In [22]:
```
## Lab -9 SVM  17162121014 Dhruv Patel
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [23]:
```
df=pd.read_csv("winequality-red.csv")
```

In [24]:
```
df.head()
```

Out[24]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcoho
0	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.

In [25]:
```
df.info()
```

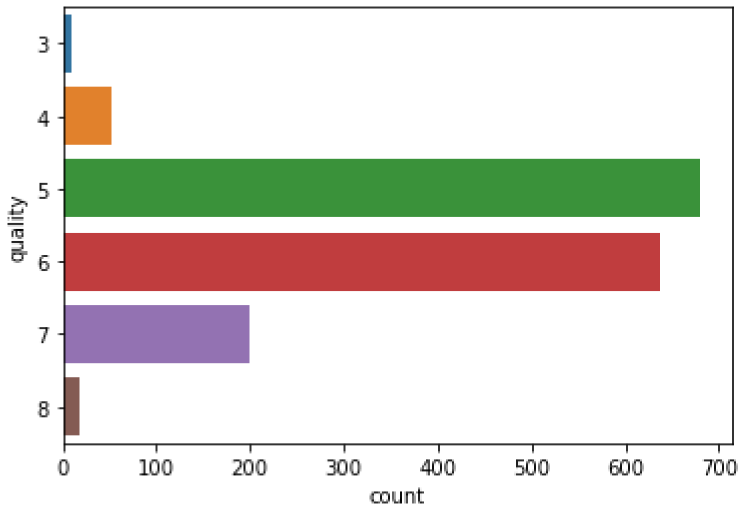
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1599 entries, 0 to 1598
Data columns (total 12 columns):
 #   Column                Non-Null Count  Dtype  
---  ------                --------------  -----  
 0   fixed acidity         1599 non-null   float64
 1   volatile acidity      1599 non-null   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
```

In [26]:
```
df["quality"].value_counts()
```

Out[26]:
```
5    681
6    638
7    199
4     53
8     18
3     10
Name: quality, dtype: int64
```

In [27]:
```
sns.countplot(data=df,y="quality")
```

Out[27]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x287f9048f88>
```



In [28]:
```
df.isnull().sum()
```

Out[28]:
```
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
```

In [110]:
```
## import model related functions
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
from sklearn.metrics import classification_report,accuracy_score,confusion_mat
rix,plot_confusion_matrix,recall_score,precision_score
from sklearn.preprocessing import StandardScaler,MinMaxScaler
```

In [30]:
```
df
```

Out[30]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alc
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
...	...	...	...	...	...	...	...	...	...	...	
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	
1596	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	

1599 rows × 12 columns

In [31]:
```
y=df["quality"]
df.drop(columns="quality",axis=1,inplace=True)
X=df
```

In [32]:
```
X
```

Out[32]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alc
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.99680	3.20	0.68	
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.99700	3.26	0.65	
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.99800	3.16	0.58	
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.99780	3.51	0.56	
...	...	...	...	...	...	...	...	...	...	...	
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.99490	3.45	0.58	
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.99512	3.52	0.76	
1596	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.99574	3.42	0.75	
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.99547	3.57	0.71	
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.99549	3.39	0.66	

1599 rows × 11 columns

In [33]:
```
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.3,random_stat
e = 0)
```

In [34]:
```
sc = StandardScaler()
```

In [35]:
```
X_train_scaled = sc.fit_transform(X_train)
X_test_scaled = sc.fit_transform(X_test)
```

In [81]:
```
svm_model = SVC(kernel="rbf",gamma=0.11,C=10,random_state=0)
```

In [82]:
```
svm_model.fit(X_train_scaled,y_train)
```

Out[82]:
```
SVC(C=10, gamma=0.11, random_state=0)
```

In [83]:
```
svm_model.score(X_test_scaled,y_test)
```

Out[83]:
```
0.61875
```

In [84]:
```
svm_model.score(X_train_scaled,y_train)
```

Out[84]:
```
0.8114387846291331
```

In [85]:
```
y_pred = svm_model.predict(X_test_scaled)
```

In [87]:
```
print(classification_report(y_test,y_pred))
```

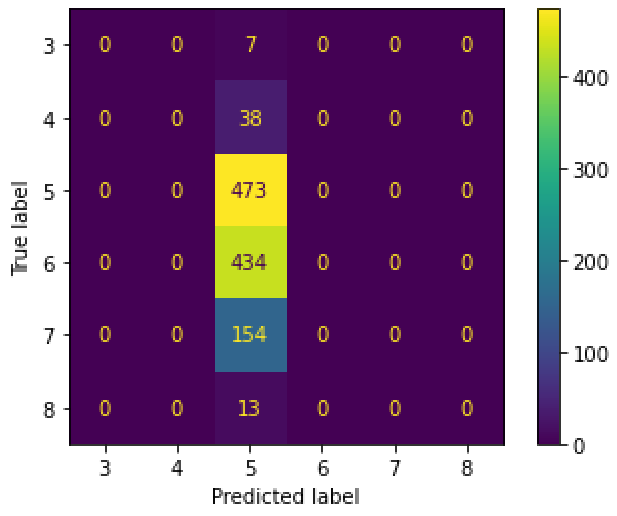
```
              precision    recall  f1-score   support

