```
In [303]: import numpy as np
          import pandas as pd
          import matplotlib.pyplot as plt
          #set plot style
          import seaborn as sns; sns.set_theme()
          sns.set_style("whitegrid", {"grid.color": ".1", "grid.linestyl
          sns.set_palette(sns.dark_palette('seagreen'),7, .50)
          #import training libraries
          from sklearn.linear_model import LinearRegression
          from sklearn.linear_model import LogisticRegression
          from sklearn.svm import SVC
          from sklearn import svm
          from sklearn.metrics import mean_absolute_error, mean_squared_erro
          r, classification report
          from sklearn.metrics import classification_report, confusion_matri
          x, accuracy_score, plot_confusion_matrix
          from sklearn.preprocessing import StandardScaler
          from sklearn.ensemble import RandomForestClassifier
          from sklearn.tree import DecisionTreeClassifier
          from sklearn.model selection import GridSearchCV
          import joblib
```

In [215]: w_wine = pd.read_csv('winequality-white.csv',sep=';')
 w_wine.head()

Out[215]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alcol
0	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	1
1	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	!
2	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10
3	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	!
4	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	!

In [216]: w_wine.shape

Out[216]: (4898, 12)

In [217]: #look for null values w_wine.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4898 entries, 0 to 4897
Data columns (total 12 columns):

#	Column	Non-Null Count	Dtype
0	fixed acidity	4898 non-null	float64
1	volatile acidity	4898 non-null	float64
2	citric acid	4898 non-null	float64
3	residual sugar	4898 non-null	float64
4	chlorides	4898 non-null	float64
5	free sulfur dioxide	4898 non-null	float64
6	total sulfur dioxide	4898 non-null	float64
7	density	4898 non-null	float64
8	рН	4898 non-null	float64
9	sulphates	4898 non-null	float64
10	alcohol	4898 non-null	float64
11	quality	4898 non-null	int64

dtypes: float64(11), int64(1)

memory usage: 459.3 KB

In [218]: w_wine.describe()

Out[218]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total di
count	4898.000000	4898.000000	4898.000000	4898.000000	4898.000000	4898.000000	4898.0
mean	6.854788	0.278241	0.334192	6.391415	0.045772	35.308085	138.3
std	0.843868	0.100795	0.121020	5.072058	0.021848	17.007137	42.4
min	3.800000	0.080000	0.000000	0.600000	0.009000	2.000000	9.0
25%	6.300000	0.210000	0.270000	1.700000	0.036000	23.000000	108.0
50%	6.800000	0.260000	0.320000	5.200000	0.043000	34.000000	134.0
75%	7.300000	0.320000	0.390000	9.900000	0.050000	46.000000	167.0
max	14.200000	1.100000	1.660000	65.800000	0.346000	289.000000	440.0

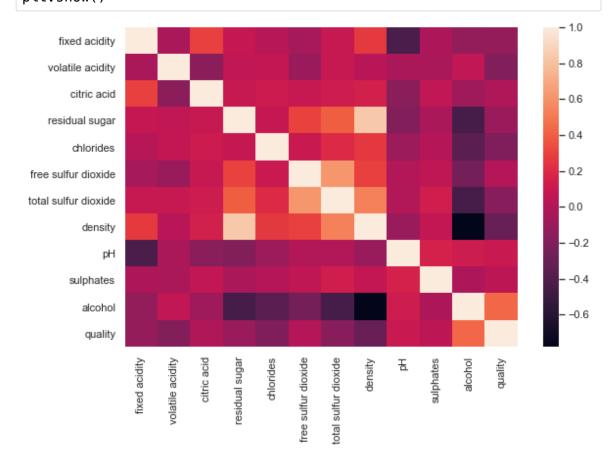
In []:

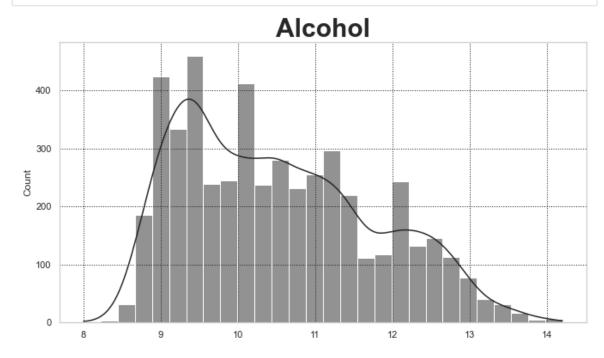
```
In [219]: #get the df correlation
wine_corr = w_wine.corr()

#plot using a heatmap
plt.figure(figsize=(9,6))

sns.heatmap(wine_corr)

#plot params
plt.show()
```



