Final Team Project

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Problem Statement

> The purpose of this project is to automate the wine selection process in order to increase profit and build on the business's reputation. This will be done by implementing a model that predicts the quality of the wine. The profit margin of restaurants is approximately 70%. This means that over half the profit of these business types come from wine. On the other hand, there are also major expenses that pertain to wine as well. From vendors to sommeliers, there are dozens of additional expenses when it comes to finding and purchasing good quality wine. The profits of the business can no longer support the expenses of the wine selection process. Within a few months, the expenses will exceed the profits of the business and the business will have to close down. The automation of the wine selection process will reduce the expenses by approximately 25%, allowing the business to build its finances and stay in business.

In [1]:

```
#Import Libraries
import pandas as pd
import numpy as np
import random
import statistics as stats
import scikitplot as skplt
import matplotlib.pyplot as plt
import statsmodels.api as sm
import seaborn as sns
import dmba
import warnings
warnings.filterwarnings("ignore")

from sklearn import preprocessing, datasets, linear_model
from sklearn.preprocessing import StandardScaler, LabelEncoder
from sklearn.model_selection import train_test_split, cross_val_score, KFold, GridSearchCV
from sklearn.metrics import accuracy_score, r2_score, plot_confusion_matrix,
from sklearn.metrics import classification_report, confusion_matrix, roc_curve
from sklearn.neighbors import NearestNeighbors, KNeighborsClassifier
from sklearn.linear_model import LogisticRegression, LogisticRegressionCV, LinearRegressio
from sklearn.tree import DecisionTreeClassifier
from sklearn.neural_network import MLPClassifier
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier
from dmba import classificationSummary, gainsChart, liftChart

from dmba.metric import AIC_score
from sklearn import svm
from sklearn.svm import SVC
from dmba import regressionSummary, adjusted_r2_score, AIC_score, BIC_score
```

In [2]:

```
#load dataset and put into a data frame
```

```
redwine_data = pd.read_csv("winequality-red.csv")

redwine_df = pd.DataFrame(redwine_data)

#Display first five rows of dataframe to confirm

redwine_df.head()
```

Out[2]:

	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
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5

Data Preprocessing

The uploaded wine dataset was preprocessed, which involved evaluating any necessary modifications needed, from outliers, correlations, or missing values, towards the dataset as a prepatory procedure for the final model. The shape of the dataset features 1,599 entries with 12 columns with no missing data detected. Since the objective is to develop a model that predicts the quality of the wine, the 'quality' predictor was designated as the target variable. There were six unique elements of an array (values 3 to 8) within the 'quality' predictor, and each element served as a scale to rate the quality of the wine. The next procedure made to the dataset was to detect any outliers within each predictor using the Z method, which also calculated the predictors' mean and standard deviation. The dataset contained many outliers, with 'total sulfur dioxide' predictor containing the most. Lastly, a heatmap was created to assess the correlations of the predictors. The 'density' predictor shared a strong positive correlation value of 0.67 with 'fixed acidity' and 'citric acid'. On the contrary, 'fixed acidity' and 'pH' shared a strong negative correlation value of -0.68.

In [3]:

```
# Check type of variables
redwine_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 [4]:

```
redwine_df.describe()
```

Out[4]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	
count	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	1599.000000	159
mean	8.319637	0.527821	0.270976	2.538806	0.087467	15.874922	46.467792	0.996747	
std	1.741096	0.179060	0.194801	1.409928	0.047065	10.460157	32.895324	0.001887	
min	4.600000	0.120000	0.000000	0.900000	0.012000	1.000000	6.000000	0.990070	
25%	7.100000	0.390000	0.090000	1.900000	0.070000	7.000000	22.000000	0.995600	
50%	7.900000	0.520000	0.260000	2.200000	0.079000	14.000000	38.000000	0.996750	
75%	9.200000	0.640000	0.420000	2.600000	0.090000	21.000000	62.000000	0.997835	
max	15.900000	1.580000	1.000000	15.500000	0.611000	72.000000	289.000000	1.003690	

In [5]:

```
# Check for data size
redwine_df.shape
```

Out[5]:

```
(1599, 12)
```

In [6]:

```
redwine_df['quality'].unique()
```

Out[6]:

```
array([5, 6, 7, 4, 8, 3], dtype=int64)
```

In [7]:

```
redwine_df.isna().sum()
```

Out[7]:

```
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 [8]:

```
redwine_df.dtypes
```

Out[8]:

```
fixed acidity           float64
volatile acidity        float64
citric acid             float64
residual sugar          float64
chlorides               float64
free sulfur dioxide     float64
total sulfur dioxide    float64
density                 float64
pH                      float64
sulphates               float64
alcohol                 float64
```

```
quality                          int64
dtype: object
```

In [9]:

```
# Removing Outliers

#based on the boxplots total sulfur dioxide has many outliers
d1= redwine_df['total sulfur dioxide']
mean = np.mean(redwine_df['total sulfur dioxide'])
std = np.std(redwine_df['total sulfur dioxide'])
print('mean of the dataset is', mean)
print('std. deviation is', std)


#z method
#total sulfur dioxide
out=[]
def Zscore_outlier(df):
    m = np.mean(df)
    sd = np.std(df)
    for i in df:
        z = (i-m)/sd
        if np.abs(z) > 3:
            out.append(i)
    print("Outliers:",out)
Zscore_outlier(redwine_df['total sulfur dioxide'])



#z method
#free sulfur dioxide
out=[]
def Zscore_outlier(df):
    m = np.mean(df)
    sd = np.std(df)
    for i in df:
        z = (i-m)/sd
        if np.abs(z) > 3:
            out.append(i)
    print("Outliers:",out)
Zscore_outlier(redwine_df['free sulfur dioxide'])
```

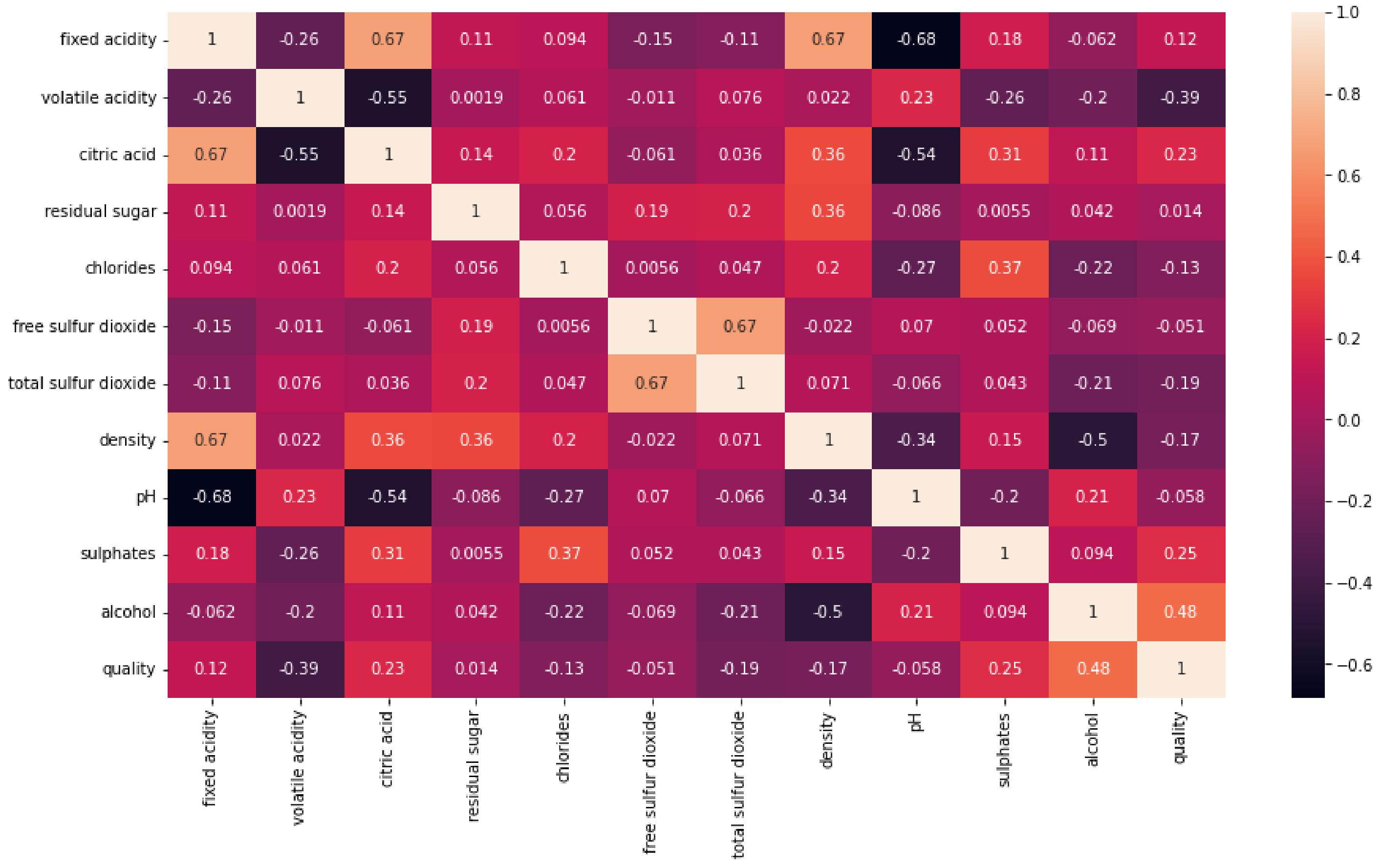
```
mean of the dataset is 46.46779237023139
std. deviation is 32.88503665178374
Outliers: [148.0, 153.0, 165.0, 151.0, 149.0, 147.0, 148.0, 155.0, 151.0, 152.0, 278.0, 28
9.0, 160.0, 147.0, 147.0]
Outliers: [52.0, 51.0, 50.0, 68.0, 68.0, 54.0, 53.0, 52.0, 51.0, 57.0, 50.0, 48.0, 48.0, 7
2.0, 51.0, 51.0, 52.0, 55.0, 55.0, 48.0, 48.0, 66.0]
```

In [10]:

```
plt.figure(figsize = (15, 8))

sns.heatmap(redwine_df.corr(), annot = True)
```

Out[10]:

```
<AxesSubplot:>
```



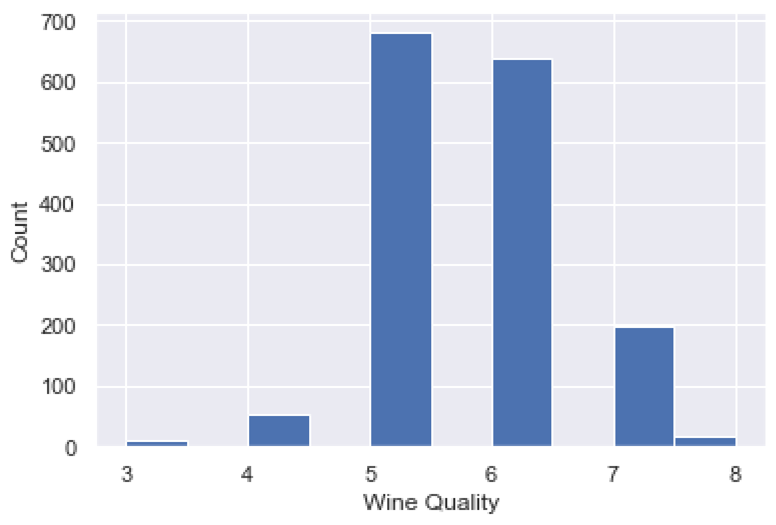
	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
fixed acidity	1	-0.26	0.67	0.11	0.094	-0.15	-0.11	0.67	-0.68	0.18	-0.062	0.12
volatile acidity	-0.26	1	-0.55	0.0019	0.061	-0.011	0.076	0.022	0.23	-0.26	-0.2	-0.39
citric acid	0.67	-0.55	1	0.14	0.2	-0.061	0.036	0.36	-0.54	0.31	0.11	0.23
residual sugar	0.11	0.0019	0.14	1	0.056	0.19	0.2	0.36	-0.086	0.0055	0.042	0.014
chlorides	0.094	0.061	0.2	0.056	1	0.0056	0.047	0.2	-0.27	0.37	-0.22	-0.13
free sulfur dioxide	-0.15	-0.011	-0.061	0.19	0.0056	1	0.67	-0.022	0.07	0.052	-0.069	-0.051
total sulfur dioxide	-0.11	0.076	0.036	0.2	0.047	0.67	1	0.071	-0.066	0.043	-0.21	-0.19
density	0.67	0.022	0.36	0.36	0.2	-0.022	0.071	1	-0.34	0.15	-0.5	-0.17
pH	-0.68	0.23	-0.54	-0.086	-0.27	0.07	-0.066	-0.34	1	-0.2	0.21	-0.058
sulphates	0.18	-0.26	0.31	0.0055	0.37	0.052	0.043	0.15	-0.2	1	0.094	0.25
alcohol	-0.062	-0.2	0.11	0.042	-0.22	-0.069	-0.21	-0.5	0.21	0.094	1	0.48
quality	0.12	-0.39	0.23	0.014	-0.13	-0.051	-0.19	-0.17	-0.058	0.25	0.48	1

Explanatory Data Analysis (EDA)

> Explorory Data Analysis recap: Exploratory Data Analysis (EDA) was implemented to evaluate the qualities of each predictor within the dataset. This procedure involved generating a number of visualizations to identify certain trends of each predictor from the dataset, test hypotheses, and evaluate assumptions

In [11]:
```python
#Create histogram on 'quality' variable
sns.set()
redwine_df.quality.hist()
plt.xlabel('Wine Quality')
plt.ylabel('Count')
```

Out[11]:
```
Text(0, 0.5, 'Count')
```



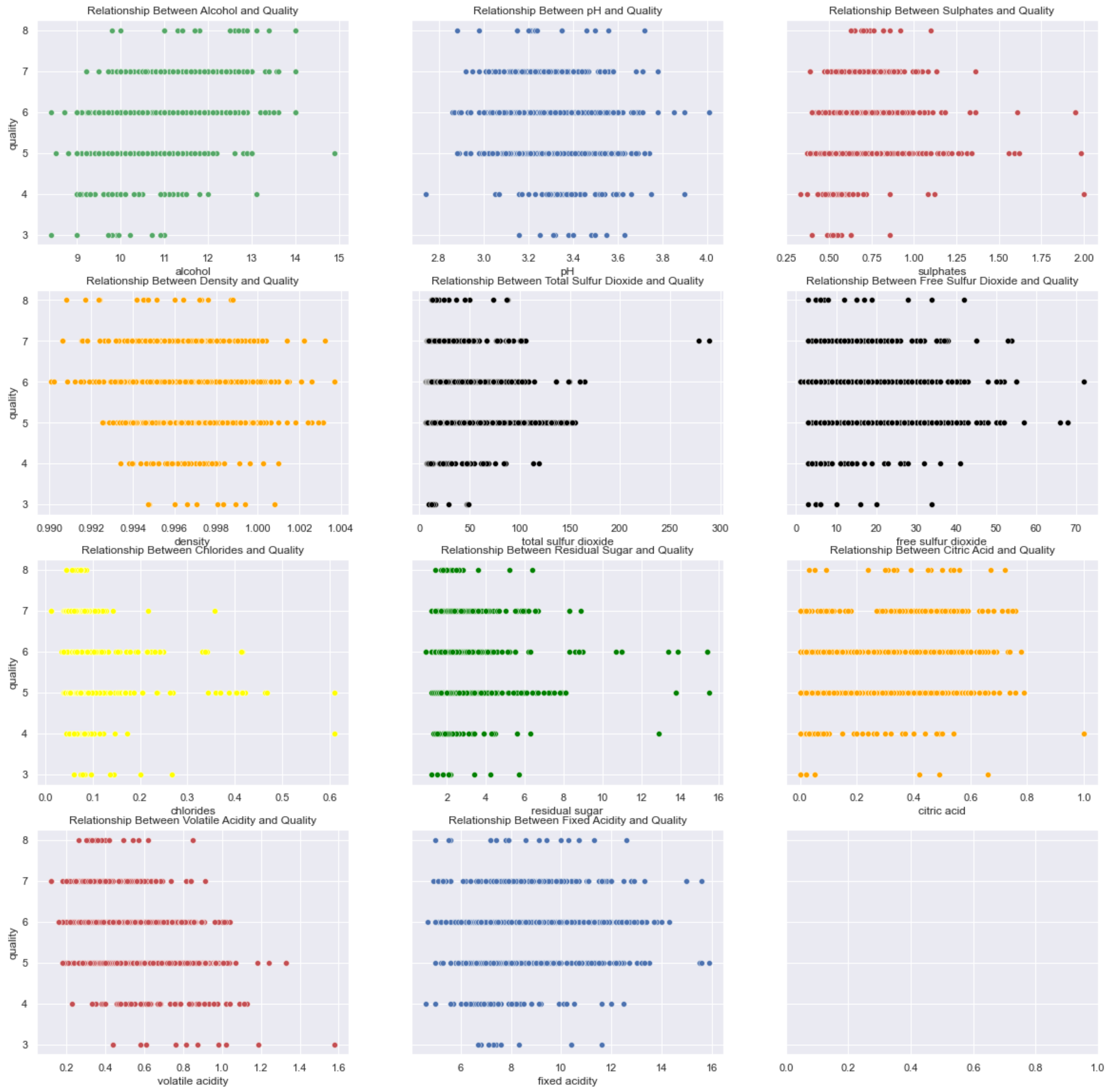
> Explanation: Explanation: The first visualization made above was a histogram, which highlights the distributed quantity of the targeted predictor 'Wine Quality' since the objective is to create a model that predicts the quality of the wine as good or bad. It was found that the average quality-type wines (rated 5 or 6) generated the highest count, which also indicates that they were most distributed among businesses. The value count function above specifies the value of wines that fit each category, which they confirm the average-rated wines being distributed the most.

In [12]:

```
# Analyze the relationships between the predictors and the target variable ('quality').


fig, axes = plt.subplots(4, 3, figsize = (20,20), sharey = True)


sns.scatterplot(ax = axes[0,0], data = redwine_df, y = "quality", x = "alcohol", color = '
axes[0,0].set_title("Relationship Between Alcohol and Quality")

sns.scatterplot(ax = axes[0, 1], data = redwine_df, y = "quality", x = "pH", color = "b")
axes[0,1].set_title("Relationship Between pH and Quality")

sns.scatterplot(ax = axes[0, 2], data = redwine_df, y = "quality", x = "sulphates", color
axes[0,2].set_title("Relationship Between Sulphates and Quality")

sns.scatterplot(ax = axes[1,0], data = redwine_df, y = "quality", x = "density", color = '
axes[1,0].set_title("Relationship Between Density and Quality")

sns.scatterplot(ax = axes[1,1], data = redwine_df, y = "quality", x = "total sulfur dioxic
axes[1,1].set_title("Relationship Between Total Sulfur Dioxide and Quality")

sns.scatterplot(ax = axes[1,2], data = redwine_df, y = "quality", x = "free sulfur dioxide
axes[1,2].set_title("Relationship Between Free Sulfur Dioxide and Quality")

sns.scatterplot(ax = axes[2,0], data = redwine_df, y = "quality", x = "chlorides", color =
axes[2,0].set_title("Relationship Between Chlorides and Quality")

sns.scatterplot(ax = axes[2,1], data = redwine_df, y = "quality", x = "residual sugar", co
axes[2,1].set_title("Relationship Between Residual Sugar and Quality")

sns.scatterplot(ax = axes[2,2], data = redwine_df, y = "quality", x = "citric acid", colo
axes[2,2].set_title("Relationship Between Citric Acid and Quality")

sns.scatterplot(ax = axes[3,0], data = redwine_df, y = "quality", x = "volatile acidity",
axes[3,0].set_title("Relationship Between Volatile Acidity and Quality")

sns.scatterplot(ax = axes[3,1], data = redwine_df, y = "quality", x = "fixed acidity", col
axes[3,1].set_title("Relationship Between Fixed Acidity and Quality")
```

Out[12]:

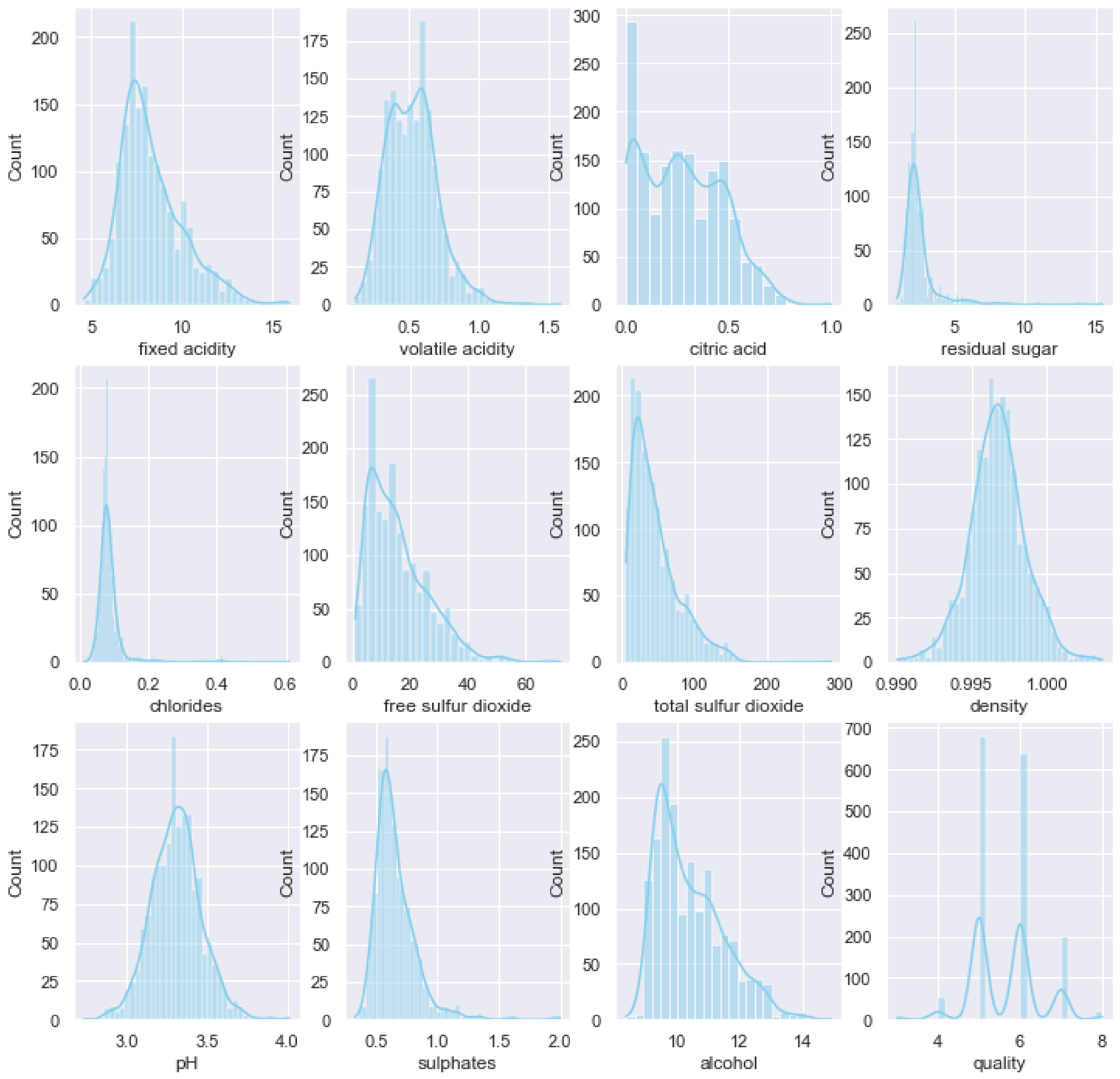
```
Text(0.5, 1.0, 'Relationship Between Fixed Acidity and Quality')
```



> Explanation: The next step was to analyze the relationships between the predictors and 'quality'. Using scatterplots to distribute a visual representation of each predictor versus 'quality', all predictors were found to have a strong relationship between the average-rated wine qualities. From the visualizations, the quality-type wines that were rated 5 or 6 garnered most of each predictor. The scatterplots also indicated a strong presence of outliers within certain predictors that includes 'sulfur dioxide', 'residual sugar', and 'chlorides'.

In [13]:
```
# Histogram

fig, axs = plt.subplots(3, 4, figsize=(12, 12))
columns = redwine_df.columns[:12]
k=0
sns.set(font_scale=1)
for i in range(3):
    for j in range(4):
```

```
    sns.histplot(data=redwine_df, x=columns[k], kde=True, color="skyblue", ax=axs[i, j
    k+=1
```

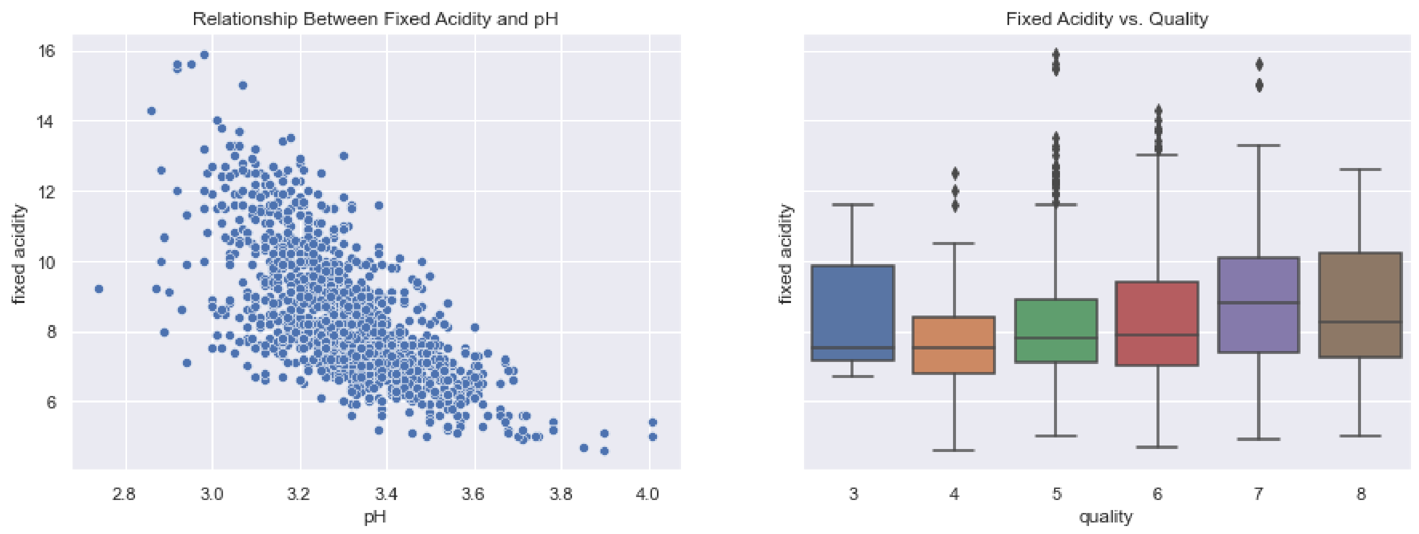


> Explanation: Explanation: Based on the histograms above we can see each columns distribution. We can see that fixed acidity, density, and PH have normal distributions. While the other columns do not follow normal distributions. Volatile acidity, citric acid, and quality appear to have more of a bimodal or multimodal distribution. One of the columns that jumps out is quality as per our objective is to automate the wine selection we can transform the quality selection to better fit a normal distribution to have a better understandment of the what makes a wine be good quality

In [14]:
```
fig, axes = plt.subplots(1, 2, figsize = (15, 5), sharey = True)

sns.scatterplot(ax = axes[0], data = redwine_df, y = "fixed acidity", x = "pH")
axes[0].set_title("Relationship Between Fixed Acidity and pH")
```

```
sns.boxplot(ax = axes[1], data = redwine_df, y = "fixed acidity", x = "quality")
axes[1].set_title("Fixed Acidity vs. Quality")
```

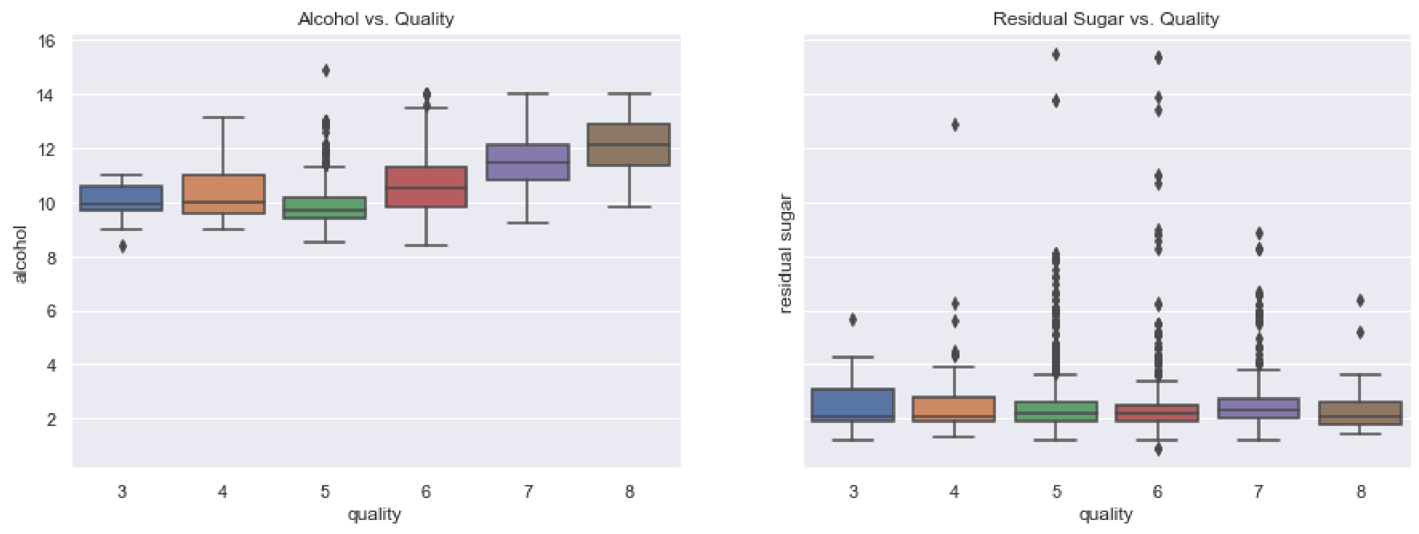
Out[14]:
```
Text(0.5, 1.0, 'Fixed Acidity vs. Quality')
```



> Explanation: The following visuals above assessed the relationship between 'fixed acidity' to 'pH' and 'quality'. For the scatterplot on the left, 'fixed acidity' and 'pH' share a strong negative correlation, where a decrease in 'fixed acidity' leads to an increse in 'pH'. For the boxplot, a majority of the wine qualities lean towards the distribution of 'fixed' acidity' and 'quality' being positively skewed. Outliers are clearly visualized for each wine quality type when assessing the relationship between 'fixed acidity' and 'quality'.

In [15]:
```
fig, axes = plt.subplots(1, 2, figsize = (15, 5), sharey = True)

sns.boxplot(ax = axes[0], data = redwine_df, y = "alcohol", x = "quality")
axes[0].set_title("Alcohol vs. Quality")

sns.boxplot(ax = axes[1], data = redwine_df, y = "residual sugar", x = "quality")
axes[1].set_title("Residual Sugar vs. Quality")
```

Out[15]:
```
Text(0.5, 1.0, 'Residual Sugar vs. Quality')
```



> Explanation: The visuals above feature boxplots that depicts the relationship of 'pH' to 'alcohol' and 'residual sugar'. The high-rated wine qualities that contain alcohol

> feature a distribution that is normally distributed while the low-rated wine qualities with alcohol are more skewed to the left. Heavy presence of outliers were detected while evaluating the relationship between 'residual sugar' and 'quality'.

Data Splitting

The wines with a score quality below or equal to 5 were changed to 0, which indicated that they were not in good quality. The wines with a score quality that were greater than or equal to 6 were changed to 1, which indicated that they were in good quality. As a result, this changes the classification from multiclass to binary.

In [16]:
```
redwine_df.head()
```

Out[16]:

	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
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	5
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	5
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	6
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	5

In [17]:
```
for idx in redwine_df.index:
    if redwine_df["quality"][idx] <=5:
        redwine_df["quality"][idx] = 0

    if redwine_df["quality"][idx] >=6:
        redwine_df["quality"][idx] = 1

redwine_df.head()
```

Out[17]:

	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	0
1	7.8	0.88	0.00	2.6	0.098	25.0	67.0	0.9968	3.20	0.68	9.8	0
2	7.8	0.76	0.04	2.3	0.092	15.0	54.0	0.9970	3.26	0.65	9.8	0
3	11.2	0.28	0.56	1.9	0.075	17.0	60.0	0.9980	3.16	0.58	9.8	1
4	7.4	0.70	0.00	1.9	0.076	11.0	34.0	0.9978	3.51	0.56	9.4	0

In [18]:
```
#Set target variable to y and the remaining predictors to x
y = redwine_df['quality'].to_numpy()
x = redwine_df.drop(columns=['quality'])
```

In [19]:
```
#Standardize the dataset
scaler = preprocessing.StandardScaler()
x_norm = scaler.fit_transform(x * 1.0)
```

In [20]:
```
#Split the full dataframe into 60/40.
train_x, test_x, train_y, test_y = train_test_split(x, y, test_size=0.4, random_state=1)
train_x.shape, test_x.shape
```

Out[20]:
```
((959, 11), (640, 11))
```

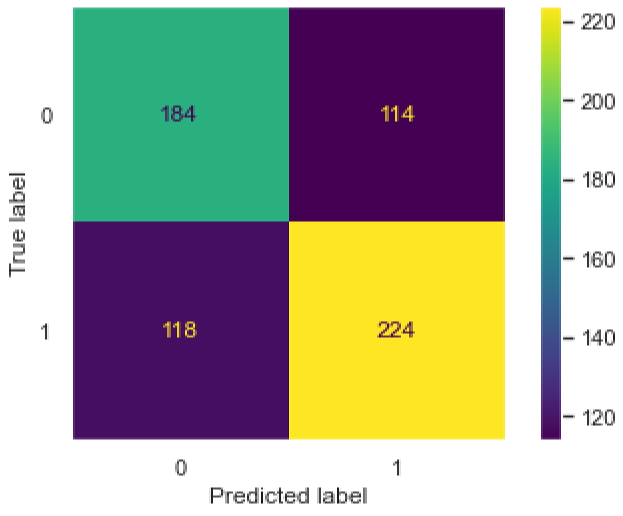
Data Modeling

K-Nearest Neighbors (KNN)

The K-Nearest Neighbors model was used as our baseline model for this project. This model, however, generated the lowest accuracy score (64%) and the lowest cross validation score (65.28%).

