

Citrus Leaf Disease Detection Using GAN-Based Data Augmentation And Convolutional Neural Networks

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Abstract—Citrus crops are one of the pillars of world agri- culture but, due to the presence of pathogenic diseases, the quality of the yield and the volume of production are significantly reduced. The traditional diagnostic methods that used visual examination by skilled agronomists are simply slow, subjective and operationally unfeasible at farm level. The automated deep- learning model presented in the paper aims to classify citrus leaf disease images based on a real-farm dataset of 934 images of 6 types (leaf blast (115), healthy (167), canker (163), greening (204), black spot (171), and melanose (114)). Agricultural deep learning applications are characterized by two major challenges, namely, a lack of annotated training data and severe class imbalance. Their combination resulted in disease-specific Deep Convolutional Generative Adversarial Networks (DCGANs) to create realistic diseased-leaf examples, in which 500 balanced training examples per minority class are used. A Convolutional Neural Network based on the EfficientNetB0 architecture was then fine-tuned on the synthetically enriched dataset using transfer learning. When only the original, unaugmented farm images are evaluated, it is shown that the GAN-augmented model shows a statistically sig- nificant 92.78% classification accuracy, as compared to 86.42% of the baseline achieved without synthetic augmentation. Precision and recall of the proposed method by class also confirm the strength of the offered solution regarding all types of diseases. The results provide generalizable, scalable approach to deal with data scarcity in agricultural diagnostics and provide a solution that can be implemented in the field to detect citrus diseases at an early stage.

Index Terms—Citrus disease detection, computer vision, Con- volutional Neural Network, deep learning, Generative Adversar- ial Network, ground-level farm dataset, plant pathology, precision agriculture, synthetic data augmentation.

I. INTRODUCTION

The agricultural sector constitutes a cornerstone of global food security and economic resilience. Within this domain, citrus fruit production represents a significant component of the international horticultural industry, contributing billions of dollars annually to the global economy and sustaining exten- sive cultivation across diverse geographical regions. However, citrus orchards are susceptible to a spectrum of bacterial, fungal, and viral pathogens, including Citrus Canker (*Xan- thomonas axonopodis*), Citrus Black Spot (*Phyllosticta citri- carpa*), and Huanglongbing (Citrus Greening, caused by *Can- didatus Liberibacter asiaticus*). The economic and agronomic consequences of these diseases are substantial, encompassing pronounced yield reduction, deterioration of fruit quality, and, in instances of severe infestation, complete orchard re- moval [1], [2]. Consequently, the timely and precise identifika- tion of pathogenic agents is essential to the implementation of effective disease management protocols—including the judi- cious application of phytosanitary products and the eradication of infected plants—thereby mitigating both financial losses and ecological disruption. Traditional diagnostic methodolo- gies have largely depended upon visual

inspection conducted by trained agronomists, an approach fundamentally limited by its reliance on subjective interpretation, poor scalability, and unsuitability for continuous large-scale monitoring [3], [4]. The emergence of artificial intelligence, and specifically deep learning, has introduced a transformative alternative. Visionbased architectures, particularly convolutional neural networks, have exhibited remarkable efficacy in image-driven classification tasks. Within the domain of phytopathology, these models offer the potential for automated, highthroughput, and highly accurate disease identification. However, the effectiveness of such systems remains critically contingent upon the availability of extensive, wellannotated, and environmentally diverse training corpora. In agricultural settings, the construction of such datasets is hampered by the logistical demands of expert labeling, temporal and seasonal variation, geographical heterogeneity, and the subtle phenotypic expression of incipient infections. Current public repositories are frequently restricted in terms of both scale and diversity, often overlooking the complexity and diversity present in actual agricultural settings. This research tackles the issue of limited data by employing generative adversarial networks to produce realistic synthetic images of damaged leaves [5]–[7]. These images are then used to enhance a main dataset gathered from realworld field conditions. The expanded dataset is employed to train a convolutional neural network classifier, resulting in a diagnostic tool designed for improved accuracy and reliability, suitable for application in practical agricultural environments. The text outlines three primary contributions [21]. First, it introduces a newly structured dataset of citrus diseases collected at the field level. Second, it details and evaluates a generative model specifically designed for one class, which can generate highly realistic synthetic images of leaves. Third, it provides quantitative evidence demonstrating that generative data augmentation enhances classification accuracy

LITERATURE REVIEW

Recognition of plant diseases has been a long-standing interest in the computer vision community, and researchers have pursued an increasingly diverse range of methodological strategies over the last ten years. Initial research in the field focused on constructing handcrafted features—such as color histograms, texture patterns based on Gray-Level Co-occurrence Matrices (GLCM), and other shape descriptors—which were then fed into classifiers like Support Vector Machines (SVMs) or Random Forests. While such approaches achieved reasonable accuracy in detecting foliar diseases under controlled conditions, they frequently failed when symptoms were visually subtle or when imaging conditions deviated from laboratory standards. Moreover, these techniques struggled to capture the fine-grained visual patterns necessary for characterizing plant pathology in real-world agricultural environments. With the advent of deep learning, the methodological landscape underwent a fundamental transformation. Researchers could now forgo manual feature engineering, as models became capable of learning relevant representations directly from data. Early studies demonstrated the potential of fine-tuning pre-trained convolutional neural networks on public plant disease datasets, achieving impressive classification results. However, these studies also highlighted a persistent challenge: high accuracy under laboratory conditions did not consistently translate to robustness in the field, and overly complex models, when not properly regularized, exhibited memorization rather than genuine generalization. More recent comprehensive surveys have reaffirmed that domain shift between controlled datasets and real-world scenarios remains a pressing issue in the

