IAES International Journal of Artificial Intelligence (IJ-AI)
Vol. 13, No. 4, December 2024, pp. 4757~4765
ISSN: 2252-8938, DOI: 10.11591/ijai.v13.i4.pp4757-4765

Enhanced detection of tomato leaf diseases using ensemble deep learning: INCVX-NET model

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Article Info

Article history:

Received Feb 10, 2024
Revised May 11, 2024
Accepted Jun 21, 2024

Keywords:

Convolutional neural network
Hybrid deep learning
Inception V2 model
Tomato plant disease
Visual geometry group-16 model
Xception model

ABSTRACT

Automated leaf disease detection quickly identifies early symptoms, and saves time on large farms. Traditional methods like visual inspection and laboratory detection are prevalent despite being labor-intensive, time-consuming, and susceptible to human error. Recently, deep learning (DL) has emerged as a promising alternative for crop disease recognition. However, these models usually demand extensive training data and face problems in generalization due to the diverse features among different crop diseases. This complexity makes it difficult to achieve optimal recognition performance across all scenarios. To solve this issue, a novel ensemble approach INCVX-Net is proposed to integrate the three DL models, 'Inception, visual geometry group (VGG)-16, and Xception' using weighted averaging ensemble for tomato crop leaf disease detection. This approach utilizes the strengths of three DL models to recognize a wide range of disease patterns and captures even slight changes in leaf characteristics. INCVX-Net achieves an impressive 99.5% accuracy in disease detection, outperforming base models such as InceptionV2 (93.4%), VGG-16 Net (92.7%), and Xception (95.2%). This significant leap in accuracy demonstrates the growing power of ensemble DL models in disease detection compared to standalone DL models. The research paves the groundwork for future advancements in disease detection, enhancing precision agriculture through ensemble models.

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1. INTRODUCTION

Agriculture is the essence of human survival: it feeds and offers a living for billions of people across the globe [1], [2]. However, the sector is associated with several threats, including adverse weather, pest attacks, and the complex spread of plant diseases [3]. Yet, the farmers are more concerned about the potential impact of diseases affecting their fields [4], particularly due to their limited knowledge regarding the symptoms of the new diseases and effective preventive measures for any such disease, remains a worrying possibility [5]. A practical approach is to employ early identification of the diseases which can help to prevent substantial losses.

When the crops are affected by pests or diseases, farmers typically attempt to identify the disease themselves or seek help from experts [6] and then turn to laboratory methods [7], which can result in delayed or incorrect disease diagnosis. For example, early blight, a tomato disease, is characterized by circular dark spots on the leaves. It was often mistaken for other leaf spot diseases. One of the wide spread fungal infections is septoria leaf spot, which looks like small dark spots with yellow halos surrounding them. It confounds experts because it mimics the symptoms of other distinct fungal infections. In laboratory methods, sample processing and analysis by the experts results in delayed detection. These challenges become more burdensome if one looks at the rural and remote areas where resources in terms of expert advice and advanced diagnostic tools are hardly available. This is where the technological advancements come into the picture to give a ray of hope in the form of a solution to the most pressing issue.

The development in information technology made the researchers employ machine learning (ML) and deep learning (DL) techniques for the efficient detection of plant diseases [8], [9]. DL, particularly has gained popularity and brought new highs to automatic feature extraction from images and new-found efficiency, joined with a high accuracy in identifying diseases [10]. The various DL models such as AlexNet, visual geometry group (VGG)Net, residual neural network (ResNet), Inception Net, custom convolutional neural network (CNN), and MobileNet are proven to provide a better performance provided a large amount of data containing information about the diseases [11]. However, in practical situations, the appearance of new diseases presents a significant challenge to the applicability of DL models particularly regarding unknown images. These models are typically trained on pre-existing datasets of leaf diseases [12], making them familiar with known conditions. But when encountering new diseases, the DL models may struggle to identify them correctly. This demands the need for a new approach that can handle evolving diseases and able to provide robust performance in real world applications.

