Feature preprocessing, CatBoost and Model Interpretability

In [1]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.preprocessing import LabelEncoder, MinMaxScaler, OneHotEr
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score, roc_curve, auc, classifica
from sklearn.metrics import ConfusionMatrixDisplay
from sklearn import tree
from sklearn.model_selection import cross_val_score, cross_validate
import imblearn
from imblearn.over_sampling import SMOTE, SMOTENC
from imblearn.pipeline import Pipeline
from sklearn.ensemble import RandomForestClassifier
from sklearn.compose import ColumnTransformer, make_column_selector
from sklearn.impute import SimpleImputer
from sklearn.model_selection import GridSearchCV
from sklearn.tree import export_text, plot_tree
from sklearn.base import BaseEstimator, TransformerMixin
from sklearn.preprocessing import FunctionTransformer
from sklearn.decomposition import PCA
from sklearn.linear_model import LinearRegression, Ridge, Lasso
from sklearn.ensemble import RandomForestRegressor
from sklearn.model_selection import GridSearchCV
from sklearn.compose import TransformedTargetRegressor
from sklearn.feature_selection import VarianceThreshold
from lime.lime_tabular import LimeTabularExplainer
from scipy.stats.mstats import winsorize
from sklearn.preprocessing import StandardScaler
from catboost import CatBoostRegressor
from sklearn.metrics import mean_absolute_error, mean_squared_error, r
import shap
```

In [2]:
```
# to show all columns
pd.set_option('display.max_columns', None) # to revert: pd.reset_optic
```

In [3]:
```
df = pd.read_csv("data/Train.csv", index_col=0)
df.head()
```

Out[3]:

ID	District	Block	CultLand	CropCultLand	LandPreparationMethod	Cro
ID_GTFAC7PEVWQ9	Nalanda	Noorsarai	45	40	TractorPlough FourWheelTracRotavator	
ID_TK40ARLSPOKS	Nalanda	Rajgir	26	26	WetTillagePuddling TractorPlough FourWheelTrac...	
ID_1FJY2CRIMLZZ	Gaya	Gurua	10	10	TractorPlough FourWheelTracRotavator	
ID_I3IPXS4DB7NE	Gaya	Gurua	15	15	TractorPlough FourWheelTracRotavator	
ID_4T8YQWXWHB4A	Nalanda	Noorsarai	60	60	TractorPlough WetTillagePuddling	

Let's calculate the yield per acre as a better measure of crop yield.

In [4]:
```
df['yield_per_acre'] = df['Yield'] / df['Acre']
df.head()
```

Out[4]:

	District	Block	CultLand	CropCultLand	LandPreparationMethod	Cro
ID						
ID_GTFAC7PEVWQ9	Nalanda	Noorsarai	45	40	TractorPlough FourWheelTracRotavator	
ID_TK40ARLSPOKS	Nalanda	Rajgir	26	26	WetTillagePuddling TractorPlough FourWheelTrac...	
ID_1FJY2CRIMLZZ	Gaya	Gurua	10	10	TractorPlough FourWheelTracRotavator	
ID_I3IPXS4DB7NE	Gaya	Gurua	15	15	TractorPlough FourWheelTracRotavator	
ID_4T8YQWXWHB4A	Nalanda	Noorsarai	60	60	TractorPlough WetTillagePuddling	

In [5]:
```
# Drop the index column
df = df.reset_index(drop=True)
```

Let's remove outliers in "Yield" in the 99th percentile

In [6]:
```
# Calculate the 99th percentile threshold for 'yield_per_acre'
yield_per_acre_threshold = df['yield_per_acre'].quantile(0.99)

# Filter out rows where 'yield_per_acre' is above the 99th percentile
df_under99 = df[df['yield_per_acre'] <= yield_per_acre_threshold]
df_under99.head()
```

Out[6]:

	District	Block	CultLand	CropCultLand	LandPreparationMethod	CropTillageDate	CropT
0	Nalanda	Noorsarai	45	40	TractorPlough FourWheelTracRotavator	2022-07-20	
1	Nalanda	Rajgir	26	26	WetTillagePuddling TractorPlough FourWheelTrac...	2022-07-18	
2	Gaya	Gurua	10	10	TractorPlough FourWheelTracRotavator	2022-06-30	
3	Gaya	Gurua	15	15	TractorPlough FourWheelTracRotavator	2022-06-16	
4	Nalanda	Noorsarai	60	60	TractorPlough WetTillagePuddling	2022-07-19	

Now we can split the data into training and testing subsets.

In [7]:
```
X = df_under99.drop(['Yield', 'yield_per_acre'], axis=1)  # Features
y = df_under99['yield_per_acre']                           # Target

# Split the data into training and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.
```

Data preprocessing

CatBoost requires minimal data preprocessing and can handle numeric and categorical features and missing values. We'll set up pipeline to convert all features to numeric for futher use of LIME.

Custom Transformer to drop the CultLand column

In [8]:
```
class DropCultLandTransformer(BaseEstimator, TransformerMixin):
    def fit(self, X, y=None):
        return self

    def transform(self, X):
        return X.drop(columns=['CultLand'], errors='ignore')  # Drop C
```

Let's extract month and day values for all date features. We don't need the year sinse the data represents 2022 season.

In [9]:
```
class DateFeatureExtractorWithScaling(BaseEstimator, TransformerMixin)
    def __init__(self, date_columns, column_to_impute_median=None):
        self.date_columns = date_columns
        self.column_to_impute_median = column_to_impute_median
        self.median_date = None
        self.scaler = StandardScaler()  # Initialize the scaler

    def fit(self, X, y=None):
        # Calculate the median date for the specified column
        if self.column_to_impute_median:
            self.median_date = pd.to_datetime(X[self.column_to_impute_

        # Fit the scaler on month and day columns after extracting the
        temp_X = self.transform(X.copy(), scale=False)  # Extract feat
        self.scaler.fit(temp_X.filter(regex='_(month|day)$'))  # Fit s
        return self

    def transform(self, X, scale=True):
        # Work on a copy of X to avoid modifying the original data
        X = X.copy()

        # Impute the specified date column with the median date if app
        if self.column_to_impute_median and self.median_date is not No
            X[self.column_to_impute_median] = pd.to_datetime(X[self.co

        # Loop through each date column to convert and extract feature
        for col in self.date_columns:
            # Ensure the column is in datetime format
            X[col] = pd.to_datetime(X[col], errors='coerce')

            # Extract month and day components
            X[f'{col}_month'] = X[col].dt.month
            X[f'{col}_day'] = X[col].dt.day

        # Drop the original date columns
```

```
        X = X.drop(columns=self.date_columns)

