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Hybrid deep learning approach for cotton leaf disease detection and management using fine-tuned VGG16 and Inception v3 models

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Abstract

Agricultural productivity is frequently threatened by crop diseases, leading to substantial economic losses and hindering the adoption of sustainable farming practices. Early detection and timely intervention are therefore critical to mitigate these risks. This paper presents a novel hybrid deep learning method (HDLM) for accurate classification of cotton leaf diseases by integrating the strengths of two fine-tuned deep learning models—Visual Geometry Group 16 and Inception v3—through a stacking ensemble strategy that combines their predictions at the output level. The model was trained and validated on a carefully curated dataset of 3,000 images, manually labeled into six classes: Aphids, Armyworm, Bacterial Blight, Powdery Mildew, Target Spot, and Healthy Leaves, with 2,400 images used for training and 600 reserved for validation. To enhance generalization and robustness against real-world variations in leaf orientation, illumination, and background, extensive data augmentation techniques were applied, including rotations, flips, zooming, translations, and brightness adjustments. The proposed HDLM achieved a classification accuracy of 98.56%, significantly outperforming benchmark models such as AlexNet, DenseNet-121, ResNet-50, LeNet-5, and a 7-layer convolutional neural network, which achieved accuracies of 90–95%. In addition, the model incorporates a disease management recommendation system that provides actionable guidance to farmers to mitigate diseases and improve crop yields. This research demonstrates the efficacy of ensemble deep learning techniques in plant disease detection, providing a scalable, robust, and practical solution for precision agriculture. Future work should focus on expanding the dataset with heterogeneous sources, integrating advanced augmentation strategies, and exploring real-time feedback mechanisms to further enhance model adaptability, predictive performance, and applicability across diverse agricultural environments.

Keywords: Cotton leaf disease detection; Hybrid deep learning; Visual Geometry Group 16; Inception v3; Ensemble learning

1. Introduction

The global economy remains anchored in agriculture's ability to supply food, fiber, and raw materials, sustaining the farmers' income worldwide. Among the world's major crops, cotton's importance to the economy lies in its contribution to the textile industry and its role in domestic supply and international trade (Bedi & Gole, 2021). The economic and agricultural system balance hinges on the crops' ability to flourish and be productive. To minimize financial losses and to maintain ostensibly high yields and fiber quality, swift and precise diagnosis of cotton leaf diseases is essential to avoid crippling the farmers and investors.

Cotton cultivation is increasingly challenged by biotic stresses, including pests and diseases such as aphids, armyworm, bacterial blight, powdery mildew, and target spot. A cotton plant cannot sustain unchecked growth, which will negatively affect the quantity and quality of its cotton fiber (Rajasekar *et al.*, 2022). Alongside these, mildew diseases, if left untreated, can severely impair cotton plant growth. The traditional approach to diagnosing the plant involves visual inspections, often conducted by trained field experts. While traditional approaches can be effective within specific domains, they are labor-intensive, costly, and difficult to scale in remote or sparsely populated areas lacking agricultural experts (Saleem *et al.*, 2020). The use of visual aids for disease diagnosis poses significant challenges. Visually diagnosable traits often reflect the principal pathogens capable of severely damaging the plant, and slight variation in environmental conditions, lighting, or plant positioning can further exacerbate these factors (Aggarwal *et al.*, 2023). Crop disease detection has become more accurate through automation and technological innovation. The rise of deep learning (DL) has made detection more efficient. Using raw data, DL convolutional neural networks (CNNs) systematically learn complex, hierarchical structures with distinct features and patterns in leaf morphology, color, and texture, capturing phenomena that are challenging for humans (Gupta & Sharma, 2024). This increased speed and accuracy lead to timely corrective actions while minimizing the need for manual evaluations.

The strength of a CNN-based architecture lies in its ability to focus on specific, often complex image features and, based solely on these features, draw meaningful conclusions. This ability, combined with the architecture's capacity for both global and local feature recognition, is crucial for its widespread application in crop disease detection (Kshirsagar *et al.*, 2022). The CNN's ability to succinctly classify numerous leaf features, thereby enhancing and distinguishing the various diseases it may have, increases the precision of the entire model. CNNs have also proven reliable tools in harsh illumination conditions and in the presence of leaf angulation and background disorder, as used in image capture for in-field applications (Kumar *et al.*, 2017).

The implementation of transfer learning has greatly improved DL's ability to pinpoint plant diseases (Chopkar *et al.*, 2024). Transfer learning is the use of existing models trained on large datasets and their modification to perform tasks, such as classifying diseases on cotton leaves. Adjustments of the Visual Geometry Group 16 (VGG16), Inception v3, and ResNet-50 fine-tune the domain of sophisticated architectures, eliminating the need for large datasets, reducing training time, and improving generalization to unseen disease patterns (Islam *et al.*, 2023). These models can effectively identify disease-related features, even with small datasets, which is advantageous for such crops, where annotated images are highly difficult to obtain. Transfer learning is, in fact, a step toward improving the model's performance on a general dataset.

To complement the performance booster for classification tasks, simple ensemble methods can be used to surpass the thresholds set by individual models and produce a single, robust output. Stacking of structure ensembles results from the covariate and conditional independence assumptions, in which each fold of the ensemble provides a different overfit complement. This yields enhanced accuracy and reliability of the model while ensuring its versatility to varying environmental and disease alterations. Furthermore, the inclusion of augmentations, such as rotation, scaling, flipping, and shifts of colors, greatly adds to the under-training set and protects the model from being too conditioned to the data set, improving the overfitting of the model and the generalization of the unsupervised data (Thivya Lakshmi *et al.*, 2024). Thus, these approaches from practicing augmented techniques improve the ability of DL models to maintain the performance threshold set in the field across varying leaf growth stages of cotton.

The proliferation of automated systems for diagnosing illnesses also supports the addition of decision-making systems for farmers. By offering practical, actionable strategies, such as targeted pest and disease interventions, these systems enable farmers to take appropriate, timely action during a disease outbreak. This helps minimize the impact of diseases on yield and enhances sustainable agriculture by reducing the inappropriate use of pesticides and environmentally unfriendly farming practices. Moreover, automated diagnostic systems enable disease surveillance across large agricultural areas without increasing the workforce (Singh & Misra, 2017).

