



Article Image-Based Leaf Disease Recognition Using Transfer Deep Learning with a Novel Versatile Optimization Module

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Abstract: Due to the projected increase in food production by 70% in 2050, crops should be additionally protected from diseases and pests to ensure a sufficient food supply. Transfer deep learning approaches provide a more efficient solution than traditional methods, which are labor-intensive and struggle to effectively monitor large areas, leading to delayed disease detection. This study proposed a versatile module based on the Inception module, Mish activation function, and Batch normalization (IncMB) as a part of deep neural networks. A convolutional neural network (CNN) with transfer learning was used as the base for evaluated approaches for tomato disease detection: (1) CNNs, (2) CNNs with a support vector machine (SVM), and (3) CNNs with the proposed IncMB module. In the experiment, the public dataset PlantVillage was used, containing images of six different tomato leaf diseases. The best results were achieved by the pre-trained InceptionV3 network, which contains an IncMB module with an accuracy of 97.78%. In three out of four cases, the highest accuracy was achieved by networks containing the proposed IncMB module in comparison to evaluated CNNs. The proposed IncMB module represented an improvement in the early detection of plant diseases, providing a basis for timely leaf disease detection.

Keywords: convolutional neural network; leaf disease classification; Mish activation function; optimization; PlantVillage dataset

1. Introduction

The growing trend of human population is a new challenge in food production, which should increase by 70% to feed the world's population in 2050 [1,2]. With the growing use of data classification, deep machine learning, and precision agriculture, we are confronted with the challenge of diagnosing diseases faster to prevent their progression and epidemic. It is necessary to eliminate the possibility of complications that arise over time by providing timely treatment for plant diseases [3]. Therefore, it is imperative to construct models that provide objective assistance to experts in decision-making and expedite the process of disease identification, such as neural networks that simulate biological organization [4]. Given the limitations of human oversight in continuously monitoring vast agricultural fields, advancements in transfer deep machine learning and remote sensing technologies are enabling the earlier and more precise terrestrial and visual detection of plant diseases [5–7]. As one of the essential food staples in the world, the global annual production value of tomatoes exceeds USD 90 billion [8]. With the global impact of climate change on overall agricultural production, causing pest and insecticide resistance, target tomato yields are at risk [9]. The climate change crop impact model forecasts a significant rise in the potential for two-spotted spider mite outbreaks across nine countries in Europe, Africa, and Asia [9]. As a result of international trade, the main concern is the competition of invasive species with native organisms as well as the spread of resistance genotypes [10]. According to



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Copyright: © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). Guedes et al. [11], the tomato pinworm *Tuta absoluta*, the well-known tomato pest, has developed resistance to close to a hundred active chemical ingredients [11,12]. Moreover, the tomato yellow leaf curl virus has recently been reported as seed-transmissible, with a potential risk of causing economic losses and decreasing agricultural production [13]. Inadequate use of pesticides can cause long-term resistance to pathogens and damage the plant's defense mechanism [14], but could be prevented by early detection, which allows targeted application of pesticides or fungicides only to infected areas or specific crops exhibiting symptoms. It could also minimize unnecessary usage of chemicals, reduce costs, and protect healthy plants from potential harm caused by broad-spectrum pesticides [15]. For diseases without visible symptoms of infection or symptoms that are noticed too late, the present treatment options cannot prevent damage to crop yield quality [16,17].

Deep learning algorithms have provided accurate and computationally efficient solutions for the early detection of plant diseases so far. They outperform existing traditional methods for diagnosing plant diseases that rely on human expertise, leading to potential delays in treatment [3]. Moreover, traditional monitoring methods are labor-intensive and cannot cover large areas effectively, allowing diseases to spread before detection [5]. The development and use of state-of-the-art transfer deep learning methods in the last decade have exponentially increased compared to classic machine learning methods [18]. This statement is also confirmed by the distribution of scientific papers indexed in the Web of Science Core Collection based on the application of deep machine learning in the detection of plant diseases since 2015 (Figure 1). In the second half of the previous decade, the number of published papers in which deep learning methods were used for recognizing plant leaf disease increased. Nevertheless, the research gap still exists regarding the optimization of presently known deep learning methods [19].



Figure 1. Distribution of papers indexed in the Web of Science Core Collection with the application of machine learning in the recognition of plant diseases from 2015 to 2022.

