Major Project - Corizo
Wine Quality Analysis

Submitted by
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In [1]:
```
#import all library which required
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score
import warnings
warnings.filterwarnings('ignore')
```

In [4]:
```
#Upload the dataset

df = pd.read_csv('C:/Users/cws/OneDrive/Desktop/Corico Data/1788410-1767134-1729261-1613779-Red_wine.csv')

df.head()
```

Out[4]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5.0
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5.0
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5.0
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6.0
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5.0

In [5]:
```
#df.shape
```

Out[5]:
```
(1599, 12)
```

In [9]:
```
#Check the missing value in the data set
df.isnull().sum()
```

Out[9]:
```
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    1
density                 0
pH                      1
sulphates               0
alcohol                 0
quality                 1
dtype: int64
```

In [17]:
```
#drop all the null values
Df=df.dropna()
```

In [20]:
```
#To check again missing value
Df.isnull().sum()
```

Out[20]:
```
fixed acidity           0
volatile acidity        0
citric acid             0
residual sugar          0
chlorides               0
free sulfur dioxide     0
total sulfur dioxide    0
density                 0
pH                      0
sulphates               0
alcohol                 0
quality                 0
dtype: int64
```

Data Analysis

In [22]:
```
Df.describe()
```

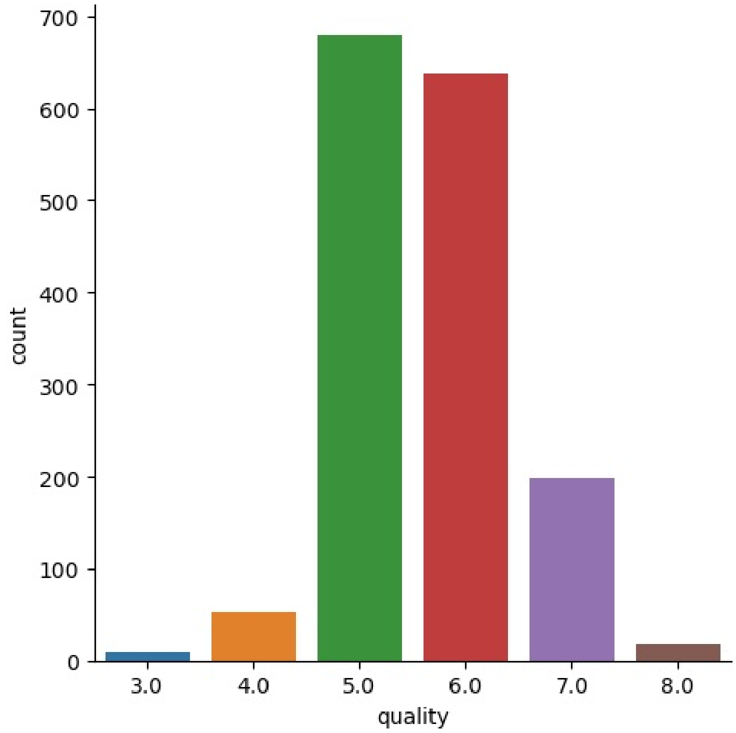
Out[22]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates
count	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000	1596.000000
mean	8.321366	0.527666	0.271128	2.536936	0.087487	15.882206	46.431078	0.996745	3.498716	0.658189
std	1.742121	0.179154	0.194847	1.408341	0.047107	10.467380	32.893072	0.001889	0.080297	0.169587
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.990070	2.740000	0.330000
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.995600	3.520000	0.550000
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.996745	3.520000	0.620000
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.997842	3.520000	0.730000
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1.003690	3.900000	2.000000

In [70]:

```
#To check number of values
plt.figure(figsize=(12,6))
sns.catplot(x='quality', data=Df, kind='count')
plt.show()
```