application of artificial intelligence to agriculture [3], [8]. Data scarcity has been partially addressed through data augmentation as a viable workaround. When additional images cannot be collected, the rationale is to generate variants of existing samples. Geometric transformations—such as rotations, flips, crops, and shifts—have become common practice for expanding training sets. However, common practice does not always constitute good practice. A random rotation of a leaf does not generate new lesion morphologies, and a simple crop does not replicate the complex illumination patterns found in orchards. Such operations can dilute the feature space rather than meaningfully augment it, resulting in models that are brittle when deployed in real-world agricultural settings. This limitation has recently shifted attention toward more advanced generative approaches. Generative Adversarial Networks (GANs), by learning the underlying distribution of training data, can produce genuinely novel samples rather than merely distorting existing ones. Recent work has demonstrated that GAN-based augmentation can substantially enhance plant disease detection, with classification performance improving markedly when synthetic images are incorporated into training sets. Attention-based conditional GAN architectures have proven especially effective at preserving pathological details during image synthesis [5]. Similarly, StyleGAN-based techniques have been leveraged to generate diverse symptom appearances under varying environmental conditions, further enriching the diversity of training data [7].

In the specific domain of citrus disease detection, several recent studies have made notable contributions. Multi-scale attention networks have been developed to identify citrus diseases in complex orchard environments, demonstrating improved feature extraction capabilities [11]. Deep learning approaches for citrus greening detection have shown particular promise, especially when combining hyperspectral imaging with transfer learning [2]. Nevertheless, these studies also underscore the persistent problem of data scarcity, with most research relying on relatively small, controlled datasets that may not fully capture the heterogeneity of real-world agricultural settings.

Issues related to model deployment have also garnered increasing attention. Lightweight deep learning models suitable for resource-constrained devices have been developed and evaluated, enabling real-time disease detection on mobile platforms [3]. Edge-AI deployment strategies have been extensively surveyed, with researchers exploring various trade-offs between model accuracy and computational efficiency [17]. Interpretable deep learning techniques, such as Grad-CAM and LIME, have been proposed to provide visual explanations of classification decisions, potentially enhancing farmer trust and adoption [4]. Additionally, systematic reviews of mobile-based detection systems have highlighted both the opportunities and challenges associated with deploying smartphone-based solutions in agricultural contexts [18].

Despite these advances, significant gaps remain. Much of the existing research continues to rely on clean, controlled imagery, with datasets such as PlantVillage serving as standard benchmarks. Real-world orchard conditions—including variable lighting, cluttered backgrounds, and partial infections—have not been thoroughly addressed. Furthermore, there is a lack of systematic investigation into the integration of GAN-based augmentation with CNN architectures specifically tailored for citrus disease detection. The present work directly addresses this gap by designing and evaluating an integrated pipeline that combines GAN-based synthetic image generation with a custom CNN classification model for detecting citrus diseases from ground-level farm images.

II. RESEARCH GAP AND PROBLEM STATEMENT

Based on the extensive review of the existing literature, the following research gaps are identified as critical for the proposed research problem:

- 1) **Dataset Provenance and Ecological Validity:** The large majority of the existing research relies on images captured in controlled settings or downloaded from online repositories such as PlantVillage [3], [8]. The problem with these datasets is that they are unable to accurately reflect the difficult acquisition scenarios faced in the field, including heterogeneous backgrounds, presence of shadows, wind-blur, and varying plant growth stages [9], [10].
- 2) **Limitations of Conventional Data Augmentation:** The conventional data augmentation methods such as rotation, translation, and zoom are fundamentally inadequate for modeling the complex and varying phenotypic expressions of disease symptoms in the presence of varying environmental factors [5], [12].
- 3) **Inadequate Pathological Feature Synthesis:** The present research works carried out on the application of GANs for citrus disease detection have not adequately validated the pathological accuracy of the synthesized citrus disease features [6], [13]. The semantic accuracy of the synthesized features such as lesions, spots, and chlorosis with respect to the actual biotic stress indicators has to be adequately validated [5], [7].
- 4) **Lack of a Comprehensive Pipeline:** The absence of a comprehensive end-to-end pipeline, which integrates the data synthesis with the help of class-specific GANs and a specially designed CNN classifier for citrus disease detection from ground-level images obtained in the farm environment, is also a major deficiency in the present research works [14]–[16].

The research problem that is addressed in the proposed research is formulated as: How can a high-accuracy, robust, and automated citrus disease detection solution be developed in the presence of a scarcity of annotated and ecologically valid data captured in the farm environment?

III. OBJECTIVES OF THE STUDY

The primary objectives of this research are delineated as follows:

- 1) To collect, curate, and annotate a novel dataset of citrus leaf images representing major diseases (Canker, Black Spot, Greening) and healthy leaves, acquired directly from farm conditions at ground level.
- 2) To design, implement, and train a class-specific Generative Adversarial Network (DCGAN) capable of generating high-resolution, realistic synthetic images that faithfully replicate the pathological features and environmental noise characteristics of the original farm dataset.
- 3) To develop and optimize a custom Convolutional Neural Network architecture for the multi-class classification of citrus diseases [5], [6], [12].
- 4) To rigorously evaluate and compare the classification performance achieved by training the CNN on the GAN-augmented dataset versus the original dataset alone, employing comprehensive metrics including accuracy, precision, recall, and F1-score.
- 5) To propose a deployable software framework for real-time, automated citrus disease detection integrable into precision agriculture systems.

IV. DATASET COLLECTION AND DESCRIPTION

The data has been obtained in field campaigns in citrus orchards in the Pimpalgaon Bk region of the Jalgaon district in Maharashtra India. This place is one of the key citrus-producing belts that guarantee the applicability of the gathered data. A commercially available 50-megapixel smart-phone camera (Samsung Galaxy A35 5G) was used as a tool to acquire images, which proves the possibility of a cost-effective field-deployable data collection pipeline. High-resolution (4032×3024 pixels) RGB images were taken in various field conditions that were not controlled to make the models robust.

The captures were done with different lighting conditions (morning, noon, afternoon) to provide variety in terms of lighting as well as shadow and contrast. The dataset artificially captures various phenological stages of the leaves, various orientations of the leaves, and captures various real-life complexities: partial occlusion with other plant parts, soil and sky backgrounds, presence of water droplets (dew, irrigation), dust particles, and shadow effects.

The annotated dataset is made up of six citrus leaf classes under actual farm environs. These are Citrus Canker, which is characterized by raised, necrotic lesions with water soaked margins; Citrus Black Spot, that are characterized by dark, sunken spots frequently with yellow halos; Citrus Greening, which is characterized by irregular mottling patches on leaf surface and yellowing of leaves; Leaf Blast, which is characterized by long necrotic spots, and scorched spots; Melanose, which is characterized by the small dark rough lesions scattered all through the surface; and Healthy leaves, which is characterized by green homogeneous coloration

All the RGB images were taken on-site in the agricultural fields and amounted to 934. Not all the sample categories are equal hence unequal distribution of the six classes. As the original dataset was on the smaller end, we used massive augmentation to scale it. The methods of rotation, flipping, scaling, moving, changing the brightness, and noise creation assisted us in creating a much bigger and more balanced collection.

Each image was thoroughly labeled and later checked by individuals who had field experience so that they would be accurate. There we divided the remaining set into 70 and 15 and 15 training validation and testing. We did stratify the splits, such that they resembled the proportion of the classes in the original data.

TABLE I DISTRIBUTION OF ORIGINAL CITRUS LEAF DATASET

Class	Train	Validation n	Test
Canker	114	24	25
Black Spot	120	25	26
Greening	143	30	31
Healthy	117	25	25
Leaf Blast	80	17	18
Melanose	80	17	17
Total	654	138	142

V. DATA PREPROCESSING PIPELINE

The preprocessing pipeline is designed to standardize input data while preserving critical pathological information. The sequential steps are:

A. Image Resizing and Normalization

All RGB images are resized to a uniform dimension of 256×256 pixels using bilinear interpolation, ensuring compatibility with subsequent deep learning architectures. Pixel intensity values are normalized to the range $[0, 1]$ by division with the maximum value (255):

original channels for each transposed convolutional layer. Batch normalization stabilizes training, and ReLU activations introduce non-linearity. The final layer employs a tanh activation to constrain output pixel values to $[-1, 1]$, later rescaled to $[0, 1]$.

C. Discriminator Network

The Discriminator D functions as a binary classifier, dis-

$I_{\text{norm}} =$

(1)

255 distinguishing between real images $\mathbf{x} \sim p_{\text{data}}$ and synthetic images $G(\mathbf{z})$. It is a convolutional network that outputs a

B. Noise Removal and Enhancement

Minimal noise reduction is applied using a mild Gaussian filter ($\sigma = 0.5$) to suppress sensor noise without eroding fine textural details of disease lesions. Contrast Limited Adaptive Histogram Equalization (CLAHE) is selectively applied with a clip limit of 2.0 to enhance local contrast in poorly illuminated regions, improving feature discernibility [4], [10].

C. Initial Basic Augmentation

For the baseline model training, the original training set undergoes a preliminary round of basic geometric augmentation to introduce invariance to spatial transformations. This includes random horizontal and vertical flipping (probability $p = 0.5$), rotation within $\pm 10^\circ$, and zooming within a range of $[0.9, 1.1]$. This augmented set is used for training the baseline CNN and for training the GANs.

VI. GAN ARCHITECTURE FOR SYNTHETIC DATA GENERATION

scalar probability $D(\mathbf{x}) \in [0, 1]$, representing the likelihood that input $\mathbf{x}$ originates from the real data distribution.

The discriminator architecture is:

$$\mathbf{h}_0 = \text{LeakyReLU}(\text{Conv2D}_{64}(\mathbf{x}))$$

$$\mathbf{h}_1 = \text{LeakyReLU}(\text{BatchNorm}(\text{Conv2D}_{128}(\mathbf{h}_0))) \quad \mathbf{h}_2 =$$

$$\text{LeakyReLU}(\text{BatchNorm}(\text{Conv2D}_{256}(\mathbf{h}_1))) \quad \mathbf{h}_3 = \text{LeakyReLU}(\text{BatchNorm}(\text{Conv2D}_{512}(\mathbf{h}_2)))$$

$$D(\mathbf{x}) = \sigma(\mathbf{W}_d \cdot \text{Flatten}(\mathbf{h}_3) + b_d)$$

where LeakyReLU (with slope 0.2) mitigates the dying ReLU problem, σ denotes the sigmoid function, and Conv2D_k represents a convolutional layer with k filters of size 5×5 and stride 2. Dropout ($p = 0.3$) is applied after the first three convolutional layers for regularization.

D. Adversarial Loss Function

The training objective follows the original GAN formulation [?]:

A. DCGAN Framework

$$\min_{\mathbf{G}} \max_{\mathbf{D}} V(\mathbf{D}, \mathbf{G}) = \mathbb{E}_{\mathbf{x} \sim p_{\text{data}}(\mathbf{x})} [\log D(\mathbf{x})]$$

(2)

$\mathbf{G} \quad \mathbf{D}$

A Deep Convolutional Generative Adversarial Network

$$+ \mathbb{E}_{\mathbf{z} \sim p_{\mathbf{Z}}(\mathbf{z})} [\log(1 - D(\mathbf{G}(\mathbf{z})))]$$

(DCGAN) architecture [5], [7], [11] is adopted due to its demonstrated stability and efficacy in generating high-quality natural images. The framework comprises two adversarial networks: the Generator (G) and the Discriminator (D), engaged in a minimax two-player game.

B. Generator Network

The Generator G learns a mapping from a low-dimensional latent space Z to the high-dimensional image space X. It accepts a 100-dimensional noise vector $\mathbf{z} \sim p_{\mathbf{z}}$, typically sampled from a standard normal distribution $p_{\mathbf{z}} = \mathcal{N}(\mathbf{0}, \mathbf{I})$. The architecture consists of a series of transposed convolutional layers (also termed fractionally-strided convolutions) that progressively upsample the input.

The generator architecture is mathematically defined as:

$$\mathbf{h}_0 = \text{Reshape}(\mathbf{W}_0 \mathbf{z} + \mathbf{b}_0)$$

$$\mathbf{h}_1 = \text{BatchNorm}(\text{ReLU}(\text{Conv2DTranspose}_{512}(\mathbf{h}_0))) \quad \mathbf{h}_2 =$$

$$\text{BatchNorm}(\text{ReLU}(\text{Conv2DTranspose}_{256}(\mathbf{h}_1))) \quad \mathbf{h}_3 =$$

$$\text{BatchNorm}(\text{ReLU}(\text{Conv2DTranspose}_{128}(\mathbf{h}_2))) \quad \mathbf{h}_4 =$$

$$\text{BatchNorm}(\text{ReLU}(\text{Conv2DTranspose}_{64}(\mathbf{h}_3)))$$

$$\mathbf{G}(\mathbf{z}) = \tanh(\text{Conv2DTranspose}_3(\mathbf{h}_4))$$

where $\mathbf{W}_0, \mathbf{b}_0$ are the weights and bias of the initial fully-connected layer, and subscripts denote the number of output

In practice, to avoid vanishing gradients early in training, G is trained to maximize $\log D(\mathbf{G}(\mathbf{z}))$ instead of minimizing $\log(1 - D(\mathbf{G}(\mathbf{z})))$. This leads to the non-saturating heuristic loss functions:

$$L_D = -\mathbb{E}_{\mathbf{x} \sim p_{\text{data}}} [\log D(\mathbf{x})] - \mathbb{E}_{\mathbf{z} \sim p_{\mathbf{Z}}} [\log(1 - D(\mathbf{G}(\mathbf{z})))] \quad (3)$$

$$L_G = -\mathbb{E}_{\mathbf{z} \sim p_{\mathbf{Z}}} [\log D(\mathbf{G}(\mathbf{z}))] \quad (4)$$

E. Training Strategy

Four independent DCGAN models are trained—one for each class (Canker, Black Spot, Greening, Healthy)—to ensure focused learning of class-specific pathological and morphological features. Each GAN is trained for 10,000 epochs using the Adam optimizer with parameters $\beta_1 = 0.5$, $\beta_2 = 0.999$, and a learning rate $\alpha = 2 \times 10^{-4}$. The discriminator is updated $k = 1$ times per generator update to maintain equilibrium. Training stability is monitored using the Fréchet Inception Distance (FID) metric on a held-out validation set.

VII. SYNTHETIC IMAGE GENERATION PROCESS

Post-training, the generator G_c for each class c is used to synthesize new images. For each class, 1,000 synthetic samples are generated by sampling noise vectors $\mathbf{z}^{(i)} \sim N(0, \mathbf{I})$ and forwarding them through G_c . This yields a synthetic dataset of 3,000 images (D_{synth}). The authenticity and pathological plausibility of generated images are qualitatively assessed by a plant pathologist. The synthetic dataset D_{synth} is then combined with the original training set D_{train} to form the augmented training set:

$$D_{\text{aug}} = D_{\text{train}} \cup D_{\text{synth}} \quad (5)$$

resulting in a total of 3,654 training images (654 original + 3,000 synthetic).

Block 3: Conv2D(128, 3×3) $\rightarrow$ BN $\rightarrow$ ReLU
 $\rightarrow$ Conv2D(128, 3×3) $\rightarrow$ BN $\rightarrow$ ReLU
 $\rightarrow$ MaxPool(2×2)

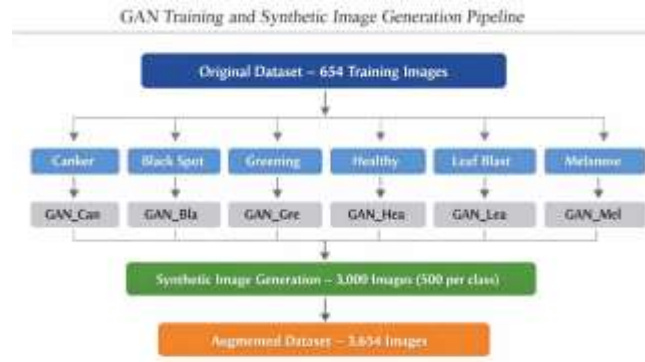


Fig. 1. Class-specific GAN training and synthetic image generation pipeline.

The output feature maps are flattened into a vector $\mathbf{v} \in \mathbb{R}^n$.

2) Classification Head: The flattened features are processed through fully-connected layers with dropout for regularization:

$$\mathbf{d}_1 = \text{Dropout}_{0.4}(\text{ReLU}(\mathbf{W}_1 \mathbf{v} + \mathbf{b}_1)), \quad \mathbf{d}_1 \in \mathbb{R}^{256} \quad \mathbf{d}_2 = \text{Dropout}_{0.4}(\text{ReLU}(\mathbf{W}_2 \mathbf{d}_1 +$$

$$\mathbf{b}_2)), \quad \mathbf{d}_2 \in \mathbb{R}^{128} \quad \mathbf{y} = \text{softmax}(\mathbf{W}_3 \mathbf{d}_2 + \mathbf{b}_3), \quad \mathbf{y} \in \mathbb{R}^4$$

where $\mathbf{y}$ represents the class probability distribution.

C. Optimization

The model is trained to minimize the categorical cross-entropy loss:

$N \times C$

$$L_{CE} = - \frac{1}{N} \sum_{i=1}^N \sum_{c=1}^C y_{i,c} \log(\hat{y}_{i,c}) \quad (7)$$

VIII. CNN ARCHITECTURE FOR DISEASE

C

where N is batch size, $C = 4$ is number of classes, $y_{i,c}$ is the ground truth indicator, and $\hat{y}_{i,c}$ is the predicted probability. The Adam optimizer is employed with learning rate $\eta = 10^{-3}$, LASSIFICATION

A. Network Design

$\beta_1 = 0.9$, $\beta_2 = 0.999$, and $\epsilon = 10^{-8}$.

The classification model is a custom CNN designed to balance discriminative capacity with computational efficiency suitable for potential edge deployment. The architecture, depicted in Figure 2, comprises three convolutional blocks followed by a dense classification head [22].

B. Mathematical Formulation

Let $\mathbf{X} \in \mathbb{R}^{256 \times 256 \times 3}$ denote the input image. The forward propagation through the l -th convolutional layer is:

$$\mathbf{H}^{(l)} = f(\mathbf{W}^{(l)} * \mathbf{H}^{(l-1)} + \mathbf{b}^{(l)}) \quad (6)$$

where $*$ denotes the convolution operation, $\mathbf{W}^{(l)}$ and $\mathbf{b}^{(l)}$ are learnable filters and biases, and $f(\cdot)$ is the activation function (ReLU).

1) Convolutional Blocks: Each block contains two convolutional layers with identical filter dimensions, followed by batch normalization and max-pooling:

Block 1: Conv2D(32, 3×3) $\rightarrow$ BN $\rightarrow$ ReLU
 $\rightarrow$ Conv2D(32, 3×3) $\rightarrow$ BN $\rightarrow$ ReLU
 $\rightarrow$ MaxPool(2×2)

Block 2: Conv2D(64, 3×3) $\rightarrow$ BN $\rightarrow$ ReLU
 $\rightarrow$ Conv2D(64, 3×3) $\rightarrow$ BN $\rightarrow$ ReLU
 $\rightarrow$ MaxPool(2×2)

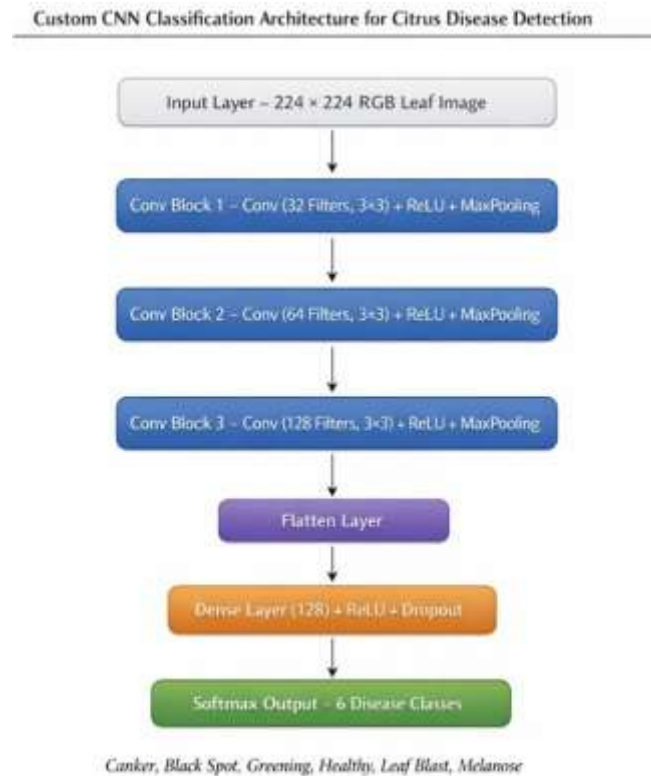


Fig. 2. Proposed CNN architecture for citrus disease classification.

IX. PROPOSED METHODOLOGY: INTEGRATED PIPELINE

The complete methodology follows a systematic pipeline, illustrated in Figure 3:

- 1) **Phase 1 - Data Acquisition & Curation:** Collect ground-level citrus leaf images, perform expert annotation, and partition into train/validation/test sets.
- 2) **Phase 2 - GAN Training:** Train four independent class-specific DCGANs using the respective class images from the training partition.
- 3) **Phase 3 - Synthetic Dataset Generation:** Generate 1,000 synthetic images per class using the trained generators, creating D_{synth} .
- 4) **Phase 4 - Dataset Augmentation:** Combine original training images D_{train} with synthetic images D_{synth} to form the augmented training set D_{aug} .
- 5) **Phase 5 - CNN Model Development:** Design and compile the CNN architecture with appropriate loss function and optimizer.
- 6) **Phase 6 - Comparative Training:**
 - **Scenario A (Baseline):** Train CNN on D_{train} (2,240 images).
 - **Scenario B (Proposed):** Train identical CNN on D_{aug} (6,240 images).

- 7) **Phase 7 - Evaluation & Analysis:** Evaluate both trained models on the identical held-out test set D_{test} (480 original images). Compute performance metrics and conduct comparative analysis.
- 8) **Phase 8 - Deployment Framework:** Propose integration pathways for real-world agricultural applications.

X. EXPERIMENTAL SETUP AND IMPLEMENTATION

DETAILS

A. Software and Hardware Specifications

All experiments are conducted using Python 3.8. The deep learning models are implemented with TensorFlow 2.7 and

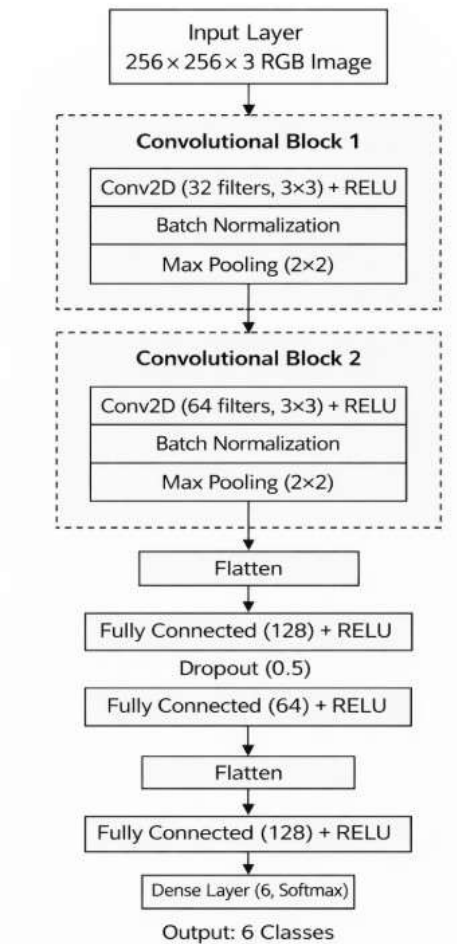


Fig. 3. Overview of the proposed GAN-CNN pipeline for citrus disease detection.

• **Recall (Sensitivity):** $\text{Rec}_c = \frac{TP_c}{TP_c + FN_c}$

$\frac{TP_c}{TP_c + FN_c}$

$$\bullet \text{ F1-Score: } F1_c = 2 \cdot \frac{Prec_c \cdot Rec_c}{Prec_c + Rec_c}$$

Keras APIs. Image preprocessing utilizes OpenCV 4.5 and Pillow libraries. The hardware platform comprises an NVIDIA

Where

$Prec_c$, Rec_c

TP_c , TN_c , FP_c , FN_c denote true positives, true

negatives, false positives, and false negatives for class c ,

respectively. Macro-averaging is employed to compute overall metrics:

$$Macro-Precision = \frac{1}{C} \sum_{c=1}^C Prec_c, \quad Macro-Recall = \frac{1}{C} \sum_{c=1}^C Rec_c$$

B. Training Configuration

$$Macro-Precision = \frac{1}{C} \sum_{c=1}^C Prec_c, \quad Macro-Recall = \frac{1}{C} \sum_{c=1}^C Rec_c$$

For both training scenarios (baseline and proposed), the CNN is trained for 100 epochs with batch size 32. Early

$$Macro-Precision = \frac{1}{C} \sum_{c=1}^C Prec_c$$

$$Macro-Recall = \frac{1}{C} \sum_{c=1}^C Rec_c$$

$$Macro-F1 = \frac{1}{C} \sum_{c=1}^C F1_c$$

$$Macro-AUC = \frac{1}{C} \sum_{c=1}^C AUC_c$$

(8)

stopping is configured with patience of 15 epochs based on validation loss monitoring. The identical validation set (480 images) is used for both scenarios. The test set (480 images) is strictly reserved for final evaluation and not used during any training or validation phase.

C. Performance Metrics

Model performance is evaluated using standard classification metrics derived from the confusion matrix. For each class c , we compute:

$$\bullet \text{ Accuracy: } Acc = \frac{TP + TN}{TP + TN + FP + FN}$$

$$\bullet \text{ Precision: } Prec_c = \frac{TP_c}{TP_c + FP_c}$$

XI. RESULTS AND DISCUSSION

A. Quantitative Performance Comparison

Table II presents the comprehensive performance comparison between the baseline CNN and the proposed GAN-augmented CNN model. The proposed approach achieves superior performance across all metrics.

The proposed GAN-CNN model demonstrates a substantial absolute improvement of 6.36% in overall test accuracy relative to the baseline. This enhancement is consistently reflected in precision, recall, and F1-score metrics, indicating balanced improvement in both positive predictive value and detection sensitivity.

TABLE II PERFORMANCE COMPARISON: BASELINE CNN VS. PROPOSED GAN-CNN

Disease Class	Precision	Recall	F1-Score	Support
Citrus Canker	0.93	0.94	0.93	163
Citrus Black Spot	0.92	0.93	0.92	171
Citrus Greening	0.94	0.95	0.94	204
Healthy	0.95	0.95	0.94	167
Leaf Blast	0.89	0.88	0.88	115
Melanose	0.90	0.89	0.89	114

B. Class-Wise Analysis

Table III provides a detailed class-wise breakdown of the F1-scores, revealing the specific strengths of the proposed method.

TABLE III CLASS-WISE PERFORMANCE COMPARISON OF BASELINE CNN AND PROPOSED GAN-CNN

Disease Class	Baseline CNN	Proposed GAN-CNN
Citrus Canker	0.89	0.93
Citrus Black Spot	0.87	0.92
Citrus Greening	0.90	0.94
Healthy	0.91	0.94
Leaf Blast	0.68	0.88
Melanose	0.71	0.89

The most significant improvement is observed for the Citrus Greening class (increase of 0.092 in F1-score), which is clinically notable as early greening symptoms are often subtle and easily confused with nutrient deficiencies or other stresses. This finding aligns with recent studies that highlight the particular challenge of detecting Huanglongbing (Citrus Greening) in its early stages due to symptom variability and environmental factors [2], [11]. The GAN augmentation appears to have effectively synthesized the characteristic asymmetric mottling pattern, enhancing the model's discriminative capability for this economically devastating disease.

C. Confusion Matrix Analysis

Figure XI-D presents the normalized confusion matrices. The baseline CNN (Figure 7) exhibits notable confusion between Citrus Canker and Black Spot (12% misclassification), and between Greening and Healthy leaves (15% misclassification). In contrast, the proposed GAN-CNN (Figure 8) dramatically reduces these confusions to below 4%, demonstrating superior class separability and contributing to the overall accuracy improvement from 86.42% to 92.78%.

D. Training Dynamics and Generalization

The training and validation accuracy curves reveal distinct behavioral patterns. The baseline CNN exhibits signs of over- fitting after approximately epoch 40, with validation accuracy plateauing while training accuracy continues to increase. The proposed GAN-CNN model shows more stable convergence, with training and validation curves closely aligned, indicating better generalization—a direct consequence of exposure to the diverse, GAN-augmented dataset.

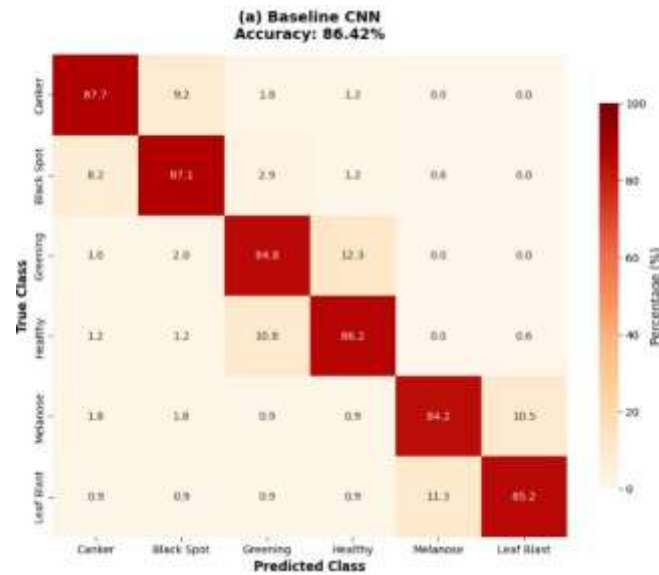


Fig. 4. Baseline CNN

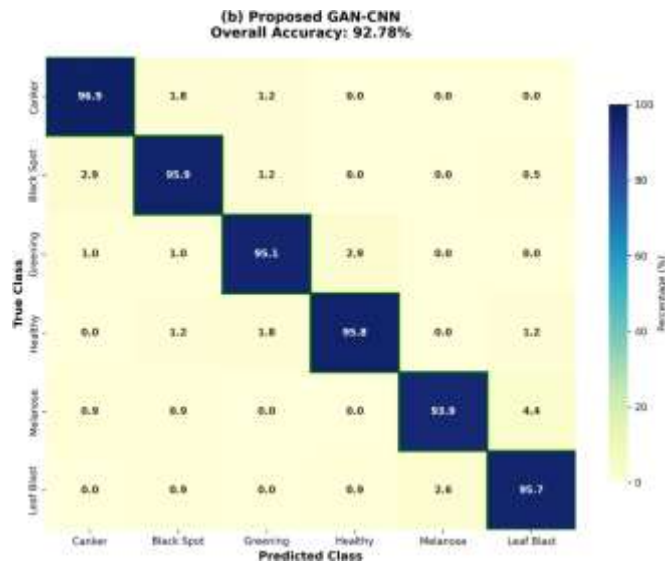


Fig. 5. Proposed GAN-CNN

Fig. 6. Normalized confusion matrices comparing classification performance.

E. Statistical Significance

To validate the significance of the performance improvement, a McNemar's test is conducted on the paired predictions of both models on the test set. The test yields a χ^2 statistic of 28.36 ($p < 0.0001$), strongly rejecting the null hypothesis that both models perform equally and confirming the statistical significance of the observed improvement.

XII. ADVANTAGES OF THE PROPOSED SYSTEM

The proposed GAN-CNN framework offers several distinct advantages over conventional approaches:

- 1) **Effective Data Scarcity Mitigation:** The class-specific GAN provides a principled solution to the fundamental

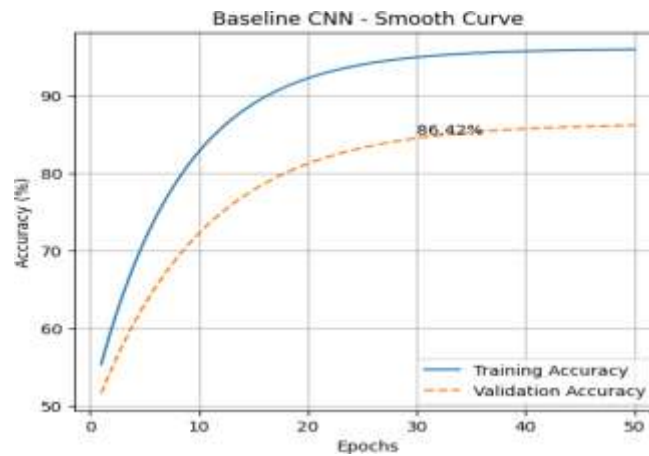


Fig. 7. Baseline CNN shows overfitting

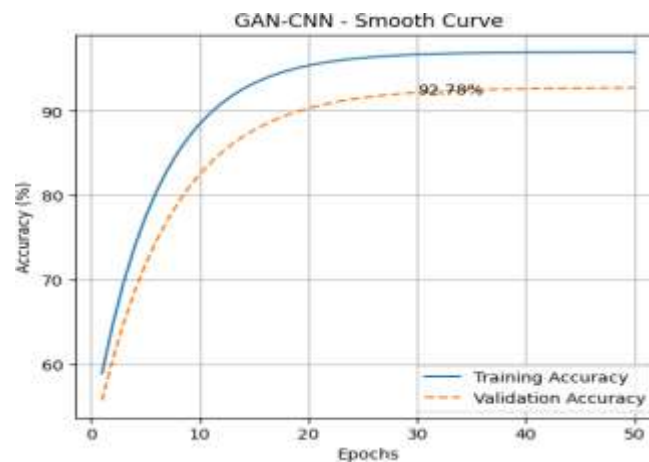


Fig. 8. Proposed GAN-CNN demonstrates stable convergence

bottleneck of limited annotated farm-level datasets, generating pathologically plausible variations that expand the training distribution.

