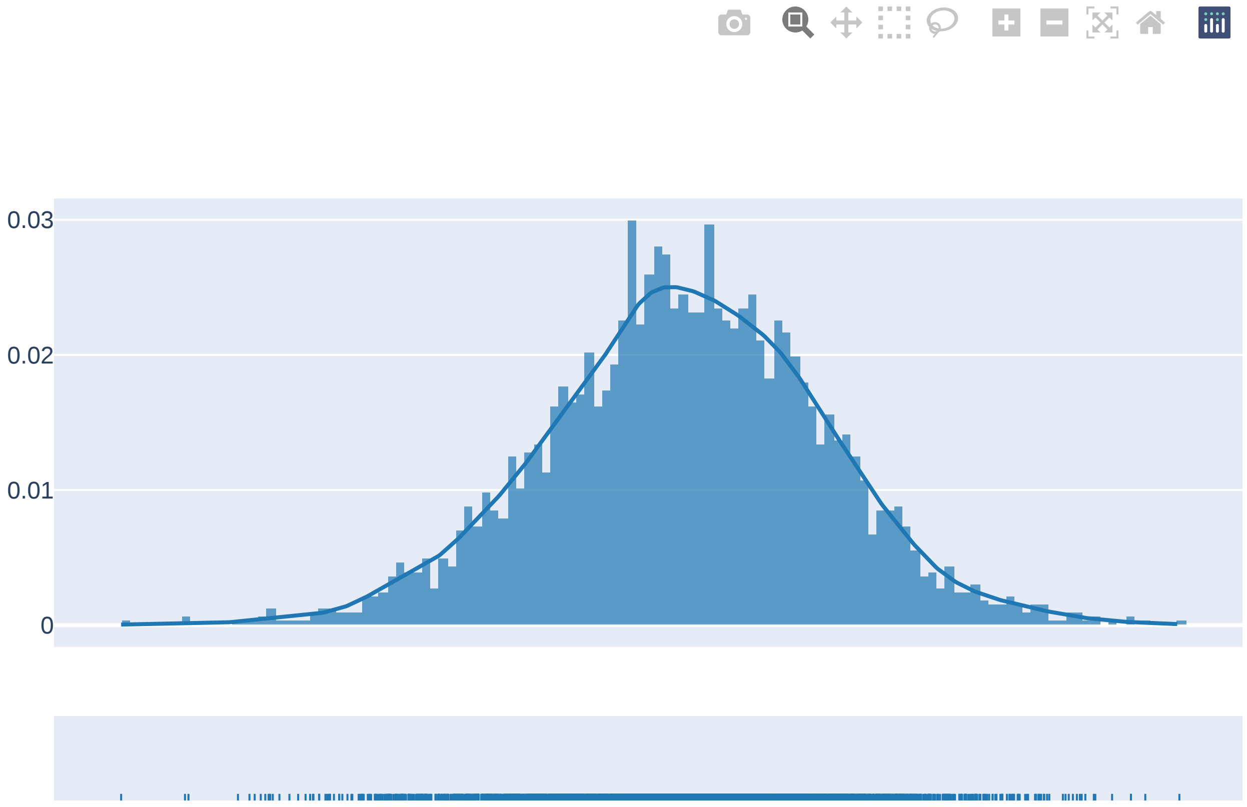


Trihalomethanes_random

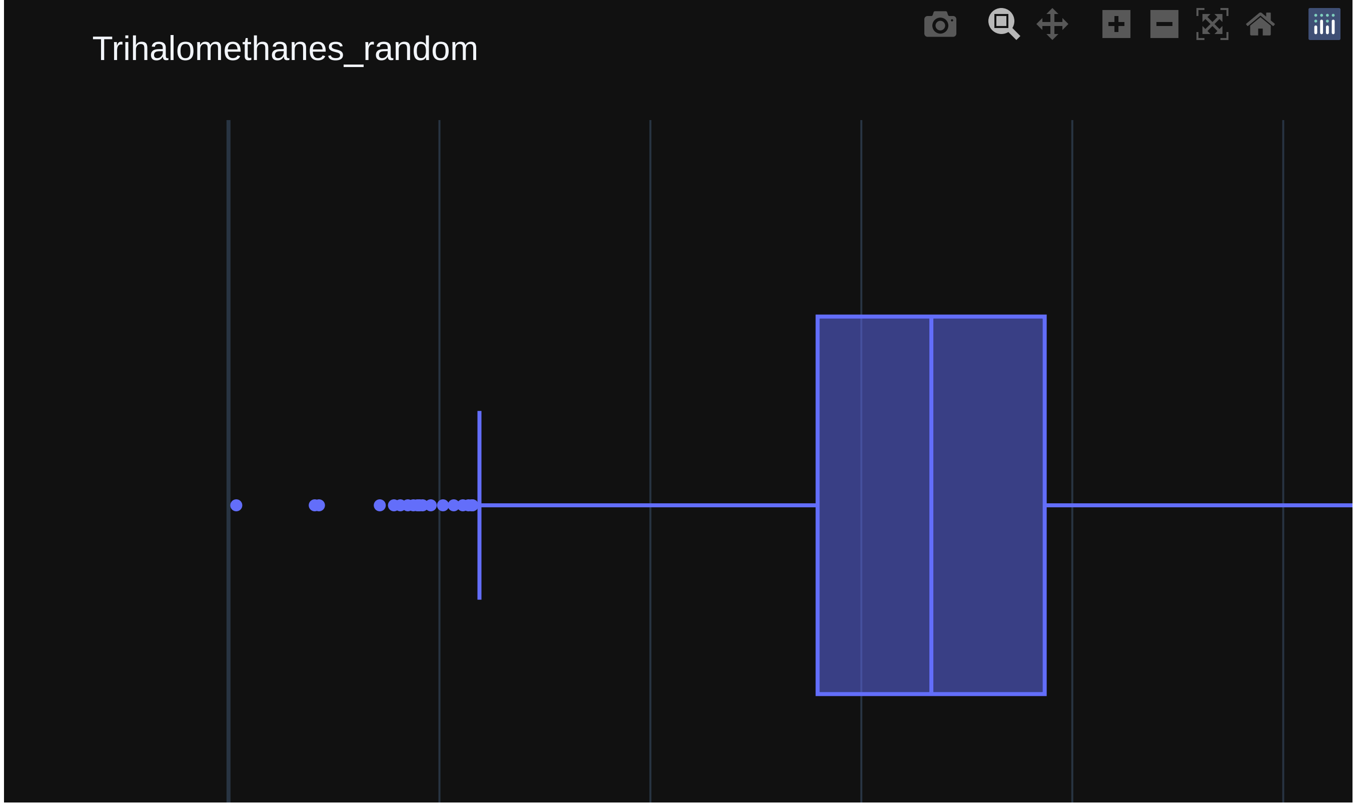
```
In [59]: data['Trihalomethanes_random'].describe()
```

