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Research Article

Determining Model Reliability for Leaf Disease Classification and Detection Approach by Evaluation of Performance Measures

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ABSTRACT

This research paper presents a comparative analysis of three deep learning architectures—VGG16, DenseNet121, and the proposed EfficientNetV2B2—for the identification of plant diseases through image classification. The study reveals distinct differences in training efficiency, convergence speed, and computational demands among the models. VGG16, characterized by its substantial parameter count of 15 million, exhibited slower convergence and signs of over fitting despite achieving high training accuracy. In contrast, DenseNet121, with only 7.3 million parameters, demonstrated remarkable efficiency and quick convergence, achieving a classification accuracy of 96.25%. The proposed EfficientNetV2B2 excelled with a classification accuracy of 99.29%, effectively handling complex disease patterns and leaf textures. All models successfully classified healthy leaf classes, attributed to their distinct visual characteristics. The findings highlight the importance of model depth, transfer learning, and data preprocessing in enhancing the reliability of automated plant disease classification. EfficientNetV2B2 stands out as the most robust and scalable model suitable for real-world precision farming applications, while the limitations and potential trade-offs of each architecture warrant further investigation across diverse plant species, diseases, and imaging conditions.

Keywords: Deep Learning, Convolutional neural networks (CNN), plant disease, VGG16, DenseNet121, EfficientNetV2B, Transfer learning, Precision agriculture.

Introduction

Agricultural biodiversity is essential to the supply of food and raw materials to humans and is an important component of human civilization [1, 2]. Diseases can occur when pathogenic organisms such as fungi, bacteria, and nematodes, soil PH, extreme temperatures, air humidity changes, and other elements continue to affect plants. Plant diseases affect the growth, function, and structure of plants and crops, and affect people who rely on them. Most farmers continue to use manual methods to identify and classify plant disorders because early detection is difficult and reduces productivity. Agricultural productivity is an important economic factor. Therefore, identifying and classifying plant diseases in the agricultural industry are essential [3]. If not taken, proper precautions, it can have serious consequences for plants by reducing the quality, quantity, or productivity of the products or services. Automatic disease detection and classification recognize symptoms early in the process, i.e., when they first appear on plant leaves, reducing the amount of labor required to monitor large-scale crops. According to [4], leaf diseases are an important problem in rice production and can harm crops and lead to a decrease in production. It is difficult to detect and classify leaf diseases in plants leaf diseases. Traditional methods of physical observation to detect and classify diseases are not always reliable, which can lead to a significant reduction in agricultural production. Plant diseases first attack leaves before infecting the whole plant, reducing the quality and quantity of production [5].

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The recent development of DL has led to the use of images of infected plants to detect and classify plant diseases [6]. Early detection and classification of plant diseases are essential to increasing agricultural productivity [7]. Plant diseases harm the crop, reducing crop yields. Identification of plant diseases is an important challenge for farmers and experts in agriculture [8]. Artificial intelligence (AI) is used to detect and classify plant leaf diseases early on before they spread to other crops on the farm and increase crop productivity. Every country needs agriculture to meet its needs and strengthen its economy. When crops are damaged by disease, production and the economy of the country are also affected [9, 10].

Convolutional neural networks (CNNs) have demonstrated remarkable success in automatically learning multi-level and high-level features from disease images, surpassing the limitations of traditional manual design methods [11, 12]. Convolutional Neural Networks (CNNs) have emerged as a powerful tool in image analysis, demonstrating exceptional capabilities in feature extraction, classification, object detection, and localization tasks. Their ability to automatically learn discriminative features from raw image data has revolutionized computer vision, enabling accurate and efficient solutions for a wide range of applications [13]. They provide considerable advantages in the diagnosis of diseases and have been studied extensively [14]. Depending on the network structure, CNN-based disease detection methods can be classified as one-stage or two-stage detectors [15-17].

Our paper focuses on early network detection using various techniques and algorithms, a technique that offers greater accuracy than many other existing techniques. This article evaluates and assesses final performance. Plant Leaf (a balanced image dataset that also includes apples, peaches, grapes, tomatoes, corn, potato, cherries, and strawberries) can be divided into training, validation, and testing. EfficientNetV2B2 architectures are used to develop and train deep learning models on the prepared training dataset; a comparative study of EfficientNetV2B2, VGG16, and DenseNet121 is conducted; the effectiveness of various transfer learning techniques (e.g., fine-tuning) to leverage pre-trained weights and improve model performance is investigated; accuracy, precision, recall, F1-score, and confusion matrix are used to assess each model's performance on the validation set.
A wide range of agricultural diseases can occur at various stages of plant development, damaging plant growth and negatively impacting crop production as a whole. Plant diseases are caused by various conditions at various stages of plant development [18]. As mentioned in [19], the variables causing crop diseases are classified into two categories: biotic factors and abiotic factors. Biochemical agents, such as viruses, fungi, bacteria, moss, and insects, cause plant diseases as a result of microbial infections, whereas the abiotic ones, such as water, temperature, radiation, and nutrition, act by constraining plant growth.

Ahmad et al. [20] Studying several DL models in detecting plant diseases, depending on the dataset and environmental parameters.

Five corn disease datasets were utilized: PlantVillage, PlantDoc, Digipathos, NLB, and a personally acquired CD&S dataset. Several combinations of datasets were used in order to train and evaluate the DL models. Transfer learning using five pre-trained architectures was used in four experiments. Performance-wise, DenseNet169 performed the best. The DenseNet169 model achieved an accuracy of 81.60% by removing backgrounds from RGBA images in the CD&S dataset and merging field and lab data to enhance generalization. These results imply that improved data diversity and quality can boost the performance of DL models for disease detection in the real world. Shovon et al.[21] study, five common rice leaf diseases and two betel leaf conditions were identified through image analysis. To overcome the difficulties presented by limited and diverse image datasets, a novel deep ensemble model, PlantDet, was developed using InceptionResNetV2, EfficientNetV2L, and Xception architectures.PlantDet comprised data augmentation, preprocessing, a Global Average Pooling layer, a Dropout mechanism, L2 regularizers, PReLU activation function, Batch Normalisation layers, and methods to increase model robustness and prevent overfitting. With an accuracy of 98.53%, the proposed model exceeded current techniques in the classification of rice leaf disease. Yang et al.[22] presented three interconnected networks forming LFC-Net, a tomato disease detection model. This approach detects informative areas in images without human annotations, utilizing a self-supervised mechanism. Combining location detection, feedback refinement, and classification, LFC-Net beats ImageNet-pretrained models

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with a remarkable accuracy of 99.7% on the tomato dataset. There may be wider uses for this novel framework in the diagnosis of plant diseases.[23] To overcome the drawbacks of controlled datasets like PlantVillage, we used a dataset that included photos of sunflower and cauliflower leaves, bulbs, and flowers taken in natural settings. To maximize the accuracy of disease classification, we investigated 38 pre-trained models. Results show that EfficientNetV2B2 and EfficientNetV2B3 consistently perform better than other models on the Agri-ImageNet, cauliflower, and sunflower datasets. Balafas et al.[24] Research is based on classification or object detection. They provide a comprehensive overview of available datasets for these tasks. To benchmark state-of-the-art techniques, we conduct extensive experiments on the PlantDoc dataset using five object detection and eighteen classification algorithms. Results demonstrate YOLOv5's superior performance in object detection and highlight the efficiency of ResNet50(accuracy 61.01%) and MobileNetv2(accuracy 59.74%) were trained for about 16 minutes for image classification.[25] Using the EfficientNet-V2 architecture, the model integrates dense layers and transfer learning to address class imbalance and improve model generalization, and it uses a spatial-channel attention mechanism to improve feature extraction. EfficientPNet is tested on the PlantVillage dataset and provides a 98.12% accuracy rate in potato leaf disease classification.

Datasets

The PlantVillage dataset, which is an open-access plant leaf image repository, was chosen as the principal source of information for this research. The Plant Village dataset comes in three color modes: color, grayscale, and segmented. For this research, the color images were chosen, as they carry the maximum amount of information for visual analysis. PlantVillage dataset, 2016, consists of 54,305 images of healthy and diseased leaves of 14 plant species. The dataset folder organizes these categories into 38 classes that combine species and diseases.

Pre-processing of the Dataset

For the sake of quality and uniformity, we excluded some of the classes from the dataset. Hence, classes representing plants with only a single disease/healthy category, such as Orange Huanglongbing, Squash Powdery Mildew, and healthy varieties of Blueberry, Raspberry and Soybean, were removed, since they may introduce noise or bias into the model. Classes containing fewer than 100 images were also removed to avoid overfitting and guarantee adequate training data. Thus, finally, we have RGB-colored Apple, Cherry, Corn, Grape, Peach, Potato, Strawberry, and Tomato at 256X256.