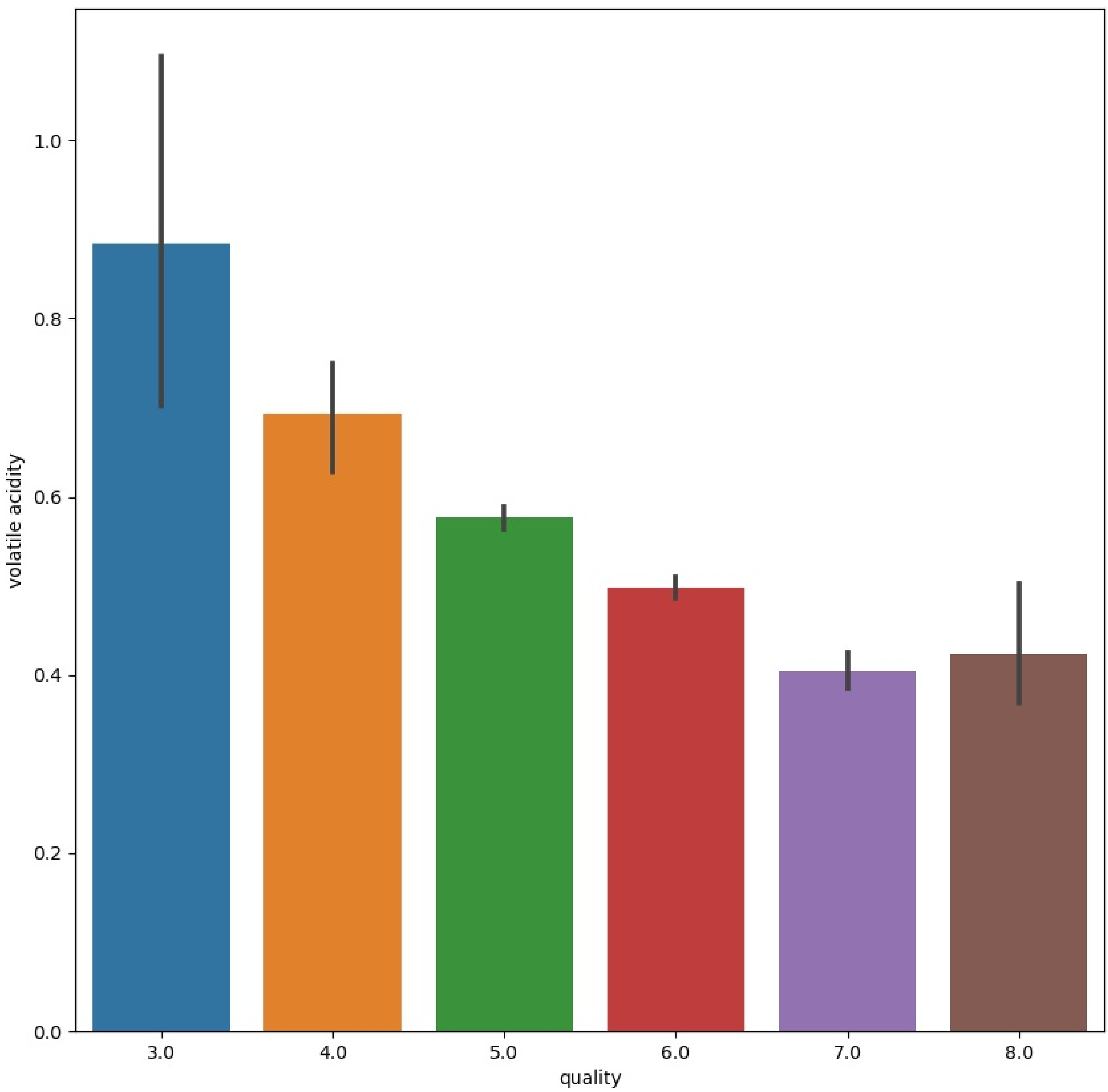
<Figure size 1200x600 with 0 Axes>



In [66]:

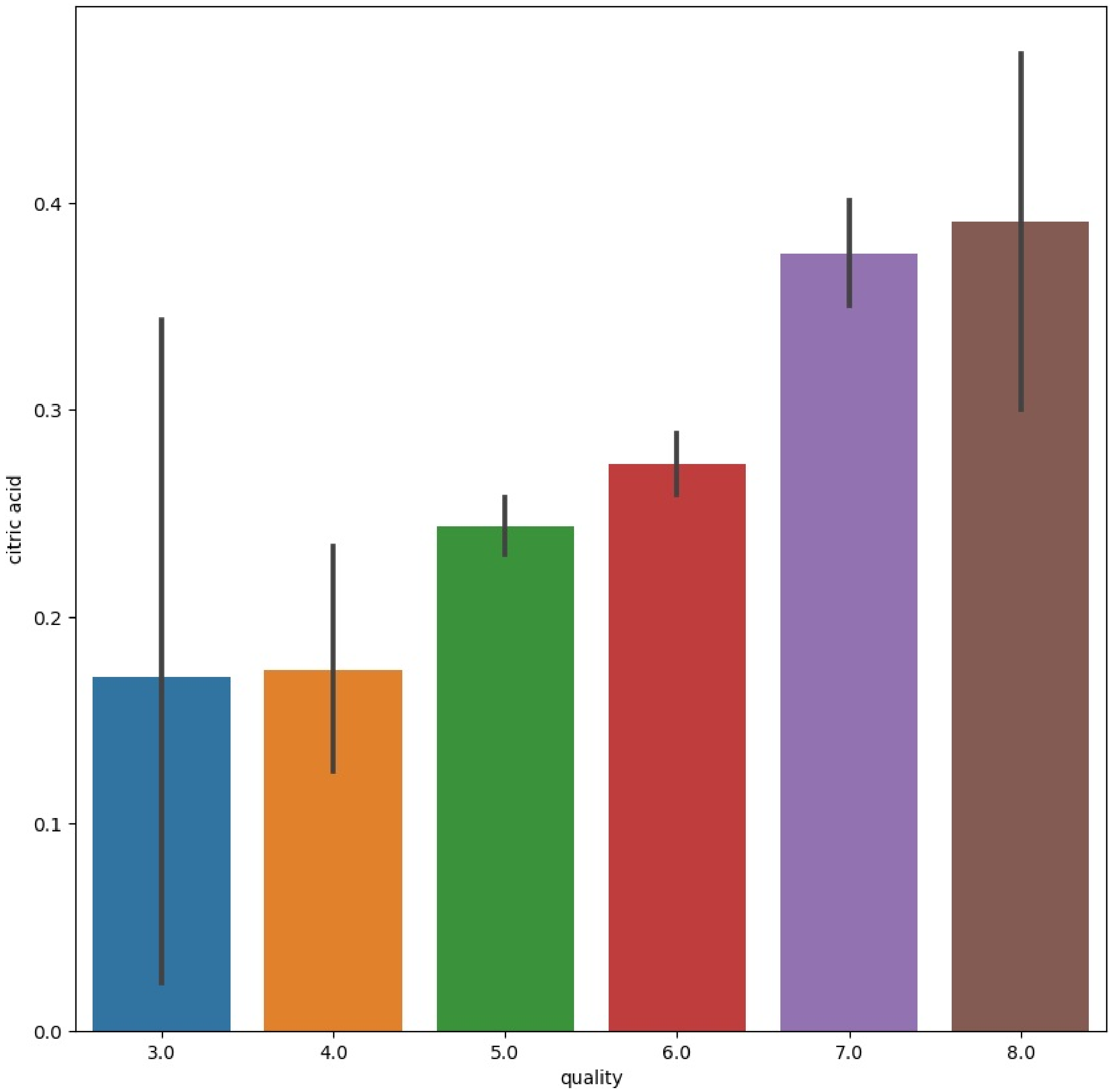
```
#volatil acidity vs quality
plot = plt.figure(figsize=(10,10))
sns.barplot(x='quality', y='volatile acidity', data = Df)
```

