

```
#Importing required packages.
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.linear_model import SGDClassifier
from sklearn.metrics import confusion_matrix, classification_report
from sklearn.preprocessing import StandardScaler, LabelEncoder
from sklearn.model_selection import train_test_split, GridSearchCV, cross_val_score
%matplotlib inline
```

```
#Loading dataset
wine = pd.read_csv('/content/archive (1).zip')
```

```
#Let's check how the data is distributed
wine.head()
```



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

```
#Information about the data columns
wine.info()
```

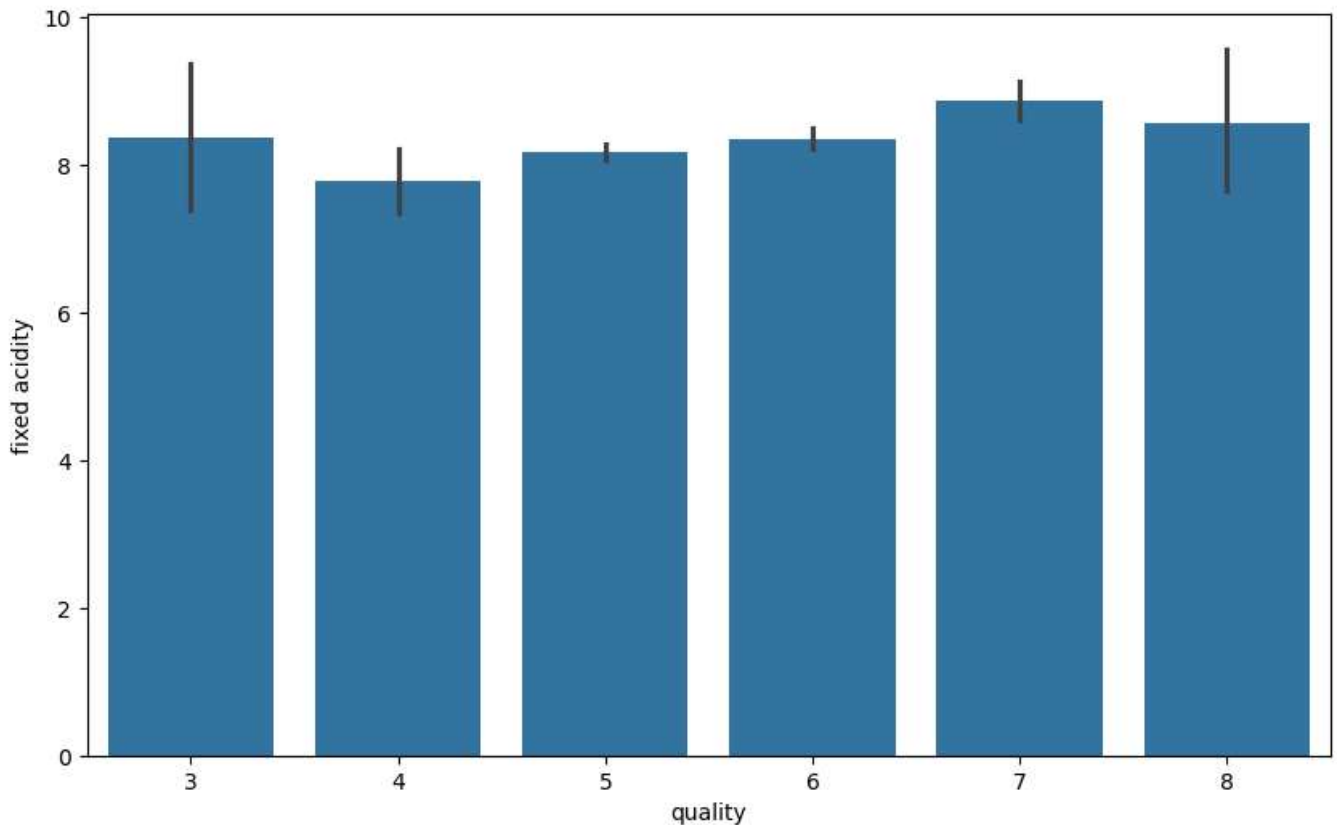
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1599 entries, 0 to 1598
Data columns (total 12 columns):
#   Column                Non-Null Count  Dtype
---  -
0   fixed acidity          1599 non-null   float64
1   volatile acidity       1599 non-null   float64
2   citric acid            1599 non-null   float64
3   residual sugar         1599 non-null   float64
4   chlorides              1599 non-null   float64
5   free sulfur dioxide    1599 non-null   float64
6   total sulfur dioxide   1599 non-null   float64
7   density                1599 non-null   float64
8   pH                    1599 non-null   float64
```

```
9  sulphates      1599 non-null  float64
10 alcohol        1599 non-null  float64
11 quality        1599 non-null  int64
dtypes: float64(11), int64(1)
memory usage: 150.0 KB
```

#Here we see that fixed acidity does not give any specification to classify the quality.

