In [1]:

```python
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

Normalization

Normalization is technique often applied as part of data preparation for machine learning. The goal of normalization is to change the values of numeric columns in the dataset to use a common scale, without distorting differences in the range of values or losing information

In [2]:

```python
#We will use only three columns of our data set and label them
df=pd.read_csv('wine_data.csv',header=None,usecols=[0,1,2])
df.columns=['Class label','Alcohol','Malic acid']
```

In [3]:

```python
df.head()
```

Out[3]:

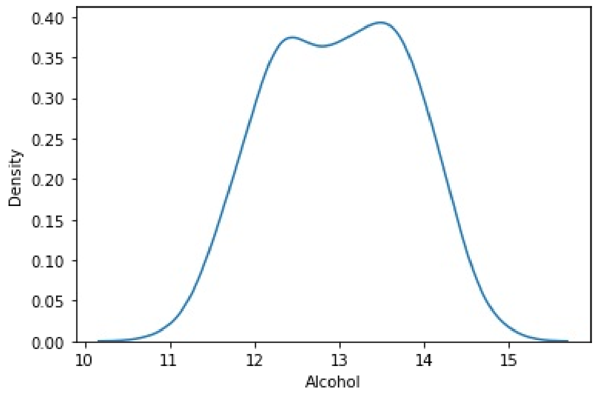
	Class label	Alcohol	Malic acid
0	1	14.23	1.71
1	1	13.20	1.78
2	1	13.16	2.36
3	1	14.37	1.95
4	1	13.24	2.59

In [4]:

```python
sns.kdeplot(df['Alcohol'])
```

Out[4]:

```
<AxesSubplot:xlabel='Alcohol', ylabel='Density'>
```

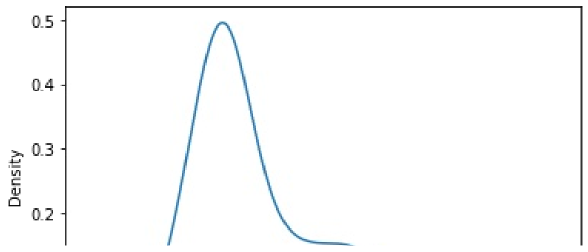


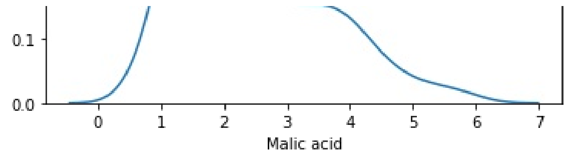
In [5]:

```python
sns.kdeplot(df['Malic acid'])
```

Out[5]:

```
<AxesSubplot:xlabel='Malic acid', ylabel='Density'>
```

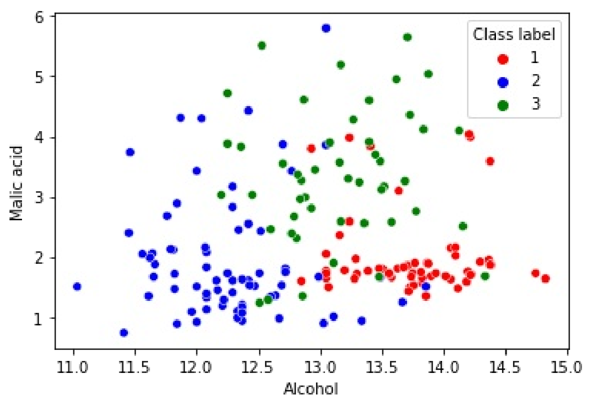




In [6]:
```
color_dict={1:'red',2:'blue',3:'green'}
sns.scatterplot(df['Alcohol'],df['Malic acid'],hue=df['Class label'],palette=color_dict)
```