In [21]:
```
kneighbors = KNeighborsClassifier().fit(train_x, train_y)
knn_pred = kneighbors.predict(test_x)

plot_confusion_matrix(kneighbors, test_x, test_y)
plt.grid(False)

print(classification_report(test_y, knn_pred))

print("Cross Val Score: ", stats.mean(cross_val_score(kneighbors, train_x, train_y, cv=5)))
```

```
              precision    recall  f1-score   support

           0       0.61      0.62      0.61       298
           1       0.66      0.65      0.66       342

    accuracy                           0.64       640
   macro avg       0.64      0.64      0.64       640
weighted avg       0.64      0.64      0.64       640

Cross Val Score:  0.6527814136125655
```



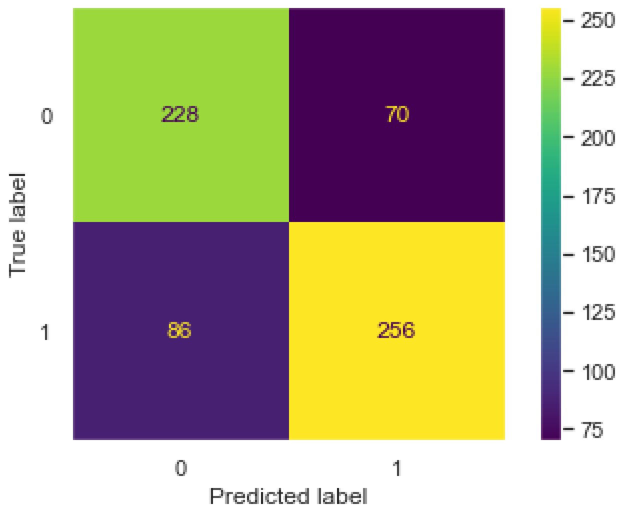
LDA

One of the reasons we chose to include linear discriminant analysis as part of the models was the simplicity and effectiveness of the model. Although regarded as simple, lda as a classification model is robust and interpretable. LDA can be used for dimensionality reducer, visualizer, and classifier. In our case, we focus on LDA as a classifying model in aims to automate wine selection. Based on our confusion matrix (below) our model's cross validation score is: 73.62%

In [22]:
```
# initializing the model with 2 components
lda = LinearDiscriminantAnalysis(n_components=1)

# fitting the dataset
X_r2 = lda.fit(x, y).transform(x)
```

In [23]:
```
lda_pred_t = lda.predict(train_x)
lda_pred_v = lda.predict(test_x)
lda_pred_prob_v = (lda.predict_proba(test_x))


#Cross Validation Score of LDA
lda_score = cross_val_score(lda, train_x, train_y, cv=5)
print(classification_report(train_y,lda_pred_t))
print("Cross Val Score: ", stats.mean(cross_val_score(lda, train_x, train_y, cv=5)))

#plot confusion matrix
plot_confusion_matrix(lda,test_x,test_y)
plt.grid(False)
```

```
              precision    recall  f1-score   support

           0       0.71      0.73      0.72       446
           1       0.76      0.74      0.75       513

    accuracy                           0.74       959
   macro avg       0.74      0.74      0.74       959
weighted avg       0.74      0.74      0.74       959

Cross Val Score:  0.7361965532286213
```



Gradient Boosting

Gradient Boosting is a great model that can be used for regression, classification, and ranking. In our case, to automate the wine process we decided to classify wines into two categories as either high (1) or low (0) quality. Gradient boosting is an excellent choise as it has methods that can enhance the algorithm's performance. In our case, we performed grid search to know the best paramenters for this model.

In [24]:
```
gradient_booster = GradientBoostingClassifier()
parameters = {
    "n_estimators":[5,50,250,500],
    "max_depth":[1,3,5,7,9],
    "learning_rate":[0.01,0.1,1,10,100]
}
```

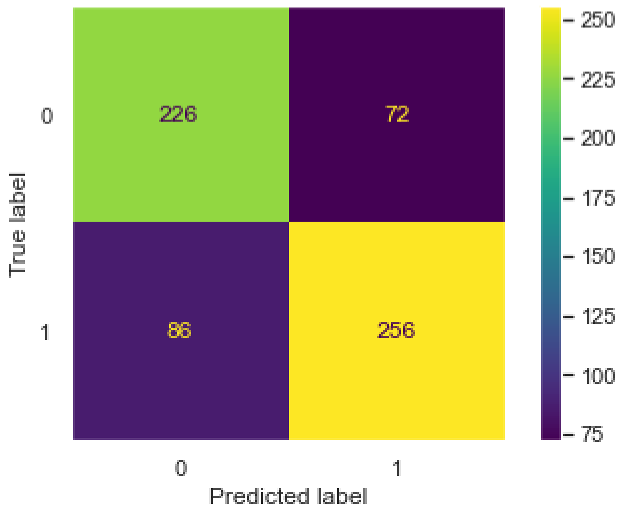
In [25]:
```
## Print out the best Parameters.
def display(results):
    print(f'Best parameters are: {results.best_params_}')
    print("\n")
    mean_score = results.cv_results_['mean_test_score']
    std_score = results.cv_results_['std_test_score']
    params = results.cv_results_['params']
    for mean,std,params in zip(mean_score,std_score,params):
        print(f'{round(mean,3)} + or -{round(std,3)} for the {params}')
```

In [26]:
```
gb = GradientBoostingClassifier(learning_rate=0.01, max_depth=3, n_estimators=250)

## Fit our model
gb.fit(train_x,train_y)
```

Out[26]:
```
▾                    GradientBoostingClassifier
GradientBoostingClassifier(learning_rate=0.01, n_estimators=250)
```

In [27]:
```
gb_pred_t = gb.predict(train_x)
gb_pred_v = gb.predict(test_x)
gb_pred_prob_v = (gb.predict_proba(test_x))


#Cross Validation Score of LDA
lda_score = cross_val_score(gb, train_x, train_y, cv=5)
print(classification_report(train_y,gb_pred_t))
print("Cross Val Score: ", stats.mean(cross_val_score(gb, train_x, train_y, cv=5)))

#plot confusion matrix
plot_confusion_matrix(gb,test_x,test_y)
plt.grid(False)
```

```
              precision    recall  f1-score   support

           0       0.81      0.82      0.82       446
           1       0.84      0.83      0.84       513

    accuracy                           0.83       959
   macro avg       0.83      0.83      0.83       959
weighted avg       0.83      0.83      0.83       959

Cross Val Score:  0.7476712478184991
```



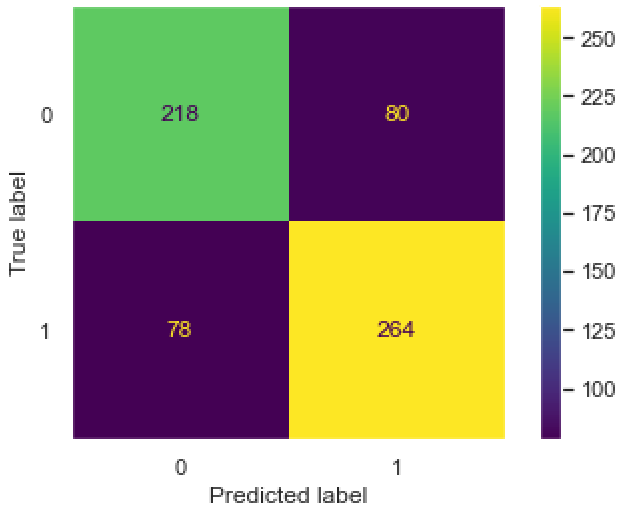
Logistic Regression

Another model that was chosen for this project was logistic regression. The main aspect that made this model relatable towards our project's goal was its ability to predict a binary outcome based on observations within a data set. It also has the ability to describe the data and to explain relationship between one dependent binary variable with additional independent variables. These aspects made the logistic regression model relatable towards our goal in predicting the wine types as either high (1) or low (0) quality. After fitting the data before making predictions with the test data set and plotting a classification report with confusion matrix, this model generated an accuracy score of 75% and a cross validation score of 73.83%.