The ensemble technique [13], [14] can mitigate the challenge associated with the emergence of new diseases in plant health management. This approach integrates DL models, each trained on various datasets, focusing on a particular area of characteristics. For example, when a DL model in the ensemble approach concentrates on fungal diseases whereas another specializes in detecting viral infections. In that case, the combined knowledge of multiple models can improve the overall disease recognition performance. In the present work, the INCVX-Net ensemble learning model for disease detection in tomato plants is proposed, which integrates the three DL models and is able to enhance the generalization ability of the classification method.

Before considering the ensemble approach, it’s necessary to know the outcomes for plant disease detection based on standalone DL models [15]–[17] and to understand the effectiveness of the ensemble method [18]–[20]. Trivedi *et al.* [15] suggested CNN to distinguish ten different classes of tomato leaves with a dataset containing 3,000 images. The proposed model with tuned hyperparameters showed 98.49% accuracy. However, achieving this level of accuracy underscores the challenges of collecting diverse data. Ahmad *et al.* [16] use both laboratory and field-based datasets ,employing four CNN architectures-VGG16, VGG19, Inception v3, and ResNet for tomato leaf disease classification. Despite promising results on the laboratory dataset, with an accuracy variation of 10 to 15%, Inception V3 is best for both datasets. Ferentinos [17] considered VGG, AlexNet, AlexNetOWTBn, GoogleNet, and Overfeat, to conduct plant disease detection on the open database including 87,848 photos of both healthy leaves and diseased plants. Among these, VGG produced a success rate of 99.53%.

Arshad *et al.* [18] propose a PLDPNet, a novel hybrid DL model, for automatic segmentation and classification of potato (3 classes), tomato (10 classes), and apple (4 classes) leaf diseases. The PLDPNet uses auto-segmentation and deep feature ensemble fusion modules to increase disease classification accuracy. The end-to-end performance of the proposed PLDPNet achieves a recorded accuracy of 98.66% with 100 epochs. Ganaie *et al.* [19] employs a novel TomConv model, a modified CNN, a classification system among the ten different kinds of tomato plant leaves. In this study 105 epochs of training were applied to the publicly available dataset Plant Village, which contains over 16,000 pictures of tomato leaves, and an accuracy of 98.19% was attained. By utilizing 3,602,506 total parameters, the suggested model performs greater than current state-of-the-art models. He *et al.* [20] introduced a novel ensembling approach ensemble learning method for crop leaf disease recognition (ELCDR), for disease detection in 4 different crops, which assigns weights to models based on their feature vectors. Experimental results demonstrate that ELCDR outperforms single model recognition and traditional voting methods, showing 98.13% apple, 95.88% corn, 98.38% grape, and 90.75% rice accuracy which validates the effectiveness of the ensembling approach in crop leaf disease recognition.

The researchers have used various well-built pre-trained DL models to recognize the diseases and get noteworthy performance.They must generalize easily to new or unseen data/features [21]. Later, in the mid-2000s, Research slowly considered integrating the multiple DL model, thus leading to the effective ensemble approach. So, the present work, emphasizes ensemble learning, by exploring efficient ensemble strategies that perform well in plant disease detection areas.The contributions of this paper involve the following core components: i) proposed an ensemble approach for tomato crop disease detection named INCVX-Net; ii) three different DL models are subjected to transfer learning, wherein the bottom layers are frozen, and each model’s performance is individually recorded; iii) incorporated weighted averaging ensemble strategy and compared the outcomes with the crop disease detection methods that are based on a single DL model; iv) the experiments consist of a tomato dataset comprising five classes, conducted on a Google Colab platform. The results showed the necessity of considering the ensemble approach. The remainder of the paper is structured as follows: section 2 discusses the methodology, section 3 presents the results and subsequent discussion, and section 4 encapsulates the concluding remarks.

2. METHOD

The research aims to improve the prediction and recognition of plant leaf disease efficiently by concatenating the features of three DL models, namely the Inception model, VGG-16 Net model, and Xception model. The basic flow of INCVX-Net comprises four stages as listed as follows and depicted in Figure 1. There are: i) dataset collection, ii) extraction of features from the base models, iii) predictions and weight averaging, and iv) validation of the model.

