Import Libraries

In [12]:
```
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns
%matplotlib inline
import time
import random

random.seed(100)
```

In [13]:
```
wine = pd.read_csv('winequality-red.csv')
wine.head()
```

Out[13]:

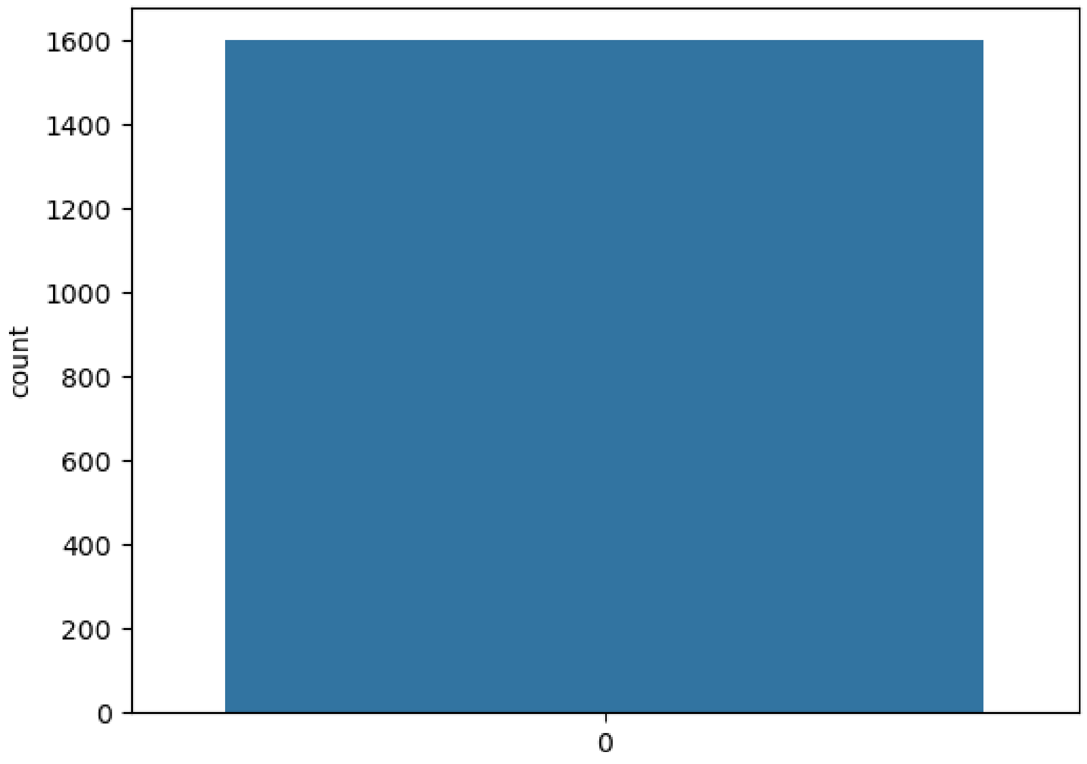
	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	qua
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970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

In [14]:
```
from sklearn.preprocessing import LabelEncoder
bins = (2, 6.5, 8)
group_names = ['bad', 'good']
wine['quality'] = pd.cut(wine['quality'], bins = bins, labels = group_names)
label_quality = LabelEncoder()
wine['quality'] = label_quality.fit_transform(wine['quality'])
wine['quality'].value_counts()
```

