Machine Learning Lab 4

Logistic Regression

In machine learning, the logistic model is a widely used statistical model that, in its basic form, uses a logistic function to model a binary dependent variable; many more complex extensions exist. Logistic Regression is a classification algorithm. It is used to predict a binary outcome (1 / 0, Yes / No, True / False) given a set of independent variables. To represent binary / categorical outcome, we use dummy variables. It can also be thought of as a special case of linear regression when the outcome variable is categorical, where we are using log of odds as dependent variable. In simple words, it predicts the probability of occurrence of an event by fitting data to a logit function.

The dataset

The dataset used to perform this experiment is the wine quality dataset, it is a combination of data on two types of wine variants, namely red wine and white wine, of the portuguese “Vinho Verde” wine. The dataset contains information on the parameters for fixed acidity, volatile acidity, citric acid, residual sugar, chlorides, free sulfur dioxide, total sulfur dioxide, density, pH, sulphates, alcohol.

Experiment

In this experiment I used the sklearn’s logistic regression algorithms to predict the quality of a wine.

Using the pandas library in I loaded the red wine and white wine datasets into the memory from their respective csv files and then merged the two datasets into one single pandas dataframe.

Using the pandas.Dataframe.describe() function in pandas I calculated the various statistical measures of each of the columns of the dataset.

For performing the experiment I started with plotting the scatter plot for each of the features in the dataset with every other feature, this helped to find if there were any features which were linearly separable. In the case of my dataset they were not.

Next used random forests to find the importance of features in the dataset and as to how much each feature contributes to the importance. The two most important features are the fixed acidity and the volatile acidity.

Finally, I applied logistic regression to the dataset using both l1 and l2 penalty and the using the saga and newton-cg solver. I was able to achieve and accuracy of 52 and 53 percent respectively. The reason for this low accuracy was the dataset being skewed with just 20 examples in class 3 and more than 2000 examples in class 6 and this skewness in the dataset was the reason for a bad performance of the logistic regression.

The code and plots can be found in the accompanying jupyter notebook.

Logistic Regression

November 1, 2018

1 Lab 4

2 Logistic Regression

2.0.1 Submitted to: Prof. Sweetlin Hemlatha

2.0.2 Submitted by: Prateek Singh (15BCE1091)

```
In [4]: import random
        import numpy as np
        import pandas as pd
        import seaborn as sn
        from sklearn import preprocessing
        from sklearn.metrics import confusion_matrix
        from sklearn.ensemble import ExtraTreesClassifier
        from sklearn.linear_model import LogisticRegression
        from sklearn.model_selection import train_test_split
        from sklearn.metrics import precision_score, recall_score

        import matplotlib.pyplot as plt
        from matplotlib.colors import ListedColormap
        %matplotlib inline
```

```
In [5]: white_wine = pd.read_csv('../Dataset/winequality-white.csv', sep=';')
        sn.set(style='ticks', color_codes=True, font_scale=1)
```

```
In [6]: white_wine.head()
```

```
Out[6]:    fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
        0            7.0              0.27         0.36            20.7      0.045
        1            6.3              0.30         0.34             1.6      0.049
        2            8.1              0.28         0.40             6.9      0.050
        3            7.2              0.23         0.32             8.5      0.058
        4            7.2              0.23         0.32             8.5      0.058

           free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
        0                 45.0                 170.0   1.0010  3.00       0.45
        1                 14.0                 132.0   0.9940  3.30       0.49
```

```
2                30.0                 97.0   0.9951  3.26        0.44
3                47.0                186.0   0.9956  3.19        0.40
4                47.0                186.0   0.9956  3.19        0.40

   alcohol  quality
0      8.8        6
1      9.5        6
2     10.1        6
3      9.9        6
4      9.9        6
```

Working with white wine dataset first, in between the assignment I realized there was no need for regression analysis. As we arealy have a dataset, we just need to apply the sklearn's logistic regression with different function.

