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Transfer Learning-based Deep Neural Networks for Rice Leaf Disease Classification: A Comparative Study of Squeeze Net and Google Net

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Abstract— **Rice is considerably impacted by various diseases, demands an early and precise diagnosis to ensure sustainable agriculture. The adaptability and scalability of traditional machine learning approaches are restricted by the use of handcrafted features. This paper analyzes deep neural networks based on transfer learning for the classification of rice leaf diseases, with particular focus on the Squeeze Net and Google Net architectures. Model's performance was assessed using a dataset of 4,834 images from field and repository data. The three main rice diseases—bacterial leaf blight, brown spot, and leaf smut—were successfully classified using both networks. Experimental results demonstrate that Google Net achieved 98.29% accuracy, outperforming Squeeze Net at 97.86%, due to its deeper architecture and multi-scale feature extraction. However, Squeeze Net, with its lightweight design, provides comparable accuracy while being computationally efficient, making it more suitable for real-time deployment. This paper establishes transfer learning as a robust approach for intelligent paddy disease diagnosis in precision agriculture.**

Index Terms— **Deep Neural Networks (DNN), Transfer Learning, Squeeze Net, Google Net, Rice Leaf Disease Classification, Precision Agriculture.**

I. INTRODUCTION

Deep Neural Networks (DNNs) have revolutionized computer vision and image recognition in recent years, demonstrating state-of-the-art performance across medical imaging, autonomous vehicles, geological image analysis, and remote sensing [1] [2]. Owing to their hierarchical learning structure, DNNs can automatically learn and extract complex features from large datasets, resembling the structure and operation of the human brain [3]. This ability enables DNNs to analyze image data of rice plants and detect subtle visual indicators associated with different diseases, thereby supporting accurate and automated disease diagnosis [4].
Rice is one of the most important crops in the world, but diseases caused by bacteria, fungi, and viruses can greatly reduce its yield [5]. Traditional approaches to disease classification often rely on handcrafted feature extraction techniques such as color analysis, gray-level co-occurrence matrix (GLCM), and texture descriptors. These methods are limited by their dependency on domain expertise, lack of robustness under varying environmental conditions, and poor adaptability to dynamic agricultural systems [6], [7].

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Also, traditional machine learning techniques like multiclass support vector machines (SVMs) use hand-crafted features to find class boundaries, which makes them less scalable and able to generalize. [8].
To overcome these limitations, deep learning–based methods, particularly transfer learning, have emerged as a promising solution. Pre-trained models such as Alex Net, ResNet, Squeeze Net, and Google Net, originally trained on large-scale datasets with images of categories, can be fine-tuned for agricultural disease classification [9], [10]. These models reduce manual feature extraction, expedite training, and outperform standard methods in accuracy [11].
This paper combines two datasets to classify rice leaf diseases using two separate pre-trained transfer learning models, Squeeze Net and Google Net. The contributions of this work are as follows: a comparative analysis of lightweight and deep architectures for paddy disease classification, and experimental validation of transfer learning–based models on real-world rice disease datasets.

II. Literature Review

The emergence of machine learning algorithms for image feature-based classification tasks has integrated computer vision techniques with machine learning algorithms [7]. Random Forest Classifier (RF) undergoes the training procedure from the input dataset, and the split method. The RF is then estimated by out-of-bag samples until the estimation error meets a threshold value or the iteration time is end [12]. Aim is to develop a robust and user-friendly system for disease classification of paddy leaves using SVM. The system classifies the query image to one of the types of paddy leaf disease using a hyper plane that separates cases of different class labels. The separating hyper plane equation is used to maximize the margin. The training image is processed using different pre-processing steps, and the feature vector of a query image is sent to the classifier. The system shows a robust performance compared to existing methods with high performance on individual and over the disease classes[13].
In order to eradicate rice plant maladies such as brown spot, bacterial leaf blight, and rice blast, a modified K-means segmentation algorithm is suggested. Intensity-based colour feature extraction (NIBCFE) is employed to extract features based on colour, shape, and texture parameters. Shape features are identified by determining the area and diameter of infected portions, while texture features are identified using gray-level co-occurrence matrix (GLCM) and bit pattern features (BPF). A support vector machine-based probabilistic neural network (NSVMBPNN) is employed to identify distinctive feature values. The proposed method outperformed other methods in terms of accuracy, achieving final accuracies of 95.20%, 97.60%, 99.20%, and 98.40% for bacterial leaf blight, brown spot, healthy leaves, and rice blast, respectively[14].
The identification and classification of rice diseases are essential for the production, quantity, and quality of rice. The unavailability of professional specialists and a lack of knowledge are frequently the reasons why farmers encounter difficulty with disease diagnosis. This paper introduces a sophisticated AI system that integrates deep Convolutional Neural Network (CNN) and SVM to classify rice diseases. The Inception V3 DCNN model is retrained using transfer-learning methods with 1080 images of nine distinct rice diseases. This process involves the extraction of one-dimensional unique features and the training of a support vector classifier. The system is fully automated for the classification of rice diseases, achieving a prediction accuracy of 97.5% and 94.6% when using CNN-Softmax [15].
The Deep Neural Network with Jaya Algorithm (DNN_JOA) is a method used to classify diseased and normal portions of farm field images. It has high accuracy in identifying common rice plant diseases like brown spot, leaf blast, bacterial blight, and sheath rot. The method involves five phases for efficient treatment [16].The pre-trained Google-Net using Neural Network Toolbox in Matlab results showed consistent accuracies on all selected plants, except cotton and soybean. Images of individual lesions and spots improved classification accuracy. The expanded dataset had diverse effects, with the number of classes and images and respective characteristics varied among crops. The model's effectiveness was minimal for most crops, with accuracies not deviating by more than 2%. However, the expanded dataset had limitations on intra-class symptom variability, diversity of conditions expected to be found in practice, and similarity with other diseases. To avoid misclassifications, more samples should be generated for underrepresented classes or reduce the training samples [17].
The Paddy Doctor uses convolutional layers and dense connectivity strategies. It uses VGG16, Mobile Net, Xception, and ResNet34 models. The ResNet34 achieves the highest F1-score, while DCNN achieves the lowest. The dataset is suitable for automated paddy disease classification tasks and further more pre-trained models using transfer learning strategies needs to evaluate [18]. The [19] uses a Nikon COOLPIX 20.1 megapixel camera to analyze real-time input images from farmer's land in Chhattisgarh state, India. It uses MATLAB

software for video to frame conversion on 1500 images includes six leaf classes, including rice blast, leaf scaled, sheath blight, brown spot, healthy leaves, and bacterial leaf blight. SegNet and RPK-means algorithm. The RPK-means algorithm achieved 2%-6% more segmentation accuracy than traditional K-means clustering, while the handmade CNN outperformed RPK-means clustering by 1-2%. The proposed approach is effective in solving crop disease problems and improving vegetable disease identification systems.
To detect plant diseases [20], Deep RNN- Deep Recurrent Neural Network for rice crop detection. The RSW algorithm is trained using the Ride-Spider Water Wave (RSW) algorithm, combining RWW and SMO algorithms for optimal weights. The RSW-based Deep RNN achieves superior performance with a maximum accuracy of 90.5%, sensitivity of 84.9%, and specificity of 95.2%. In [21] segmentation-based rice disease classification uses leaf images. The method uses local segmentation and a Convolutional Neural Network (CNN) to classify disease-affected regions. The dataset including, the one created by the Bangladesh Rice Research Institute (BRRI). The CNN architectures used include VGG, Res-Net, and Dense Net. The classification performance is analyzed and compared, showing promising results in classifying rice leaf diseases. The method is optimized using Adam, combined with Root Mean Square Propagation. The study assessed the consistency and the impact of diverse images captured in different conditions on classification performance.
The [22] 5932 on-field images of four types of rice leaf diseases, evaluated using 11 CNN models. In which the SVM with deep features performed better classification compared to transfer learning counterparts. Small CNN models like mobilenetv2 and shuffle net were examined, and statistical analysis was performed to choose the best classification model. ResNet50 plus SVM was chosen as the superior classification model with 0.9838 f1 score with in training time 69s. The statistical difference among CNN models in the transfer learning approach is nil. Mobilenetv2 plus SVM had an F1 score of 0.9796 and 48 s training time, comparable to ResNet50 plus SVM. The lab colour model distinguishes diseased and healthy leaves using entropy. Segmentation improves classification performance, with BLB and NBS having 91% and 90% accuracy, respectively. Mask and segmented images enhance disease identification, with MSVM having 92% accuracy [23].
In [24] rice disease recognition model combines convolution neural networks (CNNs) and the Support Vector Machine (SVM) to identify rice leaf diseases. The model has the highest average correct recognition rate of 96.8% when the penalty parameter is set at 1 and kernel parameter is set at 50. Deep learning is a powerful tool for crop disease classification, using Convolutional Neural Networks (CNNs) like VGG16, ResNet, and Inception. Transfer learning reduces computational cost and enhances model robustness. However, generalization to unseen data remains a challenge, prompting hybrid approaches combining deep learning with classical algorithms. Future work should focus on larger datasets, multi-organ symptoms, and improved model resilience [25].

III. METHODOLOGY

For the classification of paddy diseases, the suggested approach uses transfer learning using pre-trained convolutional neural networks (CNNs).
The four main phases of the workflow—dataset preparation, model selection, transfer learning adaption, and performance evaluation—are shown in Fig. 1.

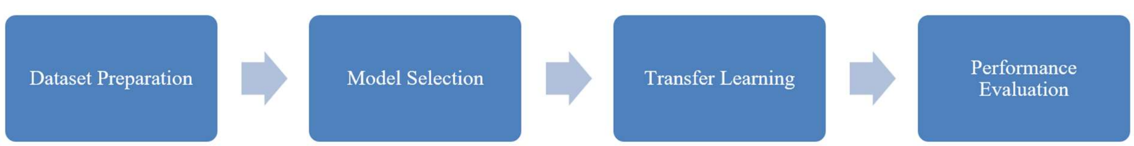

Figure 1. Methodology

A. Dataset Preparation

It comprises 4834 images of three major rice disease leaves affected by bacteria, virus and fungi. Images were collected from the field and publicly available data repositories as tabulated in Table I.

TABLE I. DATASET DESCRIPTION

Label	Natural Images	Repository Images	Total Images
Bacterial leaf blight	50	1604	1654
Brown spot	50	1620	1670
Leaf smut	50	1460	1510

B. Model Selection and Transfer Learning

Two pre-trained CNN architectures were employed: Squeeze Net and Google Net. Both models were originally trained dataset and recognized with high accuracy in image classification tasks. Instead of training from scratch, the final classification layers of these networks were fine-tuned for the three rice disease categories. This transfer learning strategy improves model generalization.

- Squeeze Net is an 18-layer deep CNN that introduces the "Fire Module," which efficiently combines 1×1 and 3×3 convolutions to reduce parameters while preserving accuracy. It further employs global average pooling to avoid overfitting.
- Google Net (Inception v1) is a 22-layer deep CNN that integrates multiple convolutional filters (1×1, 3×3, 5×5) in parallel, enabling multi-scale feature extraction. The inception modules capture both fine and coarse visual patterns crucial for disease classification.

C. Performance Evaluation

The MATLAB R2023b on an Intel Core i3 processor with 4 GB RAM was used to implement the model. The fixed number of epochs is used in training and learning rate tuned experimentally. The classification accuracy across the three rice disease classes is evaluated.

Although Squeeze Net and Google Net are well-established deep learning architectures, the novelty of this research lies in their domain adaptation for paddy disease classification. By fine-tuning these pre-trained models, the work demonstrates their applicability in the agricultural domain. Furthermore, a comparative analysis between the lightweight Squeeze Net and the deeper Google Net provides insights into the trade-offs between computational efficiency and classification accuracy. Finally, the models are validated on a dataset that combines repository images with real-world field-collected samples, enhancing robustness against environmental variations and improving the practical reliability of the proposed system for real agricultural applications.

IV. Results and Discussions

The Fig. 2 shows validation accuracy of 97.86% Squeeze Net achieved, while Google Net achieved 98.29%. The parameters of Squeeze Net and Google Net models are tabulated in Table 2. The superior performance of Google Net can be attributed to its deeper architecture and inception modules that capture features at multiple scales, whereas SqueezeNet is optimized for lightweight deployment with fewer parameters.

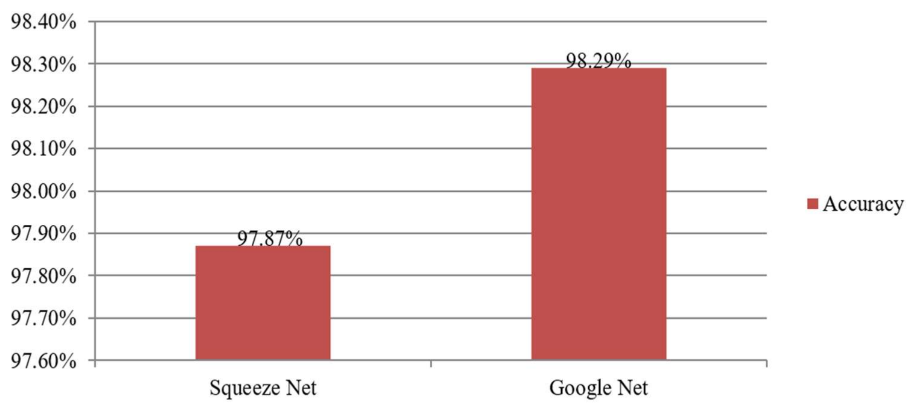

Figure 2. Models v/s Accuracy

TABLE II. PARAMETERS OF THE MODELS

Neural Network	Depth	Size	Parameters (Millions)	Image input size
Squeeze-Net	18	5.2MB	1.24	227 by 227
Google-Net	22	27 MB	7.0	224 by 224

Squeeze Net achieved 100% accuracy on bacterial leaf blight and brown spot but dropped to 99.8% on leaf smut. Google Net performed best with 99.9% accuracy on bacterial leaf blight but showed weaker performance on leaf smut with 77.7% as shown in and graphs are shown in Fig. 3, indicating sensitivity to intra-class variation in that disease category.

