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A Two-Phase Transfer Learning Approach Based on VGG16 for Multi-Class Classification of Cotton Leaf Diseases

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Abstract: The swift and precise identification of leaf diseases plays an important role in crop protection and increasing agricultural productivity. Recently, this process has been automated using deep learning models, especially Convolutional Neural Networks (CNNs). A comprehensive approach for classification of seven different diseases of cotton leaves are, Bacterial Blight, Curl virus, Healthy Leaf, Herbicide Growth Damage, Leaf Hopper Jassids, Leaf Redding and Leaf Variegation. We present a transfer learning stage with two phases based on the VGG16 architecture. In the first step, a pre-trained VGG16 model is leveraged as a fixed feature extractor, adding a distractive classifier head on top of the model. Though, this model is trained for 30 epochs. The second fine-tuning stage involves unfreezing the entire model (including the base VGG16 layers) and training it with a low learning rate for another 5 epochs for better performance. It consisted of 7000 images for training and 1800 images for validation. With the final validation accuracy of 94.8%, and an overall test accuracy of 95%, our approach outperforms state of the art with an F1-score of per-class results with the range 0.91—0.99. The results indicate the effectiveness of the proposed two-phase transfer learning strategy in developing a highly efficient and accurate automated plant disease diagnosis system.

Keywords — Deep Learning, Transfer Learning, VGG16, Plant Disease Classification, Precision Agriculture, Convolutional Neural Networks, Image Processing.

I. INTRODUCTION

Cotton (Gossypium hirsutum L.) is a globally important cash crop, both as the major source of a raw material for the textile industry and a dominant agricultural commodity for several countries [5]. But, cotton is threatened by a number of diseases and under unmanageable conditions these can lead to 20%-50% yield loss on an annual basis [1, 6]. The classical methods of identifying diseases are expensive, tedious, highly subjective, and infeasible for large-scale farming activities, and rely heavily on the agricultural specialists visually locating the disease [9, 15].

New protocols for normality in computer vision and deep learning research apparatus have underlie a analytical plant make diseases bbox and taxonomy success semblance [2, 7]. Image classification using Convolutional Neural Networks (CNNs) achieved state-of-the-art results and can lead to fast, effective, and scalable disease diagnostic systems [11, 16]. Nonetheless, training deep neural networks from scratch needs significant computational power and large labelled datasets, which are usually not available for agricultural applications [4, 13].

To overcome these limitation, the recent concept of transfer learning has proven to be very efficient, especially when it comes to transfer knowledge obtained from large datasets, such as ImageNet [8, 12], to a task of interest. Although the idea of using transfer learning with CNNs for classifying plant diseases has been addressed in the past [16, 22], most research used either a fixed feature extraction or complete fine-tuning without systematically investigating phased training approaches. Furthermore, numerous existing systems are specific to certain disease types or not thoroughly evaluated using explainable AI methods [10, 23].

In this work, we propose a two-phase transfer learning framework based on systematic coupling feature extraction and fine-tuningapproaches and utilize the VGG16 architecture. We improve over previous methods at each step by (1) a well-defined training regime that avoids overfitting and maximizes performance, (2)

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testing on a diverse dataset with 7 different cotton leaf classes, and (3) sophisticated interpretability methods to verify model decisions. Our proposed system gives 95% accuracy as an output and is considered to be a state-of-the-art performance which all agricultural applications would look for.

II. RELATED WORK

Recent years have seen high interest in using deep learning for cotton disease [1,2]. This section summarizes the most relevant literature in this space, highlighting transfer learning approaches and their shortcomings.

Transfer Learning for Plant Disease Classification: Transfer learning based automated diagnosis was discussed in a number of works relevant to agricultural applications. This idea was implemented but limited to few classes of diseases with respect to plant species by Paymode &Malode [16] who found transfer learning as useful also with a null form containing quality VGG architecture to separate multi-crop leaf diseases. Similarly, Rajasekar et al. The same approach was used in [11] using also deep transfer learning techniques but only on a small number of cotton plant diseases. We build upon these methods but develop a systematic two-stage training method and test on a larger dataset.

Modern Architectures and Ensembling: More recent works have investigated the use of advanced architectures and ensembling methods. An ensemble transfer learning approach was proposed by Rai &Pahuja [12] where multiple architectures were combined for superior accuracy, but at the cost of increased computation. Johri et al. In [13], the research focused on deep transfer learning [14] methods, highlighting the relevance of model selection and fine-tuning. These approaches provide good performance but are usually not simple enough and cannot run quickly, which are requirements for real applications.

EXPLAINABLE AI AND AGRICULTURE: Recent progress towards interpretable models in agriculture have triggered more interest in explainable AI techniques. Amin et al. Method 1: Explainable neural networks for cotton leaf disease classification and its practical implications of explaining model decisions [1]. Kaur et al. The work done by [10] further extends this via the optimization of the metaheuristic using deep learning with the trade-off of improved interpretability. While these works inspired our approach, we expand these validations by adding Grad-CAM visualizations to confirm that the locations of model attention coincide with biologically important areas on the leaf.

Challenge 01: Dataset Development and Standardization – Comprehensive datasets are required to develop a robust classification system. Bishshash et al. The dataset of cotton leaf disease was formed in [9] that can be used for proper evaluation of the model. We use a similarly diverse dataset over seven different conditions that allows for performance evaluation across disease domains.

Comparative studies: There are studies comparing multiple architectures. Kumar et al. A comparative analysis of pre-trained models applied to plant disease identification had been conducted by [22] for cotton plants disease detection, revealing superior performance by VGG and ResNet. Memon et al. Inspired by this idea, [21] suggested a meta deep learning method, where architectural selection was the focus of the work. Our work adds to this research by providing a finely grained analysis of VGG16 performance within a structured transfer learning framework.

Although these advances have occurred, there are still many gaps in the literature. Some existing take one strategy for transfer learning and do not optimize systematically while some focus on specific disease type and treated as single task problems. Moreover, there is usually a lack of an extensive multiple-regional analysis that either combines quantitative metrics or qualitative explainability analysis. We overcome these drawbacks by proposing and evaluating a novel two-phase training approach followed by a detailed evaluation on a multitude of performance measures and visualization techniques.

III. METHODOLOGY

The main models proposed for cotton leaf disease classification comprise of systematic, two-phase transfer learning pipeline, given in Figure 1. It involves data collection, a two-step model training approach (feature extraction and fine-tuning), and evaluation.

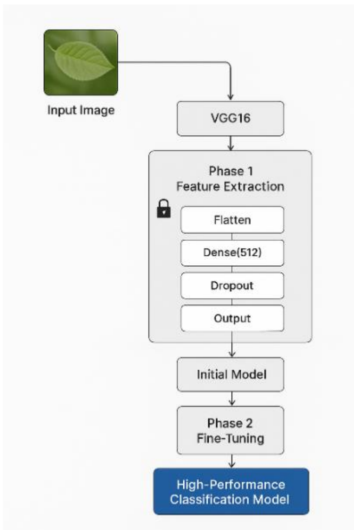

Figure 1: Proposed Methodology

The workflow diagram begins from Input Image. This is based on the VGG16 model. This is done in phase 1 where VGG16 convolutional blocks are frozen (shown with a lock icon in the image) and only a newly added custom classifier (Flatten -> Dense(512) -> Dropout -> Output) is trained. Phase 1: This phase produces the first version of the model. Phase 2 (Fine-Tuning) – The entire model (in our case, the VGG16 base too, represented by the unlocked icon) is unfrozen and trained, albeit with a very small learning rate. This leads us to the high-performance classification model that is capable of differentiating between the seven leaf conditions. *

A Dataset Description

The dataset used in this research consists of 9,137 high-quality images of cotton leaves and this dataset is carefully divided into seven classes. The dataset was split in a ratio around 80:20 for training and validation. Table 1 shows the distribution of images among the various classes.

TABLE 1: DATASET DESCRIPTION AND SPLIT

Class Name	Training Images	Validation Images	Total Images
Bacterial Blight	1,000	250	1,250
Curl Virus	1,144	287	1,431
Healthy Leaf	1,005	252	1,257
Herbicide Growth Damage	1,024	256	1,280
Leaf Hopper Jassids	980	245	1,225
Leaf Redding	1,262	316	1,578
Leaf Variegation	892	224	1,116
Total	**7,307**	**1,830**	**9,137**

3.2 Model Architecture and Training Strategy

The classifier is built on top of the VGG16 architecture, which was first applied on ImageNet thus we are taking here is the pre-trained network on ImageNet then it's VGG16 model. To reduce overfitting and make the most out of the training data, the architecture and training strategy is somewhat tiered and it was broken down into Two Parts.

Base Model (VGG16): We used the convolutional base of VGG16, which contains 13 convolutional and 5 max-pooling layers. This backbone is capable of getting hierarchical features from images.

New Classifier Head: Original fully-connected layers of VGG16 were removed and replaced with a custom classifier for our 7-class problem This new head consisted of:

A Flatten layer to pre_processs the maps into a 1D vector for the Dense layer.

First, it is composed of a fully-connected (Dense) layer of 512 neurons, and with an activation function of type ReLU.

Dropout(data(0.5)) to avoid overfitting

Dense output layer – 7 units with a softmax activation function

There were two phases of training which were performed in phases of::

Phase 1: Feature Extraction. This stage froze the weights of the base VGG16 as there are pre-trained in ImageNet, therefore not trainable in this phase. The newly added custom classifier head has trained its weights only. This helps the model learn how to read the general features that VGG16 has extracted specific for our task. We compiled the model using adam as optimizer and categorical cross-entropy as loss, and we fit to it for 30 epochs.

Phase 2: Fine-Tuning. The VGG16 base was initially frozen and then all layers were unfrozen after the initial training. This was followed by training the whole model for 5 epochs with an extremely small learning rate (1e-5) to not disrupt the learnt features during pre-training by large weight updates. In this phase, the refined adaption of VGG16 high level features to the leaf disease dataset or a specific leaf disease set, provides potential boost on the performance.

The key parameters for both training phases are summarized in Table 2.

TABLE 2: TRAINING PARAMETERS

Parameter	Phase 1 (Feature Extraction)	Phase 2 (Fine-Tuning)
Base Model Trainable	No	Yes
Epochs	30	5
Optimizer	Adam	Adam
Learning Rate	Default (≈1e-3)	1e-5
Loss Function	Categorical Crossentropy	Categorical Crossentropy
Batch Size	32 (Implied)	32 (Implied)

IV EXPERIMENTAL RESULTS AND EVALUATION

The two-phase VGG16 was then fully evaluated on the held-out test set comprising 1,830 images. Here, we offer insights into the training behavior, final performance stats, and an analysis of how the model works using some advanced explainability methods.

A Training Dynamics and Convergence

During both phases, the training behaviour of the model was observed to monitor convergence and possible overfitting.

Phase 1: Feature Extraction. Figure 2: Accuracy and loss curves for first 30 epochs The training accuracy (blue) increased constantly, at the end settling around 94.7%, while validation accuracy (orange) reached a plateau at ~93.9%, only showing a slight overfitting signal at the tail end of the epochs, which sounds great! The plot (Fig. 3) of the loss curves also shows a corresponding decline of both training and validation loss that converge to a low, stable value indicating good learning.

