

# A Soft Computing Framework for Automatic Cotton Leaf Disease Detection via Convolutional Neural Networks

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## ABSTRACT

Cotton foliar diseases and pest damage reduce yield and fiber quality, while manual diagnosis is slow and dependent on specialist experience. This paper presents an integrated soft-computing framework for automatic identification, interpretation, and prognosis of cotton leaf conditions. The system classifies images into six categories—healthy leaf, aphids, armyworm, bacterial blight, powdery mildew, and target spot—using a convolutional neural network trained with resized, normalized, contrast-enhanced, and augmented images. A complementary image-segmentation module estimates the infected-area percentage and maps it to severity levels for decision support. The MATLAB implementation combines the Deep Learning Toolbox, Image Processing Toolbox, and a graphical user interface for model training, image upload, prediction, severity visualization, and report generation. The reported confusion matrix contains 1,200 test decisions and yields 98.83% overall accuracy, 98.84% macro-precision, 98.83% macro-recall, and 98.83% macro-F1. The integrated design extends classification-only approaches by linking disease recognition with quantitative severity assessment and interpretable prognosis. The framework therefore offers a practical basis for rapid cotton-health screening and precision-agriculture decision support, while field validation remains necessary before operational deployment.

**Keywords:** convolutional neural network, cotton leaf disease, disease severity, precision agriculture, soft computing

## INTRODUCTION

Cotton is a high-value commercial crop and a principal raw material for the textile industry. Its productivity and fiber quality are threatened by foliar diseases and pest damage, including aphids, armyworm, bacterial blight, powdery mildew, and target spot. Delayed identification allows infection to spread, increases chemical use, and raises production losses. Conventional diagnosis relies on visual inspection by farmers or experts; this process is subjective, labor-intensive, and difficult to scale across large fields.

Image processing and artificial intelligence provide a route to rapid and objective crop-health assessment. Convolutional neural networks (CNNs) learn hierarchical visual representations directly from images and have achieved strong results in plant-disease recognition [1–7]. Their ability to capture color, texture, lesion, and shape patterns reduces dependence on handcrafted features.

However, classification alone does not indicate the extent of damage or the urgency of intervention.

This work addresses that gap through an integrated framework that combines six-class CNN recognition, infected-area estimation, severity categorization, prognosis, and a MATLAB graphical user interface (GUI). The main contributions are: (1) a unified workflow from image acquisition to decision support; (2) quantitative severity estimation in addition to disease classification; (3) matrix-consistent reporting of classification metrics; and (4) an interactive implementation for training, testing, visualization, and report generation.

## RELATED WORK

Mohanty et al. demonstrated that deep CNNs can identify plant diseases directly from leaf images [1], while Ferentinos compared deep architectures for disease detection and diagnosis [2]. Surveys by Kamilaris and Prenafeta-Boldú [3] and Liakos et al. [6] established deep learning and machine learning

as important components of precision agriculture. Barbedo showed that dataset size, diversity, and imaging conditions strongly affect model generalization [4], and Brahimi et al. confirmed the effectiveness of CNN-based disease classification on visually similar symptoms [5].

Comparative studies support transfer learning and deeper feature extractors for plant-disease recognition [7]. Mobile and field-oriented systems have also demonstrated the potential for practical deployment [8]. At the same time, lesion variability, background clutter, class imbalance, and symptom similarity remain important limitations [9]. Subsequent work has compared deep-learning classifiers [10], examined transfer learning [11], and reviewed the robustness requirements of crop-disease recognition [12].

Automated diagnosis has been extended to multiple crops and operating conditions [13–20]. Nevertheless, much of the literature emphasizes class labels and aggregate accuracy. Fewer systems integrate classification with infected-area measurement, severity interpretation, and an end-user interface. The present framework therefore focuses on connecting recognition output to a quantitative and interpretable prognosis pipeline.

## PROPOSED METHODOLOGY

### 3.1 Image Preparation

The dataset is organized into six labeled classes: healthy leaf, aphids, armyworm, bacterial blight, powdery mildew, and target spot. Each input is resized to  $224 \times 224$  pixels with three color channels. Preprocessing includes filtering, contrast enhancement, color normalization, and intensity normalization. Rotation, reflection, translation, and scaling are applied during augmentation to increase visual diversity and reduce overfitting.

### 3.2 CNN Classification

The CNN uses four convolutional blocks with rectified linear unit activation and  $2 \times 2$  max-pooling, followed by flattening, a 512-unit fully connected layer, and a six-class Softmax output. The Adam optimizer updates network weights to minimize classification loss. During inference, the Softmax layer assigns a probability to each class and the largest probability determines the predicted label.

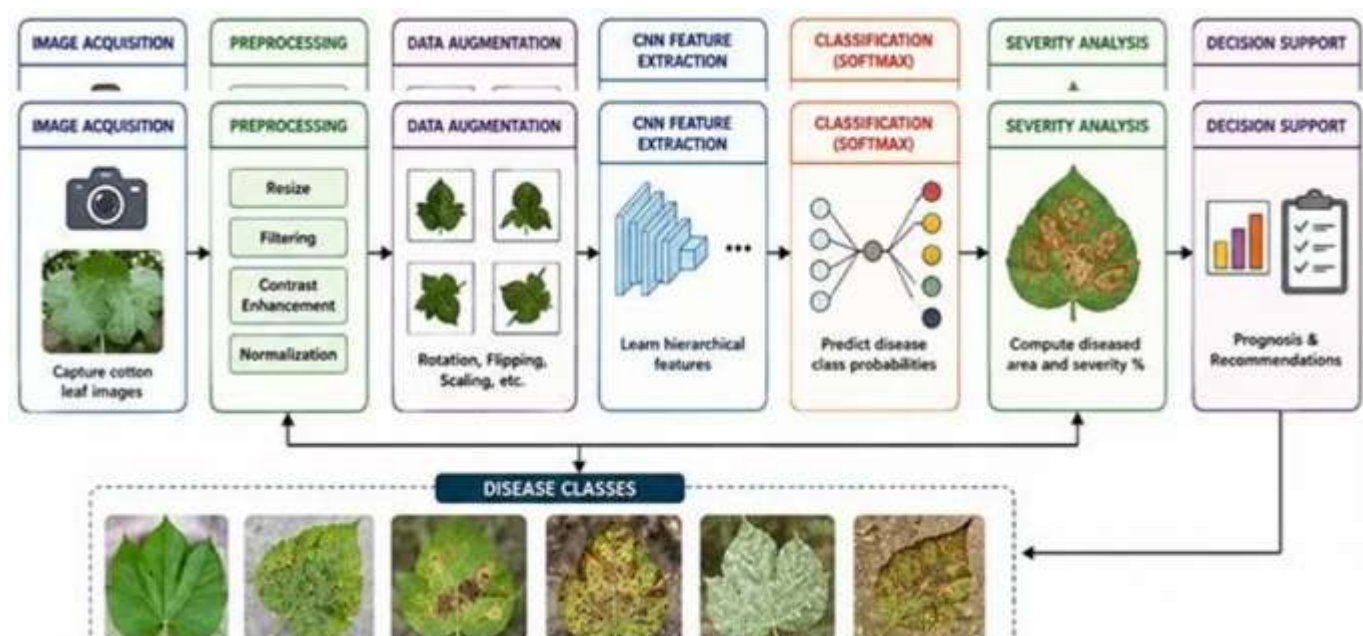


Fig. 1. End-to-end framework for cotton leaf disease analysis.

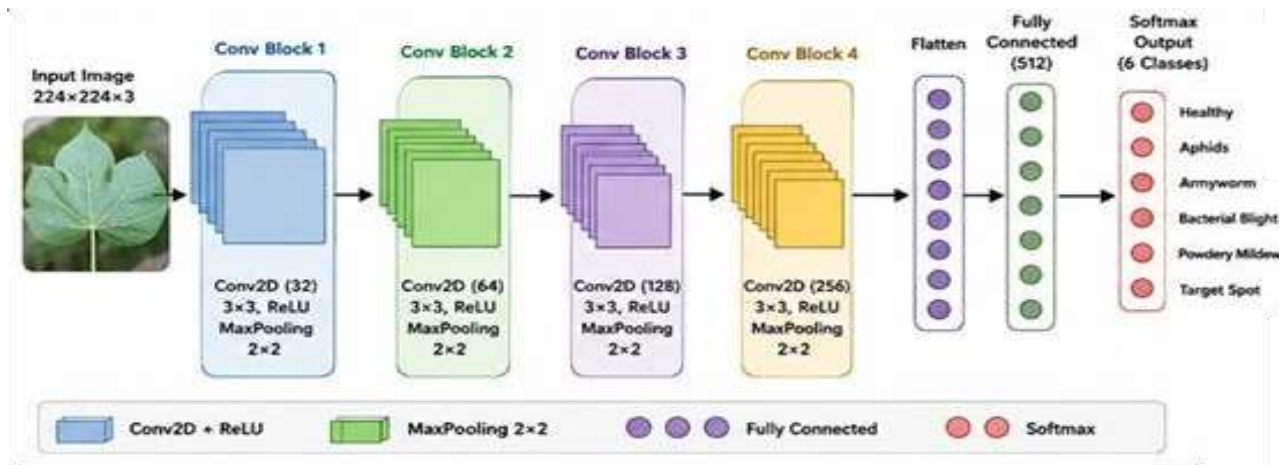


Fig. 2. CNN architecture used for six-class classification.

### 3.3 Severity Estimation and Prognosis

After classification, color analysis and threshold-based segmentation separate abnormal regions from healthy leaf tissue. Morphological operations remove isolated noise and consolidate lesion regions. Disease severity is computed from the segmented infected area and the total leaf area:

$$\text{Disease severity (\%)} = (\text{infected area} / \text{total leaf area}) \times 100.$$

The healthy-tissue percentage is 100 minus disease severity. The severity value is mapped to five qualitative levels (very low, mild, moderate, severe, and critical). The predicted class and severity level are then passed to the prognosis and report-generation modules. Treatment text is presented as decision-support output and must be confirmed against local agronomic advice, pesticide labels, crop stage, and applicable regulations.

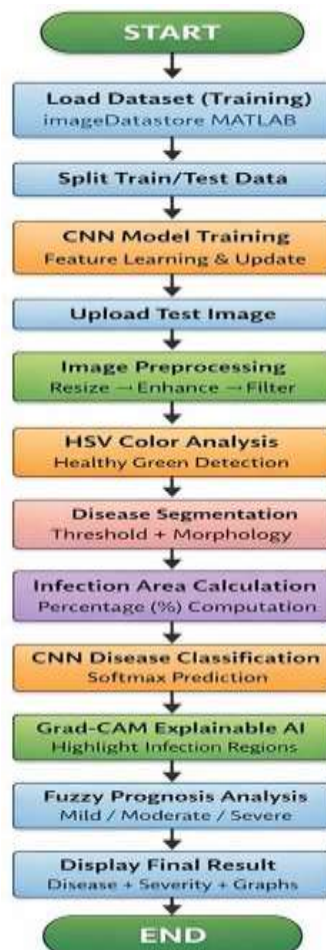


Fig. 3. Processing flow for classification, severity estimation, explainability, and prognosis.



Fig. 4. Example decision-support output.

## EXPERIMENTAL PROTOCOL

The framework was implemented in MATLAB using the Deep Learning Toolbox and Image Processing Toolbox. The GUI supports dataset loading, model training, test-image upload, preprocessing, prediction, severity estimation, result visualization, and report generation. The confusion matrix contains 200 test decisions for each of the six classes, giving 1,200 decisions in total. Because the original experimental record does not specify the random seed, batch size, or exact split ratio, these settings should be documented in future replication studies.

Table 1. Experimental configuration reported in the study

| Item           | Specification                                            |
|----------------|----------------------------------------------------------|
| Classes        | 6 (healthy + 5 disease/pest conditions)                  |
| Input          | 224 × 224 × 3 image                                      |
| Optimizer      | Adam                                                     |
| Classifier     | Six-class Softmax                                        |
| Test decisions | 1,200 (200 per class)                                    |
| Platform       | MATLAB with deep-learning and image-processing toolboxes |

## RESULTS AND DISCUSSION

### 5.1 Classification Performance

The confusion matrix in Fig. 5 shows 1,186 correct predictions from 1,200 test decisions. The resulting overall accuracy is 98.83%. Class recall ranges from 98.50% to 99.00%, while class precision ranges from 97.52% to 100.00%. Healthy leaves achieve 100% precision in the displayed matrix, whereas powdery mildew has the lowest precision because predictions from several other classes enter that column. The small

number of off-diagonal entries indicates that most errors occur between visually related symptoms rather than between healthy and diseased leaves.

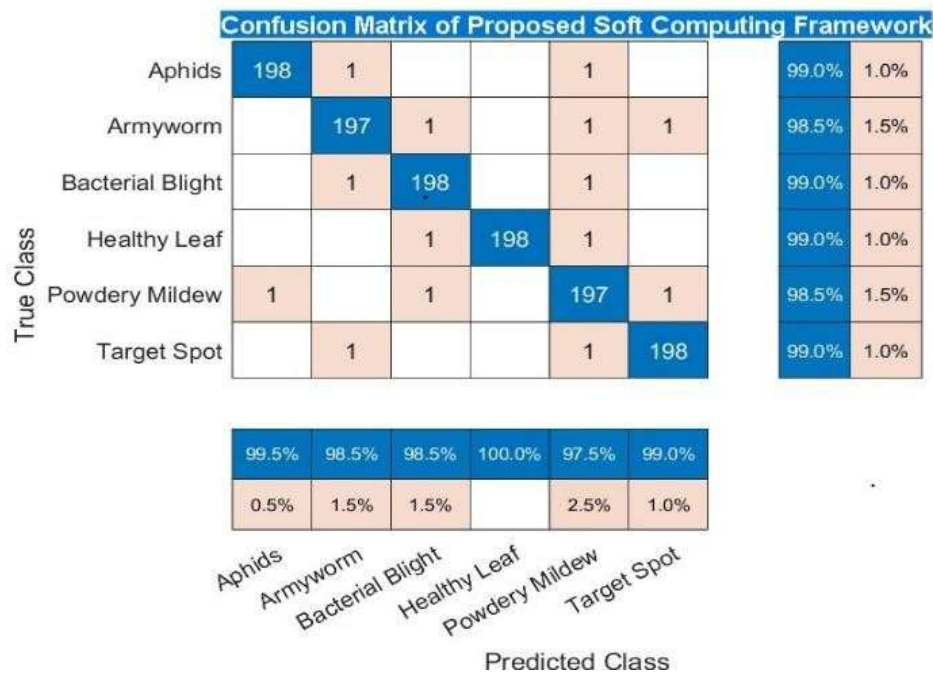


Fig. 5. Confusion matrix of the proposed framework.

| Metric          | Value (%) |
|-----------------|-----------|
| Accuracy        | 98.83     |
| Macro-precision | 98.84     |
| Macro-recall    | 98.83     |
| Macro-F1        | 98.83     |

Table 2. Matrix-consistent aggregate performance

Training accuracy rises rapidly during the first epoch and then stabilizes near the upper range, while the loss decreases sharply before converging. The remaining fluctuations suggest that reporting repeated runs, confidence intervals, and an external-field test set would provide a more reliable estimate of generalization than a single split.

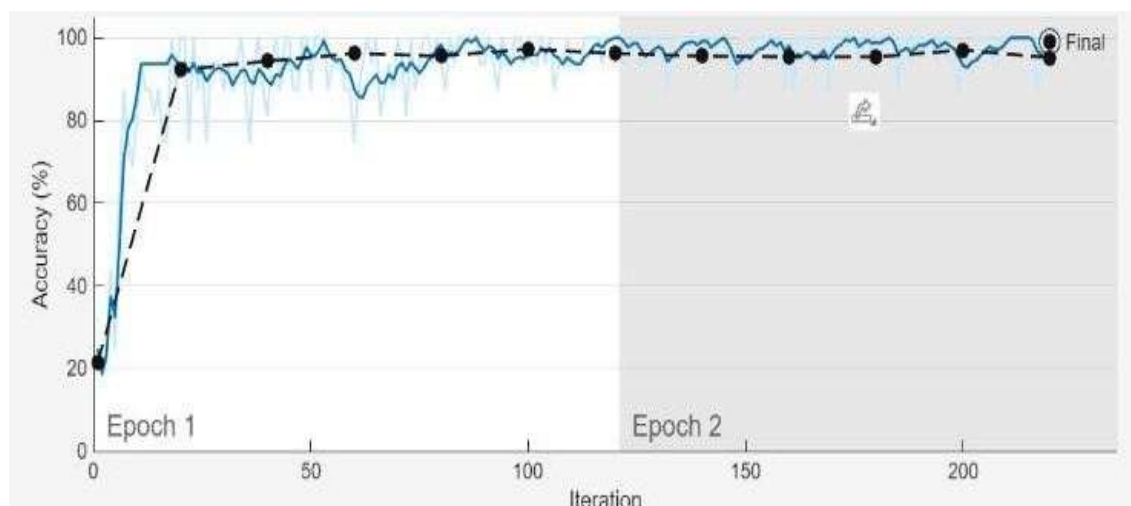


Fig. 6. Training accuracy across iterations.

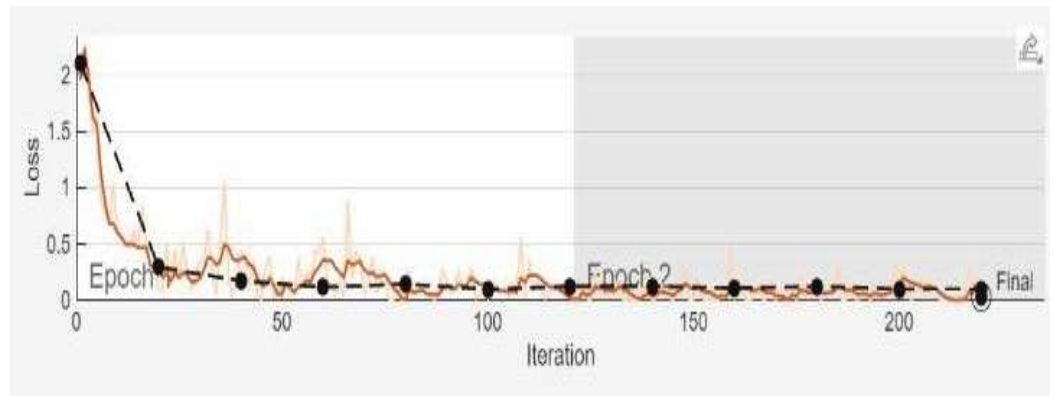


Fig. 7. Training loss across iterations.

## 5.2 Severity and Decision Support

Table 3. Severity categories used by the prognosis module

| Infected area (%) | Severity |
|-------------------|----------|
| 0–10              | Very low |
| >10–25            | Mild     |
| >25–50            | Moderate |
| >50–75            | Severe   |
| >75               | Critical |

Representative GUI outputs show severity values from 5.09% for a predominantly healthy sample to 90.61% for an armyworm sample. Applying the thresholds in Table 3 removes the inconsistent qualitative labels present in the preliminary draft and produces a reproducible mapping from infected area to severity.

