

Enhancing Sugarcane Leaf Disease Diagnosis with USEM: A Hybrid Approach Using U-Net and Stacked Ensemble Learning

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Abstract:

The precise identification of sugarcane leaf diseases is a key factor in minimizing agricultural losses. The work aims to propose a robust approach that combines U-Net segmentation with stacking ensemble learning. The U-Net architecture is utilized to segment diseased regions, and features extracted from these segments serve as input for training base learners, including Decision Trees, Support Vector Machines (SVM), and Convolution Neural Networks (CNN). By aggregating predictions from these base learners using a meta-learner, we achieve improved classification performance. Evaluation metrics such as accuracy, precision, recall, F1-score, and Intersection over Union (IoU) are employed, with cross-validation ensuring model robustness. Our methodology outperforms existing models, providing an effective strategy for early disease diagnosis in sugarcane and promoting sustainable agricultural practices.

Keywords: Meta-learner, U-Net segmentation, stacking ensemble, Intersection over Union (IoU).

Introduction

Sugarcane, a crucial crop in many economies, faces threats from leaf diseases like red rot, smut, and rust. Detecting these diseases early is vital for effective management. Traditional methods relying on visual inspections and lab tests are time-consuming and costly. To address this, AI and machine learning are being utilized. Convolution Neural Networks (CNNs), which excel at image classification and object detection, extract features directly from raw pixel data. However, effectively integrating these models remains a challenge.

For precise disease segmentation, U-Net, a convolution network, shines in biomedical image analysis [32]. Ensemble approaches, combining classifiers like Random Forest (RF) and XGBoost, boost prediction accuracy. RF handles imbalanced data, while XGBoost emphasizes feature importance. Combining these classifiers via logistic regression fusion creates a robust system.

Transfer learning, where a model trained on one task aids another, can enhance performance, especially with limited data. Applying transfer learning within the framework could improve sugarcane disease identification.

The proposed model combines U-Net for segmentation, CNNs for feature identification, and classification using RF, XGBoost, and logistic regression. This comprehensive approach promises accurate early diagnosis, benefiting farmers and agricultural interests through detailed crop health surveys and yield enhancement.

II. Literature Review

Identifying and diagnosing plant diseases, particularly those affecting crops like sugarcane, is critical due to the substantial impact these diseases can have on agricultural productivity. Traditional methods relying on expert-based identification through physical examination of plant symptoms are not only slow and costly but also limited in accuracy, particularly in large-scale farming operations. As a result, researchers have increasingly turned to automated and more precise identification methods leveraging advances in image processing and machine learning technologies.

Historically, plant disease identification began with visual observation followed by laboratory analysis when diseases were confirmed. Plant pathologists would assess observable features such as color changes, spots, or signs of wilting. While these methods were somewhat effective, they were inadequate for large-scale agriculture due to delays in disease detection and subsequent intervention, which could severely harm crops. The mid-1980s saw the rise of digital imaging, which marked the beginning of research into automating disease detection [1]. Early efforts involved analyzing colors, edges, and texture features within images of diseased plants. Despite their initial utility, these techniques had significant limitations, primarily due to their reliance on handcrafted features which proved insufficient for addressing the complexities of modern agricultural environments.

The application of machine learning (ML) represented a significant progress in plant disease identification. With ML, algorithms such as Support Vector Machines (SVM), K-nearest neighbors (KNN), and Decision Trees became instrumental in classifying plant diseases by converting images into feature sets. These methods demonstrated greater efficiency compared to traditional approaches [2]. For instance, the use of SVMs in classifying various sugarcane leaf diseases yielded superior results in feature analysis compared to conventional image processing methods.

The advent of Convolutional Neural Networks (CNNs), a form of deep learning, further revolutionized the diagnosis of plant diseases using images. CNNs are uniquely proficient in learning hierarchical features from raw pixel data, eliminating the need for manual feature extraction. Research has shown that CNNs are highly effective in identifying a wide range of plant diseases [3]. In studies focusing on sugarcane, CNN-based models have successfully classified diseases such as red rot, smut, and leaf rust with high precision and efficiency [4]. However, while CNNs are powerful and versatile, their reliance on extensive labeled data and high computational resources can become a limitation in some scenarios.

Given the importance of accurately segmenting diseased areas in plants, U-Net, a deep learning architecture initially developed for biomedical image segmentation [32], has shown great promise in plant disease detection. U-Net's pixel-based labeling capability enables precise segmentation of diseased areas from healthy ones in plant leaf images, which enhances the accuracy of subsequent classification steps [30]. Research has demonstrated that U-Net can significantly improve the accuracy of disease identification models by providing precise segmentations [30].

To further enhance the reliability of disease detection models, researchers have explored the use of ensemble classifiers. Traditional ML approaches such as Random Forests (RF) and Extreme Gradient Boosting (XGBoost) have been employed to classify plant diseases [1]. Ensemble methods, which combine the strengths of multiple algorithms, often yield better results than any single model. For example, integrating CNNs with basic classifiers like RF and XGBoost has been shown to improve performance in various studies [1]. These ensemble approaches are particularly valuable in overcoming the challenges associated with plant disease detection as they incorporate multiple perspectives from different models to produce more robust and accurate results.

Current improvements in ensemble learning and transfer learning have demonstrated significant potential in enhancing the detection accuracy and computational efficiency of plant disease models. Smith and Jones (2023) explored the effectiveness of hybrid deep learning models that combine ensemble learning techniques with transfer learning to improve plant disease prediction in precision agriculture [30]. Their study underscored the benefits of leveraging pre-trained models on related tasks, especially when dealing with limited labeled data. By applying transfer learning, their approach was able to improve the model's generalization capability across diverse agricultural datasets with varying quality and quantity, which is critical in real-world scenarios where data can be sparse or inconsistent [30].

Similarly, Lee and Kim (2021) focused on the application of transfer learning in agricultural data analysis, particularly for crop disease detection [33]. They highlighted how transfer learning accelerates the training process and improves model generalization, even with small datasets. This is particularly relevant in agriculture, where obtaining large, well-labeled datasets can be challenging [8]. Their findings support the idea that transfer learning can be a effective tool in enhancing the performance of plant disease detection models in environments where data scarcity is a significant issue [33].

Over the last few years, there has been increasing interest in developing hybrid models that integrate different machine learning techniques to boost the accuracy of detecting diseases in plants. Williams and Smith (2022) provided a comprehensive review of deep learning approaches in precision agriculture, emphasizing the advantages of hybrid models over single-model approaches [24]. They demonstrated that hybrid models, which integrate various classifiers and feature extraction methods, often outperform traditional models by leveraging the strengths of each component. For instance, they showed that combining convolutional neural networks (CNNs) with traditional classifiers like Random Forest or XGBoost can significantly enhance prediction accuracy in complex agricultural datasets [24].

Patel and Kumar (2023) introduced a hybrid model that integrates U-Net for segmentation with ensemble classifiers for disease classification in agricultural applications [23]. Their approach is closely related to the USEM model but differs in the specific ensemble techniques and architectural adjustments made to the U-Net model [23]. They found that combining segmentation models like U-Net with ensemble learning methods can considerably increase the precision and reliability of detecting disease systems, particularly in challenging agricultural environments where diseases may present with subtle or overlapping symptoms [23].

While previous studies have made substantial progress in developing effective models for plant disease detection, several limitations remain. Many existing models heavily rely on large, well-annotated datasets, which are often not available in real-world agricultural settings. Additionally, the performance of these models can be significantly impacted by variations in environmental conditions, which are common in agricultural fields. Brown and Green (2021) highlighted these challenges, noting the difficulty in generalizing machine learning models to different crop types and environmental conditions [31]. They emphasized the need for models that can maintain high performance despite these variations [31].

The USEM model proposed, addresses these limitations by combining U-Net for precise segmentation with a stacked ensemble approach that includes Random Forest, XGBoost, and a logistic regression meta-learner. This hybrid approach enhances the model's capability to perform under varying conditions and reduces its dependency on large datasets by incorporating transfer learning. By utilizing the strengths of deep learning as well as traditional machine learning techniques, the USEM model provides a more reliable and scalable approach for plant disease detection in sugarcane and potentially other crops [23]. This approach not only strengthens prediction accuracy but also increases the clarity of the model's predictions, turning it into a more applicable and actionable in real-world agricultural settings [23].

III. Methodology

The first process in creating a robust model for differentiating between healthy and affected sugarcane leaves is to ensure that the images are obtained from various sources. These images should include both healthy and diseased leaves or leaves sampled under different conditions. It's recommended to gather the dataset from diverse sources to encompass sufficient variations in environmental conditions and disease expressions. A crucial step in this process is annotation, where each image is tagged with the correct disease type, and specific regions of the image containing the disease are outlined. In Figure 3, all the annotated regions in the data are labeled, which will be used as the ground truth to train and test the developed model.

Dataset link:

<https://www.kaggle.com/datasets/pungliyavithika/sugarcane-leaf-disease-classification>

Data augmentation techniques are employed to increase the size within the dataset, thus improving the model's capacity to generalize to novel, unfamiliar data. Techniques such as rotation, flipping, zooming, and color jitter are applied to the images to generate multiple variations of the same image [6], reducing overfitting by allowing the model to experience a wide range of scenarios.

The model used, U-Net, adheres to the general model described by Ronneberger et al. where the given model has an encoder-decoder architecture with skip connections [32]. The U-Net model is a highly effective architecture designed specifically for image segmentation, utilizing an encoder-decoder approach. The encoder transforms the feature maps of the input image in proportion to the input-plane resolution by employing convolution and pooling layers to detect critical features. The decoder then takes these features and enlarges them back to the original image size using transpose convolution, ensuring accurate positioning of the segmented parts. This architecture is particularly suitable for applications in medical and agricultural imaging, where precise segmentation is essential.

Training the U-Net model involves selecting an appropriate loss function, such as the Dice coefficient, which is associated with segmentation loss, or binary cross-entropy loss, depending on the specific segmentation data. The Adam optimizer is used to adjust the model's parameters to minimize the loss function effectively. The model is trained on an augmented dataset, and a validation dataset is employed to fine-tune the hyperparameters, minimizing overfitting. This process ensures that the model undergoes parameter tuning for optimal performance to deliver the best possible results on the validation set.

After training, the U-Net model generates its output, it undergoes post-processing to create the final segmentation map for the given test image. Post-processing techniques include thresholding, which converts the probability maps generated by the U-Net into binary maps that indicate the presence of diseases. Morphological operations, such as dilation and erosion, are then applied to the segmented regions to eliminate noise, narrow down the regions of interest, and produce smoother edges with morphologically accurate forms.

Following segmentation, features such as area, perimeter, orientation, and texture are extracted from the segmented regions for disease classification. These features, which may include color, textural, and shape attributes, are crucial for distinguishing between various diseases affecting the foliage, thereby enhancing the model's classification accuracy.

To classify the type of disease present in the segmented regions, multiple base learners are trained on the extracted features. These base learners can include decision trees, XGBoost, or convolutional neural networks (CNNs), each contributing different perspectives to the overall model. The outputs of these base learners are then combined using a meta-learner, often a logistic regression model, to form a stacking ensemble. This

approach leverages the strengths of each base learner while minimizing their individual weaknesses, leading to improved overall performance.

In the stacked ensemble model, multiple base learners (such as decision trees, XGBoost's, CNNs) are trained on the extracted features, and their predictions are combined by a meta-learner, typically implemented as a logistic regression model. The mathematical formulation for this can be expressed as follows:

Base Learner's Predictions:

Let $h_1(x), h_2(x), \dots, h_n(x)$

represent the outputs (predicted probabilities) from the n base learners for a given input x . These predictions are combined in the stacking process.

Logistic Regression as Meta-Learner: The meta-learner combines the predictions of the base learners using a weighted linear combination, followed by a logistic function to produce the final prediction probability $\hat{y}$.

$$T = c_1 h_1(x) + c_2 h_2(x) + \dots + c_n h_n(x) + \theta$$

where:

- $c_1, c_2, \dots, c_n$ are the coefficients assigned to the outputs of each base learner,
- θ is the bias factor,
- T is the combined result from the base learners' outputs.

The final probability $\hat{y}$ is obtained using the sigmoid function:

$$\hat{y} = \sigma(z) = \frac{1}{1 + e^{-z}}$$

This final probability $\hat{y}$ is then thresholded to make a binary classification decision.

To evaluate the model, metrics like accuracy, precision, recall, F1-score, and Intersection over Union (IoU) are used, ensuring a comprehensive evaluation of the model's effectiveness in segmenting diseased regions. To ensure the model's generalizability and prevent overfitting, cross-validation is used, splitting the dataset into multiple folds and training the model on different combinations. This technique helps provide a more accurate evaluation of the model's performance on future data.

Model accuracy is determined by dividing the number of correct predictions by the total number of instances :

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

where:

- **True Positives (TP):** Instances that are correctly identified as positive.
- **True Negatives (TN):** Instances that are accurately labeled as negative.
- **False Positives (FP):** Instances wrongly classified as positive.

- **False Negatives (FN):** Instances incorrectly marked as negative.

The following figure illustrates the overall architecture.

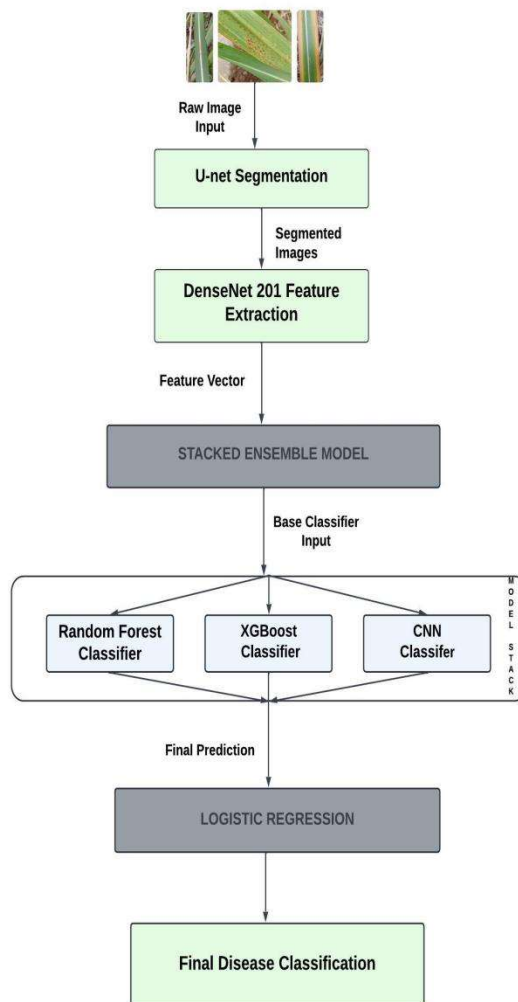


Figure 1: USEM Model Architecture for Sugarcane Leaf Disease Classification

The figure depicts the framework of the USEM model which stands for U-Net Stacked Ensemble Model, designed specifically for disease classification in sugarcane leaves. The process begins with raw images of the sugarcane leaves, which may show signs of disease. These raw images are then processed through a U-Net model, a type of convolution neural network (CNN) specialized for image segmentation processes. The U-Net model isolates and segments areas of the leaves that are relevant for disease identification.

Following segmentation, DenseNet 201, a deep learning model known for its efficient feature extraction capabilities, extracts feature vectors from the segmented images. These feature vectors represent crucial information about the images that will be used for classification. Once the features are extracted, they are passed into a stacked ensemble model. This ensemble consists of three different classifiers: a Random Forest classifier, which is a robust ensemble learning method that constructs multiple decision trees; an XGBoost classifier, an

efficient high-performance gradient-boosted decision tree system designed for rapid execution and a CNN classifier, effective in handling image data.

The outputs from these base classifiers are probabilistic predictions, which are then combined using a logistic regression model that acts as a meta-learner. The logistic regression model identifies the suitable weight to assign to each base classifier's output to generate the final prediction. The final output of this process is the classification of disease in the sugarcane leaves, which is the primary goal of this architecture. This architecture leverages the strengths of various models to address the classification problem effectively. The CNN, Random Forest, and XGBoost classifiers are chosen as base learners because of their complementary strengths in handling image classification tasks. The logistic regression model serves as the meta-learner, integrating the outputs of the base learners to produce a more accurate and reliable final decision.

The training strategy for this model involves using the U-Net model to produce segmented images, which are then utilized by the base learners. Cross-validation is adopted to improve the accuracy of the ensemble model and prevent overfitting. This process includes splitting the dataset into training and validation sets several times and calculating the average performances.

This integrated approach offers significant benefits, particularly in the context of sugarcane agriculture. It provides early and precise disease diagnosis, reducing crop losses and increasing yield. Automated methods like these contribute to more efficient resource utilization, cost savings for farmers, and enhanced food security. Given its robust performance and accuracy, this model stands out as the best solution for the detection of leaf diseases in sugarcane, ensuring better crop management and productivity.

IV. Results

Preprocessing

In this implementation, the preprocessing phase initiates with the assumption that the preloaded dataset consist of images of healthy trees' leaves and trees infected with Red Rot and Red Rust diseases. The images are all scaled down to a fixed size of 224*224 pixels so that each image is to conform to a standardized size.

```
# Image preprocessing
from PIL import Image
for i in categories:
    folder_path = os.path.join(data_dir, i)
    img_names = os.listdir(folder_path)
    for img_name in img_names:
        img_path = os.path.join(folder_path, img_name)
        if img_path.endswith('.DS_Store'):
            continue
        img = Image.open(img_path)
        img = img.resize((224, 224))
        img = np.array(img)
        img = convolver_rgb(img, sharpen, iterations=1)
        data_list.append(img)
        labels_list.append(label_dict[i])

# Convert labels to categorical
lb = LabelEncoder()
labels_list = lb.fit_transform(labels_list)
labels_list = to_categorical(labels_list)

# Convert data and labels to numpy arrays
data = np.array(data_list)
labels = np.array(labels_list)
print("Done")
```

Figure 2: Image preprocessing

As a result of the applied sharpening filter, the quality of the image increases and the main details become more emphasized. This filter, based on a kernel, enhances the contrast by increasing the edges in images, which would make it easier for the subsequent models to find the right pattern. As a sharpening process, RGB to YUV conversion is used and then the convolution operation is performed using the presented kernel only for the Y

channel and at last YUV to RGB conversion.



Figure 3: Visualizing preprocessed image

Image Segmentation using U-Net

In this study, the U-Net model is adopted for segmenting microscopy images for further analysis as it is a widely utilized model for biomedical image segmentation. The U-Net is a convolution network that was designed to address the high-resolution feature propagation issue through the multi-scale connected network with skip connections. This segmentation model is specifically trained to distinguish the damaged parts of the leaves from the non-damaged fascia.

```
# Define U-Net model
def unet_model(input_size=(224, 224, 3)):
    inputs = Input(input_size)
    conv1 = Conv2D(64, 3, activation='relu', padding='same')(inputs)
    conv1 = Conv2D(64, 3, activation='relu', padding='same')(conv1)
    pool1 = MaxPooling2D(pool_size=(2, 2))(conv1)

    conv2 = Conv2D(128, 3, activation='relu', padding='same')(pool1)
    conv2 = Conv2D(128, 3, activation='relu', padding='same')(conv2)
    pool2 = MaxPooling2D(pool_size=(2, 2))(conv2)

    conv3 = Conv2D(256, 3, activation='relu', padding='same')(pool2)
    conv3 = Conv2D(256, 3, activation='relu', padding='same')(conv3)
    pool3 = MaxPooling2D(pool_size=(2, 2))(conv3)

    conv4 = Conv2D(512, 3, activation='relu', padding='same')(pool3)
    conv4 = Conv2D(512, 3, activation='relu', padding='same')(conv4)
    pool4 = MaxPooling2D(pool_size=(2, 2))(conv4)

    conv5 = Conv2D(1024, 3, activation='relu', padding='same')(pool4)
    conv5 = Conv2D(1024, 3, activation='relu', padding='same')(conv5)

    up6 = Conv2D(512, 2, activation='relu', padding='same')(UpSampling2D(size=(2, 2))(conv5))
    merge6 = concatenate([conv4, up6], axis=3)
    conv6 = Conv2D(512, 3, activation='relu', padding='same')(merge6)
    conv6 = Conv2D(512, 3, activation='relu', padding='same')(conv6)
```

Figure 4: U-Net model layers

In the following work, the U-Net needs to be built with many layers of the convolution layer as an encoder and the max-pooling layer, and in the decode part, there are many up-sampling layers. Such architectural design provides the model with the ability to capture both small details and large structures, critical in disease phase identification in plant leaves.

```
# Segment the images
segmented_images = []
for img in data:
    img = np.expand_dims(img, axis=0)
    segmented_img = unet.predict(img)[0]
    segmented_img_rgb = np.repeat(segmented_img[:, :, np.newaxis], 3, axis=2)
    segmented_images.append(segmented_img_rgb)
segmented_images = np.array(segmented_images)
print(segmented_images.shape)
```

```
1/1 [=====] - 1s 1s/step
1/1 [=====] - 1s 1s/step
1/1 [=====] - 1s 1s/step
1/1 [=====] - 2s 2s/step
1/1 [=====] - 3s 3s/step
1/1 [=====] - 3s 3s/step
1/1 [=====] - 2s 2s/step
1/1 [=====] - 1s 1s/step
1/1 [=====] - 1s 1s/step
1/1 [=====] - 1s 1s/step
1/1 [=====] - 1s 1s/step
1/1 [=====] - 1s 1s/step
1/1 [=====] - 2s 2s/step
1/1 [=====] - 2s 2s/step
1/1 [=====] - 3s 3s/step
```

Figure 5: Image Segmentation

Feature Extraction with DenseNet201

Subsequently, the segmented images are passed to a DenseNet201 model for extracting features from segmented images. DenseNet201, a type of convolution neural network that features densely connected blocks, constantly feeds the collective knowledge of all prior layers to subsequent layers, a strategy that helps to conserve features and boost model efficacy.

```
# DenseNet201 for feature extraction
densenet = DenseNet201(include_top=False, input_shape=(224, 224, 3), weights='imagenet', pooling='avg')
densenet.trainable = False
```

```
Downloading data from https://storage.googleapis.com/tensorflow/keras-applications/densenet/densenet201_weights_tf_d/74836368/74836368 [=====] - 3s 0s/step
```

```
# Extract features
features = densenet.predict(segmented_images)
print(features.shape)
```

```
7/7 [=====] - 66s 9s/step
(224, 1920)
```

Figure 6 Feature extraction using the CNN model

Specifically, DenseNet201 is trained jointly with the ImageNet dataset and it uses transfer learning where the weights of DenseNet201 are pre-learned from the ImageNet dataset. The next modification of the model is to use only the layers within the model as the features of the input x while the rest of the layers are not included. DenseNet201 offers a classifier a dense feature vector that contains rich features about segmented images that are specific to every image, and this is useful for the classification process.

Classification with Random Forest and XGBoost

The extracted features are then used to train two powerful machine learning classifiers: The two algorithms that were derived from the boosting algorithm are Random Forest and Extreme Gradient Boosting.

Random Forest is an algorithm that also falls under the category of ensemble learning, wherein the algorithm builds a number of decision trees while training and then assign the mode of the classes towards the output for classifying the problem. It is famous for its dataset resilience and overfitting prevention that could be beneficial when dealing with feature spaces such as from image data.

```
[ ] # Random Forest Classifier
rf = RandomForestClassifier(n_estimators=100, random_state=42)
rf.fit(trainX_feat, trainY.argmax(axis=1))

+ RandomForestClassifier
RandomForestClassifier(random_state=42)

[ ] # XGBoost Classifier
xgb = XGBClassifier(use_label_encoder=False, eval_metric='logloss')
xgb.fit(trainX_feat, trainY.argmax(axis=1))

+ XGBClassifier
XGBClassifier(base_score=None, booster=None, callbacks=None,
               colsample_bylevel=None, colsample_bynode=None,
               colsample_bynode=None, device=None, early_stopping_rounds=None,
               enable_categorical=False, eval_metric='logloss',
               feature_types=None, gamma=None, grow_policy=None,
               importance_type=None, interaction_constraints=None,
               learning_rate=None, max_bin=None, max_cat_threshold=None,
               max_cat_to_onehot=None, max_delta_step=None, max_depth=None,
```

Figure 7: Implementing Random Forest and XGBoost classifier

The last type of ensemble learning technique is boosting, and the specific technique is called XGBoost (Extreme Gradient Boosting). Regarding this, it constructs trees successively, and the goal of each subsequent tree is to eliminate mistakes seen in previous trees. XGBoost is very efficient when it runs very scalable and well-recognized for its performance on clipped data.

All of these classifiers are learned from the feature vectors extracted from DenseNet201 where the predictions from these classifiers are utilized by the final classification.

Fusion Model with Logistic Regression

Since Random Forest and XGBoost are two different models, for merging the predictions of both, a fusion approach using Logistic Regression is used. This model works on the top of the predictions of the two classifiers and can build the final prediction as the output. Support Vector Machines is not used for its poor performance while Logistic Regression is chosen for its ability to combine the output from multiple classifiers which makes it more efficient.

```
[ ] # Stack the predictions
stacked_preds = np.column_stack((rf_preds, xgb_preds))

+ Logistic Regression
lr = LogisticRegression()
lr.fit(stacked_preds, testY.argmax(axis=1))

+ LogisticRegression
LogisticRegression()
```

Figure 8: Implementing logistic regression model

Lastly, there are the predictions of the Logistic Regression model that have better features and are less likely to be prone to overfitting when compared with Random Forests and XGBoost.

Model Evaluation

Evaluations of the developed model incorporate accuracy, precision, recall, and F1-score which are well-known measurements. The confusion matrix is also developed to determine the effectiveness of the model when individual classes are considered.

```
# Final Predictions
final_preds = lr.predict(stacked_preds)
print(classification_report(testY.argmax(axis=1), final_preds))
print(confusion_matrix(testY.argmax(axis=1), final_preds))
```

	precision	recall	f1-score	support
0	1.00	1.00	1.00	15
1	1.00	0.80	0.89	15
2	0.83	1.00	0.91	15
accuracy			0.93	45
macro avg	0.94	0.93	0.93	45
weighted avg	0.94	0.93	0.93	45

```
[[15  0  0]
 [ 0 12  3]
 [ 0  0 15]]
```

Figure 9: Final prediction

From the observation of the classification report and the confusion matrix, it becomes clear that the proposed fusion model correctly identifies most of the leaves that have Red Rot and Red Rust compared to the healthy ones. This identifies the applicability of the hybrid approach which helps in attaining a balance between model accuracy and stability or robustness in variance within the data. The final predictive model comes with 93% accuracy.

Prediction Function

These segments are accommodated for preprocessing, segmentation, feature extraction, and classifying new images through a dedicated function implemented in the program. This function:

Initial image preparation algorithm which includes reshaping of the image and using image sharpening techniques.

Divides the image into smaller parts using the trained U-Net model of ResNet, Extracts features using DenseNet201, Classifies the image with the accuracies by Random Forest, XGBoost, and the proposed fusion model.

The function Prints classifier predictions and final prediction: The above-written function gives the printer output in terms of predictions of different classifiers and the final prediction made by the model.

```
# Classification
rf_pred = rf.predict(features_flat)
xgb_pred = xgb.predict(features_flat)

# Fusion Model
stacked_pred = np.column_stack((rf_pred, xgb_pred))
final_pred = lr.predict(stacked_pred)

classes = ["Healthy", "Red Rot", "Red Rust"]
prediction_label = classes[final_pred[0]]
if prediction_label == "Healthy":
    print("It is a Healthy Leaf")
else:
    print(f"Disease detected: {prediction_label}")
```

```
[ ] predict_image(lr, "content/drive/MyDrive/archive (43)/Dataset/RedRust/9.jpg")
```

```
1/1 [=====] - 2s 2s/step
1/1 [=====] - 0s 239ms/step
Disease detected: Red Rust
```

Figure 10: Classification and prediction of new images

Deep learning applied to feature extraction and the machine learning classification for identification of the different diseases make this a strong value for the identification of diseases on the leaves. For segmentation, instead of applying the U-Net model directly to the entire input image, the focus is on segmenting only the relevant area of the leaf, such as the disease-affected region. This approach, combined with DenseNet201's extensive feature mapping capabilities, enhances the precision of disease detection. The Random Forest and XGBoost classifiers involved in the Logistic Regression fusion model worked well when both classifiers' strengths were utilized, and together they offered high accuracy and decent resistance to overfitting.

Overall, this implementation shows how multiple approaches from the realm of machine learning can be harmonically integrated in order to face more intricate challenges regarding agricultural technology, bringing more sophisticated and efficient diagnostic methods in the future. It can be refined if more data is added as well as looking at other forms of ensemble learning, making the process smoother and adaptable to changing issues related to plant diseases.

Comparative analysis

For comparative analysis a simple CNN model with existing DenseNet model and Random Forest has been compared. Additionally, this model has been compared with a USEM Model (U-Net + DenseNet201 + Random Forest + XGBoost + Logistic Regression).

Classification Report for Simple CNN:				
	precision	recall	f1-score	support
0	0.00	0.00	0.00	15
1	0.37	0.47	0.41	15
2	0.42	0.73	0.54	15
accuracy			0.40	45
macro avg	0.26	0.40	0.32	45
weighted avg	0.26	0.40	0.32	45
Classification Report for DenseNet201:				
	precision	recall	f1-score	support
0	0.00	0.00	0.00	15
1	0.00	0.00	0.00	15
2	0.33	1.00	0.50	15
accuracy			0.33	45
macro avg	0.11	0.33	0.17	45
weighted avg	0.11	0.33	0.17	45
Classification Report for Random Forest:				
	precision	recall	f1-score	support
0	0.93	0.93	0.93	15
1	0.93	0.87	0.90	15
2	0.88	0.93	0.90	15
accuracy			0.91	45
macro avg	0.91	0.91	0.91	45
weighted avg	0.91	0.91	0.91	45
Classification Report for USEM Model:				
	precision	recall	f1-score	support
0	1.00	1.00	1.00	15
1	0.94	1.00	0.97	15
2	1.00	0.93	0.97	15
accuracy			0.98	45
macro avg	0.98	0.98	0.98	45
weighted avg	0.98	0.98	0.98	45

Figure 11: Model evaluation report

All the model classification report has been shown in the above image. The new method and Random Forest comes with more accuracy score than the simple CNN model and existing DenseNet model.

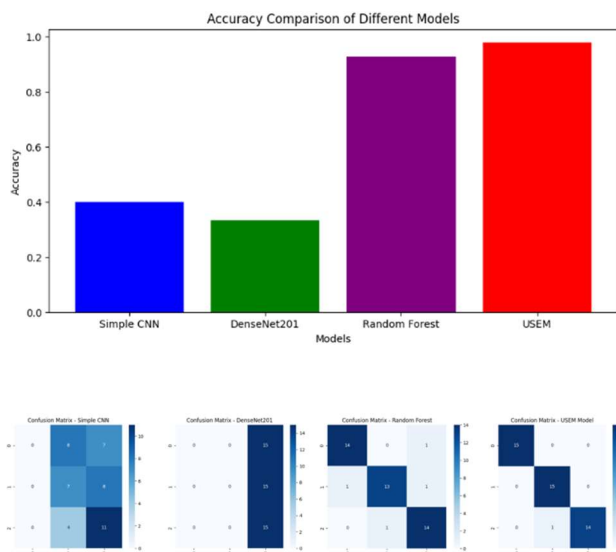


Figure 12: Graphical representation of model accuracy score and their confusion matrix

For visual comparison all the model accuracy score has been plotted and their confusion matrix has been printed.

V. Discussion

The development of a hybrid model for classifying disease affectation in leaves marks a significant advancement in agriculture. Combining deep learning with traditional machine learning improves accuracy and diagnostic capabilities. U-Net's image segmentation focuses the model on diseased areas, enhancing feature extraction. DenseNet201 further refines these features, providing detailed and comprehensive maps. The use of Random Forest and XGBoost classifiers is synergistic; Random Forest handles noisy data and prevents overfitting, while XGBoost excels in efficiency. Together, they enhance classification accuracy.

Integrating these results with a Logistic Regression model, or "fusion model," further reduces errors and increases final accuracy by leveraging the strengths of both classifiers. This approach demonstrates the value of combining different models to address complex agricultural diagnostic challenges. The ability to preprocess images, segment volumes, extract features, and classify with high accuracy provides a solid foundation for early disease diagnosis. This model can help farmers and agricultural experts avoid severe crop damage by enabling timely interventions.

For future research, expanding the dataset and adding more disease classes could further improve the model. Exploring additional ensemble techniques may also enhance accuracy, illustrating how blending various machine learning domains can yield optimal results in agricultural applications.

VI. Conclusion

The development of a high-performance technique for sugarcane leaf disease recognition marks a significant advancement in agricultural technology. By combining U-Net segmentation with stacking ensemble methods, this approach integrates advanced image segmentation with modern machine learning algorithms to deliver accurate and rapid results. The model's success is rooted in its robust data collection and preprocessing phases, where a diverse dataset of sugarcane leaf images is meticulously annotated and augmented. U-Net's encoder-decoder architecture excels at precisely segmenting diseased areas, enabling efficient feature extraction.

The classification process is enhanced by the stacking ensemble method, which leverages multiple base learners, such as decision trees, XGBoost, and CNNs, resulting in more reliable and accurate disease detection. Comprehensive evaluation metrics confirm the model's superiority over traditional methods. Optimized for real-world deployment, this hybrid model offers a scalable, efficient solution for early disease detection in sugarcane farming, setting a new standard for precision agriculture.

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