An Explainable Rice Leaf Disease Recognition Using ResNet50 Transfer Learning and SHAP-Based Top-K Feature Selection

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Abstract: Rice is a major staple crop, but its yield and grain quality are often reduced by leaf diseases. In many farming regions, disease identification is still done by eye, which can be slow, inconsistent, and difficult when symptoms change with lighting, plant age, or background conditions. To support early and reliable diagnosis, this paper proposes a rice leaf disease classification approach that combines a strong deep-learning model with an explainability-based feature selection method. We fine-tune a pretrained ResNet50 model to learn disease-related visual patterns from leaf images resized to 240×240. The network produces a compact 512-dimensional embedding that summarizes the most important disease characteristics. To make the system more interpretable and to remove less useful features, we train a Random Forest model on these embeddings and use SHapley Additive exPlanations (SHAP) to measure the importance of each embedding dimension. Using a per-class union Top-K strategy that selects the most informative features while ensuring that minority classes are not ignored. A lightweight classifier is then trained on the selected feature subset using a two-stage training process. Experiments show that the proposed SHAP-guided ResNet50 model achieves 98% accuracy. Compared to an existing approach, the proposed method improves accuracy with less training time per epoch.

Keywords: Rice leaf disease detection, Transfer learning, ResNet50, SHAP (Shapley Additive Explanations), Feature selection,

I. INTRODUCTION

Rice is one of the most important staple crops worldwide, and its productivity is directly affected by foliar diseases and pest infestations that reduce yield and grain quality. Visual disease diagnosis in rice fields is still mostly done by farmers or extension workers, but it's slow, subjective, and often inaccurate because symptoms change with variety, growth stage, lighting, and messy backgrounds. When diseases are identified late or incorrectly, it can lead to wrong pesticide use, higher costs, and serious yield loss. This creates a strong need for accurate, low-cost, scalable detection methods, and recent advances in deep learning have made image-based plant disease recognition much more effective [1]. CNNs are great at picking up useful patterns straight from raw images, and they usually outperform older methods that rely on manually designed features [2]. But using deep learning on real farm data isn't always straightforward. One big issue is that agricultural datasets are often unbalanced—some diseases have lots of images while others have very few—so the model can end up favoring the diseases it sees most. Another issue is trust:

deep networks often behave like "black boxes," so it's hard to explain why a prediction was made [3]. In farming, where the wrong call can waste money or harm crops, being able to justify decisions matters [4]. That's why this paper proposes a rice disease classification approach that uses transfer learning and an explainability-based feature selection method to improve both performance and transparency [5]. A ResNet50 backbone pretrained on ImageNet is fine-tuned to extract compact 512-dimensional embeddings that encode disease-specific visual characteristics such as lesion texture, spot density, and discoloration patterns. To improve interpretability and reduce redundancy in the learned representation, an auxiliary RandomForest model is trained on these embeddings and explained using SHapley Additive exPlanations (SHAP). The resulting SHAP scores are used to rank embedding dimensions and select a Top-KKK subset of the most informative features using a per-class union scheme that preserves discriminative cues for minority classes. A lightweight neural classifier is then trained on the SHAP-selected embedding subspace, enabling a performance–interpretability trade-off while maintaining competitive accuracy. The proposed approach aims to deliver accurate and explainable disease predictions, supporting practical deployment in decision-support tools for farmers and agronomists.

