

In [2]:

```
1 #importing libraries
2 import pandas as pd
3 import seaborn as sns
4 import matplotlib.pyplot as plt
5 import numpy as np
6 import warnings
7 warnings.filterwarnings('ignore')
```

In [3]:

```
1 #importing the dataset
2 data = pd.read_csv('f2.csv')
3 data.head()
```

Out[3]:

	Temparature	Humidity	Moisture	Soil_Type	Crop_Type	Nitrogen	Potassium	Phosphorous
0	20	83	26	Clayey	rice	90	49	36
1	25	84	32	Loamy	rice	66	59	36
2	33	64	50	Loamy	Wheat	41	0	0
3	34	65	54	Loamy	Wheat	38	0	0
4	38	72	51	Loamy	Wheat	39	0	0



In [4]:

```

1 # Define the number of augmented samples to create for each original sample
2 # increase dataset from 100 rows to 500
3
4
5 # num_augmented_samples = 3
6
7 # augmented_data = []
8
9 # for index, row in dataset.iterrows():
10 #     original_sample = row.to_dict()
11 #     augmented_samples = []
12
13 #     for _ in range(num_augmented_samples):
14 #         augmented_sample = original_sample.copy()
15 #         augmented_sample['Temparature'] += np.random.normal(0, 0.1)
16 #         augmented_sample['Humidity'] += np.random.normal(0, 0.1)
17 #         augmented_sample['Moisture'] += np.random.normal(0, 0.1)
18 #         augmented_sample['Nitrogen'] += np.random.normal(0, 0.1)
19 #         augmented_sample['Potassium'] += np.random.normal(0, 0.1)
20 #         augmented_sample['Phosphorous'] += np.random.normal(0, 0.1)
21 #         # Add more transformations for other columns as needed
22 #         augmented_samples.append(augmented_sample)
23
24
25 #     augmented_data.extend(augmented_samples)
26
27 # # Convert the augmented data to a DataFrame
28 # augmented_dataset = pd.DataFrame(augmented_data)
29
30 # # Concatenate the original dataset
31 # data = pd.concat([dataset, augmented_dataset], ignore_index=True)

```

In [5]:

```

1 data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 552 entries, 0 to 551
Data columns (total 9 columns):
 #   Column      Non-Null Count  Dtype  
--- 
 0   Temparature  552 non-null    int64  
 1   Humidity     552 non-null    int64  
 2   Moisture     552 non-null    int64  
 3   Soil_Type    552 non-null    object  
 4   Crop_Type    552 non-null    object  
 5   Nitrogen     552 non-null    int64  
 6   Potassium    552 non-null    int64  
 7   Phosphorous  552 non-null    int64  
 8   Fertilizer   552 non-null    object  
dtypes: int64(6), object(3)
memory usage: 38.9+ KB

```

```
In [6]: 1 #changing the column names
2 data.rename(columns={'Humidity ':'Humidity','Soil Type':'Soil_Type','Crop
```

```
In [7]: 1 #checking unique values
2 data.unique()
```

```
Out[7]: Temparature      21
         Humidity        34
         Moisture        41
         Soil_Type       5
         Crop_Type       17
         Nitrogen        47
         Potassium       31
         Phosphorous     36
         Fertilizer      14
         dtype: int64
```

```
In [8]: 1 #checking for null values
2 data.isna().sum()
```

```
Out[8]: Temparature      0
         Humidity        0
         Moisture        0
         Soil_Type       0
         Crop_Type       0
         Nitrogen        0
         Potassium       0
         Phosphorous     0
         Fertilizer      0
         dtype: int64
```

```
In [9]: 1 data['Fertilizer'].unique()
```

```
Out[9]: array(['Urea', 'TSP', 'Superphosphate', 'Potassium sulfate.',
   'Potassium chloride', 'DAP', '28-28', '20-20', '17-17-17',
   '15-15-15', '14-35-14', '14-14-14', '10-26-26', '10-10-10'],
   dtype=object)
```

```
In [10]: 1 data['Crop_Type'].unique()
```

```
Out[10]: array(['rice', 'Wheat', 'Tobacco', 'Sugarcane', 'Pulses', 'pomegranate',
   'Paddy', 'Oil seeds', 'Millets', 'Maize', 'Ground Nuts', 'Cotton',
   'coffee', 'watermelon', 'Barley', 'kidneybeans', 'orange'],
  dtype=object)
```

In [11]:

```

1 #statistical parameters
2 data.describe(include='all')

```

Out[11]:

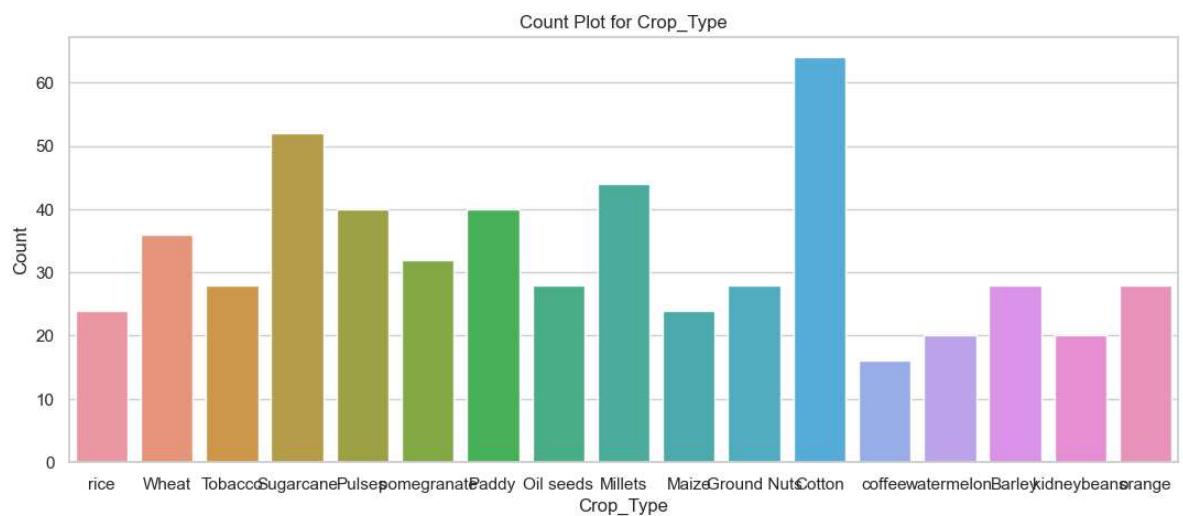
	Temparature	Humidity	Moisture	Soil_Type	Crop_Type	Nitrogen	Potassium	Ph
count	552.000000	552.000000	552.000000	552	552	552.000000	552.000000	
unique	NaN	NaN	NaN	5	17	NaN	NaN	
top	NaN	NaN	NaN	Loamy	Cotton	NaN	NaN	
freq	NaN	NaN	NaN	192	64	NaN	NaN	
mean	28.630435	64.557971	42.840580	NaN	NaN	28.521739	10.144928	
std	5.088082	11.880236	11.507275	NaN	NaN	29.121989	13.456956	
min	0.000000	50.000000	25.000000	NaN	NaN	0.000000	0.000000	
25%	26.000000	54.000000	33.000000	NaN	NaN	10.000000	0.000000	
50%	29.000000	62.000000	41.000000	NaN	NaN	15.000000	0.000000	
75%	32.000000	68.000000	51.000000	NaN	NaN	37.000000	18.000000	
max	38.000000	95.000000	65.000000	NaN	NaN	126.000000	59.000000	

In [12]:

```

1 plt.figure(figsize=(13, 5))
2 sns.set(style="whitegrid")
3 sns.countplot(data=data, x='Crop_Type')
4 plt.title('Count Plot for Crop_Type')
5 plt.xlabel('Crop_Type')
6 plt.ylabel('Count')
7 plt.show()

```



In [13]:

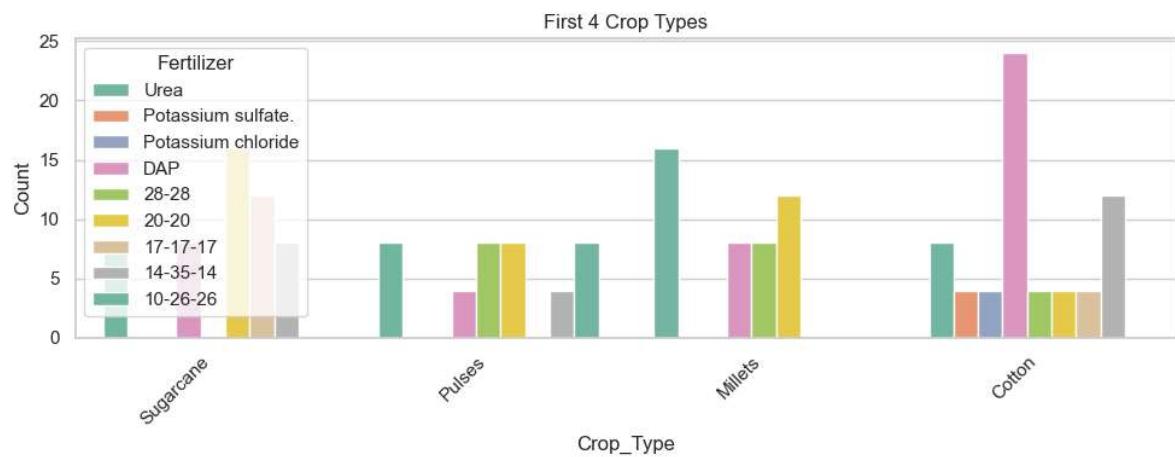
```

1 #The plot that shows the count (frequency) of each unique crop type in the
2 #The x-axis represents the different crop types.
3 #The y-axis represents the count (the number of occurrences) of each crop