           3       0.00      0.00      0.00         3
           4       0.00      0.00      0.00        15
           5       0.67      0.74      0.70       208
           6       0.62      0.56      0.59       204
           7       0.50      0.64      0.56        45
           8       0.00      0.00      0.00         5

    accuracy                           0.62       480
   macro avg       0.30      0.32      0.31       480
weighted avg       0.60      0.62      0.61       480
```

In [88]:
```
plot_confusion_matrix(svm_model,X_train,y_train)
```

Out[88]:
```
<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x287f94a48
c8>
```



In [98]:
```
##  tasks
from sklearn import datasets
cancer = datasets.load_breast_cancer()
```

In [99]:
```
# print the names of the 13 features
print("Features: ", cancer.feature_names)

# print the label type of cancer('malignant' 'benign')
print("Labels: ", cancer.target_names)
```

```
Features:  ['mean radius' 'mean texture' 'mean perimeter' 'mean area'
 'mean smoothness' 'mean compactness' 'mean concavity'
 'mean concave points' 'mean symmetry' 'mean fractal dimension'
 'radius error' 'texture error' 'perimeter error' 'area error'
 'smoothness error' 'compactness error' 'concavity error'
 'concave points error' 'symmetry error' 'fractal dimension error'
 'worst radius' 'worst texture' 'worst perimeter' 'worst area'
 'worst smoothness' 'worst compactness' 'worst concavity'
 'worst concave points' 'worst symmetry' 'worst fractal dimension']
Labels:  ['malignant' 'benign']
```

In [100]:
```
# print data(feature)shape
cancer.data.shape
```

Out[100]:
```
(569, 30)
```

In [101]:
```
print(cancer.data[0:2])
```

```
[[1.799e+01 1.038e+01 1.228e+02 1.001e+03 1.184e-01 2.776e-01 3.001e-01
  1.471e-01 2.419e-01 7.871e-02 1.095e+00 9.053e-01 8.589e+00 1.534e+02
  6.399e-03 4.904e-02 5.373e-02 1.587e-02 3.003e-02 6.193e-03 2.538e+01
  1.733e+01 1.846e+02 2.019e+03 1.622e-01 6.656e-01 7.119e-01 2.654e-01
  4.601e-01 1.189e-01]
 [2.057e+01 1.777e+01 1.329e+02 1.326e+03 8.474e-02 7.864e-02 8.690e-02
  7.017e-02 1.812e-01 5.667e-02 5.435e-01 7.339e-01 3.398e+00 7.408e+01
  5.225e-03 1.308e-02 1.860e-02 1.340e-02 1.389e-02 3.532e-03 2.499e+01
  2.341e+01 1.588e+02 1.956e+03 1.238e-01 1.866e-01 2.416e-01 1.860e-01
  2.750e-01 8.902e-02]]
```

In [102]:
```
print(cancer.target)
```

```
[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 1 0 0 0 0 0 0 0 0 1 0 1 1 1 1 1 0 0 1 0 0 1 1 1 1 0 1 0 0 1 1 1 1 0 1 0 0
 1 0 1 0 0 1 1 1 0 0 1 0 0 0 1 1 1 0 1 1 0 0 1 1 1 0 0 1 1 1 1 0 1 1 0 1 1
 1 1 1 1 1 1 0 0 0 1 0 0 1 1 1 0 0 1 0 1 0 0 1 0 0 1 1 0 1 1 0 1 1 1 1 0 1
 1 1 1 1 1 1 1 1 0 1 1 1 1 0 0 1 0 1 1 0 0 1 1 0 0 1 1 1 1 0 1 1 0 0 0 1 0
 1 0 1 1 1 0 1 1 0 0 1 0 0 0 0 1 0 0 0 1 0 1 0 1 1 0 1 0 0 0 0 1 1 0 0 1 1
 1 0 1 1 1 1 1 0 0 1 1 0 1 1 0 0 1 0 1 1 1 1 0 1 1 1 1 1 0 1 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 1 1 1 1 1 1 0 1 0 1 1 0 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1
 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 1 0 1 0 1 1 1 1 0 0 0 1 1
 1 1 0 1 0 1 0 1 1 1 0 1 1 1 1 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 0 0 1 0 0
 0 1 0 0 1 1 1 1 1 0 1 1 1 1 1 0 1 1 1 0 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1
 1 0 1 1 1 1 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 1 1 1 1 0 1 1
 0 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 0 1
 1 1 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 0 0 1 0 1 0 1 1 1 1 1 0 1 1 0 1 0 1 0 0
 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 1 1 1 1 1 1 1 0 0 0 0 0 0 1]
```

In [103]:
```
X_train, X_test, y_train, y_test = train_test_split(cancer.data, cancer.target
, test_size=0.3,random_state=109) # 70% training and 30% test
```

In [104]:
```
svm = SVC(kernel="linear",random_state=0)
```

In [105]:
```
svm.fit(X_train,y_train)
```

Out[105]:
```
SVC(kernel='linear', random_state=0)
```

In [106]:
```
y_pred = svm.predict(X_test)
```

In [108]:
```
print("Accuracy:",accuracy_score(y_test, y_pred))
```

```
Accuracy: 0.9649122807017544
```

In [111]:
```
# Model Precision: what percentage of positive tuples are labeled as such?
print("Precision:",precision_score(y_test, y_pred))

# Model Recall: what percentage of positive tuples are labelled as such?
print("Recall:",recall_score(y_test, y_pred))
```

```
Precision: 0.9811320754716981
Recall: 0.9629629629629629
```

In [ ]: