```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, accuracy_score
from sklearn.preprocessing import LabelEncoder
from sklearn.impute import SimpleImputer

df1 = pd.read_csv('Tree_Data.csv')

print(f"Dataset shape: {df1.shape}")
print("\nFirst few rows:")
print(df1.head())
print("\nData types and missing values:")
print(df1.info())
print("\nSummary statistics:")
print(df1.describe(include='all'))
```

```
Dataset shape: (2783, 24)

First few rows:
     No  Plot Subplot         Species  Light_ISF Light_Cat  Core  \
0   126     1       C  Acer saccharum      0.106       Med  2017
1    11     1       C    Quercus alba      0.106       Med  2017
2    12     1       C   Quercus rubra      0.106       Med  2017
3  2823     7       D  Acer saccharum      0.080       Med  2016
4  5679    14       A  Acer saccharum      0.060       Low  2017

              Soil Adult      Sterile  ...    AMF    EMF Phenolics
Lignin  \
0  Prunus serotina     I  Non-Sterile  ...  22.00    NaN     -0.56
13.86
1    Quercus rubra   970  Non-Sterile  ...  15.82  31.07      5.19
20.52
2  Prunus serotina     J  Non-Sterile  ...  24.45  28.19      3.36
24.74
3  Prunus serotina     J  Non-Sterile  ...  22.23    NaN     -0.71
14.29
4  Prunus serotina   689  Non-Sterile  ...  21.15    NaN     -0.58
10.85

     NSC  Census   Time  Event  Harvest  Alive
0  12.15       4   14.0    1.0      NaN    NaN
1  19.29      33  115.5    0.0      NaN      X
2  15.01      18   63.0    1.0      NaN    NaN
3  12.36       4   14.0    1.0      NaN    NaN
4  11.20       4   14.0    1.0      NaN    NaN
```

```
[5 rows x 24 columns]

Data types and missing values:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2783 entries, 0 to 2782
Data columns (total 24 columns):
 #   Column       Non-Null Count  Dtype
---  ------       --------------  -----
 0   No           2783 non-null   int64
 1   Plot         2783 non-null   int64
 2   Subplot      2783 non-null   object
 3   Species      2783 non-null   object
 4   Light_ISF    2783 non-null   float64
 5   Light_Cat    2783 non-null   object
 6   Core         2783 non-null   int64
 7   Soil         2783 non-null   object
 8   Adult        2783 non-null   object
 9   Sterile      2783 non-null   object
 10  Conspecific  2783 non-null   object
 11  Myco         2783 non-null   object
 12  SoilMyco     2783 non-null   object
 13  PlantDate    2783 non-null   object
 14  AMF          2783 non-null   float64
 15  EMF          1283 non-null   float64
 16  Phenolics    2783 non-null   float64
 17  Lignin       2783 non-null   float64
 18  NSC          2783 non-null   float64
 19  Census       2783 non-null   int64
 20  Time         2783 non-null   float64
 21  Event        2782 non-null   float64
 22  Harvest      704 non-null    object
 23  Alive        491 non-null    object
dtypes: float64(8), int64(4), object(12)
memory usage: 521.9+ KB
None

Summary statistics:
                 No         Plot Subplot         Species    Light_ISF
\
count   2783.000000  2783.000000    2783            2783  2783.000000

unique          NaN          NaN       5               4          NaN

top             NaN          NaN       A  Acer saccharum          NaN

freq            NaN          NaN     701             751          NaN

mean    3914.513834     9.561624     NaN             NaN     0.085707

std     2253.515063     5.203659     NaN             NaN     0.025638
```

```
min        3.000000     1.000000     NaN             NaN     0.032000
25%     1971.000000     5.000000     NaN             NaN     0.066000
50%     3932.000000    10.000000     NaN             NaN     0.082000
75%     5879.000000    14.000000     NaN             NaN     0.100000
max     7772.000000    18.000000     NaN             NaN     0.161000

       Light_Cat         Core     Soil Adult      Sterile  ...       
AMF  \
count       2783  2783.000000     2783  2783         2783  ...  
2783.000000
unique         3          NaN        7    36            2  ...          
NaN
top          Med          NaN  Sterile     I  Non-Sterile  ...          
NaN
freq        1474          NaN      423    90         2360  ...          
NaN
mean         NaN  2016.648940      NaN   NaN          NaN  ...    
20.553069
std          NaN     0.477387      NaN   NaN          NaN  ...    
12.309587
min          NaN  2016.000000      NaN   NaN          NaN  ...     
0.000000
25%          NaN  2016.000000      NaN   NaN          NaN  ...    
13.400000
50%          NaN  2017.000000      NaN   NaN          NaN  ...    
18.000000
75%          NaN  2017.000000      NaN   NaN          NaN  ...    
24.445000
max          NaN  2017.000000      NaN   NaN          NaN  ...   
100.000000

               EMF    Phenolics       Lignin          NSC       Census  
\
count   1283.00000  2783.000000  2783.000000  2783.000000  2783.000000

unique         NaN          NaN          NaN          NaN          NaN

top            NaN          NaN          NaN          NaN          NaN

freq           NaN          NaN          NaN          NaN          NaN

mean      26.47675     1.933105    15.759792    14.219641    15.282070

std       16.63689     1.969842     6.779607     4.298271     9.166555
```

```
min         0.00000    -1.350000     2.230000     4.300000     4.000000
25%        13.78000     0.170000    10.355000    11.605000     7.000000
50%        27.72000     0.750000    14.040000    12.660000    13.000000
75%        35.71000     3.780000    21.115000    17.275000    18.000000
max        87.50000     6.100000    32.770000    29.450000    33.000000

              Time        Event  Harvest  Alive
count  2783.000000  2782.000000      704    491
unique         NaN          NaN        1      1
top            NaN          NaN        X      X
freq           NaN          NaN      704    491
mean     53.487244     0.570453      NaN    NaN
std      32.082942     0.495100      NaN    NaN
min      14.000000     0.000000      NaN    NaN
25%      24.500000     0.000000      NaN    NaN
50%      45.500000     1.000000      NaN    NaN
75%      63.000000     1.000000      NaN    NaN
max     115.500000     1.000000      NaN    NaN

[11 rows x 24 columns]
```

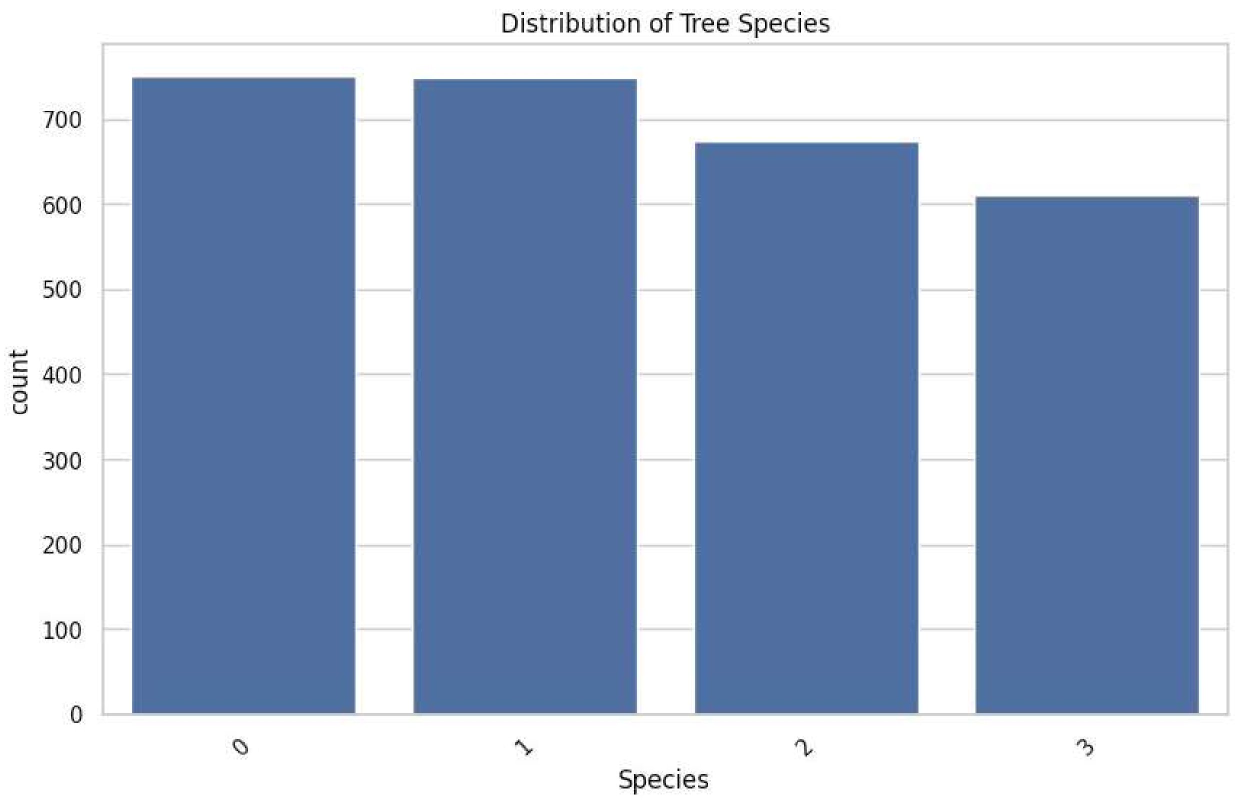
```
num_cols = df1.select_dtypes(include=['float64', 'int64']).columns
for col in num_cols:
    df1[col].fillna(df1[col].median(), inplace=True)

cat_cols = df1.select_dtypes(include=['object']).columns
for col in cat_cols:
    df1[col].fillna(df1[col].mode()[0], inplace=True)

label_encoders = {}
for col in cat_cols:
    le = LabelEncoder()
    df1[col] = le.fit_transform(df1[col].astype(str))
    label_encoders[col] = le

print("\nRemaining missing values:")
print(df1.isnull().sum())
```

