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Advancing Real-Time Plant Disease Detection by Using Lightweight Model for Pigeon Pea Crop

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Abstract

Early and accurate detection of pigeon pea leaf diseases is essential for improving crop productivity and ensuring food security, particularly under real-field agricultural conditions. This paper introduces a shallow and computationally off-the-shelf deep learning system to detect the presence of pigeon pea leaf disease with great accuracy and in real-time on resource-limited cameras. DSLR and smartphone cameras were used to make up a custom high-resolution dataset under natural field conditions, including healthy leaves and major diseases, such as Fusarium wilt, leaf spot, and powdery mildew. All the images were downsampled to 224 × 224 pixels and processed with a Gaussian smoothing filter to remove noise and a Canny edge detector to improve structural features. Disease regions were accurately isolated using a Skill Optimization Algorithm (SOA)-driven segmentation strategy that dynamically optimized threshold levels, morphological kernel sizes, and lesion area constraints to handle background clutter and illumination variations. A pretrained EfficientNet-B0 model was used to extract deep semantic features, which consisted of compact 1280-dimensional feature vectors. A novel FMDDCN approach was used to classify these features through exploiting the sensitivity to subtle disease patterns by relying on differential feature modeling and multi-layer fusion of features. The model was fitted on stochastic gradient descent with a learning rate of 1 x 10-3 and a batch size of 32, and assessed on a 60/20/20 train validation test split with 5-fold cross-validation. The results of the experiment show consistent convergence with low overfitting. The proposed framework was found to produce a classification accuracy of 94.5%, precision of 91.0%, recall of 85.5% and Matthews Correlation Coefficient of 88.5% when it was used with four optimized features. In comparison, it is demonstrated that FMDDCN performs better than traditional machine learning and deep learning models, with its F1-score of 0.965 and the overall accuracy of 0.965. The suitability of the real-time edge deployment is verified, as confirmed by the use of computational analysis to reduce inference latency and memory consumption.

Keywords:

Agricultural disease detection, deep learning, efficientnet, fmddcn, pigeon pea, real-time classification, skill optimization algorithm.

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Introduction

Agriculture is among the oldest jobs ever practiced by human beings and continues to play a central role in food sustainability and even economic stability worldwide (Narayanan & Rajan, 2024). Crop cultivation and agricultural technologies have been developed greatly over the centuries, increasing productivity and sustainability (Bhagat et al., 2024; Tomar et al., 2024). Nevertheless, the high growth in population has put strain on the available arable land, and there is a need to have new methods of farming that will yield maximum production without consuming high levels of land and resources. Plant diseases are one of the most serious problems in the modern food production sector and can negatively affect both the volume and the quality of the crops, as well as food security (Wang et al., 2025; Shoaib et al., 2025). The diseases that impact the leaf, especially, have a direct effect on photosynthesis and plant health, resulting in significant losses in terms of productivity (Altınbilek & Kızıl, 2021). Conventional types of disease identification are time-consuming, subjective, labor-intensive, and with high chances of human error because of the necessity of making visual observations by professionals (Chowdhury et al., 2021; Verma et al., 2023). These constraints have necessitated the use of smart and automatic technologies in the process of early disease detection.

The latest innovations in deep learning and computer vision have allowed using deep learning to detect plant diseases with high precision in an automated way. Traditional machine learning methods involved the use of hand-crafted features, including Gray Level Co-occurrence Matrix (GLCM), Local Binary Patterns (LBP), and texture descriptors, with the support of such classifiers as Support Vector Machines (SVM) and neural networks (Islam et al., 2021; Panchal et al., 2022). Though the techniques were successful in controlled settings, they experienced challenges in dealing with complex leaf textures, noise, variable lighting, and backdrop interference. The development of Convolutional Neural Networks (CNNs) has enhanced the quality of plant disease classification by automatically adopting discriminative features of leaf images. Deep networks, including VGG, ResNet, DenseNet, and EfficientNet Feature Map-based Differential Deep Convolutional Network (FMDDCN), and in combination with transfer learning, have shown better results on benchmark datasets. Most of these models are, however, computationally heavy, making them unsuitable for real-time and resource-constrained agricultural systems like farms, mobile systems, and edge devices. Such difficulties are particularly applicable to such crops as pigeon pea that are mostly produced by small farmers in actual field conditions.

The main aim of the proposed study is to come up with an effective and deep learning model that can be used to detect pigeon pea leaf diseases in real time. The objective of the proposed approach is to successfully detect diseased regions in a natural field under optimal conditions and still retain low computational complexity since it requires implementation on a resource-limited device.