In [28]:

```
logit_reg = LogisticRegression().fit(train_x, train_y)
y_pred = logit_reg.predict(test_x)

plot_confusion_matrix(logit_reg, test_x, test_y)
plt.grid(False)

print(classification_report(test_y, y_pred))

print("Cross Val Score: ", stats.mean(cross_val_score(logit_reg, train_x, train_y, cv = 5)
```

```
              precision    recall  f1-score   support

           0       0.74      0.73      0.73       298
           1       0.77      0.77      0.77       342

    accuracy                           0.75       640
   macro avg       0.75      0.75      0.75       640
weighted avg       0.75      0.75      0.75       640

Cross Val Score:  0.7382744328097731
```



Random Forest

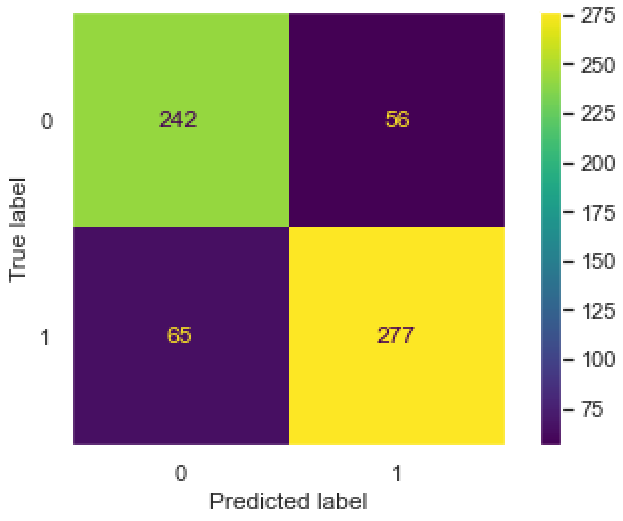
The random forest algorithm was chosen because of its ability to handle classification-type problems towards large datasets and to assess the features that contribute towards an objective. Since all the features contributed towards the objective of evaluating which wine type qualities were good or bad, they were all included to assess the accuracy level of the data set from this algorithm. The random forest algorithm generated the highest accuracy score of 81% and a cross validation score of 78.31%.

In [29]:

```
rf = RandomForestClassifier().fit(train_x, train_y)
rf_pred = rf.predict(test_x)

plot_confusion_matrix(rf, test_x, test_y)
```

```
plt.grid(False)

print(classification_report(test_y, rf_pred))

print("Cross Val Score: ", stats.mean(cross_val_score(rf, train_x, train_y, cv = 5)))
```

```
              precision    recall  f1-score   support

           0       0.79      0.81      0.80       298
           1       0.83      0.81      0.82       342

    accuracy                           0.81       640
   macro avg       0.81      0.81      0.81       640
weighted avg       0.81      0.81      0.81       640

Cross Val Score:  0.7831042757417103
```



In [ ]:

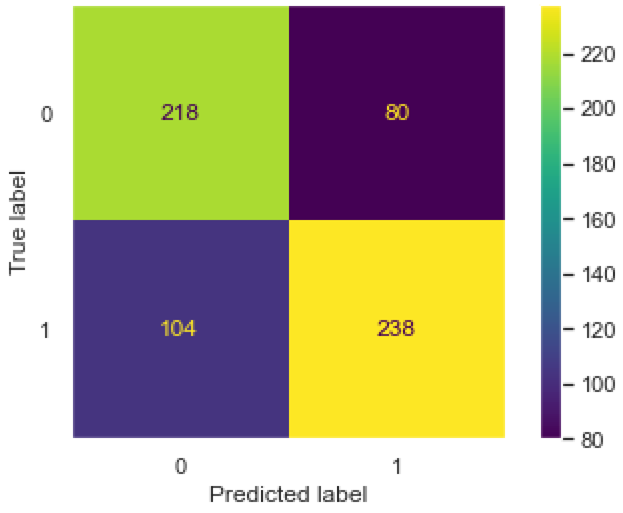
Decision Trees

One of the aspects of decision trees that was relatable to our project goal was its ability to effectively choose between various actions. For this project, supervised learning would be the best route to go. The objective is to predict which wines are low quality (0) and high quality (1). Part of the process in determining the output is understanding how the output was chosen. By using decision tree, we can examine the choices made in the process and what role the predictors played. After fitting the data, predictions were made with the testing data. A confusion matrix was plotted along with a classification report showing how well the model performed. The accuracy score for this model is 73% and the cross validation score is 71.84%. Recall gives a general overview saying of the total amount of actual good quality values, which were correctly predicted as good quality. Precision notes the number of predicted good quality values that contained a true value of 6 or higher. F1-score focuses on recall and precision simultaneously, and it also comapres the performance of the two metrics.

In [30]:
```
decisiontree = DecisionTreeClassifier().fit(train_x, train_y)
dt_pred = decisiontree.predict(test_x)
plot_confusion_matrix(decisiontree, test_x, test_y)
plt.grid(False)
print(classification_report(test_y, dt_pred))
print("Cross Val Score: ", stats.mean(cross_val_score(decisiontree, train_x, train_y, cv =
```

```
              precision    recall  f1-score   support

           0       0.68      0.73      0.70       298
           1       0.75      0.70      0.72       342
```

```
    accuracy                           0.71       640
   macro avg       0.71      0.71      0.71       640
weighted avg       0.72      0.71      0.71       640

Cross Val Score:  0.7215641361256545
```

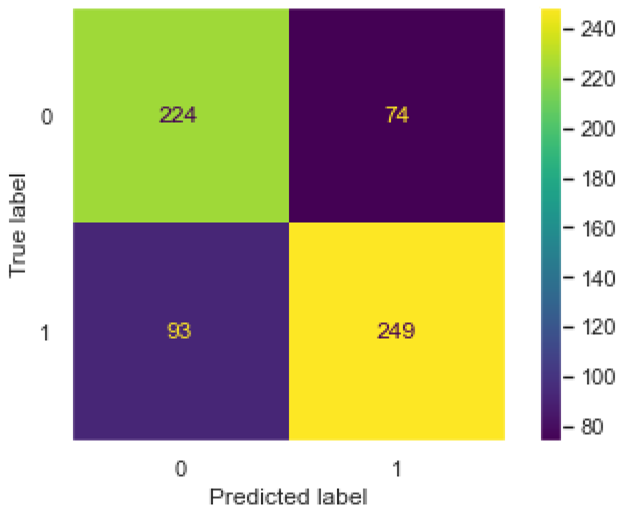


Neural Network

When looking into which wines have good or poor quality, the balance of the components play a huge role. It is not solely about if a wine was high in pH or low in sweetness, thus making it bitter. It is about the combination of each ingredient and how they complement each other. This is one of the reasons why wine tastes better with age because it gives the components time to mix and balance each other out. When creating a model to predict which wine has good or bad quality, part of the process is to determine the relationship between each predictors (the components of the wine). Neural networks meets this task.

