Wine Classification Algorithms

Importing Libraries

```
In [263]: import numpy as np
          import pandas as pd
          from sklearn import tree
          import seaborn as sns
          from sklearn.tree import DecisionTreeClassifier
          import seaborn as sns, matplotlib.pyplot as plt
          from sklearn.ensemble import RandomForestClassifier
          from sklearn import metrics #Import scikit-learn metrics module for accuracy calculation
          from sklearn.model_selection import train_test_split
          from sklearn.model_selection import cross_val_score
          from sklearn.ensemble import RandomForestClassifier
          from sklearn.neighbors import KNeighborsClassifier
          from sklearn.naive_bayes import MultinomialNB
          from sklearn.naive_bayes import GaussianNB
          from sklearn.pipeline import make_pipeline
          from sklearn.svm import SVC
          %matplotlib inline
```

Loading / Processing Data

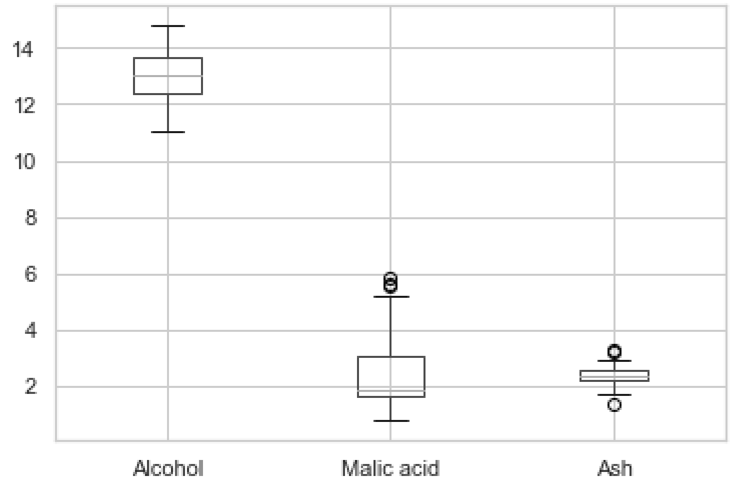
```
In [146]: #importing data
          feature_cols = ['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Flavanoi
          ds',
          'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
          e']

          col_names = ['Class', 'Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Fl
          avanoids',
          'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
          e']

          df = pd.read_csv('wine.csv', header = None, names=col_names)
          df.head()
```

Out[146]:

	Class	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	OD280/OD315 of diluted wines	Proline
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	5.64	1.04	3.92	1065
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	4.38	1.05	3.40	1050
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	5.68	1.03	3.17	1185
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	7.80	0.86	3.45	1480
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	4.32	1.04	2.93	735

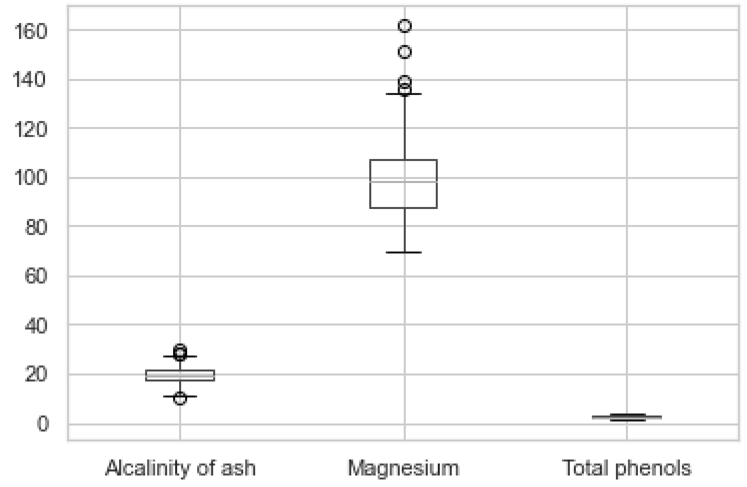
```
In [14]: # Analyzing dara


         #Checking for NaN values

         df.isna().sum()

         #No NaN Values found
```

```
Out[14]: Class                           0
         Alcohol                         0
         Malic acid                      0
         Ash                             0
         Alcalinity of ash               0
         Magnesium                       0
         Total phenols                   0
         Flavanoids                      0
         Nonflavanoid phenols            0
         Proanthocyanins                 0
         Color intensity                 0
         Hue                             0
         OD280/OD315 of diluted wines    0
         Proline                         0
         dtype: int64
```