Various investigations have documented the practical and financial benefits of using DL methods in workflows for detecting diseases in cotton. For example, recent accounts have stressed the need to maintain production sustainability to avoid losses and support global textile production by preserving the health of cotton crops (Bedi & Gole, 2021). DL-based approaches have been deployed and demonstrated the ability to accurately and reliably classify multiple leaf diseases, making them suitable for use in the agricultural sector (Chen *et al.*, 2020; Singh & Misra, 2017). These systems not only detect problems but also integrate management advice, thereby improving crop protection by providing diagnostic and practical guidance.

Figure 1 describes the significance of cotton agriculture, the threats associated with cotton leaf diseases, and the usage of DL technology for automated disease tracking and diagnostics. It describes the most prominent cotton leaf diseases and pests, such as cassava aphids, armyworms, cotton bacterial blight, cotton powdery mildew, and second cotton target spot, and highlights key cases where CNN-based DL models and mobile-based detection systems provide scalable, accurate early diagnosis and management solutions.

To conclude, integrating hybrid DL techniques, CNN-based models, transfer learning, stacking ensembles, and data augmentation offers a strong and flexible approach to automated detection of cotton leaf diseases. Such strategies address the shortcomings of manual assessments, reducing the prevalence of undiagnosed diseases and improving overall disease management, thereby increasing cotton yield and quality. The increased accessibility to labeled datasets, paired with improved computational technology, enables the application of these techniques to real-world agricultural scenarios, thereby remarkably improving cotton farming practices.

2. Literature review

The ability of DL to detect different plant diseases has been optimized for accuracy, speed, and scalability in diagnosing agricultural disorders. Achieving accurate and timely results is crucial not only for maintaining crop health and minimizing losses, but also for ensuring the long-term sustainability of agricultural practices. Improvements in computational intelligence, alongside the increasing availability of digital imagery, have led to the development of complex DL frameworks that fully automate disease diagnosis.

Deep transfer learning is one of the most effective methods for diagnosing plant diseases. Chen *et al.* (2020) reported that using disease-specific pre-trained models fine-tuned on plant datasets yields optimal identification accuracy, thereby reducing the need for annotated images. This approach allows models to adapt quickly to new crops or disease states, offering a cost-effective solution for agricultural systems. However, not all implementations are equally successful. Amin *et al.* (2022) developed a DL framework for classifying corn leaf diseases. Their pseudo-automated DL systems reduced reliance on labeled data, but at a cost of accuracy. This contrast highlights that although transfer learning can save time and resources, careful model design and dataset selection remain critical to maintain performance.

Research on early detection of plant disease has also

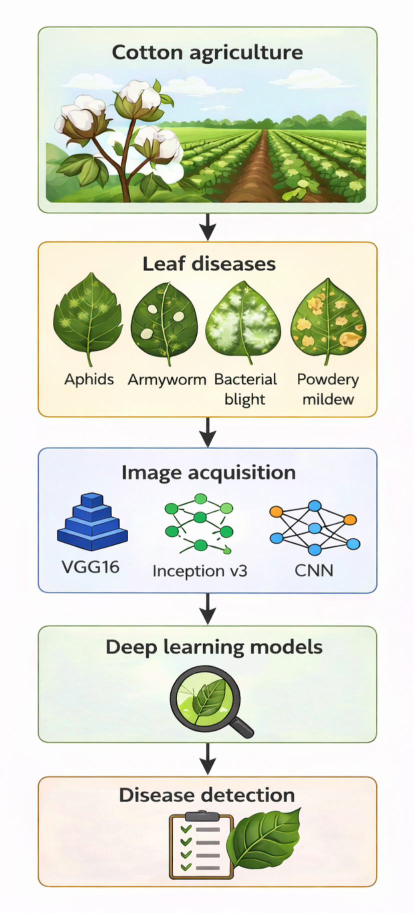

Figure 1. Overview of cotton agriculture, leaf diseases, and deep learning in disease detection

benefited from traditional image processing techniques, such as segmentation and soft computing. Singh and Misra (2017) studied isolated segmentation methods for disease classification, enabling a focus on a single class and improved classification. Wang *et al.* (2016) explored the use of context DL models in medical imaging and discussed how techniques, such as CNNs, can be applied to agricultural disease recognition, demonstrating the cross-pollination of methodologies across domains. Zhu *et al.* (2018) combined DL models with different imaging techniques, demonstrating the use of thermal and multispectral images for disease detection and diagnosis.

The boundaries of an image and its contents are crucial for automating disease analysis and treatment. Pang *et al.* (2011) introduced region-growing and local thresholding and applied them to segment diseases on leaves. Zhang *et al.* (2018) focused on the practical side of computer vision and developed an automated segmentation method for cotton leaves in uncontrolled environments. Kumar *et al.* (2017) highlighted the use of image-processing techniques to flag wheat leaf diseases and further demonstrated the impact of relevant segmentation and preprocessing techniques on improving classifier performance. Jian and Wei (2010) used support vector machines to analyze and identify diseases in cucumber leaves and demonstrated the use of image-based preprocessing techniques to serve as wrappers in traditional machine learning workflows.

Crop disease detection has relied heavily on advanced learning models, especially CNNs, because they can learn hierarchical features from raw images. Deep residual networks were introduced by Cheng *et al.* (2017) for pest detection in highly complex field backgrounds. Alfarisy *et al.* (2018) developed DL-based models for the detection and classification of paddy pests and diseases. Fujita *et al.* (2016) demonstrated the use of CNNs and the economy of robust plant diagnostic systems, while stressing the importance of developing DL modules for real-world use. In the early era, color-transform techniques were employed in automated disease-detection methods; Chaudhary *et al.* (2012) were the first to use leaf contrast and simple image features to enhance the system's detection capabilities.

It is crucial to develop disease-detection systems for cotton due to its economic impact. Using unconstrained field imagery of cotton crops, Parikh *et al.* (2016) explored approaches to detecting diseases and assessing their severity. They highlighted the importance of developing models that can adapt to real-world conditions and evolving environments. Zhang *et al.* (2021) used DL models to identify cucumber leaf diseases with limited data, underscoring the importance of approaches that work with scarce data, which is applicable to leaf datasets. To improve model generalization, augmentation techniques have been used. For instance, Liu *et al.* (2020) employed generative adversarial networks to generate synthetic grape leaf images for use with cotton disease datasets, thereby improving model performance. Lastly, Kaya *et al.* (2019) demonstrated the utility of transfer learning for plant classification, especially for reducing training time and computational load, by showing that performance in disease recognition can be greatly improved by adding specific adjustments to previously trained models.