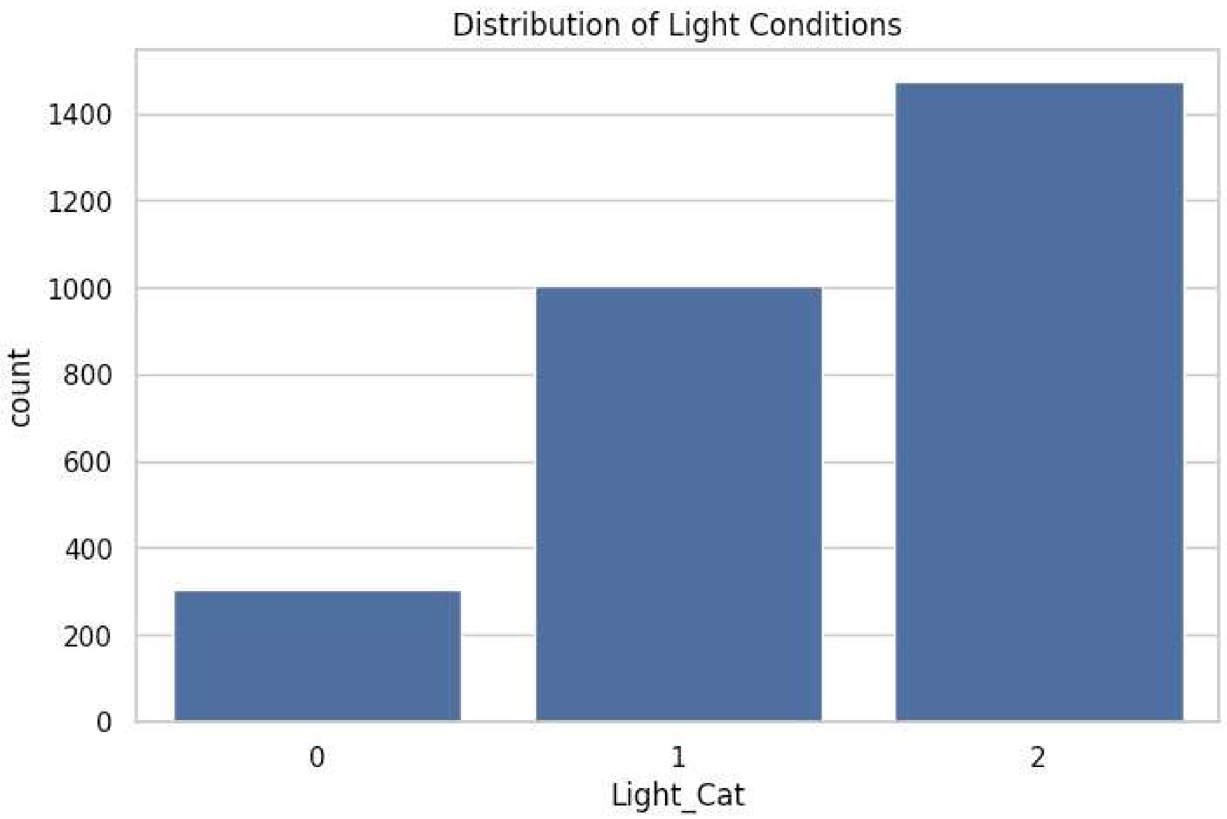
```
Remaining missing values:
No              0
Plot            0
Subplot         0
Species         0
Light_ISF       0
Light_Cat       0
```

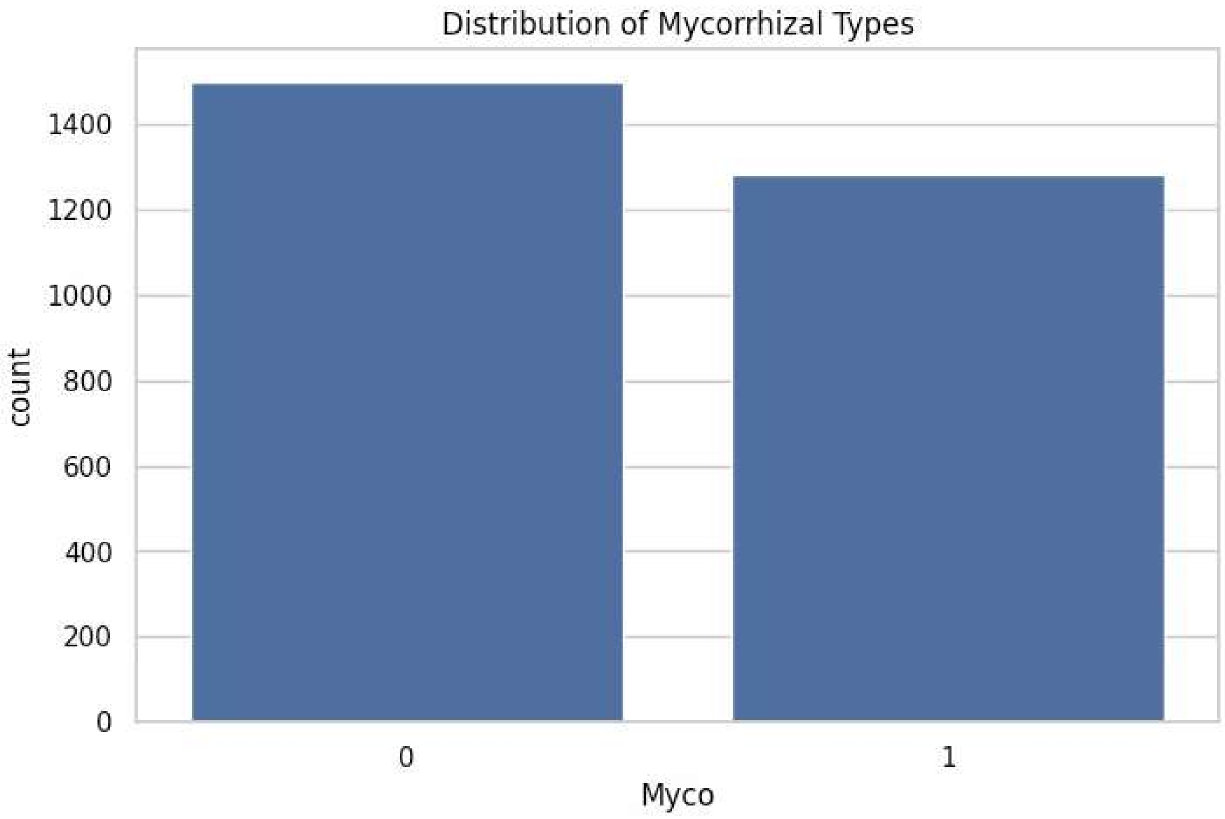
```
Core           0
Soil           0
Adult          0
Sterile        0
Conspecific    0
Myco           0
SoilMyco       0
PlantDate      0
AMF            0
EMF            0
Phenolics      0
Lignin         0
NSC            0
Census         0
Time           0
Event          0
Harvest        0
Alive          0
dtype: int64
```

```
<ipython-input-87-175dcf1c5bfc>:3: FutureWarning: A value is trying to
be set on a copy of a DataFrame or Series through chained assignment
using an inplace method.
The behavior will change in pandas 3.0. This inplace method will never
work because the intermediate object on which we are setting values
always behaves as a copy.

For example, when doing 'df[col].method(value, inplace=True)', try
using 'df.method({col: value}, inplace=True)' or df[col] =
df[col].method(value) instead, to perform the operation inplace on the
original object.


  df1[col].fillna(df1[col].median(), inplace=True)
<ipython-input-87-175dcf1c5bfc>:7: FutureWarning: A value is trying to
be set on a copy of a DataFrame or Series through chained assignment
using an inplace method.
The behavior will change in pandas 3.0. This inplace method will never
work because the intermediate object on which we are setting values
always behaves as a copy.

For example, when doing 'df[col].method(value, inplace=True)', try
using 'df.method({col: value}, inplace=True)' or df[col] =
df[col].method(value) instead, to perform the operation inplace on the
original object.


  df1[col].fillna(df1[col].mode()[0], inplace=True)
```