```
fig = plt.figure(figsize = (10,6))
sns.barplot(x = 'quality', y = 'fixed acidity', data = wine)
```

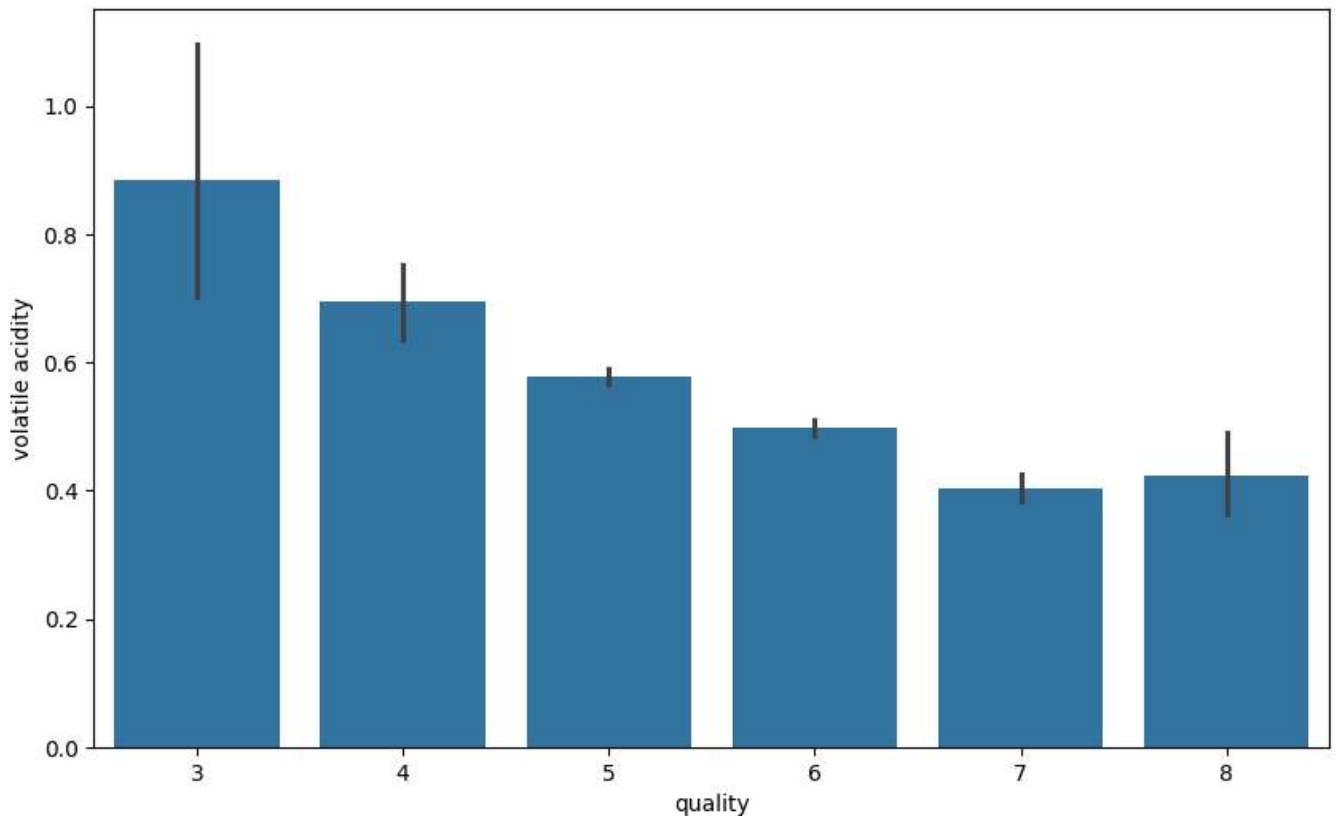
<Axes: xlabel='quality', ylabel='fixed acidity'>



#Here we see that its quite a downing trend in the volatile acidity as we go higher the qual