Most of the literature discusses the importance of DL, transfer learning, and hybrid ensemble methods for automated disease detection. Dsouza (2023) highlighted recent trends in cotton production and emphasized the importance of sustainable agricultural practices, while Nigam and Jain (2020) provided a comprehensive review of deep learning techniques for plant disease detection, demonstrating their effectiveness in improving diagnostic accuracy and automation in modern agriculture. These methods are accurate, scalable, and practical, especially for cotton, for which timely disease detection is crucial for yield and economic sustainability. The combination of advanced preprocessing techniques, segmentation, data augmentation, and the structural design of deep CNNs tackles the unique challenges posed by agricultural environments. The Hybrid DL Method (HDLM) proposed in this study integrates fine-tuned models with ensemble methods to deliver a reliable diagnosis of cotton leaf disease and actionable control measures for farmers and other stakeholders.

3. Proposed methodology

The proposed methodology integrated fine-tuned DL models with a stacking ensemble framework to achieve highly reliable cotton-leaf disease detection. The process began with dataset construction, where 3,000 high-quality images representing six classes—Healthy, Aphids, Armyworm, Bacterial Blight, Powdery Mildew, and Target Spot—were collected from agricultural repositories and online sources. Expert-validated labeling ensured class accuracy, and an 80–20 train–test split with balanced class distribution was employed to prevent model bias. High-quality, well-annotated data were essential for enabling deep models to learn discriminative patterns and produce dependable predictions.

In the preprocessing phase, images were resized to 224 × 224 pixels to match the input size of the deep architectures. Pixel normalization (0–1 scaling) was applied to accelerate convergence, followed by extensive augmentation using Keras ImageDataGenerator. Random rotations, translations, zooming, shear distortion, and horizontal/vertical flips significantly increased intra-class variation, making the model more resilient to changes in leaf orientation, lighting, and background noise. Such diversity ensured that the model generalized well to real-world field images.

Feature extraction and fine-tuning were performed using VGG16 and InceptionV3, both initialized with ImageNet weights. Early convolutional layers were frozen to retain generic feature representations, while deeper layers were retrained to learn fine-grained disease-specific patterns. Custom dense layers were added for six-class classification, and training used the Adam optimizer with a learning-rate scheduler and categorical cross-entropy loss. To enhance predictive robustness, a stacking ensemble strategy was adopted. Outputs from the base models served as input features for a logistic-regression meta-learner. Cross-validation was used during training, enabling the ensemble to learn optimal decision boundaries across folds and effectively combine complementary representations from both CNN models.

A key enhancement of the proposed system was its adaptive-learning perspective, which was conceptually aligned with feedback-based and adaptive control systems widely used in nonlinear dynamic environments. Similar to adaptive fuzzy control and fixed-time synchronization approaches used in fractional-order chaotic systems, adaptive backstepping controllers for uncertain nonlinear systems, and neural-adaptive controllers for complex multivariable dynamics, the proposed model exhibited adaptability through iterative fine-tuning and continuous error-driven optimization. The ensemble effectively behaved as an adaptive decision layer, adjusting its internal weights based on prediction feedback, comparable to output-feedback controllers that refine system response in the presence of uncertainties. This analogy highlighted the system's robustness, as the meta-learner dynamically corrected prediction deviations—akin to how adaptive controllers stabilized uncertain robotic or motor-driven systems. Therefore, the methodology established a foundation for integrating sensor-driven feedback loops, enabling real-time agricultural data to autonomously guide model updates, similar to adaptive and optimal control systems used in precision engineering.

Finally, the complete workflow was formalized in pseudocode that described data loading, augmentation, fine-tuning, cross-validated stacking, and evaluation. After training, the model computed accuracy, precision, recall, F1-score, and the area under the receiver operating characteristic curve (AUC) to evaluate performance. This adaptive, stacked learning framework ensured robust disease identification and provided a scalable foundation for future real-time precision agriculture systems.

Figure 2 depicts the sequential steps starting with dataset collection and preprocessing, followed by data augmentation, fine-tuning of VGG16 and Inception v3, and application of a stacking ensemble for final predictions. The diagram highlights the integration of multiple DL architectures, emphasizing how the ensemble combines diverse feature representations to produce robust and accurate disease classification. Each step in the figure corresponds to a phase in the methodology, clearly showing the flow from raw images to high-confidence predictions, ensuring interpretability and reproducibility.

For pseudocode representation, the input was the cotton leaf images dataset D with six classes (Aphids, Armyworm, Bacterial Blight, Powdery Mildew, Target Spot, and Healthy Leaves), and the output was predicted classes for test images and performance metrics.

4. Implementation

In brief, the methodology combined dataset curation, stepwise advanced preprocessing, DL models, and stacking ensemble learning to create a scalable and reliable disease detection model for cotton leaves. The methodology addressed each model's deficiencies and improved overall classification performance by leveraging diverse, complementary feature representations from different architectures and integrating them at a meta-learner. Each step, including model ensemble learning, data collection and augmentation, and model fine-tuning, was developed for real-world effectiveness, robustness, and accuracy as exemplified in Algorithm 1. Such a comprehensive approach strategically assisted farmers and other stakeholders in crop production by enabling timely disease identification and management, thereby promoting sustainable cotton production.

The implementation of the proposed HDLM for cotton leaf disease classification followed a systematic and reproducible approach to ensure high performance and practical applicability. The dataset used consists of 3,000 images collected from multiple sources, including publicly available agricultural datasets and online repositories. Each image was manually labeled into six classes—Aphids, Armyworm, Bacterial Blight, Powdery Mildew, Target Spot, and Healthy Leaves—by domain experts. To ensure labeling accuracy and consistency, quality control measures such as cross-verification by multiple annotators and validation of label consistency across images were applied. All images were preprocessed by resizing to 224 × 224 pixels and normalizing pixel intensities to the [0, 1] range, enabling the DL models to converge effectively. To enhance generalization and reduce the risk of overfitting,

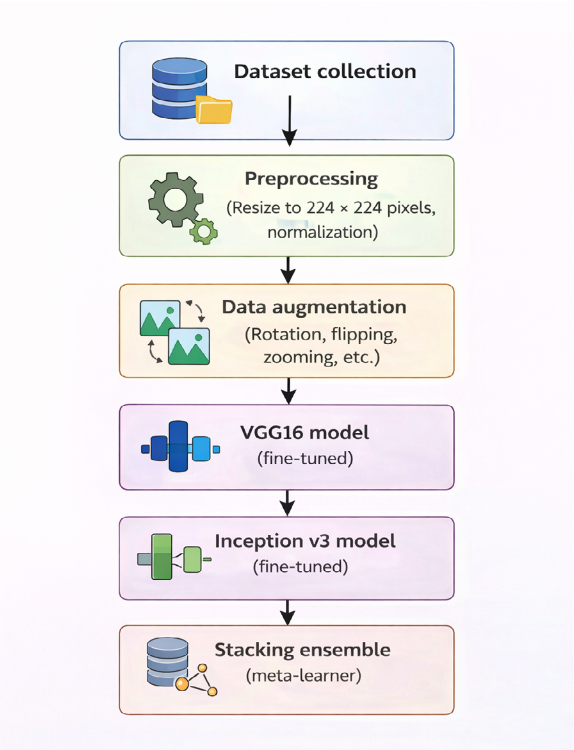

Figure 2. Proposed cotton leaf disease classification workflow
Abbreviation: VGG16: Visual Geometry Group 16.

extensive data augmentation was performed using Keras ImageDataGenerator, including random rotations, width and height shifts, zooming, horizontal and vertical flips, and brightness adjustments. These augmentation techniques introduced variations in leaf orientation, lighting conditions, and background clutter, mimicking real-world scenarios that the model would encounter in agricultural environments.

The HDLM leverages two pre-trained DL architectures—VGG16 and Inception v3—each fine-tuned on the augmented dataset to capture complementary spatial and morphological features of cotton leaf diseases. Each network incorporated a global average pooling layer followed by a fully connected dense layer with 1,024 neurons, allowing adaptation to the six-class classification task. Hyperparameters such as the learning rate (0.0001), batch size (32), optimizer (Adam), and number of epochs (20) were optimized using a grid search strategy combined with cross-validation. Early stopping based on validation loss was employed to prevent overfitting while maximizing model performance. The stacking ensemble approach was then applied to integrate the strengths of each base model, with their predictions serving as input features to a logistic regression meta-classifier. This meta-learner effectively combines outputs from individual models, thereby enhancing classification accuracy and providing a robust prediction framework that handles complex variations in cotton leaf images.

Performance evaluation was conducted using standard metrics, including accuracy, precision, recall, F1-score, and AUC, to assess classification effectiveness. Additional error analysis was conducted to identify misclassification patterns and to ensure the model's reliability across all six categories. The methodology was designed to simulate real-world agricultural scenarios in which variations in lighting, leaf orientation, and background can significantly impact prediction accuracy. Furthermore, to support transparency and reproducibility, the codebase and dataset will be made publicly available, enabling other researchers to replicate and extend the study. Overall, this implementation combines meticulous dataset preparation, advanced DL architectures, robust data augmentation, and ensemble learning to deliver a highly accurate and reliable solution for cotton leaf disease detection, demonstrating practical utility for precision agriculture and decision-making in real farming environments.

4.1. Evaluation

The final model's accuracy was evaluated by comparing the predicted labels with the true labels from the test set. The proposed HDLM model achieved an accuracy of 98.56%, demonstrating its effectiveness in classifying cotton leaf diseases.

For the proposed HDLM model for cotton leaf disease classification, several equations were included:

(i) Cross-entropy loss function: The cross-entropy loss function is widely used in classification tasks and is essential in training DL models. It evaluates the model's performance by comparing the predicted probabilities with the actual labels (**Equation 1**).

$$L = -(1/N)\,\Sigma\, y_{i,c} \log(\hat{y}_{i,c}) \quad (1)$$

where:

- N is the number of samples.
- C is the number of classes.
- $y_{i,c}$ is the binary indicator (0 or 1) if class label c is the correct classification for observation i.
- $\hat{y}_{i,c}$ is the predicted probability of observation i being of class c.

(ii) Accuracy metric: Accuracy is a fundamental metric for evaluating the performance of classification models. It is defined as the ratio of correctly predicted instances to the total instances (**Equation 2**).

Algorithm 1. Stacked ensemble for cotton leaf disease detection using fine-tuned Visual Geometry Group 16 (VGG16) and Inception v3.

Steps	Description
1	Dataset collection: Gather 3,000 images of cotton leaves—leaves showing various disease conditions (bacterial blight, powdery mildew, and target spot), leaves infected with different pests (aphids and armyworms), and healthy leaves—from online repositories and manually label them for accuracy.
2	Dataset split: Partition the dataset into 80% training and 20% for testing while maintaining class balance.
3	Preprocessing: Resize images to 224 × 224 pixels, normalize pixel values to [0,1], and handle any missing or corrupted data.
4	Data augmentation: Apply geometric transformations (rotation, shifting, scaling, zooming, and flipping) using Keras ImageDataGenerator to enhance generalization and prevent overfitting.
5	Base model selection: Select VGG16 and Inception v3 pre-trained models for feature extraction and classification.
6	Fine-tuning: Freeze the early convolutional layers and retrain the deeper layers with the cotton leaf dataset. Add custom fully connected layers for six-class classification. Use Adam optimizer and categorical cross-entropy loss function.
7	Cross-validation setup: Divide training data into *n* folds. For each fold:
7a	Train VGG16 and Inception v3 on *n*−1 folds.
7b	Predict the *n*-th fold using trained models and collect outputs as features.
8	Meta-learner training: Combine predictions from all folds to train a logistic regression meta-learner that learns the optimal combination of base model outputs.
9	Final ensemble prediction: Use a stacking ensemble (meta-learner + base models) to predict classes on the testing dataset.
10	Performance evaluation: Calculate accuracy, precision, recall, F1-score, and area under the receiver operating characteristic curve to assess model effectiveness.
11	Output: Produce final disease classification for all test images and provide actionable insights for disease management.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \quad (2)$$

Accuracy = (TP + TN) / (TP + TN + FP + FN)

where:

- TP is the correctly predicted positive observations (true positives).
- TN is the correctly predicted negative observations (true negatives).
- FP is the incorrectly predicted positive observations (false positives).
- FN is the incorrectly predicted negative observations (false negatives).

(iii) Softmax activation function: The Softmax function is used in the output layer of a multi-class classification model to convert logits (raw predictions) into probabilities (**Equation 3**).

$$\sigma(Z_i) = \hat{e}\,\{Z_i\} \,/\, \Sigma\ \hat{e}\,\{Z_j\} \quad (3)$$

where:

- Z_i is the logit or output of the network for class *i*.
- *C* is the total number of classes.

For comparative evaluation, additional deep learning models including AlexNet, DenseNet-121, ResNet-50, LeNet5, and a 7-layer CNN were implemented and trained under the same experimental conditions. These models served as benchmark architectures to evaluate the effectiveness of the proposed HDLM. Performance comparisons demonstrate that the HDLM outperformed all baseline models in terms of accuracy and robustness.

5. Results

The dataset consists of 3,000 images, evenly distributed across six categories: Aphids, Armyworm, Bacterial Blight, Powdery Mildew, Target Spot, and Healthy Leaves. Images were collected from online sources, carefully labeled, and split into 80% training and 20% testing sets. Figure 3 illustrates the distribution of the six classes in the dataset, ensuring a balanced representation for effective training and testing. Figure 4 shows that the AlexNet model's accuracy improves steadily over 20 epochs, starting at around 70% and reaching approximately 95% by the 20th epoch. Figure 5 shows a gradual improvement in the DenseNet-121 model's accuracy over 20 epochs, beginning at 66% and reaching around 93% by the final epoch. Figure 6 illustrates that the ResNet-50 model's accuracy starts at 65% and steadily improves to approximately 92% by the 20th epoch. Figure 7 shows a significant improvement in the LeNet5 model's accuracy, starting at 62% and reaching about 91% by the last epoch. Figure 8 shows consistent improvement in the accuracy of the 7-layered CNN model, reaching around 90% by the 20th epoch. Lastly, Figure 9 shows the improvement in the accuracy of the proposed hybrid model, which recorded the highest final accuracy, which is 98.56%.

Table 1 highlights the accuracy improvement across different DL models over 20 epochs, showcasing the effectiveness of each model in classifying cotton leaf diseases. Among the benchmark models, AlexNet achieved the highest final accuracy of 95%, followed closely by DenseNet-121 and ResNet-50. Each model demonstrated significant improvements in accuracy from the initial to the final epoch, indicating successful training and fine-tuning. Figure 10 compares the final accuracy of various models after training. The proposed HDLM model achieved the highest accuracy of 98.56%, surpassing other models, which range from 91% to 95%.