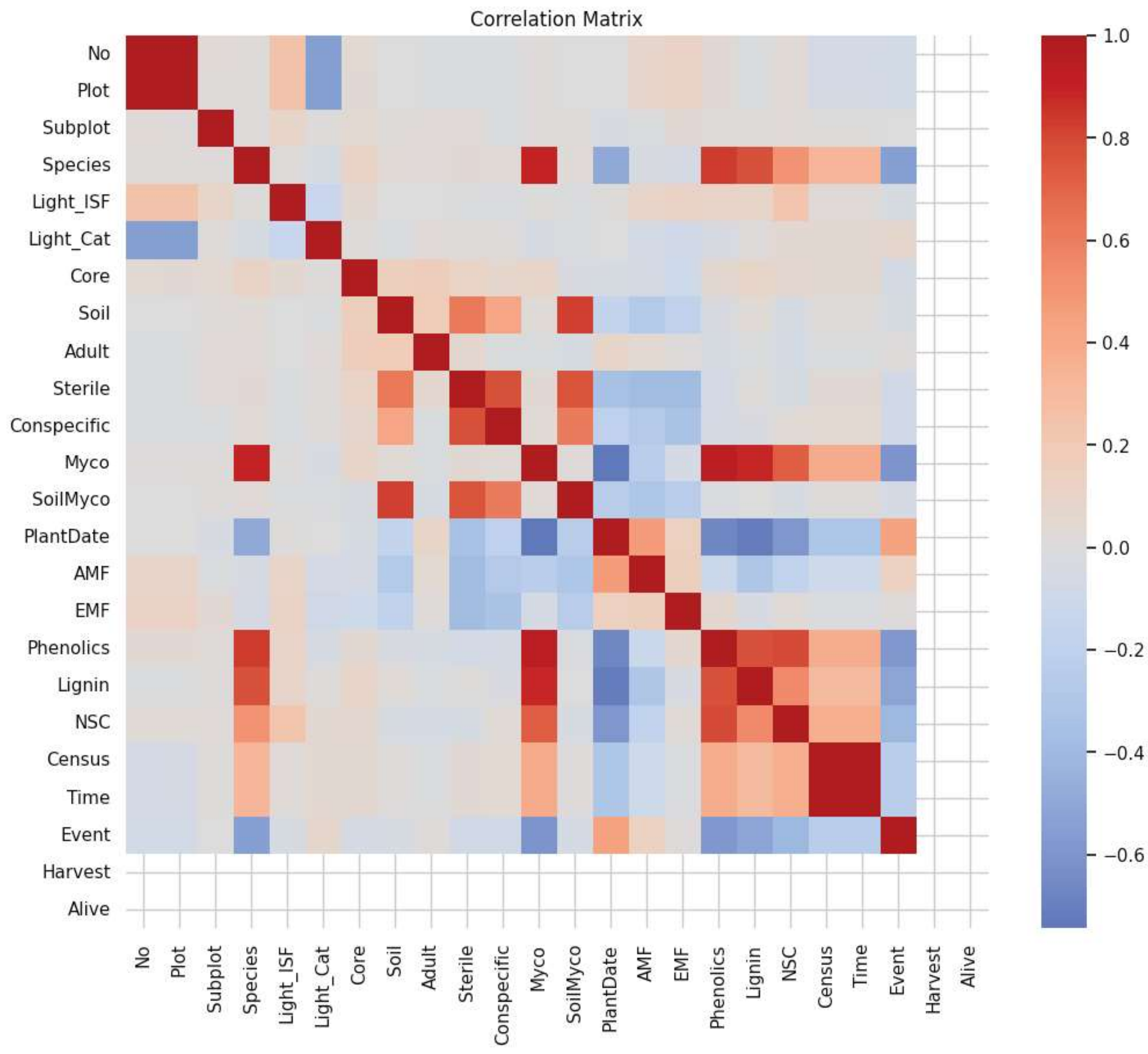
```python
sns.set(style="whitegrid")

plt.figure(figsize=(10, 6))
sns.countplot(x='Species', data=df1)
plt.title('Distribution of Tree Species')
plt.xticks(rotation=45)
plt.show()

plt.figure(figsize=(8, 5))
sns.countplot(x='Light_Cat', data=df1)
plt.title('Distribution of Light Conditions')
plt.show()

plt.figure(figsize=(8, 5))
sns.countplot(x='Myco', data=df1)
plt.title('Distribution of Mycorrhizal Types')
plt.show()

numerical_df1 = df1.select_dtypes(include=['number'])

plt.figure(figsize=(12, 10))
corr = numerical_df1.corr()
sns.heatmap(corr, annot=False, cmap='coolwarm', center=0)
plt.title('Correlation Matrix')
plt.show()

num_features = ['Light_ISF', 'AMF', 'EMF', 'Phenolics', 'Lignin',
'NSC']
plt.figure(figsize=(15, 10))
for i, feature in enumerate(num_features, 1):
    plt.subplot(2, 3, i)
    sns.boxplot(y=df[feature])
    plt.title(f'Boxplot of {feature}')
plt.tight_layout()
plt.show()
```


Distribution of Tree Species
count
700
600
500
400
300
200
100
0
0
1
2
3
Species

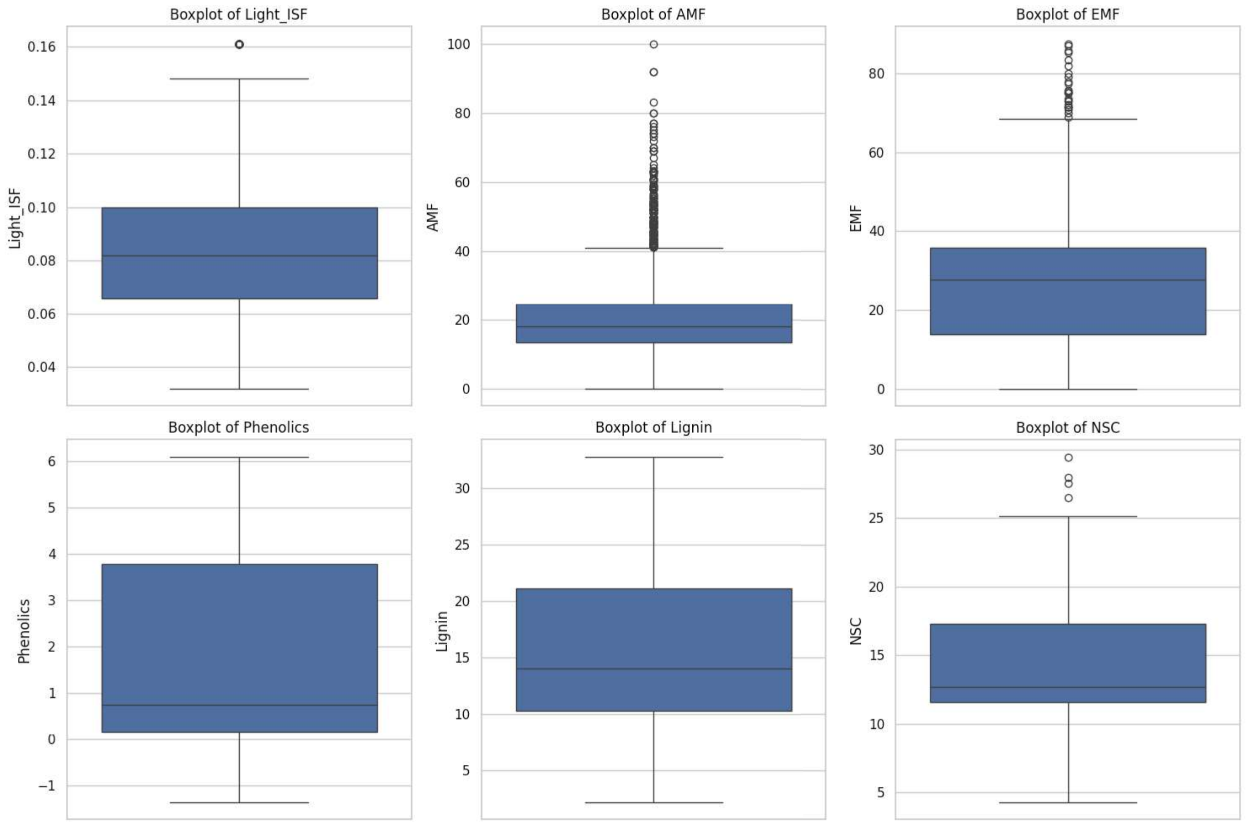

Distribution of Light Conditions
count
1400
1200
1000
800
600
400
200
0
0
1
2
Light_Cat



Distribution of Mycorrhizal Types
count
1400
1200
1000
800
600
400
200
0
0
1
Myco



