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Adaptive deep learning framework for multi-scale plant disease detection

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ABSTRACT

Plant disease detection is a critical task in modern agriculture, directly impacting crop yield, food security, and sustainable farming practices. Traditional methods rely on expert visual inspection, which is time-consuming, inconsistent, and inaccessible in remote areas. This study introduces an advanced deep learning (DL) framework, the adaptive multi-scale convolutional network (AMS-ConvNet), optimized for accurate and efficient plant disease identification. hierarchical feature extraction network (HFEN) integrates the multi-domain attention framework (MDAF) and adaptive scale fusion module (ASFM) to enhance feature extraction and address challenges such as complex natural backgrounds, non-uniform leaf structures, and varying environmental conditions. The proposed framework employs pre-trained knowledge adaptation (PTKA) techniques to improve generalization and overcome data scarcity. Comprehensive evaluations on multiple datasets demonstrate the model's better performance, achieving state-of-the-art metrics in precision, recall, F1-score, and accuracy. Furthermore, this approach ensures scalability and adaptability, making it suitable for real-field conditions. The study emphasizes the importance of robust, automated solutions in minimizing crop losses, reducing labor costs, and enhancing agricultural sustainability through precision disease management.

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1. INTRODUCTION

Finding and diagnosing plant leaf diseases is essential to maintaining crop resilience and production in contemporary horticulture and agriculture [1]. Computer vision and machine learning (ML) are two examples of advanced technologies that provide useful tools for precise illness identification. In recent years, visual symptoms on leaves, stems, and fruits have been analyzed using automated imaging systems and smartphone applications that use image recognition algorithms for quick pattern identification. Improvements in deep learning (DL) and pre-trained knowledge adaptation (PTKA) models have enhanced the capacity to identify illnesses in plant leaves. The study's main focus is on the decline in agricultural production. A plant eventually dies when a disease or other condition prevents its leaves from carrying out photosynthesis, which is necessary for the production of chlorophyll. Visual evaluations of disorders are performed by experts according to recognized standards [2]. When opposed to automated procedures, the identification of the ailment takes more time. Experts could only be available in certain nations. Image analysis-based automated plant disease detection systems must be put in place to solve this problem. A comprehensive evaluation of the condition's severity is necessary for both accurate yield prediction and the selection of the best treatment.

Internal causes of plant illnesses include pathogens, which include molds, viruses, and fungus. On the other hand, environmental elements including precipitation, humidity, and temperature may also contribute to their occurrence. These diseases can have a substantial financial impact on farmers' livelihoods. Crops are seriously threatened by plant diseases, which might result in a food catastrophe. The security and sustainability of human food systems are impacted by this issue. For agricultural disease management and intervention to be effective, plant illnesses must be identified promptly. Plant disease diagnosis requires human skill, but in rural and isolated parts of developing nations, this information has to be improved and standardized. The development of quick and precise techniques for identifying plant diseases is made easier by artificial intelligence technology. Modern image processing and pattern recognition algorithms allow farmers and agricultural experts to spot diseases using a variety of techniques. Plant diseases have been identified using a variety of methods [3]. By using ML and DL techniques to analyze visual data, models may be created to detect plant illnesses. Recent developments in agriculture have concentrated on using different DL techniques to tackle a range of problems. Insect detection, fruit and disease identification, plant leaf categorization, and leaf disease identification are among the difficulties. When using conventional ML techniques for real-time disease diagnosis, a number of challenges need to be overcome. Engineers can thus overcome these obstacles and develop the agriculture industry thanks to DL techniques. It is crucial to gather a range of photos showing various plant sections in order to create a model that can recognize plant illnesses [4], [5]. The leaves of a plant are the main area used to determine whether disease is present. Variations in leaf shape, texture, color, picture noise, and other characteristics might confound image processing techniques, which are useful for recognizing plant illnesses. It is possible to identify the main signs of illness by methodically examining photos of plant leaves. Several ML algorithms have shown to be an effective method for automated plant disease identification in precision agriculture. Plant diseases have been categorized and identified using a variety of ML techniques, such as support vector machines and K-means clustering. Potential problems in the pre-processing and feature extraction phases restrict the efficacy of these techniques in real-time illness diagnosis. Changes to traditional ML techniques are required due to the intricacy and unpredictability of real-world detecting situations. A variety of illnesses may affect crops, and each one has its own characteristics. There are several obstacles in the way of creating a reliable system that can detect different types of illnesses in a variety of crop species. It is crucial to personally check large agricultural fields for signs of illness on a regular basis [6].

Citrus, rice, cassava, PlantVillage, iBean, and AI Challenger 2018 are the most well-known plant disease datasets that contain laboratory images. The datasets were used to train the convolutional neural network (CNN), which made it easier to identify and categorize plant illnesses. The neural networks used on these datasets demonstrated a notable degree of classification accuracy throughout the training stage. However, when tested in real-world scenarios, these gadgets' efficacy dramatically declined. Unlike laboratory photography, field photography has more intricate background components, including extra leaves, stems, fruits, soil, and mulch. The main cause of declining performance in outdoor photography, according to research, is complicated backdrops. Excluding these backdrops has been shown to improve the accuracy of sickness detection [7]. The are 759 photos of both healthy and sick citrus fruits and foliage make up the citrus dataset. The information includes diseases, including melanose, canker, scab, greening, and black spot that impact citrus plants. using the help of an expert, the photographs in the dataset were manually taken using a DSLR.