```
C:\Users\DELL\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass the following variables
as keyword args: x, y. From version 0.12, the only valid positional argument will be `data`, and passing other ar
guments without an explicit keyword will result in an error or misinterpretation.
  warnings.warn(
```

Out[6]:
```
<AxesSubplot:xlabel='Alcohol', ylabel='Malic acid'>
```



Train Test split

In [7]:
```
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(df.drop('Class label',axis='columns'),df['Class label'],test_size=
```

In [8]:
```
x_train.shape,x_test.shape
```

Out[8]:
```
((124, 2), (54, 2))
```

MinMax_Scalling

Also known as min-max scaling or min-max normalization, rescaling is the simplest method and consists in rescaling the range of features to scale the range in [0, 1] or [−1, 1]. Selecting the target range depends on the nature of the data.

MinMax_Scaling

In [9]:
```
from sklearn.preprocessing import MinMaxScaler
scaler=MinMaxScaler()
scaler.fit(x_train)
x_trained_scaler=scaler.transform(x_train)
x_test_scaler=scaler.transform(x_test)
```

In [10]:

```
x_trained_scaler=pd.DataFrame(x_trained_scaler,columns=x_train.columns)
x_test_scaler=pd.DataFrame(x_test_scaler,columns=x_test.columns)
```

In [11]:

```
np.round(x_train.describe(),1)
```

Out[11]:

	Alcohol	Malic acid
count	124.0	124.0
mean	13.0	2.4
std	0.8	1.1
min	11.0	0.9
25%	12.4	1.6
50%	13.0	1.9
75%	13.6	3.2
max	14.8	5.6

In [12]:

```
np.round(x_trained_scaler.describe(),1)
```

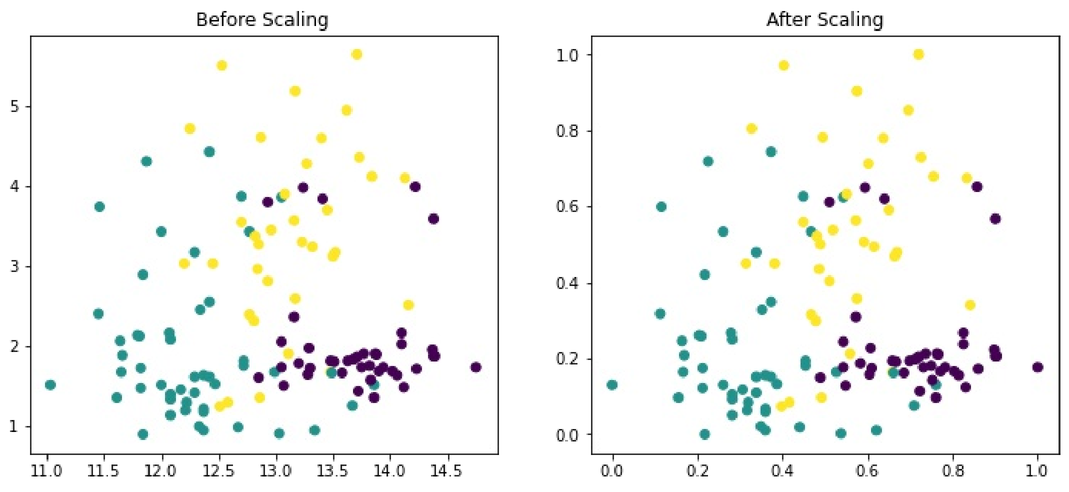
Out[12]:

	Alcohol	Malic acid
count	124.0	124.0
mean	0.5	0.3
std	0.2	0.2
min	0.0	0.0
25%	0.4	0.2
50%	0.5	0.2
75%	0.7	0.5
max	1.0	1.0

Scaling Effects

In [13]:

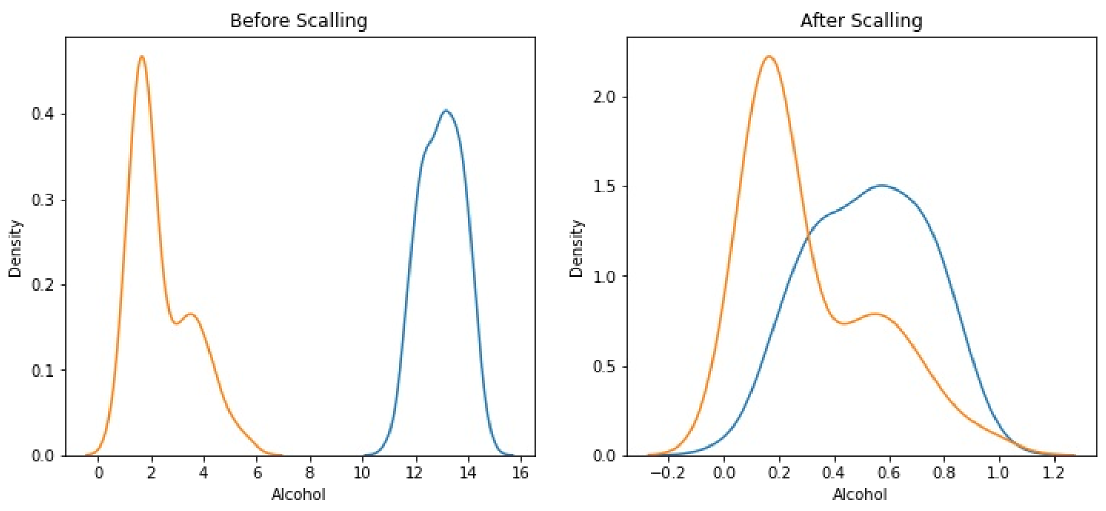
```
fig, (ax1, ax2) = plt.subplots(ncols=2, figsize=(12, 5))