Out[14]:
```
0    1382
1     217
Name: quality, dtype: int64
```

In [16]:
```
sns.countplot(wine['quality'])
```

Out[16]:
```
<Axes: ylabel='count'>
```

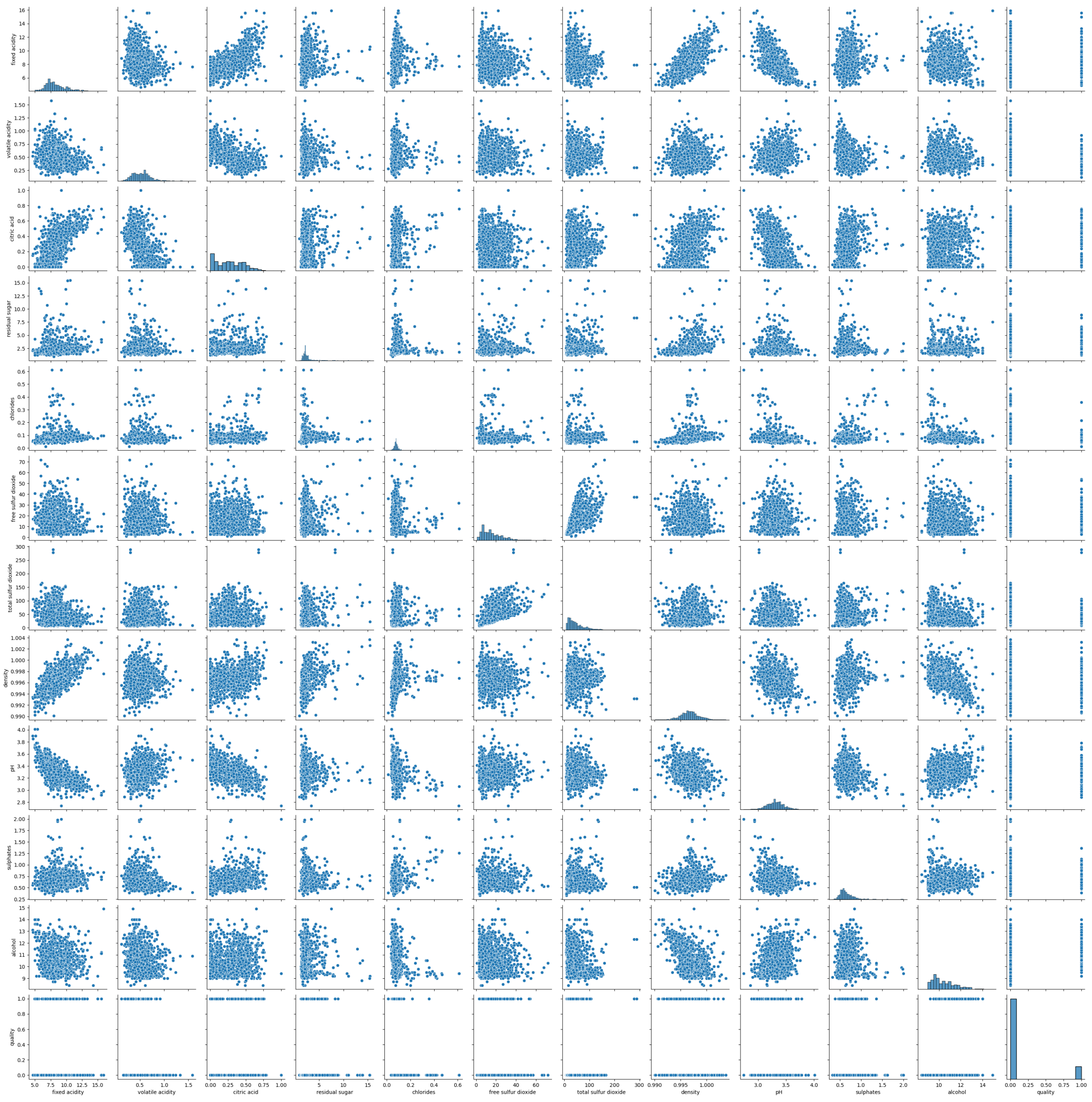


In [17]:
```
wine.columns
```

Out[17]:
```
Index(['fixed acidity', 'volatile acidity', 'citric acid', 'residual sugar',
       'chlorides', 'free sulfur dioxide', 'total sulfur dioxide', 'density',
       'pH', 'sulphates', 'alcohol', 'quality'],
      dtype='object')
```

In [18]:
```
sns.pairplot(wine)
```

Out[18]:
```
<seaborn.axisgrid.PairGrid at 0x23445ae8210>
```



In [19]:
```
wine[wine.columns[:11]].describe()
```

Out[19]:

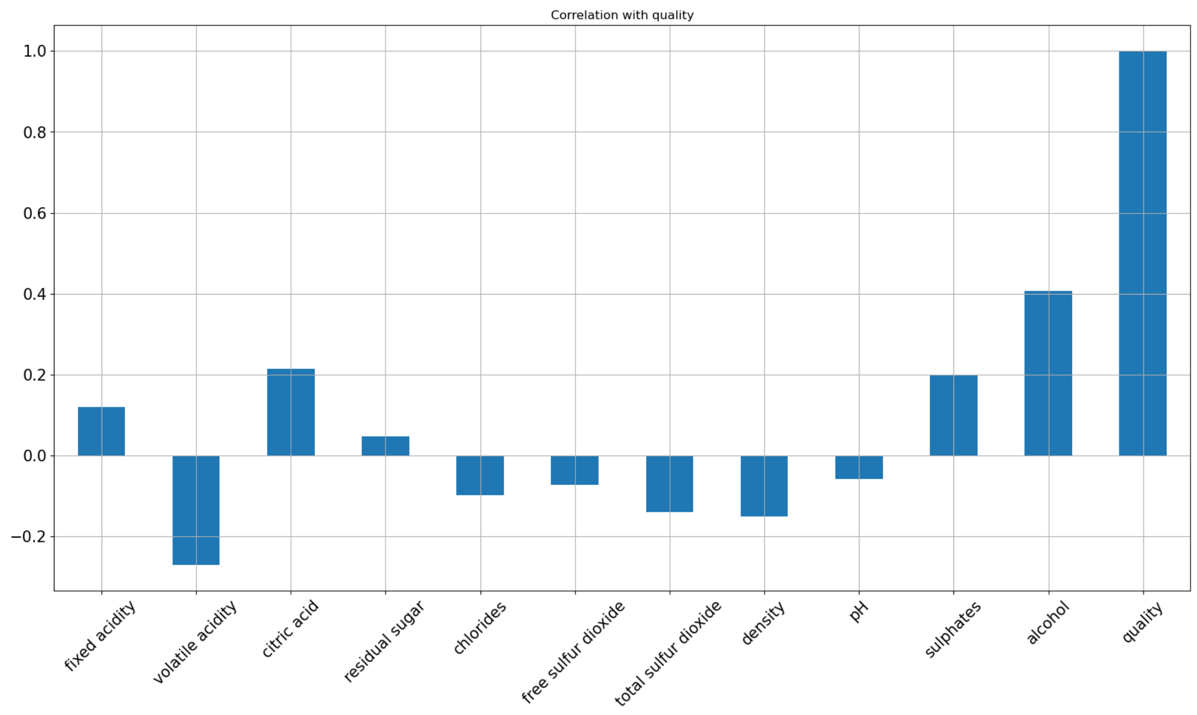
	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.467792
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000

In [20]:
```
wine.isna().any()
```

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

In [21]:
```
wine.corrwith(wine.quality).plot.bar(
        figsize = (20, 10), title = "Correlation with quality", fontsize = 15,
        rot = 45, grid = True)
```

Out[21]:
```
<Axes: title={'center': 'Correlation with quality'}>
```



In [23]:
```
sns.set(style="white")

# Compute the correlation matrix
corr = wine.corr()
corr.head()
```

Out[23]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	p
fixed acidity	1.000000	-0.256131	0.671703	0.114777	0.093705	-0.153794	-0.113181	0.668047	-0.6829
volatile acidity	-0.256131	1.000000	-0.552496	0.001918	0.061298	-0.010504	0.076470	0.022026	0.2349
citric acid	0.671703	-0.552496	1.000000	0.143577	0.203823	-0.060978	0.035533	0.364947	-0.5419
residual sugar	0.114777	0.001918	0.143577	1.000000	0.055610	0.187049	0.203028	0.355283	-0.0856
chlorides	0.093705	0.061298	0.203823	0.055610	1.000000	0.005562	0.047400	0.200632	-0.2650

Feature Engineering

In [25]:
```
X = wine.drop('quality',axis=1)
y=wine['quality']
```

In [26]:
```
X.head()
```

Out[26]:

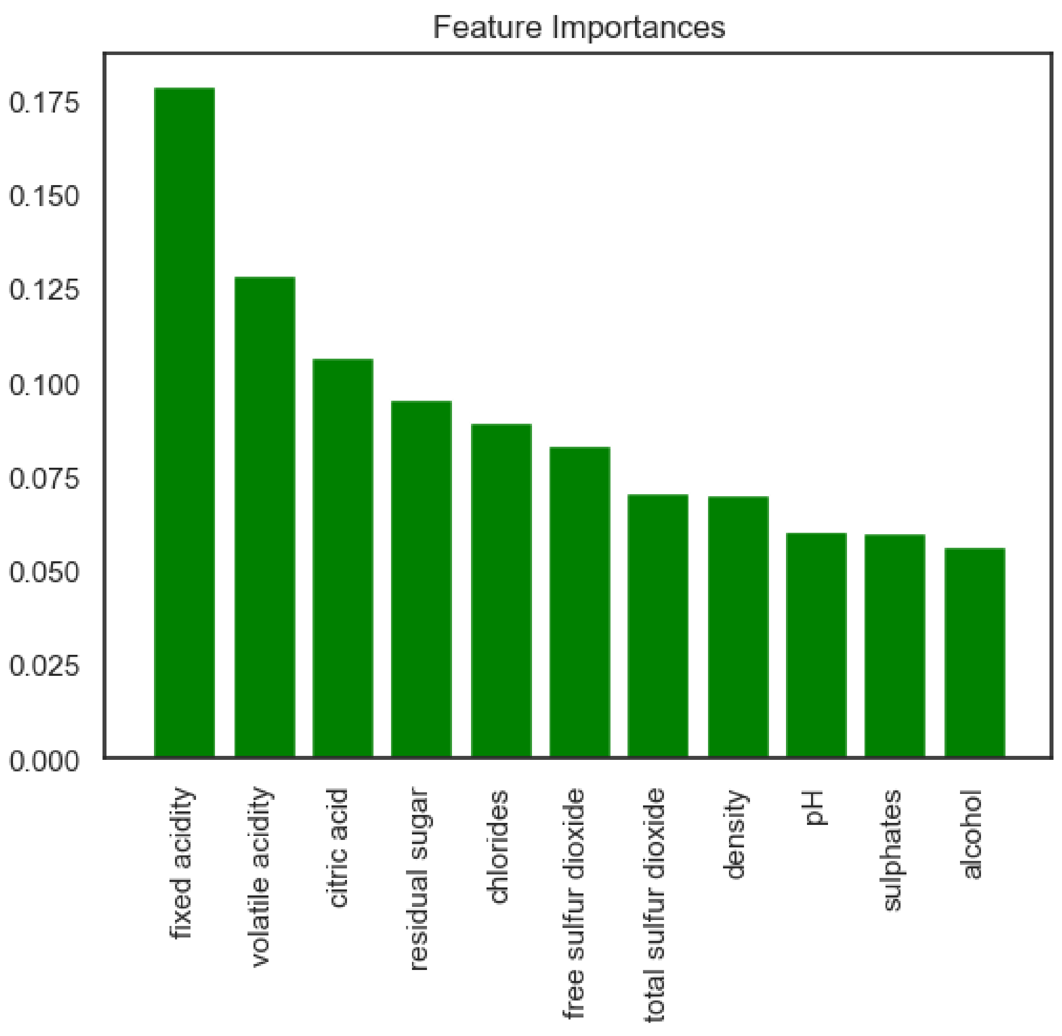
	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65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