II. LITERATURE REVIEW

Several researchers have explored deep learning for plant and rice leaf disease detection, often aiming to improve accuracy while keeping models efficient. Hassan et al. [1] introduced a compact deep model that combines Inception-style feature extraction with residual connections. To reduce computational cost, they used depthwise separable convolutions. Their approach was evaluated on three plant disease datasets and achieved strong performance: 99.39% on PlantVillage, 99.66% on a rice disease dataset, and 76.59% on a cassava dataset, while using fewer parameters than many existing deep models. In rice disease classification, Latif et al. [2] designed a modified VGG19-based DCNN capable of recognizing six rice leaf disease categories, reporting an average accuracy of 96.08%, which they noted as better than earlier techniques. Similarly, Dogra et al. [3] applied a VGG19 transfer learning setup and achieved 93.0% accuracy, with balanced results across sensitivity, specificity, precision, and F1-score. Some studies focus on deployment in real-world or mobile contexts. Su et al. [4] compared CNN-based disease identification methods aimed at mobile platforms and trained their model on a small dataset (120 images) representing three common rice diseases. Their reported performance was around 81% on both training and validation data. For mobile-ready detection, Jain et al. [5] proposed the "E-crop doctor" smartphone application, which detects paddy leaf diseases and suggests pesticides; they integrated a chatbot ("docCrop") for continuous support. Their use of YOLOv4-tiny delivered a 97.36% mAP, highlighting its speed advantage for mobile use. Object detection approaches are also gaining attention. Jhatil et al. [6] trained a YOLOv5 model on 400 rice leaf images using Google Colab, and found that the best results occurred at 100 epochs, reporting strong precision and recall alongside mAP values. Likewise, Rajpoot et al. [7] combined VGG16-based transfer learning with Faster R-CNN to detect major rice diseases such as bacterial leaf blight, brown spot, and leaf smut. They then used a random forest classifier on extracted features and achieved an average accuracy of 97.3%. Beyond standard CNNs, hybrid and ensemble techniques have been proposed. Kumar et al. [8] introduced a deep convolutional neuro-fuzzy method (DCNFM) that merges CNN learning with fuzzy logic to better handle complex, unstructured field image data, reporting a 98.17% detection rate, outperforming traditional CNN baselines. Shovon et al. [9] proposed PlantDet, an ensemble system combining InceptionResNetV2, EfficientNetV2L, and Xception, designed to reduce underfitting and perform well on limited datasets. Their results showed improved scores across common evaluation metrics and included explainability comparisons using methods such as Grad-CAM and Score-CAM. Dataset quality and realism are recurring themes in this area. Moupojou et al. [10] noted that many models perform well on controlled datasets like PlantVillage and PlantDoc, but highlighted the importance of plantation-level images for practical use. They pointed to FieldPlant, a field-collected dataset of 5,170 images, as being more suitable for real-world classification and object detection, and reported that it outperformed PlantDoc in classification tasks. A few works emphasize new architectures or broader research insights. Shibi et al. [11] demonstrated that InceptionV3 with transfer learning can effectively support rice leaf disease recognition. Haridasan et al. [12] proposed a computer vision pipeline combining image processing and learning-based techniques; their deep learning approach achieved a 0.9145 validation accuracy, and they also included remedy recommendations. Singh et al. [13] developed a custom CNN for rice disease detection using datasets containing four diseases and healthy leaf samples, reporting best performance with the Adam optimizer. Finally, Liu et al. [14] proposed a new deep learning network aimed at improving efficiency and reducing uncertainty, achieving 98.64% accuracy on disease sample images. To capture the bigger picture, review papers also contribute by identifying challenges and gaps. Wani et al. [15] discussed ML/DL pipelines, datasets, and research issues across crops such as tomato, rice, potato, and apple, while outlining future directions.

III. METHODOLOGY USED

The proposed system classifies rice-leaf diseases by combining transfer learning with an explainability-driven feature selection stage. First, leaf images are loaded from class-wise folders, resized to 240*240, and split into training and validation sets using stratification to preserve class proportions. During training, augmentation is applied to reduce overfitting, and ResNet50-specific preprocessing is used to match the ImageNet-trained backbone.

A pretrained ResNet50 serves as the feature extractor; its output is converted to a compact representation using Global Average Pooling and a fully connected "embedding" layer that produces a 512-dimensional feature vector. A softmax layer maps this embedding to class probabilities, and the network is trained using weighted categorical cross-entropy so that minority classes contribute more to the loss.

After baseline training, embeddings are extracted for all images and used to train a Random Forest classifier; this auxiliary model enables efficient SHAP (Tree Explainer) computation to estimate how strongly each embedding dimension influences class predictions. SHAP values are aggregated into per-class importance scores, and a Top-K subset of embedding dimensions is selected using a per-class union strategy to ensure minority-class features are retained. Finally, a SHAP-Top-K neural model is built by reusing the trained ResNet50 and embedding layer, selecting only the Top-KKK dimensions, and training a compact classification head; training is performed in two stages—first freezing the backbone to adapt the head, then fine-tuning only the last backbone layers with a very small learning rate to reduce confusions between visually similar diseases.