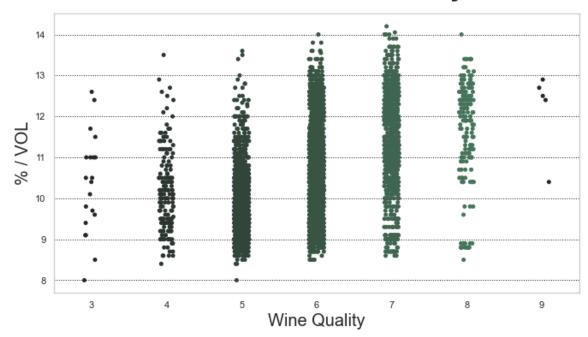


```
In [391]: #plot params
   plt.figure(figsize=(11,6))
   plt.title('Alcohol Level vs Quality',pad = 20, fontdict={'fontsize
':30,'fontweight':'bold'})

#stripplot
   sns.stripplot(data=w_wine, x='quality', y='alcohol')

#plot params
   plt.xlabel('Wine Quality', fontdict={'fontsize':20})
   plt.ylabel('% / VOL', fontdict={'fontsize':20})
   plt.show()
```

Alcohol Level vs Quality



Data Cleaning

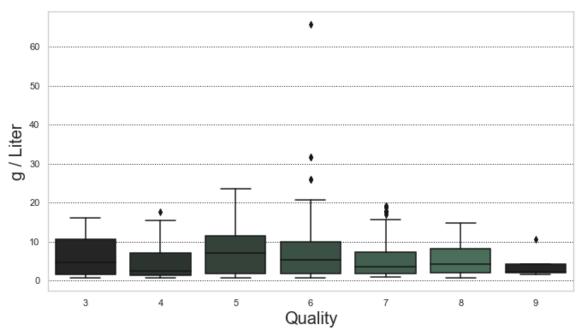
Clean the outliers for residual sugars

```
In [222]: #plot params
   plt.figure(figsize=(11,6))
   plt.title('Residual Sugar vs Quality', pad=20, fontdict={'fontsize
':30,'fontweight':'bold'})

#scatterplot
   sns.boxplot(data = w_wine, x='quality',y = 'residual sugar')

#plot params
   plt.ylabel('g / Liter',fontdict={'fontsize':20})
   plt.xlabel('Quality', fontdict={'fontsize':20})
   plt.show()
```

Residual Sugar vs Quality



Wine with the quality rating of 6 has the most apparent outliers, we will need to remove them.

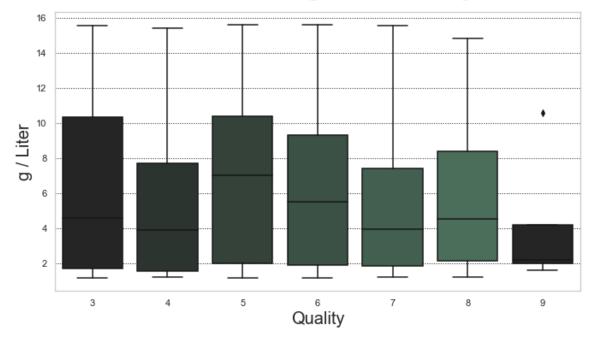
```
In [223]:
          #show stats for residual sugar
          w wine['residual sugar'].describe()
Out[223]: count
                    4898,000000
                       6.391415
          mean
          std
                       5.072058
                       0.600000
          min
          25%
                       1.700000
          50%
                       5.200000
          75%
                       9.900000
                      65.800000
          Name: residual sugar, dtype: float64
```

Residual sugar holds the mean of 6.4 grams and a standard deviation of 5, we will cut off the outliers at +2 standard deviations.

```
In [252]: #use .quantile 95% to remove outliers above 2 standard deviations
#get the lower and upper limits of residual sugar
res_sug_min, res_sug_max = w_wine['residual sugar'].quantile([.05,.
95])

#create a new dataframe without the outliers
w_wine1 = w_wine.loc[(w_wine['residual sugar']>res_sug_min) & (w_wine['residual sugar']<res_sug_max)].copy()</pre>
```

