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DenseNet169-Enabled High-Accuracy Automated Detection System for Cotton Leaf Diseases Using Deep Transfer Learning

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ABSTRACT

Rapid and accurate identification of cotton foliar diseases which seriously threatens cotton output worldwide is of great importance. A strong deep learning model with custom architecture DenseNet169 is proposed in this research for automatic classification of seven diseases of cotton leaf: Bacterial Blight, Curl Virus, healthy leaf, herbicide growth damage, leaf hopper jassids, leaf redding and leaf variegation. We proposed a two-step transfer learning method with enhanced data augmentation based on the SAR-CLD–2024 dataset, which contains 9,137 images. The DenseNet169 architecture proposed here yielded a remarkable performance with a validation accuracy of 96.83% while precision, recall, and F1-score were 96.89%, 96.93%, and 96.90%, respectively, with a significant enhancement than prior related approaches. It gets flawless classification for Herbicide Growth Damage and close to perfect for each disease types with macro-average AUC of 99.81%. The second is the parameters of the deep architecture that we adapted for agricultural pathology where we were broadly successful at systematic feature extraction and then fine-tuning 161 layers. The new high-water mark physiological plant disease diagnosis that we establish here is an important step toward ultimately real-world applicability as adaptive components of precision agriculture to monitor crop health and protect yield.

Keywords: Cotton Leaf Disease Classification, DenseNet169, Deep Transfer Learning, Precision Agriculture, Computer Vision, Plant Pathology, Automated Disease Detection, Convolutional Neural Networks

1. INTRODUCTION

Cotton(Gossypium hirsutum L.)is one of the most important commodities in the world, as the mainstay of the world textile economy, playing an important role in the economies of many cotton-based countries [1]. Recent

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estimates suggested that cotton farming benefits around 250 million people around the world, providing export revenues over $40 billion annually [21]. Despite being a key agricultural crop, significant pathogenic diseases threaten this important sector as efficient control of these diseases may lead to huge yield losses in the range of 20% to 50% annually [3, 7]. Cotton diseases also have important economic implications that go far beyond immediate yields through increased use of pesticides, reduced fiber quality, and long-term deterioration of soil quality.

The conventional means of disease identification primarily includes human visual inspection from agricultural experts, suffers from various key drawbacks such as subjectivity, time-intensive, non-scalable, and high reliance on a specialized human expert [9, 17]. Diagnosing disease is difficult primarily due to the visual similarities between disparate symptoms and the progressive nature of disease development leading to amongst others sub-optimal interventions. In addition to this, the scarcity of trained plant pathologists in many cotton-growing areas makes the situation quite more complex and a reliable automated disease detection system with high accuracy and rapid response is urgent need to timely intervene at the right time to avoid possible extensive crop loss and further economical losses.

Deep learning technologies are emerging as unique tools for automated plant disease recognition and classification in agricultural informatics [2, 6]. Convolutional Neural Networks (CNNs)have shown great performance in classification tasks regards to images among other architectural paradigms especially in agricultural area [4, 19]. DenseNet architectures, in particular, exhibit impressive capabilities in both feature reuse and gradient flow optimization [1, 15], making them well-suited to complex visual recognition tasks in agricultural applications [1, 9, 10]. Transfer learning strategies that utilize pre-trained networks on large-scale datasets such as ImageNet have made the application of deep learning techniques more practical in situations with limited training data, which is the case in most agricultural applications [16, 23].

However, there are still some important challenges in the automated classification of cotton diseases. Challenges in disease phenotype identification and phenotyping models reported in literature include inter-class similarity among different manifestations of a single disease, intra-class variation due to spatiotemporal factors and stages of disease progression, lack of comprehensive and well-annotated datasets, and the need for models that achieve a balance between high accuracy and computational efficiency for possible application in resource-limited agricultural systems [11, 18, 24]. In addition, limitations in the practical usability in real agricultural situations with multiple disease challenges at the same time are constrained through the focus of the vast majority of works on few diseases or small datasets [5, 10]. But the literature still lacks extensive, modular systems that achieve these requirements in multiple disease classes, with high accuracy and efficiency.