Dividing the dataset into training and testing classes.

```
In [7]: print('Rows in white wine dataset: ', len(white_wine.axes[0]))
        # print('Rows in red wine dataset: ', len(red_wine.axes[0]))
```

```
Rows in white wine dataset:  4898
```

Let's use the white wine dataset and we will split the dataset into training and testing

```
In [8]: # Doing some analysis over the dataset
        white_wine.head()
```

```
Out[8]:    fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
        0            7.0              0.27         0.36            20.7      0.045
        1            6.3              0.30         0.34             1.6      0.049
        2            8.1              0.28         0.40             6.9      0.050
        3            7.2              0.23         0.32             8.5      0.058
        4            7.2              0.23         0.32             8.5      0.058

           free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
        0                 45.0                 170.0   1.0010  3.00       0.45
        1                 14.0                 132.0   0.9940  3.30       0.49
        2                 30.0                  97.0   0.9951  3.26       0.44
        3                 47.0                 186.0   0.9956  3.19       0.40
        4                 47.0                 186.0   0.9956  3.19       0.40

           alcohol  quality
        0      8.8        6
        1      9.5        6
        2     10.1        6
        3      9.9        6
        4      9.9        6
```

```
In [9]: classes = sorted(white_wine.quality.unique())

        print('Number of data points for class: \n')

        for cls in classes:
            num_samples = len(white_wine.loc[white_wine.quality == cls])
            print(cls, " :", num_samples)
```

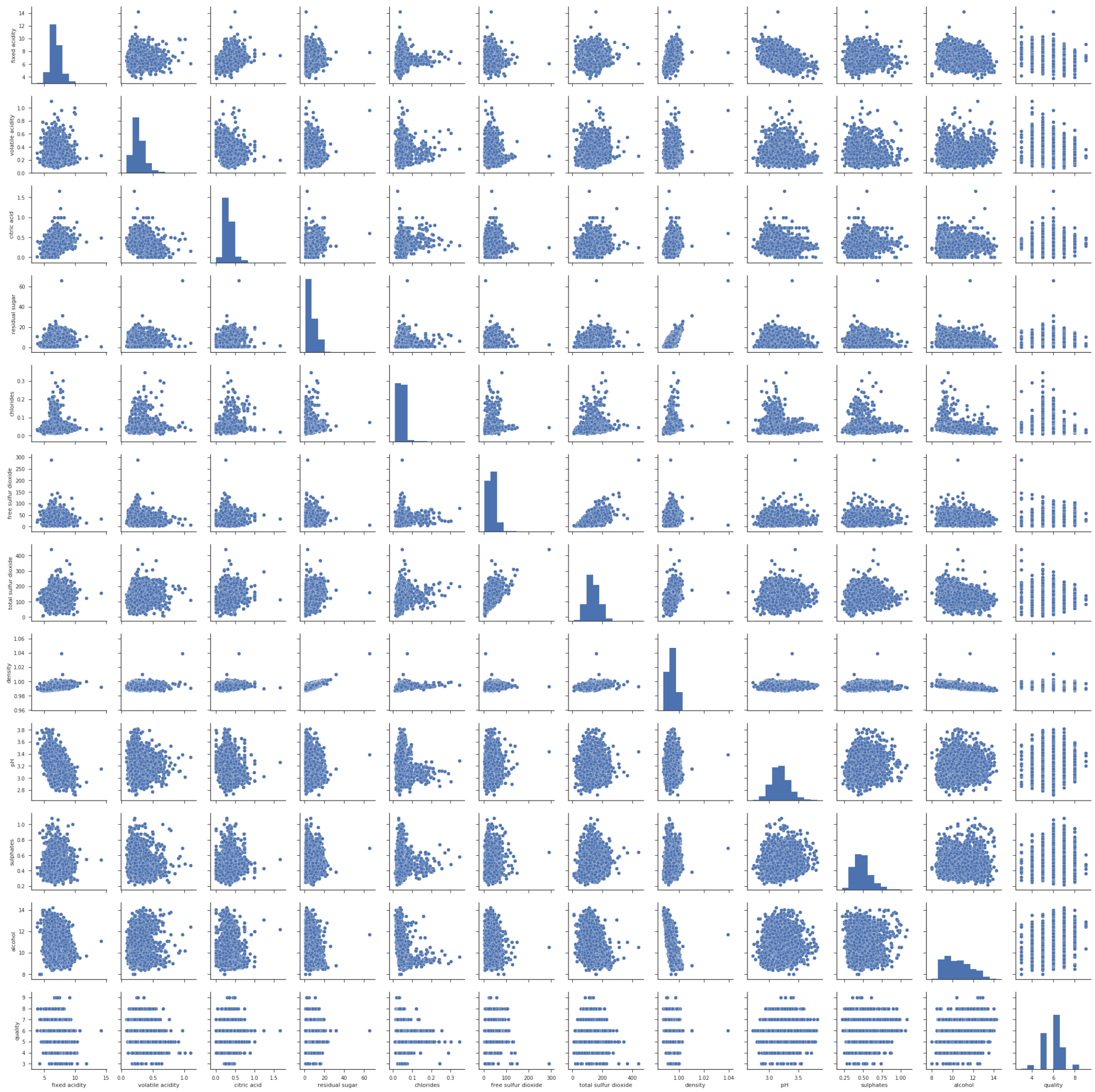
```
Number of data points for class:

3  : 20
4  : 163
5  : 1457
6  : 2198
7  : 880
8  : 175
9  : 5
```

Each data point has 11 features in total, however, we just have around 4400 training example. Moreover the dataset is very skewed with very few examples in some classes and the major concentration of examples in the other classes.

We either need to reduce the number of features that we're dealing with, by either trying to find the importance of each feature (using decision trees) or dimensionality reduction, or we need to increase the number of examples such that the dataset is less biased towards some of the classes.

```
In [10]: sn.pairplot(white_wine.dropna(), size=2.5)
```

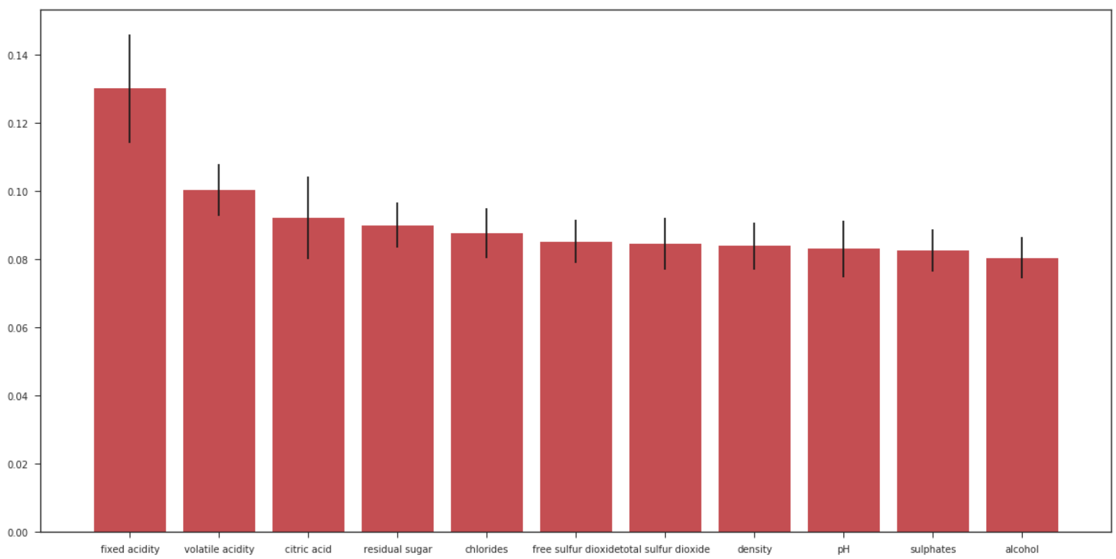
```
Out[10]: <seaborn.axisgrid.PairGrid at 0x7f973e68ca20>
```




```
In [11]: data, labels = white_wine.iloc[:, :11], white_wine.iloc[:, 11]

         forest = ExtraTreesClassifier(n_estimators=250, random_state=0)
         forest.fit(data, labels)
         importances = forest.feature_importances_
         std = np.std([tree.feature_importances_ for tree in forest.estimators_], axis=0)
         indices = np.argsort(importances)[::-1]
         cumulative_imp = np.cumsum(importances)

         print('Feature rankings')

         for f in range(data.shape[1]):
             print("%d. feature %d (%f) (%f)" % (f + 1, indices[f], importances[indices[f]], cu
```

```
plt.figure(figsize=(20, 10))
plt.bar(range(data.shape[1]), importances[indices], color="r", yerr=std[indices], alig
plt.xticks(range(data.shape[1]), list(white_wine.columns.values[:11]))
plt.xlim([-1, data.shape[1]])
plt.show()
```

```
Feature rankings
1. feature 10 (0.130143) (1.000000)
2. feature 1 (0.100346) (0.180734)
3. feature 7 (0.092182) (0.701958)
4. feature 5 (0.089962) (0.522192)
5. feature 6 (0.087584) (0.609776)
6. feature 8 (0.085251) (0.787209)
7. feature 3 (0.084598) (0.349213)
8. feature 2 (0.083881) (0.264614)
9. feature 4 (0.083017) (0.432230)
10. feature 9 (0.082648) (0.869857)
11. feature 0 (0.080387) (0.080387)
```




```
In [12]: X_train, X_test, Y_train, Y_test = train_test_split(white_wine.iloc[:, :11],
                                                             white_wine.iloc[:, 11],
                                                             test_size=0.1,
                                                             random_state=42)
         print("Size of training set: ", len(X_train.axes[0]))
         print("Size of test set: ", len(X_test.axes[0]))
```

```
Size of training set:  4408
Size of test set:  490
```

In [13]: X_train.head()

```
Out[13]:       fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
        1052            7.6              0.29         0.42             1.3      0.035
        3606            6.4              0.38         0.24             7.2      0.047
        1610            7.5              0.32         0.49             1.7      0.031
        621             6.5              0.26         0.43             8.9      0.083
        4750            6.0              0.14         0.37             1.2      0.032

              free sulfur dioxide  total sulfur dioxide  density    pH  sulphates  \
        1052                 18.0                  86.0  0.99080  2.99       0.39
        3606                 41.0                 151.0  0.99604  3.11       0.60
        1610                 44.0                 109.0  0.99060  3.07       0.46
        621                  50.0                 171.0  0.99650  2.85       0.50
        4750                 63.0                 148.0  0.99185  3.32       0.44

              alcohol
        1052     11.3
        3606      9.2
        1610     12.5
        621       9.0
        4750     11.2
```

In [14]:

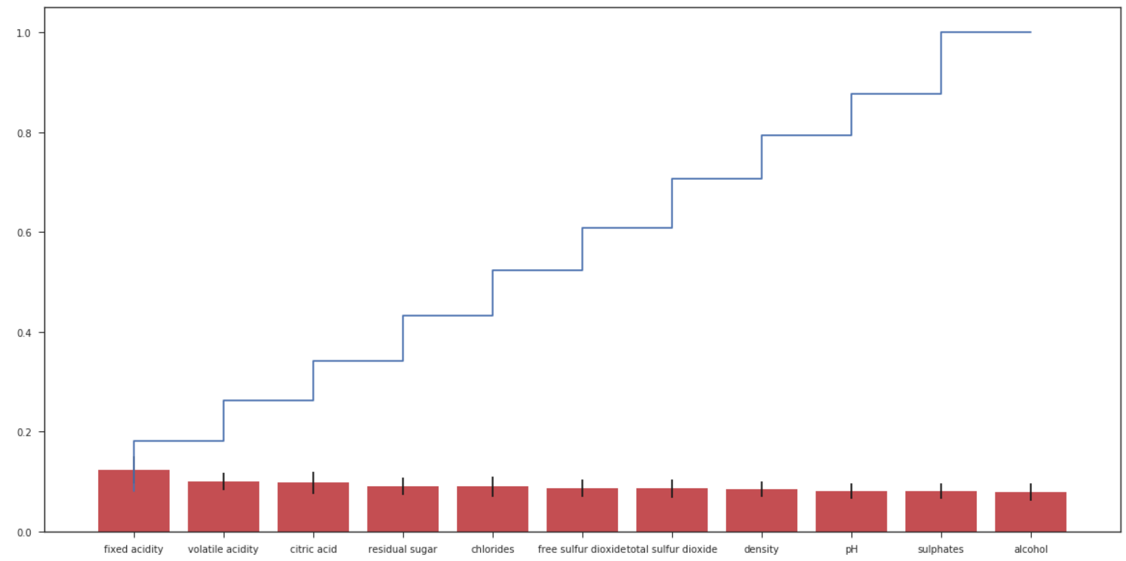
```python
# Normalizing the features in Training and testing data.
X_tr, X_tes = X_train.values, X_test.values
min_max_scaler = preprocessing.MinMaxScaler()
#X_tr_scaled = min_max_scaler.fit_transform(X_tr)
#X_tes_scaled = min_max_scaler.fit_transform(X_tes)
X_train = pd.DataFrame(min_max_scaler.fit_transform(X_tr), index=X_train.index, colum
X_test = pd.DataFrame(min_max_scaler.fit_transform(X_tes), index=X_test.index, columns

X_train.head()
```

```
Out[14]:       fixed acidity  volatile acidity  citric acid  residual sugar  chlorides  \
        1052         0.4750          0.205882     0.253012        0.010736   0.077151
        3606         0.3250          0.294118     0.144578        0.101227   0.112760
        1610         0.4625          0.235294     0.295181        0.016871   0.065282
        621          0.3375          0.176471     0.259036        0.127301   0.219585
        4750         0.2750          0.058824     0.222892        0.009202   0.068249

              free sulfur dioxide  total sulfur dioxide   density        pH  \
        1052             0.052448              0.178654  0.071139  0.245455
        3606             0.132867              0.329466  0.172161  0.354545
        1610             0.143357              0.232019  0.067284  0.318182
        621              0.164336              0.375870  0.181029  0.118182
        4750             0.209790              0.322506  0.091382  0.545455

              sulphates   alcohol
```

```
1052   0.197674  0.532258
3606   0.441860  0.193548
1610   0.279070  0.725806
621    0.325581  0.161290
4750   0.255814  0.516129
```

In [15]:
```
forest = ExtraTreesClassifier(n_estimators=250, random_state=0)
forest.fit(X_test, Y_test)
importances = forest.feature_importances_
std = np.std([tree.feature_importances_ for tree in forest.estimators_], axis=0)
cum_imp = np.cumsum(importances)
indices = np.argsort(importances)[::-1]

print('Feature rankings')

for f in range(data.shape[1]):
    print("%d. feature %d (%f)" % (f + 1, indices[f], importances[indices[f]]))

plt.figure(figsize=(20, 10))
plt.bar(range(data.shape[1]), importances[indices], color="r", yerr=std[indices], ali
plt.step(range(data.shape[1]), cum_imp, 'b')
plt.xticks(range(data.shape[1]), list(white_wine.columns.values[:11]))
plt.xlim([-1, data.shape[1]])
plt.show()
```

```
Feature rankings
1. feature 10 (0.123645)
2. feature 1 (0.100660)
3. feature 7 (0.097706)
4. feature 5 (0.090431)
5. feature 4 (0.090032)
6. feature 6 (0.086664)
7. feature 8 (0.086057)
8. feature 9 (0.083790)
9. feature 0 (0.080790)
10. feature 2 (0.080779)
11. feature 3 (0.079445)
```



From the above graph it is evident that each of the feature contributes almost eqaully to the information represented by the dataset and thus omitting any of the features from the logistic regression isn't a wise choice, Hence we will keep all the features in the dataset with us.

```
In [16]: model_l1 = LogisticRegression(penalty='l1', solver='saga', max_iter=100000, multi_clas
         model_l1.fit(X_train, Y_train)

         print("Train Score: ", model_l1.score(X_train, Y_train))
         print("Test Score: ", model_l1.score(X_test, Y_test), '\n')

         Y_pred = model_l1.predict(X_test)
         cm = confusion_matrix(Y_test, Y_pred)
         print(cm)
```

```
Train Score:  0.5410617059891107
Test Score:  0.49183673469387756

[[  0   0   0   3   0   0]
 [  0   0  11   7   0   0]
 [  0   0  34 108   1   1]
 [  0   0  14 188  13   0]
 [  0   0   3  72  18   1]
 [  0   0   0  11   4   1]]
```

```
In [17]: model_l2 = LogisticRegression(penalty='l2', solver='newton-cg', max_iter=10000, multi_
         model_l2.fit(X_train, Y_train)

         print("Train Score: ", model_l2.score(X_train, Y_train))
         print("Test Score: ", model_l2.score(X_test, Y_test), '\n')
```

```
Y_pred = model_l2.predict(X_test)
cm = confusion_matrix(Y_test, Y_pred)
print(cm)
```

```
Train Score:  0.5394736842105263
Test Score:  0.4959183673469388

[[  0   0   0   3   0   0]
 [  0   0  10   8   0   0]
 [  0   0  31 113   0   0]
 [  0   0  13 193   9   0]
 [  0   0   2  73  19   0]
 [  0   0   0  11   5   0]]
```