In [31]:
```
neuralnet = MLPClassifier(hidden_layer_sizes = (3), activation = 'logistic',
                          solver = 'lbfgs', random_state =1).fit(train_x, train_y)

nnet_pred = neuralnet.predict(test_x)

plot_confusion_matrix(neuralnet, test_x, test_y)
plt.grid(False)

print(classification_report(test_y, nnet_pred))

print("Cross Val Score: ", stats.mean(cross_val_score(neuralnet, train_x, train_y, cv=5)))
```

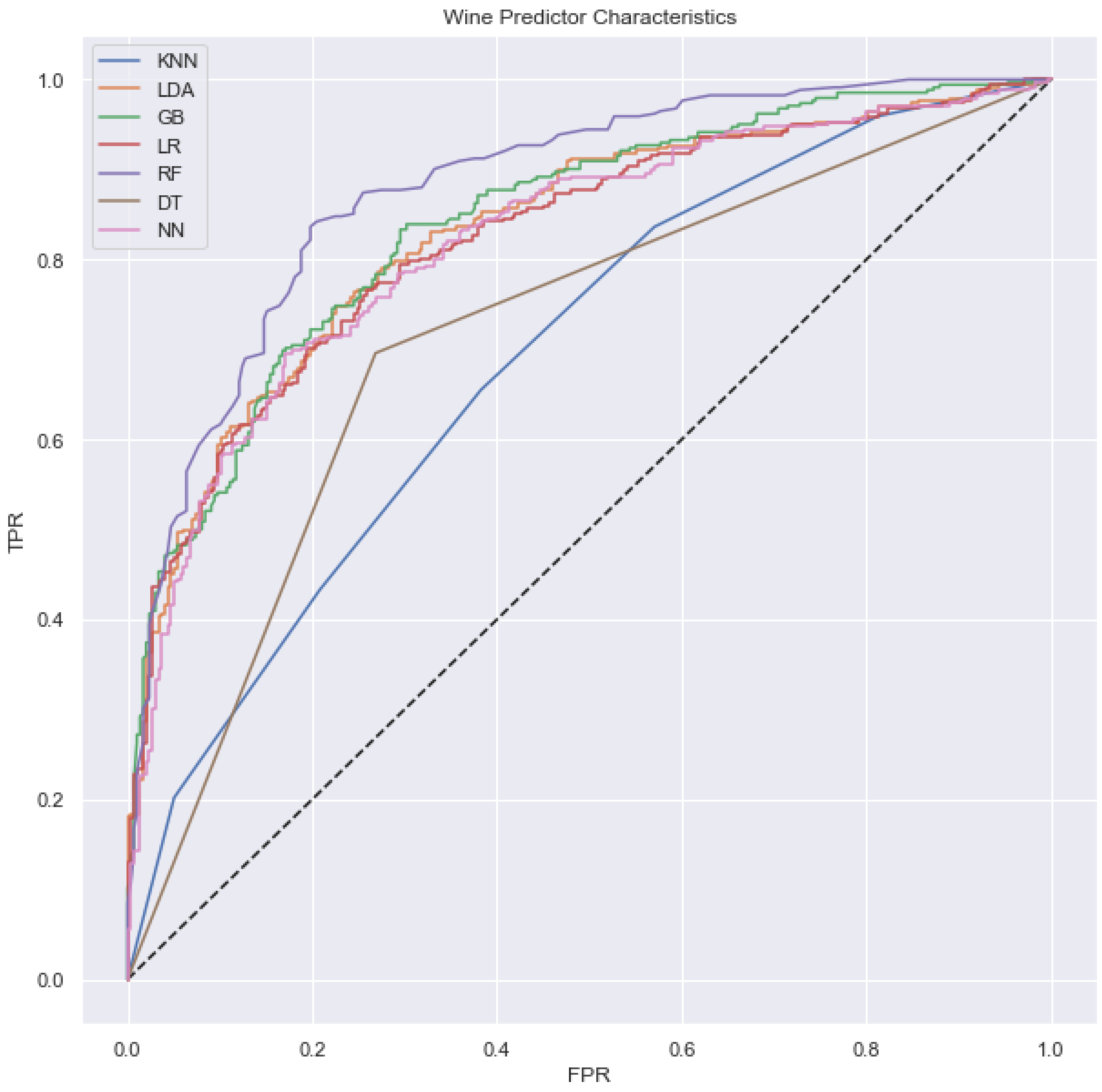
```
              precision    recall  f1-score   support

           0       0.71      0.75      0.73       298
           1       0.77      0.73      0.75       342

    accuracy                           0.74       640
   macro avg       0.74      0.74      0.74       640
weighted avg       0.74      0.74      0.74       640

Cross Val Score:  0.7268160994764398
```



Model Selection

In [32]:
```
y_pred_prob1 = kneighbors.predict_proba(test_x)[:,1]
fpr_knn, tpr_knn, thresholds_knn = roc_curve(test_y, y_pred_prob1)

y_pred_prob2 = lda.predict_proba(test_x)[:,1]
fpr_lda, tpr_lda, thresholds_lda = roc_curve(test_y, y_pred_prob2)

y_pred_prob3 = gb.predict_proba(test_x)[:,1]
fpr_gb, tpr_gb, thresholds_gb = roc_curve(test_y, y_pred_prob3)

y_pred_prob4 = logit_reg.predict_proba(test_x)[:,1]
fpr_lr, tpr_lr, thresholds_lr = roc_curve(test_y, y_pred_prob4)

y_pred_prob5 = rf.predict_proba(test_x)[:,1]
fpr_rf, tpr_rf, thresholds_rf = roc_curve(test_y, y_pred_prob5)

y_pred_prob6 = decisiontree.predict_proba(test_x)[:,1]
fpr_dt, tpr_dt, thresholds_dt = roc_curve(test_y, y_pred_prob6)

y_pred_prob7 = neuralnet.predict_proba(test_x)[:,1]
fpr_nn, tpr_nn, thresholds_nn = roc_curve(test_y, y_pred_prob7)
```

In [33]:
```
plt.figure(figsize = (10, 10))
plt.plot([0,1],[0,1], 'k--')
plt.plot(fpr_knn, tpr_knn, label = 'KNN')
plt.plot(fpr_lda, tpr_lda, label = 'LDA')
plt.plot(fpr_gb, tpr_gb, label = 'GB')
plt.plot(fpr_lr, tpr_lr, label = 'LR')
plt.plot(fpr_rf, tpr_rf, label = 'RF')
plt.plot(fpr_dt, tpr_dt, label = 'DT')
plt.plot(fpr_nn, tpr_nn, label = 'NN')
plt.legend()
plt.xlabel("FPR")
plt.ylabel("TPR")
plt.title('Wine Predictor Characteristics')
plt.show()
```



One of the downfalls with hiring people to determine which wines are good is that the process will always be partially subjective. What one would tastes as a little too bitter, the other would view as being just right. All the expenses that are being invested into the assortment of professionals is ultimately blind probability. It is a matter of if that professional is an expert, adequate, or a fraud. By taking out the subjectiveness and solely focusing on the amount of the components in the wine, one would still be able to determine the right concoction that defines good wine. Based on previously recorded data, a predictive model can be trained to do this task. Using a random forest model, good wine will be able to be predicted at an eighty percent accuracy level. This will allow the company to reduce expenses on wine professionals which will increase their revenue by approximately 25 percent.

```
In [ ]:
```