Table 1: Number of samples for each class

Class/Folder Name	**Before Preprocessing Image Count**	**After Preprocessing Image Count**
Apple___Apple_scab	500	500
Apple___Black_rot	500	500
Apple___Cedar_apple_rust	275	500
Apple___healthy	500	500
Cherry_(including_sour)___Powdery_mildew	500	500
Cherry_(including_sour)___healthy	500	500
Corn_(maize)___Cercospora_leaf_spot Gray_leaf_spot	500	500

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Corn_(maize)__*Common_rust*	500	500
Corn_(maize)___Northern_Leaf_Blight	500	500
Corn_(maize)___healthy	500	500
Grape___Black_rot	500	500
Grape___Esca_(Black_Measles)	500	500
Grape___Leaf_blight_(Isariopsis_Leaf_Spot)	500	500
Grape___healthy	423	500
Peach___Bacterial_spot	500	500
Peach___healthy	360	500
Potato___Early_blight	500	500
Potato___Late_blight	500	500
Potato___healthy	152	500
Strawberry___Leaf_scorch	500	500
Strawberry___healthy	456	500
Tomato___Bacterial_spot	500	500
Tomato___Early_blight	500	500
Tomato___Late_blight	500	500
Tomato___Leaf_Mold	500	500
Tomato___Septoria_leaf_spot	500	500
Tomato___Spider_mites Two-spotted_spider_mite	500	500
Tomato___Target_Spot	500	500
Tomato___Tomato_Yellow_Leaf_Curl_Virus	500	500
Tomato___Tomato_mosaic_virus	373	500
Tomato___healthy	500	500

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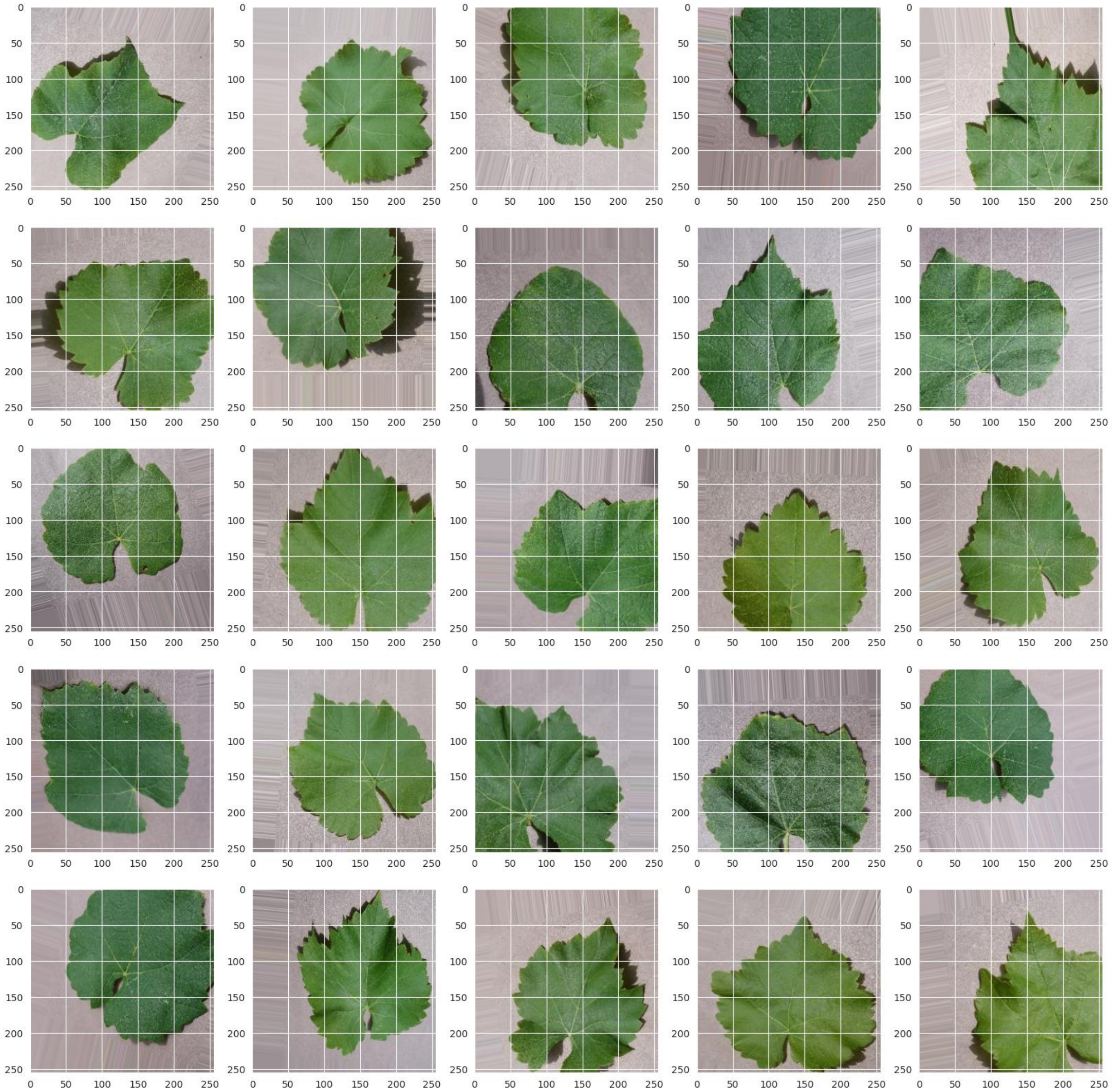