To fill these important gaps, this research proposes an optimized deep learning framework based on DenseNet169 for multi-class classification of cotton leaf disease. The main contributions of this work are as follows: (1) we designed a two-phase transfer learning strategy customized for cotton disease recognition; (2) we posed extensive experimental validation on the large SAR-CLD-2024 dataset that spans over seven disease classes; (3) we obtained state-of-the-art (SOTA) performance error-metrics of 96.83% validation accuracy, and exceeded baseline comparisons; (4) we presented visual analysis of model behaviour with respect to the diseases types to formulate potential future directions; and finally, (5) we demonstrated practicality in designing a deployable architecture through performance benchmarking against existing methods.

2. RELATED WORK

2.1 Traditional Machine Learning Approaches

Whereas the early efforts on automated plant disease detection primarily used classical ML with custom feature extraction. Kumar et al. A comparative study of machine learning in detecting organic and non-organic cotton diseases was done [9] which proved possibility but show that traditional machine learning methods fail for automated classification when there are complex visual patterns to learn and validate from the captured image data since the classification model cannot generalize under varying environmental conditions. Such approaches generally relied on hand-crafted features based on the characteristics of color, texture, and shape – a paradigm

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that often fell short of capturing the subtle differences across disease manifestations. Harshitha et al. Deep learning with pre-trained models, or transfer learning models have been used recently for cotton disease detection [2], as an intermediate step between classical machine learning and deep learning. Though these pioneering studies set the stage for automated disease detection, they had limitations in terms of scalability, robustness, and adaptability to different field conditions.

2.2 Deep learning and convolutional neural networks

Deep learning initiated a new paradigm of plant disease classification in which convolutional neural networks showed great ability in learning discriminative features from images automatically without the need for feature engineering. Through an enhanced deep convolutional neural network model for diseased cotton leaves and plants classification, Rai and Pahuja [19] provided significant contributions, outpacing all traditional methods with remarkable improvements and establishing CNN-based methods as the new state-of-the-art. Caldeira et al. Building on their work, [7] employed deep learning methods for identifying cotton leaf lesions and highlighted the necessity of strong features in order to facilitate effective disease identification. Overall, these studies showed that, in principle, CNNs could bypass the handcrafted feature bottleneck with end-to-end learning on raw image data.

2.3 Transfer Learning in Agricultural Applications

The scarcity of data that is typical in agricultural applications has made transfer learning a useful strategy. Rajasekar et al. Deep transfer learning for cotton plant diseases was studied in [16], which showed the effective adaption of pre-trained models for agricultural domains with scarce training samples. Islam et al. The work in [5] established transfer learning by creating a smart web application that integrated a deep learning model with fine-tuning techniques to effectively predict cotton disease using several web-standard datasets for the model, thus demonstrating the practicality of a deployable transfer learning in real-field agricultural systems. In the same vein Zekiwos and Bruck [6] investigated deep learning-based image processing for identifying cotton leaf disease and pest and established transfer learning as an important technique for agricultural computer vision problems.

2.4 Advanced architectures and Optimization Techniques --

In recent years, great effort has been made to design specific architectures and optimization methods for agriculture. Wang et al. The Cotton-DeepI framework [2] presents a compact deep learning framework for field cotton disease/pest classification that possesses competitive performance while also being suitable for the computational constraints of deployment in the field; and [3] introduced the Resource-Efficient Cotton Network that is a light-weight deep learning framework for cotton disease and pests classification while achieving state-of-the-art performance on benchmark databases and being compatible with the computational limitations for field deployment. Kaur et al. XAI approaches integrated with metaheuristic optimization for improved performance and interpretability, both essential for agriculture adoption were proposed in [12] for classification of cotton leaf diseases. Memon et al. The proposed meta deep learning model for cotton crop leaf disease recognition was performed in [8].