```

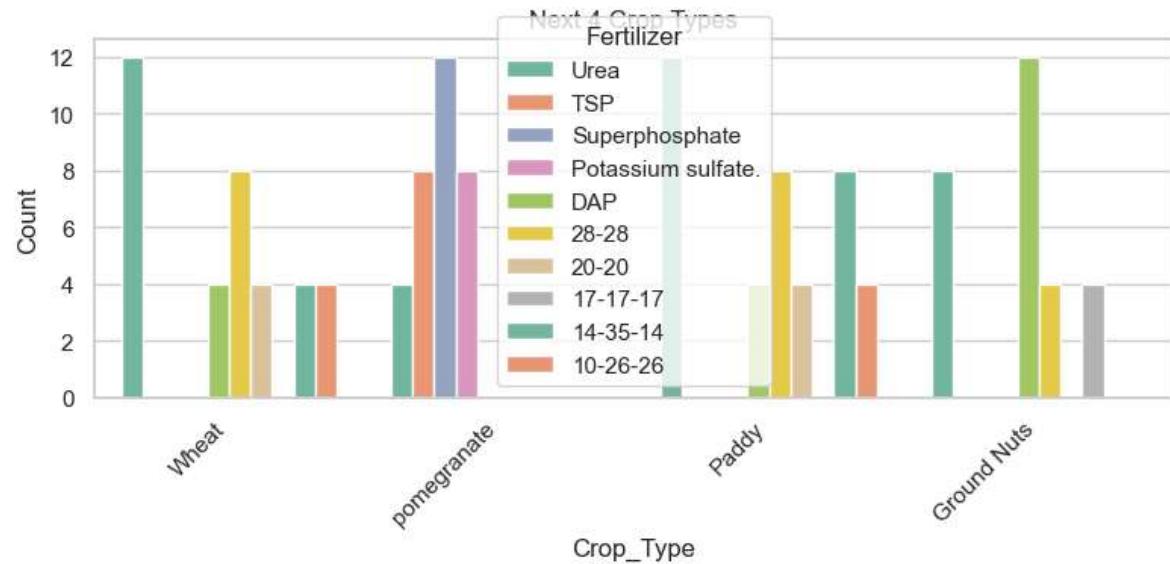
In [14]:

```
1 #first 4 crop types
2 part1_data = data[data['Crop_Type'].isin(data['Crop_Type'].value_counts())
3
4
5 # Create the first countplot
6 plt.figure(figsize=(10, 4))
7 sns.set(style="whitegrid")
8 sns.countplot(data=part1_data, x='Crop_Type', hue='Fertilizer', width=0.8)
9 plt.title('First 4 Crop Types')
10 plt.xlabel('Crop_Type')
11 plt.ylabel('Count')
12 plt.legend(title='Fertilizer')
13 plt.xticks(rotation=45, horizontalalignment='right')
14 plt.tight_layout()
15 plt.show()
16
```



In [15]:

```
1 # Split the data into three parts: next 4 crop types
2 part2_data = data[data['Crop_Type'].isin(data['Crop_Type'].value_counts())
3
4 # Create the second countplot
5 plt.figure(figsize=(8, 4))
6 sns.set(style="whitegrid")
7 sns.countplot(data=part2_data, x='Crop_Type', hue='Fertilizer', width=0.8)
8 plt.title('Next 4 Crop Types')
9 plt.xlabel('Crop_Type')
10 plt.ylabel('Count')
11 plt.legend(title='Fertilizer')
12 plt.xticks(rotation=45, horizontalalignment='right')
13 plt.tight_layout()
14 plt.show()
15
```

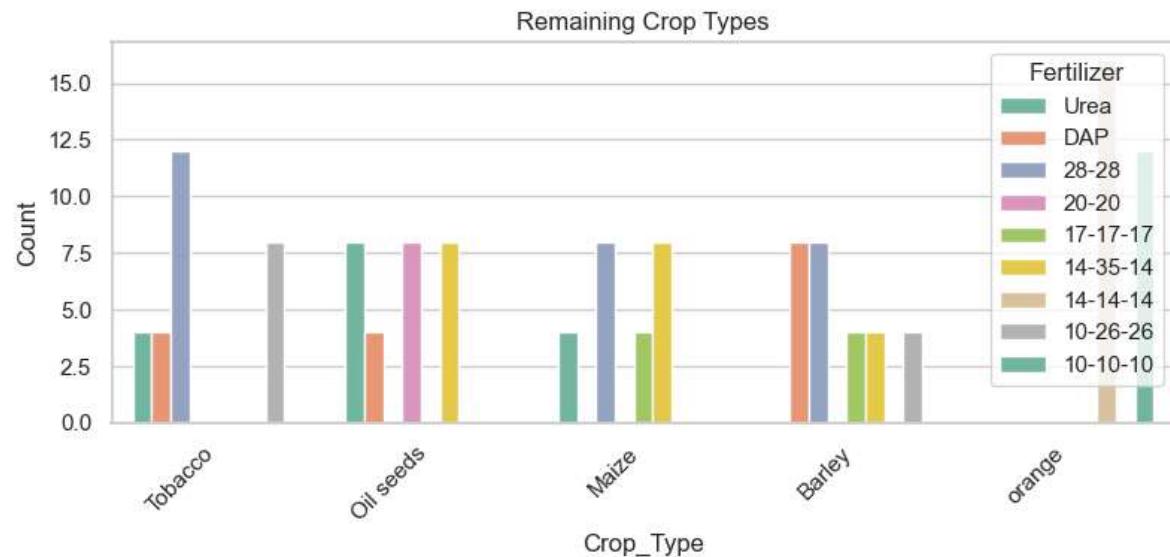


In [16]:

```

1 # Split the data into three parts: remaining crop types
2 part3_data = data[data['Crop_Type'].isin(data['Crop_Type'].value_counts())
3
4 # Create the third countplot
5 plt.figure(figsize=(8, 4))
6 sns.set(style="whitegrid")
7 sns.countplot(data=part3_data, x='Crop_Type', hue='Fertilizer', width=0.8)
8 plt.title('Remaining Crop Types')
9 plt.xlabel('Crop_Type')
10 plt.ylabel('Count')
11 plt.legend(title='Fertilizer')
12 plt.xticks(rotation=45, horizontalalignment='right')
13 plt.tight_layout()
14 plt.show()
15