        # Apply scaling to the extracted month and day columns
        if scale:
            month_day_columns = X.filter(regex='_(month|day)$').columr
            X[month_day_columns] = self.scaler.transform(X[month_day_c

        return X

# Instantiate the custom transformer with median imputation for 'RcNur
date_feature_extractor = DateFeatureExtractorWithScaling(
    date_columns=['CropTillageDate', 'RcNursEstDate', 'SeedingSowingTr
    column_to_impute_median='RcNursEstDate'
)
```

Custom Transformer for Imputation and Capping Outliers for Numeric attributes

In [10]:

```
# Fill missing values with the median, cap values at 99 percentile to
# Fill missing values with the median OR
# Fill missing values with 0, cap values at 99 percentile

# Define the columns for each transformation
columns_to_impute_and_cap = ['SeedlingsPerPit', 'TransplantingIrrigati
                             'CropCultLand','Acre']
columns_to_impute_only = ['StandingWater', 'BasalDAP', 'BasalUrea', 'H
columns_to_impute_with_zero_and_cap = ['Ganaura', 'CropOrgFYM', '1tdUr


class ImputeAndCapOutliers(BaseEstimator, TransformerMixin):
    def __init__(self, columns_to_impute_and_cap, columns_to_impute_or
        self.columns_to_impute_and_cap = columns_to_impute_and_cap
        self.columns_to_impute_only = columns_to_impute_only
        self.columns_to_impute_with_zero_and_cap = columns_to_impute_w
        self.medians = {}
        self.percentile_99 = {}

    def fit(self, X, y=None):
        # Calculate the median and 95th percentile for each column to
        for col in self.columns_to_impute_and_cap:
            self.medians[col] = X[col].median()
            self.percentile_99[col] = X[col].quantile(0.99)

        # Calculate the median for each column to impute only
        for col in self.columns_to_impute_only:
            self.medians[col] = X[col].median()

        # Calculate the 99th percentile for columns to impute with zer
```

```
        for col in self.columns_to_impute_with_zero_and_cap:
            self.percentile_99[col] = X[col].quantile(0.99)

        return self

    def transform(self, X):
        # Work on a copy of X to avoid modifying the original data
        X = X.copy()

        # Impute and cap outliers for specified columns
        for col in self.columns_to_impute_and_cap:
            # Impute missing values with the median
            X[col] = X[col].fillna(self.medians[col])
            # Cap values above the 99th percentile
            X[col] = np.where(X[col] > self.percentile_99[col], self.p

        # Impute only with median for each specified column in columns
        for col in self.columns_to_impute_only:
            X[col] = X[col].fillna(self.medians[col])

        # Impute with zero and cap values for the specified columns
        for col in self.columns_to_impute_with_zero_and_cap:
            X[col] = X[col].fillna(0)
            X[col] = np.where(X[col] > self.percentile_99[col], self.p

        return X
```

Let's process '2tdUrea', '2appDaysUrea' features separartely

In [11]:
```
# If NoFertilizerAppln equals 3 or 4 and there is a value for 2tdUrea,
# otherwise, replace missing values for 2tdUrea and 2appDaysUrea with

# Define columns and conditions for the custom transformer
columns_to_impute = ['2tdUrea', '2appDaysUrea']
condition_column = 'NoFertilizerAppln'
condition_values = [3, 4]

class ConditionalImputeUrea(BaseEstimator, TransformerMixin):
    def __init__(self, columns, condition_column, condition_values):
        self.columns = columns
        self.condition_column = condition_column
        self.condition_values = condition_values
        self.median_values = {}

    def fit(self, X, y=None):
        # Calculate the median for each column to be used for conditic
        for col in self.columns:
            self.median_values[col] = X[col].median()
        return self

    def transform(self, X):
        X = X.copy()

        # Apply conditional imputation
        for col in self.columns:
            if col == '2appDaysUrea':
                # Condition for NoFertilizerAppln in specified values
                condition = (X[self.condition_column].isin(self.condit
                # Impute missing values in 2appDaysUrea with median if
                X.loc[condition & X['2appDaysUrea'].isna(), '2appDaysU

            # For cases not meeting the condition, replace missing val
            X[col] = X[col].fillna(0)

        return X

# Instantiate the custom transformer
conditional_impute_urea = ConditionalImputeUrea(
    columns=columns_to_impute,
    condition_column=condition_column,
    condition_values=condition_values
)
```

For categorical features, let's replace missing values should be replaced with 'Unknown'

In [12]:
```
# Define the columns where missing values should be replaced with 'Unk
columns_to_impute_with_unknown = ['NursDetFactor', 'TransDetFactor', '
                                  'TransplantingIrrigationPowerSource'
                                  'OrgFertilizers', 'PCropSolidOrgFert
                                  'FirstTopDressFert', 'MineralFertApp

# Define the custom transformer for filling missing values with 'Unkno
class FillMissingWithUnknown(BaseEstimator, TransformerMixin):
    def __init__(self, columns, fill_value='Unknown'):
        self.columns = columns
        self.fill_value = fill_value

    def fit(self, X, y=None):
        return self

    def transform(self, X):
        X = X.copy()
        for col in self.columns:
            X[col] = X[col].fillna(self.fill_value)
        return X
```

For some categorical features, each value is a space separated list. Let's extract those as separate features.

In [13]:
```
# Let's create a binary (0/1) indicator column for each unique value

# usage in a pipeline for multiple columns
columns_to_binarize = ['LandPreparationMethod', 'NursDetFactor', 'Tran
                       'CropbasalFerts', 'FirstTopDressFert']

class MultiColumnMultiLabelBinarizer(BaseEstimator, TransformerMixin):
    def __init__(self, columns):
        self.columns = columns
        self.unique_labels = {}

    def fit(self, X, y=None):
        # Extract unique labels for each specified column
        for col in self.columns:
            all_labels = X[col].dropna().apply(lambda x: x.split()).su
            self.unique_labels[col] = list(set(all_labels))  # Get dis
        return self

    def transform(self, X):
        # Work on a copy of X to avoid modifying the original data
        X = X.copy()
        for col in self.columns:
            for label in self.unique_labels[col]:
                # Create a new column for each unique label
                X[f"{col}_{label}"] = X[col].apply(lambda x: 1 if pd.r

            # Drop the original column if desired
            X = X.drop(columns=[col])
        return X
```

Now we can do One Hot Encoding for the remaining categorical columns and scale remaining numeric columns

In [14]:
```
# Define the exact list of categorical columns to one-hot encode
categorical_columns = [
    'District', 'Block', 'CropEstMethod', 'TransplantingIrrigationSour
    'TransplantingIrrigationPowerSource', 'PCropSolidOrgFertAppMethod'
    'MineralFertAppMethod', 'MineralFertAppMethod.1', 'Harv_method',
    'Threshing_method', 'Stubble_use'
]

def continuous_column_selector(X):
    """Select columns for scaling: considers continuous columns with a
    continuous_columns = []
    for col in X.select_dtypes(include=['float64', 'int64']).columns:
        unique_values = X[col].unique()
        # Only consider continuous if it has more than 2 unique values
        if len(unique_values) > 2 or (len(unique_values) == 2 and abs(
            continuous_columns.append(col)
    return continuous_columns



one_hot_preprocessor = ColumnTransformer(
    transformers=[
        ('onehot', OneHotEncoder(drop='first', handle_unknown='ignore'
        ('scaler', StandardScaler(), continuous_column_selector(X))
    ],
    remainder='passthrough',  # Keep all other columns as is
    force_int_remainder_cols=False  # Use column names for remainder c
)
```

Final Pipeline

In [15]:
```
# Define the final pipeline
pipeline = Pipeline(steps=[
    #('drop_cultland', DropCultLandTransformer()),  # Step to drop Cul
    ('date_feature_extractor', date_feature_extractor),
    ('impute_and_cap_outliers', ImputeAndCapOutliers(
        columns_to_impute_and_cap=columns_to_impute_and_cap,
        columns_to_impute_only=columns_to_impute_only,
        columns_to_impute_with_zero_and_cap=columns_to_impute_with_zer
    )),
    ('conditional_impute_urea', conditional_impute_urea),
    ('fill_missing_with_unknown', FillMissingWithUnknown(columns=colum
    ('multi_column_multi_label_binarizer', MultiColumnMultiLabelBinari
    ('one_hot_preprocessor', one_hot_preprocessor),
    ('variance_threshold', VarianceThreshold(threshold=0.05))
    ])
```

Fit and transform the training data once

In [16]:
```
X_train_transformed = pipeline.fit_transform(X_train)

# Retrieve feature names after one-hot encoding and variance thresholc
if hasattr(pipeline.named_steps['one_hot_preprocessor'], 'get_feature_
    one_hot_feature_names = pipeline.named_steps['one_hot_preprocessor
else:
    one_hot_feature_names = X_train.columns

# Filter feature names according to variance threshold
filtered_feature_names = [name for idx, name in enumerate(one_hot_feat
                          if idx in pipeline.named_steps['variance_thr

# Convert the transformed output to a DataFrame with correct column na
X_train_transformed_df = pd.DataFrame(X_train_transformed, columns=fil

# Display the first few rows
X_train_transformed_df.head()
```

Out[16]:

	onehot__District_Jamui	onehot__District_Nalanda	onehot__District_Vaishali	onehot__Block_Gu
0	1.0	0.0	0.0	
1	0.0	0.0	1.0	
2	0.0	0.0	1.0	
3	1.0	0.0	0.0	
4	0.0	0.0	0.0	

Let's check the data after the transformations

In [17]:
```
X_train_transformed_df.describe()
```

Out[17]:

	onehot__District_Jamui	onehot__District_Nalanda	onehot__District_Vaishali	onehot__Bloc
count	3069.000000	3069.000000	3069.000000	306
mean	0.290648	0.305963	0.252851	(
std	0.454136	0.460889	0.434717	(
min	0.000000	0.000000	0.000000	(
25%	0.000000	0.000000	0.000000	(
50%	0.000000	0.000000	0.000000	(
75%	1.000000	1.000000	1.000000	(
max	1.000000	1.000000	1.000000	'

In [18]:
```
X_train_transformed_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 3069 entries, 0 to 3068
Data columns (total 75 columns):
 #   Column                                                         Non-Nul
l Count  Dtype
---  ------                                                         -------
-------  -----
 0   onehot__District_Jamui                                         3069 no
n-null   float64
 1   onehot__District_Nalanda                                       3069 no
n-null   float64
 2   onehot__District_Vaishali                                      3069 no
n-null   float64
 3   onehot__Block_Gurua                                            3069 no
n-null   float64
 4   onehot__Block_Jamui                                            3069 no
n-null   float64
 5   onehot__Block_Khaira                                           3069 no
n-null   float64
 6   onehot__Block_Mahua                                            3069 no
n-null   float64
 7   onehot__Block_Noorsarai                                        3069 no
n-null   float64
 8   onehot__Block_Rajgir                                           3069 no
n-null   float64
 9   onehot__Block_Wazirganj                                        3069 no
n-null   float64
 10  onehot__CropEstMethod_Manual_PuddledLine                       3069 no
n-null   float64
 11  onehot__CropEstMethod_Manual_PuddledRandom                     3069 no
```

```
n-null   float64
 12  onehot__TransplantingIrrigationSource_Canal                 3069 no
n-null   float64
 13  onehot__TransplantingIrrigationPowerSource_Electric         3069 no
n-null   float64
 14  onehot__TransplantingIrrigationPowerSource_Unknown          3069 no
n-null   float64
 15  onehot__PCropSolidOrgFertAppMethod_SoilApplied              3069 no
n-null   float64
 16  onehot__PCropSolidOrgFertAppMethod_Unknown                  3069 no
n-null   float64
 17  onehot__MineralFertAppMethod_SoilApplied                    3069 no
n-null   float64
 18  onehot__MineralFertAppMethod.1_Unknown                      3069 no
n-null   float64
 19  onehot__Harv_method_machine                                 3069 no
n-null   float64
 20  onehot__Threshing_method_machine                            3069 no
n-null   float64
 21  scaler__CultLand                                            3069 no
n-null   float64
 22  scaler__CropCultLand                                        3069 no
n-null   float64
 23  scaler__CropTillageDepth                                    3069 no
n-null   float64
 24  scaler__SeedlingsPerPit                                     3069 no
n-null   float64
 25  scaler__TransplantingIrrigationHours                        3069 no
n-null   float64
 26  scaler__TransIrriCost                                       3069 no
n-null   float64
 27  scaler__StandingWater                                       3069 no
n-null   float64
 28  scaler__Ganaura                                             3069 no
n-null   float64
 29  scaler__CropOrgFYM                                          3069 no
n-null   float64
 30  scaler__NoFertilizerAppln                                   3069 no
n-null   float64
 31  scaler__BasalDAP                                            3069 no
n-null   float64
 32  scaler__BasalUrea                                           3069 no
n-null   float64
 33  scaler__1tdUrea                                             3069 no
n-null   float64
 34  scaler__1appDaysUrea                                        3069 no
n-null   float64
 35  scaler__2tdUrea                                             3069 no
n-null   float64
 36  scaler__2appDaysUrea                                        3069 no
```