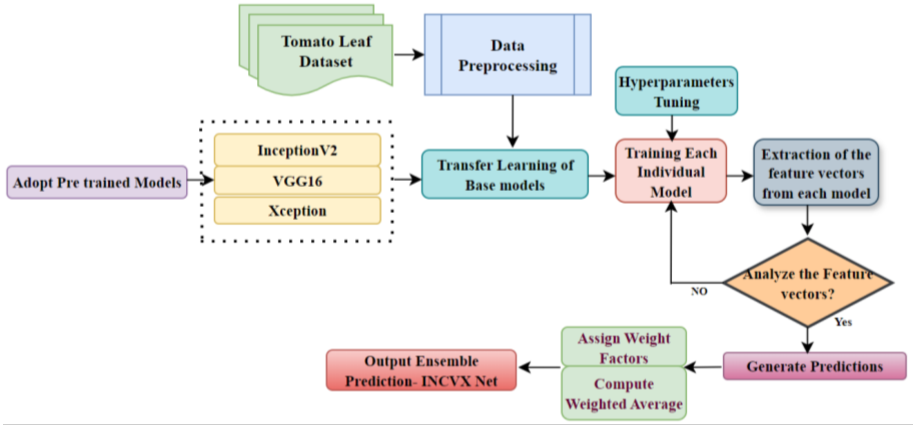


Figure 1. The overview of INCVX-Net model

2.1. Dataset collection

To achieve the research aims, tomato leaf images obtained from the plant village dataset is employed. The plant village dataset contains large scale high-resolution images that have been captured from unmanned aerial vehicle (UAV) [21]. The present dataset comprises 5,250 images from five different classes such as bacterial spot, healthy leaf, late blight, spot leafe, and yellow leaf curl virus. The images of size 256×256 pixels which are split as training, validation, and testing images as displayed in Table 1. The visualization of the sample images of the tomato leaf is shown in Figure 2.

Table 1. Dataset information of the tomato leaf

S. No.	Leaf type	Total no. of images	Training images	Validation images	Testing images
1.	Bacterial spot	1,050	900	50	100
2.	Healthy leaf	1,050	900	50	100
3.	Late blight	1,050	900	50	100
4.	Spot leafe	1,050	900	50	100
5.	Yellow leaf curl virus	1,050	900	50	100

Figure 2. Dataset description of tomato leaf dataset

Later in the process, the tomato leaf images are subjected to pre-processing step. Initially, all images are resized to a standard format of 224×224×3 pixels using open CV library in Python. Additionally, to enhance the models performance, the pixel values of the images are normalized to a range of 0 to 1. The resizing provides uniformity in image dimensions, whereas normalization minimize the effects of varying pixel intensities.

2.2. Extraction of the features from base models

The feature extraction process begins with selecting the base models from a set of pre-trained DL models. Inceptionv2, VGG-16, and Xception are chosen as a base model which is initially trained on large scale datasets such as ImageNet and comes with pre-trained weights. The models are subjected to transfer learning, which involves adjusting them by incorporating five output units into the final output layer [22], [23]. The pre-trained layers of the base models are frozen to a certain point by excluding the final classification layers, allowing only the newly added layers to be trained on the tomato leaf dataset by fine tuning the hyperparameters. The overview of transfer learning is shown in Figure 3. The hyperparameters settings of all three models are shown in Table 2. Training base models undergo a feature extraction process tailored to their architecture. Once the features are extracted, they serve as input to the prediction phase.

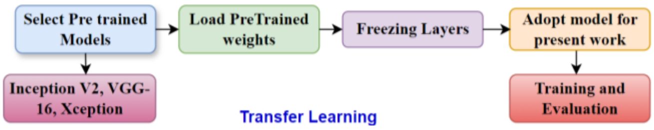


Figure 3. The overview of transfer learning

Table 2. Hyperparameters settings

Hyperparameters	Value
Epochs	8
Batch_ size	64
Activation_ function	Relu
Optimization algorithm	Adam
Loss _function	Categorical Loss Entropy
Learning rate	0.00001