```



In [17]:

```

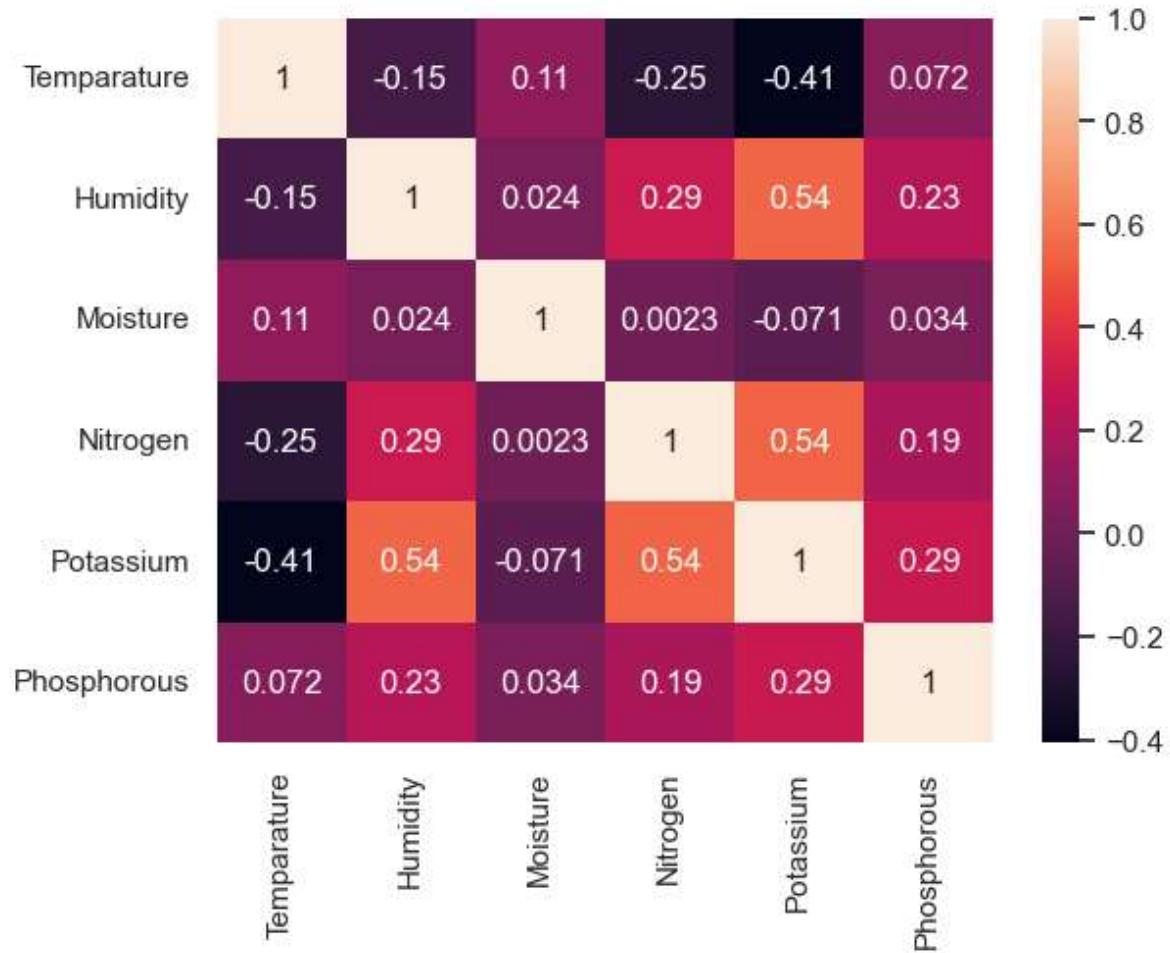
1 # this plot provides insights into how different crop types are distributed
2 # The x-axis represents the different crop types.
3 # The y-axis represents the count (the number of occurrences) of each crop type.

```

In [18]:

```
1 #Heatmap for Correlation Analysis
2 sns.heatmap(data.corr(), annot=True)
```

Out[18]: <Axes: >



In [19]:

```
1 #here is no such correlation between any of variables..
```

In [20]:

```
1 #encoding the Labels for categorical variables
2 from sklearn.preprocessing import LabelEncoder
3 #it transforming non-numeric data into a numeric format
```

In [21]:

```
1 #encoding Soil Type variable
2 encode_soil = LabelEncoder()
3
4 #fitting the label encoder
5 data.Soil_Type = encode_soil.fit_transform(data.Soil_Type)
6
7 #creating the DataFrame
8 Soil_Type = pd.DataFrame(zip(encode_soil.classes_, encode_soil.transform(
9 Soil_Type = Soil_Type.set_index('Original')
10 Soil_Type
```

Out[21]:

Encoded

Original	Encoded
Black	0
Clayey	1
Loamy	2
Red	3
Sandy	4

In [22]:

```
1 #encoding Crop Type variable
2 encode_crop = LabelEncoder()
3
4 #fitting the label encoder
5 data.Crop_Type = encode_crop.fit_transform(data.Crop_Type)
6
7 #creating the DataFrame
8 Crop_Type = pd.DataFrame(zip(encode_crop.classes_, encode_crop.transform(data.Crop_Type)))
9 Crop_Type = Crop_Type.set_index('Original')
10 Crop_Type
```

Out[22]:

Encoded

Original	Encoded
Barley	0
Cotton	1
Ground Nuts	2
Maize	3
Millets	4
Oil seeds	5
Paddy	6
Pulses	7
Sugarcane	8
Tobacco	9
Wheat	10
coffee	11
kidneybeans	12
orange	13
pomegranate	14
rice	15
watermelon	16

In [23]:

```

1 #encoding Fertilizer variable
2 encode_ferti = LabelEncoder()
3
4 #fitting the label encoder
5 data.Fertilizer = encode_ferti.fit_transform(data.Fertilizer)
6
7 #creating the DataFrame
8 Fertilizer = pd.DataFrame(zip(encode_ferti.classes_, encode_ferti.transform(
9 Fertilizer = Fertilizer.set_index('Original')
10 Fertilizer

```

Out[23]:

Encoded

Original	
10-10-10	0
10-26-26	1
14-14-14	2
14-35-14	3
15-15-15	4
17-17-17	5
20-20	6
28-28	7
DAP	8
Potassium chloride	9
Potassium sulfate.	10
Superphosphate	11
TSP	12
Urea	13

In [24]:

```

1 #splitting the data into train and test
2 from sklearn.model_selection import train_test_split
3
4 x_train, x_test, y_train, y_test = train_test_split(data.drop('Fertilizer',
5 print('Shape of Splitting :')
6 print('x_train = {}, y_train = {}, x_test = {}, y_test = {}'.format(x_trai

```

Shape of Splitting :

x_train = (441, 8), y_train = (441,), x_test = (111, 8), y_test = (111,)

In [25]:

```

1 # here 20% of the data should be used for testing (evaluation), and the re
2 #x_train and x_test = contain the features (independent variables) used fo
3 #y_train and y_test = contains the labels(dependent variable) used for tra

```

In [26]: 1 x_train.info()

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 441 entries, 213 to 37
Data columns (total 8 columns):
 #   Column      Non-Null Count  Dtype  
--- 
 0   Temperature  441 non-null    int64  
 1   Humidity     441 non-null    int64  
 2   Moisture     441 non-null    int64  
 3   Soil_Type    441 non-null    int32  
 4   Crop_Type    441 non-null    int32  
 5   Nitrogen     441 non-null    int64  
 6   Potassium    441 non-null    int64  
 7   Phosphorous  441 non-null    int64  
dtypes: int32(2), int64(6)
memory usage: 27.6 KB
```

In [27]: 1 acc = [] # TEST
2 model = []
3 acc1=[] # TRIAN

Logistic regression model

In [29]:

```
1 #importing libraries
2 from sklearn.tree import DecisionTreeClassifier
3 from sklearn.metrics import classification_report
4 from sklearn import metrics
5 from sklearn import tree
6 import warnings
7 warnings.filterwarnings('ignore')
8
9 ds = DecisionTreeClassifier(criterion="entropy",random_state=2,max_depth=1)
10 ds.fit(x_train,y_train)
11
12 predicted_values = ds.predict(x_test)
13 x = metrics.accuracy_score(y_test, predicted_values)
14 acc.append(x)
15 model.append('Decision Tree')
16
17 predicted_values = ds.predict(x_train)
18 y = metrics.accuracy_score(y_train, predicted_values)
19 acc1.append(y)
20
21 print("DecisionTrees's Accuracy is: ", x*100, y*100)
22
23 print(classification_report(y_test,predicted_values))
```

DecisionTrees's Accuracy is: 90.09009009009009 93.42403628117914

```

-----  

ValueError                                     Traceback (most recent call last)  

e:\DATA_SCIENCE_PRACTISE_FILES\Project\college_projects\New folder (2)\Fertilizer-Prediction-main\finalferti.ipynb Cell 28 line 2  

    <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X40sZmlsZQ%3D%3D?line=18'>19</a> acc1.append(y)  

    <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X40sZmlsZQ%3D%3D?line=20'>21</a> print("DecisionTrees's Accuracy is:", x*100, y*100)  

---> <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X40sZmlsZQ%3D%3D?line=22'>23</a> print(classification_report(y_test, predicted_values))  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:2310, in classification_report(y_true, y_pred, labels, target_names, sample_weight, digits, output_dict, zero_division)
    2195 def classification_report(
    2196     y_true,
    2197     y_pred,
    (...),
    2204     zero_division="warn",
    2205 ):
    2206     """Build a text report showing the main classification metrics.
    2207
    2208     Read more in the :ref:`User Guide <classification_report>`.
    (...),
    2307     <BLANKLINE>
    2308     """
-> 2310     y_type, y_true, y_pred = _check_targets(y_true, y_pred)
    2312     if labels is None:
    2313         labels = unique_labels(y_true, y_pred)  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:86, in _check_targets(y_true, y_pred)
    59 def _check_targets(y_true, y_pred):
    60     """Check that y_true and y_pred belong to the same classification task.
    61
    62     This converts multiclass or binary types to a common shape, and raises a
    (...),
    84     y_pred : array or indicator matrix
    85     """
---> 86     check_consistent_length(y_true, y_pred)
    87     type_true = type_of_target(y_true, input_name="y_true")
    88     type_pred = type_of_target(y_pred, input_name="y_pred")  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\utils\validation.py:397, in check_consistent_length(*arrays)
    395     uniques = np.unique(lengths)
    396     if len(uniques) > 1:
---> 397         raise ValueError(
    398             "Found input variables with inconsistent numbers of samples: %r"

```

```
399      % [int(l) for l in lengths]
400      )
```

ValueError: Found input variables with inconsistent numbers of samples: [111, 441]

In [30]:

```
1 from sklearn.naive_bayes import GaussianNB
2
3 NaiveBayes = GaussianNB()
4
5 NaiveBayes.fit(x_train,y_train)
6
7 predicted_values = NaiveBayes.predict(x_test)
8 x = metrics.accuracy_score(y_test, predicted_values)
9 acc.append(x)
10
11 predicted_values = NaiveBayes.predict(x_train)
12 y = metrics.accuracy_score(y_train, predicted_values)
13 acc1.append(y)
14
15 model.append('Naive Bayes')
16 print("Naive Bayes's Accuracy is: ", x,y)
17
18 print(classification_report(y_test,predicted_values))
```

Naive Bayes's Accuracy is: 0.9459459459459459 0.9138321995464853

```

-----  

ValueError                                     Traceback (most recent call last)  

e:\DATA_SCIENCE_PRACTISE_FILES\Project\college_projects\New folder (2)\Fertilizer-Prediction-main\finalferti.ipynb Cell 29 line 1  

    <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X41sZmlsZQ%3D%3D?line=14'>15</a> model.append('Naive Bayes')  

    <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X41sZmlsZQ%3D%3D?line=15'>16</a> print("Naive Bayes's Accuracy is:", x,y)  

---> <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X41sZmlsZQ%3D%3D?line=17'>18</a> print(classification_report(y_test, predicted_values))  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:2310, in classification_report(y_true, y_pred, labels, target_names, sample_weight, digits, output_dict, zero_division)
    2195 def classification_report(
    2196     y_true,
    2197     y_pred,
    (...),
    2204     zero_division="warn",
    2205 ):
    2206     """Build a text report showing the main classification metrics.
    2207
    2208     Read more in the :ref:`User Guide <classification_report>`.
    (...),
    2307     <BLANKLINE>
    2308     """
-> 2310     y_type, y_true, y_pred = _check_targets(y_true, y_pred)
    2312     if labels is None:
    2313         labels = unique_labels(y_true, y_pred)  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:86, in _check_targets(y_true, y_pred)
    59 def _check_targets(y_true, y_pred):
    60     """Check that y_true and y_pred belong to the same classification task.
    61
    62     This converts multiclass or binary types to a common shape, and raises a
    (...),
    84     y_pred : array or indicator matrix
    85     """
---> 86     check_consistent_length(y_true, y_pred)
    87     type_true = type_of_target(y_true, input_name="y_true")
    88     type_pred = type_of_target(y_pred, input_name="y_pred")  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\utils\validation.py:397, in check_consistent_length(*arrays)
    395     uniques = np.unique(lengths)
    396     if len(uniques) > 1:
--> 397         raise ValueError(
    398             "Found input variables with inconsistent numbers of samples: %r"

```

```
399      % [int(l) for l in lengths]
400      )
```

ValueError: Found input variables with inconsistent numbers of samples: [111, 441]

In [31]:

```
1 from sklearn.svm import SVC
2 # data normalization with sklearn
3 from sklearn.preprocessing import MinMaxScaler
4 # fit scaler on training data
5 norm = MinMaxScaler().fit(x_train)
6 X_train_norm = norm.transform(x_train)
7 # transform testing dataabs
8 X_test_norm = norm.transform(x_test)
9 SVM = SVC(kernel='poly', degree=3, C=1)
10 SVM.fit(X_train_norm,y_train)
11
12 predicted_values = SVM.predict(X_test_norm)
13 x = metrics.accuracy_score(y_test, predicted_values)
14 acc.append(x)
15
16 predicted_values = SVM.predict(X_train_norm)
17 y = metrics.accuracy_score(y_train, predicted_values)
18 acc1.append(y)
19
20 model.append('SVM')
21 print("SVM's Accuracy is: ", x,y)
22
23 print(classification_report(y_test,predicted_values))
```

SVM's Accuracy is: 0.990990990990991 0.9931972789115646

```

-----
```

ValueError Traceback (most recent call last)
e:\DATA_SCIENCE_PRACTISE_FILES\Project\college_projects\New folder (2)\Fertilizer-Prediction-main\finalferti.ipynb Cell 30 line 2
20 model.append('SVM')
21 print("SVM's Accuracy is: ", x,y)
---> 23 print(classification_report(y_test, predicted_values))

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics_classification.py:2310, in classification_report(y_true, y_pred, labels, target_names, sample_weight, digits, output_dict, zero_division)
2195 def classification_report(
2196 y_true,
2197 y_pred,
2198 (...),
2199 zero_division="warn",
2200):
2201 """Build a text report showing the main classification metrics.
2202
2203 Read more in the :ref:`User Guide <classification_report>`.
2204 (...)
2205 <BLANKLINE>
2206 """
-> 2207 y_type, y_true, y_pred = _check_targets(y_true, y_pred)
2208 if labels is None:
2209 labels = unique_labels(y_true, y_pred)

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics_classification.py:86, in _check_targets(y_true, y_pred)
59 def _check_targets(y_true, y_pred):
60 """Check that y_true and y_pred belong to the same classification task.
61
62 This converts multiclass or binary types to a common shape, and raises a
63 (...)
64 y_pred : array or indicator matrix
65 """
---> 66 check_consistent_length(y_true, y_pred)
67 type_true = type_of_target(y_true, input_name="y_true")
68 type_pred = type_of_target(y_pred, input_name="y_pred")

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\utils\validation.py:397, in check_consistent_length(*arrays)
395 uniques = np.unique(lengths)
396 if len(uniques) > 1:
---> 397 raise ValueError(
398 "Found input variables with inconsistent numbers of samples:
%r"
399 % [int(l) for l in lengths])