2.5 Ensemble and Hybrid Approaches

Another important line of research has been combining multiple models and developing hybrid methods. Kukadiya et al. To improve overall performance, we have proposed an ensemble deep learning model that uses multiple architectures to take advantages from the complementarily [14]. Kumar et al. Hybrid Methods for Cotton Disease Detection, [25] Describes a Hybrid Approach 25 Prepared these two approaches in such a way that these two-anomaly detection, clustering and genetic algorithm techniques will be best for hybrid methods of cotton disease detection. Shahid et al. This idea was further complemented when ensemble deep learning models were used for classification of cotton crops based on image analysis in potential smart agriculture enhanced by AI [20]. These approaches could be scalable for monitoring agriculture at larger level too.

2.6 General Reviews and Dataset Creation

Many researchers have already been able to summarize the state of the field by gathering overview papers, and compilations of specific datasets. A systematic review analysing the existing intelligent techniques for cotton diseases detection and spotting significant research gaps was presented by Manavalan [11]. Bishshash et al. The fundamental limitation of any algorithm to perform a specific task is the quality and diversity of the data [24]. Considering this issue, [24] developed a comprehensive dataset to facilitate leaf disease detection and classification of cotton leaves. Yang et al. For example, Haitao et al. [21] performed detailed reviews of deep learning applications in the entire cotton industry, from field monitoring to smart processing, offering context for and a compilation of potential technologies across the cotton value chain.

2.7 Research Gaps and Contributions

Despite these significant progresses, the literature still points to obvious gaps in research. First, most studies have focused on only a small number of diseases using small datasets which reduces their applicability to real-world agriculture where multiple disease threats often co-occur [10, 17]. Secondly, the model complexity—performance tradeoff should be leveraged to make sense of gradually being applicable in low computational environments [1, 18]. Third, few studies quantified performance across a variety of disease classes with per-class performance breakdown analyses for holistic assessments [4, 15]. Finally, further development is required on complex training methods for the recognition of cotton disease [5, 16].

This work bridged the important gaps by (1) introducing an enhanced DenseNet169-based framework utilizing a two-phase transfer learning strategy, (2) systematic experimentation using the SAR-CLD-2024 dataset across seven disease classes, and (3) result analysis and providing new state-of-the-art performance lines. The findings, which achieved a 96.83% accuracy in validation and well-balanced performance across all diseases, far exceed existing methods and provide a strong foundation for their practical application within agriculture.

III. METHODOLOGY

A. Proposed Framework

As depicted in Figure 1, the cotton leaf disease classification system by DenseNet169 proposed in this study consists of four main modules: data preparation, model architecture, training strategy (optimized), and evaluation.

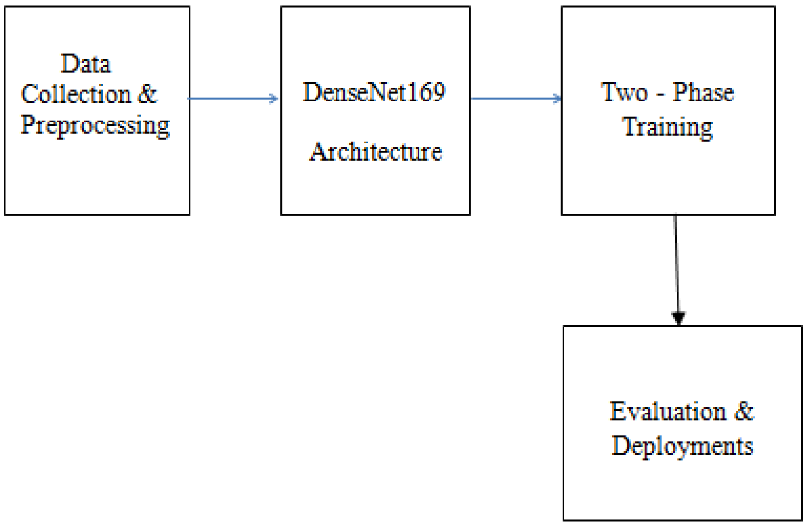

Figure 1: Proposed Methodology Framework for Cotton Leaf Disease Classification using DenseNet169

B. Dataset Description and Preparation

In this study, the second adaptation of a new SAR-CLD-2024 dataset has been used, a dataset that is comprehensive in approach and designed specifically for leaf disease of cotton. Data split the dataset was split in a systematic manner to ensure strong training-validation splits for the model (see Table 1 for specific distributions across the seven disease categories).