In [74]:
```
# Outlier analysis


df.iloc[:,1:4].boxplot()
```
Out[74]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6e11ff1c0>
```


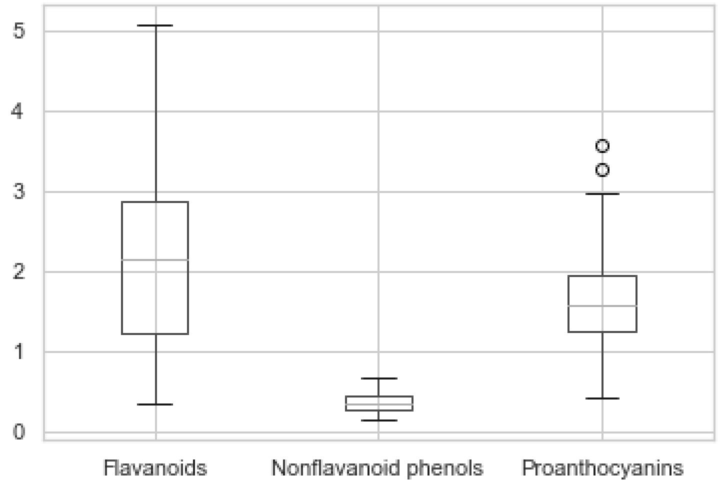
In [70]:
```
df.iloc[:,4:7].boxplot()
```

Out[70]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6e103b460>
```

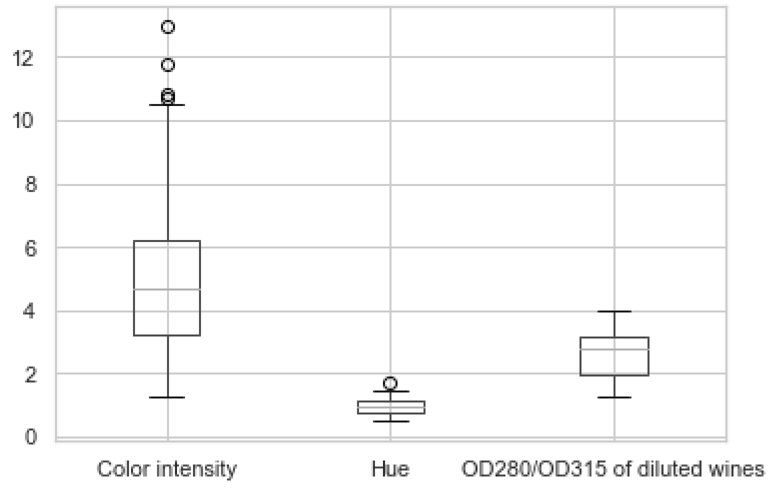


In [71]:
```
df.iloc[:,7:10].boxplot()
```

Out[71]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7fc6e11298b0>
```



```
In [72]: df.iloc[:,10:13].boxplot()

Out[72]: <matplotlib.axes._subplots.AxesSubplot at 0x7fc6e11f9d60>
```



It appears that we have outliers in the following columns:

Hue

Color Intensity

Proanthocyanins

Ash

Malic Acid

Magnesium

Alcalinity of Ash

In [147]:
```
#Removing Outliers

from scipy import stats
z_scores = stats.zscore(df)

