In [26]:
```
import pandas as pd
import statsmodels.formula.api as smf
import statsmodels.stats.multicomp as multi
import scipy.stats
import numpy as np
import seaborn
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')
%matplotlib inline
```

In [27]:
```
red = pd.read_csv('winequality-red.csv', low_memory=False, sep=';')
white = pd.read_csv('winequality-white.csv', low_memory=False, sep=';')
```

In [28]:
```
red.head()
```

Out[28]:

	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 [29]:
```
white.head()
```

Out[29]:

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.8	6
1	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.5	6
2	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.1	6
3	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	6
4	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	6

In [30]:
```
# Function to select red or white dataset
def call(functionToCall):
    print('\nRed Wine\n')
    functionToCall(red)
    print('\nWhite Wine\n')
    functionToCall(white)
```

In [31]:
```
# Remove spaces from column names
def rm(wine_set):
    wine_set.columns = [x.strip().replace(' ','_') for x in wine_set.columns]
call(rm)
```

```
Red Wine


White Wine
```

In [32]:
```
red.head()
```

Out[32]:

	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

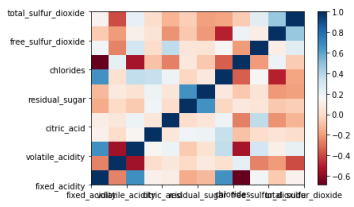
In [33]:
```
white.head()
```

Out[33]:

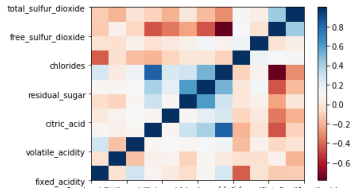
	fixed_acidity	volatile_acidity	citric_acid	residual_sugar	chlorides	free_sulfur_dioxide	total_sulfur_dioxide	density	pH	sulphates	alcohol	quality
0	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.8	6
1	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.5	6
2	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.1	6
3	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	6
4	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	6

In [34]:
```
# Covarience matrix
def covmax(wine_set):
    cov_mat = wine_set.corr(method = 'pearson')
    fig = plt.figure().add_subplot(111)
    plt.pcolor(cov_mat, cmap = 'RdBu')
    plt.colorbar()
    fig.set_xticklabels(wine_set.columns)
    fig.set_yticklabels(wine_set.columns)
    plt.show()
call(covmax)
```

```
Red Wine
```




```
White Wine
```



fixed_acidity volatile_acidity citric_acid residual_sugar chlorides free_sulfur_dioxide total_sulfur_dioxide

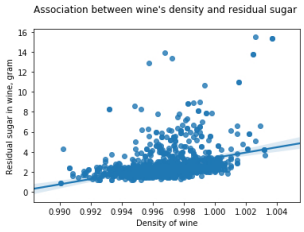
In [35]:
```
# Add a column 'quality_mark'
def add_categ_quality(wine_set):
    low = wine_set[wine_set['quality'] <= 5]
    medium = wine_set[(wine_set['quality'] == 6) | (wine_set['quality'] == 7)]
    high = wine_set[wine_set['quality'] > 7]

    low['quality_mark'] = 'low'
    medium['quality_mark'] = 'medium'
    high['quality_mark'] = 'high'

    frames = [low, medium, high]
    return pd.concat(frames)
```

In [36]:
```
# Calculating the F-statistics and associated p-value
def anova(wine_set):
    prepared_data = add_categ_quality(wine_set)
    model1 = smf.ols(formula='total_sulfur_dioxide ~ C(quality_mark)', data = prepared_data)
    results1 = model1.fit()
    print(results1.summary())

    sub = prepared_data[['total_sulfur_dioxide', 'quality_mark']]
    print("\nMeans for total sulfur dioxide by quality marks of wine \n")
    print(sub.groupby('quality_mark').mean())
    print('\nStandard deviation for total sulfur dioxide by quality marks of wine \n')
    print(sub.groupby('quality_mark').std(), '\n')

    # Perform Post hoc test
    mc1 = multi.MultiComparison(sub['total_sulfur_dioxide'], sub['quality_mark'])
    res1 = mc1.tukeyhsd()
    print(res1.summary())

call(anova)
```

```
quality_mark
high                  125.883333
low                   148.597866
medium                133.635802

Standard deviation for total sulfur dioxide by quality marks of wine

              total_sulfur_dioxide
quality_mark
high                     32.719653
low                      46.914579
medium                   39.400592

Multiple Comparison of Means - Tukey HSD,FWER=0.05
=================================================
group1 group2 meandiff  lower    upper   reject
-------------------------------------------------
 high   low   22.7145  15.0095  30.4196   True
 high  medium  7.7525   0.2275  15.2774   True
 low   medium -14.9621 -17.9621 -11.9621  True
```