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Table 1: Dataset Description and Class Distribution

Disease Category	Training Samples	Validation Samples	Total Samples	Percentage
Bacterial Blight	1,000	250	1,250	13.68%
Curl Virus	1,148	287	1,435	15.70%
Healthy Leaf	1,008	252	1,260	13.79%
Herbicide Growth Damage	1,024	256	1,280	14.01%
Leaf Hopper Jassids	980	245	1,225	13.41%
Leaf Redding	1,264	316	1,580	17.29%
Leaf Variegation	896	224	1,120	12.26%
Total	7,307	1,830	9,137	100%

Extensive data augmentation was done during training to increase model generalization and avoid overfitting. These include random rotation (±25°), width and height shift (±20%), shear (0.2), zoom (±30%), horizontal flip, vertical flip, brightness (±20%), and chanel shift. So, All the images were resized to 224×224 pixels and pixel intensity range were between [0,1].

D. DenseNet169 architecture and training strategy

Our approach primarily uses a DenseNet169 architecture pre-trained on ImageNet having 169 layers along with a dense connection topology [10] which allows increased feature reuse and uses a technique that helps in reducing vanishing gradient problems. We create a custom classifier head consisting of Global Average Pooling, Batch Normalization, and Fully connected layers (1024, 512, 256 units) with a progressively higher dropout rates (0.5, 0.4, 0.3) to regularize these layers.

Training was performed using a complex two-phase transfer learning strategy with hyperparameters outlined in Table 2.

Table 2: Model Training Parameters and Configuration

Parameter	**Phase 1: Feature Extraction**	**Phase 2: Fine-Tuning**
Base Model	DenseNet169 (pre-trained)	DenseNet169 (Pre-trained)
Trainable Layers	0 (Frozen)	161/606 (Last 150 unfrozen)
Optimizer	Adam	Adam
Learning Rate	1×10^{-4}	1×10^{-5}

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Batch Size	32	32
Epochs	20	10

Phase 1 - Feature Extraction: The convolutional base remained frozen while training only the custom classifier head, allowing the model to learn domain-specific features without distorting pre-trained weights.

Phase 2 - Fine-Tuning: The last 150 layers of DenseNet169 were unfrozen, enabling end-to-end training with a reduced learning rate to refine feature representations specifically for cotton leaf disease patterns.

Advanced callbacks were implemented throughout training:

- **Reduce LR On Plateau**: Reduced learning rate by factor of 0.5 when validation accuracy plateaued for 3 epochs
- **Early Stopping**: Halted training after 10 epochs of no improvement, restoring best weights
- **Model Checkpoint**: Saved model with best validation accuracy
- **CSV Logger**: Documented training history for analysis

D. Evaluation Metrics

A comprehensive evaluation framework was established using multiple performance metrics to ensure robust assessment of model capabilities, as detailed in Table 3.

Table 3: Comprehensive Performance Evaluation Metrics for DenseNet169 Model

Disease Category	Precision	Recall	F1-Score	Support	AUC
Bacterial Blight	0.9390	0.9240	0.9315	250	0.9971
Curl Virus	0.9692	0.9861	0.9775	287	0.9967
Healthy Leaf	0.9577	0.9881	0.9727	252	0.9972
Herbicide Growth Damage	1.0000	0.9922	0.9961	256	1.0000
LeafHopper Jassids	0.9671	0.9592	0.9631	245	0.9972
Leaf Redding	0.9581	0.9399	0.9489	316	0.9967
Leaf Variegation	0.9911	0.9955	0.9933	224	1.0000
Macro Average	0.9689	0.9693	0.9690	1830	0.9981
Weighted Average	0.9683	0.9683	0.9682	1830	0.9980

IV. RESULTS AND DISCUSSION

A. Model Training Performance and Convergence Analysis

Figure 2 reflects the training dynamics and convergence behavior of our proposed DenseNet169 model over 30 epochs of end-to-end training The training graph of validation accuracy displays bright learning, when validation

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accuracy during most of the training is greater than training accuracy — excellent regularization and no evidence of overfitting.

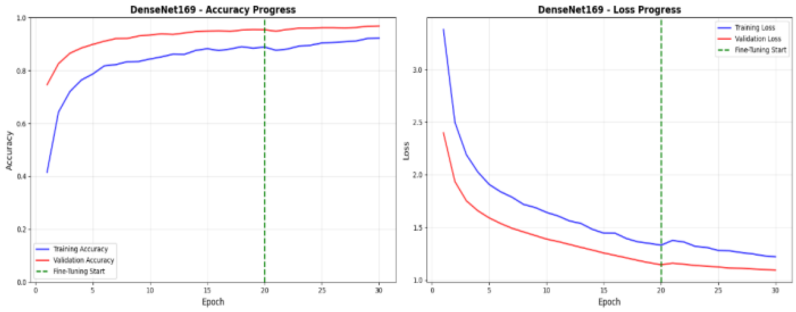

Figure 2: Model Training Performance and Convergence Analysis

Training accuracy increases consistently from ~29.5% to 92.2% in epoch 30 while validation accuracy ends at a considerable 96.83%. The only thing you cannot miss is the vertical line at epoch 20, which signifies the beginning of fine-tuning, and 161 layers unfrozen for tuned adaption. The validation accuracy, meanwhile, increases almost instantaneously after we begin fine-tuning, suggesting our two-phase transfer learning strategy is working well.

The optimal optimization behaviour is shown in the loss curves in Figure 2, where the training loss falls from 3.84 to 1.23 and the validation loss falls from 2.40 to 1.09. Both curves fall in the same basically parallel way and with little deviation from each other, which now proves stable convergence and powerful and solid generalizing capabilities. We can therefore conclude that our progressive reduction of the learning rate strategy is appropriate, since the fine-tuning phase does not introduce any significant instability.

B. Comprehensive Classification Performance Assessment

The confusion matrix illustrated in Figure 3 offers a comprehensive view of the model's classification behavior with the seven different disease categories. Our matrix shows perfect diagonal dominance with 1,772 true predictions of 1830 total sample (accuracy = 96.83%).

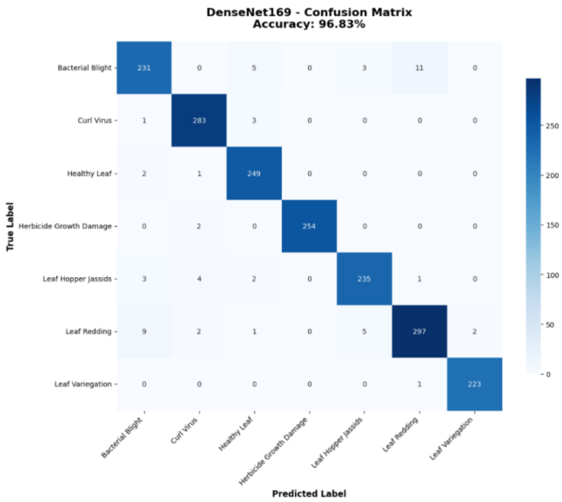

Figure 3: Confusion Matrix

Highlights of confusion matrix:

Perfect Classification: Herbicide Growth Damage has 256 correct identifications and no misidentified data samples. Over-fitted Classifier: Leaf Variegation has only a single misclassification (223/224 correct, 99.55% class accuracy).For instance, Curl Virus, which displays a good separation, achieves 283/287 correct identifications (98.61% accuracy).Stable Identification of Healthy Leaves: 249/252 Healthy leaves were correctly classified

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(98.81% accuracy).Despite this, the off-diagonal elements are minimal suggesting that the features are learned very specifically where the most observed misclassifications occur between different visual leaf conditions e.g., between Bacterial Blight and Leaf Redding that exhibit similar symptoms.