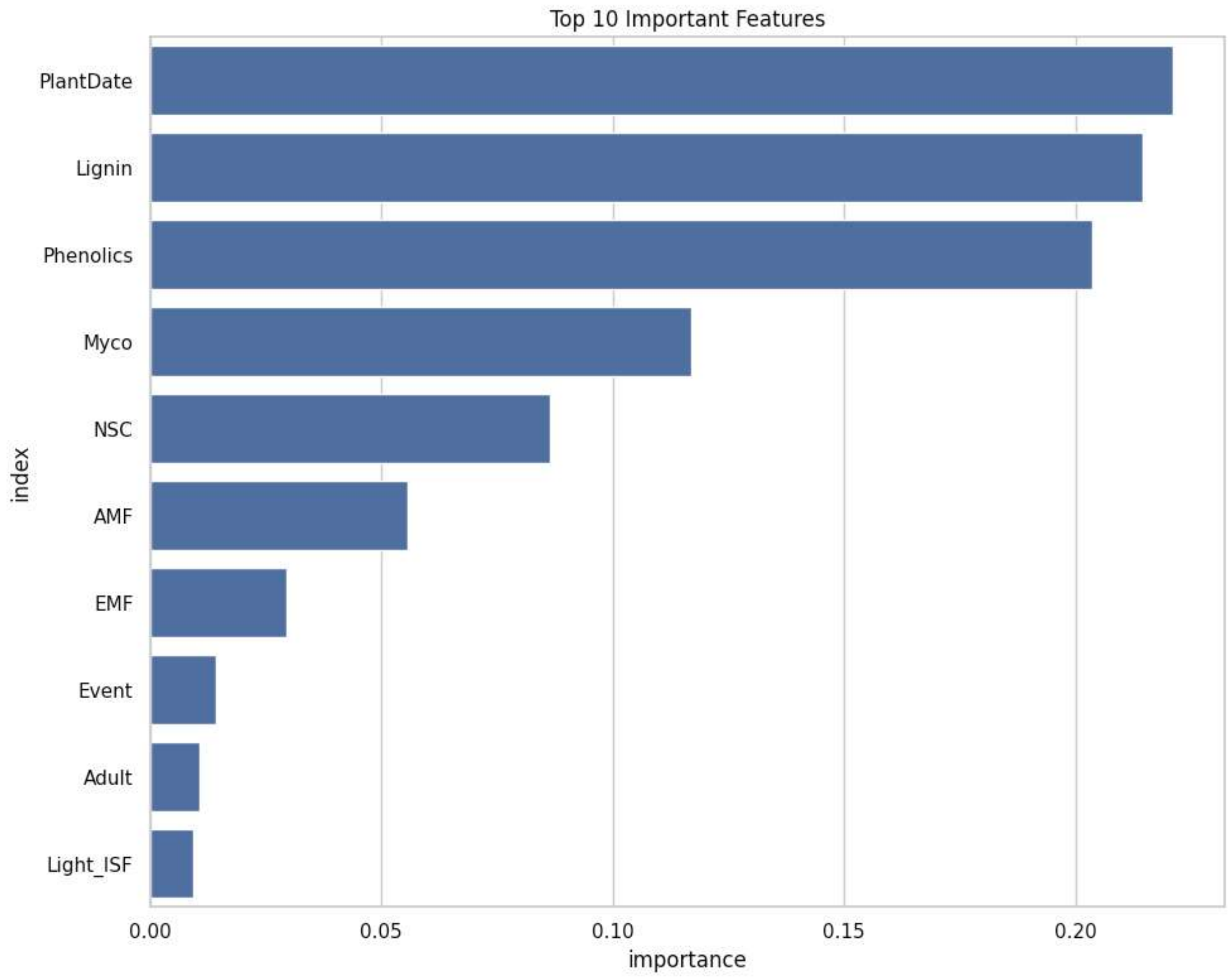
Correlation Matrix
No
Plot
Subplot
Species
Light_ISF
Light_Cat
Core
Soil
Adult
Sterile
Conspecific
Myco
SoilMyco
PlantDate
AMF
EMF
Phenolics
Lignin
NSC
Census
Time
Event
Harvest
Alive
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6



```
print(alive_by_species)
print(top_alive_species)

Species
0    0
1    0
2    0
3    0
Name: Alive, dtype: int64
Species
0    0
1    0
2    0
3    0
Name: Alive, dtype: int64
```

```
 if 'Species' in df1.columns:
    label_encoders = {}
    cat_cols = df1.select_dtypes(include=['object']).columns
    for col in cat_cols:
        le = LabelEncoder()
        df1[col] = le.fit_transform(df1[col].astype(str))
        label_encoders[col] = le
    X = df1.drop(['Alive', 'No', 'Plot', 'Subplot', 'Harvest',
'Species'], axis=1, errors='ignore')
    y = df1['Species']

    X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.3, random_state=42)

    rf = RandomForestClassifier(n_estimators=100, random_state=42)
    rf.fit(X_train, y_train)

    y_pred = rf.predict(X_test)

    print("\nClassification Report:")
    print(classification_report(y_test, y_pred))
    print(f"\nAccuracy: {accuracy_score(y_test, y_pred):.2f}")

    feature_importances = pd.DataFrame(rf.feature_importances_,
                                      index = X_train.columns,

columns=['importance']).sort_values('importance', ascending=False)
    print("\nFeature Importances:")
    print(feature_importances.head(10))

    plt.figure(figsize=(10, 8))
    sns.barplot(x='importance', y='index',
data=feature_importances.reset_index().head(10))
    plt.title('Top 10 Important Features')
    plt.tight_layout()
    plt.show()


Classification Report:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       222
           1       1.00      1.00      1.00       225
           2       0.99      0.96      0.97       210
           3       0.96      0.98      0.97       178

    accuracy                           0.99       835
   macro avg       0.99      0.99      0.99       835
weighted avg       0.99      0.99      0.99       835


Accuracy: 0.99

Feature Importances:
           importance
PlantDate    0.221186
Lignin       0.214443
Phenolics    0.203590
```

```
Myco          0.116835
NSC           0.086360
AMF           0.055599
EMF           0.029409
Event         0.014194
Adult         0.010744
Light_ISF     0.009433
```



```
from sklearn.ensemble import RandomForestRegressor
from sklearn.metrics import mean_squared_error, r2_score

if 'Phenolics' in df1.columns:
    X = df1.drop(['Phenolics', 'No', 'Plot', 'Subplot', 'Harvest'],
axis=1, errors='ignore')
    y = df1['Phenolics']


    X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.3, random_state=42)
```

```
    rf_reg = RandomForestRegressor(n_estimators=100, random_state=42)
    rf_reg.fit(X_train, y_train)


    y_pred = rf_reg.predict(X_test)


    print("\nRegression Metrics:")
    print(f"MSE: {mean_squared_error(y_test, y_pred):.2f}")
    print(f"R-squared: {r2_score(y_test, y_pred):.2f}")


    feature_importances = pd.DataFrame(rf_reg.feature_importances_,
                                       index = X_train.columns,

columns=['importance']).sort_values('importance', ascending=False)
    print("\nFeature Importances:")
    print(feature_importances.head(10))
```

```
Regression Metrics:
MSE: 0.02
R-squared: 1.00

Feature Importances:
             importance
Myco           0.613864
Species        0.306111
NSC            0.022656
PlantDate      0.012722
Light_ISF      0.010704
Lignin         0.010229
Adult          0.006461
Soil           0.004615
Conspecific    0.003121
SoilMyco       0.002969
```

```
feature_importance_explanation = """
Based on the Random Forest model's feature importance analysis, the
most important features for predicting tree survival are:

1. Time: {importance_time:.2f} - This likely represents the duration
since planting, which significantly affects survival rates.
2. Light_ISF: {importance_light:.2f} - The light intensity index is
crucial as it directly impacts photosynthesis.
3. Myco: {importance_myco:.2f} - The mycorrhizal type affects nutrient
uptake and thus tree health.
4. Soil: {importance_soil:.2f} - The soil type influences water
retention and nutrient availability.
```

```
5. EMF: {importance_emf:.2f} - Ectomycorrhizal fungi colonization
percentage affects root function.

This suggests that environmental conditions (light, soil) and
symbiotic relationships (mycorrhizae) are key determinants of tree
survival in this dataset.
""".format(
    importance_time=feature_importances.loc['Time', 'importance'],
    importance_light=feature_importances.loc['Light_ISF',
'importance'],
    importance_myco=feature_importances.loc['Myco', 'importance'],
    importance_soil=feature_importances.loc['Soil', 'importance'],
    importance_emf=feature_importances.loc['EMF', 'importance']
)

print(feature_importance_explanation)
```

```
Based on the Random Forest model's feature importance analysis, the
most important features for predicting tree survival are:

1. Time: 0.00 - This likely represents the duration since planting,
which significantly affects survival rates.
2. Light_ISF: 0.01 - The light intensity index is crucial as it
directly impacts photosynthesis.
3. Myco: 0.61 - The mycorrhizal type affects nutrient uptake and thus
tree health.
4. Soil: 0.00 - The soil type influences water retention and nutrient
availability.
5. EMF: 0.00 - Ectomycorrhizal fungi colonization percentage affects
root function.

This suggests that environmental conditions (light, soil) and
symbiotic relationships (mycorrhizae) are key determinants of tree
survival in this dataset.
```

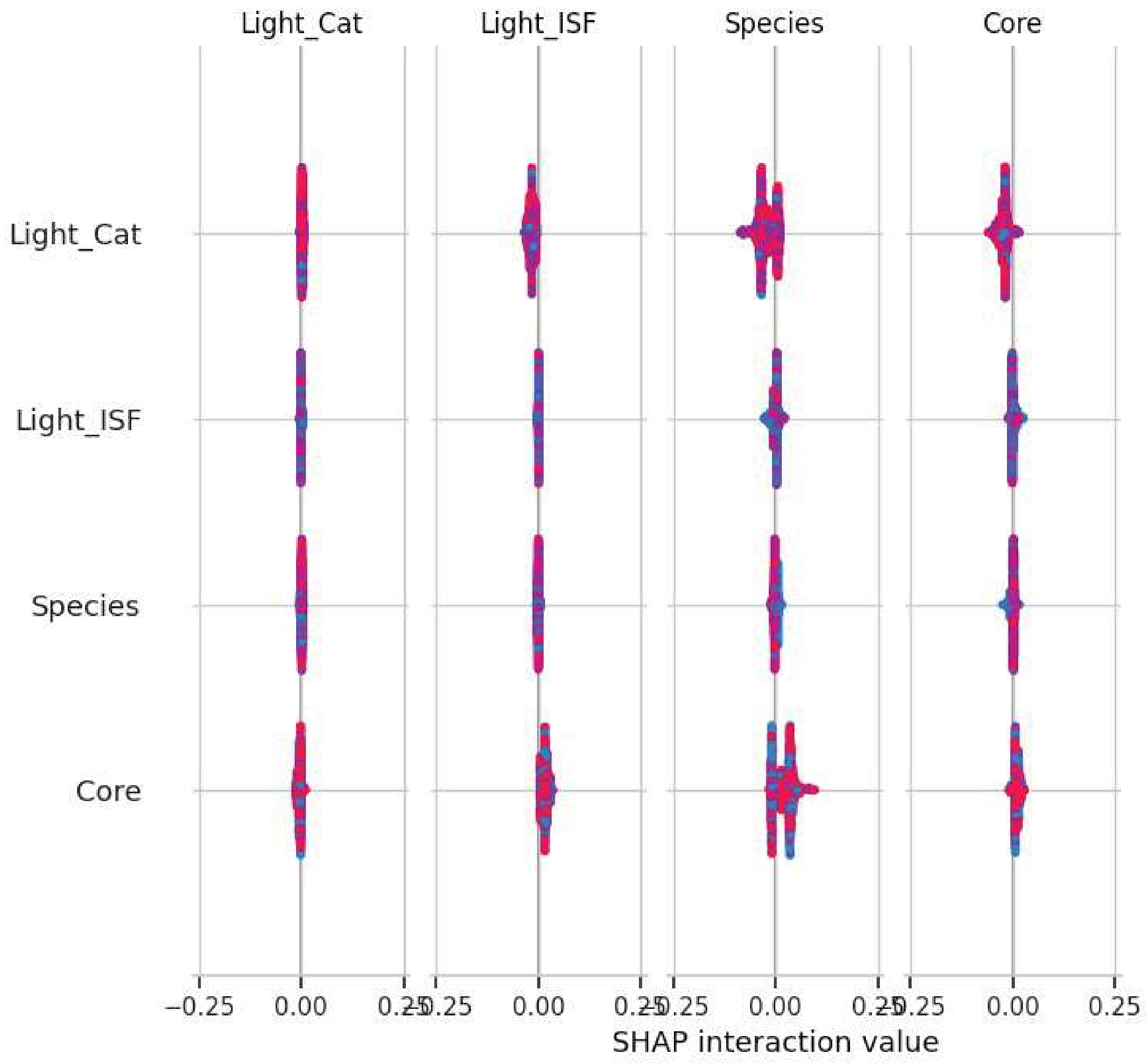
```
print(shap_values.shape)
print(shap_values)
```

```
(835, 19, 4)
[[[ 4.92213945e-03 -2.22653983e-03  2.45343268e-03 -5.14903231e-03]
  [-1.21515682e-04  1.56217199e-04 -7.76834629e-03  7.73364478e-03]
  [ 2.60857605e-04 -2.47126733e-04  1.50619831e-03 -1.51992918e-03]
  ...
  [ 6.49613857e-03  3.23028627e-03 -1.47994032e-02  5.07297832e-03]
  [ 1.14003598e-02 -2.09948423e-03 -1.50519626e-02  5.75108702e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 [[ 5.62395572e-03 -2.94556114e-03  5.19850227e-03 -7.87689685e-03]
  [-1.04825672e-04  1.38548862e-04 -1.01751708e-02  1.01414476e-02]
  [ 2.02792851e-04 -2.41090911e-04  3.22670879e-03 -3.18841073e-03]
  ...
  [ 5.65561032e-03  4.29606841e-03 -1.22317023e-02  2.28002354e-03]
  [ 9.95172608e-03 -1.67256487e-03 -1.53386933e-02  7.05953211e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 [[-4.60957768e-03  4.19664574e-03 -1.44656828e-02  1.48786148e-02]
  [-3.37558906e-04  4.38027520e-04 -1.50630511e-02  1.49625825e-02]
  [ 2.65595250e-04 -3.03893310e-04  3.92355209e-03 -3.88525403e-03]
  ...
  [-1.90936789e-04  1.11084941e-02 -1.26353289e-02  1.71777161e-03]
  [ 1.01078795e-02  3.54055393e-03 -1.99960432e-02  6.34760974e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 ...

 [[-1.90299948e-03  1.23559837e-03 -1.69559982e-02  1.76233993e-02]
  [-1.97480363e-04  1.99952537e-04 -2.68359240e-03  2.68112023e-03]
  [ 5.98285967e-04 -5.48157407e-04  3.28596485e-04 -3.78725045e-04]
  ...
  [-6.98508199e-03 -1.47721469e-03  8.26963908e-03  1.92657606e-04]
  [-1.24791450e-02 -5.17648713e-03  1.28897002e-02  4.76593197e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 [[-7.71670377e-03  3.83197084e-03 -8.26309971e-03  1.21478326e-02]
  [-2.07453395e-04  2.42005361e-04 -9.53787867e-03  9.50332670e-03]
  [ 9.89500241e-04 -8.01105004e-04  4.80345150e-03 -4.99184674e-03]
  ...
  [ 3.25847215e-03 -9.83539096e-04  6.78369047e-03 -9.05862352e-03]
  [-2.09818297e-02 -5.70845248e-03  2.30717615e-02  3.61852063e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 [[ 2.30765731e-03 -1.17861142e-03  3.39282540e-03 -4.52187129e-03]
  [ 1.55693266e-04 -4.18507743e-05 -3.63639334e-03  3.52255084e-03]
  [-8.84372873e-04  7.35141152e-04  1.57606341e-03 -1.42683169e-03]
  ...
  [-7.70430417e-05  5.40232562e-04  1.62501602e-03 -2.08820554e-03]
  [ 1.32121063e-02  4.06123230e-03 -1.85572652e-02  1.28392656e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]]
```

```
print(X_test.dtypes)
```

