

Hybrid Deep Learning Framework for Cashew Leaf Disease Classification Using Model Concatenation

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Abstract

In this paper, we propose a novel deep learning-based method for the accurate classification of cashew leaf diseases, utilizing a hybrid MobileNet-VGG19 Con concatenated model trained on the CCMT cashew disease dataset. Detecting cashew leaf diseases is particularly challenging due to the wide variability in texture, color, and structural patterns. To overcome these complexities, our model integrates the lightweight efficiency of MobileNet with the deep feature extraction strength of VGG19, achieving a powerful balance between computational speed and representational depth. The proposed model outperforms its standalone counterparts, achieving impressive results: 98.20% training accuracy, 96.23% test accuracy, 96% precision, 95% recall, and an F₁-score of 96%. Beyond accuracy, the model demonstrates strong robustness and generalizability, making it highly suitable for real-world applications in precision agriculture. Our findings highlight the potential of hybrid deep learning models to revolutionize plant disease detection, supporting sustainable, automated, and intelligent crop management practices.

Keywords

Agriculture, Cashew, Disease, Leaf, MobileNet-VGG19 Con, Plant.

INTRODUCTION

Cashew (Anacardium occidentale) is a critical cash crop cultivated primarily in tropical regions and serves as a significant economic resource for many developing countries. The productivity and quality of cashew crops, however, are severely impacted by various diseases that affect leaves, which is a primary concern for farmers and agricultural industries alike [1]. Efficient and accurate disease detection is essential for timely intervention, ultimately supporting yield improvement and reducing economic losses. Traditional methods identification are often labor-intensive, prone to human error, and typically rely on the expertise of agronomists, which may not be readily accessible in all regions [2].

Deep learning has emerged as a powerful tool for image-based disease classification, achieving high accuracy in tasks such as plant disease detection through advanced convolutional neural networks (CNNs) [3]. Nonetheless, single models, while effective, often struggle with the balance between computational efficiency and the need for high feature richness, particularly in datasets with complex disease patterns. MobileNet and VGG19, two widely adopted CNN architectures, offer complementary strengths: MobileNet is highly efficient and lightweight, making it suitable for real-time applications, while VGG19 is known for its depth and ability to capture intricate patterns [4].

This study introduces a hybrid approach by concatenating MobileNet and VGG19, leveraging both architectures to create a model capable of detecting cashew leaf diseases effectively. The CCMT cashew disease dataset, a curated collection of labeled images covering multiple disease classes, serves as the benchmark for evaluating the proposed model [5]. Our aim is to achieve robust classification

performance while maintaining a model size that supports deployment in practical agricultural settings. Through comprehensive experiments, we assess the impact of this concatenated architecture on test accuracy with 96.23%, training accuracy with 98.20%, and the potential of the model to support disease management practices in the cashew industry.

LITERATURE REVIEW

The development of automated systems for plant disease detection has gained substantial interest in recent years, with deep learning-based image classification models leading the way in precision agriculture. Many studies have leveraged Convolutional Neural Networks (CNNs) to classify plant diseases with promising results. However, single CNN models often struggle to achieve a balanced trade-off between model complexity, computational efficiency, and feature extraction depth, particularly when used in agricultural contexts where real-time application is crucial.

Several researchers have explored MobileNet for plant disease classification due to its lightweight architecture and capacity for mobile deployment. For example, Howard introduced MobileNet as a computationally efficient CNN model, specifically designed for mobile and embedded vision applications MobileNet's depthwise [6]. convolutions allow it to significantly reduce computational costs while maintaining competitive accuracy. Studies by Ahmed have further demonstrated the model's effectiveness resource-constrained environments, such as rural agricultural fields where hardware limitations are common [7]. Despite its advantages in efficiency, MobileNet often faces limitations in capturing complex textures and patterns characteristic of certain diseases [8].



On the other hand, VGG19, proposed by Simonyan and Zisserman, remains a popular choice for its depth and simplicity, achieving impressive results in numerous image classification tasks [9]. With its 19-layer deep structure, VGG19 is highly capable of capturing intricate visual features, which is crucial for distinguishing among visually similar disease types in plant leaves. However, VGG19's high parameter count and computational intensity restrict its practical applications in environments with limited processing power, such as handheld or field-deployable devices.