abs_z_scores = np.abs(z_scores)
filtered_entries = (abs_z_scores < 3).all(axis=1)
new_df = df[filtered_entries]
```

In [149]:
```
#dataset without outliers, 10 rows have been removed.
new_df
```

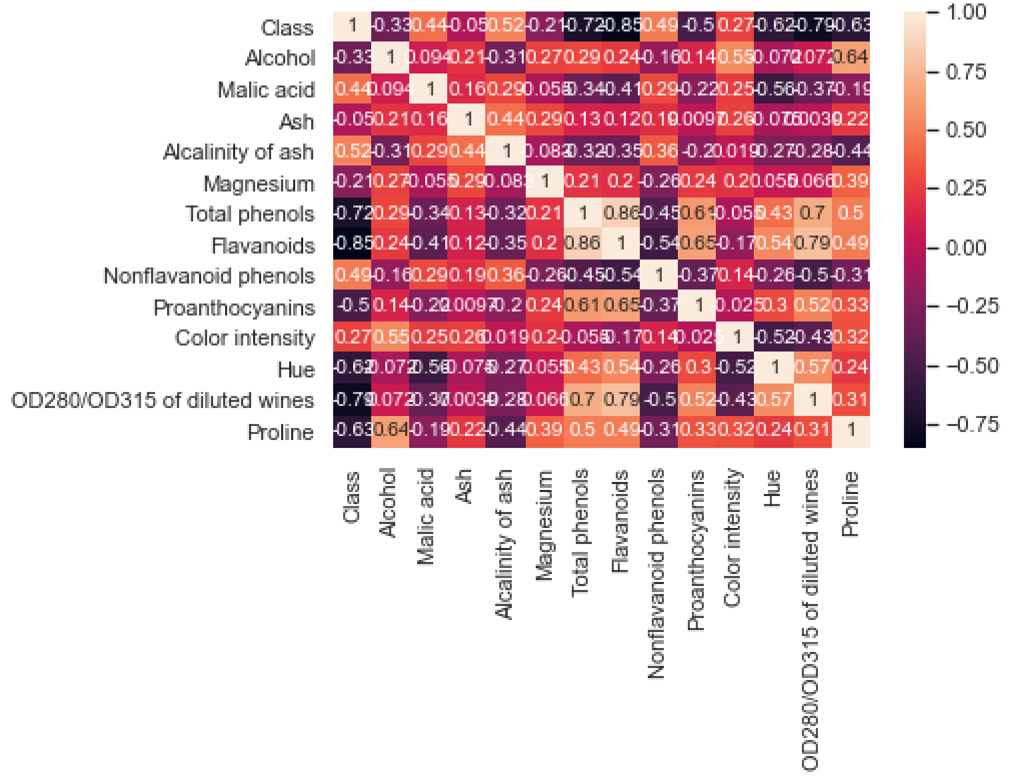
Out[149]:

	Class	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	OD280/OD315 of diluted wines	Prolin
0	1	14.23	1.71	2.43	15.6	127	2.80	3.06	0.28	2.29	5.64	1.04	3.92	106
1	1	13.20	1.78	2.14	11.2	100	2.65	2.76	0.26	1.28	4.38	1.05	3.40	105
2	1	13.16	2.36	2.67	18.6	101	2.80	3.24	0.30	2.81	5.68	1.03	3.17	118
3	1	14.37	1.95	2.50	16.8	113	3.85	3.49	0.24	2.18	7.80	0.86	3.45	148