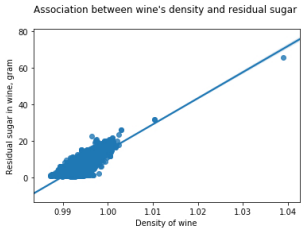
In [37]:
```
# Pearson Correlation
def pearson(wine_set):
    scat1 = seaborn.regplot(x = "density", y = "residual_sugar", fit_reg = True, data = wine_set)
    plt.xlabel("Density of wine")
    plt.ylabel("Residual sugar in wine, gram")
    plt.title("Association between wine's density and residual sugar \n")
    plt.show()

    print(scipy.stats.pearsonr(wine_set['density'], wine_set["residual_sugar"]))

call(pearson)
```

Red Wine



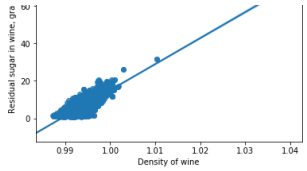
(0.3552833709833765, 9.013041728296711e-49)

White Wine



(0.8389664549045837, 0.0)

In [38]:
```
# Exploring Statistical Interactions
def explore(wine_set):
    low = wine_set[wine_set['quality'] <= 5]
    medium = wine_set[(wine_set['quality'] == 6) | (wine_set['quality'] == 7)]
    high = wine_set[wine_set['quality'] > 7]

    print('association between wine`s density and residual sugar for wines \nof `low` quality')
    print(scipy.stats.pearsonr(low['density'], low["residual_sugar"]))
    print('\nof `medium` quality')
    print(scipy.stats.pearsonr(medium['density'], medium["residual_sugar"]))
    print('\nof `high` quality')
    print(scipy.stats.pearsonr(high['density'], high["residual_sugar"]))

    scat0 = seaborn.regplot(x="density", y="residual_sugar", fit_reg=True, data=low)
    plt.xlabel("Density of wine")
    plt.ylabel("Residual sugar in wine, gram")
    plt.title("Association between wine's density and residual sugar for wines of `low` quality")
    plt.show()

    scat0 = seaborn.regplot(x="density", y="residual_sugar", fit_reg=True, data=medium)
    plt.xlabel("Density of wine")
    plt.ylabel("Residual sugar in wine, gram")
    plt.title("Association between wine's density and residual sugar for wines of `medium` quality")
    plt.show()

    scat0 = seaborn.regplot(x="density", y="residual_sugar", fit_reg=True, data=high)
    plt.xlabel("Density of wine")
    plt.ylabel("Residual sugar in wine, gram")
    plt.title("Association between wine's density and residual sugar for wines of `high` quality\n")
    plt.show()

call(explore)
```



Association between wine's density and residual sugar for wines of `high` quality

In [39]:
```
def basicInfo(wine_set):
    print(len(wine_set))
    print(len(wine_set.columns))
    print(list(wine_set.columns.values))
    print(wine_set.ix[:10,:4])
    print('\n')
    print("-------------describe the data----------------")
    print('\n')
    print(wine_set.describe())

call(basicInfo)
```

```
Red Wine

1599
12
['fixed_acidity', 'volatile_acidity', 'citric_acid', 'residual_sugar', 'chlorides', 'free_sulfur_dioxide', 'total_sulfur_dioxide', 'density', 'pH', 'sulphates', 'alcohol', 'quality']
    fixed_acidity  volatile_acidity  citric_acid  residual_sugar
0             7.4              0.70         0.00             1.9
1             7.8              0.88         0.00             2.6
2             7.8              0.76         0.04             2.3
3            11.2              0.28         0.56             1.9
4             7.4              0.70         0.00             1.9
5             7.4              0.66         0.00             1.8
6             7.9              0.60         0.06             1.6
7             7.3              0.65         0.00             1.2
8             7.8              0.58         0.02             2.0
9             7.5              0.50         0.36             6.1
10            6.7              0.58         0.08             1.8


-------------describe the data----------------


       fixed_acidity  volatile_acidity  citric_acid  residual_sugar  \
count    1599.000000       1599.000000  1599.000000     1599.000000
mean        8.319637          0.527821     0.270976        2.538806
std         1.741096          0.179060     0.194801        1.409928
min         4.600000          0.120000     0.000000        0.900000
25%         7.100000          0.390000     0.090000        1.900000
50%         7.900000          0.520000     0.260000        2.200000
75%         9.200000          0.640000     0.420000        2.600000
max        15.900000          1.580000     1.000000       15.500000

         chlorides  free_sulfur_dioxide  total_sulfur_dioxide      density  \
count  1599.000000          1599.000000           1599.000000  1599.000000
mean      0.087467            15.874922             46.467792     0.996747
std       0.047065            10.460157             32.895324     0.001887
min       0.012000             1.000000              6.000000     0.990070
25%       0.070000             7.000000             22.000000     0.995600
50%       0.079000            14.000000             38.000000     0.996750
75%       0.090000            21.000000             62.000000     0.997835
max       0.611000            72.000000            289.000000     1.003690

                pH    sulphates      alcohol      quality
count  1599.000000  1599.000000  1599.000000  1599.000000
mean      3.311113     0.658149    10.422983     5.636023
std       0.154386     0.169507     1.065668     0.807569
min       2.740000     0.330000     8.400000     3.000000
25%       3.210000     0.550000     9.500000     5.000000
50%       3.310000     0.620000    10.200000     6.000000
75%       3.400000     0.730000    11.100000     6.000000
max       4.010000     2.000000    14.900000     8.000000

White Wine

4898
12
['fixed_acidity', 'volatile_acidity', 'citric_acid', 'residual_sugar', 'chlorides', 'free_sulfur_dioxide', 'total_sulfur_dioxide', 'density', 'pH', 'sulphates', 'alcohol', 'quality']
    fixed_acidity  volatile_acidity  citric_acid  residual_sugar
0             7.0              0.27         0.36            20.70
1             6.3              0.30         0.34             1.60
2             8.1              0.28         0.40             6.90
3             7.2              0.23         0.32             8.50
4             7.2              0.23         0.32             8.50
5             8.1              0.28         0.40             6.90
6             6.2              0.32         0.16             7.00
7             7.0              0.27         0.36            20.70
8             6.3              0.30         0.34             1.60
9             8.1              0.22         0.43             1.50
10            8.1              0.27         0.41             1.45


-------------describe the data----------------


       fixed_acidity  volatile_acidity  citric_acid  residual_sugar  \
count    4898.000000       4898.000000  4898.000000     4898.000000
mean        6.854788          0.278241     0.334192        6.391415
std         0.843868          0.100795     0.121020        5.072058
min         3.800000          0.080000     0.000000        0.600000
25%         6.300000          0.210000     0.270000        1.700000
50%         6.800000          0.260000     0.320000        5.200000
75%         7.300000          0.320000     0.390000        9.900000
max        14.200000          1.100000     1.660000       65.800000

         chlorides  free_sulfur_dioxide  total_sulfur_dioxide      density  \
count  4898.000000          4898.000000           4898.000000  4898.000000
mean      0.045772            35.308085            138.360657     0.994027
std       0.021848            17.007137             42.498065     0.002991
min       0.009000             2.000000              9.000000     0.987110
25%       0.036000            23.000000            108.000000     0.991723
50%       0.043000            34.000000            134.000000     0.993740
75%       0.050000            46.000000            167.000000     0.996100
max       0.346000           289.000000            440.000000     1.038980

                pH    sulphates      alcohol      quality
count  4898.000000  4898.000000  4898.000000  4898.000000
mean      3.188267     0.489847    10.514267     5.877909
std       0.151001     0.114126     1.230621     0.885639
min       2.720000     0.220000     8.000000     3.000000
25%       3.090000     0.410000     9.500000     5.000000
50%       3.180000     0.470000    10.400000     6.000000
75%       3.280000     0.550000    11.400000     6.000000
max       3.820000     1.080000    14.200000     9.000000
```