In Inception V2, features are extracted from intermediate Convolutional layers. These layers capture both high level and low level visual patterns in the input data, providing a rich representation at various levels of abstraction. The VGG-16 features are obtained from the second to last fully connected layer or the global average pooling layer. These layers captures complex patterns and structures while abstracting away specific pixel level details. On the other hand, in Xception, features are extracted from intermediate depth wise separable Convolutional layers. These layers enable the model to learn rich representations with various levels of abstraction. The distribution of the extracted features is analyzed using gradient-weighted class activation mapping (Grad-Cam) [24] to ensure they are rich in all possible features, if not, the models should be retrained to capture a more comprehensive set of features. Thus, extracting features from pre-trained DL models harnesses the power of learned representations to capture essential characteristics of the input data. This allows us to reduce the need for extensive labeled data and also enables us to leverage the knowledge encoded in these models from their training on large-scale datasets like ImageNet.

2.3. Predictions and weight averaging

The extracted features are passed through a final classification layer of the models with a softmax activation function. The final layer generates predictions in the form of class probabilities for each input sample. Weights are assigned to each model's prediction, to reflect the importance placed on each models predictions. For each class C, a weighted average of the predicted probabilities from all models is calculated using (1).

$$F_C = \sum_{i=1}^{n} Wi * P_{i,c} \tag{1}$$

Where, F_c is final probability for each class C, Wi is weight assigned to each model I, $P_{i,c}$ is predicted probability of class C by model I. Three DL models may extract different features from the same dataset. The weights are assigned [25] to the predictions depending on factors such as model performance on different classes of data. The name INCVX-Net is coined to indicate the combined prediction of the Inception, VGG16, and Xception models.

2.4. Validation of the model

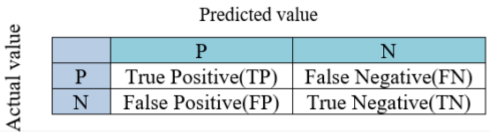
The performance of the proposed model is evaluated by using various performance metrics such as precision, recall, accuracy and F1-measure [26]. The confusion matrix is a two dimensional table, as shown in Figure 4, and is used to calculate the above mentioned metrics. In this matrix actual values are on the column side and predicted values are on the row side. Let true positive (TP), true negative (TN), false positive (FP), and false negative (FN) denote the number of TP, TN, FP, and FN respectively. The TP is an outcome where the models correctly predict the positive class. The TN is an outcome where the models correctly predict the negative class. The FP is an outcome where the models incorrectly predict the positive class. The FN is an outcome where the models incorrectly predict the negative class [27]. The metrics are calculated using (2) to (5).

$$\text{Accuracy} = (\text{TP} + \text{TN})/(\text{TP} + \text{TN} + \text{FP} + \text{FN}) \tag{2}$$

$$\text{Precision} = \text{TP}/(\text{TP} + \text{FP}) \tag{3}$$

$$\text{Recall} = \text{TP}/(\text{TP} + \text{FN}) \tag{4}$$

$$\text{F1} - \text{Measure} = 2/(1/\text{precision} + 1/\text{Recall}) \tag{5}$$