Although one can say that much progress has been made in the area of automated plant disease detection, multiple research gaps can be identified that restrict the practical application of the available strategies. The vast majority of existing models are also trained and tested on controlled benchmark datasets like PlantVillage, and these models are not very capable of generalizing well to the real-world field conditions of background clutter, variable illumination, and different leaf orientations. Traditional handcrafted feature-based techniques also lack richness against noise, variations in illumination, and complicated backgrounds, leading to poor performance in the natural environment. Deep CNN architectures have proven to be highly accurate classifiers, but due to the large computational and memory footprint, they are not always feasible to run in real time, especially on low-resource devices deployed in farm environments. Also, not much research has been dedicated to the specific application of lightweight and scalable deep learning models to detect pigeon pea crop disease (Hridoy et al., 2022; Lin et al., 2024). Various methods used also do not take into account the accurate segmentation of diseased areas, which minimizes the accuracy of the detection in cases when the leaves are in cluttered or nonhomogeneous backgrounds. All these limitations help to realize that there is a need to design a computationally efficient, but still precise, disease detection system that is specially designed to be used in agriculture in real-time (Duhan et al., 2025).

A deep learning network with optimized disease region segmentation and feature extraction based on transfer learning would be a lightweight model, capable of producing high classification accuracy on pigeon pea leaf diseases and, at the same time, be computationally efficient enough to be deployed in real-time.

The key contributions of this research are summarized as follows:

- Reduction of a weightless framework of plant disease detection that is specific to the pigeon pea crop in a real-life scenario.
- A combination of a segmentation scheme based on optimization and the Skill Optimization Algorithm (SOA) to precisely isolate the diseased leaf regions.
- Transfer learning-based robust and compact deep feature extraction using pretrained EfficientNet-B0.
- Development of a tailor-made high-resolution image dataset of pigeon pea leaves that have been taken under natural lighting conditions with DSLR photography.
- Greater resistance to the background noise, variations in illumination, and inter-class similarity.
- Reduced computational costs: Accurate, improved classification is obtained with reduced computational costs, facilitating the use of the method in real-time and field-deployable agricultural systems.

The paper is organized in a way that it shows a thorough and systematic research on the real-time pigeon pea leaf disease detection with a lightweight deep learning framework. The paper starts with the Introduction describing the importance of automated detection of plant diseases, limitations of current methods, and the goals and contributions of the research. There is a thorough Literature Survey, overviews of the recent developments in the field of deep learning, lightweight architectures, segmentation methods, and real-time deployment of agriculture, with an emphasis on the research gaps existing at the time of the publication. The section under Materials and Methods presents the suggested SOA-optimized EfficientNet-(FMDDCN framework, such as data collection in real-field conditions, preprocessing and segmentation, feature extraction, architectural model, training plan, and assessment guidelines. The results section gives the findings of the experiment, performance measures, ablation experiments, and the comparison with the existing classifiers. The results are interpreted in a comprehensive Discussion that explains the effectiveness, strength, and computational efficiency of the suggested approach. Lastly, the Conclusion will conclude the main findings and suggest ways of future research to move towards scalable, real-time agricultural disease management.

Literature Survey

The latest innovations in computer vision and artificial intelligence have greatly transformed automated plant disease diagnosis and provided scalable methods of enhancing agricultural productivity and food security (Kavitha & Subramani, 2025). In-depth articles by (Upadhyay et al., 2025; Wang et al., 2025; Shoaib et al.,

2025) point to the development of feature-based methods that require handcrafting to deep convolutional neural networks (CNNs) that can learn hierarchical representations when presented with leaf images (Altinbi maintains this direction, 2022; Ahamed et al., 2024). Although the initial methods used textural descriptors, which included GLCM, LBP, and morphological features in addition to classical classifiers, they were restricted by the inability to generalize in changing illumination, background noise, and clutter. Most of these problems have been solved with the adoption of deep learning architectures that allow end-to-end learning and feature extraction. It has been proven that CNN-based models are effective in plant disease classification, using benchmark datasets. AlexNet and GoogLeNet were also trained on the PlantVillage data by (Kaur et al., 2024) and their accuracy of classification was above 99 % and they did not have to use manual feature engineering. On the same note, (Chowdhury et al., 2021; Panchal et al., 2022) excelled greatly in various crop-disease situations using deep CNNs (Leema & Balakrishnan, 2024). Nevertheless, their impressive performance was reported to decline when tested with field images, even though they had excellent results, which were affected by the background complexity, change in lighting, and the leaf orientation, which is a limitation to their application in agriculture (Mustapha et al., 2016).

To improve the localization of disease-affected regions, segmentation-based approaches have been explored. Islam et al., 2021 used segmentation with local thresholding and deep CNNs to identify rice leaf disease and showed better results related to the focus on the infected areas. (Nawaz et al., 2022) added the localization of the disease with classification, which increases resilience during cluttered backgrounds. However, these segmentation pipelines can be expensive in computational terms, and thus, real-time operation is difficult, especially in resource-constrained systems. Deep learning models that are lightweight have become one of the potential solutions to real-time work in the agricultural industry. Architectures Mobile Net-based architectures have been extensively studied because they have fewer parameters and fewer computations. The models based on MobileNetV2 have been found to be competitive, as they can be deployed on mobile and edge devices, as Liu et al. (2023) show. The application they suggest to monitor the peanut leaf disease is the lightweight CNN, which implies using the application that is run in real-time (Dhurgadevi & Nandhini, 2022). Similarly, Hartono et al., 2025 used a lightweight CNN and integrated it with an Android resp. An Android application to identify rice leaf disease (AltinbiLek & Kizil, 2022). The efficiency of these models is notwithstanding the fact that many of them do not target diseased areas explicitly, thus restricting their capability to precisely target diseased areas in complicated field setups.