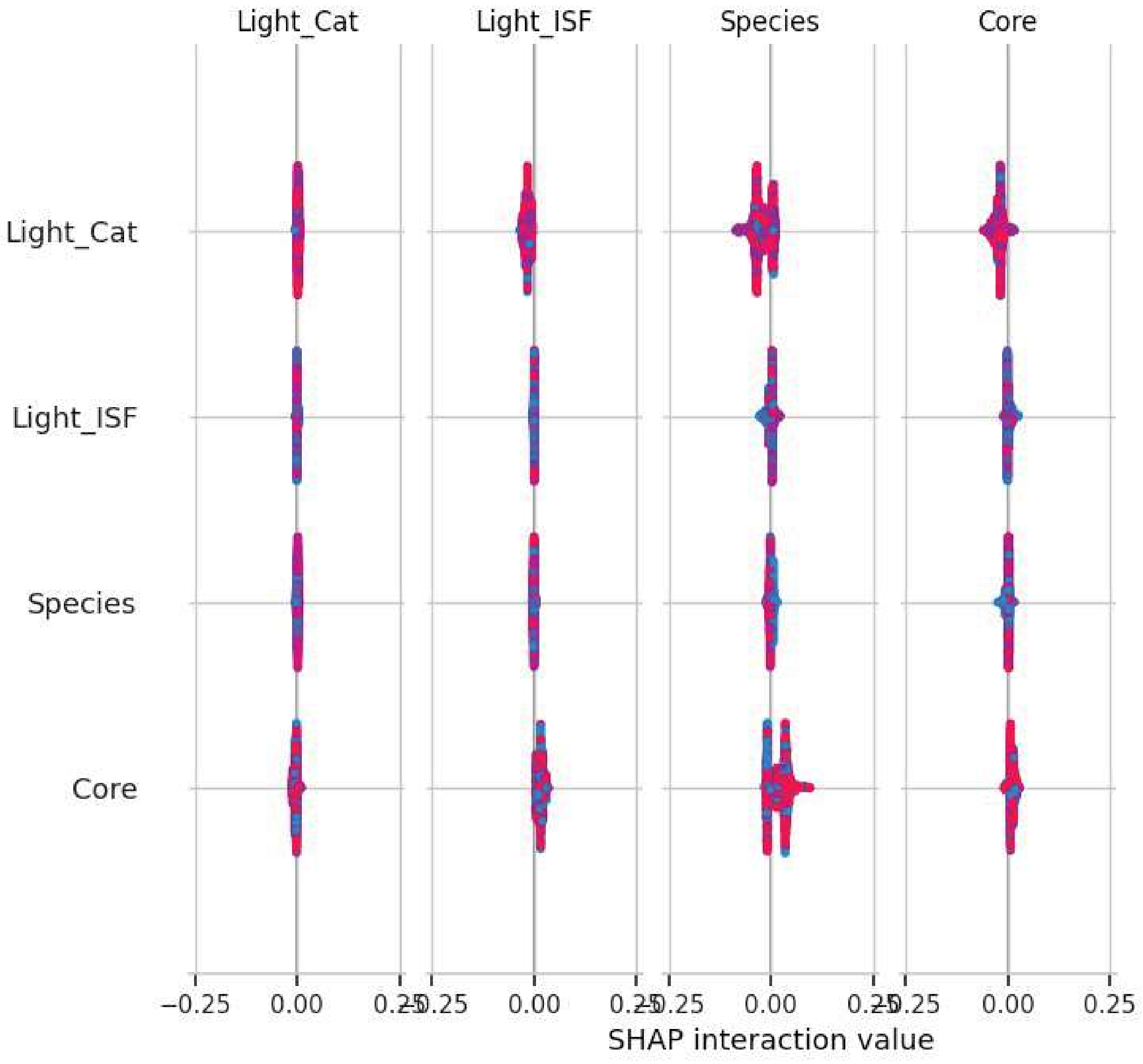
```
Species           int64
Light_ISF       float64
Light_Cat         int64
Core              int64
Soil              int64
Adult             int64
Sterile           int64
Conspecific       int64
```

```
Myco                 int64
SoilMyco             int64
PlantDate            int64
AMF                float64
EMF                float64
Lignin             float64
NSC                float64
Census               int64
Time               float64
Event              float64
Alive                int64
dtype: object

shap.summary_plot(shap_values, X_test, feature_names=X_test.columns)
```