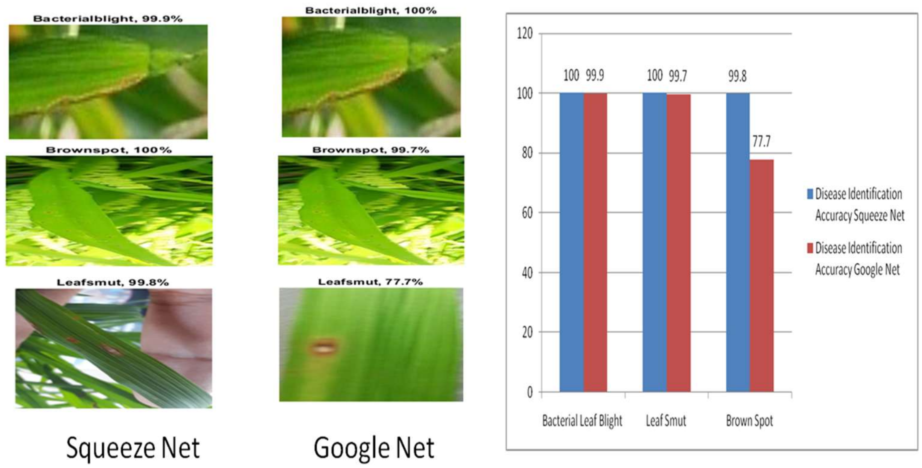

Figure 3. Validation Accuracy

The relatively lower accuracy of Google Net for leaf smut can be explained by the visual similarity between diseased and healthy regions under varying light conditions that is intra-class variability cab be avoided by dataset augmentation.

When compared with traditional machine learning methods such as feature-based SVM classifiers [7], the proposed deep learning models show clear improvements. Conventional methods typically report accuracies in the range of 85–92% for rice disease classification [5], whereas our models consistently exceed 97%. This demonstrates the effectiveness of transfer learning in eliminating manual feature engineering and enhancing robustness.

Squeeze Net, being lightweight (5.2 MB vs. Google Net's 27 MB), is better suited for deployment on low-resource devices such as mobile and edge systems in agricultural fields. On the other hand, Google Net's deeper architecture provides slightly higher accuracy but requires more computational resources. This trade-off suggests that Squeeze Net is preferable for real-time applications in the field, while Google Net is suitable for high-performance offline analysis.

In summary, the comprehensive evaluation demonstrates that transfer learning with Squeeze Net and Google Net significantly outperforms conventional approaches. While Google Net offers marginally higher accuracy, Squeeze Net provides an optimal balance between accuracy and computational efficiency, making it highly practical for precision agriculture

V. Conclusion and Future Work

This article investigated the application of transfer learning–based deep neural networks for the classification of rice leaf diseases, focusing on Squeeze Net and Google Net architectures. Both models were fine-tuned on a dataset comprising repository and field-collected images to ensure practical relevance. The results revealed that Google Net achieved a marginally higher accuracy of 98.29%, compared to 97.86% for Squeeze Net, highlighting the effectiveness of deeper architectures for fine-grained disease classification. Class-wise analysis demonstrated strong performance for bacterial leaf blight and brown spot across both models, while leaf smut remained comparatively challenging.

A comprehensive evaluation using multiple performance metrics confirmed the superiority of the proposed transfer learning approach over traditional machine learning methods based on handcrafted features. Importantly, this study emphasizes the trade-off between accuracy and computational efficiency, Google Net provides slightly higher accuracy but requires more resources, whereas SqueezeNet offers competitive accuracy with significantly reduced model size and computational cost, making it more suitable for real-time and resource-constrained environments.

Future research can extend this work in several directions. First, expanding the dataset with more disease categories and diverse environmental conditions will improve model generalization and resilience to real-world variability. Second, integrating data augmentation and synthetic dataset generation can help address class imbalance, particularly for diseases like leaf smut. Third, exploring hybrid models that combine lightweight and deep architectures may provide a better balance between efficiency and accuracy. Finally, deploying these models on mobile or edge devices and validating them under field conditions will be critical for developing scalable, intelligent plant disease diagnostic systems to support precision agriculture.

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