Out[59]:
```
count    3276.000000
mean       66.419200
std        16.184832
min         0.738000
25%        55.861675
50%        66.639068
75%        77.384166
max       124.000000
Name: Trihalomethanes_random, dtype: float64
```

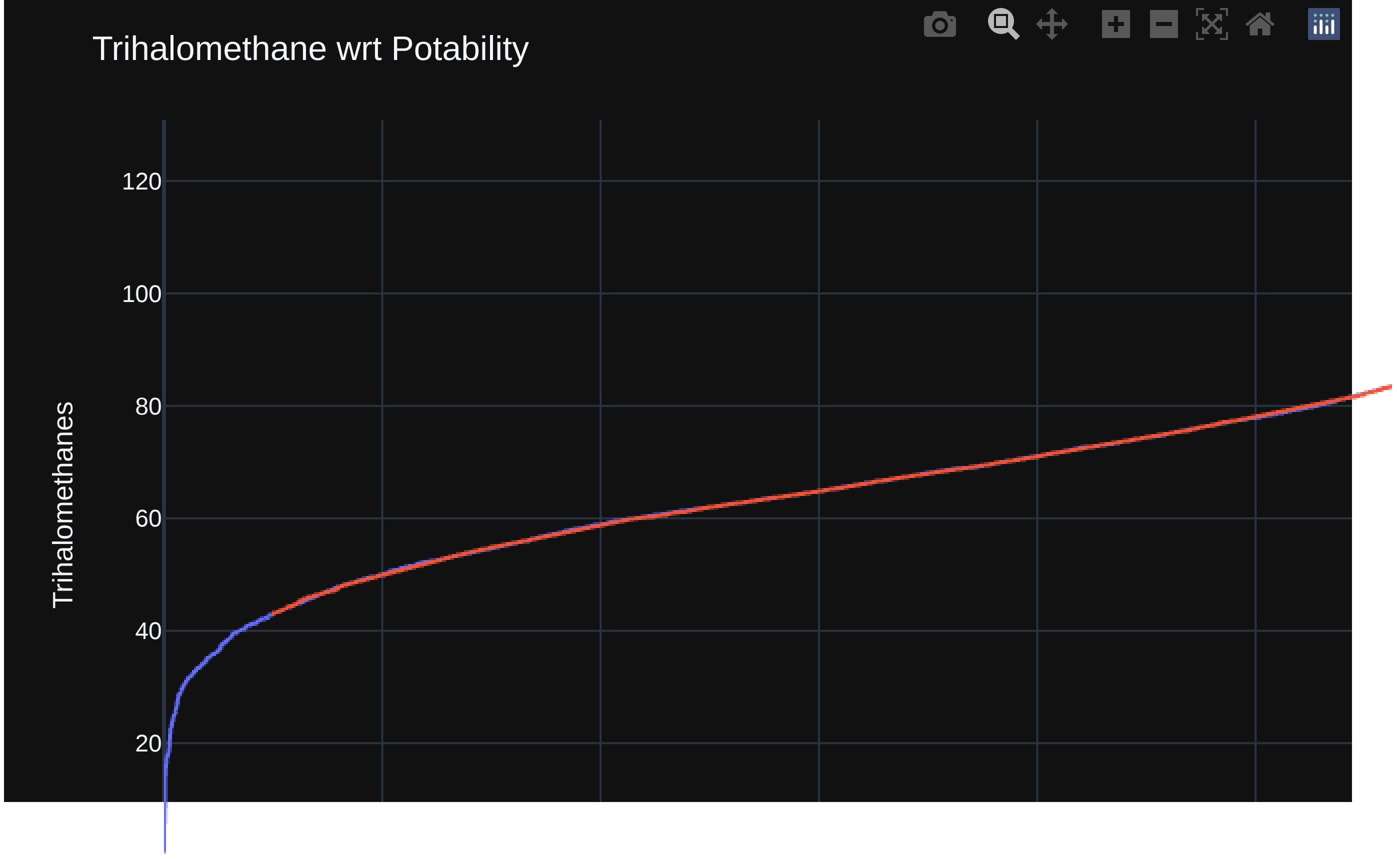
In [60]:
```
group_labels = ['Trihalomethanes_random'] # name of the dataset

fig = ff.create_distplot([data['Trihalomethanes_random']], group_labels)
fig.show()
```



