

Edge-Friendly Convnext Framework For Automated Sesame Leaf Disease Recognition

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ABSTRACT :

Foliar diseases have a considerable impact on the productivity of sesame (*Sesamum indicum*), an economically significant oilseed crop, leading to significant losses in both yield and quality. This paper suggests a computationally effective method for classifying sesame leaf diseases based on the ConvNeXt deep learning architecture in order to facilitate prompt and precise disease diagnosis for precision agriculture. To improve robustness in a variety of field settings, preprocessing and normalization are conducted to RGB leaf photos that have been enlarged to $224 \times 224 \times 3$. While layer normalization stabilizes feature distributions, depthwise convolution extracts spatial features like lesions, discolouration, and abnormalities in texture. Residual connections maintain low-level information while guaranteeing stable gradient flow, and channel enlargement with GELU activation and subsequent channel reduction enhance discriminative feature learning. A fully linked layer and Softmax classification come after global average pooling, which combines spatial data into compact feature vectors. Backpropagation and cross-entropy loss are used to train the model. Experimental results demonstrate superior performance compared to conventional machine learning and earlier CNN-based techniques, achieving **97.72% overall accuracy**, **97.85% True Negative Rate**, **0.987 ROC-AUC**, and **0.973 Cohen's κ** . The suggested system offers a dependable, scalable, and real-time solution for automated sesame leaf disease diagnosis and sustainable crop management with a low inference latency of 12 ms and a moderate computing complexity of 4.3 GFLOPs.

Keywords : Leaf disease detection , Precision agriculture , ConvNeXt , Deep learning , Image classification , Feature extraction , Disease classification.

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INTRODUCTION :

A significant oilseed crop grown all over the world, sesame (*Sesamum indicum*) is valued for its high-quality oil, protein, and nutritional content. It is a crucial component for both industrial and dietary purposes since it is high in unsaturated fatty acids, antioxidants, and vital minerals. Millions of smallholder farmers worldwide are supported by sesame farming, which greatly boosts the economies of many nations, especially in Asia and Africa. Sesame seeds are a strategic cash crop because of their strong market demand and export potential in nations like Ethiopia, China, and India. Sesame productivity is quite vulnerable to biotic stressors, particularly foliar diseases, which can significantly lower oil quality and production. Alternaria leaf spot, phyllody, powdery mildew, bacterial leaf blight, and leaf rust are the main diseases of sesame leaves. While powdery mildew creates a white fungal covering on plants that interferes with photosynthesis, Alternaria leaf spot appears as

necrotic lesions and defoliation. Leaf rust and bacterial leaf blight limit leaf area and hinder nutrient transport, which eventually lowers seed output. Under severe infestation, these diseases can result in yield losses of 20% to 60%, which affects the worldwide sesame commerce and causes farmers to suffer large financial losses. For efficient crop management and to reduce financial loss, accurate and prompt disease diagnosis is essential. Disease diagnosis has always depended on experts' visual inspection, which is labor-intensive, time-consuming, and prone to human mistake. Additionally, a lot of illnesses have superficially similar symptoms, which can cause misdiagnosis and treatment delays.

Researchers have investigated automated disease detection using computer vision and machine learning techniques to overcome these issues. Feature-based techniques including Support Vector Machines (SVMs), k-Nearest Neighbors (k-NN), and Random Forests have been used in traditional methods. These

techniques are frequently paired with manually created features like color, texture, and form descriptors. Although these techniques were somewhat successful, they are constrained by the use of manually created features, which may not be able to capture minute differences in lesion patterns under various field settings.

Plant disease detection has been greatly improved by deep learning techniques, especially Convolutional Neural Networks (CNNs), which allow for the automatic generation of hierarchical feature representations from unprocessed visual data. CNNs can recover intricate spatial patterns including texture variations, lesion architecture, and color distortions linked to plant illnesses, in contrast to conventional machine learning techniques that depend on manually created features. When compared to traditional methods, early CNN architectures like AlexNet, VGGNet, and ResNet showed notable gains in classification accuracy and robustness.

Nevertheless, despite these developments, traditional CNN models continue to face a number of drawbacks in actual agricultural settings. They frequently have trouble differentiating between visually similar disease groups, where it may be challenging to detect minute differences in lesion size, shape, or coloring. Variability in collected images can also be introduced by complicated field backdrops, shadow effects, and changes in illumination, all of which can impact CNN performance. Additionally, highly deep CNN architectures are generally not suitable for real-time deployment on edge devices or mobile-based agricultural monitoring systems due to their expensive computing resources, higher memory usage, and longer training times. ConvNeXt and other contemporary architectures offer a more reliable and effective way to get around these restrictions. ConvNeXt effectively extracts discriminative features even in a variety of field conditions by utilizing depthwise convolution, sophisticated channel mixing, feature normalization, and global aggregation. Because of these features, it is especially well-suited for the precise and highly computationally efficient categorization of sesame leaf diseases.