4	1	13.24	2.59	2.87	21.0	118	2.80	2.69	0.39	1.82	4.32	1.04	2.93	73
...	...	...	...	...	...	...	...	...	...	...	...	...	...	.
173	3	13.71	5.65	2.45	20.5	95	1.68	0.61	0.52	1.06	7.70	0.64	1.74	74
174	3	13.40	3.91	2.48	23.0	102	1.80	0.75	0.43	1.41	7.30	0.70	1.56	75
175	3	13.27	4.28	2.26	20.0	120	1.59	0.69	0.43	1.35	10.20	0.59	1.56	83
176	3	13.17	2.59	2.37	20.0	120	1.65	0.68	0.53	1.46	9.30	0.60	1.62	84
177	3	14.13	4.10	2.74	24.5	96	2.05	0.76	0.56	1.35	9.20	0.61	1.60	56

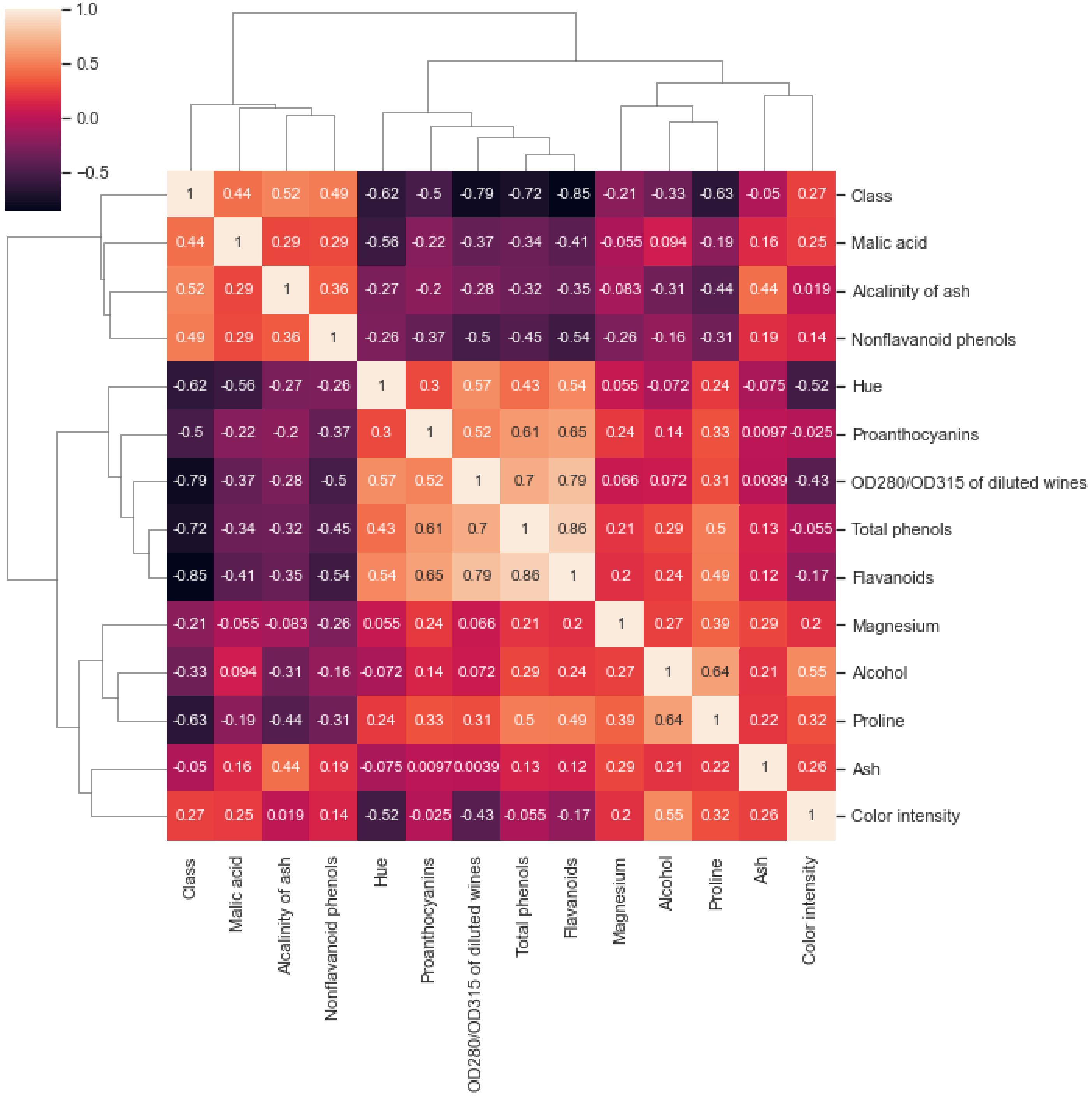
168 rows × 14 columns

In [219]:
```
#Checking for highly correlated features, removing those features may improve performance