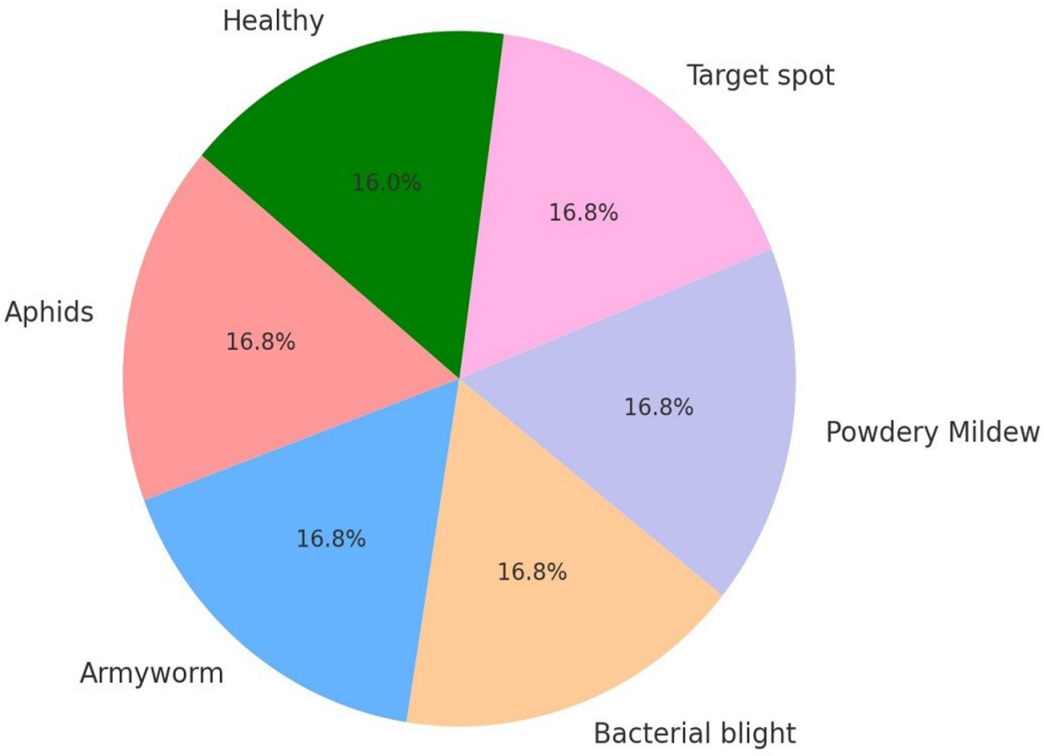

Figure 3. Dataset distribution

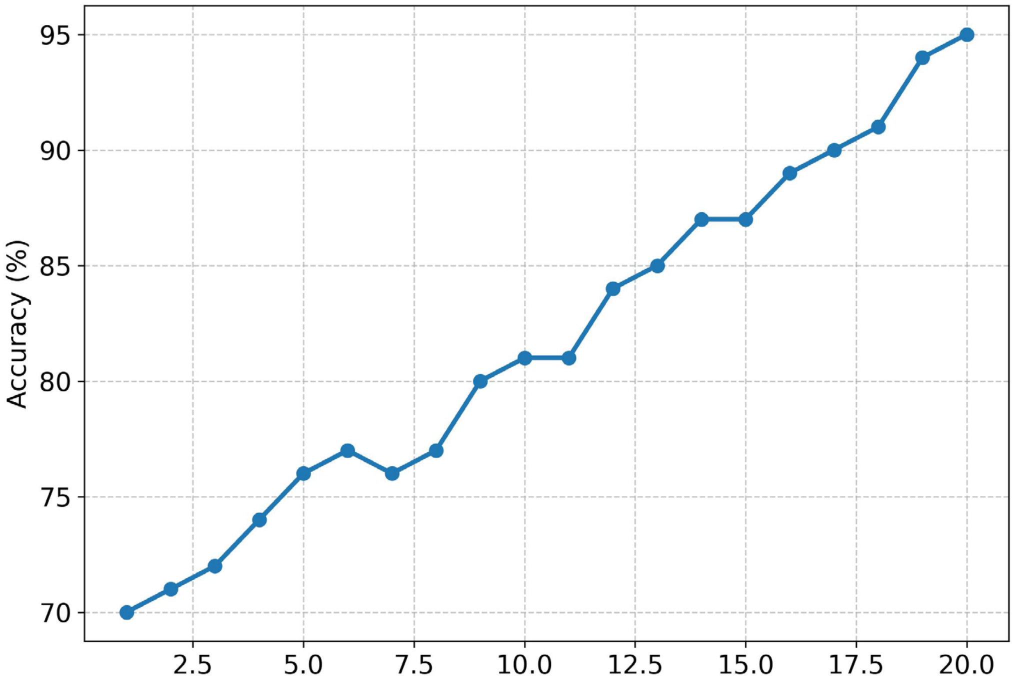

Figure 4. Accuracy vs. Epochs plot for AlexNet model

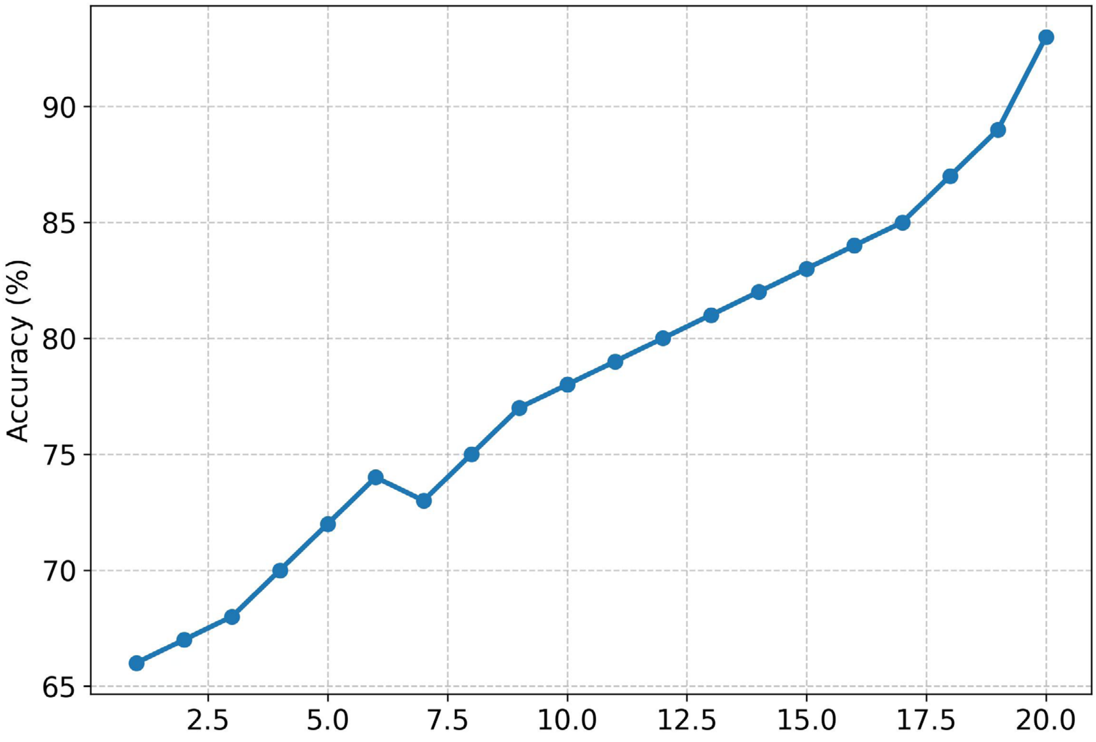

Figure 5. Accuracy vs. Epochs plot for DenseNet-121 model

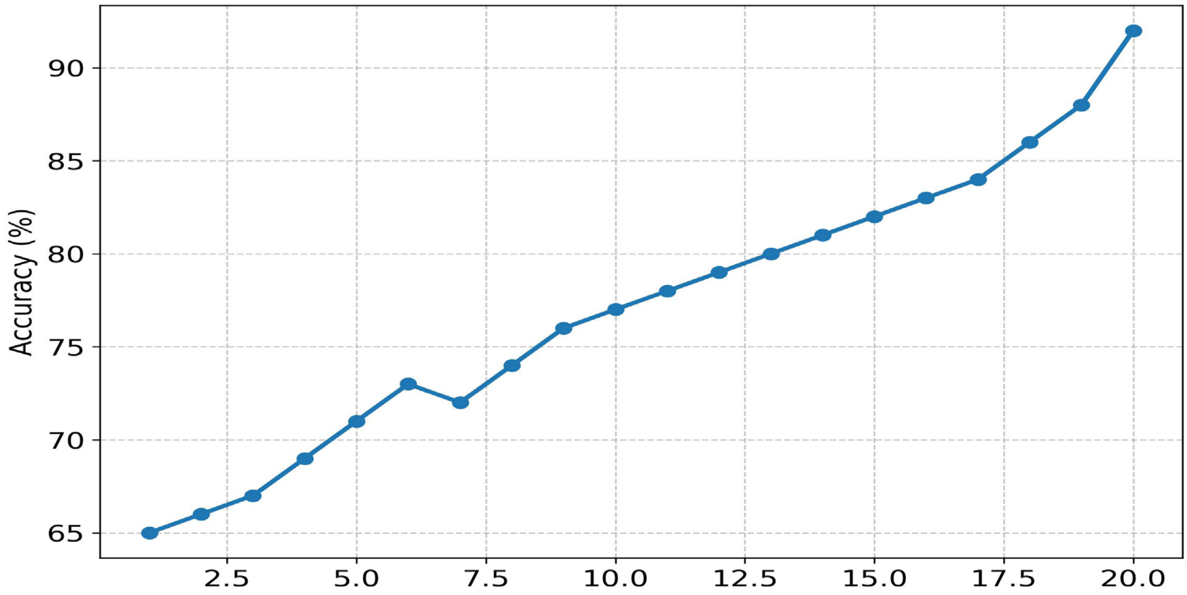