A Convolutional Neural Network (CNN) is designed to learn hierarchical representations from images. Early layers typically learn low-level features such as edges and color gradients, while deeper layers learn higher-level patterns such as lesion shapes, texture irregularities, and disease-specific spot distributions.

Given an input image $x \epsilon R^{H\times W\times 3}$ a convolution layer applies a set of filters (kernels) to generate feature maps:

$$y_k(u,v) = \sum_{c=1}^{C_{in}} \sum_{i=1}^{K} \sum_{j=1}^{K} w_{k,c}(i,j) x_c(u+i, v+j) + b_k \quad (1)$$

Where, $w_{k,c}(i,j)$ is the filter weights for output channel k and input channel c, b_k is bias and $K \times K$ is the kernel size. Non-linearity is maintained by the ReLU activation, $ReLU(t) = max(0,t)$. CNNs are well suited for leaf disease classification because diseases often manifest as local texture and color changes (spots, blight patches, lesions) that convolution captures effectively.

Training a deep CNN from scratch typically requires a very large labelled dataset. In agricultural datasets, labelled images are often limited and imbalanced. Transfer learning addresses this by leveraging a model pretrained on a large dataset such as ImageNet.

The idea is that pretrained CNNs learn generic visual primitives that are transferable:

- early layers learn edges, blobs, and simple textures
- later layers learn more structured patterns

2.1.1 Feature Reuse Hypothesis

Let $\phi(\cdot)$ be a pretrained feature extractor. Transfer learning assumes there exists a mapping such that: $z = \phi(x)$ is a good representation for the new task, and only a smaller classifier $g(\cdot)$ must be learned:

$$\hat{y} = g(z) = g(\phi(x)) \tag{2}$$

This reduces data requirement, training time and risk of overfitting.

When networks become very deep, training can become harder. Even if deeper networks should represent more complex functions, optimization may degrade due to gradient issues. ResNet introduces skip connections to learn residual functions:

$$\hat{y} = g(z) = g(\phi(x)) \tag{3}$$

Instead of directly learning $H(x)$, the block learns:

$$F(x) = H(x) - x \Rightarrow H(x) = F(x) + x \tag{4}$$

So the residual block outputs:

$$y = F(x) + x \tag{5}$$

This helps gradient flow because the derivative includes an identity path.

$$\frac{dy}{dx} = \frac{dF(x)}{dx} + I \tag{6}$$

The identity term I stabilizes learning and enables deeper architectures like ResNet50 to be optimized effectively. Rice disease patterns can be subtle and fine-grained (e.g., Brown Spot vs BLB-like lesions). Deep residual networks preserve important information across many layers, enabling learning of subtle discriminative patterns.

Global Average Pooling (GAP) and Embedding Representation

GAP converts the final convolution feature maps into a vector by spatial averaging:

$$g_d = \frac{1}{H'W'} \sum_{u=1}^{H'} \sum_{v=1}^{W'} h_d(u, v) \tag{7}$$

where $h_d(u, v)$ is the activation for the channel d. This will reduce parameters vs flattening, reduce overfitting, and make features more spatially robust.

2.1.2 Embedding Layer

The dense "embedding" layer projects pooled features into a compact feature vector:

$$Z = \sigma(W_e g + b_e) \in R^{512} \tag{8}$$

This vector acts as a learned descriptor of disease characteristics. Then dropout layer is also added that will randomly disables units during training, approximating an ensemble of subnetworks and this discourages co-adaptation and improves generalization. After that label Smoothing is also applied that will prevents over-confident predictions and improves calibration. This makes the classifier less sensitive to noise and improves generalization. When classes are imbalanced, minimizing empirical risk can bias toward majority classes. A model can achieve high accuracy even if minority classes are misclassified. In this approach an weighted loss approximates "balanced" learning by modifying the expected risk is used. Softened/capped weights are used to avoid extreme behavior where rare classes cause too many false positives.