```
fig = plt.figure(figsize = (10,6))
sns.barplot(x = 'quality', y = 'volatile acidity', data = wine)
```

<Axes: xlabel='quality', ylabel='volatile acidity'>

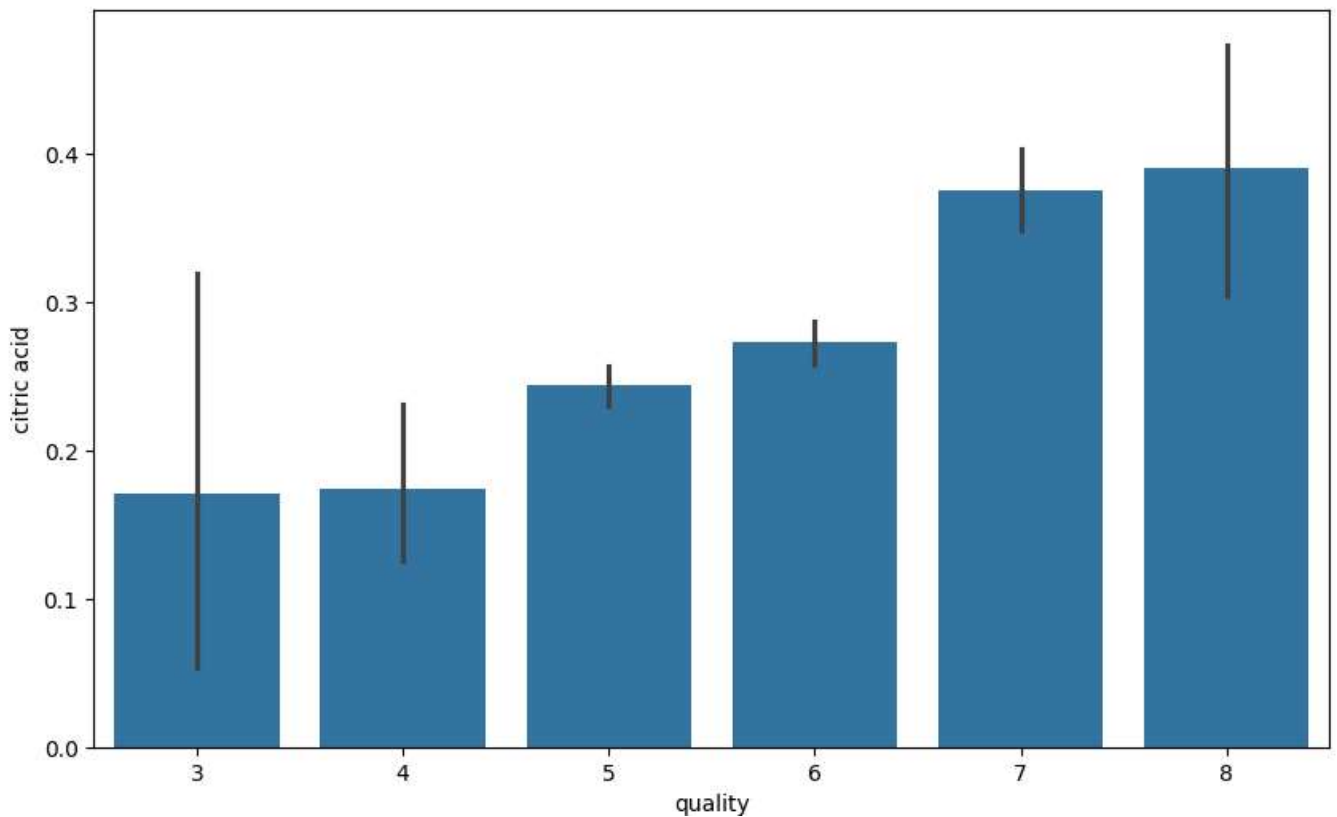


#Composition of citric acid go higher as we go higher in the quality of the wine