In [61]:
```
fig = px.box(x = 'Trihalomethanes_random', data_frame = data, template = 'plotly_dark')
fig.update_layout(title='Trihalomethanes_random')
fig.show()
```



```
In [62]: fig = px.line(x=range(data['Trihalomethanes_random'].count()), y=sorted(data['Trihalomet
                             'x': "Count",
                             'y': "Trihalomethanes",
                             'color':'Potability'

                         }, template = 'plotly_dark')
         fig.update_layout(title='Trihalomethane wrt Potability')
         fig.show()
```

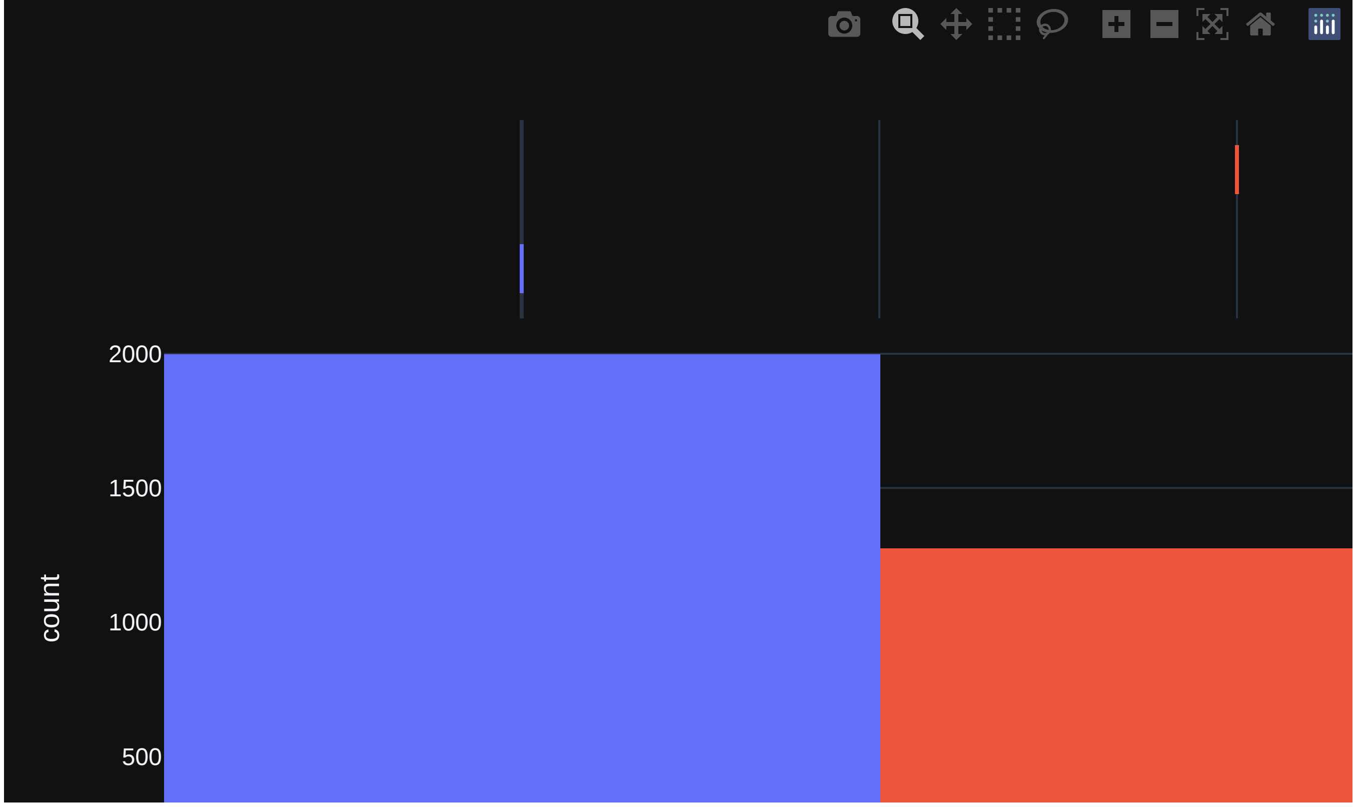


Potability

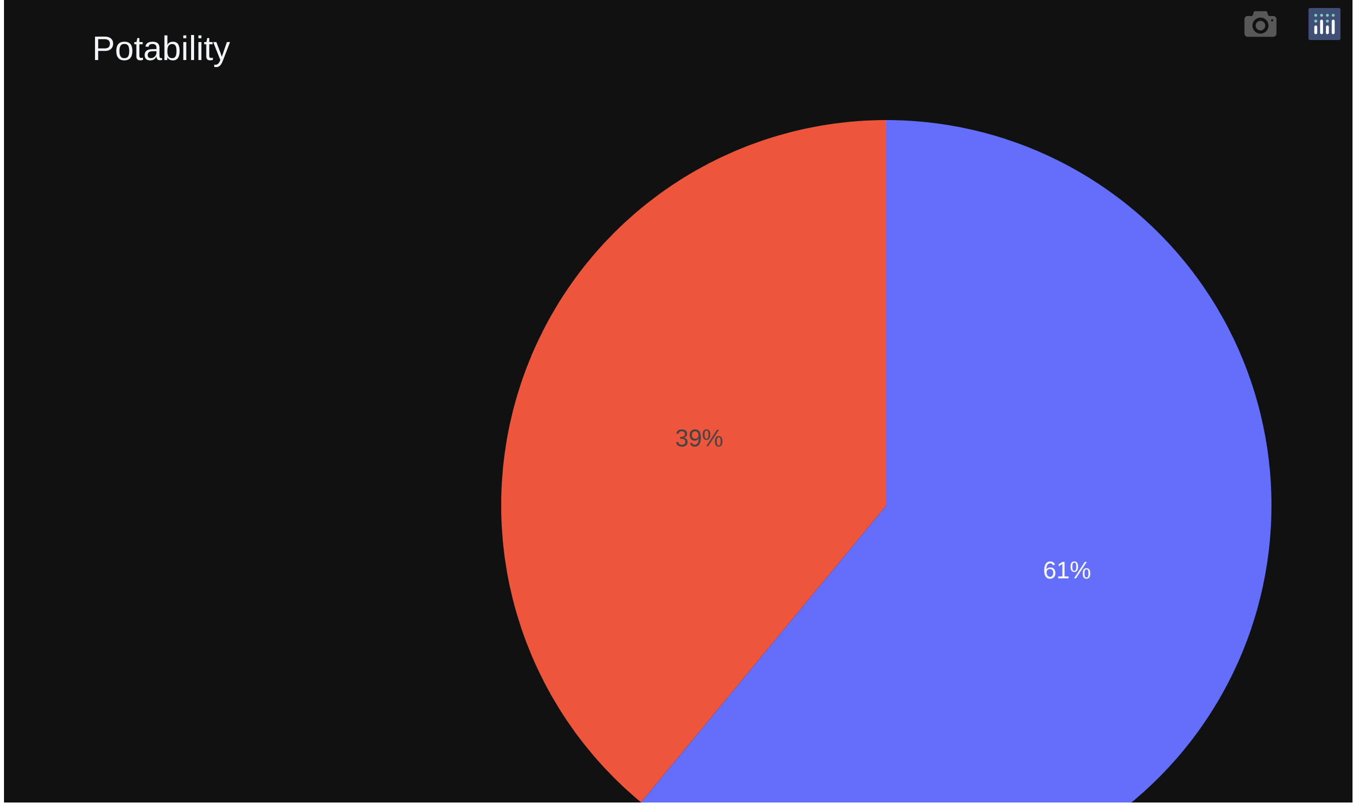
```
In [63]: data['Potability'].describe()
```

```
Out[63]: count    3276.000000
         mean        0.390110
         std         0.487849
         min         0.000000
         25%         0.000000
         50%         0.000000
         75%         1.000000
         max         1.000000
         Name: Potability, dtype: float64
```

```
In [64]: px.histogram(data_frame = data, x = 'Potability', color = 'Potability', marginal = 'box'
                      template = 'plotly_dark')
```



```
In [65]: fig = px.pie(data,
                      values=data['Potability'].value_counts(),
                      names=data['Potability'].value_counts().keys(),
                     )
         fig.update_layout(
             title='Potability',
             template = 'plotly_dark'
         )
         fig.show()
```



Data Preprocessing

```
In [66]: from sklearn.preprocessing import StandardScaler
         from sklearn.model_selection import train_test_split
```

```
In [67]: X=data.drop(['Potability'],axis=1)
         y=data['Potability']
```

Since the data is not in a uniform shape, we scale the data using standard scalar

```
In [68]: scaler = StandardScaler()
         x=scaler.fit_transform(X)
```

```
In [69]: # split the data to train and test set
         x_train,x_test,y_train,y_test = train_test_split(x,y,train_size=0.85,random_state=42)


         print("training data shape:-{} labels{} ".format(x_train.shape,y_train.shape))
         print("testing data shape:-{} labels{} ".format(x_test.shape,y_test.shape))
```

```
training data shape:-(2784, 9) labels(2784,)
testing data shape:-(492, 9) labels(492,)
```