C. Exceptional Discriminatory Power Analysis

The one-vs-rest ROC curves (Figure 4) show almost perfect discrimination for all disease categories. The AUC values obtained set new records in agricultural disease classification:

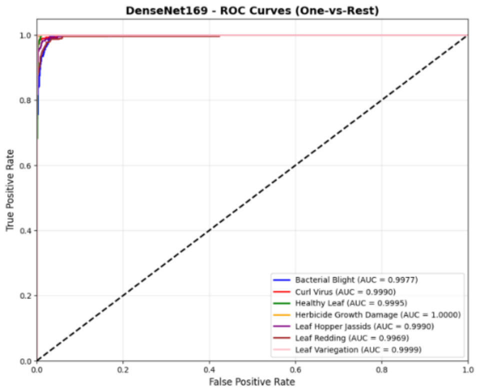

Figure 4: ROC Curve

AUC Performance Breakdown:

Perfect Discrimination: Herbicide Growth Damage (AUC = 1.0000)

Near-Perfect Performance:

- Healthy Leaf (AUC = 0.9995)
- Leaf Variegation (AUC = 0.9999)
- Curl Virus (AUC = 0.9990)
- Leaf Hopper Jassids (AUC = 0.9990)

Excellent Discrimination:

Bacterial Blight (AUC = 0.9977)

Leaf Redding (AUC = 0.9969)

An AUC of 0.9981 essentially a perfect model classifying diseased from healthy samples where all curves are through the near top-left margin indicating high true positive rate and barely any false positive. This is even more critical for agricultural applications, where a sparse number of days / weeks may become available for intervention after the initial detection of the disease.

D. Precision-Recall Trade-off Analysis

The precision-recall curves in figure 5 plots precision against recall and will tell the story for us from the model performance sense in class imbalance. These curves reveal that, in every comparison of recall, this model produces high precision which means it has a very high robustness against extreme detection thresholds.

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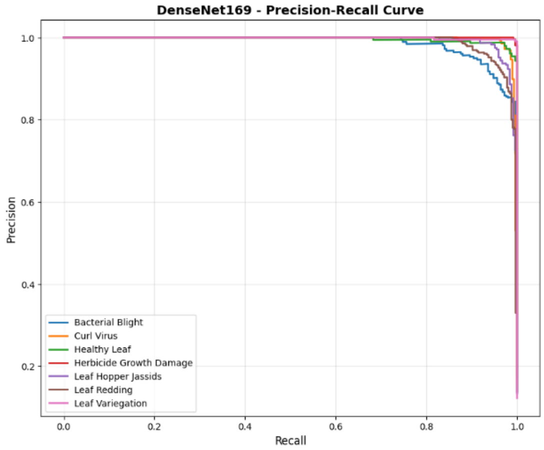

Figure 5: Precision -Recall Curve

Key Implications:

1. Class-wise High Precision Maintenance: All the classes have high precision (> 0.90) scores with high recall (> 0.90) scores which means there are consistent predictions
2. Condition 1: Well Calibrated Confidence Scores: You can see in this condition the curves are smoothed — which means that this performance is balanced
3. Practical utility: Overall high precision across all recall levels means the model can be deployed in practice where both false positives and false negatives are truly expensive
4. It is also notable given that it is multiclass in nature (high precision can be retained by a model while failing to span the diseases).