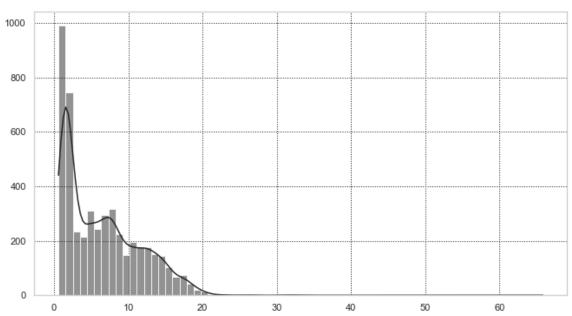
Residual Sugar vs Quality



```
In [388]: #plot the residual sugar distribution
   plt.figure(figsize=(11,6))
   plt.title('Residual Sugar', pad=20, fontdict={'fontsize':30,'fontweight':'bold'})
   sns.histplot(data=w_wine, x='residual sugar',kde=True)

plt.ylabel('')
   plt.xlabel('')
   plt.show()
```

Residual Sugar



The outliers for residual sugar have been removed but we keep a postitive distribution.

```
In [255]: w_wine1.describe()
```

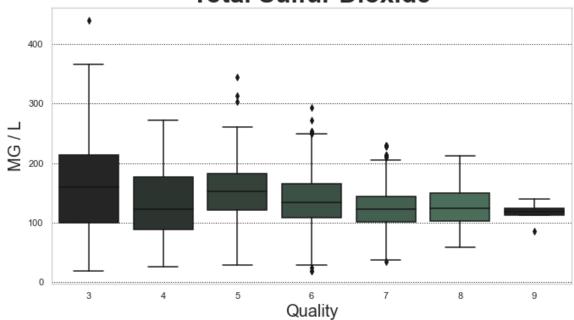
Out [255]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total di
count	4332.000000	4332.000000	4332.000000	4332.000000	4332.000000	4332.000000	4332.0
mean	6.860446	0.280015	0.332537	6.118779	0.045761	35.497576	139.3
std	0.828572	0.100428	0.117848	4.289680	0.022290	17.057093	41.9
min	3.800000	0.080000	0.000000	1.150000	0.009000	2.000000	18.0
25%	6.300000	0.210000	0.270000	1.900000	0.036000	24.000000	109.0
50%	6.800000	0.260000	0.310000	5.300000	0.043000	34.000000	135.0
75%	7.300000	0.320000	0.380000	9.200000	0.050000	46.000000	168.0
max	11.800000	1.100000	1.660000	15.600000	0.346000	289.000000	440.0

Clean sulfur dioxide outliers

```
In [256]: #plot params
    plt.figure(figsize=(11,6))
    plt.title('Total Sulfur Dioxide',fontdict={'fontsize':'30','fontwei
    ght':'bold'})
    sns.boxplot(data=w_wine1, y='total sulfur dioxide',x='quality')
    plt.xlabel('Quality',fontdict={'fontsize':20})
    plt.ylabel('MG / L',fontdict={'fontsize':20})
    plt.show()
```

Total Sulfur Dioxide

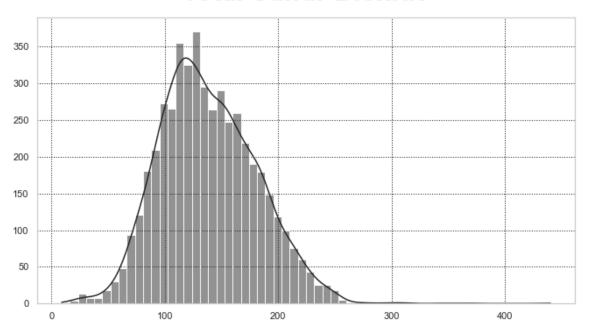


```
In [257]: #plot the total sulfur dioxide distribution
    plt.figure(figsize=(11,6))
    plt.title('Total Sulfur Dioxide', pad=20, fontdict={'fontsize':30,'
    fontweight':'bold'})

sns.histplot(data=w_wine, x='total sulfur dioxide',bins=60,kde=Tru
    e)

plt.ylabel('')
    plt.xlabel('')
    plt.show()
```