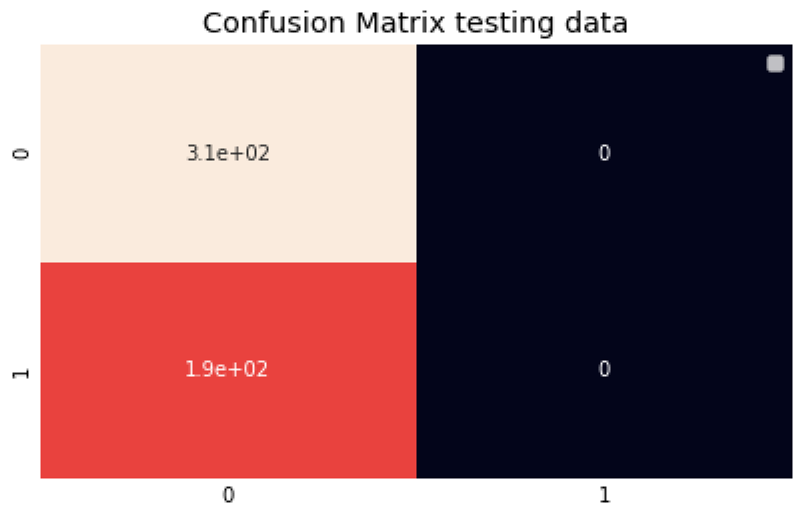
Modeling

Logistic Regression

In [70]:
```
from sklearn.linear_model import LogisticRegression
log = LogisticRegression(random_state=0).fit(x_train, y_train)
log.score(x_test, y_test)
```

Out[70]:
```
0.6219512195121951
```

In [71]:
```
#  Confusion matrix
from sklearn.metrics import confusion_matrix
# Make Predictions
pred1=log.predict(np.array(x_test))
plt.title("Confusion Matrix testing data")
sns.heatmap(confusion_matrix(y_test,pred1),annot=True,cbar=False)
plt.legend()
plt.show()
```

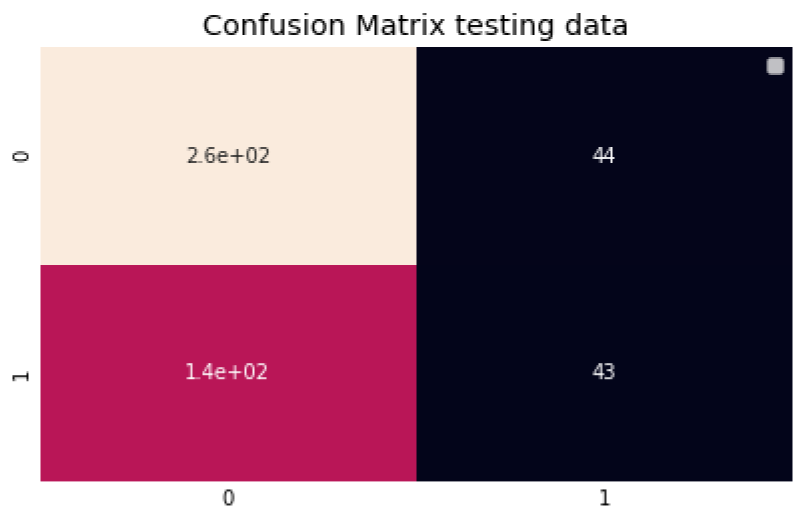


K Nearest Neighbours

In [72]:
```
from sklearn.neighbors import KNeighborsClassifier
```

In [73]:
```
knn = KNeighborsClassifier(n_neighbors=2)
# Train the model using the training sets
knn.fit(x_train,y_train)

#Predict Output
predicted= knn.predict(x_test) # 0:Overcast, 2:Mild
```

In [74]:
```
#  Confusion matrix
from sklearn.metrics import confusion_matrix
# Make Predictions
pred1=knn.predict(np.array(x_test))
plt.title("Confusion Matrix testing data")
sns.heatmap(confusion_matrix(y_test,pred1),annot=True,cbar=False)
plt.legend()
plt.show()
```



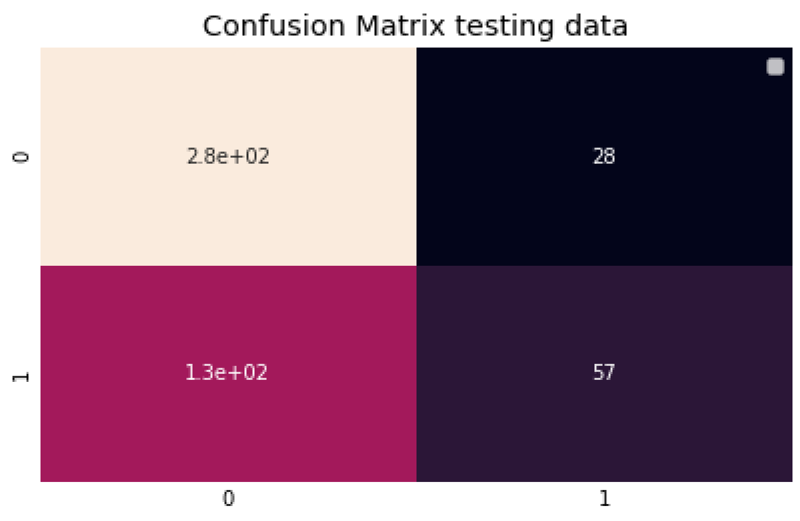
SVM

```
In [75]: from sklearn import svm
         from sklearn.metrics import accuracy_score
```

```
In [76]: svmc = svm.SVC()
         svmc.fit(x_train, y_train)

         y_pred = svmc.predict(x_test)
         print(accuracy_score(y_test,y_pred))
```

```
0.6808943089430894
```

```
In [77]: #  Confusion matrix
         from sklearn.metrics import confusion_matrix
         # Make Predictions
         pred1=svmc.predict(np.array(x_test))
         plt.title("Confusion Matrix testing data")
         sns.heatmap(confusion_matrix(y_test,pred1),annot=True,cbar=False)
         plt.legend()
         plt.show()
```