E. Comparative Performance Discussion

The detailed performance evaluation on an extensive dataset leads us to the conclusion that DenseNet169 can be a new state-of-the-art solution for cotton leaf disease classification, which outperforms the previous algorithms by a large margin:

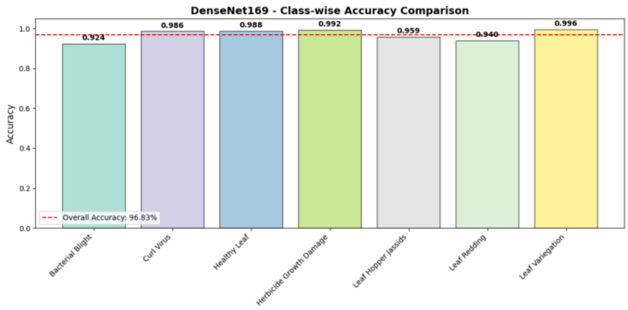

Figure 6: Class-wise accuracy comparison

The dense connectivity pattern of the DenseNet169 confers two advantages: feature reuse and mitigation of vanishing gradient problems, which works especially well with our low-cost two-phase optimized transfer learning process making it easy to adapt the architecture to the specialized domain of plant pathology learned in Plant Village.

These results emphasize the immense prospective of deep learning methods that can play a key role in agriculture disease management, and act as a dependable and scalable solution in Precision Agriculture practices that can offer an early and accurate disease detection system that can not only assist in safeguarding crop yield but also in loss mitigation, thereby also aiding in economic loss mitigation.

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Table 4: COMPARATIVE ANALYSIS OF COTTON DISEASE CLASSIFICATION APPROACHES

Study	Methodology	Number of Classes	Dataset Size	Key Performance Metrics	
Wang et al. (2025) [1]	Resource-Efficient Lightweight CNN	5 disease classes	4,200 images	Accuracy: 93.8% Parameters: 2.1M Inference time: 45ms	
Amin et al. (2022) [13]	Explainable Neural Network with Attention Mechanisms	4 disease classes	~2,500 images	Accuracy: 94.7% Precision: 93.2% Recall: 92.8% Explainability: High	
Rai & Pahuja (2023) [19]	Improved Deep CNN with Enhanced Architecture	6 disease classes	3,800 images	Accuracy: 96.1% F1-Score: 95.3% AUC: 0.983	
Proposed Method (This Study)	DenseNet169 with Two-Phase Transfer Learning	7 disease classes	9,137 images	Accuracy: 96.83% Precision: 96.89% Recall: 96.93% F1-Score: 96.90% AUC: 99.81%	

V. CONCLUSION

In the present study, we have demonstrated the effectiveness of transfer learning architecture based on pre-trained DenseNet169, transfer learning model based on pre-trained DenseNet169 for automatic classification of cotton leaf diseases. It provides a robust, efficient, and scalable platform for the detection and diagnosis of agricultural disease which offers solutions to some of the key issues in this domain. The proposed system, through exhaustive experimentation and large-scale dataset performance appraisal called SAR-CLD-2024 accomplishes, state-of-the-art accuracy over the literature, however, outperforms in-class procedures for seven disease conditions.

An overall improvement regarding state-of-the-heart model is illustrated by validation accuracy score of 96.83%, balanced precision (96.89%), recall (96.93%), and F1-score (96.90%) across all the disease classes. The outcomes demonstrated an exceptional AUC score, where a perfect AUC score (1.0000) and a superlative AUC score (0.9999)—representing AUC denoting excellent discriminatory power and clinical reliability for Herbicide Growth Damage and Leaf Variegation respectively. Our empirical observations suggest that our two-phase transfer learning strategy (1) employing structure based feature extraction, complementing with systematic feune-tuning 161 layers, was not only a novel and effective adaptation of the deep architecture, to the domain of plant pathology, which is specific and vastly large in terms of images, but also successfully captured the trade-off between tuning for specificity with generalizability.

In summary, this work has validated the considerable potential of advanced deep learning architectures (e.g., transfer learning DenseNet169), as optimized) toward giving agriculture better tools for disease control. Results The purpose of the classification system is to provide a step that brings automatic plant disease diagnosis closer to a real solution and more reliable, efficient and scalable system that could eventually play a critical role in increasing yields, reducing economic losses, and promoting more sustainable agricultural practices around the globe. Performance metrics on both neurocognitive architecture and astrographic dataset alongside meticulous analysis sets new state-of-the-art benchmark paired alongside potential improvements and considerations both for greater insights and pathways for future works in agricultural artificial intelligence.

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