Figure 1: Augmented Images

After augmentation, dataset was divided into three distinct subsets: a training set comprising 80% of the data, a validation set representing 10% of the data, and a testing set comprising the remaining 10% of the data. The number of photos for each disease is displayed in Table 1

Methodologies

Deep learning is nowadays one of the key image-classification techniques. In this approach, multilayer neural networks are generated and trained with labeled data to obtain feature representations for the purpose of improving classification and prediction accuracy.

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VGG16

VGG16 is a simple and effective convolutional neural network (CNN) architecture and has been widely adopted. It was proposed by Simonyan and Zisserman in the paper "Very Deep Convolutional Networks for Large-Scale Image Recognition" in 2014 and was the foundation of the ILSVRC (ImageNet Large Scale Visual Recognition Competition) winning image classification networks in 2014 of 2015. VGG16 uses a deep architecture with 16 layers of convolutions and can therefore model complex features in the input images. The network utilizes 3x3 filters in all convolutional layers.

Load Pre-trained Model:

We loaded the pre-trained VGG16 model from ImageNet and removed the final classification layer, allowing us to insert our custom output layers easily. Max pooling shrinks the size of the feature maps (in terms of their spatial dimensions), which in turn can help make your architecture computationally more efficient and reduce the risk of overfitting. The initial 15 layers of the VGG16 model are pre-trained and are frozen in training. This leads to improved generalization and faster training.

Experimenting with additional layers:

We obtain the one-dimensional vector of the feature maps by flattened. The dense layers for extracting abstract features at higher levels and to reduce dimensionality. A dropout used to introduce randomness to minimize the risk of overfitting. The last dense layer computes the probability of each class of disease using a sigmoid as activation. Hyperparameter Search Experiment with other hyperparameters like the learning rate, batch size, and weight decay in order to fine-tune the model for higher performance. Transfer Learning tries and leverage the idea of transfer learning by finetuning the VGG16 model on the leaf disease dataset.

Optimizer is a method for reducing the loss of the loss function during training by updating the weights of the model. Adamax is a popularized version of Adam that is based on the infinity norm. Use early stopping with an appropriate patience value of 3 to save time. Longer patience may cause overfit, and importantly, reset best weights to True to ensure that the model's weights are restored to the epoch with the best validation performance. This network has 7,511,455 trainable parameters.

DenseNet121

One major strength of DenseNets is the reduction in the vanishing gradient problem. In general, the vanishing gradient problem occurs when gradients from backpropagation have less magnitude with each iteration so much so that the model cannot learn well. DenseNet combats this by connecting each layer to all layers that come after it. This gives gradients a direct path to flow through them, thereby allowing information to flow better within a network.