In [27]:
```
features_label = wine.columns[:11]
```

In [28]:
```
from sklearn.ensemble import RandomForestClassifier
classifier = RandomForestClassifier(n_estimators = 200, criterion = 'entropy', ran
classifier.fit(X, y)
importances = classifier.feature_importances_
indices = np. argsort(importances)[::-1]
for i in range(X.shape[1]):
    print ("%2d) %-*s %f" % (i + 1, 30, features_label[i],importances[indices[i]])
```

```
 1) fixed acidity                  0.178690
 2) volatile acidity               0.128748
 3) citric acid                    0.106496
 4) residual sugar                 0.095718
 5) chlorides                      0.089280
 6) free sulfur dioxide            0.083482
 7) total sulfur dioxide           0.070669
 8) density                        0.070104
 9) pH                             0.060459
10) sulphates                      0.060048
11) alcohol                        0.056307
```

In [29]:
```
plt.title('Feature Importances')
plt.bar(range(X.shape[1]),importances[indices], color="green", align="center")
plt.xticks(range(X.shape[1]),features_label, rotation=90)
plt.xlim([-1, X.shape[1]])
plt.show()
```



In [30]:
```
from sklearn.model_selection  import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.20, random
```

In [31]:
```
# Feature Scaling
from sklearn.preprocessing import StandardScaler
sc = StandardScaler()
X_train2 = pd.DataFrame(sc.fit_transform(X_train))
X_test2 = pd.DataFrame(sc.transform(X_test))
X_train2.columns = X_train.columns.values
X_test2.columns = X_test.columns.values
X_train2.index = X_train.index.values
X_test2.index = X_test.index.values
X_train = X_train2
X_test = X_test2
```

In [32]:
```
#Using Principal Dimensional Reduction
from sklearn.decomposition import PCA
pca = PCA(n_components = 4)
X_train = pca.fit_transform(X_train)
X_test = pca.transform(X_test)
explained_variance = pca.explained_variance_ratio_
print(pd.DataFrame(explained_variance))
```

```
          0
0  0.281687
1  0.171462
2  0.143245
3  0.114765
```

In [33]:
```
from sklearn.linear_model import LogisticRegression
classifier = LogisticRegression(random_state = 0)
classifier.fit(X_train, y_train)

# Predicting Test Set
y_pred = classifier.predict(X_test)
from sklearn.metrics import confusion_matrix, accuracy_score, f1_score, precision_
acc = accuracy_score(y_test, y_pred)
prec = precision_score(y_test, y_pred)
rec = recall_score(y_test, y_pred)
f1 = f1_score(y_test, y_pred)

results = pd.DataFrame([['Logistic Regression', acc, prec, rec, f1]],
               columns = ['Model', 'Accuracy', 'Precision', 'Recall', 'F1 Score'])
print(results)
```

```
                 Model  Accuracy  Precision   Recall  F1 Score
0  Logistic Regression   0.86875        0.6  0.26087  0.363636
```