According to recent research, the new DL approach outperforms conventional hand-engineered feature approaches when data volume exceeds a certain threshold. The use of CNN techniques might make it easier to exclude important sources that significantly affect the major elements shown in pictures. In order to properly diagnose a variety of plant diseases, recent research has focused on developments in deep learning, image fusion techniques, encoder-decoder network designs, and computer vision approaches [8]. Detection techniques based on vision improve precision and dependability in agricultural applications. It is anticipated that the application of these techniques will improve crop quality, reduce labor expenses, and eliminate time inefficiencies. The application of suitable management techniques improves the efficacy of disease control, especially when guided by prior experiences in an infected setting. Plant disease identification by image analysis is a multi-step procedure with a number of obstacles to overcome. These problems include illnesses with similar symptoms, the possibility of many diseases affecting the same crop, and symptoms with different visual features [9]. Picture processing methods including feature engineering, preprocessing, classification, and picture segmentation have been used in recent breakthroughs in the diagnosis of plant diseases. Picture fusion algorithms have been investigated by researchers as a potential disease diagnosis technique. Furthermore, sophisticated CNN-based DL techniques were widely used by researchers to identify plant illnesses [10]. The study team focused on improving the group's categorization accuracy, which produced favorable results. On the other hand, it will classify the different illnesses that affect a single leaf or several types.

The motivation for this research lies in addressing the pressing challenges of plant disease detection, which is critical for ensuring crop resilience, productivity, and food security in modern agriculture. Traditional diagnostic methods are constrained by limitations such as time-intensive processes, dependency on expert availability, and inconsistent outcomes, particularly in remote or resource-limited regions. These limitations underscore the need for advanced, automated, and scalable solutions. Leveraging cutting-edge developments in DL and computer vision, this research aims to overcome challenges such as non-uniform leaf structures, complex natural backgrounds, and varying environmental conditions, which often impede real-world applicability of disease detection systems. This study focuses on the development of a robust and optimized DL framework that bridges the gap between laboratory-grade accuracy and field-level deployment, facilitating precise, real-time plant disease identification and classification. By addressing these challenges, this work contributes significantly to the advancement of precision agriculture, enabling proactive disease management and sustainable crop production.

- Development of an enhanced DL framework: The study introduces a robust adaptive multi-scale convolutional network (AMS-ConvNet) integrated with advanced attention mechanisms such as the multi-domain attention framework (MDAF) and the adaptive scale fusion module (ASFM). These innovations significantly improve feature extraction, focusing on diverse scales of lesion characteristics and addressing challenges posed by complex natural backgrounds in plant disease detection.
- Integration of advanced image processing techniques: The proposed method incorporates augmented convolutional block attention modules and depthwise separable convolutions, optimizing computational efficiency while maintaining high accuracy. These modifications effectively enhance disease classification performance, especially in real-field conditions where existing approaches often fail due to environmental complexities.
- Extensive evaluation and adaptation for practical deployment: The proposed framework is thoroughly validated on multiple datasets, showcasing significant improvements in precision, recall, F1-score, and overall accuracy compared to state-of-the-art models. Furthermore, the method is designed with scalability and robustness, ensuring its adaptability to real-field conditions, thereby advancing the practical implementation of automated plant disease detection systems in precision agriculture.

The research work is organized in 4 sections: the first section gives a brief description of the overview and background of plant disease detection and classification. The second section gives a brief description of the related work, the third section discusses the proposed methodology. The fourth section discusses the performance evaluation where the results are displayed in the form of graph and tables.

2. RELATED WORK

There has been plenty of related work developed in the past for individual leaf disease detection using the DL and some of them included multiple plants; considering our research some of them are discussed. The DAC-PPYOLOE model was created by [11] to increase the accuracy of apple pest diagnosis under difficult circumstances. This model recognizes small objects using both shallow and deep feature maps using an adaptive feature fusion method that combines deep separable convolution and residual connectivity. [12] presented the enhanced SE-YOLOv5 network for tomato disease and pest detection. The SE attention mechanism overcomes the limitations of existing feature screening and model generalization methods by enhancing critical feature extraction. In [13] developed an enhanced R-CNN model employing federated learning (FL) to solve issues with data imbalance, variety, and complex detection settings in traditional plant disease and pest detection. This paradigm reduces communication and data storage expenses by leveraging FL's distributed computing characteristics. Additionally, ResNet-101 enhances multiscale detection accuracy for a range of diseases and pests by substituting VGG-16 in the convolutional layer. To increase the detection accuracy of maize diseases, in [14] proposed a technique for corn leaf disease diagnosis utilizing fuzzy C-means (FCM) and long short-term memory (LSTM) algorithms. The gray-level co-occurrence matrix was used to extract texture information from illness pictures. The LSTM algorithm was then used to classify these texture properties. The accuracy rating obtained by using this strategy was 80.24%. In [15] created an edge feature guidance (EFG) module to enhance the model's ability to extract local edge features in order to get over the challenges presented by complex plant disease characteristics and sparse datasets. The overall performance of the model may be improved by including multiscale features and edge information by integrating the EFG module into vision transformers like ViT and Swin.[16]

The diagnosis of plant diseases has been transformed by recent advances in deep learning, which have also introduced new methods for a variety of crops, including maize, potatoes, tomatoes, sugarcane, and groundnuts. According to research, AI-powered models can effectively address significant agricultural issues including the prompt and precise identification of diseases. A thorough assessment of more than 160 studies on deep learning-based plant disease detection highlighted the need of diverse, high-quality datasets in developing reliable models that can detect diseases early. With this method, farmers and agricultural experts may employ quick and efficient management strategies. Real-time disease detection systems based on mobile devices have emerged as promising alternatives, particularly for maize. A study [17] demonstrated how to integrate object recognition and transfer learning methods to develop a system that effectively detects diseases in maize leaves. These instruments enhance disease management and expedite field decision-making by providing farmers with instant feedback. The combination of artificial intelligence and the internet of things (IoT) has significantly altered large-scale agricultural surveillance. Drones equipped with advanced imaging technology and artificial intelligence might swiftly and precisely identify diseases over vast agricultural areas, optimizing resource utilization and reducing crop losses.

Sugarcane illnesses are being managed with the use of advanced AI technology. Researchers in [18] described a technique that employs multispectral satellite imagery and artificial intelligence to detect Ratoon Stunting Disease in sugarcane. This satellite-based method facilitates the early detection of disease hotspots on big plantations by permitting targeted treatments and stopping the spread of diseases. Furthermore, advancements in AI frameworks are making it simpler to identify diseases in crops like potatoes and tomatoes. Researchers are employing ML and DL models to detect agricultural illnesses in order to solve significant issues such as varying climatic conditions and diverse disease presentations. The combination of cutting-edge AI technology with practical applications highlights the potential of these tools to transform modern agriculture. As AI-powered systems advance, they might enhance food security, disease prevention, and crop monitoring, facilitating the widespread adoption of more resilient and sustainable agricultural practices. In [19], [20] proposes a novel lightweight deep CNN model to learn high-level hidden feature representations. Local texture information is extracted from plant leaf images using deep features and conventionally constructed local binary pattern (LBP) features. Three openly accessible datasets, apple leaf, tomato leaf, and grape leaf, are used to train and assess the proposed model. The proposed technique achieves validation accuracies of 99%, 96.6%, and 98.5% and test accuracies of 98.8%, 96.5%, and 98.3% across the three datasets. Pajany *et al*. [21] proposed a model ensemble method for accurately identifying and classifying plant diseases based on field pictures. The segment anything model allows for the recognition and delineation of any discernible item inside an image. The highlighted components are then extracted from the original image using image processing techniques. The fully convolutional data description is an explainable deep one-class classification model for anomaly detection. It aids in differentiating between background objects and actual leaf things. Finally, a categorization model created by Plantvillage is used to infer conclusions from the selected leaves. Taji *et al.* [22] recommend utilizing UAV-based remote sensing data in combination with optimal fuzzy deep neural networks (OFDNN-PDDC) to identify and categorize plant illnesses. The OFDNN-PDDC method may be used to efficiently identify and classify a range of plant diseases.

The hybrid framework employed in this study is based on a hybrid preprocessing technique that incorporates an ensemble features engineering phase that focuses on texture features together with two distinct forms of deep feature extraction [23]. The LBP characteristics are integrated with the CNN qualities. Three distinct meta-heuristic algorithms the binary dragonfly algorithm (BDA), the ant colony optimization technique, and the moth flame optimization method (MFO) are used to optimize the ensemble feature vector. Modern ML methods are used to classify the enhanced feature vector.

3. PROPOSED METHODOLOGY

AMS-ConvNet enhances the superior feature extraction capabilities and reduced training requirements. It performs better than the bulk of traditional CNN models as well as a few of transformer models. The AMS-ConvNet is made up of a feature extraction layer at the head, a feature classification layer at the end, and four stacked AMS-ConvNet blocks of varying sizes in the center. The intra-layer architecture and stacking technique of AMS-ConvNet are different from those of the general architecture. Among the modifications are the following: In each of the four stages, three, four, six, and three blocks are stacked, resulting in a ratio of around 1:1:2:1. AMS-ConvNet employs a block stacking ratio of 1:1:3:1 and modifies the stacking to 3, 3, 9, and 3, drawing inspiration from the transformer idea.

AMS-ConvNet performs the Patchify process in parallel, substituting a 4 x 4 convolutional kernel size and a stride of 4 for the Stem. Dimensionality expansion follows dimensionality reduction in the bottleneck design of CNN, and feature extraction follows. Using an inverted bottleneck, AMS-ConvNet performs feature extraction first, followed by dimensionality reduction and dimensionality increase. A depth-separable convolution is also employed, which is comparable to the Transformer's Self-attention and the the activation function is employed infrequently. In the normalizing layer, layer normalization has taken the role of batch normalization, and the frequency of normalization applications has decreased. AMS-ConvNet incorporates a downsampling layer with layer normalization and a convolution operation with a kernel size of

2 and a stride of 2 at the same time. AMS-ConvNet employs a 7x7 convolution kernel rather than the 3x3 convolution kernel.

3.1. Architecture

The background of the plant disease dataset is complex, and characteristics like tiny, dispersed disease spot patches make disease classification more challenging. To address this, this study suggests a high-performance plant disease classification network that makes use of an improved AMS-ConvNet architecture. The augmented convolutional block attention module is first included after the second 1×1 convolution of the AMS-ConvNet Block and at the conclusion of each Stage in order to improve the network's emphasis on diseased spot information and lessen the influence of unrelated elements. Second, to improve the network's capacity to extract feature information related to illnesses of varied sizes. In the end, the AMS-ConvNet Block model's repetition count is decreased in order to lower the model's complexity. Figure 1 shows the AMS-ConvNet and Figure 2 shows the proposed model.

3.2. MDAF

MDAF is an attention module consisting of spatial and channel mechanisms. The attention is levied on channel information within the position target information, this is embedded within the CNNs with added computation. The channel attention module performs information combination through average max pooling operations, then forwards it to a shared network, which creates a channel attention map by combining the input feature maps and compressing their spatial dimensions, however like this the channel attention model is evaluated.

$$O_e(H) = \vartheta\left(MLP\big(AvgPool(H)\big) + MLP\big(MaxPool(H)\big)\right)$$
$$\vartheta(Y_1\left(Y_o\big(H^e_{avg}\big)\right) + Y_1\big(Y_o(H^e_{max})\big) \quad (1)$$

In (1) H denotes the input feature map, ϑ denotes the activation function, MLP depicts multilayer perceptron, $AvgPool$ is the average pooling operation, $MaxPool$ is the maximum pooling operation, $\frac{Y_0 \epsilon TE}{t} * E, \frac{Y_1 \epsilon TE}{t} * E$. H^e_{avg} and H^e_{max} upon compression of spatial feature map by global max pool and global average pool. The spatial attention module considers the importance of pixels at different locations in the same channel, compresses the channel, and performs average pooling and maximum pooling in the channel dimension to concentrate the information at the spatial locations of important features. The spatial attention module is calculated as follows.

$$O_e(H) = \vartheta(h^{7*7}([AvgPool(H), MaxPool(H)]))$$
$$\vartheta(h^{7*7}\big(\big[H^u_{avg}, H^u_{max}\big]\big)) \quad (2)$$

Here in (2) O_e denotes the feature map, as a result of the spatial attention module, H is the input feature map, ϑ is the sigmoid function, h^{7*7} depicts the convolution operation and the convolutional kernel of size 7, $AvgPool$ depicts the pooling operation and $max\ pool$ depicts the maximum pooling operation. The MDAF channel attention module and the spatial attention module are serially connected. Channel attention is carried out prior to the application of spatial attention. The latter's input comes from the previously altered features, which will affect how spatial features are learned and might cause the attention module to function erratically. Multilayer perceptrons (MLPs) are used in tandem to reduce the dimensionality of channel attention, which results in a loss of features and an increase in the number of parameters. By switching from a serial connection to a parallel connection, this study addresses the difficulties found and enhances MDAF. This ensures that channel attention and spatial attention inputs come from the same source, continue to be non-interfering, and provide better feature weight information. To increase the model's cross-channel interaction capabilities, simplify the algorithm, improve information sharing across channels, and reduce feature degradation, a one-dimensional convolution operation simultaneously serves as the perceptron layer.

The feature extraction procedure successfully resolves the interference problems brought on by the network's intricate natural environment by allowing the network to concentrate on lesion characteristics via the attention mechanism. An improved MDAF attention module that is included into the AMS-ConvNet model is shown in this work. Focusing on the extraction of visual data, allocating weights between sick patches and background information optimally, and enhancing adaptation to a variety of contexts are all crucial for improving network identification accuracy. The number of model parameters stays roughly constant.

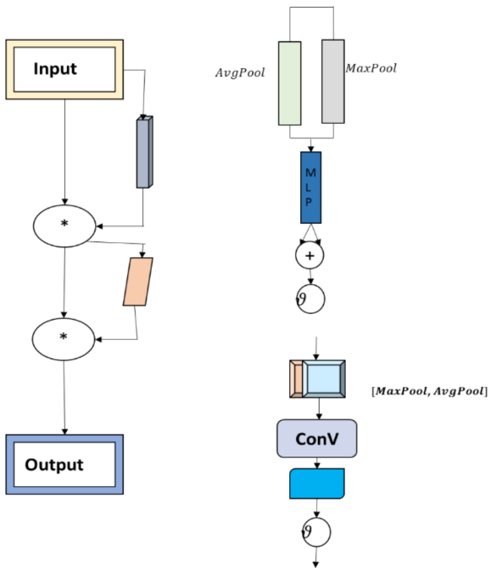

Figure 1. AMS-ConvNet

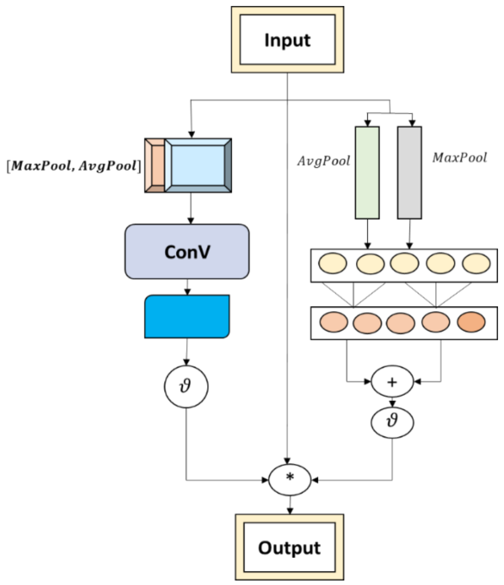

Figure 2. Proposed model

3.3. ASFM

This module increases the network width upon replacing the sparse and dense structures that enhances network performance by voiding computational time. the input further extracts various features through various sizes of convolutional kernels in the adjacent branches, the four branches are then spliced in channel dimension and is further fused with the feature matrix is given as output. The model's size may be decreased and the computational complexity decreased via depthwise separable convolution, which includes depthwise and point-wise convolution. Assume that the input feature matrix's width and height correspond to the convolution kernel's size, that the input feature matrix's number of channels is O, and that the output matrix's number of channels is P.

$$F_M * F_M * O * P * F_H * F_H \tag{3}$$

$$F_M * F_M * O * F_H * F_H + O * P * F_H * F_H \tag{4}$$

$$(F_M * F_M * O * P * F_H * F_H)/(F_M * F_M * O * F_H * F_H + O * P * F_H * F_H) = \frac{1}{P} + \frac{1}{F_M * F_M} = \frac{1}{P} + \frac{1}{9} \tag{5}$$

In (3) denotes the amount of convolutional computation, in (4) is a seperable convolution computation. in the (5) represents separate convolution that saves more parameters in comparison with the conventional convolutional computation. The ASFM structure implemented in this study is founded on depthwise separable convolution and the Inception architecture. Initially, the 1 × 1 and 3 × 3 ordinary convolutions in Inception are substituted with a 3 × 3 depthwise convolution and a 1 × 1 point-wise convolution. Subsequently, a 5 × 5 convolution is replaced by two 3 × 3 convolutions. Lastly, multiple small-kernel convolution operations can introduce increased nonlinearities while maintaining the same receptive field with reduced computational requirements. The model encounters challenges in extracting lesion characteristics within a complex natural environment, which affects recognition accuracy. Enhancing the process is challenging; however, it is equally difficult to improve the extraction of disease information using only a single convolutional kernel size is utilized due to the variability in size and shape of the disease spots. This study represents a ASFM module designed to extract deeper characteristics of illness pictures. The performance of the AMS-ConvNet network can be improved through the integration of the ASFM module, which facilitates the extraction of diverse scales of illness spot information. Figure 3 shows the HFAM model.

3.4. PTKA

The model is vulnerable to issues like overfitting and poor generalization ability in the field of disease recognition since it is challenging to gather further citrus disease leaf data. A technique for moving pre-training weights from the source domain to the target domain is called PTKA, and it can help with small sample issues and enhance network performance. Usually, a sizable dataset is utilized as the source domain to first train the model. A data collection that you wish to apply to a limited number of samples is known as the target domain. ImageNet is the biggest image recognition database and is frequently used for picture categorization, detection, and placement. To pre-train the model in this study, the ImageNet data set was used as the source domain. Then, among freezing and fine-tuning techniques, the PTKA approach appropriate for diagnosing plant disease dataset was used. Freezing is the process of setting the weights in the source domain's network model, freezing all of the network's convolutional layers, and only modifying the fully connected ones. Fine-tuning is the process of keeping some of the network's convolutional and fully connected layers for additional training and fine-tuning while freezing some of the network's convolutional layers. Figure 4 shows the PTKA mechanism.

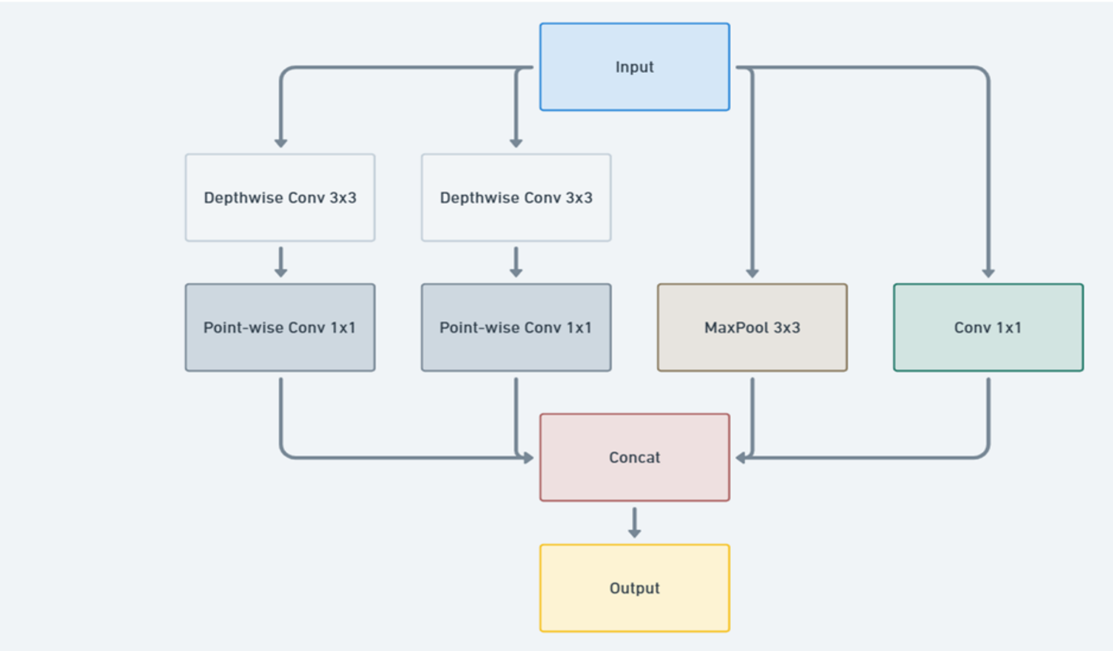

Figure. 3 HFAM model

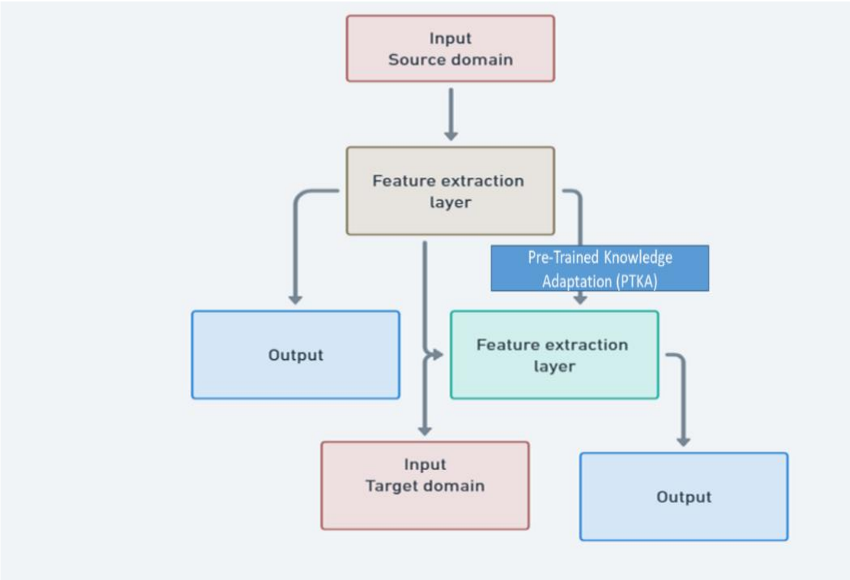

Figure 4. PTKA mechanism

4. RESULTS AND DISCUSSION

The performance evaluation reveals that models achieve varying levels of effectiveness across different datasets, with metrics such as precision, recall, F1-score, and accuracy reflecting the complexity of the tasks. Datasets like sugarcane leaf disease show relatively lower performance, indicating challenges in accurate detection, while better results are observed for Corn, Potato, and Groundnut datasets. Advanced architectures like MobileNetV2 and EfficientNetB5 demonstrate strong performance, showcasing the benefits of modern designs.

4.1. Dataset details

- Groundnut dataset [23]: The dataset used for this research includes digital images of groundnut leaves captured under varying weather conditions and diverse lighting environments in the Koppal area of Karnataka, India. It consists of a total of 10,361 images, which have been divided into separate training and test sets. The test dataset, on the other hand, consists of 2,451 photos, with each class including, depending on the category, 409 or 405 images.
- Sugarcane leaf disease dataset [24]: the sugarcane leaf disease dataset comprises 2,567 images distributed across five distinct classes: Healthy, Mosaic, Red Rot, Rust, and Yellow. This dataset is designed to capture a wide variety of visual features associated with these conditions, offering a comprehensive resource for the development of ML models for disease classification. The inclusion of diverse disease types ensures robust training and testing capabilities for algorithms targeting sugarcane leaf health.
- Corn (or maize) leaf disease dataset [25]: the corn (or maize) leaf disease dataset contains 4,188 images categorized into four groups: Common Rust, Gray Leaf Spot, Blight, and Healthy. This dataset provides a rich and diverse set of visual patterns for disease and healthy leaf identification. It plays a critical role in advancing precision agriculture, enabling the development of accurate and efficient models for early disease detection and effective crop management in maize farming.
- Potato leaf disease dataset [26]: the potato leaf disease dataset consists of 4,062 images classified into three categories: early blight, late blight, and healthy. It serves as a vital tool for studying the visual distinctions between different types of blights and healthy potato leaves. This dataset is instrumental in facilitating the development of automated disease detection systems, helping to reduce crop loss and improve productivity in potato cultivation.

4.2. Metrics comparison

4.2.1. Precision

Precision measures the proportion of correctly identified positive instances among all instances predicted as positive by the model. It focuses on the accuracy of positive predictions and is particularly important in scenarios where false positives carry significant consequences. For example, in spam detection, a high precision means the model effectively avoids labeling legitimate emails as spam. Precision provides insight into the reliability of the model's positive predictions, indicating how well the model discriminates between relevant and irrelevant positive classifications.

4.2.2. Recall

Recall, also known as sensitivity or the true positive rate, evaluates the model’s ability to correctly identify all actual positive instances in the dataset. It measures how well the model captures positive cases and is crucial in applications where missing a positive instance can have severe consequences, such as in medical diagnoses or fraud detection. A high recall indicates the model successfully identifies most of the true positives, ensuring that critical cases are not overlooked, even if it includes some irrelevant positives.

4.2.3. F1-Score

F1-score is the harmonic mean of precision and recall, providing a balanced evaluation of a model's performance when dealing with imbalanced datasets. It is particularly useful when both false positives and false negatives carry significant consequences, and a balance between precision and recall is needed. A high F1-score indicates that the model maintains a good trade-off, capturing most positive cases while minimizing incorrect predictions. This metric is ideal for applications like medical diagnoses or spam detection, where both types of errors must be carefully managed.

4.2.4. Accuracy

Accuracy is the proportion of correctly predicted instances (both positive and negative) out of the total instances in the dataset. It is a straightforward and widely used metric that measures the overall effectiveness of a model. However, it can be misleading in imbalanced datasets where one class significantly outweighs the other. For example, in a dataset with 95% negatives, a model predicting all negatives achieves

95% accuracy but fails to identify positives. Thus, while accuracy is a helpful metric for balanced datasets, it is often supplemented by other metrics like precision, recall, and F1-score to provide a more comprehensive evaluation of model performance.

4.3. Groundnut dataset results

Table 1 and Figure 5 illustrate the precision rates (%) of various models in a comparative analysis. It shows that traditional models like VGG16 exhibit relatively lower precision (85.863%), while advanced architectures like DenseNet161, EfficientNetB5, and MobileNetV2 demonstrate improved performance, with MobileNetV2 achieving 93.852%. EfficientNetB5 shows slightly less precision (93.155%) than MobileNetV2. Remarkably, the custom or experimental models labeled ES and PS achieve significant precision improvements, with ES reaching 97.365% and PS achieving the highest precision at 98.34%. This analysis suggests that while modern DL architectures enhance performance, custom models like PS and ES outperform standard pre-trained models, indicating potential optimizations tailored to the specific dataset or task.

Table 1. Metric comparison on groundnut dataset

Model	Precision (%)	Recall (%)	F1-Score (%)	Accuracy (%)
DenseNet161	92.145	91.84	91.83	91.84
EfficientNet	93.155	94.084	94.064	94.084
VGG16	85.863	85.597	85.422	85.597
MobileNetV2	93.852	93.798	95.588	93.798
InceptionResNetV2	88.471	88.29	88.255	88.29
ES	97.365	97.756	97.225	97.225
PS	98.34	98.76	98.98	98.43

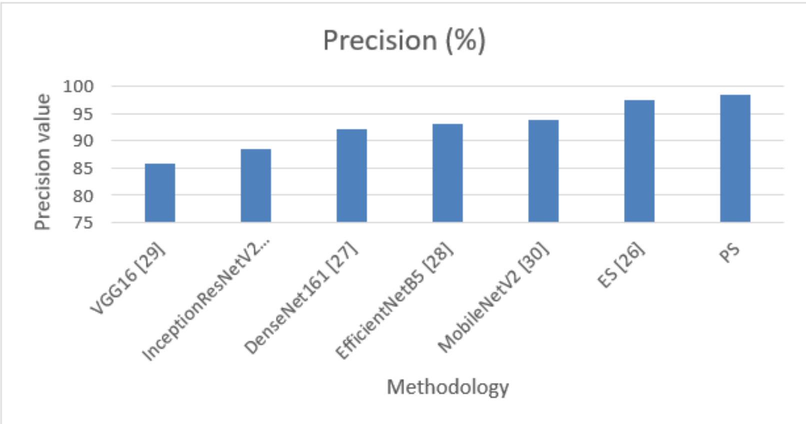

Figure 5. Precision metric comparison on groundnut dataset

Figure 6 presents the recall (%) performance of various DL models. Among the listed models, VGG16 demonstrates the lowest recall at 85.597%, while newer architectures like InceptionResNetV2 (88.29%) and DenseNet161 (91.84%) show incremental improvements. MobileNetV2 and EfficientNetB5 achieve notable recall values of 93.798% and 94.084%, respectively, indicating their effectiveness in identifying true positives. The custom models ES and PS significantly outperform the standard architectures, with ES achieving an impressive 97.756% recall and PS attaining the highest recall of 98.76%. This analysis highlights the evolution of model performance and underscores the superior recall achieved by the specialized models, suggesting their adaptation to specific dataset characteristics or task requirements.

Figure 7 showcases the F1-score performance of various DL models. The F1-score, which balances precision and recall, indicates that VGG16 has the lowest performance at 85.422%. Improvements are observed with InceptionResNetV2 (88.255%) and DenseNet161 (91.83%), while EfficientNetB5 and MobileNetV2 demonstrate strong performance at 94.064% and 95.588%, respectively. However, the custom models ES and PS significantly outperform these standard architectures, with ES achieving 97.225% and PS reaching an exceptional 98.98%. This analysis underscores the superior balance achieved by the custom models, especially PS, suggesting their enhanced optimization and suitability for the specific dataset or task compared to the traditional architectures.

Figure 8 summarizes the accuracy (%) of different DL models. VGG16 exhibits the lowest accuracy at 85.597%, indicating room for improvement in its performance. InceptionResNetV2 and DenseNet161 demonstrate better results, with accuracy values of 88.29% and 91.84%, respectively. MobileNetV2 and EfficientNetB5 show even greater accuracy at 93.798% and 94.084%, showcasing the impact of advancements in architecture design. The custom model PS significantly surpasses all other models, achieving an exceptional accuracy of 98.43%, highlighting its superior adaptability and optimization for the specific dataset or task. This analysis underscores the evolutionary performance improvements, with PS emerging as the most effective model.

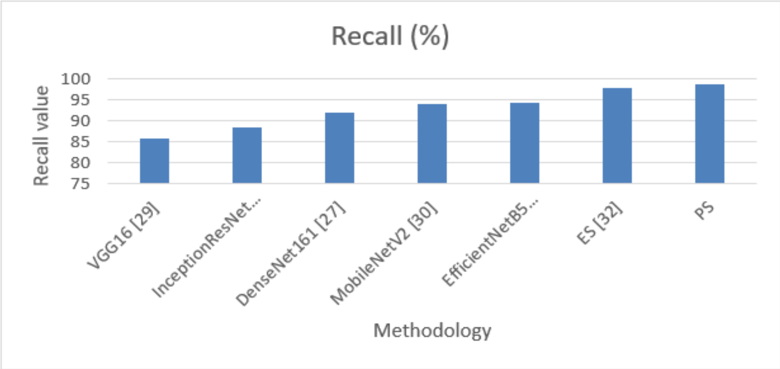

Figure 6. Recall metric comparison on groundnut dataset

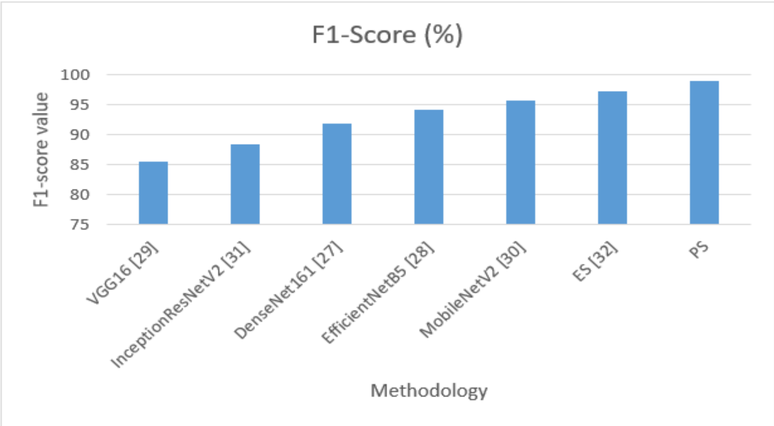

Figure 7. F1-score metric comparison on groundnut dataset

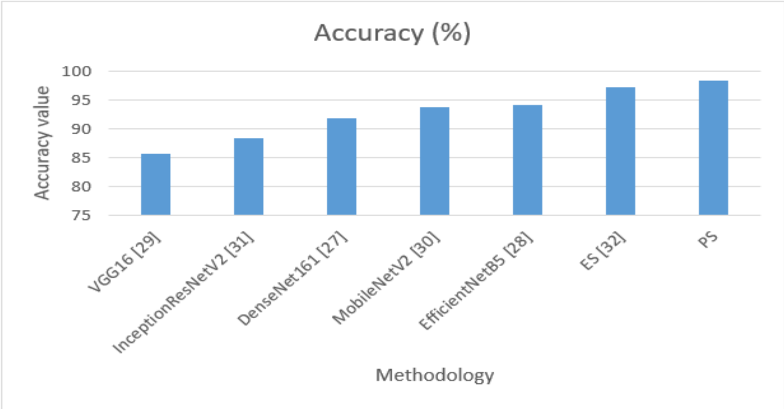

Figure 8. Accuracy metric comparison on groundnut dataset

4.4. Dataset comparison

Specifically, the precision for sugarcane leaf disease [PS] is 84.76%, an improvement over sugarcane [ES] at 83.127%. Similarly, recall improves from 82.669% for sugarcane [ES] to 84.54% for sugarcane leaf disease [PS], indicating better detection of relevant instances. The F1-Score, a harmonic mean of precision and recall, shows a notable increase from 82.61% to 84.65%, highlighting a better balance between precision and recall in sugarcane leaf disease [PS]. Finally, accuracy improves marginally from 82.669% to 83.87%, reflecting the overall enhancement in correctly classified samples. Table 2 and Figure 9 show the sugarcane dataset comparison.

Table 2. Sugarcane dataset

Dataset	Precision (%)	Recall (%)	F1-Score (%)	Accuracy (%)
Sugarcane leaf disease [ES] [24]	83.127	82.669	82.61	82.669
Sugarcane leaf disease [PS]	84.76	84.54	84.65	83.87

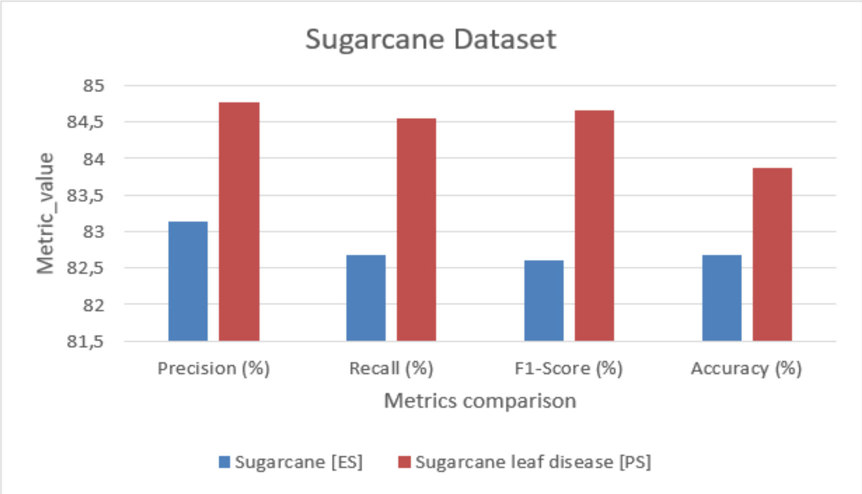

Figure 9. Metric comparison on sugarcane dataset

The comparison of metrics for corn or maize leaf dataset across two scenarios reveals a clear improvement in the second case (PS). Precision increased from 89.204% to 91.87%, indicating better identification of true positives among predicted positives. Similarly, recall rose from 89.354% to 90.57%, showcasing the model's enhanced ability to detect actual positive cases. The F1-Score, which balances precision and recall, improved significantly from 89.262% to 91.65%, reflecting a more robust performance in handling both false positives and false negatives. Furthermore, accuracy climbed from 89.354% to 91.86%, signifying an overall increase in correct predictions. Table 3 and Figure 10 shows the corn or maize leaf dataset comparison.

Table 3. Corn or maize leaf dataset comparison

Dataset	Precision (%)	Recall (%)	F1-Score (%)	Accuracy (%)
Corn or maize leaf disease [ES] [25]	89.204	89.354	89.262	89.354
Corn or maize leaf disease [PS]	91.87	90.57	91.65	91.86

The analysis of potato leaf disease performance metrics between the two scenarios shows significant improvements in the PS. Precision increased from 94.68% to 95.31%**,** reflecting a higher accuracy in predicting true positives among the predicted cases. Recall showed a more substantial rise from 94.567% to 96.12%**,** demonstrating an enhanced ability to identify all true positive instances. This improvement in both precision and recall is further validated by the increase in the F1-Score from 94.584% to 95.54%, indicating a better balance between precision and recall in the second scenario. Additionally, the accuracy improved from 94.567% to 95.86%, highlighting the model's overall enhanced ability to make correct predictions. Table 4 and Figure 11 shows the potato leaf comparison.

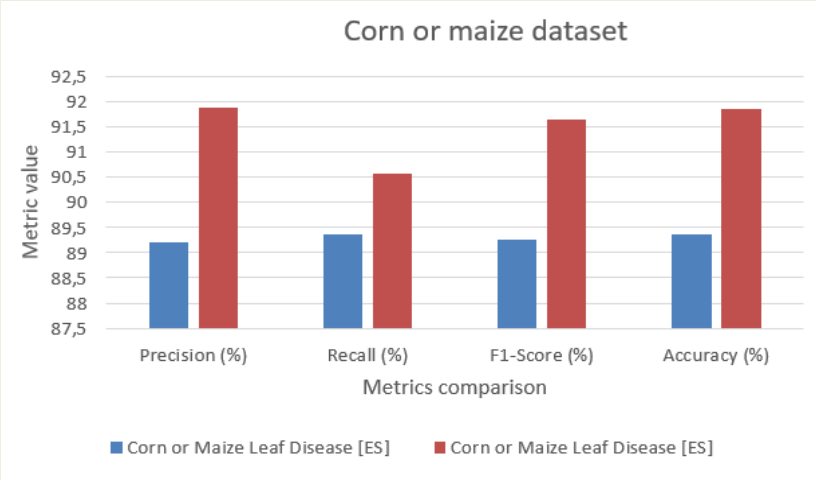

Figure 10. Metric comparison on corn or maize dataset

Table 4. Potato leaf disease comparison

Dataset	Precision (%)	Recall (%)	F1-Score (%)	Accuracy (%)
Potato leaf disease [ES] [26]	94.68	94.567	94.584	94.567
Potato leaf disease [PS]	95.31	96.12	95.54	95.86

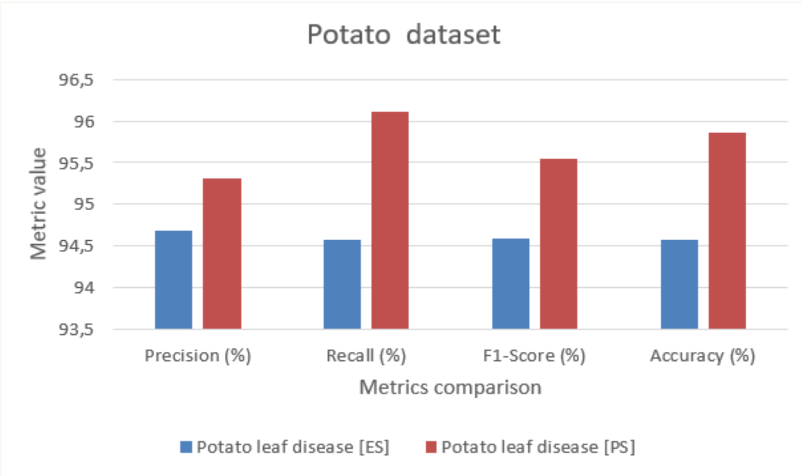

Figure 11. Metrics comparison on potato leaf disease

5. CONCLUSION

This study addresses the critical challenges in plant disease detection by proposing a novel DL framework, the AMS-ConvNet. By incorporating advanced modules such as the MDAF and ASFM, the proposed framework demonstrates enhanced capability in extracting disease-specific features, even in complex real-world conditions. The integration of PTKA further improves the model's generalization, enabling effective utilization of limited dataset sizes and adapting to diverse crop diseases. Comprehensive evaluations across multiple datasets validate the framework's superiority, achieving state-of-the-art metrics in precision, recall, F1-score, and accuracy. These results underscore the model’s potential to bridge the gap between laboratory-grade performance and real-field applicability. This study not only contributes to precision agriculture by offering a robust and scalable solution but also highlights the role of advanced AI techniques in ensuring food security and sustainable farming practices. Future work will focus on further optimizing the framework to handle a broader range of crops and environmental conditions, fostering greater adoption of automated plant disease detection systems in diverse agricultural settings.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST

Author declares no conflict of interest.

DATA AVAILABILTY

Dataset is utilized in this research mentioned in reference [23]-[26].

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