Predicted value

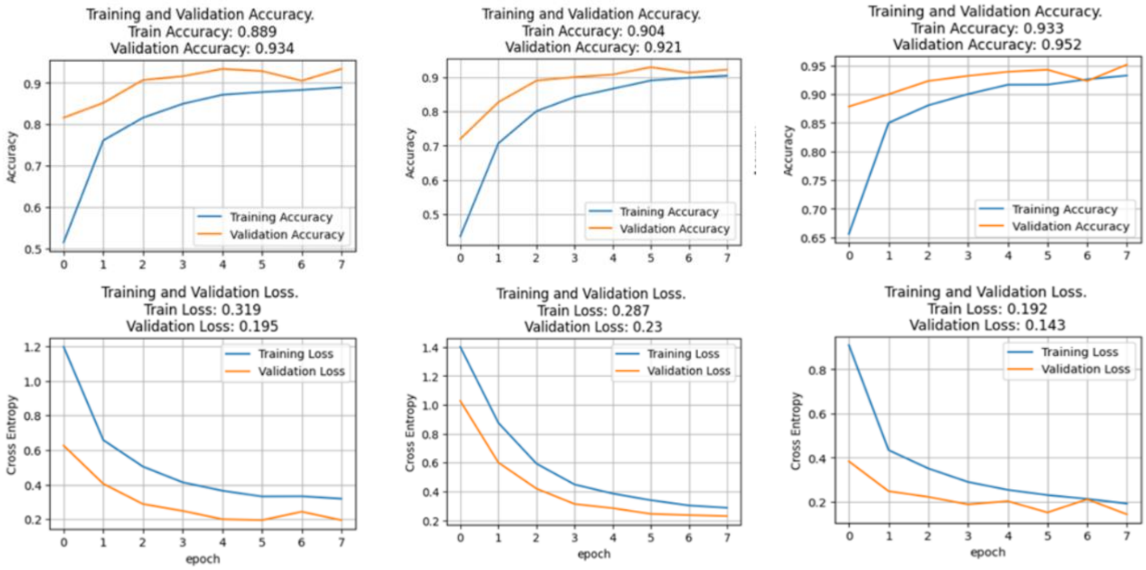
Actual value

	P	N
P	True Positive(TP)	False Negative(FN)
N	False Positive(FP)	True Negative(TN)

Figure 4. Confusion matrix

3. RESULTS AND DISCUSSION

The work employed three DL models: inception, VGG-16 Net, and Xception model individually, to recognize various tomato leaf diseases. The experiments were conducted on a Python 3 Google Compute Engine back end (GPU) using a Jupyter Notebook and various DL libraries including OpenCV, NumPy, Matplotlib, scikit-learn, Keras, and TensorFlow. Google Colab, running on an Intel (R) Core (TM) i7-8700 CPU @ 3.20 GHz with 8.00 GB of RAM, was utilized for execution. The training accuracy and loss of the base models Inception, VGG16, and Xception are shown in Figures 5(a) to 5(c) respectively. As the number of epochs increases, there is a gradual reduction in loss and a corresponding rise in accuracy.



(a) (b) (c)

Figure 5. Classification accuracy and loss of (a) InceptionV2, (b) VGG-16, and (c) Xception models

The confusion matrix was utilized to calculate various performance metrics. Figures 6 and 7 show the confusion matrix of the base models and the proposed INCVX-NET model. In InceptiontV2, VGG-16, and Xception models some of the classes are misclassified. For example, in the confusion matrix of the VGG-16 model, late blight is misclassified as healthy leaf and spot leaf. Hence, to improve the tomato leaf disease prediction further the three models namely InceptionV2, VGG-16, and Xception model are combined at the decision level by weighted averaging method. After the integration, the resulted model INCVX-Net able to identify more correct images than the base models as shown in Figure 7. The accuracy of the ensemble approach reached 99.5%, with 99.1% precision, 99.4% recall, and 99.25% F1-score. Figure 8 shows the performance comparison of the ensemble model with three base models. The findings of this study are compared with those of previous works carried out within the same application domain, as detailed in Tables 3 and 4.

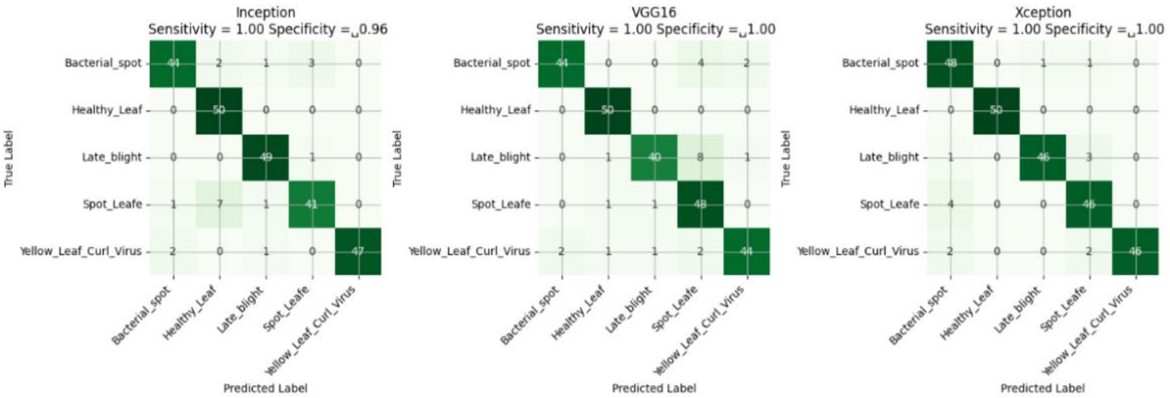


Figure 6. Confusion matrix of InceptionV2, VGG-16 net and xception model

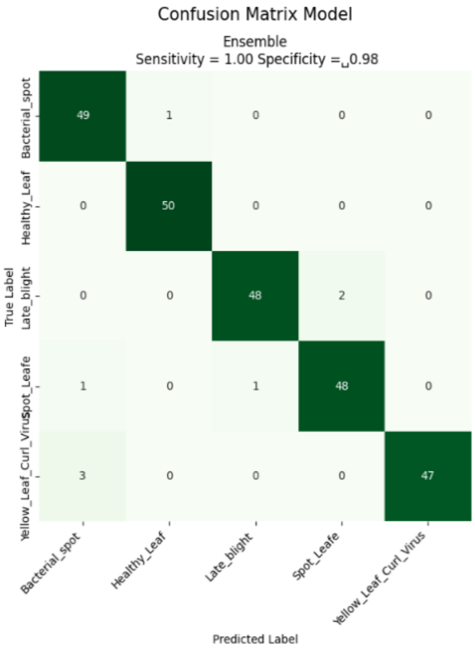


Figure 7. Confusion matrix of INCVX-Net model

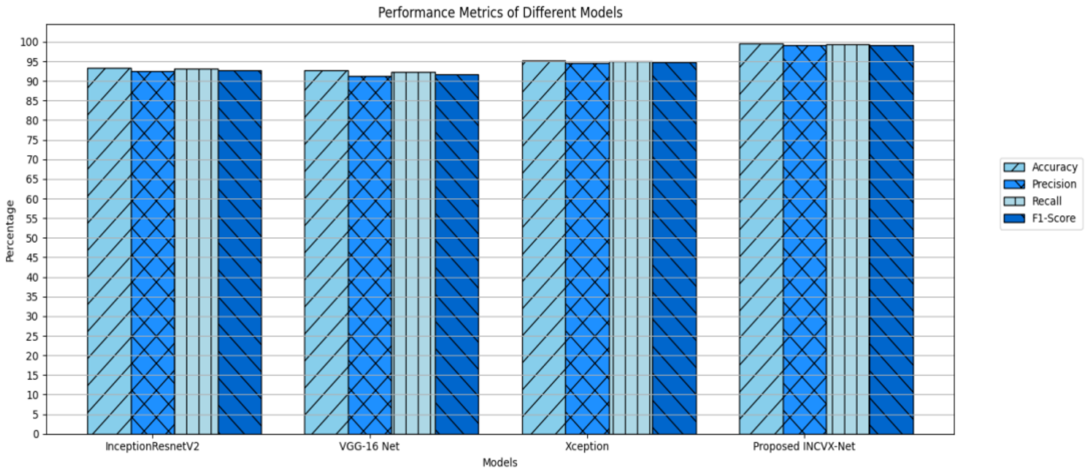


Figure 8. Performance comparison of INCVX-Net with the base model

Table 3. Performance comparison of proposed model with the base models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
InceptionResnetV2 Model	93.4	92.6	93.1	92.75
VGG-16 Net Model	92.7	91.25	92.4	91.7
Xception Model	95.2	94.7	95.1	94.8
Proposed INCVX-Net Model	99.5	99.1	99.4	99.25