Figure 6. Accuracy vs. Epochs plot for ResNet-50 model

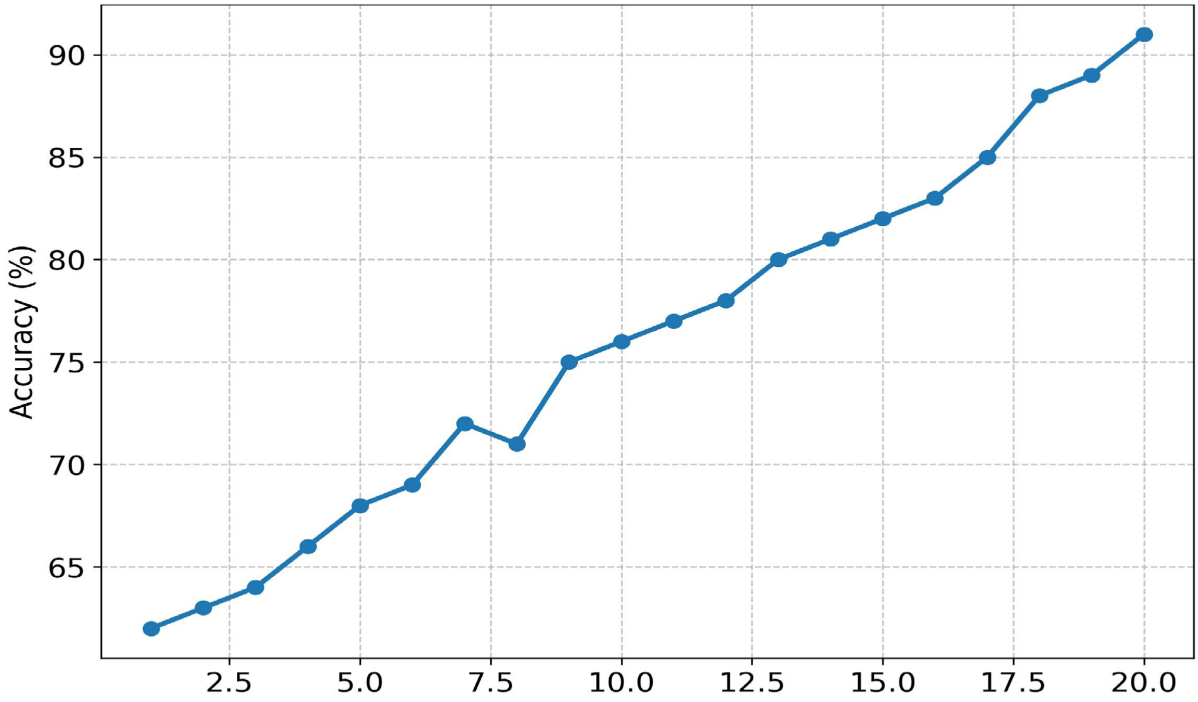

Figure 7. Accuracy vs. Epochs plot for LeNet5 model

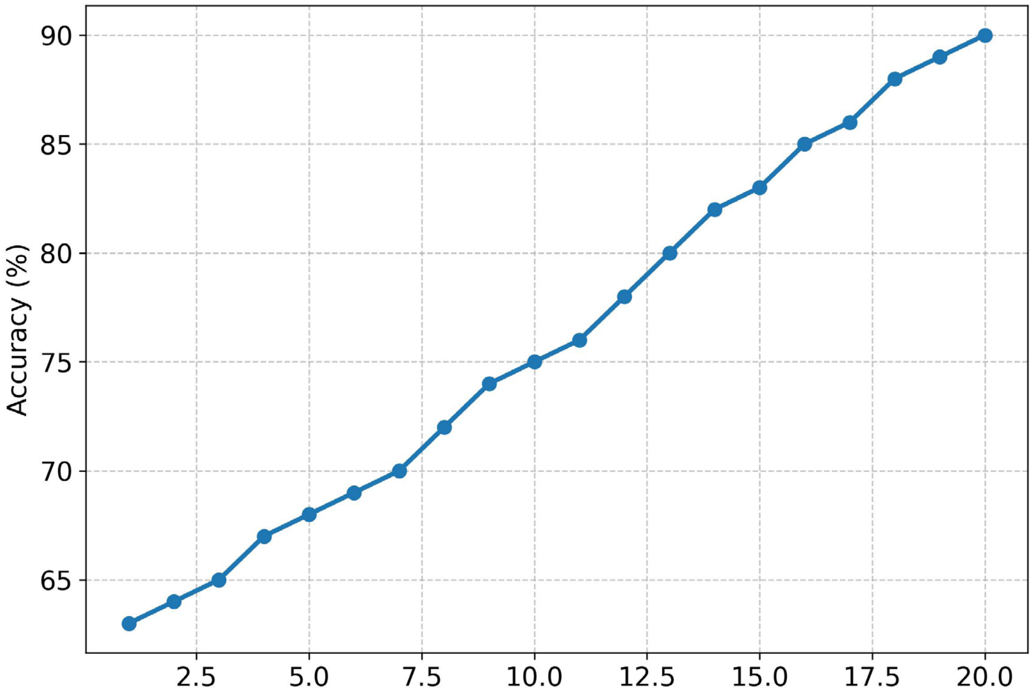

Figure 8. Accuracy vs. Epochs plot for a 7-layered convolutional neural network model