In [40]:
```
# print frequency distributions of wines' quality
def frequencyDists(wine_set):
    print("This is the frequency distribution of the wines' quality.")
    print(wine_set.groupby("quality").size()*100 / len(wine_set))
    print()

call(frequencyDists)
```

```
Red Wine

This is the frequency distribution of the wines' quality.
```

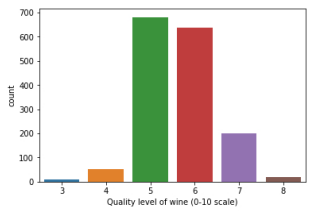
```
quality
3     0.625391
4     3.314572
5    42.589118
6    39.899937
7    12.445278
8     1.125704
dtype: float64


White Wine

This is the frequency distribution of the wines' quality.
quality
3     0.408330
4     3.327889
5    29.746835
6    44.875459
7    17.966517
8     3.572887
9     0.102082
dtype: float64
```

In [41]:
```
# print quartile split of the quality variable
def quartileSplit(wine_set):
    print("This is the quartile split of the wines' quality. I-st column contains the intervals of wines' quality;")
    print("II-nd - the number of wine samples with the quality in the corresponding interval.")
    wine_set["quality_quart"] = pd.qcut(wine_set["quality"], 3)
    print(wine_set.groupby("quality_quart").size())

call(quartileSplit)
```

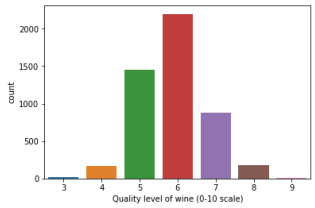
```
Red Wine

This is the quartile split of the wines' quality. I-st column contains the intervals of wines' quality;
II-nd - the number of wine samples with the quality in the corresponding interval.
quality_quart
(2.999, 5.0]    744
(5.0, 6.0]      638
(6.0, 8.0]      217
dtype: int64

White Wine

This is the quartile split of the wines' quality. I-st column contains the intervals of wines' quality;
II-nd - the number of wine samples with the quality in the corresponding interval.
quality_quart
(2.999, 5.0]    1640
(5.0, 6.0]      2198
(6.0, 9.0]      1060
dtype: int64
```

In [42]:
```
# Visualization  with countplots and factorplots
def countplots(wine_set):
    wine_set["quality"] = pd.Categorical(wine_set["quality"])
    seaborn.countplot(x="quality", data=wine_set)
    plt.xlabel("Quality level of wine (0-10 scale)")
    plt.show()

call(countplots)
```

Red Wine



White Wine



In [50]:
```
from sklearn.neighbors import KNeighborsClassifier
from sklearn import svm
import time
from sklearn.linear_model import LogisticRegression

from sklearn.model_selection import train_test_split
import pandas as pd
from sklearn.tree import DecisionTreeClassifier, export_graphviz
import sklearn
from sklearn.ensemble import RandomForestClassifier, ExtraTreesClassifier
import matplotlib.pyplot as plt
import operator
from sklearn import preprocessing
from sklearn.linear_model import LassoLarsCV
import numpy as np
from sklearn.metrics import mean_squared_error
from sklearn.cluster import KMeans
from scipy.spatial.distance import cdist
from sklearn.decomposition import PCA
import statsmodels.formula.api as smf
import statsmodels.stats.multicomp as multi

from sklearn.naive_bayes import GaussianNB
from sklearn.naive_bayes import MultinomialNB
from sklearn.naive_bayes import BernoulliNB

from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
import warnings
warnings.filterwarnings('ignore')
```