```
n-null   float64
 37  scaler__Harv_hand_rent                                3069 no
n-null   float64
 38  scaler__Residue_length                                3069 no
n-null   float64
 39  scaler__Residue_perc                                  3069 no
n-null   float64
 40  scaler__Acre                                          3069 no
n-null   float64
 41  remainder__CropTillageDate_month                      3069 no
n-null   float64
 42  remainder__CropTillageDate_day                        3069 no
n-null   float64
 43  remainder__RcNursEstDate_month                        3069 no
n-null   float64
 44  remainder__RcNursEstDate_day                          3069 no
n-null   float64
 45  remainder__SeedingSowingTransplanting_month           3069 no
n-null   float64
 46  remainder__SeedingSowingTransplanting_day             3069 no
n-null   float64
 47  remainder__Harv_date_month                            3069 no
n-null   float64
 48  remainder__Harv_date_day                              3069 no
n-null   float64
 49  remainder__Threshing_date_month                       3069 no
n-null   float64
 50  remainder__Threshing_date_day                         3069 no
n-null   float64
 51  remainder__LandPreparationMethod_WetTillagePuddling      3069 no
n-null   float64
 52  remainder__LandPreparationMethod_TractorPlough           3069 no
n-null   float64
 53  remainder__LandPreparationMethod_BullockPlough           3069 no
n-null   float64
 54  remainder__LandPreparationMethod_FourWheelTracRotavator  3069 no
n-null   float64
 55  remainder__NursDetFactor_CalendarDate                 3069 no
n-null   float64
 56  remainder__NursDetFactor_Unknown                      3069 no
n-null   float64
 57  remainder__NursDetFactor_SeedAvailability             3069 no
n-null   float64
 58  remainder__NursDetFactor_PreMonsoonShowers            3069 no
n-null   float64
 59  remainder__NursDetFactor_LabourAvailability           3069 no
n-null   float64
 60  remainder__NursDetFactor_IrrigWaterAvailability       3069 no
n-null   float64
 61  remainder__TransDetFactor_LaborAvailability           3069 no
```

```
n-null   float64
 62  remainder__TransDetFactor_CalendarDate                    3069 no
n-null   float64
 63  remainder__TransDetFactor_Unknown                         3069 no
n-null   float64
 64  remainder__TransDetFactor_SeedlingAge                     3069 no
n-null   float64
 65  remainder__TransDetFactor_IrrigWaterAvailability          3069 no
n-null   float64
 66  remainder__TransDetFactor_RainArrival                     3069 no
n-null   float64
 67  remainder__OrgFertilizers_Unknown                         3069 no
n-null   float64
 68  remainder__OrgFertilizers_FYM                             3069 no
n-null   float64
 69  remainder__OrgFertilizers_Ganaura                         3069 no
n-null   float64
 70  remainder__CropbasalFerts_Urea                            3069 no
n-null   float64
 71  remainder__CropbasalFerts_DAP                             3069 no
n-null   float64
 72  remainder__FirstTopDressFert_Unknown                      3069 no
n-null   float64
 73  remainder__FirstTopDressFert_Urea                         3069 no
n-null   float64
 74  remainder__FirstTopDressFert_DAP                          3069 no
n-null   float64
dtypes: float64(75)
memory usage: 1.8 MB
```

In [19]:

```
# Transform the test data and convert it to a DataFrame with the same
X_test_transformed = pipeline.transform(X_test)
X_test_transformed_df = pd.DataFrame(X_test_transformed, columns=filte
X_test_transformed_df.head()
```

Out[19]:

	onehot__District_Jamui	onehot__District_Nalanda	onehot__District_Vaishali	onehot__Block_Gu
0	0.0	0.0	1.0	
1	0.0	1.0	0.0	
2	0.0	0.0	0.0	
3	1.0	0.0	0.0	
4	0.0	0.0	1.0	

CatBoost

Wrap CatBoost with TransformedTargetRegressor for target scaling

In [20]:
```
model = TransformedTargetRegressor(
    regressor=CatBoostRegressor(iterations=500, learning_rate=0.1, dep
    transformer=StandardScaler()
)

# Fit the model on the transformed training data with scaled target
model.fit(X_train_transformed_df, y_train)

# Predict using the transformed test data
y_pred = model.predict(X_test_transformed_df)
```

```
0:      learn: 0.9531624        total: 60ms     remaining: 29.9s
100:    learn: 0.4689018        total: 173ms    remaining: 682ms
200:    learn: 0.3970226        total: 282ms    remaining: 419ms
300:    learn: 0.3469275        total: 391ms    remaining: 258ms
400:    learn: 0.3070368        total: 497ms    remaining: 123ms
499:    learn: 0.2735642        total: 606ms    remaining: 0us
```

Evaluate the model using original target values

In [21]:
```
mae = mean_absolute_error(y_test, y_pred)
print(f"Mean Absolute Error (MAE): {mae}")

mse = mean_squared_error(y_test, y_pred)
print(f"Mean Squared Error (MSE): {mse}")

r2 = r2_score(y_test, y_pred)
print(f"R-squared (R²): {r2}")
```

```
Mean Absolute Error (MAE): 186.49572742956306
Mean Squared Error (MSE): 83389.75080490908
R-squared (R²): 0.6894206377689867
```

Our model achieved a Mean Absolute Error of 192 and an R-squared score of 0.67, meaning it explains about 67% of the variation in crop yields. This provides a reasonably accurate prediction but still leaves room for improvement.

Model Interpretability

To understand our model's predictions, we used interpretability tools, LIME and SHAP. LIME helps us understand why the model made a specific prediction, which can help farmers understand why a certain yield is predicted for their specific plot. SHAP, on the other hand, gives a more general view of which attributes are consistently important for predicting yield across all data.

LIME

LIME (Local Interpretable Model-agnostic Explanations) helps explain individual predictions by creating simpler, interpretable models around each specific instance. It perturbs the instance slightly, observes how the model's prediction changes, and builds a linear model to approximate the behavior locally. This provides insights into which features influence the prediction for that instance the most, making complex models more understandable.

In [22]:
```
# Set up LIME explainer
explainer = LimeTabularExplainer(
    training_data=X_train_transformed_df.values,  # LIME requires data
    feature_names=X_train_transformed_df.columns.tolist(),
    mode='regression'
)

# Define the prediction function for LIME
predict_fn = model.predict

# Choose an instance from the test set to explain
i = 0  # Index of the instance in X_test_transformed_df to explain
instance = X_test_transformed_df.iloc[i].values  # Extract a single in

# Generate explanation for the selected instance
exp = explainer.explain_instance(
    data_row=instance,
    predict_fn=predict_fn
)

# Display the explanation
exp.show_in_notebook(show_all=False)
```

In [23]:
```
# Display the explanation as text
explanation = exp.as_list()
for feature, value in explanation:
    print(f"{feature}: {value}")
```