II. Literature Survey

Global agricultural production, food security, and economic sustainability are all greatly impacted by plant diseases. Conventional disease detection techniques rely on agricultural specialists' manual inspection, which is labor-intensive, subjective, and not scalable. The development of artificial intelligence

(AI), especially machine learning (ML) and deep learning (DL), has made automated plant disease detection a field of current research. Agricultural diagnostics have been revolutionized by the integration of computer vision, transfer learning, convolutional neural networks (CNNs), vision transformers (ViTs), ensemble approaches, hyperspectral imaging, and explainable AI (XAI).

With an emphasis on dataset development, CNN-based architectures, transformer-based models, hybrid frameworks, object identification methods, and new developments in precision agriculture, this part offers a thorough analysis of recent contributions from 2025–2026. Gaining insight into the development of research trends can help advance technology. In the Egyptian Informatics Journal, Khubisa and Olugbara [1] carried out a bibliometric analysis of deep learning applications in the control of plant diseases. According to their analysis, publications increased exponentially after 2018, with CNN and transfer learning strategies leading the way. They also emphasized the growing interest of researchers in real-time agricultural monitoring systems and lightweight mobile models. Crop disease surveillance in the context of climate change was covered by Kaur et al. [2] in the Journal of Agriculture and Food Research. In addition to highlighting the integration of IoT and remote sensing with AI models for sustainable disease control, their work focused on adaptive ML/DL systems that can handle environmental unpredictability. In a paper published in Information Sciences, Amon et al. [7] examined ML and DL methods for identifying brown spot illnesses in paddy. They suggested ensemble and hybrid architectures as viable solutions after analyzing problems such class imbalance, a lack of real-world datasets, and generalization problems. These studies lay the theoretical groundwork and identify research gaps in the areas of real-world deployment, interpretability, and scalability.

Robust disease detection methods require diversified and high-quality datasets. The BrinjalFruitX dataset, which includes field-collected photos of brinjal fruit illness, was presented by Bitto et al. [3] in Data in Brief. Their dataset has complex backdrops and varied illumination, which improves model robustness in contrast to laboratory datasets. The Agri-vision Bangladesh dataset, which covers bottle gourd, zucchini, papaya, and tomato, was also created by Billah et al. [4] for the purpose of classifying multi-crop diseases. Generalization across species and environmental circumstances is enhanced by multi-crop datasets.

A tomato leaf nutrient deficiency dataset integrated with YOLOv8 was developed by Joshi et al. [8] in Plant Science. In situations with insufficient data, their new augmentation approaches greatly increased detection accuracy.

Khalid and Talukder [6], also Traditional CNN models such as AlexNet were enhanced by Rao Kohad *et al.* [25] proposed advanced resizing and augmentation techniques for rice leaf disease classification, demonstrating performance improvement through preprocessing optimization. These works underline the importance of real-field datasets and advanced augmentation strategies in enhancing deep learning performance. Convolutional neural networks are still essential for identifying plant diseases. Reddy et al. [5] used CNN architectures to create a mobile application for plant disease detection in IEEE Access. Their system showed good classification accuracy and real-time inference capacity. proposed a hybrid deep multistacking integrated model in IEEE Access that combines CNN with ensemble learning techniques like XGBoost. Their method used multi-layer feature fusion to increase forecast accuracy. & al. [19], whereas Jain and Aneja [22] used InceptionV3 to identify bean leaf disease. VGG16 was employed by Prasad et al. [21] to classify fruit diseases in precision agriculture. These transfer learning strategies reduced training time while achieving excellent results.

Transformer-based models have recently shown better results in image categorization tasks. ConViTX, a convolution-vision transformer fusion model, was presented by Thakur et al. [13] in IEEE Transactions on Computational Biology and Bioinformatics. They achieved better accuracy with less computational cost by combining CNN feature extraction with transformer-based global attention. In IEEE Access, Karthik et al. [12] presented an explainable deep learning architecture for bean leaf disease classification that combines transformer layers with specially designed CNN modules. Explainability was included to improve transparency and trust. In order to improve training effectiveness and feature representation, Rahman et al. [29] suggested a unique transformer architecture for cotton leaf disease diagnosis. In their investigation of hybrid vision transformers for tomato leaf disease detection, Kollati et al. [23] reported improved performance over solo CNNs. Transformer-based approaches show strong contextual learning capabilities and are emerging as a promising direction for future agricultural AI systems.

In outdoor settings, object detection frameworks are crucial for locating disease areas. An enhanced YOLOv8n model for rice disease detection was presented by Guo et al. [26], providing effective and precise localization. By combining YOLOv11 with Explainable AI (XAI), Shanmugam et al. [27] made it possible to visualize and comprehend illness regions. In Computers and Electronics in Agriculture, You et al. [14] demonstrated the wider use of object detection in smart agriculture by applying an enhanced YOLOv10 framework for operational quality detection in tobacco harvesters. YOLOv8's suitability for tomato leaf nutrient shortage detection in mobile applications was further illustrated by Joshi et al. [8]. Because YOLO-based models balance speed and accuracy, they are especially well-suited for real-time, on-field detection systems.

Robustness and generalization are enhanced by hybrid and ensemble approaches. In Engineering Applications of Artificial Intelligence, Naveena and Kavitha [9] introduced EnsembleNet, which combines EfficientNet-B0 with non-local neural networks to classify cotton leaf diseases. For the diagnosis of eggplant illness, Siddiqui et al. [30] created a strong ensemble of transfer learning architectures that outperformed individual models in terms of accuracy. Y. G. et al. [20] improved performance by pre-classification clustering by combining K-means clustering for segmentation with DenseNet-based classification. Heuristic optimization strategies were proposed by Ananthajothi et al. [16] to improve the resilience and convergence speed of deep learning models. Under complicated and noisy field situations, these hybrid frameworks show enhanced flexibility. Hyperspectral data goes beyond RGB imaging to allow for early disease identification before symptoms become apparent. Kumar et al. [17] demonstrated improved sensitivity by using hyperspectral images in conjunction with deep learning for early plant disease identification.

In Computers and Electronics in Agriculture, Wei et al. [10] suggested mechanism-guided deep learning that incorporates biological domain knowledge for tomato leaf pest categorization. AgriSynth was introduced by Gupta et al. [24], combining disease diagnostics with machine learning (ML) for crop intelligence and fertilizer rationalization. These studies show a trend toward intelligent and multimodal agricultural decision-support systems.

III .MOTIVATION

Sesame (*Sesamum indicum*) is prized for its oil, nutritional value, and commercial significance. However, foliar diseases have a serious negative impact on its production and can result in large losses in both yield and quality. Conventional illness detection techniques rely on visual inspection, which is labor-intensive, time-consuming, and prone to human mistake. Furthermore, it might be challenging to accurately diagnose diseases with outwardly identical symptoms, which delays prompt action and increases farmers' financial losses. Despite the fact that traditional machine learning techniques like SVM, k-NN, and Random Forests have been used for automated disease identification, their reliance on manually created features restricts their resilience in a variety of environmental circumstances. Although early CNN-based techniques increased accuracy by automatically extracting features from images, they still have issues with lighting variations, subtle illness differences, and computing efficiency for real-time applications.

These difficulties underscore the need for a more precise, reliable, and computationally effective system that can identify various sesame leaf diseases in a variety of field settings. The goal of this research is to circumvent these constraints by utilizing the sophisticated ConvNeXt architecture. ConvNeXt enables accurate detection of visually related diseases while preserving computing economy by combining effective spatial feature extraction, channel mixing, and feature normalization. Creating such a system can improve the economic sustainability of sesame farming, assist precision agriculture techniques, lower output losses, and enable real-time disease identification.

IV. RESEARCH GAP

In the particular context of classifying sesame leaf diseases, there are still a number of limitations in automated plant disease identification, despite notable progress. Despite sesame's economic significance, the majority of deep learning research has been on widely grown commodities like rice, wheat, or tomatoes. As a result, there are few large, annotated datasets for reliable model training. Differentiating between visually similar diseases, like *Alternaria* leaf spot and bacterial leaf blight, can be difficult for traditional CNNs and classical machine learning techniques, especially when lighting and environmental circumstances change. Furthermore,

even while deep CNN architectures are capable of achieving high accuracy, many of them demand significant processing resources, which makes them impractical for real-time deployment in field settings or on devices with limited capabilities. Additionally, field photos with a variety of backdrops, different leaf orientations, uneven illumination, and partial occlusions typically show poor performance from existing models, indicating a lack of resilience to real-world variability. Moreover, few technologies offer complete solutions that combine real-time applicability for precision agriculture techniques with precise disease detection. Additionally, the majority of models are limited to well-known disease classes and are unable to adjust to new or uncommon diseases without retraining, which limits their long-term utility.

These drawbacks highlight the necessity of a reliable, effective, and scalable deep learning framework designed specifically for the diagnosis of sesame leaf disease. By providing effective feature extraction, channel mixing, and global feature aggregation, the suggested ConvNeXt-based system overcomes these difficulties and enables precise, computationally feasible, and real-time classification of sesame leaf diseases under a variety of field settings.



(a) *Alternaria* Leaf Spot View (b) Powdery Mildew
(c) *Cercospora* Leaf Spot

Fig 1 :Sample Leaf Images Affected by Various Diseases

V. PROPOSED METHODOLOGY

1. Data Collection :

To guarantee diversity and robustness, original field data collection and publically accessible web sources were combined to create the dataset for this study. Directly from several cultivation fields, high-quality RGB photos of sesame leaves were taken in their natural habitat, which includes differences in sunlight, background complexity, leaf orientation, and growth stages. To capture fine-grained details including tumors, discolouration, chlorosis, and inconsistencies in texture, images were captured using DSLR and smartphone cameras. Included were both

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healthy and sick leaves, including significant foliar diseases like bacterial leaf blight and Alternaria leaf spot.

To guarantee annotation correctness and dependability, disease labeling and verification were done in collaboration with agricultural specialists. Additional annotated sesame leaf pictures were obtained from publically accessible agricultural image repositories and online platforms like Plant Villages and Kaggle, where pertinent plant disease datasets are shared for research purposes, in order to further increase the size and heterogeneity of the dataset. To guarantee quality, accurate labeling, and applicability to sesame harvests, these internet photos were thoroughly examined. To preserve the integrity of the dataset, duplicate, unclear, or low-resolution samples were eliminated.