The proposed method for tomato disease detection was based on the color and structure of the leaf, since most often the first symptoms of the disease appear on the tomato leaves. To improve the present transfer deep learning models, the goal of this study was to develop a module based on the Inception module, Mish activation function, and Batch normalization (IncMB), which represents a versatile module that can be embedded in deep neural networks to optimize CNNs while achieving higher accuracy. In the comparison of pre-trained CNNs, CNNs with SVM, and CNNs with the IncMB module, the hypothesis is that the approach of the deep network with the IncMB module is the most accurate for the detection of tomato leaf disease.

2. Related Works

While significant progress has been made in automated tomato plant disease recognition using deep learning techniques, the scalability and robustness of these models in real-world agricultural settings remain areas of active research and development. Previous research had moderate success in optimizing deep learning methods for the detection of plant leaf diseases.

Albattah et al. [20] presented a new approach using deep machine learning in the detection and classification of plant diseases by introducing a robust classification system based on the publicly available PlantVillage dataset [21]. While DenseNet-77 served to extract key features and summarize them, the CenterNet network enabled the detection and categorization of plant diseases [20]. Lee et al. [22] presented methods for the detection and classification of plant diseases using CNNs based on pre-trained models. They examined the performance of pre-trained models and models trained only on the observed dataset, after which they discovered that the best performance was achieved by the pre-trained model based on transfer learning. They also confirmed that the isolated features do not necessarily indicate a classified disease due to the difference in symptoms during plant development. Ramcharan et al. [23] used transfer learning to train a CNN to successfully recognize three diseases and two pests that affect the cassava plant, which is one of the three largest sources of carbohydrates in Sub-Saharan Africa. The used dataset contained images of cassava diseases in different stages of growth with the observation of different genotypes. By analyzing the performance of the InceptionV3 network with the Inception softmax layer, the SVM method, and the k-nearest neighbor method (k = 3), the best model achieved an accuracy of 93.00% and was implemented on Android devices [23]. Chen et al. [24] created a model based on transfer learning and CNNs for detecting lesions on plant leaves at an early stage, as well as detecting diseases in general. They expanded the PlantVillage dataset with self-collected images, which consisted of diseased examples of rice and corn. Using a pre-trained VGGNet model, they achieved an accuracy of 91.83% for recognizing the diseases available in the PlantVillage dataset, while the accuracy of identifying examples within the self-collected database was 92.00%. Saeed et al. [25] used two pretrained CNNs, InceptionV3 and InceptionResNetV2, which were trained on 5225 images from the PlantVillage dataset [21] to classify healthy and unhealthy tomato leaves. They investigated the impact of using different dropout rates and concluded that the best results were achieved using InceptionV3 with a 50% dropout rate and InceptionResNetV2 with a 15% dropout rate, with an accuracy of 99.22%. Attallah [26] proposed a pipeline for the automatic identification of tomato leaf diseases using three compact CNNs. The results showed that the K-nearest neighbor and support vector machine achieved the highest accuracies of 99.92% and 99.90%, respectively, using as few as 22 and 24 features, demonstrating competitive performance compared to previous studies in tomato leaf disease classification.

While these studies proved the superiority of transfer deep learning models in crop disease detection in comparison to conventional approaches, there is still potential for future optimization to ensure a balance between computational complexity and improved model performance. To effectively minimize crop losses from plant diseases, there is a need for novel leaf recognition methods. Therefore, this study proposes a universal module to enhance network performance by ensuring early detection of tomato leaf diseases, which can be embedded in convolutional neural networks.

3. Materials and Methods

The proposed transfer deep learning method based on the novel IncMB module for tomato leaf disease detection consisted of the following three steps (Figure 2): (1) input data preparation for six tomato leaf diseases based on the PlantVillage dataset; (2) evaluation of deep learning models, including four transfer deep learning models (InceptionV3, InceptionResNetV2, MobileNetV2, and DenseNet201) and a novel IncMB module; and (3) tomato leaf disease detection and accuracy assessment.



Figure 2. The study workflow for tomato disease classification based on transfer deep learning and a novel IncMB module in the following three steps: (1) input data preprocessing with six tomato leaf disease images; (2) evaluation of deep learning base models and their combination with SVM and the proposed IncMB module; and (3) tomato leaf disease classification and accuracy assessment of evaluated deep learning approaches.

3.1. Data Preprocessing and Experimental Setup

The PlantVillage dataset [21] is a public dataset that is widely used in crop disease detection research as it consists of more than 50,000 images of plant diseases and healthy plants. A total of 3300 images of six tomato leaf diseases were used for the training and validation of CNN algorithms. The selected tomato diseases were early blight (lat. *Alternaria solani*), late blight (lat. *Phytophthora infestans*), septoria leaf spot (lat. *Septoria lycopersici*), spider mite (lat. *Tetranychus urticae*), tomato mosaic virus (lat. *Tobamovirus*), and tomato yellow leaf curl virus (lat. *Begomovirus*). Each class consisted of 550 images of diseased leaves, for which a stratified random split in a 70:30 ratio was performed to create training and validation datasets. To avoid overfitting, a training dataset consisted of a uniform number of images per tomato disease. Moreover, data preprocessing in the form of image stretching, mirroring, rotation, enhancing contrast, and changing brightness was applied to expand the dataset, as recommended in previous studies [27–29]. Images were resized to 224 × 224 pixels during preprocessing.

For preprocessing and data augmentation, as well as for implementing CNN models, the Keras-GPU [30] and TensorFlow-GPU [31] platforms were used in the Python programming language. Models were trained and validated using an open-access Google Colab cloud computing platform, which provided NVIDIA Tesla K80 graphics processing units with 12 GB of memory. Each network was trained for 30 epochs with a batch size of 32. Adam was used as the main optimization algorithm, while the learning rate was automatically determined and adjusted during training.

3.2. Structure of Transfer Deep Learning Networks for Tomato Leaf Disease Recognition

CNNs are commonly used algorithms for the development of automated systems for identifying plant diseases by detecting the symptoms on leaves [22]. As a method of deep machine learning, CNN represents the most promising solution to this problem due to its precise approach of extracting visual features without the use of segmentation [32–34]. It usually consists of convolution layers with different values of the kernel, which can be in parallel and activation functions, followed by pooling layers and fully connected layers [22,35–37].

The purpose of the activation function was to introduce nonlinearity into the network, which can then learn from data, perform complex calculations, and make predictions. It is preceded by a linear transformation of each mathematical operation performed during model learning [38,39]. Activation functions also have an integral role while representing a mathematical filter between neurons in the current and next layers [40]. By definition, the Mish function is similar to the Swish activation function, but due to its more accurate performance and simpler implementation, it is a more common choice when building deep machine learning models. In addition to increasing the classification accuracy, the smoothed and non-monotonic Mish function allows setting a lower value of the learning rate when training the model [41]. The Mish function was implemented in the deep learning classification method according to Formula (1):

$$f(x) = x * tanh (softplus(x)) = x * tanh (ln(1+ex))$$
(1)

After pretraining, the transfer learning models contained already-learned weights, which enabled the creation of feature maps before training the model on a specialized dataset. This approach ensured a drastic reduction in processing time for training as well as the ability to train for a relatively small amount of input data [35,42,43].

3.3. Structure of the Novel IncMB Module

The idea of implementing the IncMB module is to create a unique system of layers that can be embedded into all CNNs to achieve better performance and accuracy during the classification process. The IncMB module includes the most important parts of the block system, using the Inception module as a base, the Mish activation function in a separate layer, and the Batch normalization layer. To evaluate the efficiency of the proposed IncMB module, tomato leaf disease classification was evaluated for CNNs with the IncMB module, as well as pre-trained CNNs and CNNs with SVM. Figure 3 displays the evaluated deep learning approaches for tomato leaf disease detection. The Inception module was introduced in 2015 as part of GoogleNet architecture [44], which is upgraded in later studies with the idea to minimize the computational cost without effect on the network generalization [22,45–47]. Such an architecture combines filters of different sizes (5 \times 5, 3×3 , 1×1) for feature extraction and regulation of computations. The Inception module was used as the base of the IncMB module for feature extraction. After the module, the Mish activation function was applied in a separate layer. The batch normalization was used to decrease training time, prevent the vanishing gradient problem, and reduce the chance of overfitting. Feature maps were then reduced with a global pooling layer, and smaller feature maps were created. Finally, the dense layer constituted the ending layer of the proposed module.



Figure 3. The architecture of the evaluated transfer deep learning approaches and the proposed IncMB module.

3.4. Tomato Leaf Disease Accuracy Assessment

The statistic metrics used for the accuracy assessment of evaluated deep learning approaches for tomato leaf detection were precision, recall, F1-score, and accuracy. All of the stated metrics were calculated through the values of the confusion matrix according to the Formulas (2)–(5):

$$Precision = \frac{TP}{TP + FP},$$
(2)

$$Recall = \frac{TP}{TP + FN'}$$
(3)

$$F1-score = 2 * \frac{Precision * Recall}{Precision + Recall'}$$
(4)

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN'}$$
(5)

where *TP* (true positive) represents the number of leaves that are correctly classified as infected. They are usually yellow or brown and have changes in leaf shape, such as hollowness. The *FN* (false negative) represents the number of leaves that are incorrectly

classified as healthy when, in reality, they belong to one of the disease-determining classes. The *FP* (false positive) represents the number of leaves misclassified as diseased when, in reality, they are healthy. The *TN* (true negative) represents the number of correctly classified leaves that are healthy and do not belong to any disease-determining class.

4. Results

The accuracy assessment results of tomato leaf disease detection based on four different network architectures using transfer deep machine learning are presented in Table 1. The experiment was conducted using 3300 images to identify six different tomato leaf diseases. The best performance was achieved by the InceptionV3 network containing the IncMB module, with an accuracy of 97.78%. Following were the InceptionResNetV2 and MobileNetV2 network architectures, both combined with the IncMB module. Comparing each network with its version with the IncMB module and the version with the SVM, in three out of four cases the highest accuracy was achieved by the network with the IncMB module. In the remaining case, the accuracy of the DenseNet201 network version with the IncMB module was 92.00%, while in combination with the SVM, it was 92.44%. In the comparison of other methods, it was observed that the network with the IncMB module achieved superior results and increased the performance of the classifier in recognizing tomato diseases. The precision, recall, and F-score confirmed the observations that were made based on the analysis of accuracy values.

Table 1. Accuracy assessment of evaluated transfer deep learning classification variants for tomato leaf disease detection.

Transfer Deep Learning Model	Classification Approach	Accuracy	F1-Score	Precision	Recall
InceptionV3	Base model	0.9333	0.9329	0.9338	0.9335
	with SVM	0.8889	0.8866	0.8976	0.8888
	with IncMB	0.9778	0.9778	0.9779	0.9778
InceptionResNetV2	Base model	0.9667	0.9662	0.9673	0.9667
	with SVM	0.9311	0.9309	0.9337	0.9312
	with IncMB	0.9733	0.9733	0.9734	0.9733
MobileNetV2	Base model	0.9156	0.9125	0.9325	0.9155
	with SVM	0.8444	0.8443	0.8829	0.8445
	with IncMB	0.9500	0.9496	0.9502	0.9500
DenseNet201	Base model	0.8589	0.8569	0.8610	0.8588
	with SVM	0.9244	0.9247	0.9288	0.9246
	with IncMB	0.9200	0.9195	0.9198	0.9200
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The highest accuracy assessment metrics per transfer deep learning model are bolded.

Although the dataset used in the study was balanced considering the number of used images per tomato leaf disease, the F1-score was evaluated for a particular tomato disease to present an objective indicator of test accuracy due to the harmonic mean of precision and recall. Table 2 contains the obtained F1-score values for every tomato disease for classification trained on CNN with the IncMB module. According to the obtained results, the highest value of the F1-score was achieved in the class of individuals affected by the mosaic virus, followed by the tomato yellow leaf curl virus.

Tomato Leaf Disease	InceptionV3	InceptionResNetV2	MobileNetV2	DenseNet201
Early blight	0.9498	0.9533	0.8993	0.8407
Late blight	0.9637	0.9530	0.9408	0.8829
Septoria leaf spot	0.9797	0.9701	0.9199	0.9247
Spider mite	0.9834	0.9835	0.9610	0.9373
Mosaic virus	0.9967	0.9865	0.9933	0.9699
Yellow leaf curl virus	0.9934	0.9934	0.9835	0.9615

Table 2. The F1-score values for analyzed tomato leaf diseases per classification variant based on the novel IncMB module.

The highest F1-scores per tomato leaf disease are in bold.

To ensure that there was no overfitting or underfitting during model training and validation, Table 3 also displays the training and validation accuracy values and validation losses over 15 and 30 epochs. While comparing performances within the models, it was noticed that InceptionV3 consistently achieved the highest training accuracy across all approaches (CNN, CNN with a support vector machine, and CNN with the proposed IncMB module). MobileNetV2 demonstrated strong performance, particularly with IncMB, achieving high training and validation accuracy with lower validation loss compared to other models at 30 epochs. InceptionResNetV2 and DenseNet201 showed improvement with additional techniques (SVM, IncMB) but generally fell behind InceptionV3 and MobileNetV2. While increasing epochs from 15 to 30, it generally led to improved performance training and validation accuracy for most models, particularly InceptionV3 and Inception-ResNetV2. However, MobileNetV2 showed minimal improvement in validation accuracy as the number of epochs increased. While SVM integration improved validation accuracy slightly for InceptionV3 and InceptionResNetV2 at 30 epochs, it could negatively impact performance for MobileNetV2. This suggested SVM might not be universally beneficial. On the other side, the IncMB module consistently improved performance across all models, leading to higher training and validation accuracy and lower validation loss at 30 epochs.

Transfer Deep Learning Model	Classification Approach	15 Epochs			30 Epochs		
		TA	VA	VL	TA	VA	VL
InceptionV3	Base model	0.9529	0.8650	1.2822	0.9859	0.9330	0.3108
	with SVM with IncMB	0.9890	0.8349 0.9143	0.5262	0.9956	0.8884 0.9762	0.3553
InceptionResNetV2	Base model with SVM with IncMB	0.8813 0.9496 0.9325	0.8125 0.8411 0.8578	0.6906 0.8032 1.3071	0.9862 0.9950 0.9983	0.9665 0.9344 0.9733	0.2297 0.0567 0.1889
MobileNetV2	Base model with SVM with IncMB	0.9892 0.8908 0.9235	0.9167 0.8074 0.8750	1.0077 0.4561 0.4299	0.9967 0.8935 0.9693	0.9156 0.8380 0.9489	0.5614 0.3068 0.2386
DenseNet201	Base model with SVM with IncMB	0.6874 0.8154 0.8104	0.6060 0.8811 0.8678	0.5483 0.4195 0.4792	0.9122 0.9063 0.8942	0.8583 0.9244 0.9200	0.4427 0.2126 0.2657

Table 3. Accuracy and validation loss during 15 and 30 epochs of training.

(TA) training accuracy; (VA) validation accuracy; and (VL) validation loss.

The confusion matrix presented in Figure 4 contains the absolute and relative numbers of corrected classified individuals for the approach in which the IncMB module is embedded in the CNN. The best performance and the largest number of correctly classified examples were achieved by the InceptionV3 network with the IncMB module, followed by the



InceptionResNetV2 network with the IncMB module. The least accurate performance was achieved by the DenseNet201 network version with the IncMB module.

Figure 4. Confusion matrix for CNN with proposed IncMB module. (A) early blight; (B) late blight; (C) septoria leaf spot; (D) spider mite; (E) tomato mosaic virus; and (F) tomato yellow leaf curl virus. The upper number per square indicates classified values, while the lower number indicates the percentage of classified values per leaf disease.

5. Discussion

From the author's knowledge based on searching the Web of Science Core Collection, there were no similar studies with the same set of evaluated deep learning networks. However, the study by Chen et al. [24] confirmed that the InceptionV3 network was more accurate than DenseNet. Despite lower individual performance, DenseNet201 combined with SVM achieved moderate accuracy in tomato leaf disease detection. This was likely achieved due to its specific architecture, in which the feature maps of each layer are connected to the previous one, so the network contains replicated data multiple times. The connectivity of DenseNet could be particularly advantageous for capturing the subtle visual patterns characteristic of plant diseases, providing the SVM with a richer set of features for accurate classification [48–50].While SVM is a classical machine learning method, recent research showed that combining SVM with deep learning methods could improve overall classification accuracy. [51,52]. The performance of the MobileNetV2 network with the IncMB module opened up the possibility of implementing the model on mobile devices to facilitate its use by agricultural experts and ensure the early detection of tomato diseases. In the study by Minango et al. [53], it was observed that the MobileNet architecture was

also used in deployment. During the training process, the accuracy and validation loss values were evaluated to prevent overfitting or underfitting of the models. By increasing the number of epochs, training, and validation, accuracy values increased, which in almost all cases are significantly lower than those of training. At the same time, increasing the epochs reduced the validation loss, which confirmed the learning trend of the algorithm.

Deep machine learning models achieved significant levels of accuracy and high performance, although their implementation is more time-consuming and hardwaredemanding [36,54,55]. The feature extraction process was fully automated with deep machine learning methods because it was already built into the algorithm itself. In the examples of diseased and healthy plant individuals whose life cycle takes place under controlled conditions, it was demonstrated that previously trained models of CNNs achieved results with greater accuracy compared to models trained for the first time. Furthermore, the dependence on background features in the classification of plant diseases has been noted, so background removal by segmentation methods is not performed because it reduces the efficiency of the model [27]. It was observed that evaluated approaches better recognize examples of the individuals affected by the mosaic virus and tomato yellow leaf curl virus. This likely occurred due to the specificity of the symptoms of viral diseases. Namely, in individuals infected with these viruses, the main symptom is yellowing of the leaves, while in the case of the tomato yellow leaf curl virus, the curvature of the leaf surface also occurs [13,56,57]. In the case of other observed diseases, the main symptoms are black dots and/or black circles of an irregular shape, so due to over-lapping symptoms, as well as the presence of the same in different stages of development, the algorithms have a harder time recognizing what an individual tomato is infected with [13,16,56]. Moreover, while analyzing the results from the confusion matrix, the number of misclassified individuals was the lowest for the mosaic virus and the tomato yellow leaf curl virus.

The proposed models could be further applied with other state-of-the-art technologies, such as hyperspectral imaging sensors, for improving plant disease recognition. By analyzing the spectral signatures of plants, CNNs could identify signs of disease even before visible symptoms appear, potentiate early intervention, and minimize crop loss [58]. Moreover, proposed CNN models could automatically learn and extract relevant features from the hyperspectral data while eliminating the need for manual feature engineering, which can be a time-consuming and expertise-intensive process [58,59]. The proposed models could also be optimized for faster processing on powerful hardware and analyze images captured by smartphones or embedded systems in the field, enabling real-time disease identification [60]. The lightweight MobileNetV2 with IncMB module, developed in this research, has the potential to be used through a mobile application offering real-time disease detection support to agricultural experts [61,62].

The availability of a larger dataset for training deep machine learning models could likely improve the performance of the model. In addition to diseased tomato individuals, the dataset could be expanded with other examples of diseased tomato leaves as well as healthy ones, enabling the creation of a dataset containing examples of diseased leaves of other crops to expand the scope of the proposed IncMB module. Enriching the used dataset with new images would also give insight into the current breadth of application areas and assist experts in crop management decisions. To achieve better performance, it is planned to improve the IncMB module in future studies by including the additional convolutional layers and expanding the application of state-of-the-art activation functions that have been proven to contribute to the accuracy of the model.

6. Conclusions

The conventional early identification of plant diseases requires intense human supervision, and without proper automatic identification, sufficient food production according to 2050 forecasts may not be achievable. For the recognition of tomato leaf diseases, the deep machine learning method, CNN, was used together with transfer learning to take advantage of pre-trained networks in this study. To optimize their performance, a unique block of layers with built-in CNNs was proposed, labeled the IncMB module, and designed to perform image classification for tomato leaf diseases, thus achieving higher accuracy than base networks. In the experiment, the performance of pre-trained CNNs with the IncMB module was superior to pre-trained CNNs without the module and to CNNs with the SVM method.

The IncMB module presented a novel technique for improving the performance of CNNs for image classification. Experimental results showed that the best performance was achieved by the InceptionV3 network containing the IncMB module, with an accuracy of 97.78%. While evaluating the results for tomato disease recognition, it was observed that the CNN with the IncMB module nevertheless achieves notable results, and it is possible to increase them by expanding the used dataset. For future improvements and to enhance the universal applicability of the IncMB module, its effectiveness will be investigated across a wider range of similar plant disease datasets. This will involve testing the proposed models on various plant disease datasets beyond tomato diseases. However, the MobileNetV2 network with the IncMB module, developed in this study, has demonstrated promising results for real-world use. As a lightweight network, its efficiency will make it ideal for embedding within a mobile application. This application could function as a valuable virtual assistant for agricultural experts by providing real-time plant disease detection support in the field.

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