```
0.00 < onehot__District_Vaishali <= 1.00: -147.5127703213237
-0.10 < scaler__CropOrgFYM <= -0.10: -114.4972038174662
remainder__Harv_date_month <= 0.12: -72.94520629200125
0.00 < onehot__PCropSolidOrgFertAppMethod_SoilApplied <= 1.00: 58.394
14407728574
onehot__Block_Mahua > 0.00: -57.43392013054956
onehot__Block_Wazirganj <= 0.00: -56.05870309934107
remainder__FirstTopDressFert_DAP <= 0.00: -49.538090681026915
-0.16 < scaler__Residue_length <= 1.10: 46.28745951951423
scaler__TransIrriCost > 0.15: -40.20907059986689
scaler__Ganaura <= -0.15: 38.04305912661807
```

Predicted Value: LIME shows a predicted value of 1856.98 for the selected instance, with a range of potential predictions between 1098.35 and 2485.21 based on the perturbations LIME generated around this instance.
Feature Contributions:

- **Negative (Blue)**: Features that reduce the prediction. For example, onehot__District_Vaishali and scaler__CropOrgFYM (with a value of -0.10) are pulling the prediction down.
- **Positive (Orange)**: Features that increase the prediction. For instance, onehot__PCropSolidOrgFertAppMethod_SoilApplied (with a value of 1.00) and onehot__CropEstMethod_Manual_PuddledLine (with a value of 0.00) are pushing the prediction up.\

Feature and Value Section: This shows each feature’s contribution and the actual value of the feature in the chosen instance.

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Let's inspect another instance

In [24]:
```
# Choose an index for the instance you want to explain
i = 5  # Replace 5 with any other index you want to analyze

# Select the instance from the test data
instance = X_test_transformed_df.iloc[i].values  # in array format for

# Generate explanation for the selected instance
exp = explainer.explain_instance(
    data_row=instance,
    predict_fn=predict_fn
)

# Display the explanation (either as a visual or as text)
exp.show_in_notebook(show_all=False)

# Or, display as text for full feature names
explanation = exp.as_list()
for feature, value in explanation:
    print(f"{feature}: {value}")
```

```
0.00 < onehot__District_Vaishali <= 1.00: -149.80272373736724
remainder__Harv_date_month <= 0.12: -83.56127299659198
onehot__PCropSolidOrgFertAppMethod_SoilApplied <= 0.00: -63.696082036
75751
onehot__Block_Wazirganj <= 0.00: -55.97255328959717
-0.16 < scaler__Residue_length <= 1.10: 53.98493777908282
onehot__Block_Mahua > 0.00: -48.34606064666703
remainder__FirstTopDressFert_DAP <= 0.00: -46.55757285626126
onehot__CropEstMethod_Manual_PuddledLine <= 0.00: 45.757816044806376
scaler__Ganaura <= -0.15: 43.29037262936673
scaler__BasalUrea <= -0.24: 35.55533825085507
```

Predicted Value: The model predicted a value of 2139.02 for this particular instance. LIME provides a range (960.63 to 2560.52) based on the perturbations it created to test the feature contributions.

Positive and Negative Contributions:

- **Positive (Orange)**: Features that push the prediction value higher. For instance: onehot__MineralFertAppMethod_SoilApplied and onehot__CropEstMethod_Manual_PuddledLine both contribute positively to the prediction, adding 71.72 and 48.40 units, respectively. scaler__2appDaysUrea contributes 29.96 units to the prediction.
- **Negative (Blue)**: Features that pull the prediction value down. For example: onehot__District_Vaishali has a large negative impact, reducing the prediction by 143.09. onehot__PCropSolidOrgFertAppMethod_SoilApplied reduces it by 44.39.

Feature Values: On the right, each feature's value is shown for this specific instance. For example, onehot__District_Vaishali has a value of 1.0 (indicating this instance is in the district of Vaishali), and scaler__BasalUrea has a value of -0.24.

We can retrieve the row in the original test DataFrame

In [25]:
```python
original_row = X_test.iloc[i]

print("Original Row in the Dataset:")
print(original_row)
```

```
Original Row in the Dataset:
District
Vaishali
Block
Mahua
CultLand
5
CropCultLand
5
LandPreparationMethod                  WetTillagePuddling TractorPloug
h FourWheelTrac...
CropTillageDate
2022-07-13
CropTillageDepth
5
CropEstMethod                                                       Ma
nual_PuddledRandom
RcNursEstDate
```

```
RcNursEstDate
2022-07-15
SeedingSowingTransplanting
2022-08-08
SeedlingsPerPit

2.0
NursDetFactor                                                   Irri
gWaterAvailability
TransDetFactor                                                  Irri
gWaterAvailability
TransplantingIrrigationHours
2.0
TransplantingIrrigationSource
Boring
TransplantingIrrigationPowerSource
Electric
TransIrriCost
300.0
StandingWater
2.0
OrgFertilizers
NaN
Ganaura
NaN
CropOrgFYM
NaN
PCropSolidOrgFertAppMethod
NaN
NoFertilizerAppln
3
CropbasalFerts
DAP
BasalDAP
5.0
BasalUrea
NaN
MineralFertAppMethod
SoilApplied
FirstTopDressFert
Urea
1tdUrea
4.0
1appDaysUrea
35.0
2tdUrea
4.0
2appDaysUrea
65.0
MineralFertAppMethod.1
Broadcasting
```

```
Harv_method
hand
Harv_date
2022-11-05
Harv_hand_rent
200.0
Threshing_date
2022-11-10
Threshing_method
hand
Residue_length
30
Residue_perc
10
Stubble_use
plowed_in_soil
Acre
0.090909
Name: 221, dtype: object
```

SHAP

SHAP (SHapley Additive exPlanations) is a method that explains a model's predictions by calculating the contribution of each feature to the prediction. It's based on game theory and assigns a "SHAP value" to each feature, representing its impact on the predicted outcome. SHAP values are consistent, meaning they fairly allocate the prediction across features, helping to understand both global and individual feature importance.

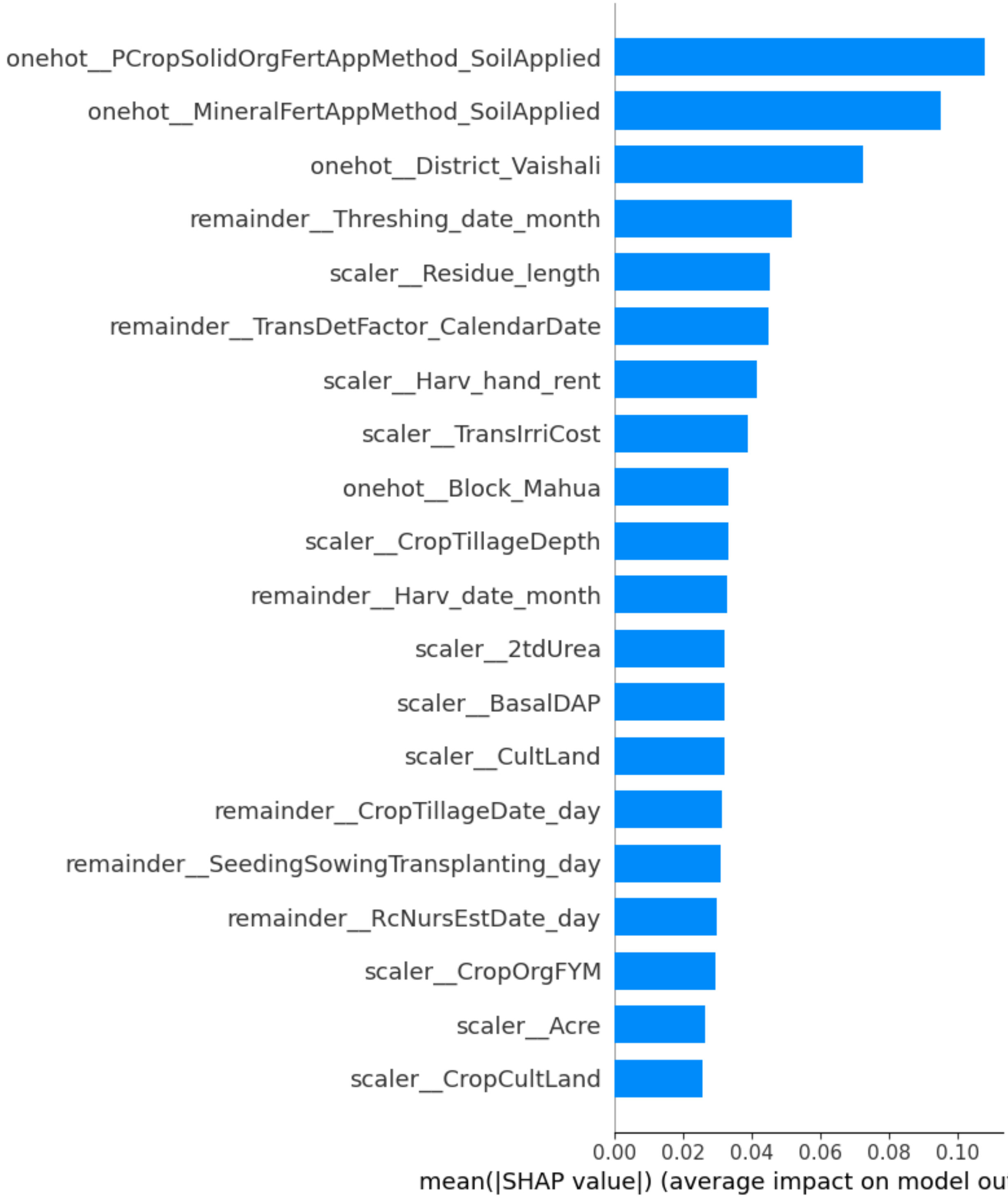
In [26]:

```
# Create the SHAP explainer for the CatBoost model

# Access the underlying CatBoost model for SHAP
explainer = shap.TreeExplainer(model.regressor_)

# Calculate SHAP values for the test set
shap_values = explainer.shap_values(X_test_transformed_df)
```

Bar Plot

- **Purpose**: Provides a simple bar chart of feature importance by showing the mean absolute SHAP values for each feature.
- **Interpretation**: Similar to the summary plot but without details on individual instances. Useful for a quick overview of global feature importance.

In [27]:
```
# Now you can use SHAP plots, e.g., summary plot
shap.summary_plot(shap_values, X_test_transformed_df, plot_type="bar")
```



This SHAP summary plot shows the average impact of each feature on the model's predictions across all instances in the test dataset. Here's a breakdown of what it means:

Feature Importance: The features are ranked from top to bottom based on their average SHAP values, which represent each feature's contribution to the model's predictions. Higher mean SHAP values indicate that the feature has a larger impact on predictions.

Top Features:

- onehot__PCropSolidOrgFertAppMethod_SoilApplied and onehot__MineralFertAppMethod_SoilApplied are the most influential features, meaning they play a significant role in determining the predicted outcome.
- onehot__District_Vaishali and scaler__Residue_length also have considerable impacts, indicating that the model relies heavily on these features for its predictions.

Interpretation of SHAP Values:

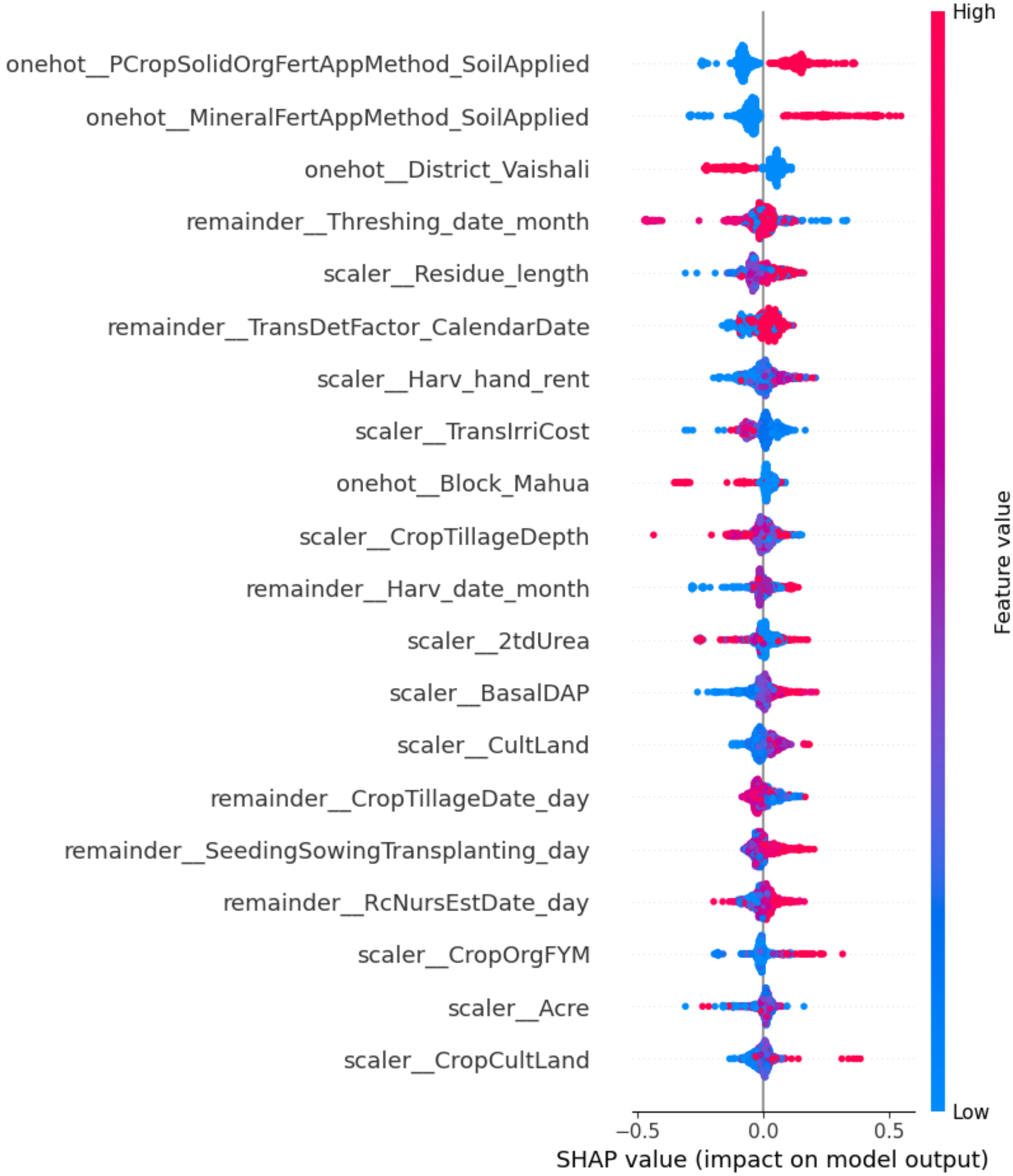
- Each bar's length represents the mean (average) absolute SHAP value for that feature across all samples, reflecting its average impact.
- Features with longer bars contribute more to the variability in predictions, meaning the model's predictions are sensitive to changes in these features.

Here, the top feature is one-hot encoded PCropSolidOrgFertAppMethod - Method of applying organic fertilizer in your previous crop during land preparation (which was soil applied).

Summary Plot (Bee Swarm Plot)

- **Purpose**: Shows both feature importance and the distribution of SHAP values for each feature across all instances.
- **Interpretation**: Each dot represents an instance. The position along the x-axis shows the impact on the model output, and the color shows whether the feature value is high (red) or low (blue).

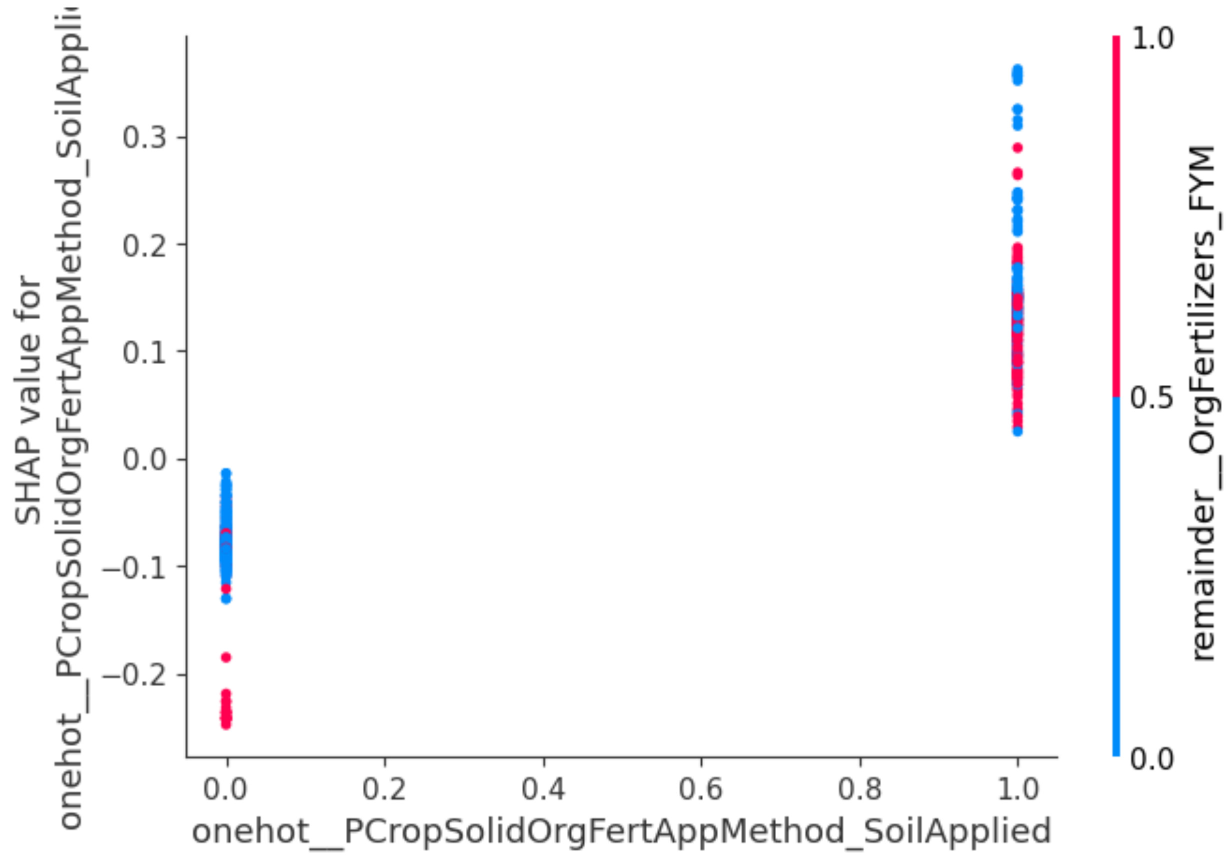
In [28]:
```