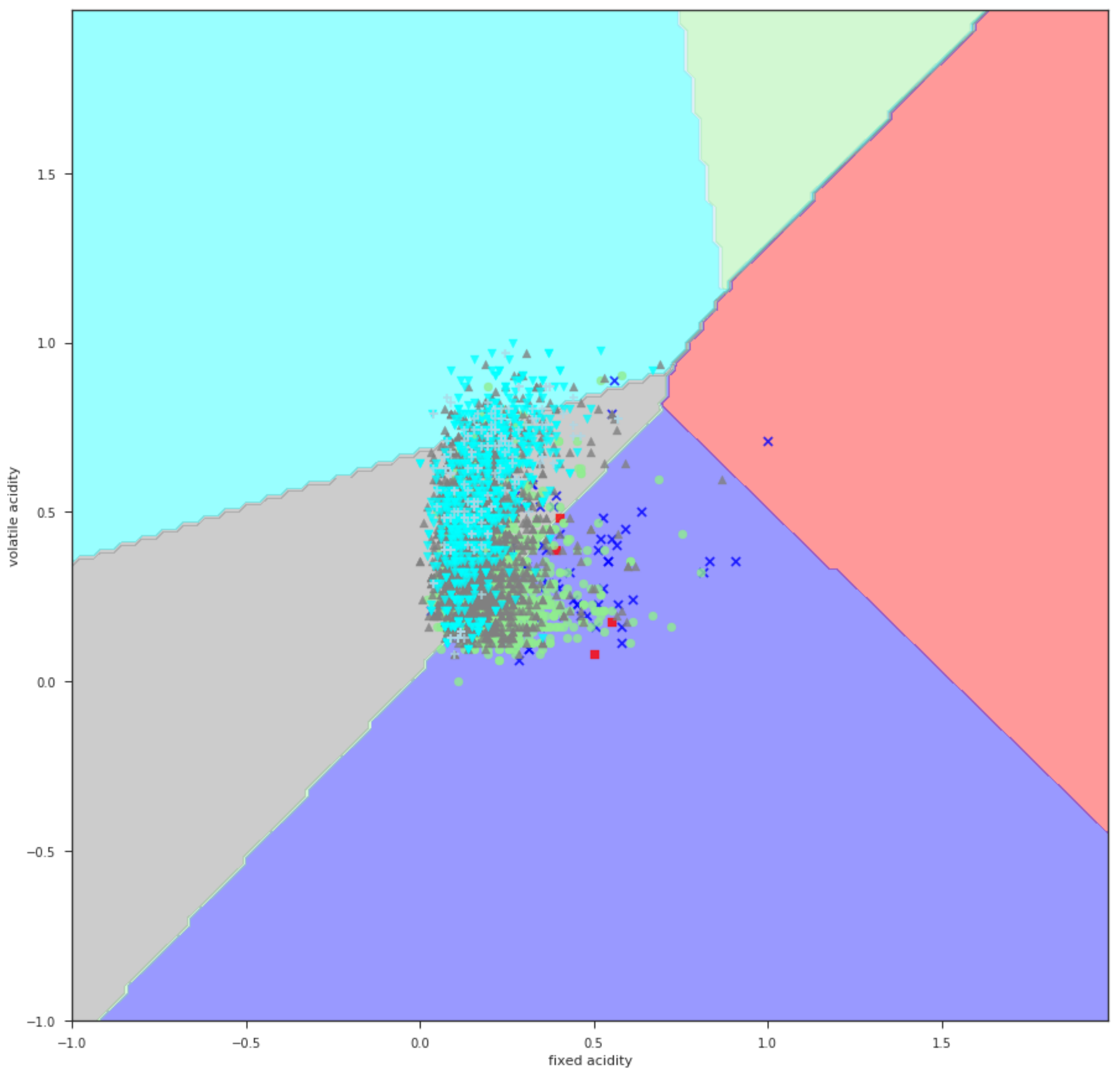
In [18]:
```
def plot_decision_surface(X, y, classifier, test_idx=None, resolution=0.02):

    markers = ('s', 'x', 'o', '^', 'v', '+', '.')
    colors = ('red', 'blue', 'lightgreen', 'gray', 'cyan', 'lightblue', 'lightgreen')
    cmap = ListedColormap(colors[:len(np.unique(y))])

    x1_min, x1_max = X[:, 0].min() - 1, X[:, 0].max() + 1
    x2_min, x2_max = X[:, 1].min() - 1, X[:, 1].max() + 1
    xx1, xx2 = np.meshgrid(np.arange(x1_min, x1_max, resolution), np.arange(x2_min, x2

    plt.figure(figsize=(15, 15))
    Z = classifier.predict(np.array([xx1.ravel(), xx2.ravel()]).T)
    Z = Z.reshape(xx1.shape)

    plt.contourf(xx1, xx2, Z, alpha=0.4, cmap=cmap)
    plt.xlim(xx1.min(), xx1.max())
    plt.ylim(xx2.min(), xx2.max())
    plt.xlabel('fixed acidity')
    plt.ylabel('volatile acidity')

    X_test, y_test = X[test_idx, :], y[test_idx]
    for idx, cl in enumerate(np.unique(y)):
        plt.scatter(x=X[y == cl, 0], y=X[y == cl, 1],
        alpha=0.8, c=cmap(idx),
        marker=markers[idx], label=cl)
        if test_idx:
            X_test, y_test = X[test_idx, :], y[test_idx]
            plt.scatter(X_test[:, 0], X_test[:, 1], c='',
            alpha=1.0, linewidth=1, marker='o',
            s=55, label='test set')
```

In [19]:
```
model_l2 = LogisticRegression(penalty='l2', solver='newton-cg', max_iter=10000, multi_
model_l2.fit(X_train.iloc[:, [1, 10]], Y_train)
```

```
print("Train Score: ", model_l2.score(X_train.iloc[:,[1, 10]], Y_train))
print("Test Score: ", model_l2.score(X_test.iloc[:, [1, 10]], Y_test), '\n')

Y_pred = model_l2.predict(X_test.iloc[:, [1, 10]])
cm = confusion_matrix(Y_test, Y_pred)
print(cm)
```

```
Train Score:  0.5249546279491834
Test Score:  0.5061224489795918

[[  0   0   2   1   0   0]
 [  0   1  12   5   0   0]
 [  0   0  90  53   1   0]
 [  0   0  64 141  10   0]
 [  0   0  15  63  16   0]
 [  0   0   1  11   4   0]]
```

```
In [20]: a = X_train.iloc[:, [1, 10]].values
         plot_decision_surface(X=a, y = np.array(Y_train.values), classifier=model_l2)
```


volatile acidity
fixed acidity
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.0
−0.5
0.0
0.5
1.0
1.5