```
400      )
```

ValueError: Found input variables with inconsistent numbers of samples: [111, 441]

In [32]:

```
1 from sklearn.linear_model import LogisticRegression
2
3 LogReg = LogisticRegression(random_state=2)
4
5 LogReg.fit(x_train,y_train)
6
7 predicted_values = LogReg.predict(x_test)
8 x = metrics.accuracy_score(y_test, predicted_values)
9 acc.append(x)
10
11 predicted_values = LogReg.predict(x_train)
12 y = metrics.accuracy_score(y_train, predicted_values)
13 acc1.append(y)
14
15 model.append('Logistic Regression')
16 print("Logistic Regression's Accuracy is: ", x,y)
17
18 print(classification_report(y_test,predicted_values))
```

Logistic Regression's Accuracy is: 0.7837837837837838 0.909297052154195

```

-----  

ValueError                                     Traceback (most recent call last)  

e:\DATA_SCIENCE_PRACTISE_FILES\Project\college_projects\New folder (2)\Fertilizer-Prediction-main\finalferti.ipynb Cell 31 line 1  

    <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X43sZmlsZQ%3D%3D?line=14'>15</a> model.append('Logistic Regression')  

    <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X43sZmlsZQ%3D%3D?line=15'>16</a> print("Logistic Regression's Accuracy is: ", x,y)  

---> <a href='vscode-notebook-cell:/e%3A/DATA_SCIENCE_PRACTISE_FILES/Project/college%20projects/New%20folder%20%28%29/Fertilizer-Prediction-main/finalferti.ipynb#X43sZmlsZQ%3D%3D?line=17'>18</a> print(classification_report(y_test, predicted_values))  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:2310, in classification_report(y_true, y_pred, labels, target_names, sample_weight, digits, output_dict, zero_division)
    2195 def classification_report(
    2196     y_true,
    2197     y_pred,
    (...),
    2204     zero_division="warn",
    2205 ):
    2206     """Build a text report showing the main classification metrics.
    2207
    2208     Read more in the :ref:`User Guide <classification_report>`.
    (...),
    2307     <BLANKLINE>
    2308     """
-> 2310     y_type, y_true, y_pred = _check_targets(y_true, y_pred)
    2312     if labels is None:
    2313         labels = unique_labels(y_true, y_pred)  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:86, in _check_targets(y_true, y_pred)
    59 def _check_targets(y_true, y_pred):
    60     """Check that y_true and y_pred belong to the same classification task.
    61
    62     This converts multiclass or binary types to a common shape, and raises a
    (...),
    84     y_pred : array or indicator matrix
    85     """
---> 86     check_consistent_length(y_true, y_pred)
    87     type_true = type_of_target(y_true, input_name="y_true")
    88     type_pred = type_of_target(y_pred, input_name="y_pred")  

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\utils\validation.py:397, in check_consistent_length(*arrays)
    395     uniques = np.unique(lengths)
    396     if len(uniques) > 1:
---> 397         raise ValueError(
    398             "Found input variables with inconsistent numbers of samples:
    %r"

```

```
399      % [int(l) for l in lengths]
400      )
```

ValueError: Found input variables with inconsistent numbers of samples: [111, 441]

In [33]:

```
1 from sklearn.ensemble import RandomForestClassifier
2
3 RF = RandomForestClassifier(n_estimators=20, random_state=0)
4 RF.fit(x_train,y_train)
5
6 predicted_values = RF.predict(x_test)
7 x = metrics.accuracy_score(y_test, predicted_values)
8 acc.append(x)
9
10 predicted_values = RF.predict(x_train)
11 y = metrics.accuracy_score(y_train, predicted_values)
12 acc1.append(y)
13
14 model.append('RF')
15 print("RF's Accuracy is: ", x,y)
16
17 print(classification_report(y_test,predicted_values))
```

RF's Accuracy is: 1.0 1.0