Total Sulfur Dioxide

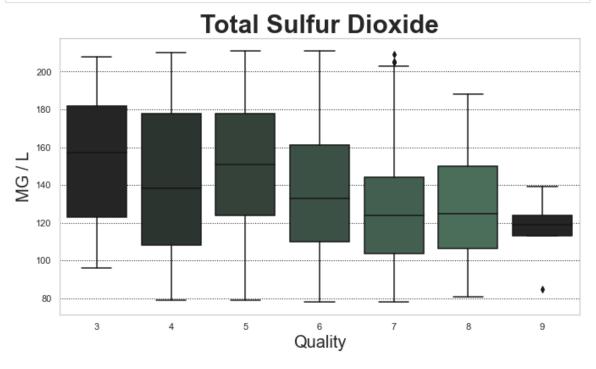


```
#show stats for total sulfur dioxide
In [258]:
          w_wine1['total sulfur dioxide'].describe()
Out [258]: count
                    4332.000000
                     139.319483
          mean
                      41.902354
          std
                      18.000000
          min
          25%
                     109.000000
          50%
                     135.000000
          75%
                     168.000000
                     440.000000
          max
          Name: total sulfur dioxide, dtype: float64
```

We will remove anything above 2 standard deviations from total sulfur dioxide.

```
In [259]: #use .quantile 95% on total sulfur dioxide to remove outliers
#so2 = sulfur dioxide
so2_min,so2_max = w_wine1['total sulfur dioxide'].quantile([.05,.9 5])

w_wine2 = w_wine1.loc[(w_wine1['total sulfur dioxide']>so2_min) &
    (w_wine1['total sulfur dioxide']<so2_max)].copy()</pre>
```



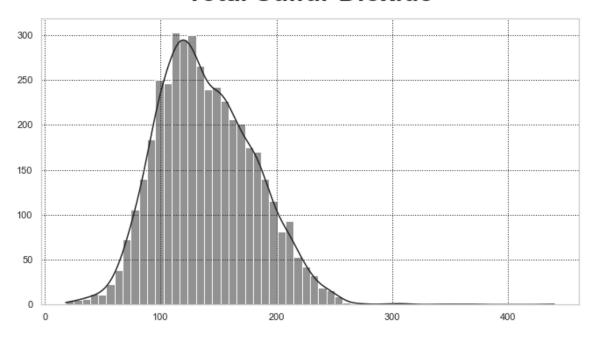
The outliers for Sulfur Dioxide have been removed.

```
In [386]: #plot the total sulfur dioxide distribution
    plt.figure(figsize=(11,6))
    plt.title('Total Sulfur Dioxide', pad=20, fontdict={'fontsize':30,'
    fontweight':'bold'})

sns.histplot(data=w_wine1, x='total sulfur dioxide',bins=60,kde=Tru
    e)

plt.ylabel('')
    plt.xlabel('')
    plt.show()
```

Total Sulfur Dioxide



The distribution for Total Sulfur Dioxide stayed roughly the same.

```
In [262]: w_wine2.describe()
```

Out [262]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total di
count	3888.000000	3888.000000	3888.000000	3888.000000	3888.000000	3888.000000	3888.0
mean	6.854231	0.277667	0.332217	6.075116	0.045684	35.541795	138.3
std	0.820197	0.098100	0.117592	4.267172	0.021608	15.487129	33.3
min	3.800000	0.080000	0.000000	1.150000	0.009000	2.000000	78.0
25%	6.300000	0.210000	0.270000	1.900000	0.036000	24.000000	112.0
50%	6.800000	0.260000	0.310000	5.200000	0.043000	34.000000	134.5
75%	7.300000	0.320000	0.380000	9.100000	0.050000	45.000000	164.0
max	11.800000	1.100000	1.660000	15.600000	0.346000	124.000000	211.0