2.1.3 Random Forest Theory on Deep Embeddings

A Random Forest is an ensemble of decision trees trained on bootstrapped samples and random feature subsets. It is used for embedding such that trees can model non-linear decision boundaries in embedding space. Tree-based SHAP (TreeExplainer) is efficient and well-defined because RF provides a stable, interpretable mapping from features → class decisions. In the proposed method, RF is primarily an explainability vehicle to compute feature importance of the learned embeddings.

2.1.4 Shapley Values for Model Explanation

SHAP explains predictions by attributing the model output to input features. It is based on Shapley values from cooperative game theory. Let features be players in a game and model output be the payout. For feature j, the Shapley value is:

$$\emptyset_j = \sum_{S \subseteq N\{j\}} \frac{|S|!\,(|N| - |S| - 1)!}{|N|!} [f(S \cup \{j\}) - f(s)] \quad (9)$$

This is the average marginal contribution of feature j over all subsets S.

For tree models, SHAP can be computed efficiently without enumerating all subsets. For multiclass output, SHAP returns:

$$\emptyset^c \epsilon \mathrm{R}^{\mathrm{N \times F}} \quad (10)$$

and global importance $\mathrm{I_j}$ is computed. If classes are imbalanced, global average importance:

$$\mathrm{G_j} = \frac{1}{\mathrm{C}} \sum_{\mathrm{c=1}}^{\mathrm{C}} \mathrm{I_j} \quad (11)$$

can still favor features useful for majority classes. This causes a drop in minority recall when Top-K pruning removes minority-specific dimensions. To preserve minority discriminative features, select Top-M per class.

2.1.5 Data Augmentation and Input Preprocessing

To improve generalization under varying illumination, pose, and scale, we perform online augmentation during training. Each training image is transformed by a stochastic augmentation operator $T(\cdot)$, yielding:

$$xi' = T(xi) \quad (12)$$

Augmentations include random horizontal flips, rotations, translations, zoom, and contrast adjustments. For ResNet50 transfer learning, we apply the model-specific preprocessing $g(\cdot)$ after augmentation.

Proposed Algorithm

Input: Trained baseline model with embeddings layer (512-D)

Training set and validation set

Parameters: M (top features per class), K (final features), class weights class_weight

Output:

Selected indices topk_indices

Trained SHAP-Top-K model shap_model

Steps:

Extract embeddings:

Compute Z_train = Embeddings(X_train)

and Z_val = Embeddings(X_val)

from the baseline model's embeddings layer.

Train a RandomForest classifier RF using (Z_train, y_train_int).

Use TreeExplainer(RF) to compute SHAP values on a stratified subset of Z_train.

For each class c and feature j,

Compute I_c[j] = mean(|SHAP_c[:, j]|).

For each class c, pick S_c = topM(I_c).

Union: U = union(S_c for all c).

If |U| > K, keep the best K features in U using global score G[j] = mean_c(I_c[j]).

If |U| < K, add highest G[j] features until size becomes K.

Return topk_indices.

Reuse baseline input → embedding output (512-D) → select topk_indices → small dense head → softmax.

Train with class_weight and evaluate on validation set.

IV. RESULTS AND DISCUSSIONS

This section describes the training setup used for the proposed hybrid rice plant disease detection model. All experiments were implemented in Python and carried out for multi-class classification. The dataset was split into training and testing sets using a 70:30 ratio. For multi-class classification, experiments were conducted using ten classes. All input images were resized to 240×240 pixels using a batch size of 32 for up to 100 epochs, with mean squared error (MSE) as the loss function. Due to the computational requirements of the model, training was conducted using Google Colab with high-performance GPU resources. Therefore, this model was trained on the computing service provided by Google i.e., Google Colab. The dataset is taken from the following three sources:

The first dataset contains 1426 images of rice diseases & it was collected from paddy fields of Bangladesh Rice Research Institute (BRRI) [16]. The second dataset contains 5932 diseased rice leaf images of four varieties & it was captured from different rice field of western Odisha

[17]. The third dataset contains 5447 images of rice diseases & it was collected from Kaggle [18].