```
fig = plt.figure(figsize = (10,6))
```

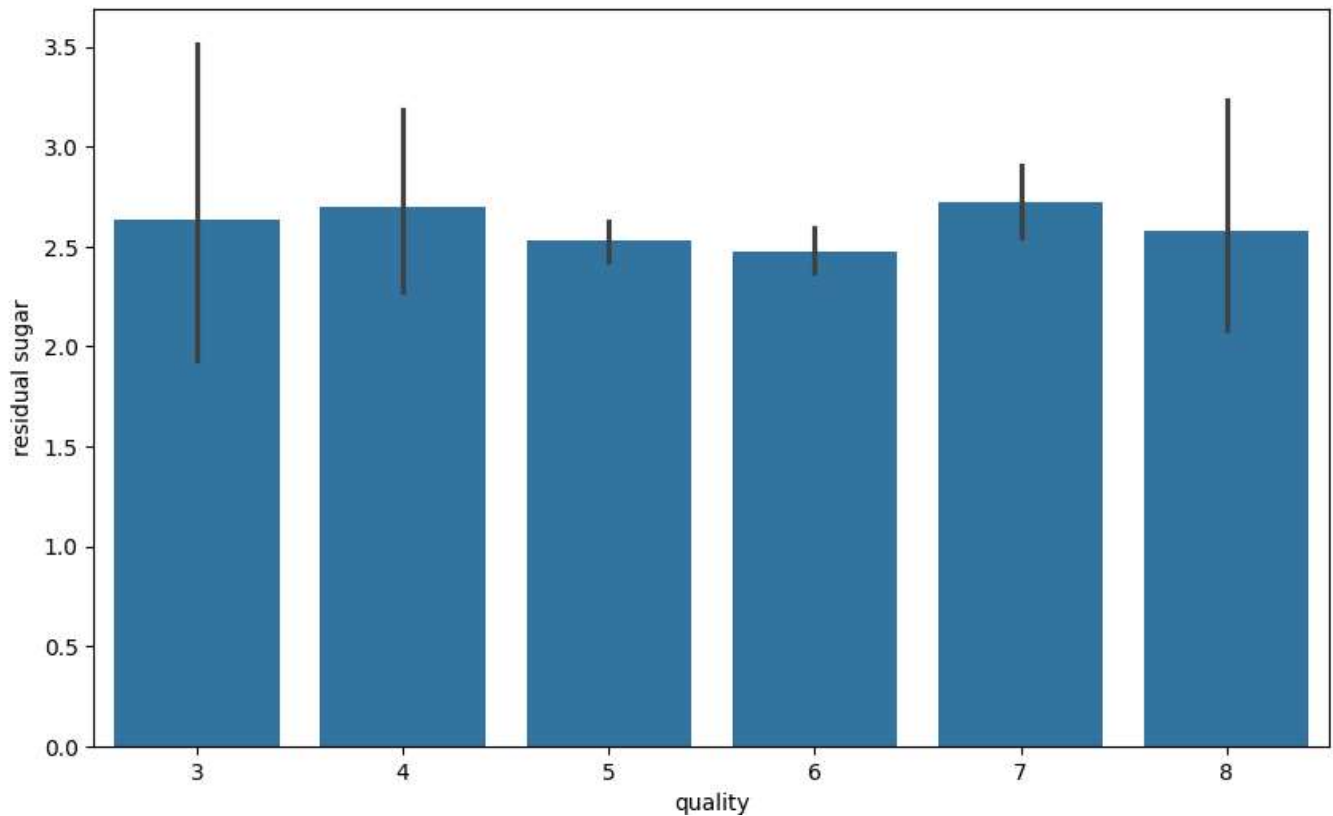
```
sns.barplot(x = 'quality', y = 'citric acid', data = wine)
```

<Axes: xlabel='quality', ylabel='citric acid'>



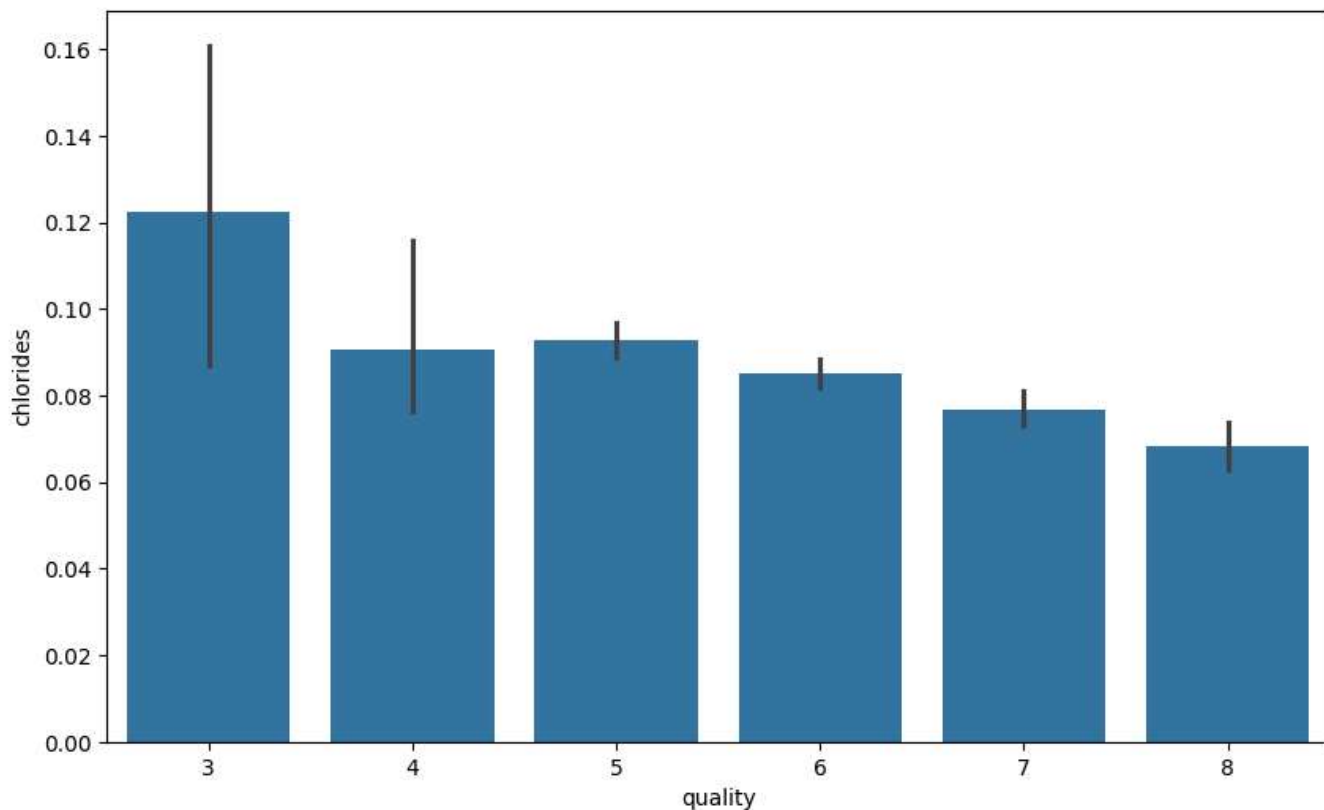
```
fig = plt.figure(figsize = (10,6))  
sns.barplot(x = 'quality', y = 'residual sugar', data = wine)
```

<Axes: xlabel='quality', ylabel='residual sugar'>



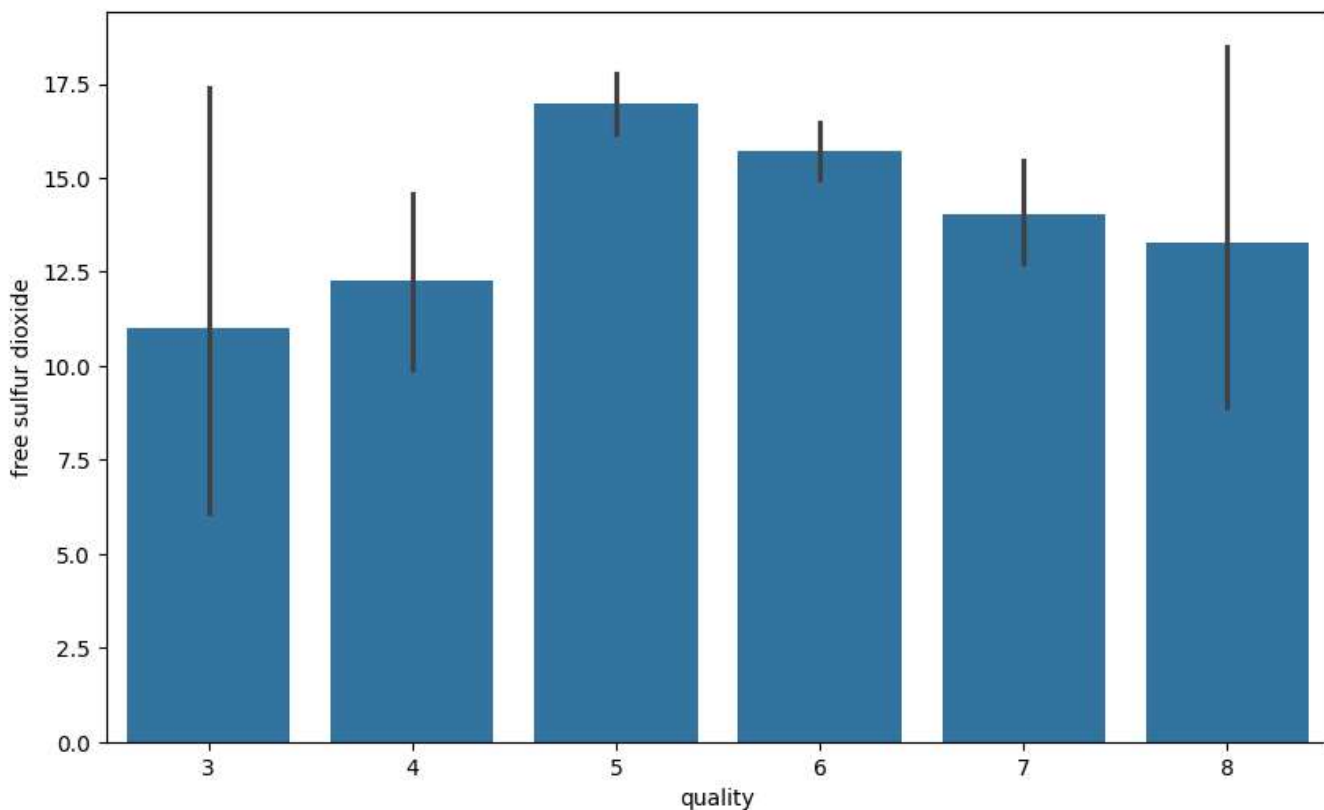