shap.summary_plot(shap_values, X_test_transformed_df)
```

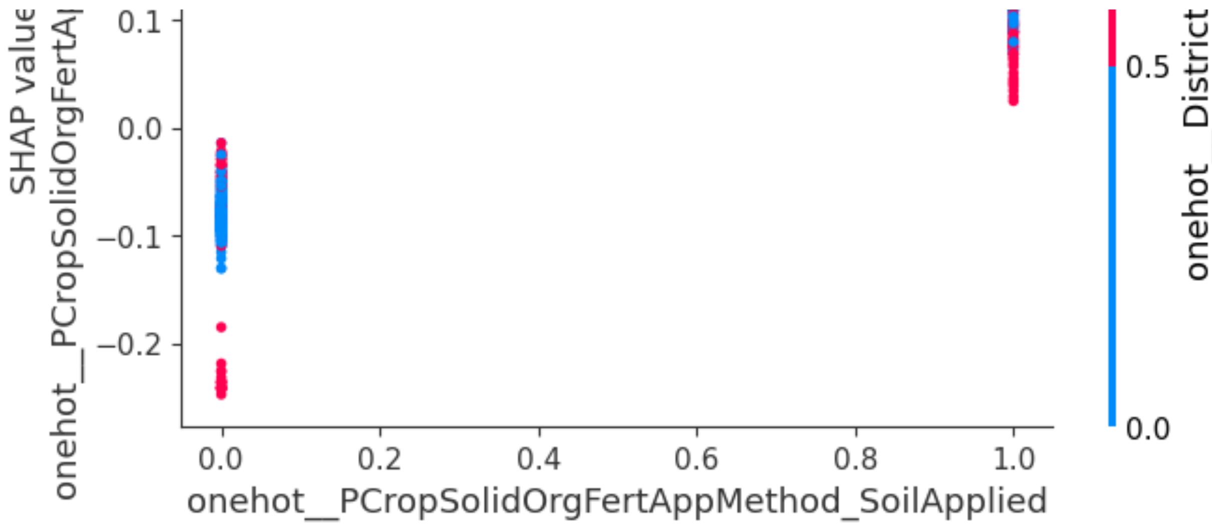


Dependence Plot

- **Purpose**: Shows the relationship between a single feature and its SHAP values, indicating how different values of that feature affect the model's prediction. It can also show interactions between features.
- **Interpretation**: Helps understand how changing a specific feature's value impacts the prediction. You can add a second feature to show interaction effects.

In [29]:
```
shap.dependence_plot('onehot__PCropSolidOrgFertAppMethod_SoilApplied',
# For interactions with another feature
shap.dependence_plot('onehot__PCropSolidOrgFertAppMethod_SoilApplied',
```

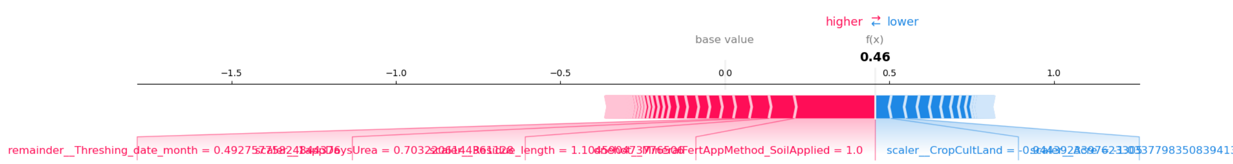




Force Plot

- **Purpose**: Visualizes the contribution of each feature to an individual prediction, showing how the SHAP values push the prediction from the baseline. -**Interpretation**: Useful for understanding how specific features affect a single prediction, especially for local interpretability.

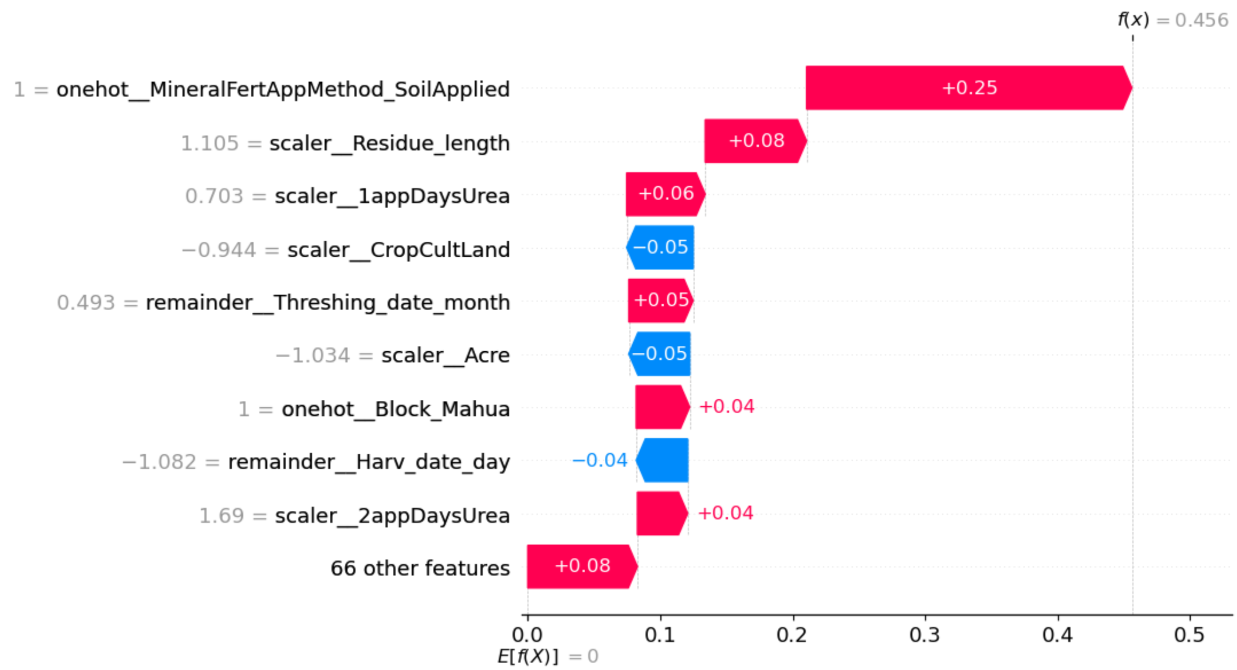
In [30]:
```
# For a single prediction (e.g., index 5)
shap.force_plot(explainer.expected_value, shap_values[5], X_test_trans
```



Waterfall Plot

- **Purpose**: Provides a detailed breakdown of the SHAP values for a single prediction, starting from the model's expected value and adding or subtracting contributions from each feature.
- **Interpretation**: Shows exactly how the model arrives at a specific prediction for an instance, making it useful for case-by-case analysis.

In [31]:
```
shap.waterfall_plot(shap.Explanation(values=shap_values[5], base_value
```



Here, the baseline here is zero, representing the average starting point of the prediction. Each feature then either adds-to Or subtracts-from this baseline. Positive contributions are shown in red, they increase yields. For example, 'Mineral Fertilizer Application by 'soil adds 0.23 on average, confirming its effectiveness. Negative contributions are shown in blue, they reduce yields.

Recommendations

Based on these insights, we can recommend promoting effective fertilizer methods, especially mineral soil applications. We can also suggest targeted support for regions like Vaishali that face challenges. Finally, educating farmers on specific land preparation methods can also boost productivity. By sharing these findings, we can help farmers make better-informed decisions for sustainable farming.