```

-----
```

ValueError Traceback (most recent call last)
e:\DATA_SCIENCE_PRACTISE_FILES\Project\college_projects\New folder (2)\Fertilizer-Prediction-main\finalferti.ipynb Cell 32 line 1
14 model.append('RF')
15 print("RF's Accuracy is: ", x,y)
---> 17 print(classification_report(y_test, predicted_values))

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics_classification.py:2310, in classification_report(y_true, y_pred, labels, target_names, sample_weight, digits, output_dict, zero_division)
2195 def classification_report(
2196 y_true,
2197 y_pred,
2198 (...),
2199 zero_division="warn",
2200):
2201 """Build a text report showing the main classification metrics.
2202
2203 Read more in the :ref:`User Guide <classification_report>`.
2204 (...)
2205 <BLANKLINE>
2206 """
-> 2310 y_type, y_true, y_pred = _check_targets(y_true, y_pred)
2311 if labels is None:
2312 labels = unique_labels(y_true, y_pred)

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\metrics_classification.py:86, in _check_targets(y_true, y_pred)
59 def _check_targets(y_true, y_pred):
60 """Check that y_true and y_pred belong to the same classification task.
61
62 This converts multiclass or binary types to a common shape, and raises a
63 (...)
64 y_pred : array or indicator matrix
65 """
---> 66 check_consistent_length(y_true, y_pred)
67 type_true = type_of_target(y_true, input_name="y_true")
68 type_pred = type_of_target(y_pred, input_name="y_pred")

File c:\Users\msi1\anaconda3\lib\site-packages\sklearn\utils\validation.py:397, in check_consistent_length(*arrays)
395 uniques = np.unique(lengths)
396 if len(uniques) > 1:
---> 397 raise ValueError(
398 "Found input variables with inconsistent numbers of samples:
%r"
399 % [int(l) for l in lengths])

400)

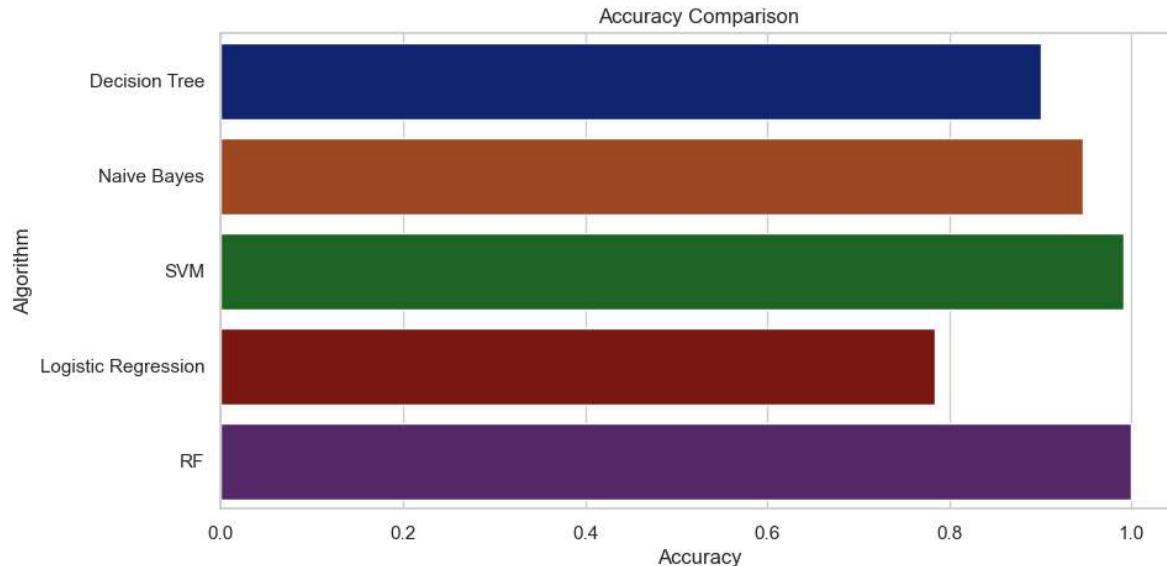
ValueError: Found input variables with inconsistent numbers of samples: [111, 441]

```
In [ ]: 1 from sklearn.model_selection import cross_val_score
2
3 score = cross_val_score(RF,data,data.Fertilizer,cv=5)
4 print("Cross-validation score of RF is:",score)
5 score = cross_val_score(LogReg,data,data.Fertilizer,cv=5)
6 print("Cross-validation score of LogReg is:",score)
7 score = cross_val_score(SVM,data,data.Fertilizer,cv=5)
8 print("Cross-validation score of SVM is:",score)
9 score = cross_val_score(NaiveBayes,data,data.Fertilizer,cv=5)
10 print("Cross-validation score of NaiveBayes is:",score)
11 score = cross_val_score(ds, data, data.Fertilizer,cv=5)
12 print("Cross-validation score of ds is:",score)
```

Cross-validation score of RF is: [1. 1. 1. 1. 1.]
 Cross-validation score of LogReg is: [0.97297297 0.94594595 0.91818182 0.88181818 0.87272727]
 Cross-validation score of SVM is: [0.96396396 0.92792793 0.91818182 0.88181818 0.98181818]
 Cross-validation score of NaiveBayes is: [1. 1. 1. 1. 1.]
 Cross-validation score of ds is: [1. 1. 1. 1. 1.]

```
In [ ]: 1 plt.figure(figsize=[10,5],dpi = 100)
2 plt.title('Accuracy Comparison')
3 plt.xlabel('Accuracy')
4 plt.ylabel('Algorithm')
5 sns.barplot(x = acc,y = model,palette='dark')
```

Out[35]: <Axes: title={'center': 'Accuracy Comparison'}, xlabel='Accuracy', ylabel='Algorithm'>



```
In [ ]: 1 #pickling the file  
2 import pickle  
3 pickle_out = open('classifier.pkl','wb')  
4 pickle.dump(RF,pickle_out)  
5 pickle_out.close()
```

```
In [ ]: 1 model = pickle.load(open('classifier.pkl','rb'))  
2 model.predict([[34,67,62,0,1,7,0,30]])
```

Out[37]: array([6])

```
In [ ]: 1 model = pickle.load(open('classifier.pkl','rb'))  
2 model.predict([[25,78,43,4,1,22,26,38]])
```

Out[38]: array([10])

```
In [ ]: 1 #pickling the file  
2 import pickle  
3 pickle_out = open('fertilizer.pkl','wb')  
4 pickle.dump(encode_ferti,pickle_out)  
5 pickle_out.close()
```

```
In [ ]: 1 ferti = pickle.load(open('fertilizer.pkl','rb'))  
2 ferti.classes_[1]
```

Out[41]: '10-26-26'

```
In [ ]: 1
```

```
In [ ]: 1
```