In [51]:
```
def log_regression(wine_set):
    # local variable to identify if the wine_set red or white
    w = wine_set


    # recode quality (response variable) into 2 groups: 0:{3,4,5}, 1:{6,7,8,9}
    recode = {3: 0, 4: 0, 5: 0, 6: 1, 7: 1, 8: 1, 9: 1}
    wine_set['quality_c'] = wine_set['quality'].map(recode)


    # split into training and testing sets
    predictors = wine_set[["sulphates", 'alcohol']]
    targets = wine_set.quality_c
```

```
    pred_train, pred_test, tar_train, tar_test = train_test_split(predictors, targets, test_size=.4)

    # build model on training data
    classifier = LogisticRegression()
    classifier = classifier.fit(pred_train, tar_train)

    predictions = classifier.predict(pred_test)

     # print the confusion matrix and accuracy of the model
    print('Confusion Matrix:\n',sklearn.metrics.confusion_matrix(tar_test, predictions))
    print('Accuracy:',sklearn.metrics.accuracy_score(tar_test, predictions))

    print ('Score:', classifier.score(pred_test, tar_test))
    print ('RMSE:', mean_squared_error(predictions, tar_test) ** 0.5)

print('----------------Logistic Regression-----------------------')
call(log_regression)
```

```
----------------Logistic Regression-----------------------

Red Wine

Confusion Matrix:
 [[202 101]
 [ 89 248]]
Accuracy: 0.703125
Score: 0.703125
RMSE: 0.5448623679425842

White Wine

Confusion Matrix:
 [[ 232  380]
 [ 195 1153]]
Accuracy: 0.7066326530612245
Score: 0.7066326530612245
RMSE: 0.5416339602893965
```

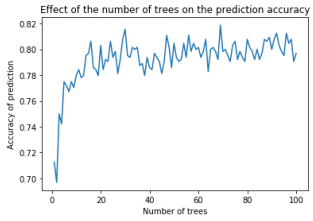
In [52]:
```
def decis_tree(wine_set):
    # Local variable to identify if the wine_set red or white
    w = wine_set


    # recode quality (response variable) into 2 groups: 0:{3,4,5}, 1:{6,7,8,9}
    recode = {3: 0, 4: 0, 5: 0, 6: 1, 7: 1, 8: 1, 9: 1}
    wine_set['quality_c'] = wine_set['quality'].map(recode)


    # split into training and testing sets
    predictors = wine_set[["residual_sugar", 'alcohol']]
    targets = wine_set.quality_c

    pred_train, pred_test, tar_train, tar_test = train_test_split(predictors, targets, test_size=.4)

    # build model on training data
    classifier = DecisionTreeClassifier()
    classifier = classifier.fit(pred_train, tar_train)

    predictions = classifier.predict(pred_test)

     # print the confusion matrix and accuracy of the model
    print('Confusion Matrix:\n',sklearn.metrics.confusion_matrix(tar_test, predictions))
    print('Accuracy:',sklearn.metrics.accuracy_score(tar_test, predictions))

    print ('Score:', classifier.score(pred_test, tar_test))
    print ('RMSE:', mean_squared_error(predictions, tar_test) ** 0.5)

print('----------------Decision Tree-----------------------')
call(decis_tree)
```

```
----------------Decision Tree-----------------------

Red Wine

Confusion Matrix:
 [[201  84]
 [137 218]]
Accuracy: 0.6546875
Score: 0.6546875
RMSE: 0.5876329636771579

White Wine

Confusion Matrix:
 [[387 272]
 [319 982]]
Accuracy: 0.698469387755102
Score: 0.698469387755102
RMSE: 0.5491180312509306
```