Table 4. Representative diagnosis and prognosis outputs

| Condition        | Severity (%) | Level    | Displayed action              |
|------------------|--------------|----------|-------------------------------|
| Healthy leaf     | 5.09         | Very low | Monitor                       |
| Powdery mildew   | 56.70        | Severe   | Fungicide advice              |
| Target spot      | 67.38        | Severe   | Fungicide advice              |
| Bacterial blight | 65.23        | Severe   | Disease-control advice        |
| Armyworm         | 90.61        | Critical | Immediate pest-control advice |

*Note: Actions are interface outputs, not agronomic prescriptions; operational use requires local expert validation.*

## 5.3 Practical Significance

The main advantage of the framework is functional integration. A user can move from a raw image to a predicted condition, localized infected regions, a severity percentage, and a readable report within one interface. This design is more useful for screening than a classification-only model because it connects recognition to the extent of damage. It can help prioritize samples for expert inspection, but it does not replace laboratory confirmation.

## **LIMITATIONS AND FUTURE WORK**

The current evidence is based on a single reported test matrix and does not establish performance under unseen farms, devices, seasons, cultivars, lighting conditions, or mixed infections. Dataset provenance, class counts before augmentation, split strategy, random seed, and computational cost should be reported explicitly. The segmentation threshold may also be sensitive to leaf color, background, shadows, and image quality. These factors limit direct claims of field readiness.

Future work should use farm-level partitioning to prevent image leakage, repeated stratified experiments, an external field dataset, and comparisons with transfer-learning and vision-transformer baselines. Explainability can be strengthened through quantitative localization evaluation, while severity estimation should be validated against expert-annotated lesion masks. A lightweight mobile implementation and calibrated uncertainty estimates would further improve responsible deployment.

## **CONCLUSION**

This paper presented an integrated soft-computing framework for six-class cotton leaf analysis. The system combines CNN-based recognition, infected-area measurement, severity mapping, prognosis, visualization, and report generation in MATLAB. Recalculation from the displayed confusion matrix gives 98.83% accuracy and approximately 98.83% macro-averaged precision, recall, and F1-score. The results demonstrate the feasibility of connecting high-accuracy image classification with interpretable severity assessment. Broader field validation and complete experimental documentation are required before deployment, but the framework provides a practical foundation for precision-agriculture screening and decision support.

## **DECLARATIONS**

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### **Conflicts of Interest/Competing Interests**

The authors declare that they have no conflicts of interest or competing interests that could have influenced the research, analysis, interpretation of the results, or preparation of this manuscript.

### **Availability of Data and Material (Data Transparency)**

The dataset used in this study consists of cotton leaf images representing six classes: Healthy Leaf, Aphids, Armyworm, Bacterial Blight, Powdery Mildew, and Target Spot. The data used for the experiments were collected and organized for the purpose of cotton leaf disease identification and classification.

The availability of the dataset is subject to the permissions and conditions associated with its source. Where permitted, the relevant dataset and supporting information can be made available from the corresponding author upon reasonable request. Any restrictions on the sharing of the data will be communicated to prospective users.

### **Code Availability**

The MATLAB R2024a source code developed for image pre-processing, leaf segmentation, disease segmentation, feature extraction, Convolutional Neural Network (CNN)-based classification, disease severity assessment, and diagnostic reporting is custom research code developed by the authors.

The source code can be made available from the corresponding author upon reasonable request, subject to institutional and research-use considerations.

## Authors' Contributions

Deepak Ramkrishna Khadse: Conceptualization, methodology, data collection and preparation, image preprocessing, MATLAB implementation, development of the proposed soft computing framework, CNN-based disease classification, experimentation, analysis of results, visualization, and manuscript preparation.

Dr. Pankaj H. Zope: Research supervision, conceptual guidance, methodology review, critical evaluation of the experimental work, interpretation of results, and critical revision of the manuscript.

Both authors reviewed and approved the final version of the manuscript and agreed to be accountable for all aspects of the work.

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