Fine-tuning of pretrained deep models has also been shown to increase the performance of plant disease detection using EfficientNet models, especially because depth, width, and resolution can be mixed to make it efficient. The work of (Liu et al., 2023; Prashanthi et al., 2025; Subramanian et al., 2022) has reported that the architecture using Efficient Net can be more accurate and converge much faster with increased depth, width, and resolution. Mechanisms of discrimination feature have also been suggested to enhance feature discrimination that are exposed by Pawar & Virupakshappa, 2025; Padshetty, 2025, but these models may be expensive in computational cost. Despite these developments, the scarcity of crop-specific research, particularly on pigeon pea, has been one of the most valuable pulse crops that is cultivated in actual field conditions. To fill this gap, Bhagat et al., 2024 proposed an effective and easy-to-use deep learning model and a new pigeon pea dataset that proves that it is possible to identify diseases in real-time. They recommended the use of their own datasets that were obtained under natural lighting and field conditions in order to enhance model robustness. Nonetheless, more investigation is needed to increase the accuracy of segmentation, computation, and scalability to be used by a large number of smallholder farmers.

The edge-based, real-time deployment considerations have become more and more popular in recent literature. Ahamed et al., 2024 proved the applicability of CNN-based disease detection systems to operate on edge devices, whereas Saha et al., 2023 emphasized the efficiency of lightweight models like MobileNetV3 to be used in real-time in agriculture. These articles focus on the significance of accuracy and efficiency balance in order to ensure that they are realistic to be applied in a discipline. In general, the existing literature justifies the application of deep learning to the problem of plant disease detection, yet also suggests that some problems, including the complexity problem, the possibility of generalizing and applying the proposed solutions to real-life situations, and crop-specific generalization, are present (Hoque et al., 2024). Although lightweight models and transfer learning have been promising, it is evident that there is a research gap in the area of creating an efficient, segmentation-aware, and crop-specific framework in detecting real-time pigeon pea disease. To fill the gap, it is necessary to apply a synergistic combination of lightweight deep learning frameworks, effective segmentation strategies, and real-world data, which is the basis of the proposed study.

Materials and Methods

This is a methodology that describes a pipeline to detect real-time pigeon pea leaf disease. The method is based on image preprocessing, disease area segmentation, deep feature, and classification, which is favorable to real-life agricultural scenarios. It is aimed at a trade-off of high diagnostic accuracy with low computational complexity so that it can be efficiently deployed.

Dataset Collection

A set of custom data was gathered with the help of a DSLR and smartphone cameras in different areas of agriculture in a field. The data contains pictures of diseased and healthy pigeon pea leaves with symptoms such as fusarium wilt, leaf spot, and powdery mildew. Images were captured under varying environmental conditions, such as sunny, cloudy, and shaded scenarios, to ensure real-world variability in terms of background, illumination, and leaf orientation.