In [*]:
```
def random_forests(wine_set):
    # recode quality (response variable) into 2 groups: 0:{3,4,5}, 1:{6,7,8,9}
    recode = {3: 0, 4: 0, 5: 0, 6: 1, 7: 1, 8: 1, 9: 1}
    wine_set['quality_c'] = wine_set['quality'].map(recode)

    # split into training and testing sets
    predictors = wine_set[["density", 'alcohol', 'sulphates', 'pH', 'volatile_acidity', 'chlorides', 'fixed_acidity',
                           'citric_acid', 'residual_sugar', 'free_sulfur_dioxide', 'total_sulfur_dioxide']]


    targets = wine_set.quality_c

    pred_train, pred_test, tar_train, tar_test = train_test_split(predictors, targets, test_size=.4)

    # build model on training data#
    classifier = RandomForestClassifier(n_estimators=25)
    classifier = classifier.fit(pred_train, tar_train)

    predictions = classifier.predict(pred_test)
    # print the confusion matrix and accuracy of the model
    print('Confusion matrix:\n', sklearn.metrics.confusion_matrix(tar_test, predictions))
    print('Accuracy:', sklearn.metrics.accuracy_score(tar_test, predictions))

    # to display the relative importance of each predictive variable
    model = ExtraTreesClassifier()
    model.fit(pred_train, tar_train)

    print('\nImportance of predictors:')
    dct = dict()
    for c in range(len(predictors.columns)):
        dct[predictors.columns[c]] = model.feature_importances_[c]
    print(sorted(dct.items(), key=operator.itemgetter(1), reverse=True))

    # run different numbers of trees to see the effect of the number on the accuracy of the prediction
    n = 100
    accuracy = [0]*n

    for i in range(n):
        classifier = RandomForestClassifier(n_estimators=i+1)
        classifier = classifier.fit(pred_train, tar_train)
        predictions = classifier.predict(pred_test)
        accuracy[i] = sklearn.metrics.accuracy_score(tar_test, predictions)

    plt.plot(range(1, n+1), accuracy)
    plt.xlabel("Number of trees")
    plt.ylabel("Accuracy of prediction")
    plt.title("Effect of the number of trees on the prediction accuracy")
    plt.show()

    print(accuracy)

print('----------------Random Forests-----------------------')
call(random_forests)
```

```
----------------Random Forests-----------------------

Red Wine
```

```
Confusion matrix:
 [[230  75]
 [ 57 278]]
Accuracy: 0.79375

Importance of predictors:
[('alcohol', 0.17957489430325 73), ('sulphates', 0.11634591523206055), ('total_sulfur_dioxide', 0.1112596487288919), ('volatile_acidity', 0.10171401061757764), ('citric_acid', 0.0766465372496247), ('densit
y', 0.07409727469760094), ('residual_sugar', 0.0700852330682216), ('fixed_acidity', 0.06812872786338389), ('pH', 0.0680366920237497), ('free_sulfur_dioxide', 0.06721408900421241), ('chlorides', 0.06689697
721141934)]
```




```
[0.7125, 0.696875, 0.75, 0.7421875, 0.775, 0.771875, 0.7671875, 0.775, 0.7703125, 0.7796875, 0.784375, 0.778125, 0.7796875, 0.7953125, 0.796875, 0.80625, 0.7859375, 0.784375, 0.7796875, 0.803125, 0.78437
5, 0.7921875, 0.790625, 0.80625, 0.79375, 0.7984375, 0.78125, 0.7921875, 0.8078125, 0.815625, 0.7953125, 0.79375, 0.8015625, 0.8, 0.8015625, 0.7875, 0.7890625, 0.7796875, 0.79375, 0.7859375, 0.784375, 0.7
96875, 0.79375, 0.790625, 0.78125, 0.790625, 0.8109375, 0.8015625, 0.7859375, 0.8046875, 0.79375, 0.790625, 0.7921875, 0.8046875, 0.79375, 0.8109375, 0.7984375, 0.8046875, 0.8, 0.8015625, 0.79375, 0.79843
75, 0.8078125, 0.7828125, 0.8, 0.8015625, 0.7984375, 0.7921875, 0.81875, 0.7984375, 0.8, 0.7953125, 0.790625, 0.803125, 0.80625, 0.7921875, 0.7984375, 0.79375, 0.790625, 0.8078125, 0.8015625, 0.7984375,
0.7921875, 0.8, 0.7921875, 0.796875, 0.8078125, 0.80625, 0.809375, 0.8, 0.8078125, 0.8125, 0.803125, 0.7984375, 0.7953125, 0.8125, 0.8046875, 0.8078125, 0.790625, 0.796875]

White Wine

Confusion matrix:
 [[ 439  219]
 [ 119 1183]]
Accuracy: 0.8275510204081633

Importance of predictors:
[('alcohol', 0.14113095486745628), ('volatile_acidity', 0.11056241239923792), ('density', 0.10627005239721632), ('free_sulfur_dioxide', 0.09116643791964407), ('citric_acid', 0.08824582096326065), ('residu
al_sugar', 0.08557151607183484), ('chlorides', 0.08082538834483728), ('total_sulfur_dioxide', 0.07668923034660174), ('sulphates', 0.07552211663131696), ('pH', 0.07255036986831495), ('fixed_acidity', 0.071
46570019027894)]
```

In [ ]: