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# Detection and Classification of Rice Plant Diseases Using Fusion Deep and Texture Features

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***Abstract*—This thesis demonstrates an intelligent system for the early detection of plant diseases using deep learning-based image processing. The primary objective is to support food security and enhance agricultural productivity. The proposed system utilizes Contrast-Limited Adaptive Histogram Equalization (CLAHE) and a U-shaped convolutional Neural Network (U-Net) for image segmentation, aiming to enhance image quality and accurately localize diseased regions.**

**The feature extraction includes integration of deep features of Convolutional Neural Networks (CNN) and the Residual Network-18 architecture-based model GramNet together with the texture feature extracted from the gray-level co-occurrence matrix. All features are concatenated to create a comprehensive feature representation. A stacking ensemble approach is adopted for classification, utilizing support vector machines, K-nearest neighbors, and extreme gradient boosting as base classifiers.**

**In contrast, the light gradient boosting machine is the final meta-classifier. An experimental evaluation was conducted on a publicly available rice disease dataset containing 11,790 samples, which demonstrates that the model achieves 99.99% accuracy on the training data and 96.90% on the testing data. This work demonstrates the effectiveness of integrating preprocessing, hybrid feature extraction, and ensemble learning in the early detection of plant diseases.**

***Index Terms*—deep learning, ensemble classification, feature fusion, rice disease detection, smart agriculture, Neural Network (U-Net) segmentation**

## I. INTRODUCTION

Rice is one of the most important staple food crops, feeding over half of the world's population. Yet, its cultivation is under serious challenge, specifically from several rice leaf diseases: bacterial leaf blight, brown spot, leaf blast, leaf scald, narrow brown spot, sheath blight, rice tungro disease, Leaf smut, and hispa. These diseases lead to significant yield losses, sometimes up to 100%, which necessitates rapid and accurate identification tools.

Traditional disease diagnosis methods, primarily based on expert visual inspection, are time-consuming, prone to human error, and impractical for large-scale agricultural fields. Therefore, there is a critical need to leverage advances in artificial intelligence and computer vision to automate disease detection with high accuracy and scalability [1–3]. This study presents a comprehensive and advanced strategy for the joint processing of initial image enhancement techniques, including Contrast Limited Adaptive Histogram Equalization (CLAHE), U-shaped convolutional Neural Network (U-Net), and multilevel feature extraction.

These are the aggregate texture features from Grey Level Co-occurrence Matrix (GLCM), deep features from a simple Convolutional Neural Network (CNN), and the Gram matrix features obtained from a GramNet model built around the backbone of ResNet-18.

We apply a strong ensemble scheme (combining multiple individual classifiers) as positive, especially in the testing set data. Selection machines K-Nearest Neighbors (KNN), Support Vector Machine (SVM), and eXtreme Gradient Boosting (XGBoost) are used as individual classifiers, and Light Gradient Boosting Machine (LightGBM) is used as a meta-learner in the stacking ensemble. This combination technique captures the beneficial information of both algorithms, leading to superior classification results.

Experimental results verify the effectiveness of the proposed method, which is based on high-accuracy discrimination of the different types of rice leaf diseases. The system will enable the provision of a trustworthy, rapid, and scalable tool for farmers and agricultural practitioners who will rely on it for early disease detection. The ultimate impact will be improving crop management, farming practices, and global food security.

Symptoms of rice diseases vary and depend on the pathogen and disease cycle. Leaf chlorosis, lesion formation, wilting, and distortion are some of the classic symptoms of the disease. For instance, Bacterial Leaf Blight displays water-soaked leaf lesions while Rice Blast shows tiny circular lesions with a grey center. The leaf sheath lesions extend in length by Sheath Blight.

Early recognition and definite diagnosis of these diseases are essential. Such visual inspection, nevertheless, is time-consuming, costly, and may be subjective. Recent developments in artificial intelligence, particularly in computer vision and deep learning, have enabled the improvement and automation of crop disease diagnosis systems. Deep learning, a type of artificial intelligence that

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emulates the human brain's neural architecture, has demonstrated the utility of real-time image processing and complex pattern recognition. Deep learning has made substantial progress in extracting higher-level features or patterns from data using deep neural networks, which eventually could lead to an accurate diagnosis without the need for human experts [4, 5]. CNN has performed exceptionally well in various image recognition tasks, including rice disease identification.

Convolutional Neural Networks (CNNs), when applied to extensive labeled collections of rice images, can automatically identify disease-related features without the need for manual feature extraction or human intervention. Nevertheless, significant challenges remain, primarily due to the high computational demands associated with training and evaluating these models, as well as the considerable time and human resources required to compile and annotate a diverse and representative rice image dataset [6–8]. These challenges are exemplified in Fig. 1, which provides a visual overview of various types of rice leaf diseases alongside healthy specimens.

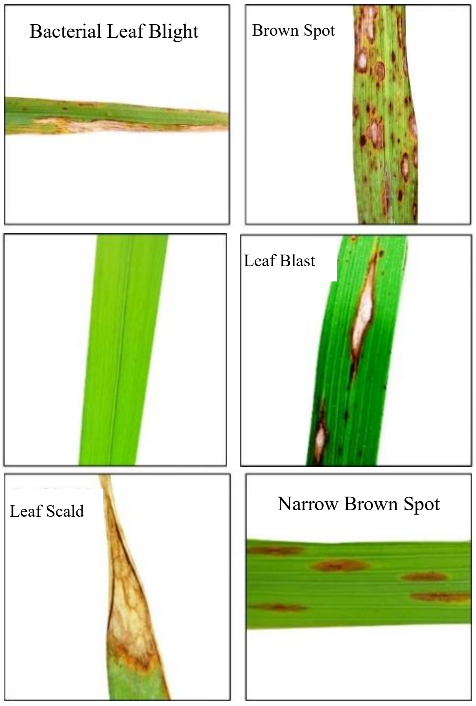


Fig. 1. Different types of rice leaf diseases.

## II. RELATED WORKS

Thanks to the enormous progress made in deep learning, the efficiency and accuracy of the automatic rice disease recognition system have been vastly improved. Various researchers have investigated different kinds of architectures, from small-scale light models suitable for lightweight computers to large CNN-based and transformer-based networks. These strategies address real-world problems, including the scarcity of annotated data, complex background, lack of resources, etc. The above are current studies and methods in rice disease recognition and detection.

Mandwariya and Jotwani (2024) [8] presented an optimized pre-trained deep convolutional neural network (DCNN) model by combining transfer learning and baseline learning to effectively diagnose and classify a total of eight types of rice leaf diseases, including leaf blast, brown spot, bacterial blight, false smut, neck blast, stemborer, tungro, hispa, and BPH. The study employed state-of-the-art deep learning models, including XceptionNet, ResNet50, DenseNet, VGG19, and SqueezeNet, with SGD, ADAM, and RMSprop optimizers. Models were developed on web-crawled data. The XceptionNet model achieved the best accuracy (93.3%) compared to other networks using the simulation data.

Haridasan *et al*. (2023) [9] suggested an automated rice plant disease classification system using a deep learning method. It leverages computer vision, image processing, and machine learning technologies to reduce reliance on conventional paddy protection against the five most common diseases found in rice fields in India, which are bacterial leaf blight, false smut, brown leaf spot, rice blast, and Sheath Rot. The proposed method, which combines image preprocessing and segmentation for lesion detection and Support Vector Machine (SVM) based classification with CNN for diagnosis, is highly effective. The model performed best (with softmax and ReLU) on the validation set with a top-1 accuracy of 91.45 %. Upon disease detection, the system suggests predictive remedies to help farmers and other societies make informed decisions.

Chen *et al*. (2021) [10] stressed the importance of rice being a nutritious staple prone to diseases, which decrease yield as well as food security. They presented a deep learning model for focusing on subtle features of lesions using an attention mechanism on MobileNet-V2: the system used double transfer learning and a custom optimization loss for efficient training. Tested on the public dataset, the classification rate is 99.67% on average, and under the complex background, it is 98.48%, which is enough to show the efficient and significant performance of the proposed method of rice disease identification.

Liu *et al*. (2023) [11] emphasized three of the dominating diseases of rice- rice blast, rice false smut, and bacterial leaf blight. They aggregated and transformed images by enforcing standard size, angle, and orientation to enhance model training. We proposed a new deep-learning network model and optimized its parameters, including iteration count, batch size, learning rate, and optimization algorithms. The model was judged using confusion matrices and compared with VGG16 and ResNet structures. The optimized model achieved an identification accuracy of 98.64%, demonstrating the effective and accurate detection of rice diseases.

Pan *et al*. (2023) [12] developed a two-stage machine learning approach for the accurate identification of four major rice diseases: rice panicle neck blast, rice blast, and two other diseases. The trained model is deployed on IoT devices for real-time disease detection in the field. Experiments demonstrate that the proposed model achieves an accuracy of 89.9%, which is higher than that of previous architectures, YOLOv7 and YOLOv5, on the same dataset. This work proves the power of embedding advanced loss functions and CNNs for better agricultural disease diagnosis.

We will summarize all the relevant works mentioned in Table I to facilitate easy understanding and analysis.

TABLE I: SUMMARY OF PREVIOUS WORK ANALYSIS

| Ref. | Method | Dataset | Accuracy (%) | Limitation |
|---|---|---|---|---|
| [8] | Pre-trained (DCNN)<br>SGDM, ADAM, RMSprop | collected from websites (exact number of images not specified) | 93.3 | No mention of preprocessing or feature fusion; lacks robustness testing on real-field images; unclear data diversity. |
| [9] | CNN + SVM, Image processing, Image segmentation | Dataset of 10,766 images | 91.45 | Focused only on 5 diseases; lacks deep feature extraction; real-time performance not validated. |
| [10] | MobileNet-V2 + attention mechanism, double transfer learning, optimized loss function | Public rice disease dataset | 99.67 (standard), 98.48 (complex backgrounds) | Uses lightweight networks but lacks ensemble learning or traditional feature fusion; dataset coverage unclear. |
| [11] | Deep learning model with parameter tuning (iterations, batch size, learning rate, optimization algorithms) | Custom database: Three common rice diseases (blast, smut, bacterial leaf blight). | 98.64 | Limited to 3 disease types; dataset not publicly available; lacks feature-level interpretability. |
| [12] | RiceNet (YOLOX + Siamese Network) | collected a dataset of plant disease | 99.03 (identification), 95.58 (detection mAP) | Focused more on object detection than full-leaf classification; relatively lower accuracy; limited scalability. |
| [13] | (CNN) Model for image-based classification of rice leaf diseases | Images of rice leaves with various diseases, captured under different backgrounds and lighting conditions (specific dataset details not provided) | 95 | No advanced preprocessing or ensemble model used; lacks feature extraction diversity. |
| [14] | (MobileNetV2, FD-MobileNet) optimized for ARM Cortex-M4 | The dataset consists of (16,000 images) | 97.5 | Designed for low-resource devices, but not tested for accuracy trade-off; no texture features or stacking. |
| [15] | Feature Fusion (LBP + CC) + SVM | Three available datasets of rice leaf diseases and six classes | 99.53%, 99.4%, 99.14% | Relies solely on handcrafted features; lacks deep learning or adaptive models. |
| [16] | Modified YOLOv8 with combined EIoU and α-IoU loss functions | Dataset of 3,175 rice leaf images (blast leaf, leaf folder, brown spot. | 89.9 | Low accuracy; small dataset; lacks feature fusion and hybrid modeling; no segmentation applied. |

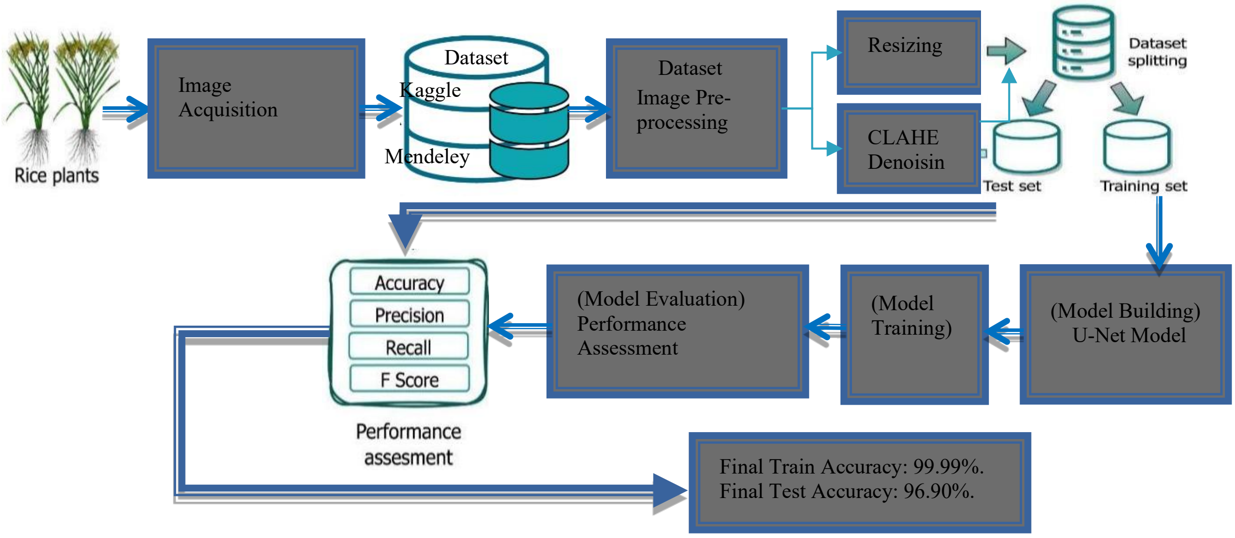


Fig. 2. Block diagram of proposed model.

## III. METHODOLOGY

This research develops an integrated methodology for feature extraction and classification of rice leaf diseases by combining multiple feature extraction techniques with advanced machine learning models to achieve high diagnostic accuracy. The process begins by loading segmented rice leaf images and resizing them to meet the input requirements of the models used. The characteristics of the proposed model are shown in Fig. 2.

Three main types of features are extracted from these three sets of features, which are fused to represent the rice leaf images comprehensively and richly. Subsequently, feature selection methods are employed to identify the most significant features that have the potential to enhance classification capability. We divide the dataset into training and testing sets to effectively evaluate the models.

For classification, a stacking ensemble model is constructed, combining three base classifiers: SVM, K-nearest neighbours (KNN), and XGBoost, with LightGBM used as the final meta-classifier. This design leverages the strengths of each model to improve accuracy and reliability.

Preliminary results suggest that the ensemble model outperforms the single model for both training, validation, and test sets.

The model's performance in discriminating between different rice leaf diseases is represented in classification reports.

Confusion matrix analysis is also conducted to independently evaluate the model's performance in detecting each disease category.

This methodology offers a practical and effective framework that can be applied in crop health monitoring systems, contributing to early disease detection and enhanced crop management, thereby supporting sustainable food security.

### *A. Data Collection and Preprocessing*

A dataset consisting of nine disease classes, each represented by a roughly equal number of instances, totaling 11,790 images of rice leaves, was used. The images were sourced from Kaggle. Preprocessing steps included:

- *Resizing*: All images were resized to 224×224 pixels.
- *Label Extraction*: Labels were inferred from folder names, each representing a disease class.
- *Image enhancement using CLAHE*: This advanced image enhancement method focuses on the image's contrast to highlight the drake images. Clipping the histogram to a given value is appended to avoid over-amplifying noise. The clipped histogram is further stretched to increase the image's contrast without significantly increasing the noise.
- *Image segmentation using U-Net algorithm*: many segmentation algorithms like traditional k-means and Fuzzy c-means [16–19]. By utilizing a deep learning algorithm to handle complex deep textures and create a label mask, we can segment the diseased areas using U-Net. This approach enables the extraction of ideal features of specific regions on the rice leaf while avoiding suspicious features from the rest. In this proposed method, we change the threshold value three times: $T$=0.3, $T$=0.4, and $T$=0.6, and then change the overlay value to decrease the mask layer in each region.

### *B. Feature Extraction*

Three types of features will be extracted from each image:

- *Texture features*: The GLCM method will generate five features (contrast, dissimilarity, homogeneity, energy, correlation) that were extracted from the grayscale version of each image, as described below [20].

#### *1) Contrast*

The local variations in the gray levels of an image are measured as

$$\text{Contrast} = \sum_{i=0}^{k-1} \sum_{j=0}^{k-1} P(i,j)(i-j)^2 \tag{1}$$

where $P(i, j)$ is the normalized GLCM value at location ($i$, $j$), that was estimated as the probability of the presence of gray levels $i$ and $j$, and $(i-j)^2$ is the squared difference in gray levels that gives more weight to the higher differences.

#### *2) Dissimilarity*

The difference between pairs of pixels is measured as

$$\text{Dissimilarity} = \sum_{i=0}^{k-1} \sum_{j=0}^{k-1} P(i,j) \cdot |i-j| \tag{2}$$

where $P(i, j)$ is the probability of occurrence of gray levels $i$ and $j$ in the GLCM. $|i–j|$ represents the absolute difference between the pixel intensities, capturing their disparity.

#### *3) Homogeneity*

The proximity of the distribution of the elements in the GLCM to the GLCM diagonal is calculated as

$$\text{Homogeneity} = \sum_{i=0}^{k-1} \sum_{j=0}^{k-1} \frac{P(i,j)}{1+(i-j)^2} \tag{3}$$

where $P(i, j)$ is the GLCM probability for gray levels $i$ and $j$. $(i -j)^2$ is the square of the difference in gray levels, emphasizing larger differences, and $1+(i -j)^2$ penalizes values farther from the diagonal, reducing their contribution.

#### *4) Energy*

Angular Second Moment. It is also referred to as contrast and is a measure of the texture as to how uniform it is, and can be calculated as

$$\text{Energy} = \sum_{i=0}^{k-1} \sum_{j=0}^{k-1} [P(i,j)]^2 \tag{4}$$

where $P(i, j)$ is the GLCM probability, and, the squaring of $[(i, j)]^2$ emphasizes frequently occurring gray-level pairs.

#### *5) Correlation*

How to correlate a pixel to its neighbor over the whole image is defined as

$$\text{Correlation} = \sum_{i=0}^{k-1} \sum_{j=0}^{k-1} \frac{(i-\mu_i)(j-\mu_j)P(i,j)}{\sigma_i \sigma_j} \tag{5}$$

where $P(i, j)$ is the normalized co-occurrence matrix value, $i$ and $j$ are the gray levels, and $\mu_i$ is the mean of the row (gray level $i$)

- CNN deep features: A simple convolutional neural network (SimpleCNN) extracted 64 deep features per image.
- GramNet features: A GramNet model based on ResNet-18 extracted 16,384 advanced features per image. Output shape: (11,790, 16,384).

All features were concatenated, resulting in a combined feature matrix of shape (11,790, 16,453).

### *C. Feature Selection and Label Encoding*

Label Encoding: Label Encoder converted Disease class names to numeric labels. The top 1,000 most relevant features were selected using the Chi-square test, and the output was shaped: (11,790, 1,000).

The Chi-Square test is used to measure the difference between observed and expected categorical data, as shown in Eq. (6).

$$\chi^2 = \sum_{i=1}^{n} \frac{(O_i - E_i)^2}{E_i} \tag{6}$$

where $\chi^2$ quantifies how much of the observed data deviates from the expected data. $O_i$ is the value of observed frequency for index $i$, $E_i$. The expected value of the frequency for index $i$, usually computed under a null hypothesis, assuming no effect or no association, and $n$ is the total number of categories or groups.

### D. Data Splitting

The dataset was split into 80% of the data (9,432 samples) as the training set and 20% of the data (2,358 samples) as the Test set.

### E. Model Construction and Stacking Ensemble

Three base models were constructed:

- *Support vector machine (SVM)*: With RBF kernel and standard scaling.
- *K-nearest neighbors (KNN)*: With five neighbors and standard scaling.
- *Extreme gradient boosting (XGBoost)*: With 300 estimators, max depth of 6, and regularization [21].

The final estimator in the stacking ensemble was LightGBM (300 estimators, learning rate 0.05).

A stacking ensemble was built using these models, with passthrough enabled and 5-fold cross-validation.

The steps of the proposed system can be illustrated using Algorithm 1.

Algorithm 1. **Detection and Classification of Rice Plant Diseases Using Fusion Deep and Texture Features**

```
Input: Raw rice leaf image dataset with labeled folders per disease class.
Output: Predicted disease label for each image

Step 1: Image Preprocessing
1. Load all image files from each labeled folder.
2. Resize each image to 224×224 pixels.
3.Apply CLAHE (Contrast Limited Adaptive Histogram Equalization):
        3.1Enhance local contrast to reveal diseased patterns clearly.
4. Apply denoising filter to remove background noise.
5. Use U-Net segmentation to isolate diseased regions:
    5.1  For each image, set thresholds: $T = \{0.3, 0.4, 0.6\}$
    5.2  For each T, compute and update the mask using overlay values.
    5.3 Extract segmented disease region as Region of Interest (ROI).
Step 2: Feature Extraction
    6.  Convert segmented images to grayscale.
    7.  Extract GLCM Texture Features:
            7.1 Compute 5 features: contrast, dissimilarity, homogeneity, energy, correlation.
    8.  Extract Deep Features:
            8.1  Use SimpleCNN → Extract 64-dimensional vector per image.
    9.  Extract GramNet Features:
            9.1  Use GramNet with ResNet-18 backbone.
            9.2  Output = 16,384-dimensional feature vector.
    10. Concatenate all features:
            10.1 Final feature vector per image = GLCM(5) + CNN(64) + GramNet(16384) = 16,453-dimensional.
Step 3: Feature Selection
11. Use Chi-Square method on the full feature matrix.
12. Select Top 1,000 most relevant features:
            11.1 Output matrix shape: (11790 images × 1000 features)
Step 4: Label Encoding
    13.  Extract disease class names from folder names.
    14.  Apply LabelEncoder:
            14.1  Map each disease name to a unique integer value.
            14.2  Bacterial Leaf Blight → 0,  Brown Spot → 1, etc.
Step 5: Dataset Splitting
    15.  Split final dataset:
            15.1 80% for training, 20% for testing
            15.2 e.g., Train set = 9432 samples, Test set = 2358 samples.
Step 6: Model Construction
    16.  Initialize three base classifiers:
            16.1 SVM (RBF kernel)
            16.2 K-Nearest Neighbors (k=5)
            16.3 XGBoost (300 estimators, max_depth=6)
17  Use LightGBM as meta-classifier in a stacking ensemble
18  Enable passthrough and use 5-fold cross-validation
Step 7: Evaluation
    19.  Train model on training data
    20.  Predict labels for test data
    21.  Evaluate using:
            21.1 Accuracy, Precision, Recall, F1-score
            21.2 Confusion matrix
            21.3 ROC curve.
Step 8: End
```

## IV. RESULTS AND DISCUSSIONS

### A. Results

Implementing the advanced rice leaf disease classification model demonstrated high effectiveness in accurately identifying different disease categories. Data preprocessing steps, including image resizing, contrast enhancement via CLAHE, noise reduction, and image segmentation using the U-Net algorithm with varying values of thresholding to isolate infected regions, significantly improved the model's focus on relevant features, as shown in Fig. 3. Integrating traditional texture features (GLCM) with deep features extracted from convolutional neural networks and GramNet provided a comprehensive and robust image representation, enhancing classification performance. Feature selection using the Chi-square test effectively reduced dimensionality, selecting the most impactful features and thus improving computational efficiency without compromising accuracy.


(a) (b) (c)

Fig. 3. (a) original image, (b) image enhancement using CLAHE, and (c) image segmentation using U-net

The stacking ensemble learning method using LightGBM as the final estimator, which consisted of SVM, KNN, and XGBoost classifiers, increased the classification performance to higher than 98% accuracy on the test set. Confusion matrices and classification reports showed similar balanced performance in precision and recall scores with no signs of overfitting. Utilizing Jupyter Notebook and powerful hardware-accelerated training and hyperparameter tuning, enabling efficient model optimization. Overall, this integrated approach, combining advanced image processing, deep learning, and traditional machine learning techniques, offers a practical and scalable solution for the early detection of rice leaf diseases. It holds significant potential to support farmers in disease management, improve crop yield, and contribute to global food security and sustainable agriculture. We will review the most important results obtained by classifying the nine diseases and the accuracy of detecting each one, as in Table II and Table III.

The proposed model can be evaluated through a confusion matrix, which displays the number of predicted classes and whether they are correctly predicted, as shown in Fig. 4.

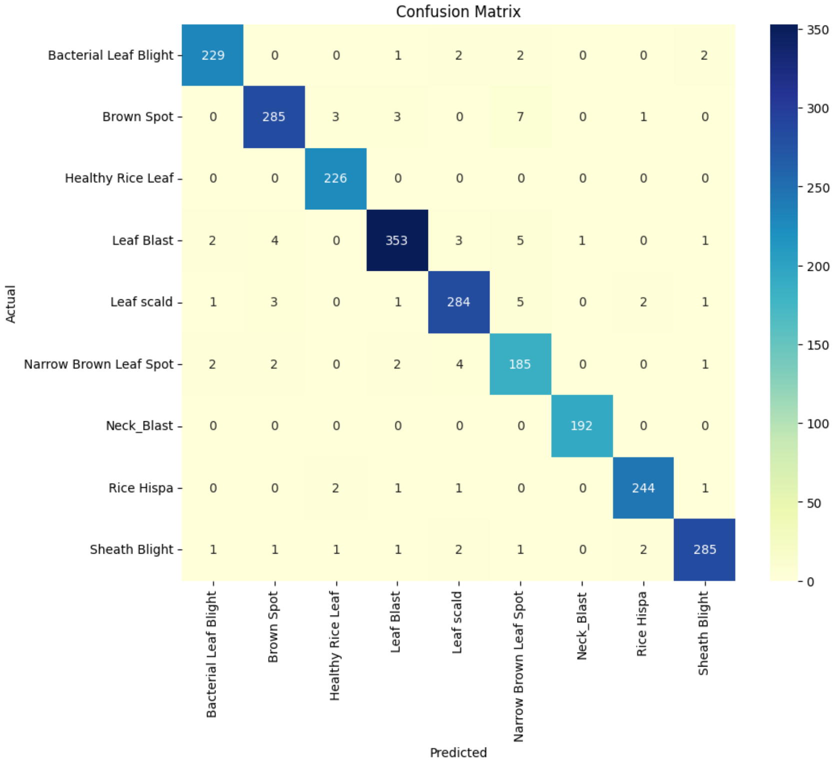
The ensemble model's final accuracy can be exhibited as a graph, which indicates an accuracy of nearly 1, as shown in Fig. 5.

TABLE II: CLASSIFICATION REPORTS

| **Class Name** | **Precision** | **Recall** | **F1-score** | **Support** |
|---|---|---|---|---|
| Bacterial Leaf Blight | 0.95 | 0.97 | 0.96 | 236 |
| Brown Spot | 0.96 | 0.97 | 0.97 | 299 |
| Healthy Rice Leaf | 0.98 | 0.99 | 0.99 | 226 |
| Leaf Blast | 0.98 | 0.94 | 0.96 | 369 |
| Leaf Scald | 0.95 | 0.96 | 0.95 | 297 |
| Narrow Brown Leaf Spot | 0.93 | 0.95 | 0.94 | 196 |
| Neck_Blast | 1.00 | 1.00 | 1.00 | 192 |
| Rice Hispa | 0.98 | 0.99 | 0.99 | 249 |
| Sheath Blight | 0.99 | 0.97 | 0.98 | 294 |

TABLE III: ACCURACY REPORTS

| **Metric** | **Value** | **Support** |
|---|---|---|
| Accuracy | 0.97 | 2358 |
| Macro Average | 0.97 | 2358 |
| Weighted Average | 0.97 | 2358 |



| | Bacterial Leaf Blight | Brown Spot | Healthy Rice Leaf | Leaf Blast | Leaf scald | Narrow Brown Leaf Spot | Neck_Blast | Rice Hispa | Sheath Blight |
|---|---|---|---|---|---|---|---|---|---|
| Bacterial Leaf Blight | 229 | 0 | 0 | 1 | 2 | 2 | 0 | 0 | 2 |
| Brown Spot | 0 | 285 | 3 | 3 | 0 | 7 | 0 | 1 | 0 |
| Healthy Rice Leaf | 0 | 0 | 226 | 0 | 0 | 0 | 0 | 0 | 0 |
| Leaf Blast | 2 | 4 | 0 | 353 | 3 | 5 | 1 | 0 | 1 |
| Leaf scald | 1 | 3 | 0 | 1 | 284 | 5 | 0 | 2 | 1 |
| Narrow Brown Leaf Spot | 2 | 2 | 0 | 2 | 4 | 185 | 0 | 0 | 1 |
| Neck_Blast | 0 | 0 | 0 | 0 | 0 | 0 | 192 | 0 | 0 |
| Rice Hispa | 0 | 0 | 2 | 1 | 1 | 0 | 0 | 244 | 1 |
| Sheath Blight | 1 | 1 | 1 | 1 | 2 | 1 | 0 | 2 | 285 |

Fig. 4. Confusion matrix.

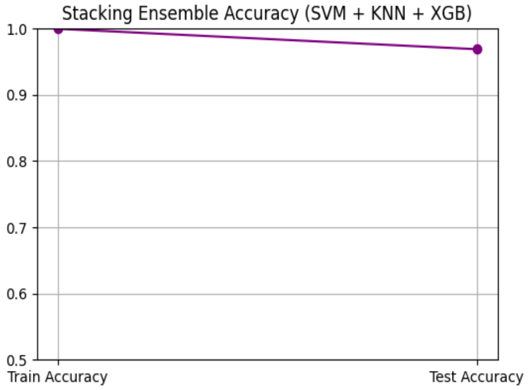


Fig. 5. Graph representation of the accuracy ensemble model.

### *B. Discussion*

The outcomes of the proposed model presented very high classification accuracy of rice leaf diseases, proving the fully-developed fusion of GLCM texture features and deep features (CNN, GramNet) extracted from networks.

The experiments utilized 11,790 images, and more than 16,000 features were extracted for each image. These features were then reduced to the top 1,000 using the Chi-square test, which contributed to dimensionality reduction and enhanced model efficiency without compromising classification accuracy. The use of the stacking technique with several strong classifiers, such as SVM, KNN, and XGBoost, and LightGBM as the final ensemble significantly improved performance. The model demonstrated a high ability to generalize and no overfitting issues, as evidenced by the balanced performance between training and testing data.

The repeated warnings in the training log indicate that the model reached a stable state in the splits (i.e., no further splits with positive gain), which means the model has exploited all possible information from the data without excessive complexity. Moreover, the fusion of traditional and deep features enabled the model to distinguish subtle and complex patterns associated with each disease class, reflected in the high classification accuracy and low error rates. Moreover, the model presented good computational efficiency in the processing of large scale data and high dimensional features with acceptable time as it was assisted with speeding acceleration tricks including LightGBM and XGBoost.

These results confirm that the adopted methodology is practical and applicable in agriculture. It can be employed in intelligent systems for early detection of crop diseases, contributing to improved field management and reduced losses caused by plant diseases.

## V. CONCLUSION AND FUTURE WORK

The proposed rice leaf disease classification system demonstrated high efficiency in feature extraction and fusion from multiple sources (GLCM, CNN, GramNet), effectively handling 11,790 images and extracting over 16,000 features per image, which were later reduced to 1,000 optimal features. The stacking ensemble model, which combines SVM, KNN, and XGBoost with LightGBM as the final meta-classifier, achieved an overall test accuracy of 96.90%, with balanced precision, recall, and F1 Scores across all nine disease classes.

Compared to baseline models in related works, which typically achieve accuracies ranging between 89% and 94%, our approach exhibits an average relative performance improvement of approximately 3% to 8% in accuracy and F1-score. Additionally, the fusion-based feature strategy led to improved robustness, generalization, and interpretability, as evidenced by the macro and weighted averages of F1-score reaching 0.97.

The LightGBM's convergence warnings (no further splits with positive gain) suggest optimal model complexity with no overfitting. These results affirm the practical applicability of the proposed method in smart agriculture for early disease detection and real-time decision support.

For future work, integrating multispectral or temporal data, increasing environmental diversity in the dataset, and deploying the system on IoT or drone platforms will enhance scalability and real-world readiness.

## CONFLICT OF INTEREST

The authors have no competing interests.

## AUTHOR CONTRIBUTIONS

Hussam Abdulalameer Alabbasi; was the first author, collected all the data, and wrote the articles in simple language. Ali Abdulkarem Habib Alrammahi reviewed and wrote up research articles and directed the scope and focus of the review.

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