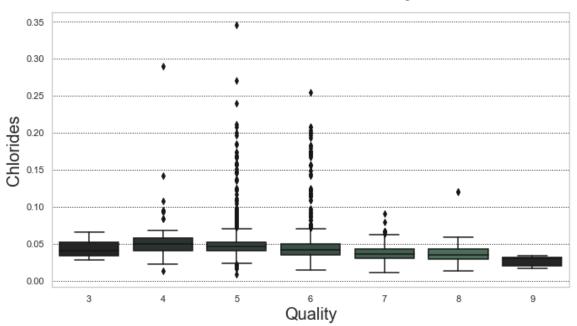
Clean Chloride outliers

```
In [263]: #Chloride vs quality
   plt.figure(figsize=(11,6))
   plt.title('Chloride vs Quality', pad= 20, fontdict={'fontsize':30})

#plot
   sns.boxplot(data=w_wine2, x='quality', y='chlorides')

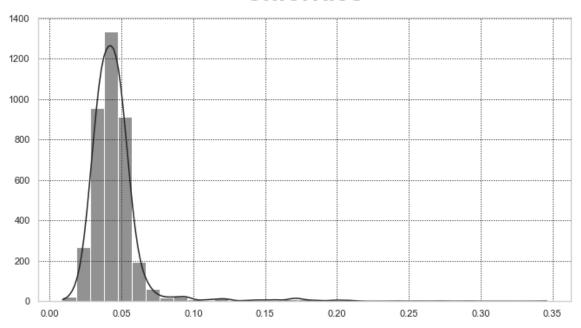
#label params
   plt.ylabel(ylabel='Chlorides', fontdict={'fontsize':20})
   plt.xlabel(xlabel='Quality', fontdict={'fontsize':20})
   plt.show()
```

Chloride vs Quality



```
In [264]: #plot the cloride distribution
   plt.figure(figsize=(11,6))
   plt.title('Chlorides', pad=20, fontdict={'fontsize':30,'fontweight
   ':'bold'})
   sns.histplot(data=w_wine2, x='chlorides',bins=35,kde=True)
   plt.ylabel('')
   plt.xlabel('')
   plt.show()
```

Chlorides



```
In [265]: w_wine.chlorides.describe()
```

```
Out[265]: count
                    4898.000000
           mean
                       0.045772
           std
                       0.021848
                       0.009000
           min
           25%
                       0.036000
           50%
                       0.043000
           75%
                       0.050000
          max
                       0.346000
```

Name: chlorides, dtype: float64

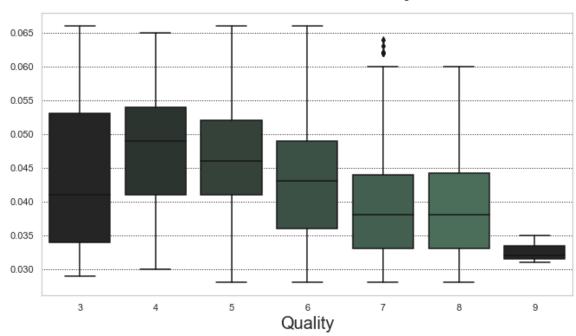
We will be removing outliers above 3 standard deviations.

```
In [385]: #Chloride plot
   plt.figure(figsize=(11,6))
   plt.title('Chloride vs Quality', pad= 20, fontdict={'fontsize':30})

#plot
   sns.boxplot(data=w_wine3, x='quality', y='chlorides')

#label params
   plt.ylabel('')
   plt.xlabel(xlabel='Quality', fontdict={'fontsize':20})
   plt.show()
```

Chloride vs Quality

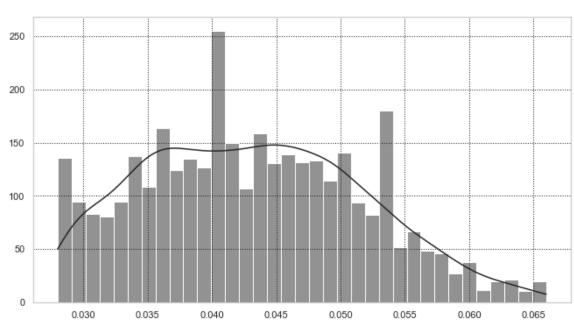


```
In [394]: #plot the total sulfur dioxide distribution
plt.figure(figsize=(11,6))
plt.title('Chlorides', pad=20, fontdict={'fontsize':30,'fontweight
':'bold'})

sns.histplot(data=w_wine3, x='chlorides',bins=35,kde=True)

plt.ylabel('')
plt.xlabel('')
plt.show()
```

Chlorides



Now that the outliers for the chlorides have been removed, the distribution looks a lot more normal.

```
In [269]: w_wine3.describe()
```

Out [269]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total di
count	3467.000000	3467.000000	3467.000000	3467.000000	3467.000000	3467.000000	3467.0
mean	6.867969	0.274254	0.331085	6.193640	0.043206	35.818575	139.0
std	0.822808	0.097020	0.113624	4.322791	0.008593	15.607268	33.2
min	3.800000	0.080000	0.000000	1.150000	0.028000	2.000000	78.0
25%	6.300000	0.210000	0.270000	1.900000	0.036000	25.000000	113.0
50%	6.800000	0.260000	0.310000	5.400000	0.043000	34.000000	136.0
75%	7.400000	0.320000	0.380000	9.450000	0.049000	46.000000	164.0
max	11.800000	1.100000	0.910000	15.600000	0.066000	124.000000	211.0

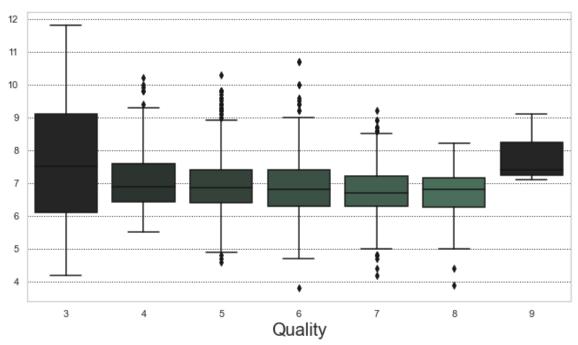
Clean Fixed Acidity outliers

```
In [270]: #fixed acidity vs quality
    plt.figure(figsize=(11,6))
    plt.title('Fixed Acidity vs Quality', pad= 20, fontdict={'fontsize
    ':30})

#plot
    sns.boxplot(data=w_wine3,x='quality',y='fixed acidity')

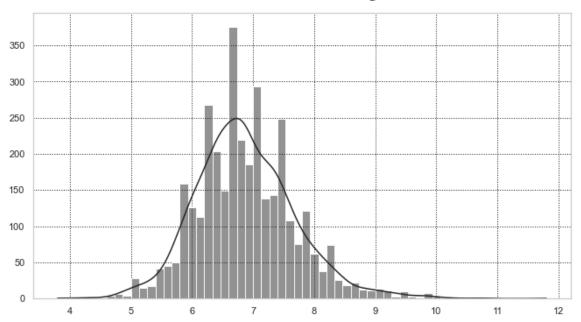
#label params
    plt.ylabel('')
    plt.xlabel(xlabel='Quality',fontdict={'fontsize':20})
    plt.show()
```

Fixed Acidity vs Quality



```
In [271]: #plot the fixed acidity distribution
    plt.figure(figsize=(11,6))
    plt.title('Fixed Acidity', pad=20, fontdict={'fontsize':30,'fontweit ght':'bold'})
    sns.histplot(data=w_wine3, x='fixed acidity',bins=60,kde=True)
    plt.ylabel('')
    plt.xlabel('')
    plt.show()
```

Fixed Acidity



```
In [272]: w_wine3['fixed acidity'].describe()
```

```
Out[272]: count
                    3467.000000
           mean
                        6.867969
           std
                        0.822808
           min
                        3.800000
           25%
                        6.300000
           50%
                        6.800000
           75%
                        7.400000
                       11.800000
           max
```

Name: fixed acidity, dtype: float64

```
In [273]: #use .quantile(.95) to remove anything above 2 standard deviations
FA_min,FA_max = w_wine3['fixed acidity'].quantile([.05,.95])

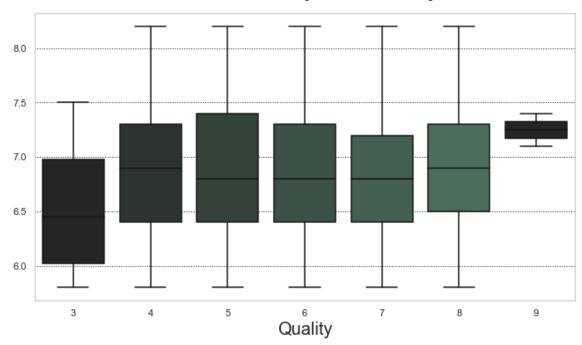
w_wine4 = w_wine3.loc[(w_wine3['fixed acidity']>FA_min) & (w_wine3
['fixed acidity']<FA_max)].copy()</pre>
```

```
In [395]: #fixed acidity vs quality
    plt.figure(figsize=(11,6))
    plt.title('Fixed Acidity vs Quality', pad= 20, fontdict={'fontsize
':30})

#plot
    sns.boxplot(data=w_wine4,x='quality',y='fixed acidity')

#label params
    plt.ylabel('')
    plt.xlabel(xlabel='Quality',fontdict={'fontsize':20})
    plt.show()
```

Fixed Acidity vs Quality



plot the fixed acidity distribution

```
plt.figure(figsize=(16,8)) plt.title('Fixed Acidity', pad=20, fontdict={'fontsize':30,'fontweight':'bold'})
sns.histplot(data=w_wine4, x='fixed acidity',bins=25,kde=True)
plt.ylabel('') plt.xlabel('') plt.show()
```

```
In [276]: w_wine4.describe()
Out[276]:
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total di
count	3068.000000	3068.000000	3068.000000	3068.000000	3068.000000	3068.000000	3068.0
mean	6.857415	0.272275	0.331708	6.310104	0.043487	36.352999	140.0
std	0.594316	0.092433	0.109394	4.352951	0.008591	15.533872	33.4
min	5.800000	0.080000	0.000000	1.200000	0.028000	2.000000	78.0
25%	6.400000	0.210000	0.270000	2.000000	0.037000	25.000000	114.0
50%	6.800000	0.260000	0.310000	5.700000	0.043000	35.000000	137.0
75%	7.300000	0.320000	0.380000	9.600000	0.050000	47.000000	166.0
max	8.200000	1.100000	0.910000	15.600000	0.066000	112.000000	211.0

Feature Engineering

We will split the wine quality into two categories of low and high quality. The threshold for low quality wine is any wine less than or equal to 6 and anything above 6 will be high quality wine.

```
In [277]: | w_wine4.head(1)
Out [277]:
                                                              total
                                                       free
                fixed volatile citric residual
                                                             sulfur density pH sulphates alcoho
                                           chlorides
                                                      sulfur
               acidity acidity
                              acid
                                     sugar
                                                     dioxide dioxide
                  6.3
                         0.3
                              0.34
                                       1.6
                                               0.049
                                                       14.0
                                                              132.0
                                                                     0.994 3.3
                                                                                   0.49
                                                                                            9.
            #add a column 'rating' to the dataframe
In [280]:
            #any value in the quality column <= 6 = 0 and >6 = 1
            w_wine4['rating'] = np.where(w_wine4['quality']>6,1,0)
            w_wine4.head()
```

Out [280]:

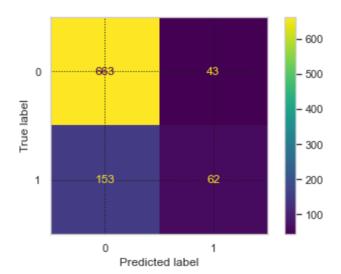
	fixed cidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alcol
 1	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	!
2	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	11
3	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	!
4	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	!
5	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10

When we split the data, we will have to drop both 'quality' and 'rating'. We will use 'rating' as our target variable.

Logistic Regression

```
In [293]: #choosing target and features
          #drop rating and quality
          #rating will be the target variable
          X = w_wine4.drop(['rating','quality'],axis=1)
          y = w_wine4.rating
          #train test spllit
          X_train,X_test,y_train,y_test = train_test_split(X,y, test_size=.3,
          random_state=101 )
In [294]: #scale the data
          sc = StandardScaler()
          X_train = sc.fit_transform(X_train)
          X_test = sc.transform(X_test)
In [295]: #Train using LinearRegression
          LG_model=LogisticRegression()
          LG_model.fit(X_train,y_train)
          LG_model.score(X_test,y_test)
Out [295]: 0.7871878393051032
In [296]: #hold prediction results
          LG_pred=LG_model.predict(X_test)
In [301]: | confusion_matrix(y_test,LG_pred)
Out[301]: array([[663,
                 [153, 62]], dtype=int64)
```

In [306]: plot_confusion_matrix(LG_model,X_test,y_test)



With a logistic regression score of .79, we get 663 true positive and 43 false positive. We also get 153 false negatives and 62 true negatives.

In [309]: print(classification_report(y_test,LG_pred))

	precision	recall	f1-score	support	
0 1	0.81 0.59	0.94 0.29	0.87 0.39	706 215	
accuracy macro avg weighted avg	0.70 0.76	0.61 0.79	0.79 0.63 0.76	921 921 921	

```
In [297]: #create a function for MAE, MSE, and RMSE using the predicted value
s
def error_calc(test,pred):
    MAE = mean_absolute_error(test,pred)
    MSE = mean_squared_error(test,pred)
    RMSE = np.sqrt(MSE)
    return MAE,MSE,RMSE
```

```
In [345]: #use the function to calculate the error metrics for the logistics
    regression model
    LG_MAE,LG_MSE,LG_RMSE = error_calc(y_test,LG_pred)
    print('Logistic Regression Metrics:\nMAE: {}\nMSE: {}\n'.
    format(LG_MAE,LG_MSE,LG_RMSE))
```

Logistic Regression Metrics: MAE: 0.21281216069489686 MSE: 0.21281216069489686 RMSE: 0.4613156844232557

SVM

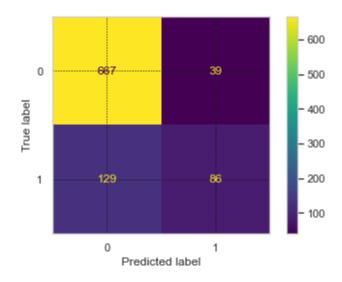
```
In [321]: #train using SVC()
    svc_model= SVC()
    svc_model.fit(X_train,y_train)
    #print the score of the model
    svc_model.score(X_test,y_test)
```

Out[321]: 0.8175895765472313

```
In [319]: svc_pred = svc_model.predict(X_test)
    print(confusion_matrix(y_test,svc_pred))
```

[[667 39] [129 86]]

```
In [324]: plot_confusion_matrix(svc_model,X_test,y_test)
```



```
In [325]: #print classification report
          print(classification_report(y_test,svc_pred))
                         precision
                                       recall f1-score
                                                           support
                                         0.94
                      0
                              0.84
                                                   0.89
                                                               706
                      1
                              0.69
                                         0.40
                                                   0.51
                                                               215
                                                   0.82
                                                               921
              accuracy
                                                   0.70
                                         0.67
                                                               921
             macro avg
                              0.76
          weighted avg
                              0.80
                                         0.82
                                                   0.80
                                                               921
```

Looks like we got a better score with SVM.

Grid Search

Out [340]:

	model	best_score	best_params
0	svm	0.780635	{'C': 20, 'kernel': 'linear'}
1	random_forest	0.771168	{'n_estimators': 10}
2	logistic_regression	0.774767	{'C': 5}
3	decision_tree	0.724895	{'criterion': 'entropy'}

Looks like SVM has the best score.

Final Model

```
In [368]: print(classification_report(y_test,final_pred))
                         precision
                                       recall f1-score
                                                            support
                                         0.92
                      0
                               0.87
                                                    0.89
                                                                706
                      1
                               0.68
                                         0.54
                                                    0.60
                                                                215
                                                    0.83
                                                                921
               accuracy
                               0.77
                                         0.73
                                                    0.75
                                                                921
              macro avg
          weighted avg
                                                    0.83
                                                                921
                               0.82
                                         0.83
```

Export model to a .pkl file

```
In [371]:
           import pickle
           #use pickle.dump to export model
           pickle.dump(final_model,open('wine_svc.pkl','wb'))
In [374]: #load the model
           load_model=joblib.load('wine_svc.pkl')
           load_model
Out [374]: SVC(C=20)
In [373]: | w_wine.head(1)
Out [373]:
                                                   free
                                                         total
               fixed volatile citric residual
                                        chlorides
                                                  sulfur
                                                         sulfur density pH sulphates alcoholic
              acidity acidity
                            acid
                                  sugar
                                                 dioxide dioxide
                                           0.045
                                                         170.0
           0
                 7.0
                       0.27
                            0.36
                                   20.7
                                                   45.0
                                                                1.001 3.0
                                                                             0.45
                                                                                     8.
In [381]:
           #predict using the values in the head of the dataframe
           #create a function to predict the quality of wine
           def wine_pred(var):
               prediction = load_model.predict(var)
               if prediction == 0:
                    print("Low Quality Wine")
               else:
                    print("High Quality Wine")
           #create a list of values
In [384]:
           values = [[7.0, 0.27, 0.36, 20.7, 0.045, 45.0, 170.0, 1.001, 3.0,
           0.45, 8.8]]
           #call the function to predict the values in the list
           wine_pred(values)
           Low Quality Wine
```

In []:			

The quality in the first entry of the dataframe is 6, the SVC model predicted a 0 for Low Quality.