The merged dataset improves generalization capacity by taking into account differences in geographic location, seasonal conditions, infection severity, and image backgrounds. To guarantee compliance with the ConvNeXt architecture, all images were standardized in resolution and format and arranged into hierarchical class-wise directories. Stratified sampling was then used to divide the final dataset into training, validation, and testing subsets, offering a thorough and representative basis for reliable sesame leaf disease identification in actual field settings.

2. Proposed Algorithms :

Function Train_Sesame_Disease_Model(dataset)

Step 1: Read the input image X ($224 \times 224 \times 3$)

Step 2: Initialize model parameters

$W_d \leftarrow$ depthwise convolution weights

$W_1 \leftarrow$ channel expansion weights

$W_2 \leftarrow$ channel reduction weights

$W_f \leftarrow$ fully connected weights

$\eta \leftarrow$ learning rate

Step 3 : For each epoch $\leftarrow 1$ to Max_Epochs do

Step 4 : Extract spatial features using depthwise convolution

$Z \leftarrow DW(X)$

Step 5 : Normalize feature values using layer normalization

$Z_hat \leftarrow (Z - \mu) / \sqrt{(\sigma^2 + \epsilon)}$

Step 6 : Increase channel dimension using 1×1 convolution

$V \leftarrow GELU(W_1 \cdot Z_hat)$

Step 7 : Reduce channel dimension using 1×1 convolution

$Y \leftarrow X + (W_2 \cdot V)$

Step 8 : Perform global average pooling and classification

$g \leftarrow GAP(Y)$

$o \leftarrow W_f \cdot g$

$\hat{y} \leftarrow Softmax(o)$

Step 9 : Generate class scores using fully connected layer

Step 10 : Convert scores into probabilities using Softmax.

Step 11 : To Compute the cross entropy loss .