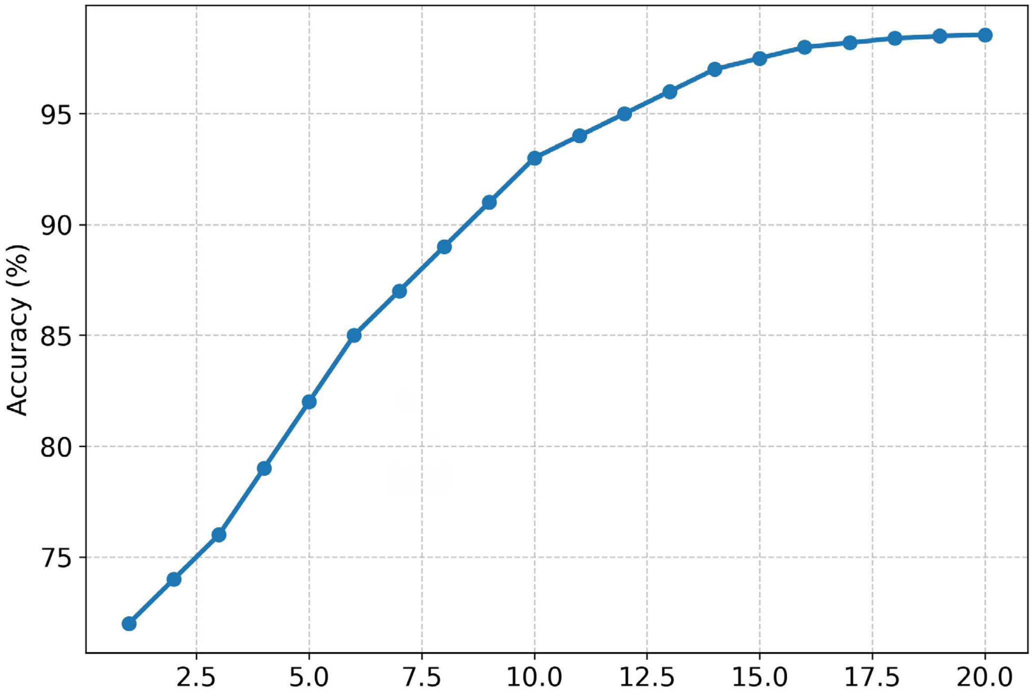

Figure 9. Accuracy vs. Epochs plot for the proposed hybrid model

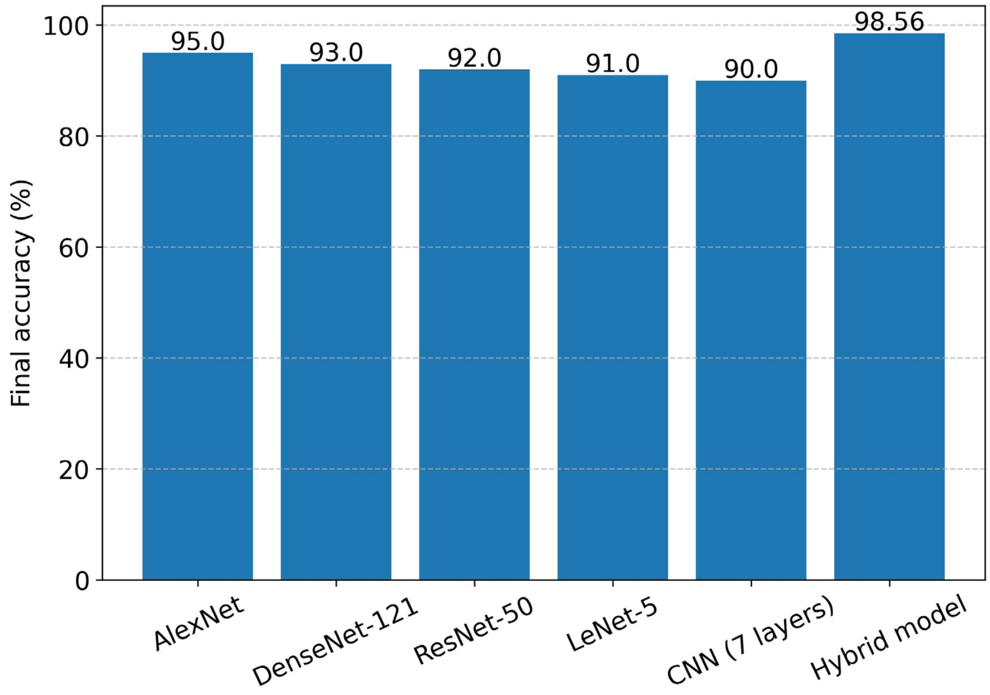

Figure 10. Final accuracy comparison between models

Table 1. Summary of model performance

Model	Initial accuracy (epoch 1)	Final accuracy (epoch 20)
AlexNet	70%	95%
DenseNet-121	66%	93%
ResNet-50	65%	92%
LeNet5	62%	91%
CNN (7 layers)	63%	90%
Hybrid model	72%	98.56%

Abbreviation: CNN: Convolutional neural network.

6. Discussion

The findings of this study demonstrate that the proposed HDLM is highly effective for cotton leaf disease detection and management. By integrating fine-tuned deep learning models within a stacking ensemble framework, the system achieved a classification accuracy of 98.56%, significantly outperforming conventional deep learning architectures and standalone models. This improved performance is attributed to transfer learning–based feature extraction, extensive data augmentation that enhanced robustness to real-world variations, and ensemble learning that captured both fine-grained texture patterns and global structural features of diseased leaves. The model successfully distinguished six disease and pest categories, enabling timely and precise diagnosis. Moreover, integrating a disease management recommendation module enhances practical applicability by providing actionable guidance to farmers, thereby transforming the system into a decision-support tool for precision agriculture. Despite these promising results, the dataset represents limited geographic and environmental variability, and the ensemble architecture increases computational complexity, which may affect deployment on resource-constrained devices. Future work should focus on expanding heterogeneous datasets, optimizing lightweight deployment for mobile and edge platforms, and incorporating real-time monitoring to further improve adaptability and field usability. Overall, the proposed framework offers a scalable, accurate, and practical solution for early cotton disease detection, contributing to improved crop productivity and sustainable farming practices.

7. Conclusion

Cotton, as a cash crop, holds both economic and environmental significance, and timely detection of its associated diseases is critical for reducing crop losses and promoting sustainable agriculture. The proposed HDLM demonstrated exceptional performance, achieving 98.56% accuracy in controlled experiments and outperforming state-of-the-art models, including AlexNet, DenseNet-121, ResNet-50, LeNet-5, and conventional CNN architectures. Beyond classification, the integrated disease management recommendation system provides actionable guidance, enabling farmers to make informed decisions and implement effective disease mitigation strategies. In future studies, the HDLM can be further enhanced by integrating additional DL models, heterogeneous datasets, and advanced augmentation techniques, thereby improving its generalization across varied field conditions. Inspired by adaptive and feedback-based control systems, future work envisions real-time sensor integration and continuous learning loops, allowing the model to dynamically update predictions, optimize recommendations, and autonomously respond to evolving disease patterns. Such enhancements will strengthen precision, reliability, and scalability, ultimately supporting sustainable cotton farming through robust, data-driven, and adaptive disease management.

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Conflict of interest

The authors declare that they have no conflict of interest.

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Availability of data

The dataset used in this study was manually collected and annotated for research purposes. The data may be made available from the corresponding author upon reasonable request for academic and research use.

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