ax1.scatter(x_train['Alcohol'], x_train['Malic acid'],c=y_train)
ax1.set_title("Before Scaling")
ax2.scatter(x_trained_scaler['Alcohol'], x_trained_scaler['Malic acid'],c=y_train)
ax2.set_title("After Scaling")
plt.show()
```



In [14]:

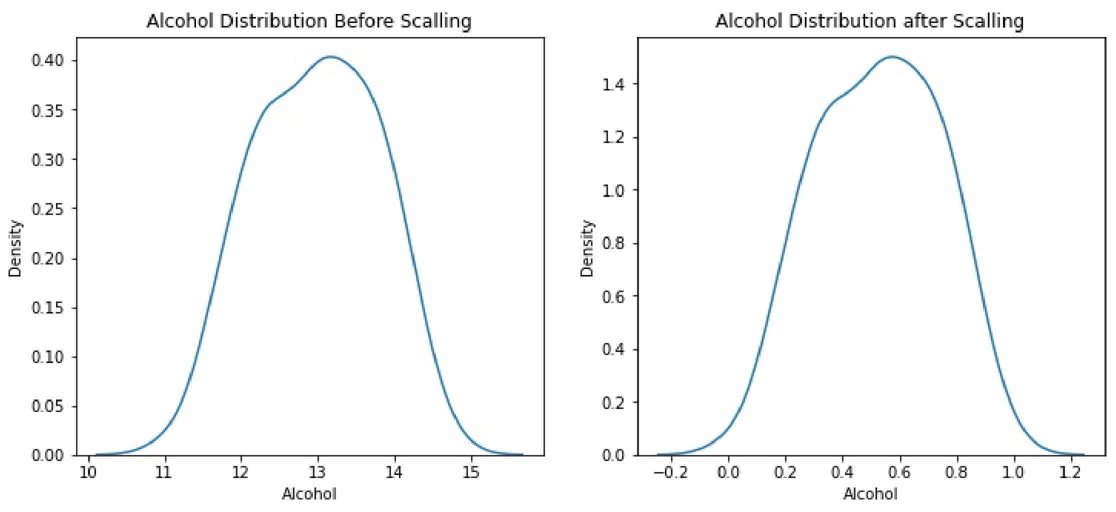
```
fig, (ax1, ax2) = plt.subplots(ncols=2, figsize=(12, 5))

#Before scalling
ax1.set_title('Before Scalling')
sns.kdeplot(x_train['Alcohol'],ax=ax1)
sns.kdeplot(x_train['Malic acid'],ax=ax1)
```

```
#After scalling
ax2.set_title('After Scalling')
sns.kdeplot(x_trained_scaler['Alcohol'],ax=ax2)
sns.kdeplot(x_trained_scaler['Malic acid'],ax=ax2)
plt.show()
```



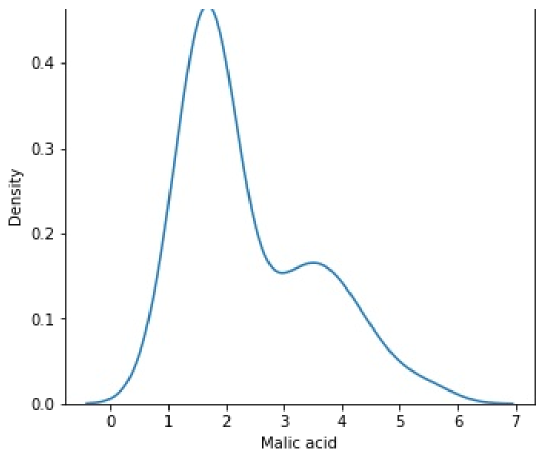
Individual Effects

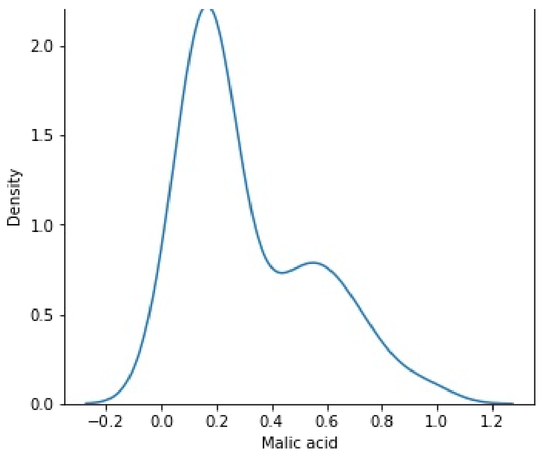
In [15]:
```
fig, (ax1, ax2) = plt.subplots(ncols=2, figsize=(12, 5))

#Before scalling
ax1.set_title('Alcohol Distribution Before Scalling')
sns.kdeplot(x_train['Alcohol'],ax=ax1)


#After scalling
ax2.set_title('Alcohol Distribution after Scalling')
sns.kdeplot(x_trained_scaler['Alcohol'],ax=ax2)

plt.show()
```



In [16]:
```
fig, (ax1, ax2) = plt.subplots(ncols=2, figsize=(12, 5))

#Before scalling
ax1.set_title('Malic acid Distribution Before Scalling')
sns.kdeplot(x_train['Malic acid'],ax=ax1)


#After scalling
ax2.set_title('Malic acid Distribution after Scalling')
sns.kdeplot(x_trained_scaler['Malic acid'],ax=ax2)

plt.show()
```

Malic acid Distribution Before Scalling
Malic acid Distribution after Scalling





Applying Logistic Regression

In [17]:
```
from sklearn.linear_model import LogisticRegression
```

In [18]:
```
Lr=LogisticRegression()
Lr_scaled=LogisticRegression()
```

In [19]:
```
Lr.fit(x_train,y_train)
Lr_scaled.fit(x_trained_scaler,y_train)
```

Out[19]:
```
LogisticRegression()
```

In [20]:
```
y_pred=Lr.predict(x_test)
y_pred_scaled=Lr_scaled.predict(x_test_scaler)
```

In [21]:
```
from sklearn.metrics import accuracy_score
```

In [22]:
```
print('Actual : ',accuracy_score(y_test,y_pred))
print('Scalled : ',accuracy_score(y_test,y_pred_scaled))
```

```
Actual :  0.7592592592592593
Scalled :  0.7962962962962963
```

Thank you

Author

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