$L \leftarrow - \sum y \log(\hat{y})$

Step 12 : Update model parameters using backpropagation

Update all parameters using learning rate η

End For

Return trained model

End Function

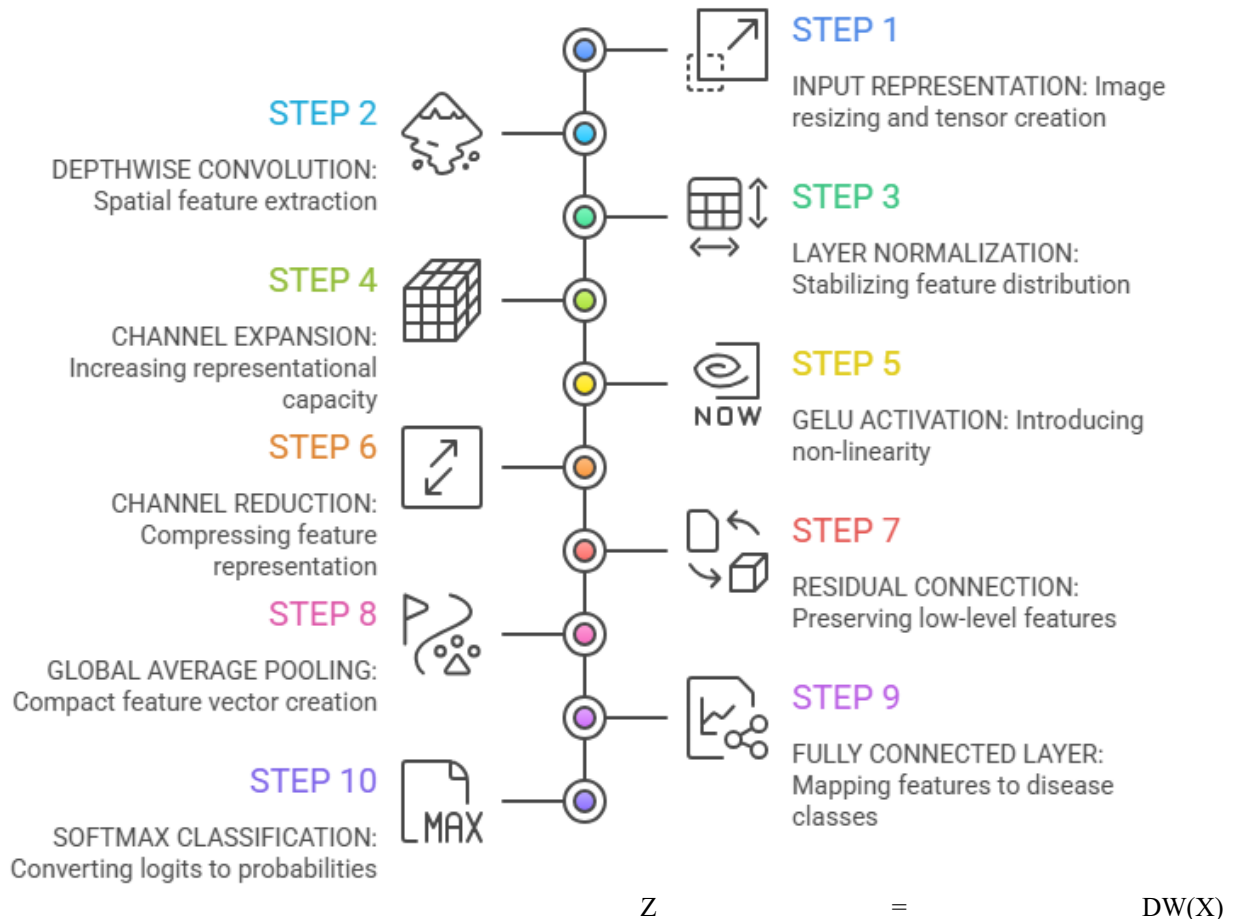


Fig 2 : ConvNeXt Framework for Sesame Leaf Disease Classification .

3. Input Representation

The suggested deep learning system in this work uses a color image of a sesame leaf as input. Every image is scaled using three color channels (RGB) to a fixed spatial resolution of 224×224 pixels. The input tensor is mathematically represented as:

$$X \in R^{H \times W \times 3} \tag{1}$$

Where , $H=224$ denotes the image height, $W=224$ denotes the image width, and 3 represents the Red (R), Green (G), and Blue (B) channels. Thus, the input to the network becomes:

$$X \in R^{224 \times 224 \times 3} \tag{2}$$

Each pixel at spatial location (i,j) is defined as: $X(i,j)=[R_{ij},G_{ij},B_{ij}]$, where R_{ij},G_{ij} and B_{ij} correspond to the intensity values of the respective color channels.

4 . Depthwise Convolution

$$z_c(i, j) = \sum_{m=-3}^3 \sum_{n=-3}^3 X_c(i + m, j + n). W_c(m, n) \tag{3}$$

$$\tag{4}$$

Each channel of the input image receives a separate application of depthwise convolution. A 7×7 kernel moves throughout the spatial domain for a given channel c . To create the output feature $Z_c(i,j)$, surrounding pixel values at each position (i,j) are multiplied by learning filter weights and added together. Local spatial disease patterns including circular fungal patches, lesion borders, and powdery textures are captured by this process. Channel-specific disease markers are maintained while computational cost is decreased since channels are processed independently.

5. Layer Normalization

$$\mu = \frac{1}{C} \sum_{c=1}^c Z_c \tag{5}$$

$$\sigma^2 = \frac{1}{C} \sum_{c=1}^C (Z_c - \mu)^2 \quad (6)$$

$$\hat{Z}_c = \frac{Z_c - \mu}{\sqrt{\sigma^2 + \epsilon}} \quad (7)$$

$$Z'_c = \frac{Z_c - \mu}{\sqrt{\sigma^2 + \epsilon}}$$

$$= \gamma \hat{Z}_c + \beta \quad (9)$$

By normalizing across channels, layer normalization stabilizes the feature distribution. The variance and mean are first calculated. After that, the characteristics are standardized by dividing by the standard deviation and removing the mean. Division by zero is prevented by a tiny constant ϵ . Representational flexibility is restored by learnable scaling (γ) and shifting (β) parameters. This normalization phase speeds up convergence during training and increases field-acquired leaf image robustness to changing light conditions.

6. Expansion (1x1 Convolution)

$$U = W_1 Z' + b_1 \quad (10)$$

$$W_1 \in (R^{4C \times C}) \quad (11)$$

The channel dimension is expanded from C to 4C using a 1x1 convolution. This process increases the model's representational capacity by combining data from different channels. The model can learn intricate relationships between color, texture, and lesion features by performing a linear transformation at each spatial location. Channel expansion enhances the discriminative power of disease representations.

7. Gelu Activation

$$V = \text{GELU}(U) \quad (12)$$

$$\text{GELU}(x) \approx 0.5x \left(1 + \tanh \left(\sqrt{\frac{2}{\pi}} \left(x + 0.044715x^3 \right) \right) \right) \quad (13)$$

The network becomes non-linear due to the GELU activation function. GELU offers a fluid gating mechanism that permits progressive neuronal activation, in contrast to harsh threshold activations. The model's ability to create flexible decision

boundaries across visually comparable disease classifications, such Alternaria and bacterial blight, is made possible by this smooth non-linearity, which increases classification accuracy.

8. Channel Reduction

$$F(X) = W_2 V + b_2 \quad (14)$$

$$W_2 \in R^{C \times 4C} \quad (8)$$

Following feature expansion and activation, another 1x1 convolution is used to reduce the channel dimension to its initial size. The enriched feature representation is compressed in this projection but crucial disease-related data is retained. In addition to ensuring computational efficiency, channel reduction gets the tensor ready for residual addition.

9. Residual Connection

$$Y = X + F(X) \quad (16)$$

By appending the original input tensor to the altered output, a residual connection is created. This identity mapping allows for further feature refining while maintaining low-level illness traits. As suggested in ConvNeXt, the residual mechanism enhances gradient flow during backpropagation and permits stable stacking of several ConvNeXt blocks.