# calculate the correlations
correlations = df.corr()

# plot the heatmap
sns.heatmap(correlations, xticklabels=correlations.columns, yticklabels=correlations.columns, annot=True)


sns.clustermap(correlations, xticklabels=correlations.columns, yticklabels=correlations.columns, annot=True)
```

```
Out[219]: <seaborn.matrix.ClusterGrid at 0x7fc6e3b9b0d0>
```



Class
Alcohol
Malic acid
Ash
Alcalinity of ash
Magnesium
Total phenols
Flavanoids
Nonflavanoid phenols
Proanthocyanins
Color intensity
Hue
OD280/OD315 of diluted wines
Proline
1.00
0.75
0.50
0.25
0.00
−0.25
−0.50
−0.75



	Class	Malic acid	Alcalinity of ash	Nonflavanoid phenols	Hue	Proanthocyanins	OD280/OD315 of diluted wines	Total phenols	Flavanoids	Magnesium	Alcohol	Proline	Ash	Color intensity
Class	1	0.44	0.52	0.49	-0.62	-0.5	-0.79	-0.72	-0.85	-0.21	-0.33	-0.63	-0.05	0.27
Malic acid	0.44	1	0.29	0.29	-0.56	-0.22	-0.37	-0.34	-0.41	-0.055	0.094	-0.19	0.16	0.25
Alcalinity of ash	0.52	0.29	1	0.36	-0.27	-0.2	-0.28	-0.32	-0.35	-0.083	-0.31	-0.44	0.44	0.019
Nonflavanoid phenols	0.49	0.29	0.36	1	-0.26	-0.37	-0.5	-0.45	-0.54	-0.26	-0.16	-0.31	0.19	0.14
Hue	-0.62	-0.56	-0.27	-0.26	1	0.3	0.57	0.43	0.54	0.055	-0.072	0.24	-0.075	-0.52
Proanthocyanins	-0.5	-0.22	-0.2	-0.37	0.3	1	0.52	0.61	0.65	0.24	0.14	0.33	0.0097	-0.025
OD280/OD315 of diluted wines	-0.79	-0.37	-0.28	-0.5	0.57	0.52	1	0.7	0.79	0.066	0.072	0.31	0.0039	-0.43
Total phenols	-0.72	-0.34	-0.32	-0.45	0.43	0.61	0.7	1	0.86	0.21	0.29	0.5	0.13	-0.055
Flavanoids	-0.85	-0.41	-0.35	-0.54	0.54	0.65	0.79	0.86	1	0.2	0.24	0.49	0.12	-0.17
Magnesium	-0.21	-0.055	-0.083	-0.26	0.055	0.24	0.066	0.21	0.2	1	0.27	0.39	0.29	0.2
Alcohol	-0.33	0.094	-0.31	-0.16	-0.072	0.14	0.072	0.29	0.24	0.27	1	0.64	0.21	0.55
Proline	-0.63	-0.19	-0.44	-0.31	0.24	0.33	0.31	0.5	0.49	0.39	0.64	1	0.22	0.32
Ash	-0.05	0.16	0.44	0.19	-0.075	0.0097	0.0039	0.13	0.12	0.29	0.21	0.22	1	0.26
Color intensity	0.27	0.25	0.019	0.14	-0.52	-0.025	-0.43	-0.055	-0.17	0.2	0.55	0.32	0.26	1

Removing outliers causes a decrease in test_set accuracy for both train-test validation approach and 10 fold cross validation approach when making decision trees. Therefore I will be moving forward with the original dataset.

Decision Trees

Train Test Split Approach

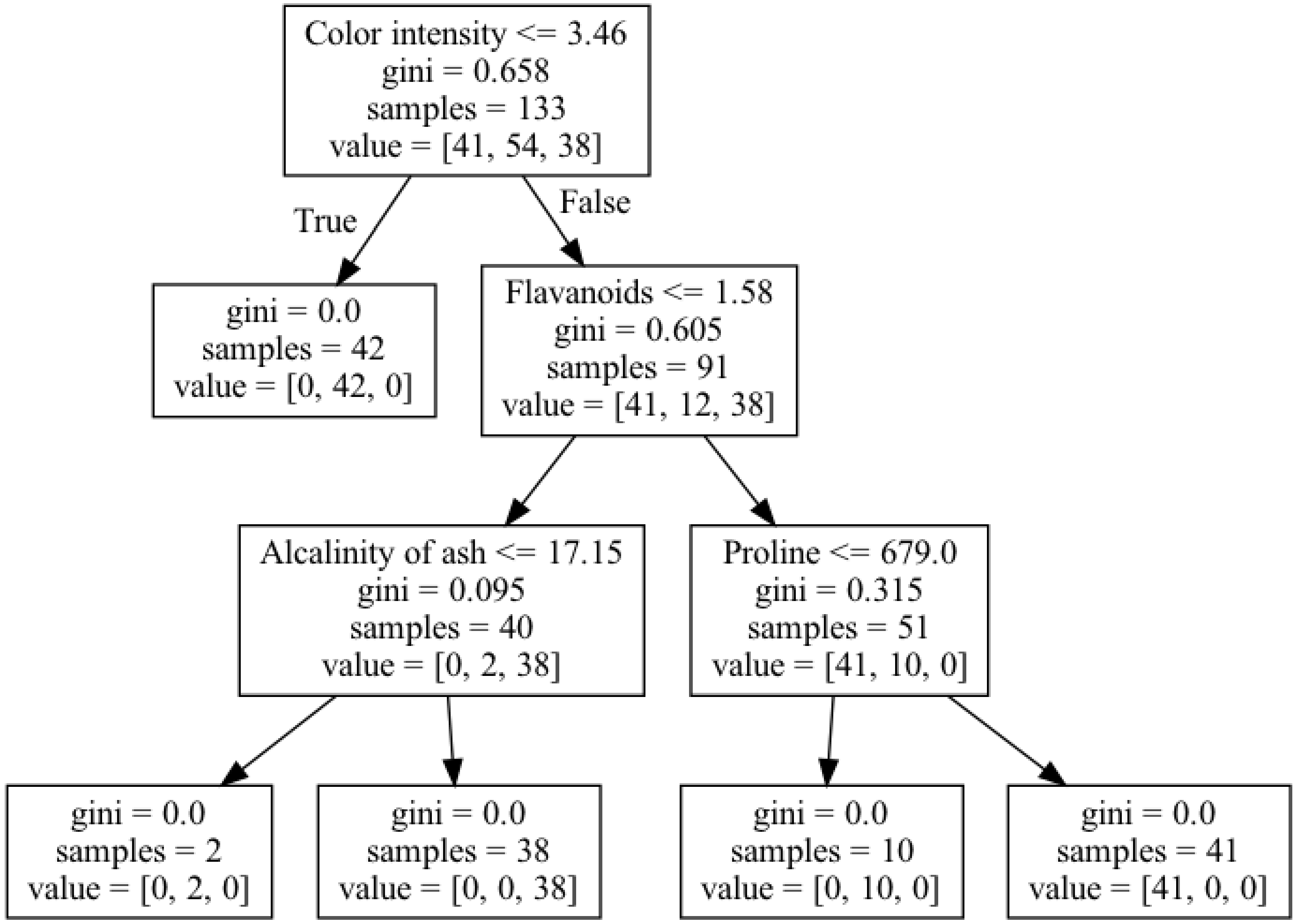
In [248]:
```
#split dataset in features and target variable
feature_cols = ['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Flavanoi
ds',
'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
e']
X = df[feature_cols] # Features
y = df['Class'] # Target variable