Recent studies have proposed hybrid approaches to leverage the strengths of both lightweight and deep CNN architectures. For instance, Chen explored a combined MobileNet-ResNet architecture for leaf disease detection in apples, reporting improved accuracy over standalone models [10]. A. K. Jain investigated a multi-model concatenation approach using EfficientNet and DenseNet for cassava leaf disease classification, achieving an effective trade-off between efficiency and accuracy [11]. Such hybrid models offer a promising solution for challenging datasets, such as those with high intra-class variation and subtle disease manifestations [12].

The CCMT cashew disease dataset, used in this study, includes diverse and complex cases of cashew leaf diseases, which are difficult to classify accurately due to variations in color, texture, and shape. Although the literature on cashew disease classification remains limited, similar studies have been conducted on other crops such as coffee, maize, and potatoes, showcasing the potential of multi-model concatenate architectures [13]. A. K. Jain introduced a MobileNet-DenseNet Concate model for detecting multiple diseases in sugarcane leaves. The model demonstrated excellent performance, achieving 96% accuracy, precision, recall, and F₁-score through the application of transfer learning [14]. The MobileNet-VGG19 Con concatenate model proposed here aligns with this trend, aiming to combine MobileNet's efficiency with VGG19's feature extraction capacity to achieve a robust and deployable solution for cashew disease detection.

In conclusion, this review highlights the limitations of single CNN models for agricultural applications and the growing trend of hybrid models that leverage multiple architectures [15]. The MobileNet-VGG19 Con concatenate approach offers a promising balance between computational efficiency and deep feature extraction, potentially setting a new standard for precision agriculture in resource-limited environments.

PROPOSED WORK

The proposed model architecture utilizes a hybrid approach by combining MobileNetV2 and VGG19 to capture a broad spectrum of features critical for accurate cashew disease classification as shown in Figure 1. MobileNetV2 model features 1280 depth channels and spatial dimensions of (7, 7). Renowned for its lightweight and efficient

architecture, MobileNetV2 leverages depthwise separable convolutions to excel at extracting distinct features such as shape, edges, and color. VGG19 model comprises 512 channels and (7, 7) spatial dimensions. VGG19 is a deep convolutional model with 19 layers, using 3x3 filters and max pooling to progressively reduce spatial dimensions, capturing hierarchical features with increasing filters (64 to 512) for accurate image classification. Initially, the input images are fed into both MobileNetV2 and VGG19 models separately, where each network processes the images through its unique architecture to extract high-level features. MobileNetV2, known for its lightweight design, processes data efficiently through depth-wise separable convolutions, emphasizing computationally effective feature extraction. VGG19, with its deep 19-layer structure, captures fine-grained details and complex patterns. After passing through these networks, the output of each model is pooled using a GlobalAveragePooling2D layer, which reduces the spatial dimensions while retaining essential information.

The outputs of (1, 1, 1280) and (1, 1, 512) from the GlobalAveragePooling2D layers of both MobileNetV2 (7, 7, 1280) and VGG19 (7, 7, 512) are then concatenated (1792) to form a unified feature representation. This concatenated output combines the efficient, compact features from MobileNetV2 with the richer, more detailed features from VGG19, providing a comprehensive feature map. Following concatenation, the combined feature map is passed through an additional convolution layer, which enables the model to learn complementary features and further refines the concatenated representations. Finally, the output of this convolutional layer is fed into a fully connected layer that performs the final classification, yielding the model's predictions for cashew leaf diseases.

This design effectively balances the depth and efficiency of the model, aiming for accurate, real-time disease detection that is suitable for practical agricultural deployment. In combining the outputs of MobileNetV2 and VGG19 through concatenation within a neural network, the process can be mathematically described based on the operations applied to the feature maps generated by each model. After processing an input image, each network produces its own set of feature maps. By concatenating these outputs, we effectively combine the distinct learned features from MobileNetV2 and VGG19 into a single representation, enhancing the model's ability to capture various aspects of the input data.

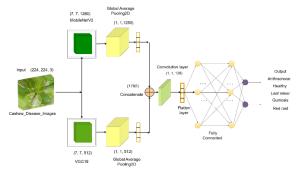


Figure 1. Proposed model



Feature Extraction: Let M and V represent the feature maps produced by MobileNetV2 and VGG19, respectively:

$$M = MobileNetV2(X)$$
 (1)

$$V = VGG19(X) \tag{2}$$

Concatenation: The concatenation operation combines feature maps along the channel dimension. Assuming that the feature maps have the same height and width (often achieved through pooling or resizing), the resulting concatenated feature map, C can be represented as follows:

$$C = Concate (M, V)$$
 (3)

Further Processing: The concatenated feature map C is then passed through subsequent layers, such as fully connected layers or additional convolutional layers, to perform classification or other tasks.

$$Y = Classifier (C)$$
 (4)

RESULTS

CCMT Cashew Disease Dataset

This study was on CCMT cashew disease dataset [16]. The CCMT cashew disease dataset is a specialized collection designed for the classification and analysis of cashew leaf diseases as shown in Figure 2 available at Kaggle dataset [17]. It includes a diverse array of images capturing various diseases that affect cashew plants, each labeled to represent different disease categories as anthracnose, gummosis, leaf miner, red rust, and healthy. This dataset serves as a valuable resource for researchers aiming to develop automated systems for identifying and classifying cashew diseases. Given the complexity of cashew diseases, which often exhibit subtle differences in texture, color, and leaf morphology, the dataset provides high-resolution images to help models learn fine-grained distinctions.



Figure 2. CCMT cashew disease dataset

In this study, the CCMT cashew disease dataset supports the training and evaluation of a MobileNet-VGG19 Con concatenate model by offering representative samples across disease classes. The diversity within the dataset challenges the model to learn features that distinguish between healthy and diseased leaves effectively, making it suitable for developing robust models for precision agriculture. This dataset also contributes to advancements in cashew disease management, facilitating early diagnosis and efficient intervention strategies in the agricultural sector.

Hyper-Parameters

The MobileNet-VGG19 Con concatenate model's training on the CCMT cashew disease dataset relies on carefully selected hyperparameters to optimize performance and maintain model generalizability. A learning rate of 0.001 is initially set to ensure stable convergence, with a decay

schedule gradually reducing the rate for fine-tuning as training progresses. The batch size is 32 or 64, balancing computational efficiency and model stability. The Adam optimizer supports adaptive learning, effectively accommodating the hybrid model's gradient demands [18]. Early stopping is applied within a 50–100 epoch range based on validation loss to prevent overfitting, while a dropout rate of 0.3-0.5 adds further regularization. ReLU activation is used throughout with a softmax layer in the output to generate disease class probabilities. Initialization aids in training efficiency, while data augmentation (including rotation, flipping, and brightness adjustments) diversifies the dataset. These hyperparameters together enhance the model's ability to accurately classify cashew diseases and generalize well across varied data.

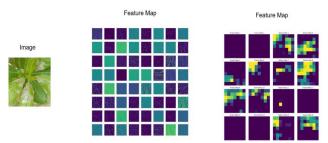


Figure 3. Feature activation map

Confusion Matrix

A confusion matrix is an essential tool for evaluating the performance of classification models, providing a detailed breakdown of how well the model's predictions align with the true labels. It is organized as a square matrix where rows correspond to actual classes and columns represent predicted classes. Key components include True Positives (TP), which denote cases where the model correctly identifies a positive instance, and True Negatives (TN), where it accurately predicts the negative class. Conversely, False Positives (FP) occur when the model incorrectly labels a negative instance as positive (often called a Type I error), while False Negatives (FN) happen when the model fails to recognize a positive instance, mistakenly classifying it as negative (Type II error). This breakdown enables the calculation of critical performance metrics, such as accuracy, precision, recall, and F₁-score, each offering unique insights into different aspects of the model's predictive power. By highlighting areas where the model misclassifies, a confusion matrix is particularly helpful for imbalanced dataset, revealing which classes are most challenging to distinguish and guiding efforts to improve overall classification accuracy.

Classification Report

The classification report is a performance metric that shows each class's precision, recall, F₁-score, accuracy.

During model training, irrelevant or background features can sometimes be included, leading to seemingly reasonable accuracy. Activation maps can help identify such cases by highlighting which features the model is focusing on. By analyzing these maps, we can assess how effectively the



model is targeting the relevant features as shown in Figure 3.

The cashew precision Table 1 shows that red rust and leaf miner show good Results, but anthracnose shows low results on proposed model. In this study, recall and F₁-score are also good in red rust and gumosis.

Table 1: Proposed model precision, recall and F₁-score comparison table

Leaf Disease	Precision	Recall	F ₁ -score
Healthy	94%	98%	96%
Anthracnose	90%	95%	92%
Gumosis	96%	100%	98%
Leaf Miner	98%	87%	93%
Red Rust	100%	99%	99%

Cashew Leaf Disease Precision, Recall, and F1score comparison

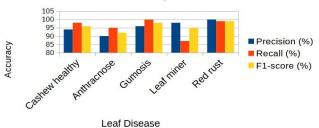


Figure 4. Cashew leaf disease precision, recall, and F1-score comparison

Table 2: Model accuracy comparison on Cashew (CCMT) datasets [17] table

Model	CCMT Dataset	Test Accuracy
Babu [19]	Cashew, Cassava, Maize	90.85%
Wang [20]	All	95.35%
R. Karthik [21]	All	95.68%
S. Palaniappan [22]	Cashew	81.70%
Proposed model	Cashew	96.23%

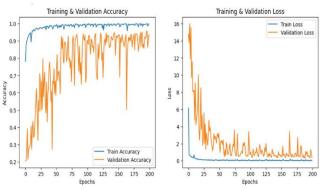


Figure 5. Model accuracy and loss graph

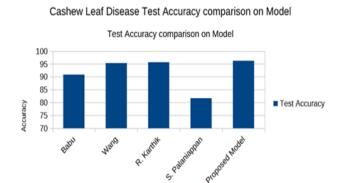


Figure 6. Test accuracy comparison on model

Figure 5 illustrates the model's accuracy progression, which begins at a high level and steadily improves, ultimately reaching a peak of 98.20%. In contrast, the loss graph exhibits a consistent decline as the number of epochs increases, stabilizing after 100 epochs. In concatenate models, loss spikes frequently occur due to inconsistencies in feature fusion across multiple architectures. These fluctuations arise from feature mismatches, gradient conflicts, and redundant or overlapping features, leading to instability in weight updates. To achieve a consistently low and well-regularized loss, the proposed model incorporates L_2 regularization with a parameter of $\lambda=0.1$ in the fully connected layer.

Our proposed model was compared with the Babu with test accuracy 90.85%, Wang with test accuracy 95.35%, R. Karthik with test accuracy 95.68%, S. Palaniappan with test accuracy 81.70% [19] [20] [21] [22]. In this comparison, our proposed models were good compared to other models, and purposed model MobileNet-VGG19 Con Model with 96.23% test accuracy and 98.20% training accuracy shown in Figure 6

Ablation Study

The figure 7 presents the heat map of the second last layer and last layer of the proposed MobileNet-VGG19 Con model.

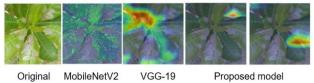


Figure 7. Ablation study

MobileNetV2 is good in big shape features and VGG19 is good in medium and small shape. Due to this reason, MobileNetV2 model extract is good in gummosis and leaf miners with medium color while VGG19 model extract is good in anthracnose, healthy, and red rust with rich color. The proposed model has both model's features. The proposed model captures more detailed features, resulting in improved classification performance.



CONCLUSION

In this study, we proposed a hybrid MobileNetV2-VGG19 Con concatenate model to address the complex task of cashew leaf disease classification using the CCMT cashew disease dataset. By leveraging the complementary strengths of MobileNetV2's computational efficiency and VGG19's depth and feature extraction capabilities, our model effectively test accuracy with 96.23% and training accuracy with 98.20%, precision with 96%, recall with 95%, and F₁-score with 96%. The model's architecture, which combines the outputs of both networks through Global Average Pooling and further refines them with an additional convolutional layer, demonstrates strong performance in identifying diverse disease patterns with high accuracy. The hyperparameter tuning and data augmentation strategies further improved generalization, allowing the model to perform robustly across varied disease presentations. This work underscores the potential of multi-model architectures in precision agriculture, offering a viable solution for real-time, accurate disease detection. Future work can explore model deployment on mobile devices and further adaptation of the architecture to other crop disease dataset, enhancing the practical applications of this hybrid approach in agricultural disease management.

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