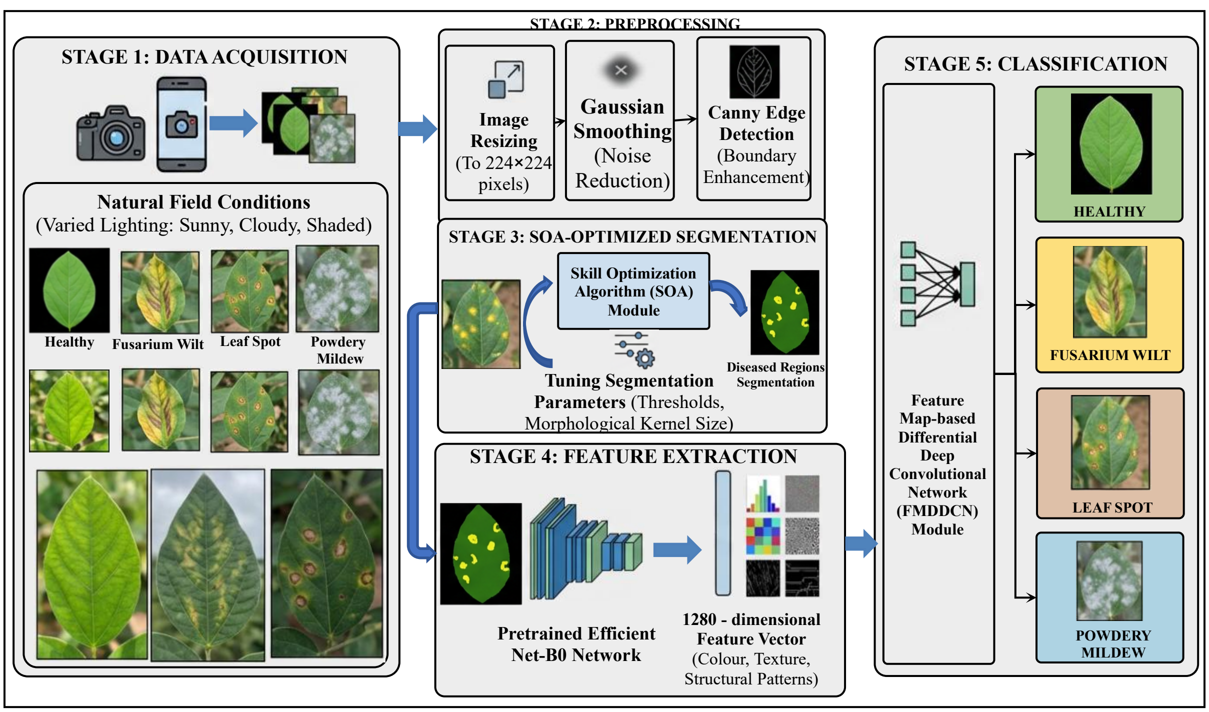

Figure 1. Workflow of the proposed soa-optimized efficientnet–fmddcn framework for real-time pigeon pea leaf disease detection

Figure 1 illustrates the complete workflow of the proposed SOA-optimized EfficientNet– Feature Map-based Differential Deep Convolutional Network (FMDDCN) framework for real-time pigeon pea leaf disease detection. It starts with the data collection and captures images of the leaf with the DSLR and smartphone cameras at the natural field conditions that include variability in lighting, background, and leaf position, and includes healthy leaves along with fusarium wilt, leaf spot, and powdery mildew infections. During the preprocessing phase, the images are cropped to 224 x 224 with Gaussian smoothing to remove noise and Canny edge detection to increase the boundaries of the leaves and the lesion features. The Skill Optimization Algorithm (SOA) then dynamically optimizes the parameters of segmentation in order to precisely isolate diseased areas in the presence of intricate backgrounds. A trained EfficientNet-B0 model is then used to extract a small but discriminative 1280-dimensional deep feature vector on the segmented regions. Last but not least, the Feature Map-based Differential Deep Convolutional Network (FMDDCN) categorizes the features into disease classes, and this process allows the real-time disease identification to be accurate and computationally efficient, and can be deployed in the field.

Preprocessing

A preprocessing method is important to improve the quality of the image by reducing noise and highlighting the structures of interest in the disease. Preprocessing: The images are resized, i.e., to 224x224 pixels, to make them compatible with the EfficientNet-B0 backbone.

Two important operations are used in the preprocessing stage: Gaussian smoothing and Canny edge detection. The Gaussian smoothing stage eliminates noise at high frequencies and leaves significant structural information of the leaf. In order to do Gaussian smoothing, we do a convolution of the image I(x,y) and the Gaussian kernel G(x,y). Convolution operation entails the multiplication of each pixel in the image by the respective value in the kernel and adding the values. Mathematically, it is given as follows:

$$I_{smooth}(x, y) = \sum_{i,j} G(i, j) \cdot I(x + i, y + j) \qquad (1)$$

In the following equation (1), I(x,y) is the value of the image at point (x,y), and G (i, j) is the value of the Gaussian kernel at points with coordinates (i,j) compared to the point where the current pixel is. The summation is a calculation of the weighted mean of the adjacent pixels with weights based on the values of the Gaussian kernel.

The next step involves canny edge detection that identifies sharp intensity changes to identify lesions, leaf veins, and disease spots. The gradient magnitude for edge detection is calculated using:

$$Edge\ Magnitude = \sqrt{(I_x)^2 + \left(I_y\right)^2} \qquad (2)$$

In equation 2, Ix and Iy represent the gradients in the x and y directions.

These actions lead to clean edge maps, which identify structures of interest in the disease, and the images are ready to be segmented.

Segmentation

This is done by isolating diseased areas of the leaf background through the use of segmentation. In order to achieve better accuracy of segmentation in different field conditions, the Skill Optimization Algorithm (SOA) is used to optimize segmentation parameters dynamically. In particular, the SOA maximizes the intensity threshold level, morphological kernel size, and minimum lesion area constraints. Through the optimization process, lesions are accurately isolated in the case of background clutter and illumination variations. SOA optimization parameters are as follows:

- **Threshold Level**: Ranging from 0.1 to 0.9
- **Morphological Kernel Size**: Ranging from 3×3 to 11×11
- **Lesion Area**: Between 50 and 500 pixels

Feature Extraction with EfficientNet-B0

To extract the features, a pretrained EfficientNet-B0 model is used, which is also associated with computational efficiency. The solution of EfficientNet-B0 offers a middle ground approach with scaling depth, width, and resolution in order to perform better but at a lower computational cost. The model derives high semantic information of the underlying convolutional layers that encode local and global disease patterns. The input images of the model are downscaled to 224 by 224 pixels, and once through the network, the result is an output of a 1280-dimensional feature vector. This feature is a representation of important data on texture, color, form, and disease-related structure that is vital in differentiating healthy and diseased leaf patterns. A conceptualized feature space is used to give an interpretable view of the extracted deep representations by splitting up the feature space into different types of visual features as a summary in Table 1. These are the major visual indicators that apply to the analysis of pigeon pea leaf disease.

Table 1. Conceptual feature categories extracted from pigeon pea leaf images for disease classification

Conceptual Feature Name	Description
Color Intensity Pattern	Captures red/green/yellow pigmentation in the leaf.
Edge Density Pattern	Captures leaf edges and vein boundaries.
Pattern of the disease	Spots/blotches/symptoms of infection.
Micro-features of the texture	Fine-grain texture of the infected areas.
Shape Deformation Cues	Malformed shape/curves as a result of infection.
Signals of vein structure	Abnormal vein development or obstruction.
Leaf Margin Transitions	Smooth vs jagged edges
Lighting Reflectance	Wetness or fungus.
Spatial Frequency	Patterns related to how texture varies across the leaf.
Color Histogram Pattern	Global color distribution.

Classification with FMDDCN

For classification, a novel Feature Map-based Differential Deep Convolutional Network (FMDDCN) is employed. FMDDCN produces the differential feature maps that capture the difference between spatial and contextual variations in adjacent feature representations. This increases sensitivity to finer patterns of disease, increasing class separability and resistance to intra-class variation, noise, and changes in illumination. The FMDDCN model operates with lightweight convolutional and depth wise separable filters in order to reduce the amount of computation without reducing accuracy.

CNN Architecture Design

The CNN structure, which took in the proposed Feature Map-based Differential Deep Convolutional Network (FMDDCN), is a multiple-layered structure that has a series of convolution and pooling operations on different layers to extract hierarchical features. The CNN design with the number of feature maps, stride, kernel size, and the type of corresponding layer is indicated in Table 2.

Table 2. CNN architecture design for FMDDCN model

Sum of Feature Maps	Stride	Kernel Size	Size of Feature Maps	Layer
5	1	2	250 × 250 × 60	Conv (2)
1	2	6	125 × 125 × 60	Pooling (2)
1	1	5	250 × 250 × 12	Pooling (1)
1	1	3	18 × 18 × 600	Conv (5)
1	1	6	6 × 6 × 600	Pooling (5)
5	1	3	120 × 120 × 300	Conv (3)
1	2	3	40 × 40 × 300	Pooling (3)
2	1	2	40 × 40 × 600	Conv (4)
1	3	3	20 × 20 × 600	Pooling (4)
Sum of Feature Maps			**21,600**	**F1**

The architecture has captivating hierarchical properties and provides an opportunity to classify diseases in terms of computational efficiency.

Model Training

The model is trained using Stochastic Gradient Descent (SGD) with the following hyperparameters:

Learning rate: 1×10^{-3}

Momentum: 0.9

Batch size: 32

Epochs: 100 (with early stopping after 10 epochs)

To increase model generalization, a complete data augmentation pipeline is employed, namely random rotations, horizontal flipping, brightness scaling, and Gaussian blurring.

Evaluation and Robustness Testing

Stratified 60/20/20 train/validation/test split and five-fold cross-validation are used to evaluate model performance. The performance measures are accuracy, precision, recall, F1-score, and Matthews Correlation Coefficient (MCC). Ablation and robustness analyses are performed to prove the applicability and usefulness of the offered framework. The ablation study contrasts the full pipeline with various variants, such as segmentation-only models, raw (non-segmented) inputs, and alternative backbones, such as MobileNetV2 and ResNet50, but trained under the same conditions. Domain-shift experiments are performed by training on DSLR-captured images and testing on smartphone-captured images, and vice versa. Additional robustness tests are performed by introducing synthetic perturbations, such as Gaussian noise, brightness variation, and occlusion masking of leaf areas.

Computational Efficiency

Computational performance: Inference latency, peak RAM use, model size, and FLOPs are measured on a desktop CPU (Intel Core i5) and edge device (Raspberry Pi 4). This makes sure that the model can be deployed in real-time systems for detecting agricultural diseases.

Reproducibility and Transparency

All the training and evaluation scripts, pretrained weights, SOA configuration files, and annotated segmentation masks will be publicly available to maintain transparency and make it easier to replicate them. Working records will also be documented to facilitate accurate reproduction of all the reported experiments and findings.

Results

Experimental Setup

All experiments were conducted on a system equipped with an Intel Core i5-7200 CPU operating at 2.7 GHz with 8 GB RAM under Windows 10. Model training, validation, and testing were performed using Python 3.7 in a Jupyter Notebook environment, while a specialized user interface (UI) was used to evaluate real-time inference feasibility. This setup reflects the targeted deployment conditions for practical agricultural disease detection.

Training and Convergence Analysis

The training and validation loss curves of the proposed SOA-optimized EfficientNet, FMDDCN model are shown as given in Figure 2. Both curves show a consistent and smooth decrease, converging steadily over training epochs. The fact that training and the validation loss are close to each other implies that learning behaviour is constant, and there is little overfitting.

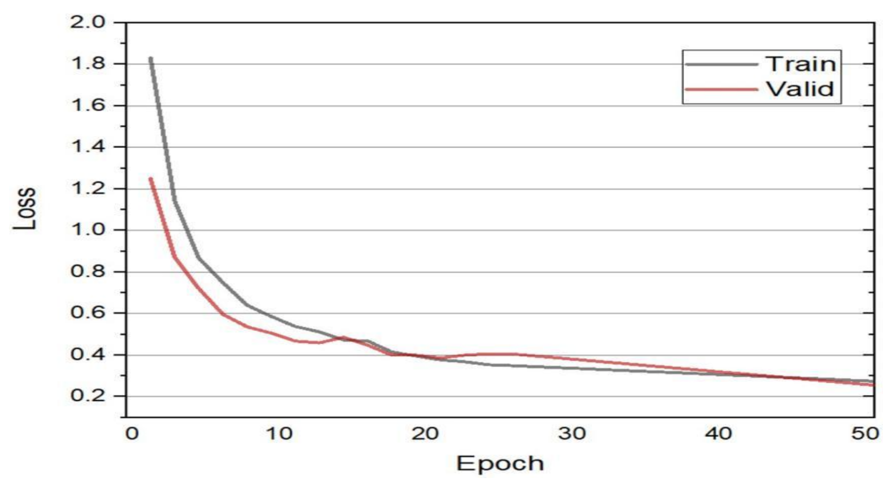

Figure 2. Loss of the proposed classical model

Evaluation Metrics

The performance of the classification models was evaluated using Accuracy, Precision, Recall, F1-score, and Matthews Correlation Coefficient (MCC). These metrics are derived from the confusion matrix and are defined as follows.

Accuracy:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \qquad (3)$$

Precision:

$$Precision = \frac{TP}{TP + FN} \qquad (4)$$

Recall:

$$Recall = \frac{TP}{TP + FN} \qquad (5)$$

F1-Score:

$$F1 - Score = \frac{2 \times Precision \times Recall}{Precision + Recall} \qquad (6)$$

Matthews Correlation Coefficient (MCC):

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \qquad (7)$$

In the above equation (3-7), the confusion matrix summarizes the relationship between actual and predicted class labels. When the actual class is positive, and the model correctly predicts it as positive, the outcome is referred to as a True Positive (TP). If the actual class is positive but the model incorrectly predicts it as negative, the result is a False Negative (FN). Conversely, when the actual class is negative, and the model incorrectly predicts it as positive, the outcome is classified as a False Positive (FP). Lastly, a True Negative (TN) is achieved when the model labels the actual negative prediction as negative (Mohanraj et al., 2025).

Feature-Set Validation Results

The aspect of dimensionality of features on classification was tested by employing three sets of configurations, namely, the full dataset, 10 optimized features, and four optimized features. Table 3 summarizes the quantitative results, and Figure 3 represents the same.

Table 3. Performance comparison across different feature sets

Metric	4 Features	10 Features	Full Dataset
MCC	88.50%	84.50%	81.00%
Recall	85.50%	87.00%	88.00%
Precision	91.00%	91.50%	92.00%
Accuracy	**94.50%**	92.50%	90.50%

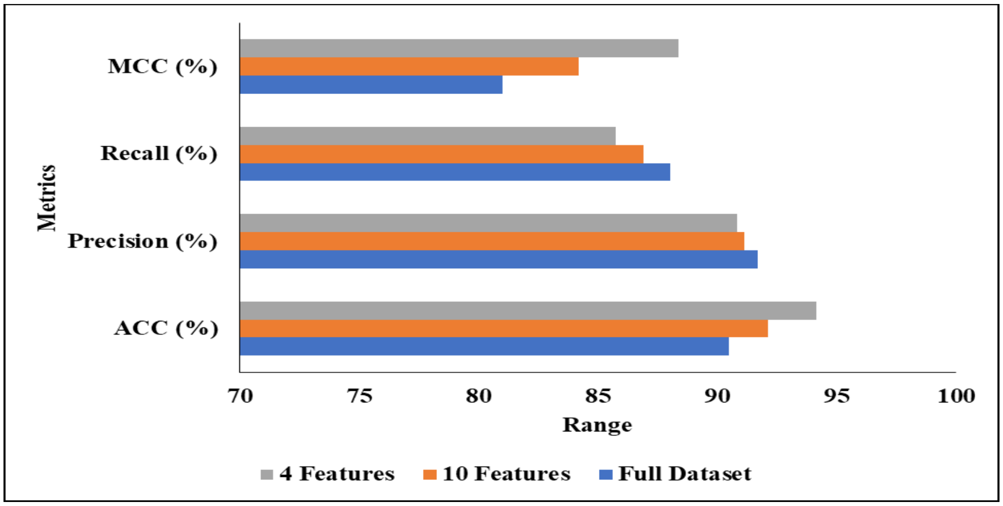

Figure 3. Performance comparison of the proposed model using different feature sets

Comparative Classifier Performance

The suggested FMDDCN classifier was compared to various machine learning and deep learning models. Table 4 and Figure 4 show the results of the comparative performance.

Table 4. Comparative performance of classifiers

Classifier	F1-Score	Recall	Precision	Accuracy
XGBoost	0.872	0.862	0.885	0.872
ELM	0.895	0.898	0.875	0.895
DBN	0.940	0.902	0.882	0.940
LSTM	0.932	0.948	0.848	0.932
CNN	0.940	0.968	0.888	0.940
FMDDCN	**0.965**	**0.985**	**0.950**	**0.965**

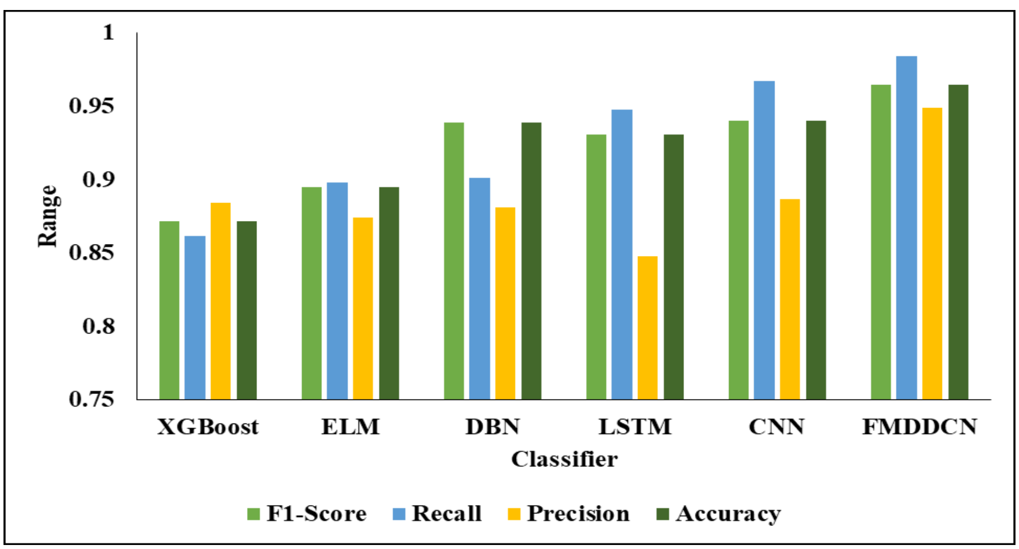

Figure 4. Comparative analysis of the proposed model

FMDDCN Feature Map Generation and Classification Results

This may be explained by the fact that the proposed FMDDCN classifier has a well-organized process of feature map generation, differential feature modeling, and fusion-based classification. The subsection is the mathematical formulation of the operations of the FMDDCN and their connection with the classification results observed.

Feature Map Generation

The first stage is FMDDCN, which produces feature maps of the input image with the help of regular convolutional layers. These layers use learnable kernels to obtain low-level and mid-level features like edges, textures, and disease patterns. Mathematically, the convolution function can be represented as:

$$F_{out}(x,y) = \sum_{i,j} I\,(x+i, y+j) \cdot K(i,j) \quad (8)$$

The equation (8) Fout (x, y) is the output feature map at the spatial position (x,y), I (x +i, y +j) is the intensity of the input image, and K(i,j) is the convolution kernel. In this operation, the hierarchy of feature maps depicting spatial variations in diseased and healthy leaf areas is generated.

Differential Feature Map Generation

The essence of novelty of FMDDCN is that it can produce differential feature maps, feature maps that capture spatial and contextual variations between neighboring feature representations. The use of differences between adjacent feature maps causes the network to be highly sensitive to fine lesion boundaries, texture discontinuities, and pattern-specific characteristics of a disease.

The differential feature map is defined as:

$$\Delta F_{differential}(x,y) = F_{adjacent}(x,y) - F_{current}(x,y) \quad (9)$$

Fadjacent(x,y) and Fcurrent(x,y) in equation (9) are feature maps of the adjacent layers or adjoining spatial locations. This is a differential operation that highlights fine-grained variations and suppresses redundant background information, which directly leads to the increased recall and MCC values in Table 4.

Feature Map Fusion

In order to increase the discriminative ability, multiple layers of different feature maps are merged together to produce a richer representation. The fusion process accumulates the information at various levels of the network to obtain the lesion characteristics at the local level and structural patterns at the global level. The fused feature map is computed as:

$$F_{fused}(x,y) = \sum_{l=1}^{L} \alpha_l \cdot F_l(x,y) \quad (10)$$

In equation (10), Fl(x,y) denotes the feature map from layer l, αl is the corresponding weighting factor, and L is the total number of layers involved. This combination approach enhances the robustness of features, and this is the reason why FMDDCN has balanced precision and recall performance.

Classification Using Softmax

The expanded feature map is then forwarded to the classification layer, which is modeled by a softmax function to approximate the probability of a given class. The likelihood that an input image x is in class k is as indicated:

$$P(class\ k|x) = \frac{e^{W_k^T F_{fused}(x)+b_k}}{\sum_{i=1}^{C} e^{W_i^T F_{fused}(x)+b_i}} \quad (11)$$

In equation (11), Wk and bk are the weights of classes k and the bias of classes, respectively, and C is the total number of disease classes. This formula can be used to classify the diseases of pigeon pea leaves accurately in a probabilistic manner.

Impact on Classification Performance

The combination of differential feature modeling with fusion helps a great deal in increasing the separability between classes. All of the comparative results allow stating that FMDDCN has the best F1-score (0.965), recall (0.985), precision (0.950), and accuracy (0.965) of all the considered classifiers (Table 4). These findings confirm the usefulness of the FMDDCN mathematical model to describe the delicate patterns of diseases and enhance the strength of the model under realistic field conditions.

Discussion

The training and validation loss curves of the SOA-optimized EfficientNet frameworks FMDDCN showed a gradual and steady decrease, which reveals convergence stability and little overfitting. The fact that these curves are almost perfectly fitting is testimony to the usefulness of the preprocessing pipeline, which consists of the Gaussian smoothing, the Canny edge detector, and the Skill Optimization Algorithm (SOA) in the context of the segmentation. This discriminative preprocessing technique facilitated network training of discriminative features, which resulted in the stable training of the model by minimizing the noise in the background and enhancing the disease-influential structures. The model was evaluated through the aid of many performance indicators, including Accuracy, Precision, Recall, F1-score, and Matthews Correlation Coefficient (MCC), which provide a comprehensive view of the performance in terms of classification. The confusion matrix puts these values into perspective by indicating how many cases are actually predicted to be positives or negatives and how many are actually predicted to be false positives or false negatives. The high MCC values with various sets of features and classifiers are indications that the proposed framework is also highly predictive even when the features contain class imbalance, which is a frequent case in agricultural data when healthy leaves are presented in large numbers compared to the diseased leaves.

Comparison of the various feature sets indicated that it is possible to introduce fewer features to enhance performance. It is interesting to note that the highest accuracy of 94.5% and MCC of 88.5% was obtained with four optimized features. This indicates that the SOA-guided segmentation effectively isolates disease-relevant regions, allowing the EfficientNet-B0 backbone to extract the most discriminative deep features, while redundant information in the full dataset may slightly lower performance. These results highlight the role of feature optimization to deploy it efficiently and resource-saving-wise. Further comparative analysis with the traditional machine learning and normal deep learning models further proved the strengths of the FMDDCN classifier. Models like LSTM and CNN were very high recall but had low precision, which implied that they were sensitive to background noise and within-class variance. Conversely, FMDDCN recorded a balanced performance with the highest F1-score of 0.965 and accuracy of 0.965, which indicates its capability to detect subtle patterns of lesions and the lowest false positives.

FMDDCN has been shown to have a better performance because its feature map generation is structured, feature modeling is differentiated, and fusion is multi-layered. On the one hand, convolutional layers produce hierarchical feature maps that capture low and mid-level features, including edges, textures, local disease patterns, and so on. Computation of the difference feature maps is then done to capture spatial and contextual variation between the adjacent maps and to be more sensitive to small lesions and subtle textural alterations that directly lead to the improved recall and MCC. Later, the feature maps of the various layers are combined to produce a fused set that combines local lesion features with global structural features to enhance the ability to separate classes and maintain a balanced precision-recall capability. Lastly, the fused representations go through a softmax classifier, which gives probabilistic results, which allow the proper identification of disease, even in adverse environmental factors, such as changes in illumination and background noise. All these findings illustrate that the offered SOA-optimized EfficientNet-FMDDCN framework is correct and computationally efficient, which means that it can be deployed into the field in real-time. The capability to operate with the system with limited features and high performance can propose a possibility of implementation on resource-limited gadgets, e.g., smartphones or portable agriculture diagnostic devices. Moreover, the modeling of the differential feature and the fusion strategy can be used as a guarantee of the stability to variations in the appearance of the leaves, the severity of the disease, and the environmental noise, which are crucial in the real-world agricultural use.

Although promising results have been demonstrated by the framework, it is now concentrated on pigeon pea leaf diseases in particular field conditions. Future developments might involve such extensions as multi-crop disease detection, multi-spectral imaging, and long-term generalization to new geographical locations. Besides, the model might be more useful in precision agriculture and automated plant health management systems through the inclusion of temporal monitoring of disease progression.

Conclusion

The suggested SOA-optimized EfficientNet-FMDDCN model presents robust and accurate results in the detection of pigeon pea leaf diseases in field conditions. A combination of Skill Optimization Algorithm (SOA)-informed preprocess, EfficientNet-based features extraction, and FMDDCN-structured feature map creation, with either the use of differential modeling and multi-layer fusion, the network can effectively learn subtle disease patterns. The results of the experiments show that there is stable convergence with small overfitting, and the extensive analysis with the help of measures like Accuracy, Precision, Recall, F1-score, and Matthews Correlation Coefficient (MCC) proves the great reliability of the framework. The optimization of features proved to be more effective, and the four optimized features yielding the highest accuracy (94.5%) and MCC (88.5%) demonstrate the necessity to choose the information that is relevant to the disease, but not the redundant information. The comparative results with the traditional machine learning models and deep learning models also confirm the higher ability of FMDDCN to trade off precision and recall, being able to address the variability within the individual classes and background noise. All in all, the suggested framework is computationally efficient and can be deployed in real-time on hardware with limited resources and is resistant to changes in the environment, thereby making it a viable solution to automated management of agricultural diseases. The further development of work can be the expansion of the framework on multi-crop identification, multi-spectral imaging, temporal disease tracking, and expanded geographic generalization, which would make it more useful in precision agriculture and effective crop management.

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Both authors share equal contributions in developing this work.

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The authors declare that they have no conflict of interest.

Compliance with Ethical Standards

The authors declare that the results of study do not involve humans and/or animals rights.

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