```
#Composition of chloride also go down as we go higher in the quality of the wine  
fig = plt.figure(figsize = (10,6))  
sns.barplot(x = 'quality', y = 'chlorides', data = wine)
```

<Axes: xlabel='quality', ylabel='chlorides'>



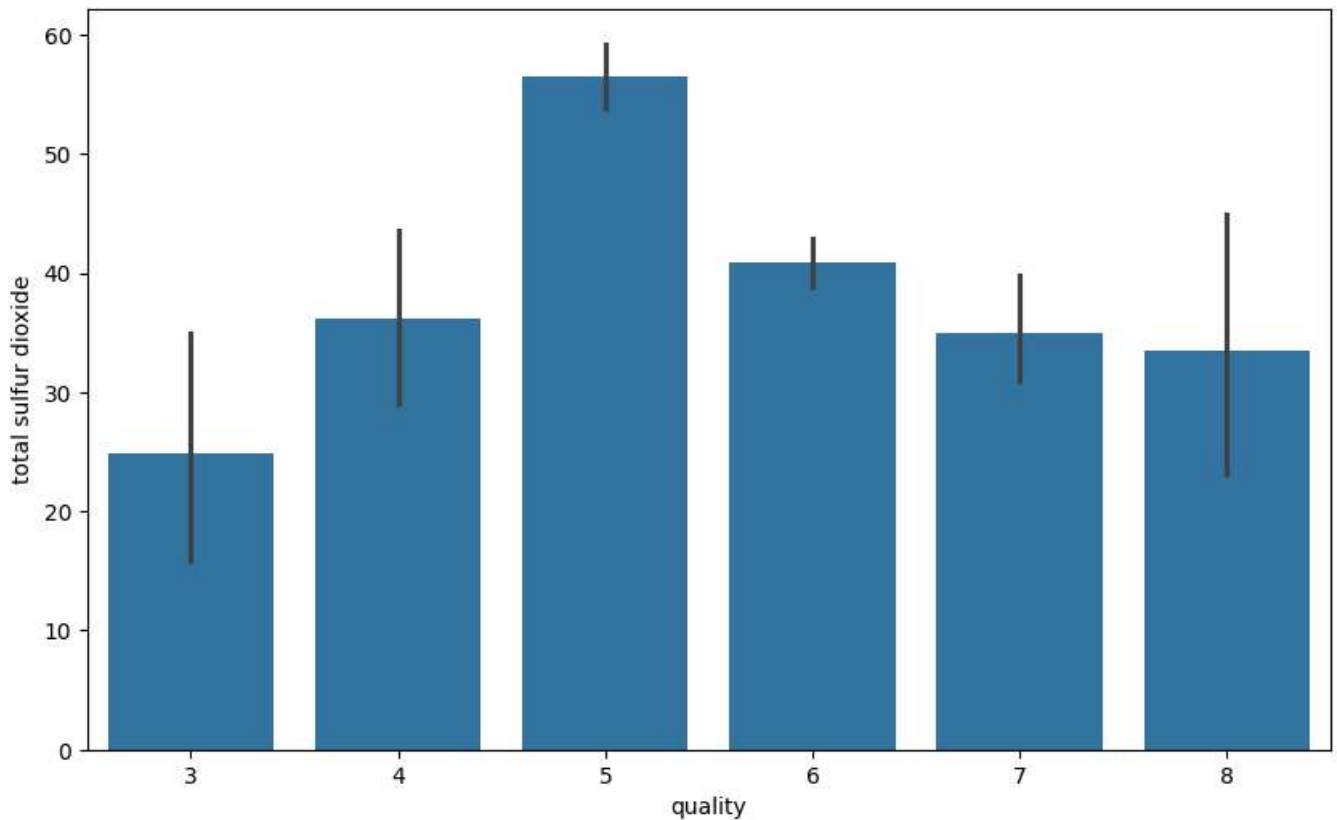
```
fig = plt.figure(figsize = (10,6))  
sns.barplot(x = 'quality', y = 'free sulfur dioxide', data = wine)
```

<Axes: xlabel='quality', ylabel='free sulfur dioxide'>



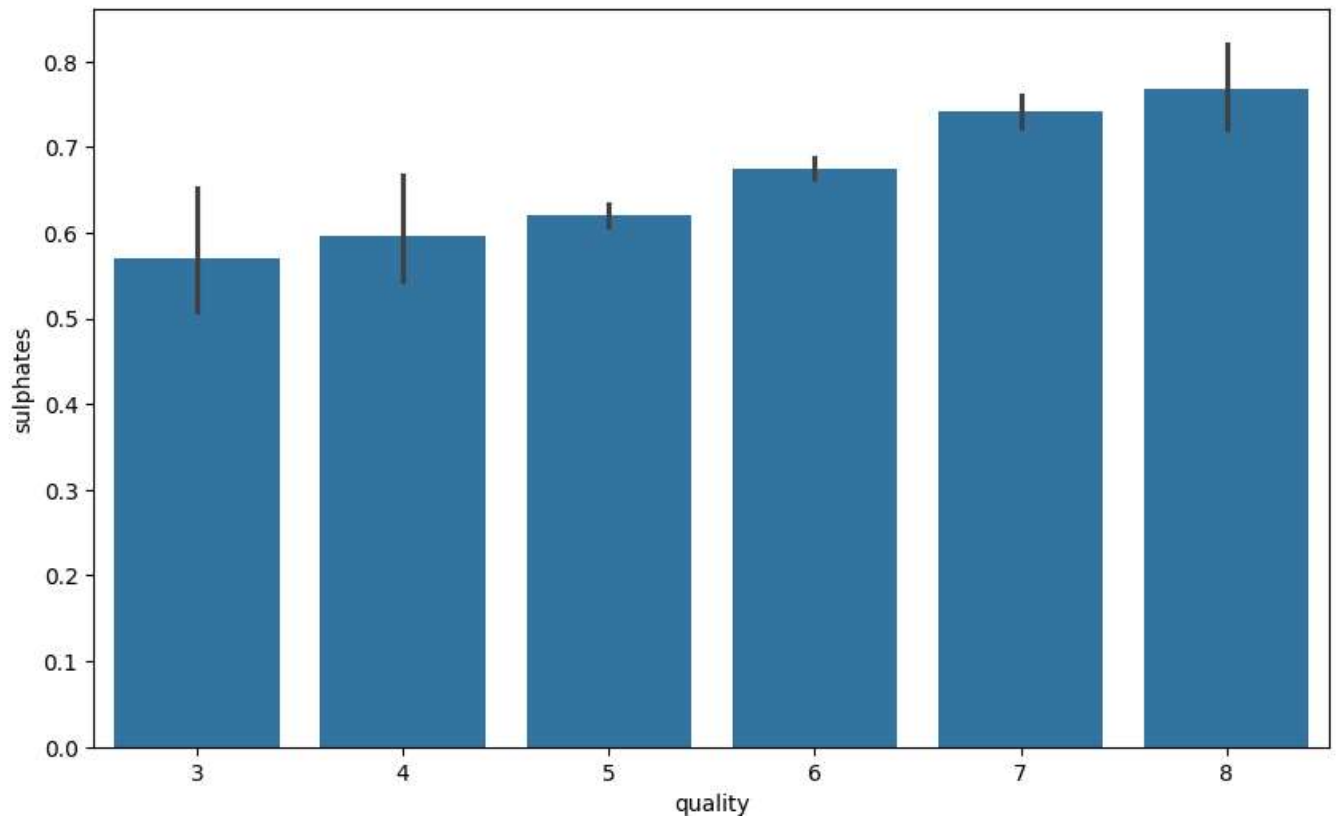
```
fig = plt.figure(figsize = (10,6))  
sns.barplot(x = 'quality', y = 'total sulfur dioxide', data = wine)
```

<Axes: xlabel='quality', ylabel='total sulfur dioxide'>



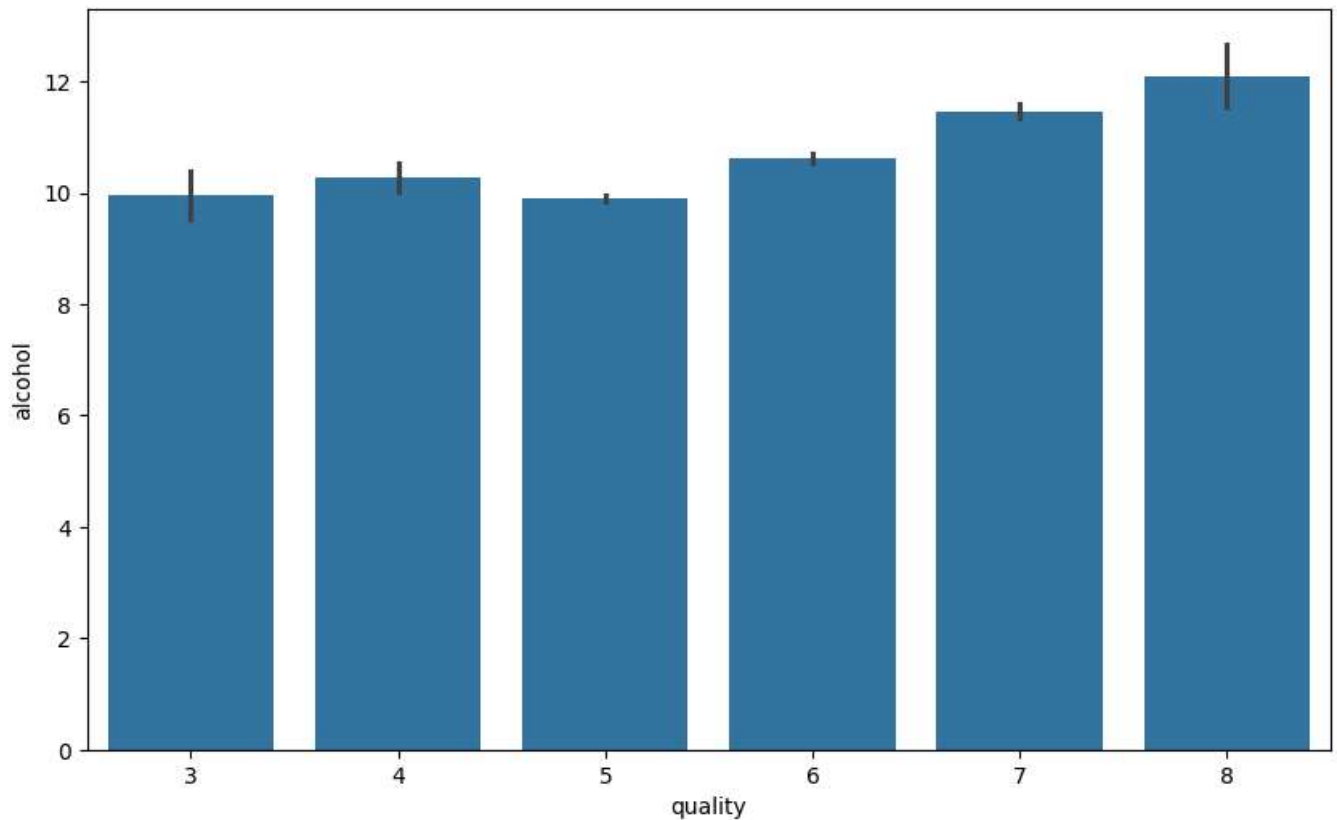
```
fig = plt.figure(figsize = (10,6))  
sns.barplot(x = 'quality', y = 'sulphates', data = wine)
```

<Axes: xlabel='quality', ylabel='sulphates'>