Following performance parameters are used:

$$\text{Accuracy } A = \frac{TP+TN}{TP+TN+FP+FN} \quad (13)$$

$$\text{precision } P = \frac{TP}{TP+FP} \quad (14)$$

$$\text{recall } R = \frac{TP}{TP+FP} \quad (15)$$

$$\text{f1-score } F1 = 2 * \frac{P*R}{P+R} \quad (16)$$

The proposed SHAP reduced ResNet50 model shows strong and consistent performance, as presented in table 1, across most rice disease categories, achieving an overall accuracy of 98% with an average precision of 95%, recall of 94%, and F1-score of 94% that indicates the SHAP-selected embedding subspace retains most of the discriminative capability of the deep model. Several classes are classified almost perfectly, demonstrating that these diseases have highly separable visual patterns in the learned feature space. Moderate but still reliable results are observed for Neck Blast, Sheath Blight/Rot, and Stemborer (F1 around 95–96%), suggesting good generalization with limited confusion. The main weaknesses appear in BLB and False Smut: BLB has high recall (96%) but lower precision (79%), meaning the model detects most BLB cases but tends to over-predict BLB for some non-BLB samples, leading to more false positives. False Smut shows the lowest performance (precision 68%, recall 79%), indicating higher visual similarity with other spot-like diseases and/or limited and variable training samples. Healthy Plant remains strong (precision 96%, recall 94%), though its slightly reduced accuracy suggests occasional confusion with mild disease symptoms. Overall, the results confirm that incorporating SHAP-based feature selection maintains high classification accuracy while highlighting that classes with overlapping symptom characteristics remain the primary sources of misclassification.

Table 1. Class-wise Performance of the Proposed Model on the Rice Leaf Disease Dataset

Class	Accuracy	Precision	Recall	F1-score
BLB	98.00%	79.00%	96.00%	87.00%
Bacterial Blight		99.00%	100.00%	99.00%
Blast		98.00%	97.00%	98.00%
Brown Spot		99.00%	98.00%	98.00%
False Smut		93.00%	68.00%	79.00%
Healthy Plant		92.00%	96.00%	94.00%
Hispa		100.00%	93.00%	96.00%
Neck Blast		96.00%	96.00%	96.00%
Sheath Blight Rot		93.00%	98.00%	96.00%
Stemborer		95.00%	95.00%	95.00%
Tungro		100.00%	100.00%	100.00%
Average	**98.00%**	**95.00%**	**94.00%**	**94.00%**

Table 2. Comparative State of Art

Models	Trainable params	Accuracy	Training Time
Existing [19]	Less	97.6%	48s/epoch
Proposed	Very High	98%	10s/epoch

Table 2 shows that the proposed model achieves a slightly higher accuracy (98%) compared to the existing approach (97.6%), indicating an improvement in predictive performance. However, this gain comes with a clear computational trade-off: the proposed model has very high trainable parameters and requires 48 seconds per epoch, whereas the existing model uses fewer parameters and trains much faster at 10 seconds per epoch. In other words, your proposed method provides a ~0.4% absolute accuracy improvement. The existing model also shows approximately 4.8× higher training time per epoch and increased model complexity. This suggests the proposed model is suitable for resource-constrained environments or rapid training and experimentation.

V. CONCLUSION

In this work, a rice leaf disease classification system is presented that aims to be both accurate and easier to understand. The proposed model started with a ResNet50 model pretrained on ImageNet and fine-tuned it to recognize rice diseases. The model learns a strong 512-dimensional embedding representation, and used a weighted loss function to reduce the impact of class imbalance so that rare diseases are not neglected. To add explainability and reduce redundant information, it trained a Random Forest classifier on these embeddings and applied SHAP to identify which embedding dimensions contribute most to the predictions. Instead of selecting features only based on global importance, it used a per-class union Top-K approach to make sure important features from minority classes are also retained. The final SHAP-Top-K model achieved 98% overall accuracy, showing that SHAP-based selection can maintain strong performance while improving interpretability. It also shows 4.8 times lower time consumption as compared to existing. In future this work will be extended on remote sensing applications.

Conflict of Interest: The corresponding author, on behalf of second author, confirms that there are no conflicts of interest to disclose.

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