Out[66]: <Axes: xlabel='quality', ylabel='volatile acidity'>



In [76]:
```
#volatil acidity vs quality
plt.figure(figsize=(10,10))
sns.barplot(x='quality', y='citric acid', data = df)
```

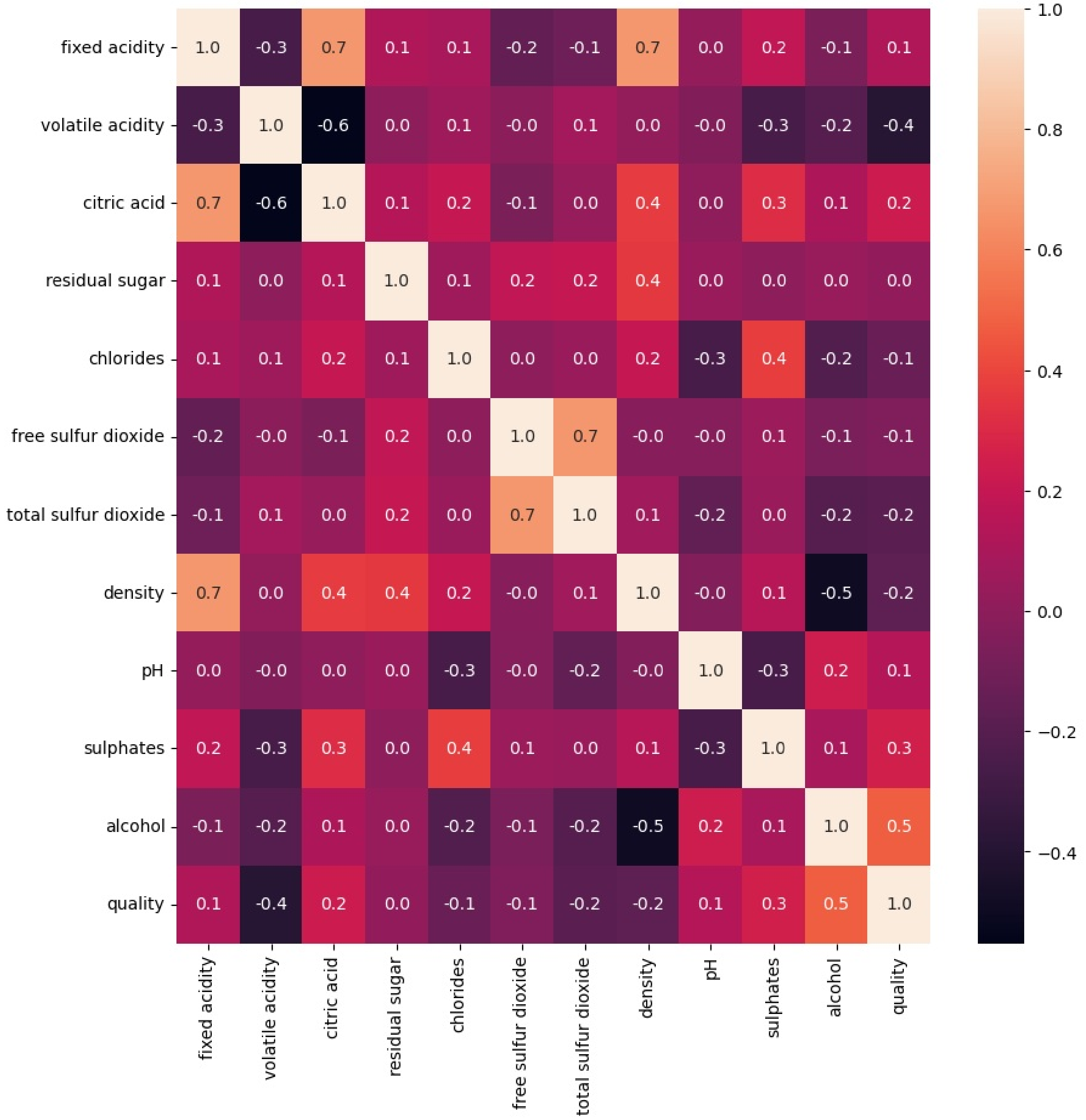
Out[76]: <Axes: xlabel='quality', ylabel='citric acid'>