```
fig = plt.figure(figsize = (10,6))  
sns.barplot(x = 'quality', y = 'alcohol', data = wine)
```

<Axes: xlabel='quality', ylabel='alcohol'>



```
#Making binary classificaion for the response variable.  
#Dividing wine as good and bad by giving the limit for the quality  
bins = (2, 6.5, 8)  
group_names = ['bad', 'good']  
wine['quality'] = pd.cut(wine['quality'], bins = bins, labels = group_names)
```

```
#Now lets assign a labels to our quality variable  
label_quality = LabelEncoder()
```

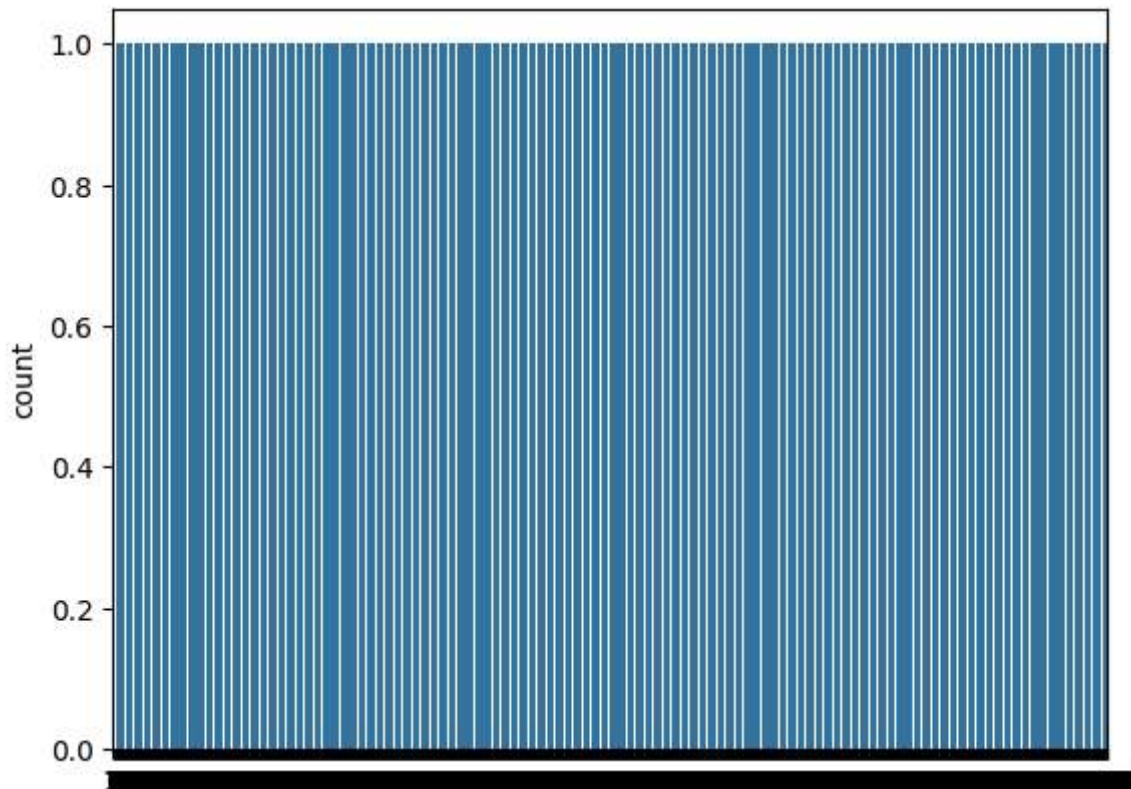
```
#Bad becomes 0 and good becomes 1  
wine['quality'] = label_quality.fit_transform(wine['quality'])
```