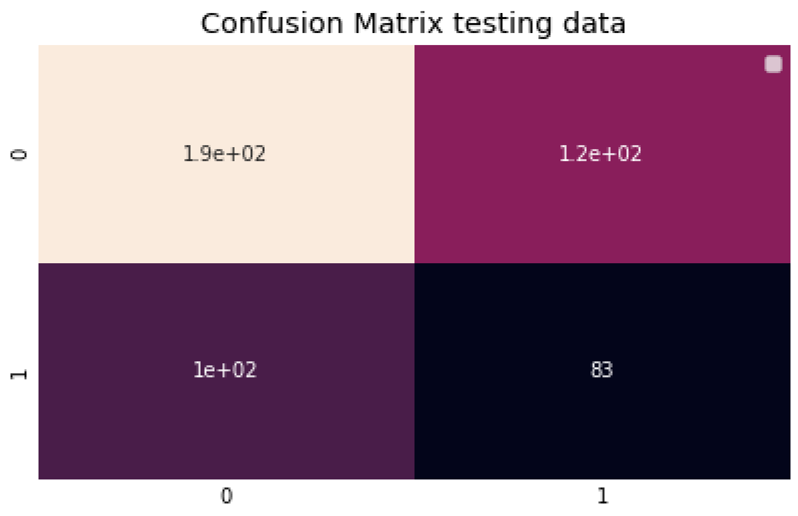
Decision Tree

```
In [78]: from sklearn import tree
         from sklearn.metrics import accuracy_score
```

In [79]:
```
tre = tree.DecisionTreeClassifier()
tre = tre.fit(x_train, y_train)

y_pred = tre.predict(x_test)
print(accuracy_score(y_test,y_pred))
```

```
0.5487804878048781
```

In [80]:
```
#  Confusion matrix
from sklearn.metrics import confusion_matrix
# Make Predictions
pred1=tre.predict(np.array(x_test))
plt.title("Confusion Matrix testing data")
sns.heatmap(confusion_matrix(y_test,pred1),annot=True,cbar=False)
plt.legend()
plt.show()
```



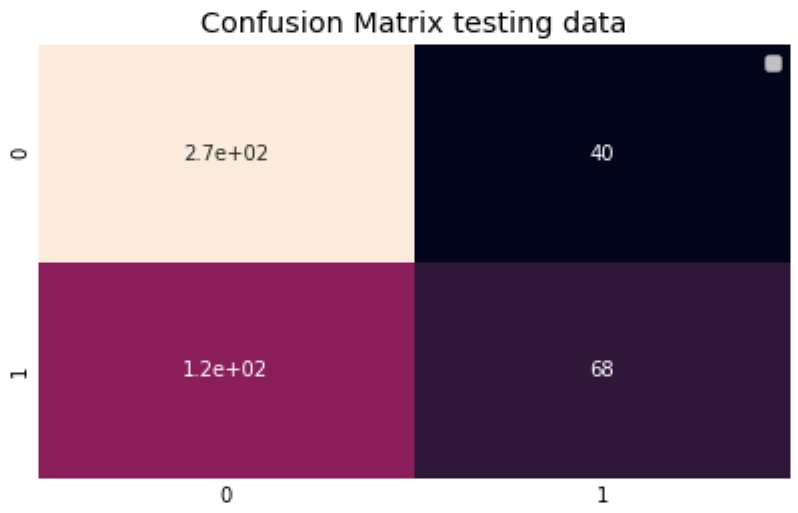
Random Forest

In [81]:
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score
```

In [82]:
```
# create the model
model_rf = RandomForestClassifier(n_estimators=500, oob_score=True, random_state=100)


# fitting the model
model_rf=model_rf.fit(x_train, y_train)

y_pred = model_rf.predict(x_test)
print(accuracy_score(y_test,y_pred))
```

```
0.6788617886178862
```

In [83]:
```
#  Confusion matrix
from sklearn.metrics import confusion_matrix
# Make Predictions
pred1=model_rf.predict(np.array(x_test))
plt.title("Confusion Matrix testing data")
sns.heatmap(confusion_matrix(y_test,pred1),annot=True,cbar=False)
plt.legend()
plt.show()
```



XG Boost

In [84]:
```
from xgboost import XGBClassifier
from sklearn.metrics import r2_score