In [72]:
```
#correlation between variables
correlation = df.corr()
```

In [73]:
```
#constructing heatmap to see the correlation
plt.figure(figsize=(10,10))
sns.heatmap(correlation, annot = True, fmt = '0.1f')
```

Out[73]:
```
<Axes: >
```



Data Processing

In [78]:
```
#seprate the data and label
x=df.drop('quality',axis=1)
```

```
print(x)
```

```
      fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
0               7.4             0.700         0.00             1.9      0.076
1               7.8             0.880         0.00             2.6      0.098
2               7.8             0.760         0.04             2.3      0.092
3              11.2             0.280         0.56             1.9      0.075
4               7.4             0.700         0.00             1.9      0.076
...             ...               ...          ...             ...        ...
1594            6.2             0.600         0.08             2.0      0.090
1595            5.9             0.550         0.10             2.2      0.062
1596            6.3             0.510         0.13             2.3      0.076
1597            5.9             0.645         0.12             2.0      0.075
1598            6.0             0.310         0.47             3.6      0.067

      free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
0                    11.0                  34.0  0.99780  3.51       0.56
1                    25.0                  67.0  0.99680  3.20       0.68
2                    15.0                  54.0  0.99700  3.26       0.65
3                    17.0                  60.0  0.99800  3.16       0.58
4                    11.0                  34.0  0.99780  3.51       0.56
...                   ...                   ...      ...   ...        ...
1594                 32.0                  44.0  0.99490  3.52       0.58
1595                 39.0                  51.0  0.99512  3.52       0.76
1596                 29.0                  40.0  0.99574  3.52       0.75
1597                 32.0                  44.0  0.99547  3.52       0.71
1598                 18.0                  42.0  0.99549  3.52       0.66

      alcohol
0         9.4
1         9.8
2         9.8
3         9.8
4         9.4
...       ...
1594     10.5
1595     11.2
1596     11.0
1597     10.2
1598     11.0

[1596 rows x 11 columns]
```

In [79]:
```
#Label encoding
y = df['quality'].apply(lambda y_value: 1 if y_value>=7 else 0)
print(y)
```

```
0       0
1       0
2       0
3       0
4       0
       ..
1594    0
1595    0
1596    0
1597    0
1598    0
Name: quality, Length: 1596, dtype: int64
```

Train & Test Split

In [80]:
```
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2, random_state = 3)
print(y.shape, y_train.shape, y_test.shape)
```

```
(1596,) (1276,) (320,)
```

Model Training : Random Forest# Model Training : Random Forest

In [81]:
```
model = RandomForestClassifier()
```

In [82]:
```
from colorsys import yiq_to_rgb
model.fit(x_train, y_train)
```

Out[82]:
```
▾ RandomForestClassifier
RandomForestClassifier()
```

Model evaluation

In [83]:
```
#Accuracy Score
x_test_prediction = model.predict(x_test)
test_data_accuracy = accuracy_score(x_test_prediction, y_test)

print('Accuracy: ', test_data_accuracy)
```

```
Accuracy:  0.909375
```

Building a Prediction System

In [85]:
```
input_data = (7.8,0.58,0.02,2,0.073,9,18,0.9968,3.36,0.57,9.5)

#changing input data into numpy array
input_data_as_numpy_array = np.asarray(input_data)

#reshaping the data as we are predicting the label for only one instance
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

prediction = model.predict(input_data_reshaped)
print(prediction)

if (prediction[0]==1):
  print("Good Quality Wine")
else:
  print("Bad Quality Wine")
```

```
[1]
Good Quality Wine
```

Thanks