# Split dataset into training set and test set
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_state=1)

# Create Decision Tree classifer object
clf = DecisionTreeClassifier()

# Train Decision Tree Classifer
clf = clf.fit(X_train,y_train)
```

In [250]:
```
#Evaluation
#Predict the response for test dataset
y_pred = clf.predict(X_test)

score = metrics.accuracy_score(y_test, y_pred)
print('Accuracy =', round(score,3)*100,'%')
```

```
Accuracy = 95.6 %
```

In [133]:
```python
from IPython.display import Image
from six import StringIO
import pydotplus

dot_data = StringIO()
tree.export_graphviz(clf, out_file=dot_data,
                     feature_names=feature_cols)
graph = pydotplus.graph_from_dot_data(dot_data.getvalue())
Image(graph.create_png())
```

Out[133]:



10 Fold Cross Validation Approach

```
In [251]: #feature_cols = ['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Flavano
          ids',
          #'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
          e']

          '''
          Adjusting for the variables with higher predictive power results in higher accuracy.
          Therefore only these variables are used in the 10-fold cross validation resulting in an
          accuracy greater than 90%.

          '''

          feature_cols = ['Alcalinity of ash' , 'Flavanoids', 'Color intensity','Proline']

          X = df[feature_cols] # Features
          y = df['Class'] # Target variable

          # Create Decision Tree classifer object
          clf = DecisionTreeClassifier()


          score = np.mean(cross_val_score(clf, X, y, cv=10, scoring = 'accuracy'))

          print('Accuracy =', round(score,3)*100,'%')
```

```
Accuracy = 92.7 %
```

Ensemble Random Forest

```
In [252]: feature_cols = ['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Flavanoi
          ds',
          'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
          e']
          X = df[feature_cols] # Features
          y = df['Class'] # Target variable

          clf = RandomForestClassifier(n_estimators=10)

          score = np.mean(cross_val_score(clf, X, y, cv=10, scoring = 'accuracy'))
          print('Accuracy =', round(score,3)*100,'%')
```

```
Accuracy = 95.5 %
```

Random forest performs better than decision tree classifier because it prevents overfittiing by using multiple trees. While decision trees are less computationally expensive, they are not as accurate as random forests.

In this code, decision tree classifier accuracy is around 90%-95%, whereas ensemble random forest gives accuracy up to 97%.

KNN

In [253]:
```
'''
Preparing the dataset by normaliziing features.
'''

feature_cols = ['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Flavanoi
ds',
'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
e']
X = df[feature_cols] # Features
y = df['Class'] # Target variable