xgb = XGBClassifier(colsample_bylevel= 0.9,
                    colsample_bytree = 0.8,
                    gamma=0.99,
                    max_depth= 5,
                    min_child_weight= 1,
                    n_estimators= 8,
                    nthread= 5,
                    random_state= 0,
                    )
xgb.fit(x_train,y_train)
```

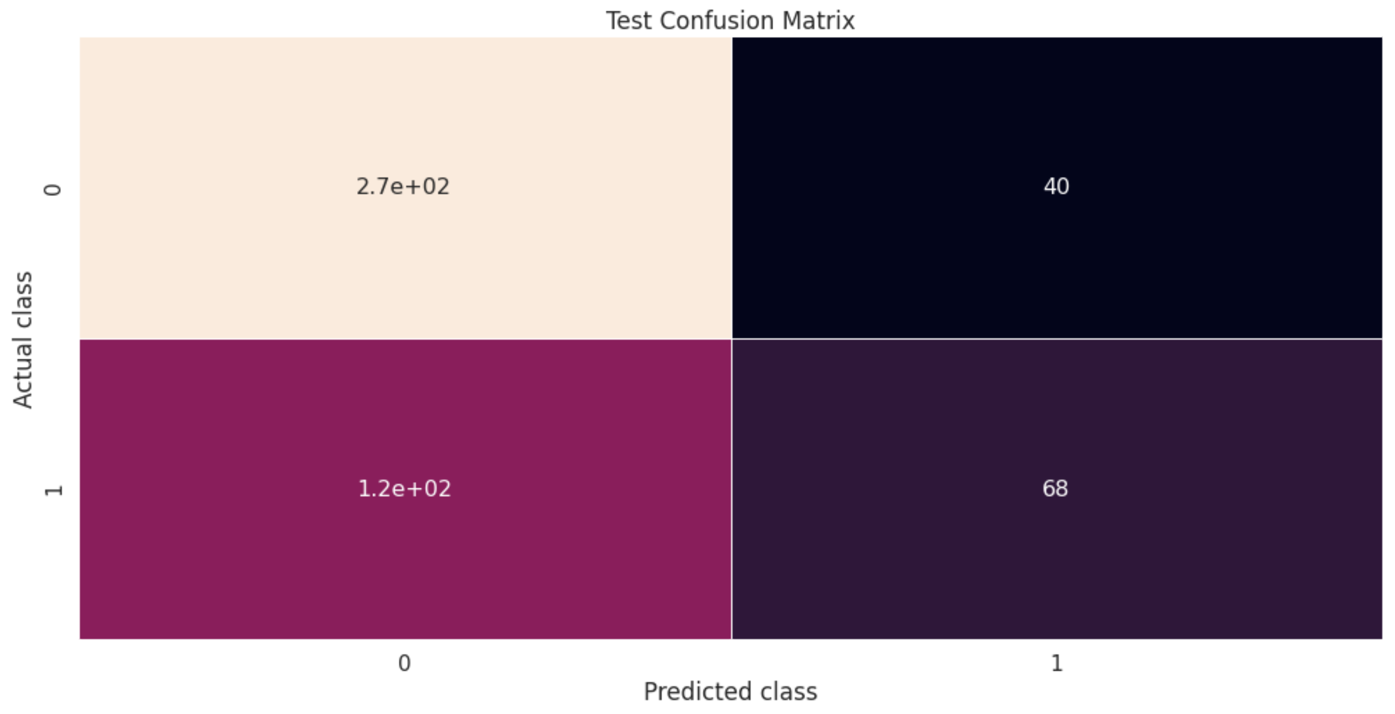
```
[14:31:40] WARNING: ../src/learner.cc:1095: Starting in XGBoost 1.3.0, the default evalu
ation metric used with the objective 'binary:logistic' was changed from 'error' to 'logl
oss'. Explicitly set eval_metric if you'd like to restore the old behavior.
```

Out[84]:
```
XGBClassifier(base_score=0.5, booster='gbtree', colsample_bylevel=0.9,
              colsample_bynode=1, colsample_bytree=0.8, gamma=0.99, gpu_id=-1,
              importance_type='gain', interaction_constraints='',
              learning_rate=0.300000012, max_delta_step=0, max_depth=5,
              min_child_weight=1, missing=nan, monotone_constraints='()',
              n_estimators=8, n_jobs=5, nthread=5, num_parallel_tree=1,
              random_state=0, reg_alpha=0, reg_lambda=1, scale_pos_weight=1,
              subsample=1, tree_method='exact', validate_parameters=1,
              verbosity=None)
```

In [85]:
```
print('Accuracy of XGBoost classifier on training set: {:.2f}'
     .format(xgb.score(x_train, y_train)))
print('Accuracy of XGBoost classifier on test set: {:.2f}'
     .format(xgb.score(x_test, y_test)))
```

```
Accuracy of XGBoost classifier on training set: 0.72
Accuracy of XGBoost classifier on test set: 0.63
```

In [86]:
```
from sklearn.metrics import confusion_matrix