```
wine['quality'].value_counts()
```

```
quality  
0    1382  
1     217  
Name: count, dtype: int64
```

```
sns.countplot(wine['quality'])
```

<Axes: ylabel='count'>



```
#Now separate the dataset as response variable and feature variabes  
X = wine.drop('quality', axis = 1)  
y = wine['quality']
```



```
#Train and Test splitting of data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_state = 42)

#Applying Standard scaling to get optimized result
sc = StandardScaler()

X_train = sc.fit_transform(X_train)
X_test = sc.fit_transform(X_test)

rfc = RandomForestClassifier(n_estimators=200)
rfc.fit(X_train, y_train)
pred_rfc = rfc.predict(X_test)

#Let's see how our model performed
print(classification_report(y_test, pred_rfc))
```

	precision	recall	f1-score	support
0	0.90	0.96	0.93	273
1	0.64	0.38	0.48	47
accuracy			0.88	320
macro avg	0.77	0.67	0.71	320
weighted avg	0.86	0.88	0.86	320

```
#Confusion matrix for the random forest classification
print(confusion_matrix(y_test, pred_rfc))
```

```
[[263  10]
 [ 29  18]]
```

```
#Stochastic Gradient Decent Classifier
sgd = SGDClassifier(penalty=None)
sgd.fit(X_train, y_train)
pred_sgd = sgd.predict(X_test)
```

```
print(classification_report(y_test, pred_sgd))
```

	precision	recall	f1-score	support
0	0.89	0.97	0.93	273
1	0.62	0.32	0.42	47
accuracy			0.87	320
macro avg	0.76	0.64	0.68	320
weighted avg	0.85	0.87	0.85	320

```
print(confusion_matrix(y_test, pred_sgd))
```

```
[[264   9]
 [ 32  15]]
```

```
#Support vector classifier
```

```
svc = SVC()
```

```
svc.fit(X_train, y_train)
```

```
pred_svc = svc.predict(X_test)
```

```
print(classification_report(y_test, pred_svc))
```

	precision	recall	f1-score	support
0	0.88	0.98	0.93	273
1	0.71	0.26	0.37	47
accuracy			0.88	320
macro avg	0.80	0.62	0.65	320
weighted avg	0.86	0.88	0.85	320

```
#grid search CV
```

```
#Finding best parameters for our SVC model
```

```
param = {
```

```
    'C': [0.1,0.8,0.9,1,1.1,1.2,1.3,1.4],
```

```
    'kernel':['linear', 'rbf'],
```

```
    'gamma' :[0.1,0.8,0.9,1,1.1,1.2,1.3,1.4]
```

```
}
```