Table 4.performance comparison of INCVX-Net with previous works

Ref.	Model	Dataset	Epochs	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
[20]	EDCLR	8,000, multi-crop	60	Apple: 98.13 Corn: 95.88 Grape: 98.3 Rice: 90.75	98.14 96 98.39 91.86	98.13 95.88 98.38 90.75	98.13 95.94 98.38 91.30
[28]	Hybrid CNN	9,027, Grapes	92	98.7	98	99	94
[29]	SE-ResNet50	22,925 tomato	150	96.81	96.77	96.81	96.79
[30]	Resnet50-CBAM+SVM	-	50	97.2	---	---	---
[31]	Attention-dilated CNN and Logistic regression	15,989 Tomato	100	100	100	100	100
[32]	ResNet50+MobileNet	5,400 Olive	100	97.08	97.61	97.11	96.86
[33]	EfficientNetB3+MobileNet	32,535, Tomato	20	99.92	-	-	-
[34]	Ensemble hydra model (CNN+VGG19)	15,600, Cotton	50	95	95	94	93
	Proposed INCVX-Net Model	5,250, Tomato	8	99.5	99.1	99.4	99.25

3.1. Discussion

This study investigated the effectiveness of an ensembling approach on disease recognition of plants. While most of the previous studies have examined the impact of single DL models on well-established datasets, they still need to address how these models work when encountering a limited dataset, and their adaptability to new images which are common in real world applications remains under explored. Stand-alone DL models operate independently, yet there’s limited investigation into the potential benefits of integrating multiple DL models.

The proposed INCVX-Net model, is an integration of the three base models Inception V2, VGG-16, and Xception to classify the diseases in tomato plants with a limited dataset. The study employed the feature vectors extracted by the base models, since in the context of disease detection in plants using DL models, there is a strong relation between the features extracted from the images and how the model learns these features to classify the diseases. Grad-cam is employed to visualize and interpret the areas of the images that contribute most to the classification decision. An easy and efficient ensembling approach known as weighted average is used to combine predictions from three models to produce final predictions. The results demonstrate the success and effectiveness of the proposed ensemble approach, INCVX-Net, which attains a predictive accuracy of 99.5% for recognizing five classes of tomato leaf disease. Unlike the single DL model, the INCVX-Net achieves significant performance even with limited data, offering a promising avenue for applications with restricted data availability.

Despite the promising results from the INCVX-Net model, there are a couple of limitations to consider. Firstly, how well ensemble methods works depends on choosing the right base models and the right way to put them together with the help of suitable aggregation technique. Secondly, implementing these methods practically might face challenges due to the computational complexities involved, which could require additional research to find viable solutions. Hence, it is important to focus on improving ensemble techniques to enhance predictive accuracy while minimizing computational demands. Additionally, investigating the applicability of ensemble approaches across diverse domains and datasets could provide valuable insights into their generalization and scalability. This study underscores the effectiveness of ensemble methods in image recognition applications which helps to mitigate the challenges like over-fitting, data variability, and model instability.

4. CONCLUSION

The farmers can minimize crop losses by taking timely preventive actions against the diseases. This is possible only when they can identify the diseases correctly at their early stage. Adopting a DL model to classify plant diseases is emerged as a promising solution. State-of-the-art DL models extract features from the training images, which they learn to classify the diseases. However, it is uncertain that the extracted features are not consistent among all models. This is where the concept of integrating multiple DL models arises. The resultant model will effectively identify the diseases by aggregating different viewpoints that help to find hidden or small features of diseases more effectively. In the proposed INCVX-Net model the feature vectors are extracted from the base models, which are validated with GRAD-cam and combined using the weighted average Ensembling technique. To prevent over-fitting, techniques such as dropout, and batch normalization were employed. The INCVX-Net model exhibits promising outcomes in recognizing and categorizing five different tomato plant diseases with a remarkable accuracy rate of 99.5% with minimal classification error. The results are evaluated by comparing with the outcomes of the base models, that the proposed model shows good performance, proves the adoption of the ensembling technique. Despite its potential as an automatic detector for early identification of tomato crop leaf diseases, it is necessary to acknowledge the limitations of the study, including the need for further validation across different tomato/plant species thereby potentially increasing production. Furthermore, real-world validation with field-collected data under diverse conditions such as varying lighting, weather, and image quality is essential to accurately assess the ensemble's effectiveness. The INCVX-Net model could be deployed on compact computing platforms, transforming it into a standalone device. This would facilitate easier integration with various systems, potentially enhancing accessibility and usability in real-world applications.

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