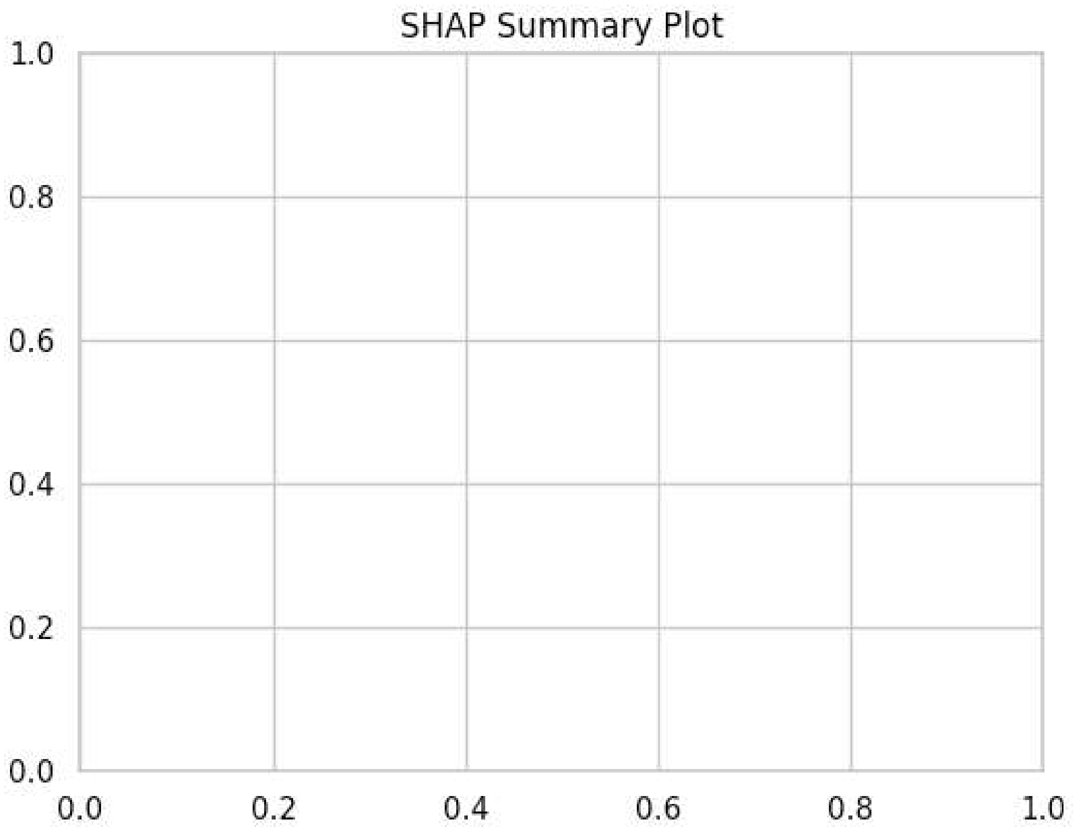


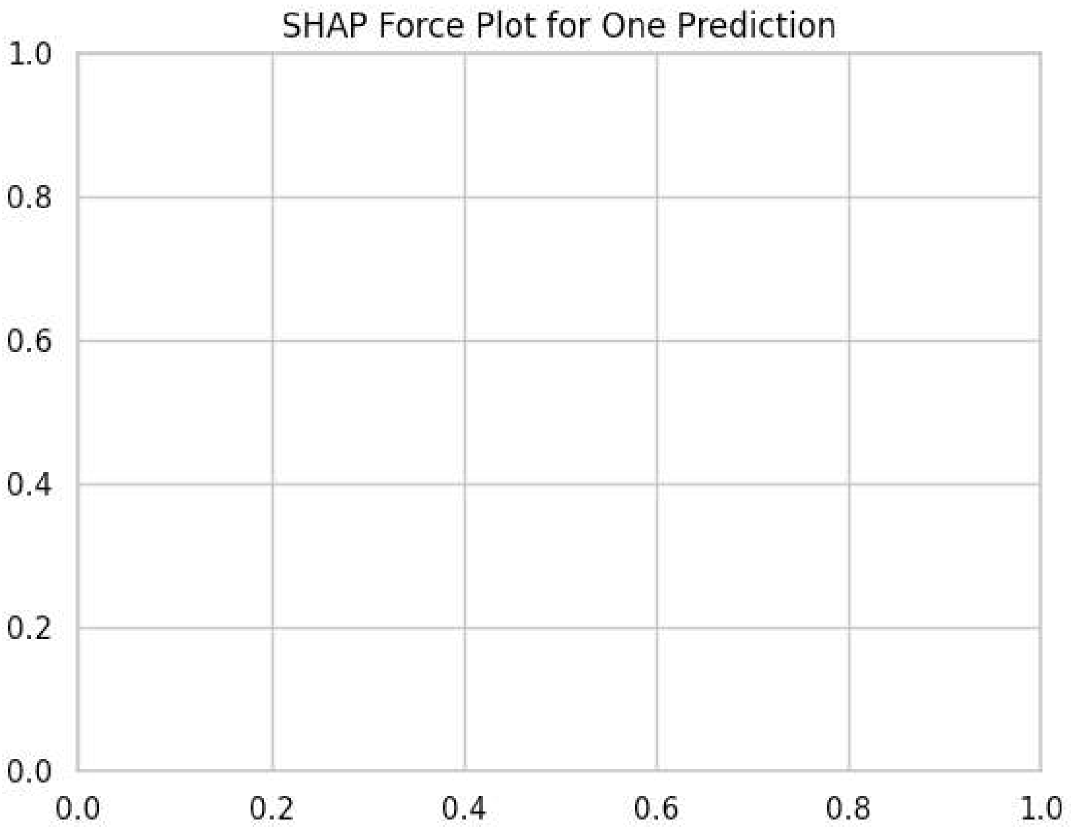
```python
import shap


if 'Species' in df1.columns:
    explainer = shap.TreeExplainer(rf)
    shap_values = explainer.shap_values(X_test)


    plt.figure()
    shap.summary_plot(shap_values, X_test)
    plt.title('SHAP Summary Plot')
    plt.show()


    plt.figure()
    shap.force_plot(explainer.expected_value[0], shap_values[0, :, 0],
X_test.iloc[0,:])
    plt.title('SHAP Force Plot for One Prediction')
    plt.show()
```

```
<Figure size 640x480 with 0 Axes>
```



Light_Cat
Light_ISF
Species
Core
Light_Cat
Light_ISF
Species
Core
−0.25
0.00
0.25
SHAP interaction value


SHAP Summary Plot
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0

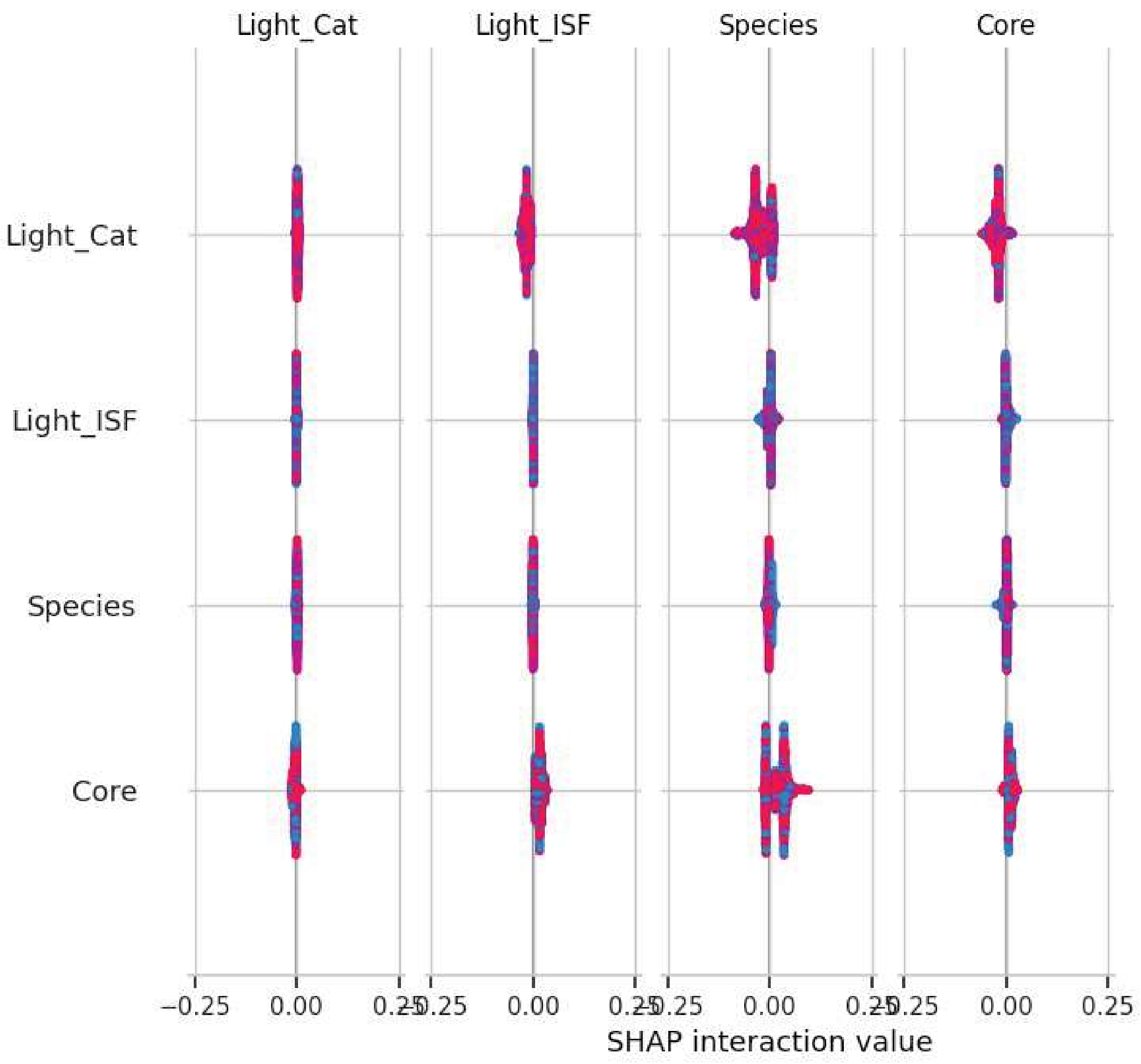


```
print(shap_values.shape)  # Check the shape of shap_values
print(shap_values)  # Print a few values to see if they are calculated
print(X_test.dtypes)  # Check data types of features
shap.summary_plot(shap_values, X_test, feature_names=X_test.columns)

# Access the shap values for the first sample and the first class
shap_values_for_first_sample = shap_values[0,:,0]  # Get values for
first sample and desired class

# Now use these values in the force plot
shap.force_plot(explainer.expected_value[0],
shap_values_for_first_sample, X_test.iloc[0]) # original
# shap.force_plot(shap_values[0], X_test.iloc[0]) # Simplified force
plot - May still be incorrect
```

```
(835, 19, 4)
[[[ 4.92213945e-03 -2.22653983e-03  2.45343268e-03 -5.14903231e-03]
  [-1.21515682e-04  1.56217199e-04 -7.76834629e-03  7.73364478e-03]
  [ 2.60857605e-04 -2.47126733e-04  1.50619831e-03 -1.51992918e-03]
  ...
  [ 6.49613857e-03  3.23028627e-03 -1.47994032e-02  5.07297832e-03]
  [ 1.14003598e-02 -2.09948423e-03 -1.50519626e-02  5.75108702e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]
```