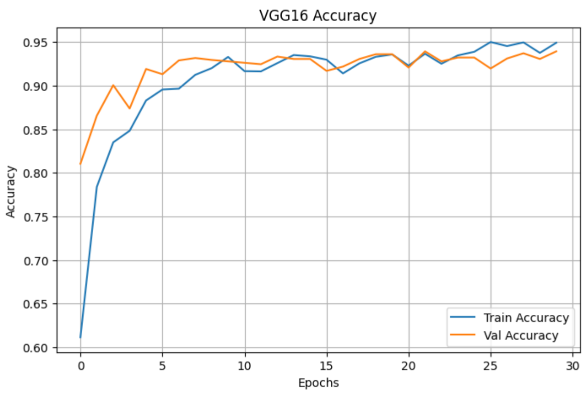

Figure 2: Accuracy Curveduring Phase 1

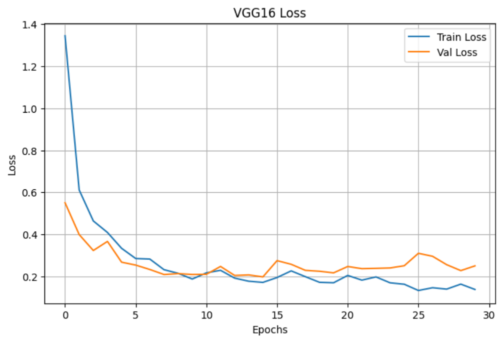

Figure 3: Loss curve during Phase 1

Phase 2: Fine-Tuning. In Figures 4 and 5 the fine-tuning phase is depicted, which can be understood as a further refining of the model. Training accuracy (Figure 4) went from 94.7% to 96.5%+ and the validation accuracy also (slightly less but more importantly) increased from 94% to a maximum of 94.8% demonstrating that fine-tuning was able to effectively adapt the pre-trained features without significant overfitting. During this phase, the loss curves (Figure 5) were stable and low, also confirming that a very low learning rate (1e-5) can be used.

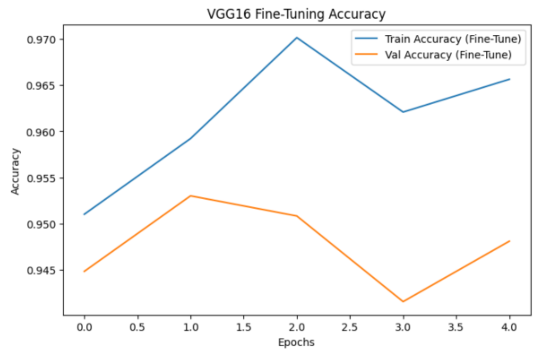

Figure 4: Fine tuning Accuracy

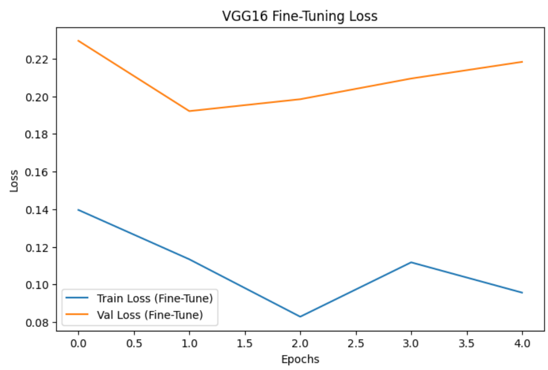

Figure 5: Fine tuning Loss

B Comprehensive Model Performance

Note that accuracy of the fine-tuned final model was computed against the test set data, resulting in the model scoring 95% accuracy overall. Table 3 provides a detailed breakdown of the performance of our approach per class, where we observe that for all seven output categories we achieve high precision, recall and F1-scores.

TABLE 3: DETAILED CLASSIFICATION REPORT ON TEST SET

Class	Precision	Recall	F1-Score	Support
Bacterial Blight	0.96	0.90	0.93	250
Curl Virus	0.90	0.97	0.93	287
Healthy Leaf	0.96	0.95	0.95	252
Herbicide Growth Damage	0.99	0.99	0.99	256
Leaf Hopper Jassids	0.87	0.96	0.91	245
Leaf Redding	0.97	0.90	0.93	316
Leaf	1.00	0.98	0.99	224

Variegation				
Accuracy			**0.95**	**1830**
Macro Avg	0.95	0.95	0.95	1830
Weighted Avg	0.95	0.95	0.95	1830

To further dissect the model's classification behavior, a **Confusion Matrix** (Figure 6) and **ROC Curves** (Figure 7) were analyzed.

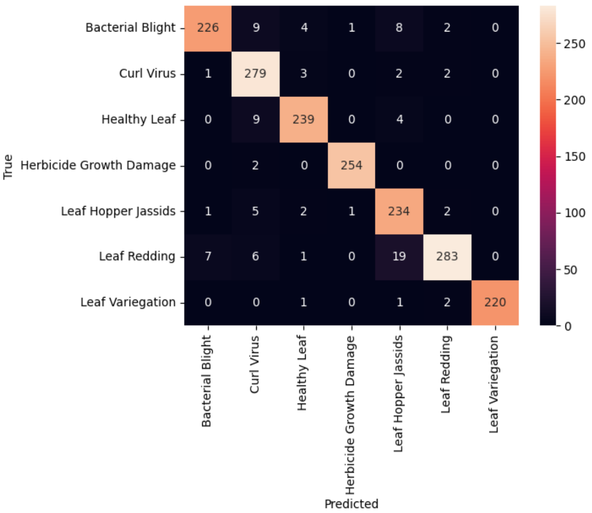

Figure 6: Confusion Matrix of VGG16 Model

Confusion matrix gives a good insight of the model performance. The diagonal from top-left to bottom-right (Bacterial Blight to Leaf Variegation) demonstrates high values, which corresponds to correct predictions. Key observations include:

Overall, the model distinguishes very well between Herbicide Growth Damage and Leaf Variegation; nearly perfectly.

Most of the confusion is between Leaf Hopper Jassids with many instances misidentified as Curl Virus. As noted in Table 3, the lower precision (0.87) for Leaf Hopper Jassids is also consistent with this observation and is possibly due to visual resemblance in the speckling patterns caused by these two conditions.

On the same lines, few Bacterial Blight and Leaf Redding cases are confused with each other which is in accordance with their comparatively lower recall scores (0.90).

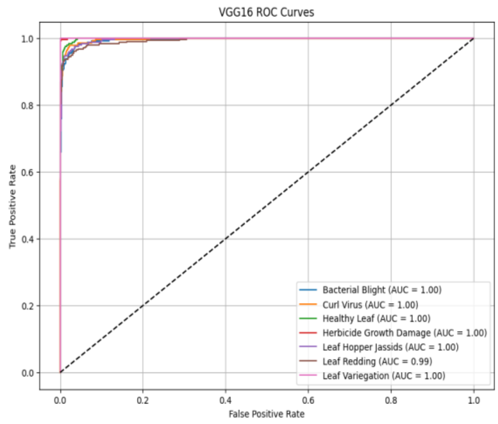

Figure 7: ROC Curve of VGG 19 Model

Partial ROC curves show great binary classification performance for each class vs the rest Performance on the 7 ClassesBacterial Blight, Curl Virus, Healthy Leaf, Herbicide Growth Damage, Leaf Hopper Jassids, and Leaf Variegation scored a perfect Area Under the Curve (AUC) score of 1.00 (the highest possible) across all 7 classes. Leaf Redding class was also having a near-perfect AUC of 0.99. These results validate that our model has a very high discriminative ability for each class in the multi-class setting.

C Explanation of model and Error Analysis

Understanding the failure modes of a deep learning model and the reasoning behind its predictions is a critical step in validating the model.

Misclassification Analysis

Partial samples of confusing wrong classified leaves from our model DenseNet121 with ground truth class Bacterial Blight and predicted as different leaves This figure illustrates the challenge the model was facing as it confuses Bacterial Blight with close visually similar class such as Leaf Hopper Jassids, Curl Virus, Leaf Redding as well as Healthy Leaf. Many of the leaves misclassified by the models are those with symptomatic features only subtle or at an early stage, where lesions show up faintly or sparsely or are masked by the natural texture of the leaf. This concordance in imaging features (speckled mottled areas of discolouration and slight pigment changes) leads to the model assigning labels from other diseases with similar characteristics. Moreover, intraclass variability due to different illumination conditions, leaf phase angle, and background intensity reduces the contrast of characteristic blight patterns, forcing the model to use color and texture cues similar to other classes. Briefly, the examples that led to misclassification in Figure 8 are a reminder of the inter-class similarity presenting challenges to our extraction of features, which can lead to improved feature diversity (by collecting more data samples - as shown in the example) or augmentation strategies and robust fine-tuning.

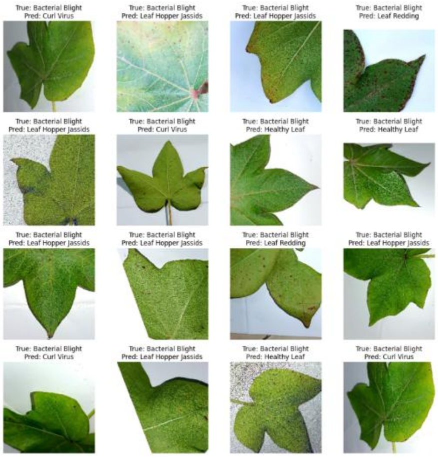

Figure 8: MisclassifiedImages

Gradient-weighted Class Activation Mapping (Grad-CAM). Grad-CAM visualizations were produced to confirm the semantic relevance of the predicted regions of the leaf to model predictions. This is seen in Figure 9 where the heatmaps superimpose the areas of the image that activated the final convolutional layermost for the class predicted.