#normalizinig the dataset
X = X.apply(lambda x: (x - np.min(x)) / (np.max(x) - np.min(x)))
X
```

Out[253]:

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	OD280/OD315 of diluted wines
0	0.842105	0.191700	0.572193	0.257732	0.619565	0.627586	0.573840	0.283019	0.593060	0.372014	0.455285	0.970696
1	0.571053	0.205534	0.417112	0.030928	0.326087	0.575862	0.510549	0.245283	0.274448	0.264505	0.463415	0.780220
2	0.560526	0.320158	0.700535	0.412371	0.336957	0.627586	0.611814	0.320755	0.757098	0.375427	0.447154	0.695971
3	0.878947	0.239130	0.609626	0.319588	0.467391	0.989655	0.664557	0.207547	0.558360	0.556314	0.308943	0.798535
4	0.581579	0.365613	0.807487	0.536082	0.521739	0.627586	0.495781	0.490566	0.444795	0.259386	0.455285	0.608059
...	...	...	...	...	...	...	...	...	...	...	...	...
173	0.705263	0.970356	0.582888	0.510309	0.271739	0.241379	0.056962	0.735849	0.205047	0.547782	0.130081	0.172161
174	0.623684	0.626482	0.598930	0.639175	0.347826	0.282759	0.086498	0.566038	0.315457	0.513652	0.178862	0.106227
175	0.589474	0.699605	0.481283	0.484536	0.543478	0.210345	0.073840	0.566038	0.296530	0.761092	0.089431	0.106227
176	0.563158	0.365613	0.540107	0.484536	0.543478	0.231034	0.071730	0.754717	0.331230	0.684300	0.097561	0.128205
177	0.815789	0.664032	0.737968	0.716495	0.282609	0.368966	0.088608	0.811321	0.296530	0.675768	0.105691	0.120879

178 rows × 13 columns

KNN with 10 Nearest Neighbours

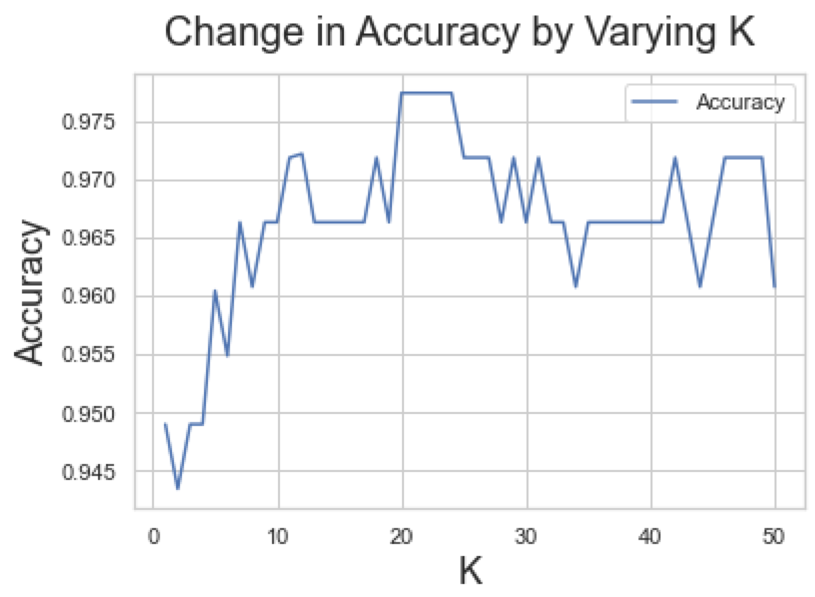
```
In [254]: '''
          KNN with 10 nearest neighbours and 10 fold cross validation
          '''

          knn_1 = KNeighborsClassifier(n_neighbors=10)

          score = np.mean(cross_val_score(knn_1, X, y, cv=10))

          print('Accuracy =', round(score,3)*100,'%')
```

```
Accuracy = 96.6 %
```

KNN with Varying values of K (1 - 50)

In [255]:

```
acc = list()
K = list()


for k in range (50):
    k += 1
    knn_1 = KNeighborsClassifier(n_neighbors=k)
    K.append(k)
    score = np.mean(cross_val_score(knn_1, X, y, cv=10, scoring = 'accuracy'))
    acc.append(score)


plt.plot(K, acc)
plt.legend(['Accuracy', 'K'])
plt.suptitle('Change in Accuracy by Varying K', fontsize=20)
plt.xlabel('K', fontsize=18)
plt.ylabel('Accuracy', fontsize=18)
plt.show()


max_K = acc.index(max(acc))+1
print('Highest Accuracy =', round(max(acc), 3)*100, '% is Achieved when K =',max_K)
```



```
Highest Accuracy = 97.7 % is Achieved when K = 20
```

Varyinig K makes a substantial difference when going from K=1 to K=10.

Naive Bayes

Multinomial NB

```
In [256]: #startinig off by using all features

          feature_cols = ['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Flavanoi
          ds',
          'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
          e']
          X = df[feature_cols] # Features
          y = df['Class'] # Target variable


          nb1 = MultinomialNB(alpha = 0.1)

          #laplace smoothing parameter (alpha) set to 0.1 leads to highest accuracy

          score = np.mean(cross_val_score(nb1, X.values, y.values, cv=10, scoring = 'accuracy'))

          print('Accuracy =', round(score,3)*100,'%')
```

```
Accuracy = 86.1 %
```

Gaussian NB

```
In [233]: feature_cols = ['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Flavanoi
          ds',
          'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
          e']
          X = df[feature_cols] # Features
          y = df['Class'] # Target variable


          nb2 = GaussianNB()

          score = np.mean(cross_val_score(nb2, X.values, y.values, cv=10, scoring = 'accuracy'))

          print('Accuracy =', round(score,3)*100,'%')
```

```
Accuracy = 97.8 %
```

GaussianNB appears to perform better than MultinomialNB. Likely because we have numerical data in decimal form whereas MultinomialNB works better with discrete/categorical data.

Support Vector Classifier (SVC)

In [262]:
```
'''
Preparing the dataset by normaliziing features.
'''

feature_cols = ['Alcohol', 'Malic acid', 'Ash', 'Alcalinity of ash' , 'Magnesium', 'Total phenols', 'Flavanoi
ds',
'Nonflavanoid phenols', 'Proanthocyanins', 'Color intensity', 'Hue', 'OD280/OD315 of diluted wines', 'Prolin
e']
X = df[feature_cols] # Features
y = df['Class'] # Target variable