conf_matrix = confusion_matrix(y_true=y_test, y_pred=y_pred)
plt.figure(figsize = (15, 8))
sns.set(font_scale=1.4) # for label size
sns.heatmap(conf_matrix, annot=True, annot_kws={"size": 16},cbar=False, linewidths = 1)
plt.title("Test Confusion Matrix")
plt.xlabel("Predicted class")
plt.ylabel("Actual class")
plt.savefig('conf_test.png')
plt.show()
```



SVM tuned

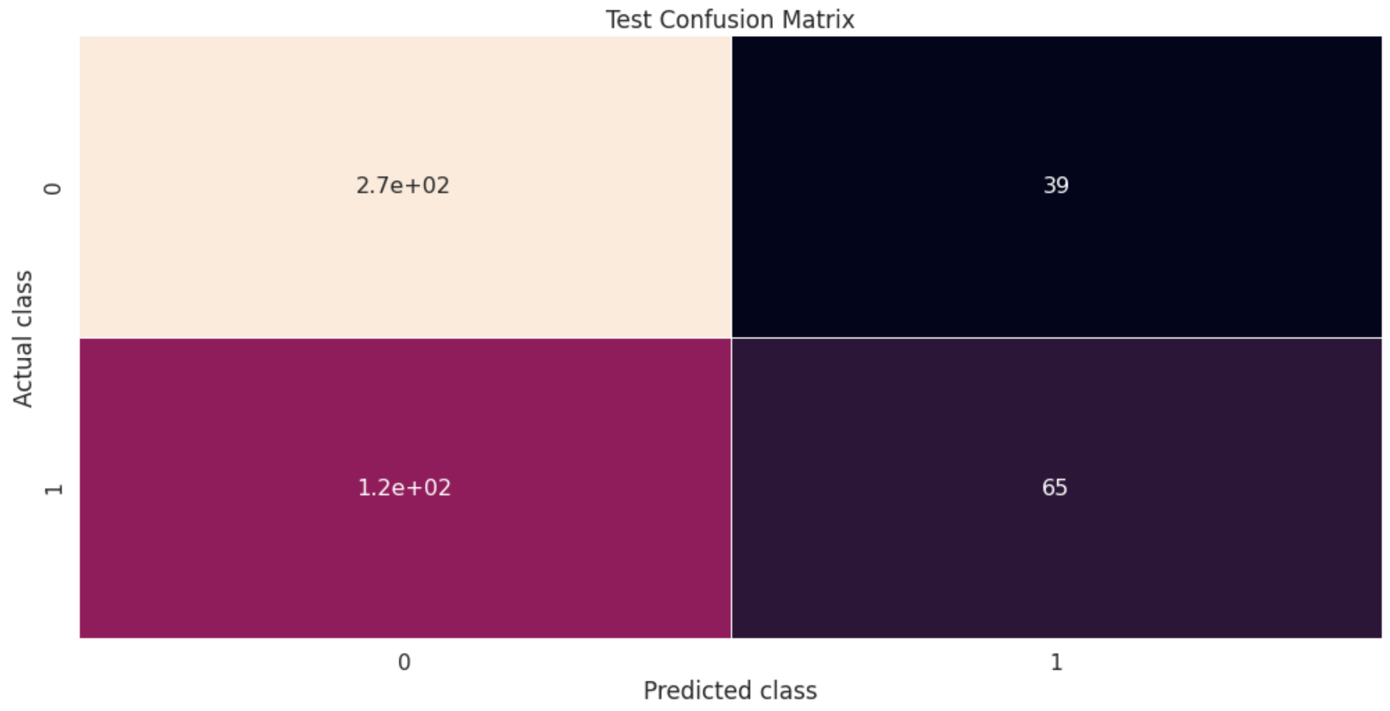
In [87]:
```
from sklearn.svm import SVC
from sklearn.model_selection import GridSearchCV
svc=SVC()
param_grid={'C':[1.2,1.5,2.2,3.5,3.2,4.1],'kernel':['linear', 'poly', 'rbf', 'sigmoid'],
gridsearch=GridSearchCV(svc,param_grid=param_grid,n_jobs=-1,verbose=4,cv=3)
gridsearch.fit(x_train,y_train)
```

```
Fitting 3 folds for each of 240 candidates, totalling 720 fits
```

```
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 4 concurrent workers.
[Parallel(n_jobs=-1)]: Done  17 tasks      | elapsed:    2.9s
[Parallel(n_jobs=-1)]: Done  90 tasks      | elapsed:    7.5s
[Parallel(n_jobs=-1)]: Done 213 tasks      | elapsed:   15.3s
[Parallel(n_jobs=-1)]: Done 384 tasks      | elapsed:   26.8s
[Parallel(n_jobs=-1)]: Done 605 tasks      | elapsed:   42.5s
[Parallel(n_jobs=-1)]: Done 720 out of 720 | elapsed:   51.0s finished
```

Out[87]:
```
GridSearchCV(cv=3, estimator=SVC(), n_jobs=-1,
             param_grid={'C': [1.2, 1.5, 2.2, 3.5, 3.2, 4.1],
                         'degree': [1, 2, 4, 8, 10], 'gamma': ['scale', 'auto'],
                         'kernel': ['linear', 'poly', 'rbf', 'sigmoid']},
             verbose=4)
```

In [88]:
```
y_pred=gridsearch.predict(x_test)
from sklearn.metrics import confusion_matrix

conf_matrix = confusion_matrix(y_true=y_test, y_pred=y_pred)
plt.figure(figsize = (15, 8))
sns.set(font_scale=1.4) # for label size
sns.heatmap(conf_matrix, annot=True, annot_kws={"size": 16},cbar=False, linewidths = 1)
plt.title("Test Confusion Matrix")
plt.xlabel("Predicted class")
plt.ylabel("Actual class")
plt.savefig('conf_test.png')
plt.show()
```


Test Confusion Matrix
2.7e+02
39
1.2e+02
65
0
1
Actual class
0
1
Predicted class