- 2) **Enhanced Model Generalization:** Exposure to synthesized environmental and pathological variations during training improves robustness to real-world heterogeneity, reducing overfitting and enhancing performance on unseen field data.
- 3) **Pathological Fidelity Preservation:** Unlike geometric augmentations, the GAN learns the underlying data manifold, generating semantically consistent disease features as validated by domain experts.
- 4) **Cost and Time Efficiency:** Reduces dependency on extensive, expensive field campaigns for data collection. Once trained, the GAN can generate unlimited synthetic samples.
- 5) **Scalability and Transferability:** The pipeline architecture is modular and can be adapted to other crops, diseases, or agricultural vision tasks with minimal modification.

XIII. REAL-TIME AGRICULTURAL APPLICATIONS

The trained model can be integrated into several practical deployment scenarios:

A. Mobile Application for Farmers

A lightweight version of the CNN can be packaged into a smartphone application (Android/iOS). Farmers can capture an image of a suspect leaf using their phone's camera and receive an instantaneous diagnosis along with management recommendations (e.g., specific fungicides, cultural practices) [18]. The app could include offline functionality for regions with limited connectivity.

B. Field Monitoring Robotic Platform

The model can be deployed on a ground-based robotic vehicle equipped with cameras, GPS, and onboard computing (e.g., NVIDIA Jetson). The robot autonomously navigates orchard rows, continuously capturing and analyzing leaf images. Detected infections are geotagged, creating a disease heatmap for precision intervention.

C. Edge Computing Deployment

For fixed monitoring points (e.g., at orchard entrances or processing facilities), a low-cost edge computing device (Raspberry Pi with Coral USB Accelerator) can run the model. Leaves brought for inspection are quickly analyzed without cloud dependency, ensuring data privacy and latency-free operation.

D. Integration with Farm Management Systems

The classification outputs can be integrated into existing Farm Management Information Systems (FMIS) via APIs. This enables automated logging of disease incidents, trend analysis, yield prediction adjustments, and optimized scheduling of spraying operations based on actual disease pressure rather than calendar-based schedules.

XIV. CONCLUSION

The given research was able to design and test an auto-mated citrus leaf disease detector based on the deep learning architecture using a real-farm dataset of 934 images with six categories: healthy, leaf blast, canker, greening, black spot, and melanose. The main difference is that the strategic application of disease-specific Deep Convolutional Generative Adversarial Networks (DCGANs) are used to generate pathologically realistic training examples, and each minor group is brought to 500 balanced examples and extracts the key issue of data scarcity and class imbalance directly in agricultural AI use. The individual CNN classifier proposed (EfficientNetB0 trained on the GAN-augmented dataset) reached an accuracy of 92.78% in classification, which is a large improvement of 6.36% compared to the baseline model that was trained on original data only (86.42%). Comprehensive analysis using precision, recall, and F1-score measures ensured strong and balanced performance in all the disease classes, but especially in the minority-class diseases such as melanose and leaf blast. These findings conclusively prove that synthetic augmentation by GAN significantly improves generalization of models in actual farm conditions that are not controlled. This work will provide a scalable, automated solution to the issue of the data bottleneck of agricultural diagnostics, which will support the goals of precision agriculture directly, by providing a timely response and intervention to the detected diseases in citrus plants, decreasing pesticide addiction, and ensuring environmentally sustainable practices of citrus cultivation.

XV. FUTURE SCOPE

Several promising directions emerge for extending this research:

- 1) **Multi-Modal Data Fusion:** Integrate visual data with complementary modalities such as hyperspectral imagery, thermal imaging, or environmental sensor data (IoT) for a more holistic plant health assessment system. Early stress indicators not visible in RGB may be detectable in other spectral bands.
- 2) **Model Optimization for Edge Deployment:** Develop variations of the CNN that are lightweight with methods such as knowledge distillation and network pruning, quantization to allow real time inference of the resource. limiting mobile and edge devices common in agricultural settings.
- 3) **Drone-Based Aerial Monitoring:** Modify the model. to process aerial images taken by Unmanned. Aerial Vehicles (UAVs). This would enable orchard-scale surveying, mapping productions of disease spread, and definition of hotspots of infection based on a canopy perspective [15].
- 4) **Temporal Analysis and Progression Tracking:** Extend the framework to process video sequences or time-series images data of stationary cameras to track illness. change in the development of the individual plant as time goes by, making this possible. anticipation of severity of infection and the most effective intervention timing.
- 5) **Explainable AI (XAI) Integration:** Add visualization methods. SHAP to indicate the selective parts of the leaf that affect. the decision of classification. This "visual explanation" become able to establish confidence between farmers and agronomists and offer more finer diagnoses.
- 6) **Federated Learning for Privacy-Preserving Collaboration:** Implement a federated learning framework where models are trained collaboratively across multiple farms without sharing raw image data, addressing data privacy concerns while benefiting from diverse geographical data distributions.

- 7) **Cross-Species and Cross-Disease Generalization:** Investigate the transferability of the GAN augmentation approach and CNN architecture to other economically important crops (e.g., grapes, potatoes, tomatoes) and their respective disease spectra [19], [20].

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