#normalizinig the dataset
X = X.apply(lambda x: (x - np.min(x)) / (np.max(x) - np.min(x)))
X.head()
```

Out[262]:

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue	OD280/OD315 of diluted wines	
0	0.842105	0.191700	0.572193	0.257732	0.619565	0.627586	0.573840	0.283019	0.593060	0.372014	0.455285	0.970696	(
1	0.571053	0.205534	0.417112	0.030928	0.326087	0.575862	0.510549	0.245283	0.274448	0.264505	0.463415	0.780220	(
2	0.560526	0.320158	0.700535	0.412371	0.336957	0.627586	0.611814	0.320755	0.757098	0.375427	0.447154	0.695971	(
3	0.878947	0.239130	0.609626	0.319588	0.467391	0.989655	0.664557	0.207547	0.558360	0.556314	0.308943	0.798535	(
4	0.581579	0.365613	0.807487	0.536082	0.521739	0.627586	0.495781	0.490566	0.444795	0.259386	0.455285	0.608059	(

10 Fold CV with rbf (default scikit-learn) kernel

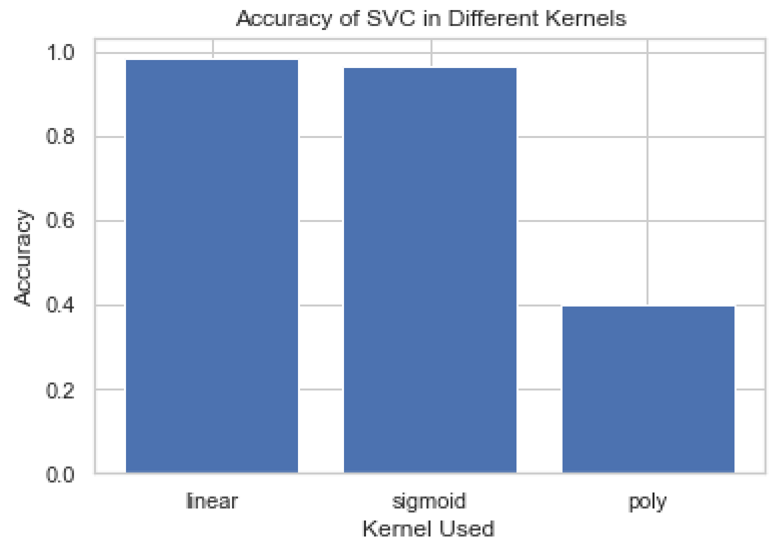
In [267]:
```
svc1 = SVC(gamma='auto')
score = np.mean(cross_val_score(svc1, X.values, y.values, cv=10, scoring = 'accuracy'))

print('Accuracy =', round(score,3)*100,'%')
```

```
Accuracy = 97.8 %
```

Varying kernels for SVC

In [284]:
```
kernels = ['linear', 'sigmoid', 'poly']
acc = list()

for i in kernels:
    svc2 = SVC(kernel = i, gamma='auto')
    score = np.mean(cross_val_score(svc2, X.values, y.values, cv=10, scoring = 'accuracy'))
    acc.append(score)
```

```
In [289]: plt.bar(kernels, acc, width=0.8, bottom=None, align='center')
          plt.xlabel('Kernel Used')
          plt.ylabel('Accuracy')
          plt.title('Accuracy of SVC in Different Kernels')

Out[289]: Text(0.5, 1.0, 'Accuracy of SVC in Different Kernels')
```



```
In [302]: print('Accuracy with Linear Kernal =', round(acc[0],3)*100, '%')
          print('Accuracy with Sigmoid Kernal =', round(acc[1],3)*100, '%')
          print('Accuracy with Poly Kernal =', round(acc[2],2)*100, '%')

          Accuracy with Linear Kernal = 98.3 %
          Accuracy with Sigmoid Kernal = 96.7 %
          Accuracy with Poly Kernal = 40.0 %

In [ ]:
```

Results

SVC with the linear kernel gives a 98.3% accuracy with 10 fold cross validation which is the highest accuracy among all the models tested.

```
In [ ]:
```