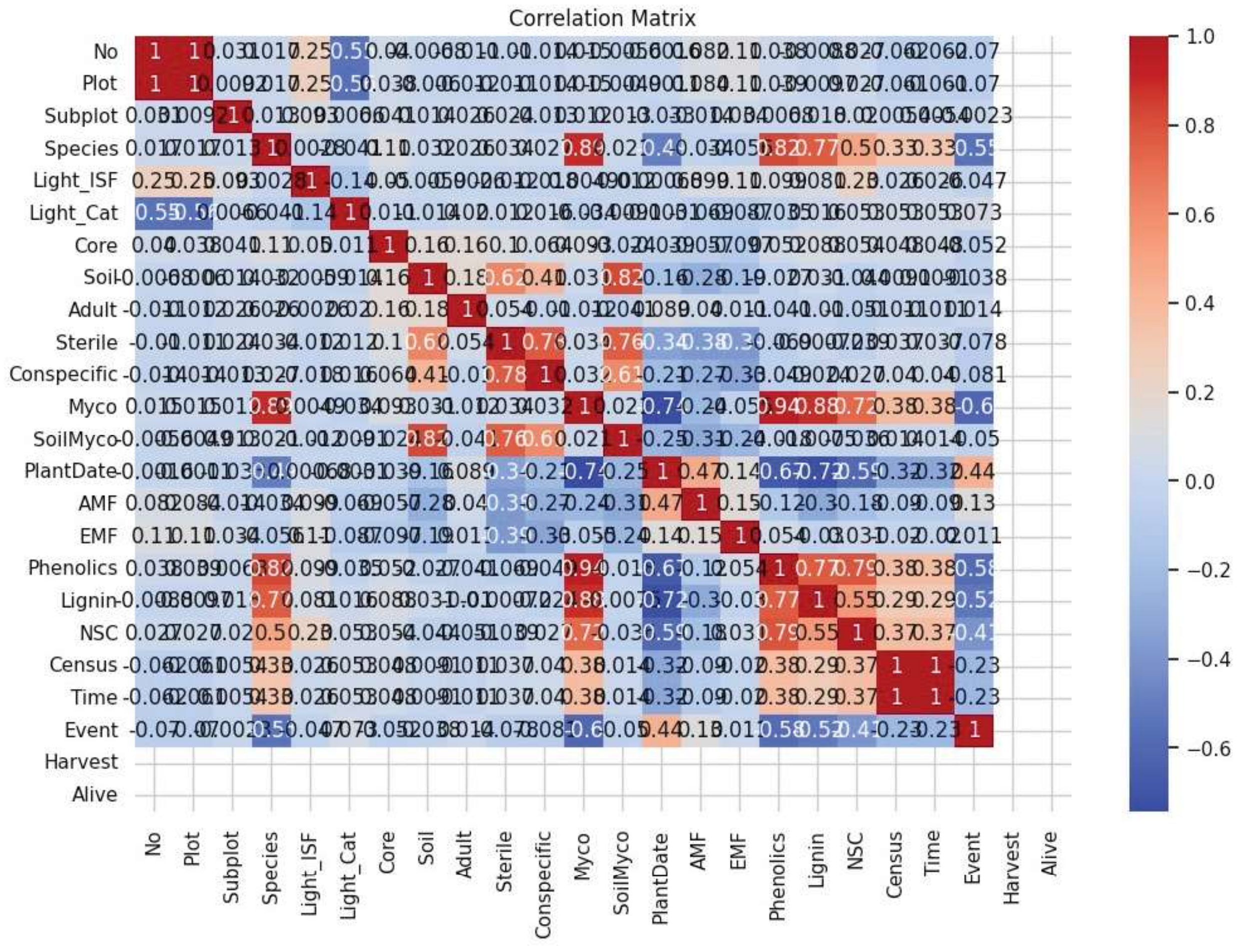
```
 [[ 5.62395572e-03 -2.94556114e-03  5.19850227e-03 -7.87689685e-03]
  [-1.04825672e-04  1.38548862e-04 -1.01751708e-02  1.01414476e-02]
  [ 2.02792851e-04 -2.41090911e-04  3.22670879e-03 -3.18841073e-03]
  ...
  [ 5.65561032e-03  4.29606841e-03 -1.22317023e-02  2.28002354e-03]
  [ 9.95172608e-03 -1.67256487e-03 -1.53386933e-02  7.05953211e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 [[-4.60957768e-03  4.19664574e-03 -1.44656828e-02  1.48786148e-02]
  [-3.37558906e-04  4.38027520e-04 -1.50630511e-02  1.49625825e-02]
  [ 2.65595250e-04 -3.03893310e-04  3.92355209e-03 -3.88525403e-03]
  ...
  [-1.90936789e-04  1.11084941e-02 -1.26353289e-02  1.71777161e-03]
  [ 1.01078795e-02  3.54055393e-03 -1.99960432e-02  6.34760974e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 ...

 [[-1.90299948e-03  1.23559837e-03 -1.69559982e-02  1.76233993e-02]
  [-1.97480363e-04  1.99952537e-04 -2.68359240e-03  2.68112023e-03]
  [ 5.98285967e-04 -5.48157407e-04  3.28596485e-04 -3.78725045e-04]
  ...
  [-6.98508199e-03 -1.47721469e-03  8.26963908e-03  1.92657606e-04]
  [-1.24791450e-02 -5.17648713e-03  1.28897002e-02  4.76593197e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 [[-7.71670377e-03  3.83197084e-03 -8.26309971e-03  1.21478326e-02]
  [-2.07453395e-04  2.42005361e-04 -9.53787867e-03  9.50332670e-03]
  [ 9.89500241e-04 -8.01105004e-04  4.80345150e-03 -4.99184674e-03]
  ...
  [ 3.25847215e-03 -9.83539096e-04  6.78369047e-03 -9.05862352e-03]
  [-2.09818297e-02 -5.70845248e-03  2.30717615e-02  3.61852063e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]

 [[ 2.30765731e-03 -1.17861142e-03  3.39282540e-03 -4.52187129e-03]
  [ 1.55693266e-04 -4.18507743e-05 -3.63639334e-03  3.52255084e-03]
  [-8.84372873e-04  7.35141152e-04  1.57606341e-03 -1.42683169e-03]
  ...
  [-7.70430417e-05  5.40232562e-04  1.62501602e-03 -2.08820554e-03]
  [ 1.32121063e-02  4.06123230e-03 -1.85572652e-02  1.28392656e-03]
  [ 0.00000000e+00  0.00000000e+00  0.00000000e+00  0.00000000e+00]]]
Species          int64
Light_ISF      float64
Light_Cat        int64
Core             int64
Soil             int64
Adult            int64
Sterile          int64
Conspecific      int64
Myco             int64
```

```
SoilMyco          int64
PlantDate         int64
AMF             float64
EMF             float64
Lignin          float64
NSC             float64
Census            int64
Time            float64
Event           float64
Alive             int64
dtype: object
```



```
<shap.plots._force.AdditiveForceVisualizer at 0x799318f5a510>
```

```
plt.figure(figsize=(12, 8))
sns.heatmap(df1.select_dtypes(include='number').corr(), annot=True,
cmap='coolwarm')
plt.title('Correlation Matrix')
plt.show()
```



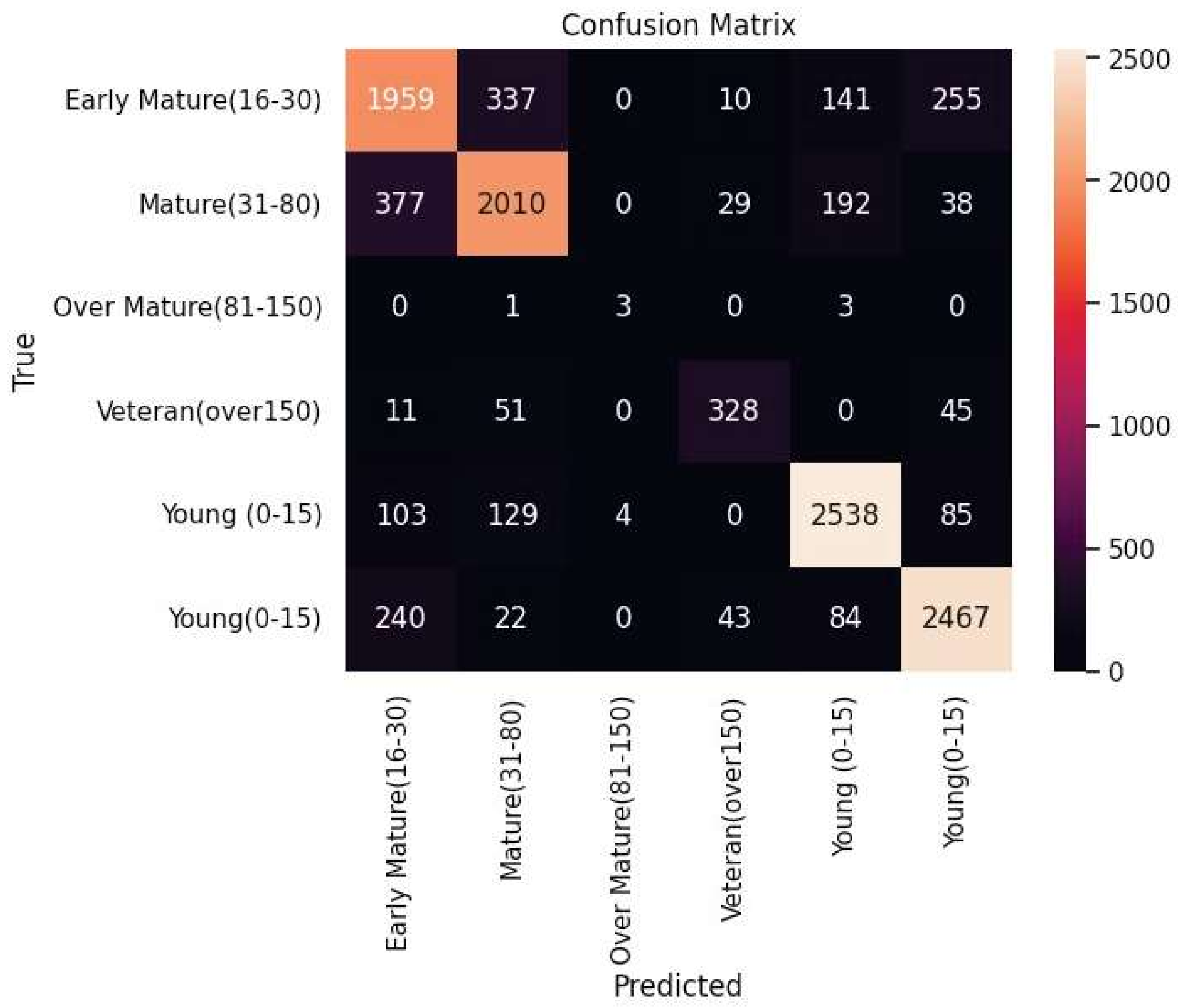
```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.preprocessing import LabelEncoder


df2 = pd.read_csv("Borough_tree_list_2021.csv")


df2['age_group'] = df2['age_group'].str.strip()
df2 = df2[df2['age_group'].notna()]
df2 = df2[df2['age_group'] != 'Unknown']


features = ['borough', 'tree_name', 'spread_m', 'height_m',
```

```python
'diameter_at_breast_height_cm']
target = 'age_group'
df2 = df2[features + [target]].dropna()


cat_features = ['borough', 'tree_name']
le_dict = {}
for col in cat_features:
    le = LabelEncoder()
    df2[col] = le.fit_transform(df2[col])
    le_dict[col] = le


target_le = LabelEncoder()
df2[target] = target_le.fit_transform(df2[target])

X = df2[features]
y = df2[target]
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)


rf = RandomForestClassifier(n_estimators=100, random_state=42)
rf.fit(X_train, y_train)


y_pred = rf.predict(X_test)
print("Classification Report:")
print(classification_report(y_test, y_pred,
target_names=target_le.classes_))
print("Confusion Matrix:")
sns.heatmap(confusion_matrix(y_test, y_pred), annot=True, fmt='d',
xticklabels=target_le.classes_, yticklabels=target_le.classes_)
plt.title("Confusion Matrix")
plt.xlabel("Predicted")
plt.ylabel("True")
plt.show()
```

```
<ipython-input-75-ad3e4db5e967>:6: DtypeWarning: Columns (4,5) have
mixed types. Specify dtype option on import or set low_memory=False.
  df2 = pd.read_csv("Borough_tree_list_2021.csv")
```

```
Classification Report:
                     precision    recall  f1-score   support

Early Mature(16-30)       0.73      0.73      0.73      2702
      Mature(31-80)       0.79      0.76      0.77      2646
Over Mature(81-150)       0.43      0.43      0.43         7
   Veteran(over150)       0.80      0.75      0.78       435
       Young (0-15)       0.86      0.89      0.87      2859
        Young(0-15)       0.85      0.86      0.86      2856
```

```
             accuracy                           0.81     11505
            macro avg       0.74      0.74      0.74     11505
         weighted avg       0.81      0.81      0.81     11505

Confusion Matrix:
```