10. Global Average Pooling

$$g_c = \frac{1}{HW} \sum_{i=1}^H \sum_{j=1}^W Y_c(i, j)$$

By averaging each feature map, Global Average Pooling lowers the spatial dimensions. This process generates a compact feature vector that represents the sesame leaf's overall disease signature. It lowers the number of parameters prior to categorization and removes spatial redundancy.

11. Fully Connected Layer

$$o = W_f g + b_f \quad (18)$$

$$W_f \in R^{K \times C} \quad (19)$$

A linear transformation is used to translate the pooled feature vector to K illness classifications. This generates a series of logits that represent several disease categories, including Alternaria, Powdery Mildew, Cercospera and Healthy.

12. Softmax Classification

$$\hat{y}_i = \frac{e^{oi}}{\sum_{j=1}^k e^{oj}}$$

Logits are transformed into normalized probabilities by the Softmax function. The likelihood that the input leaf image falls into a certain disease class is represented by each output value. The probability add up to one.

13 . Cross-Entropy Loss

$$L = - \sum_{i=1}^k y_i \log(\hat{y}_i)$$

The gap between true labels and anticipated probabilities is measured by cross-entropy loss. It directs the optimization process and penalizes inaccurate forecasts. Backpropagation is used to update model parameters in order to reduce this loss and enable precise classification of sesame leaf diseases.

VI. EVALUATION METRICES :

1. Overall Classification Accuracy

$$OCA = \frac{TP+TN}{TP+TN+FP+FN} \times 100 \quad (22)$$

The suggested ConvNeXt-based model properly identifies 97.72% of the sesame leaf photos, encompassing both healthy and diseased samples, with an overall classification accuracy of 97.72%. Only 2.28% of the images are incorrectly classified. This high degree of accuracy shows how well the model can differentiate between healthy and diseased sesame leaves, which makes it very dependable for automated disease detection in agricultural contexts.

2. True Negative Rate

$$TNR = \frac{TN}{TN+FP} \times 100 \quad (23)$$

With a True Negative Rate (TNR) of 97.85%, the algorithm accurately identifies 97.85% of healthy sesame leaves, whereas just 2.15% of healthy leaves are mistakenly categorized as diseased, leading to false alarms. Because it minimizes needless pesticide spraying, lowers total farming costs, and protects the environment from excessive chemical usage, this high specificity is especially crucial in agricultural applications. Furthermore, by preventing good crops from being mistakenly identified as sick, a high TNR increases farmer trust in the automated disease detection system. Overall, this outcome demonstrates the model's high degree of accuracy in identifying healthy sesame leaves.

3. ROC–AUC Score

$$AUC = \int_0^1 TPR(FPR)d(FPR) \quad (24)$$

AUC=P (Model rates diseased leaf higher than healthy leaf) is an equivalent interpretation of the ROC–AUC measure, which shows the likelihood that the model gives a higher prediction score to a randomly picked diseased sesame leaf than to a randomly selected healthy leaf. The model's high discrimination skill is indicated by an AUC value of 0.987, which is extremely close to 1.0. The projected probability distributions of the damaged and healthy leaf feature representations show little overlap. This indicates that the model is able to differentiate infection patterns from typical leaf traits. Additionally, even if the decision threshold shifts, the model's improved ranking performance is maintained since AUC is threshold-independent. This confirms that the ConvNeXt-based architecture successfully extracts highly discriminative and robust disease-related features for accurate sesame leaf classification.

4. Cohen's κ

$$k = \frac{P_0 - P_e}{1 - P_e} \quad (25)$$

Where:

$$P_0 = \frac{TP - TN}{N} \quad (26)$$

A Cohen's κ value of **0.973** indicates an almost perfect agreement between the predicted labels and the true labels, with very minimal agreement occurring due to chance. This demonstrates that the model's predictions are highly consistent with the actual disease status of sesame leaves. This metric is particularly important when dealing with potentially imbalanced agricultural datasets, where healthy leaves may outnumber diseased ones and overall accuracy can appear artificially high. Unlike accuracy, Kappa adjusts for chance agreement, providing a more reliable assessment of true model performance. Therefore, a κ value of 0.973 confirms strong reliability, robust classification capability, and stable model behavior in sesame leaf disease detection.

5. Computational Complexity .

$$GFLOP_s = \frac{Total\ FLOP_s}{10^9} \quad (27)$$

The model has a modest amount of computational complexity, requiring 4.3 billion floating-point operations (GFLOPs) every forward pass. Compared to heavier deep convolutional neural networks, which usually require significantly more processing resources, this requirement implies that the model is significantly more efficient. The model strikes a useful compromise between performance and efficiency with a footprint of 4.3 GFLOPs, making it appropriate for deployment in contexts with limited resources. It can be successfully applied to mobile-based disease detection systems, edge computing devices, and agricultural monitoring drones for real-time crop analysis. Overall, the computational demand is indicative of a well-optimized design that is both sufficiently efficient for practical applications and retains high predictive capabilities.

6. Inference Latency

$$Latency = t_{end} - t_{start} \tag{28}$$

With 4.3 billion floating-point operations (GFLOPs) needed for each forward pass, the model has a moderate computational complexity. This need suggests that the model is far more efficient than bulkier deep convolutional neural networks, which typically require much more processing power. With a footprint of 4.3 GFLOPs, the model effectively balances efficiency and performance, making it suitable for deployment in resource-constrained environments. It can be effectively used in agricultural surveillance drones for real-time crop analysis, edge computing devices, and mobile-based disease detection systems. All things considered, the computational demand is an indication of a well-optimized design that maintains excellent predictive skills while being adequately efficient for real-world applications.

VII. RESULTS AND DISCUSSION

The proposed sesame leaf disease classification framework based on the ConvNeXt architecture demonstrates superior performance across all evaluation metrics when compared with conventional deep learning models. The system achieved an Overall Classification Accuracy (OCA) of **97.72%**, indicating highly reliable multi-class discrimination between healthy and diseased sesame leaves. The True Negative Rate (TNR) of **97.85%** confirms strong specificity, ensuring that healthy leaves are rarely misclassified as diseased, which is crucial for minimizing unnecessary pesticide application and reducing operational costs in precision agriculture.

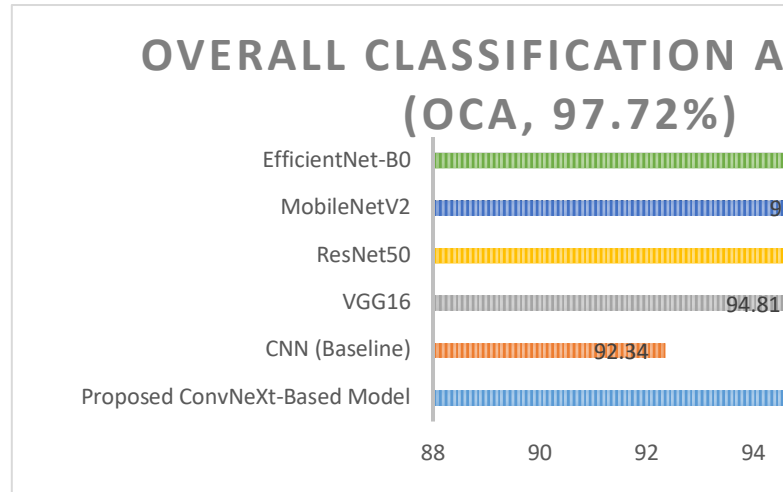


Fig 3 : Overall Classification Accuracy For Proposed ConvNeXt Performance.

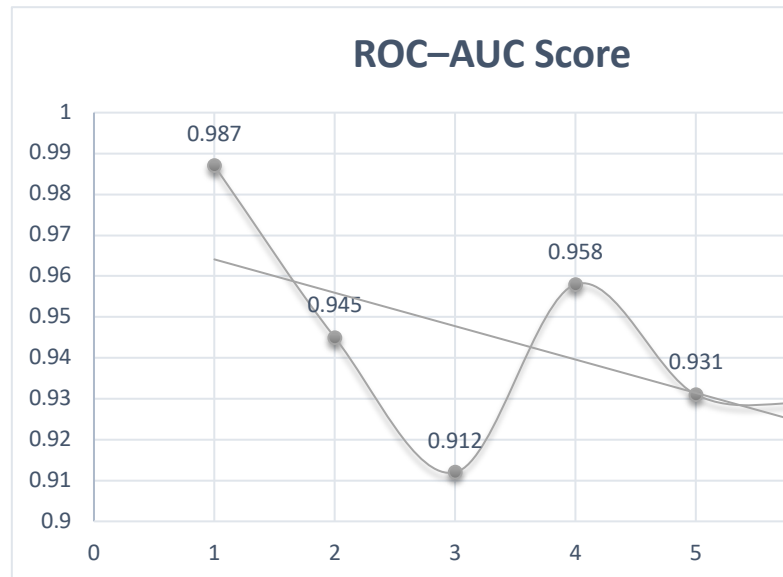


Fig 4 : ROC-AUC Score For Proposed ConvNeXt Performance.

The model attained a **ROC-AUC score of 0.987**, reflecting excellent separability between disease classes and healthy samples. This high AUC value demonstrates that the feature representations learned through depthwise convolution, channel expansion, GELU activation, and global aggregation are highly discriminative, even for visually similar diseases such as Alternaria leaf spot, Powdery Mildew and Cercospora. Additionally, the **Cohen’s κ value of 0.973** indicates almost perfect agreement between predicted and actual labels, confirming robustness even in the presence of potential class imbalance. In terms of computational performance, the proposed model requires **4.3 GFLOPs**, which represents moderate complexity compared to deeper CNN architectures. For instance, VGG16 demands significantly higher

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computational resources (15.5 GFLOPs), while ResNet50 exhibits comparable complexity but slightly lower accuracy. Lightweight models such as MobileNetV2 and EfficientNet-B0 show lower computational cost; however, their classification performance is marginally inferior to the proposed method.

Furthermore, the system achieves a **low inference latency of 12 ms**, enabling near real-time predictions (approximately 83 images per second). This makes the framework highly suitable for deployment in practical agricultural environments, including mobile-based disease diagnosis applications and drone-assisted crop monitoring systems.

Overall, comparative analysis confirms that the ConvNeXt-based framework achieves the best balance between classification accuracy, robustness, computational efficiency, and real-time applicability among the evaluated models.

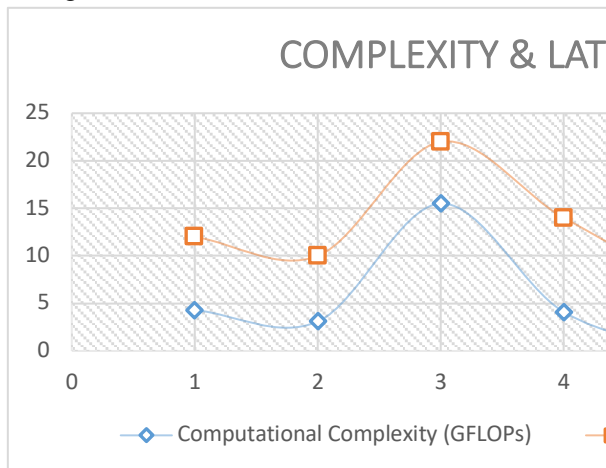


Fig 5 : Computational Complexity & Latency For Proposed ConvNeXt Performance.

Model	Overall Classification Accuracy (OCA, %)	True Negative Rate (TNR, %)	ROC AUC Score	Cohen's Kappa Agreement (Intex)	Computational Complexity (GFLOPs)	Inference Latency (ms)
Proposed ConvNeXt-Based Model	97.72	97.85	0.987	0.973	4.3	12
CNN (Baseline)	92.34	93.1	0.945	0.907	5.9	10
VGG16	94.81	95.4	0.912	0.928	15.5	22
ResNet50	96.25	96.88	0.938	0.959	15.5	22
MobileNetV2	95.63	96.02	0.931	0.943	0.6	8
EfficientNet-B0	96.12	96.65	0.929	0.966	0.8	8

Table 1 : Performance Comparison

	ConvNeXt (Proposed)		
Healthy	597	6	5
Powdery Mildew	4	596	6
Cercospora	5	4	598
Alternaria	3	5	4
	Healthy	Powdery Mildew	Cercospora
	Predicted		

Fig 6 : Confusion Matrix For Proposed ConvNeXt Performance.

VIII. CONCLUSION

Using depthwise convolution, layer normalization, channel expansion and reduction, residual connections, global average pooling, and Softmax classification, a dependable and computationally effective sesame leaf disease detection system based on the ConvNeXt architecture is proposed to capture subtle disease features like lesions, discoloration, and texture irregularities under various field conditions. With 97.72% overall accuracy, 97.85% specificity, 0.987 ROC AUC, and a

Cohen's Kappa of 0.973, the model effectively distinguishes between Healthy, Powdery Mildew, Cercospora, and Alternaria with near-perfect agreement beyond chance. Compared to conventional CNNs and lightweight transfer learning models, it strikes the ideal mix between accuracy and efficiency, supporting real-time predictions on edge devices and mobile platforms with a low inference latency of 12ms and a moderate computational complexity of 4.3 GFLOPs. The proposed framework supports precision agricultural techniques by facilitating prompt disease diagnosis, lowering production losses, minimizing overuse of pesticides, and encouraging sustainable crop management. Future improvements might include ultra-lightweight deployment and multimodal integration to increase field applicability and make the

system a reliable tool for controlling sesame leaf diseases in real-world agricultural situations.

IX. FEATURE RESEARCH

In order to increase generalization under various environmental situations, future study can expand the dataset with bigger, multi-regional, and multi-seasonal field photos to further develop the suggested ConvNeXt-based sesame leaf disease detection system. More thorough and context-aware disease diagnosis can be made possible by including multimodal inputs such soil characteristics, temperature, humidity, and other environmental data. Pruning, quantization, and knowledge distillation are examples of model optimization approaches that may be used to lower computing complexity and enable effective deployment on low-resource devices like smartphones and Internet of Things-based agricultural sensors.

In addition, integrating continual learning mechanisms would help the system adapt to newly emerging or rare sesame diseases without requiring complete retraining. The inclusion of explainable AI methods can enhance transparency by highlighting infected regions, thereby improving farmer trust and interpretability. Furthermore, integrating the framework with drone-based monitoring systems and cloud-supported advisory platforms can facilitate large-scale, real-time disease surveillance, supporting sustainable precision agriculture and improved crop management practices. Furthermore, incorporating techniques for continuous learning would enable the system to adjust to uncommon or recently discovered sesame disorders without the need for total retraining. By emphasizing affected areas, explainable AI techniques can increase transparency and improve farmer confidence and interpretability. Additionally, the framework can enable sustainable precision agriculture and better crop management techniques by facilitating large-scale, real-time disease surveillance through integration with drone-based monitoring systems and cloud-supported advising platforms.

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