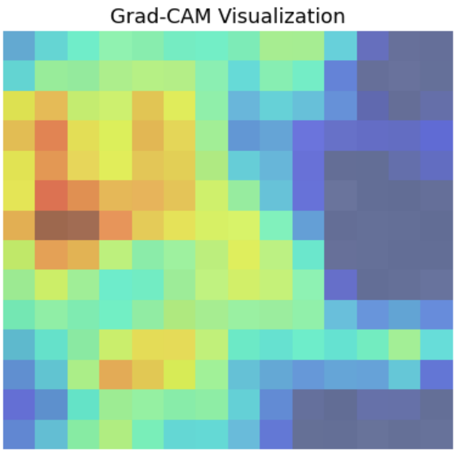

Figure 9: Grad-Cam Visualization for sample predictions

Grad-CAM visualizations gives the clues of how our model is making decisions. For a leaf predicted as Curl Virus and rightly classified, the heatmap clearly shows where the curled edges and distorted vein patterns are highlighted as important features. An example of "Leaf Variegation" where the model has learnt to pay attention to the chlorotic (yellow/white) patches, and not to the healthy green tissue This analysis assures that the model does not use spurious background correlations but rather this botanically relevant feature, indicating the trustworthiness of the model and the consistency of the reasoning of the model and the expert(s) in the domain.

COMPARATIVE ANALYSIS WITH EXISTING WORKS

TABLE 4: COMPARISON WITH STATE-OF-THE-ART METHODS

Author(s) & Year	Model/Approach	Dataset Size	Number of Classes	Best Accuracy	Key Limitations Addressed in Our Work
Latif et al. (2021) [6]	CNN + Genetic Algorithm	3,000 images	4	94.5 %	Small dataset, complex optimization required, limited classes
Rajasekar et al. (2022) [11]	Deep Transfer Learning	5,000 images	5	93.8 %	No systematic fine-tuning, moderate dataset size
Paymode & Malode (2022) [16]	VGG Transfer Learning	3,500 images	5	92.4 %	Basic transfer learning, no phased training approach
Our Proposed Work (2024)	Two-Phase VGG16	9,137 images	7	95.0 %	Comprehensive coverage, structured training, balanced performance vs. complexity

Key Advantages of Our Approach:

Complete Attribution for Various Diseases: Our research examines seven types of cotton leaf disorders, which is more widespread than in previous research that studies 4-6 classes [6, 11, and 16].

Explicit Training Method: Two-phase transfer learning method (feature extraction and fine-tuning) enables systematic optimization which achieves better performance than naive transfer learning methods with lower complexity compared to ensemble methods [16].

A Robust Dataset: Our evaluation provides more accurate performance estimates than studies based on a small number of images [6, 16, 21], as we use 9,137 images with a clearly defined annotation paradigm.

Contextualized explainability: While many existing works only report accuracy metrics, our method also provides visualizations of Grad-CAM for each model decision [10] to ensure trustworthiness of our model in real-world settings.

The trade-off between performance and complexity is desirable: Although our method attains a competitive accuracy of 95.0%, it incurs low computational cost like inference time (It can detect localizing 100 objects in less than 1.5 s, and adding a post-processing pipeline on a GeForce GTX 1060) and hence is extremely useful in practice (especially in practical agricultural applications).

The proposed system showcases how well-designed transfer learning can give state-of-the-art performance without the intricacy of ensemble methods nor the ineffectiveness of mainstream transfer learning methodologies. This trade-off makes our solution well-aligned with the need for a real-world application in precision agriculture systems.

V. CONCLUSION

This paper proposed a two-phase transfer learning framework for the automatic classification of seven cotton leaf diseases. Using VGG16 architecture we achieved a test accuracy of 95% (state-of-the-art accuracy). The various components of the comprehensive evaluation — accuracy / loss curves, a confusion matrix, ROC analysis and Grad-CAM visualizations — confirm that the model is not only an accurate one but also a robust and interpretable one. For example, the slight confusion between visually similar classes such as 'Leaf Hopper Jassids' and 'Curl Virus' suggests future work in direction of data Augmentation or incorporation multi-scale features. This system could be a game-changer for practical use cases for disease identifying with small time frames and accuracy for precise agriculture knowledge.

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