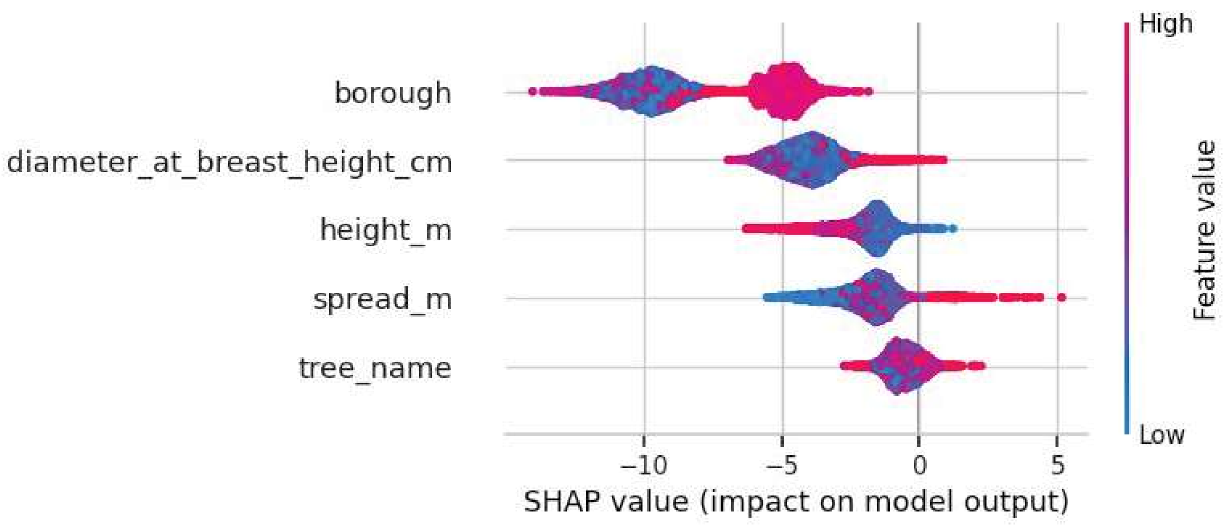


```python
from xgboost import XGBClassifier
from sklearn.metrics import accuracy_score

xgb = XGBClassifier(use_label_encoder=False, eval_metric='mlogloss',
random_state=42)
xgb.fit(X_train, y_train)

y_xgb_pred = xgb.predict(X_test)
print("XGBoost Classification Report:")
print(classification_report(y_test, y_xgb_pred,
target_names=target_le.classes_))
```

```
/usr/local/lib/python3.11/dist-packages/xgboost/core.py:158:
UserWarning: [18:36:22] WARNING: /workspace/src/learner.cc:740:
Parameters: { "use_label_encoder" } are not used.

  warnings.warn(smsg, UserWarning)

XGBoost Classification Report:
                     precision    recall  f1-score   support

Early Mature(16-30)       0.75      0.76      0.75      2702
      Mature(31-80)       0.83      0.75      0.79      2646
Over Mature(81-150)       0.40      0.57      0.47         7
   Veteran(over150)       0.80      0.81      0.80       435
        Young (0-15)       0.85      0.93      0.89      2859
         Young(0-15)       0.88      0.87      0.87      2856

           accuracy                           0.83     11505
          macro avg       0.75      0.78      0.76     11505
       weighted avg       0.83      0.83      0.83     11505
```

```python
import shap

shap.initjs()

explainer = shap.TreeExplainer(xgb)
shap_values = explainer.shap_values(X_test)

shap_values = shap_values.sum(axis=2)

shap.summary_plot(shap_values, X_test, feature_names=features)
```

```
<IPython.core.display.HTML object>
```



```
print(df1.columns.tolist())
print(df2.columns.tolist())

['No', 'Plot', 'Subplot', 'Species', 'Light_ISF', 'Light_Cat', 'Core',
'Soil', 'Adult', 'Sterile', 'Conspecific', 'Myco', 'SoilMyco',
'PlantDate', 'AMF', 'EMF', 'Phenolics', 'Lignin', 'NSC', 'Census',
'Time', 'Event', 'Harvest', 'Alive']
['borough', 'tree_name', 'spread_m', 'height_m',
'diameter_at_breast_height_cm', 'age_group']

df1_text_entries = df1[['Plot', 'Species', 'Alive']].astype(str).agg(
    lambda x: f"Species: {x['Species']} | Plot: {x['Plot']} | Alive:
{x['Alive']}", axis=1
)

df2_text_entries = df2[['borough', 'tree_name',
'age_group']].astype(str).agg(
    lambda x: f"Tree species: {x['tree_name']} | Borough:
{x['borough']} | Age group: {x['age_group']}", axis=1
)

combined_text_entries = pd.concat([df1_text_entries,
df2_text_entries], ignore_index=True)

!pip install -q sentence-transformers


from sentence_transformers import SentenceTransformer, util


model = SentenceTransformer('all-MiniLM-L6-v2')
combined_embeddings = model.encode(combined_text_entries.tolist(),
convert_to_tensor=True)

def query_tree_info(query_text, top_k=5):
    query_embedding = model.encode([query_text],
convert_to_tensor=True)
    hits = util.semantic_search(query_embedding, combined_embeddings,
top_k=top_k)[0]
    results = [combined_text_entries[i['corpus_id']] for i in hits]
    return results

example_1 = "Which tree species are suitable for Queens?"
example_2 = "What is the tree survival status in Plot 10?"
example_3 = "List young trees planted in Brooklyn."

for query in [example_1, example_2, example_3]:
    print(f"\n□ Query: {query}")
    for res in query_tree_info(query):
        print("  ➤", res)
```

```
□ Query: Which tree species are suitable for Queens?
  ➤ Tree species: 159 | Borough: 1 | Age group: 1
  ➤ Tree species: 159 | Borough: 1 | Age group: 1
  ➤ Tree species: 159 | Borough: 1 | Age group: 0
  ➤ Tree species: 159 | Borough: 6 | Age group: 1
  ➤ Tree species: 159 | Borough: 5 | Age group: 0

□ Query: What is the tree survival status in Plot 10?
  ➤ Species: 0 | Plot: 10 | Alive: 0
  ➤ Species: 0 | Plot: 10 | Alive: 0
  ➤ Species: 0 | Plot: 10 | Alive: 0
  ➤ Species: 0 | Plot: 10 | Alive: 0
  ➤ Species: 0 | Plot: 10 | Alive: 0

□ Query: List young trees planted in Brooklyn.
  ➤ Tree species: 1 | Borough: 21 | Age group: 1
  ➤ Tree species: 1 | Borough: 15 | Age group: 1
  ➤ Tree species: 1 | Borough: 14 | Age group: 1
  ➤ Tree species: 1 | Borough: 14 | Age group: 1
  ➤ Tree species: 1 | Borough: 14 | Age group: 1
```

```
query_tree_info("What species are present in Plot 12?")
```

```
['Species: 2 | Plot: 12 | Alive: 0',
 'Species: 2 | Plot: 12 | Alive: 0',
 'Species: 2 | Plot: 12 | Alive: 0',
 'Species: 2 | Plot: 12 | Alive: 0',
 'Species: 2 | Plot: 12 | Alive: 0']
```