Load Pre-trained Model:

We are loading the pre-trained DenseNet121 model, which was originally trained on ImageNet. However, when loading this model for the plant leaf dataset, the top-most classification layer is erased so that it does not interfere with the unique task of image classification. The model weights of the base model are set to non-trainable so that the pre-trained features from ImageNet remain intact and are not updated during the initial training process on the target dataset. By freezing the weights, we utilize the knowledge and patterns learned from ImageNet, which should aid in recognizing relevant features in images of plant leaf diseases.

Experimenting with additional layers:

Now, the next step is to create a custom classification head. This head will be responsible for learning the specific characteristics of plant leaf diseases and mapping the extracted features to the appropriate disease categories. A custom classification head is added, comprising several layers: a batch normalization layer, a dense layer, dropout layer, and finally, a dense layer with the number of class counts as neurons and softmax activation for output probability distribution. After adding a custom classification head, the model has 299,551 trainable parameters.

EfficientNetV2B2

EfficientNets, a family of eight neural network architectures, has recently achieved state-of-the-art performance on the ImageNet dataset. A key innovation in EfficientNets is the introduction of the Swish activation function. Swish, defined as f(x) = x * sigmoid(x), has demonstrated superior performance to ReLU in various neural network architectures and datasets[26]. EfficientNet architectures were developed using neural architecture search (NAS) to optimize the scaling of depth, width, and input resolution. This approach enables EfficientNets to achieve optimal performance while maintaining computational efficiency. By systematically scaling these dimensions, EfficientNets effectively balance accuracy and resource constraints, making them highly suitable for a wide range of applications.

Load Pre-trained Model:

We are loading the pre-trained EfficientNetV2B2 model, which was originally trained on the ImageNet dataset. However, for the plant leaf dataset, the top classification layer is excluded to avoid interference with the specific task of classifying images.

Experimenting with additional layers:

To adapt the model to the plant leaf disease task, a custom classification head is built on top of the pre-trained EfficientNetV2B2. This head consist global average pooling layer that summarizes the overall information from the extracted features and perform batch normalization to improve the training process stability. The Dense layer is used with 128 and 32 neurons using the ReLU activation function. To further enhance regularization, we added a Dropout layer with a dropout rate of 0.5 and 0.2, which randomly drops 50% and 20% of the neurons during training to prevent over fitting. This configuration aims to balance learning capacity and generalization by progressively refining the representations learned by the model. Finally, a dense layer with the number of disease categories as neurons and a softmax activation function is added. This final layer produces probability distributions for each disease class, enabling the model to predict the most likely disease present in a given leaf image.

After defining model architecture, the code configures it for training by specifying Adamax as the optimizer, a loss function, and evaluation metrics to be considered. Optimization is run by using the Adam optimizer with a learning rate setting of 0.0001. Categorical cross-entropy is picked as the loss function, which is appropriate for multi-class classification tasks such as this. The model is trained on the prepared training set for 50 epochs. Callbacks might be activated during training to watch the training process with a 'patience' parameter set to 3.

Table 2: Model configuring and training parameters

↓Hyper parameter/ Model→	**VGG16**	**DenseNet121**	**EfficientNetV2B2**
Learning rate	0.0001	0.0001	0.0001
Optimizer	Adamax	Adam	Adamax
Batch size	64	64	64

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↓Hyper parameter/ Model→	VGG16	DenseNet121	EfficientNetV2B2
Epochs	50	50	50
Activation Function at	Relu and Softmax at the output layer	Relu and Softmax at the output layer	Relu and Softmax at the output layer
Freeze/Unfreeze layers	Freeze the first 15 layers of the Base model	The base model is fully frozen	Base model fully Unfreeze
Input size	256 X 256 X 3	256 X 256 X 3	256 X 256 X 3
No. of total parameters	15,146,719	7,339,615	8,961,149
No. of Trainable Parameters	7,511,455	299,551	8,875,725

Results and Discussions

Experiment Setup

The present system development was done using Python and TensorFlow/Keras libraries. The dataset to be used in the experiment was the PlantVillage one, which originally had 54,306 images in 38 classes. For this study, only 31 relevant classes from 8 plant species were selected. The dataset was cleaned during preprocessing, which also involved the removal of extraneous classes. Each image was resized to 256×256, and after that, data augmentation techniques like rotation, flipping, and zooming were applied to help fine-tune the model. The entire dataset was further split with 80% given for training, 10% for validation, and the remaining 10% for testing.

Training

Three deep learning models were selected for performance evaluation, i.e., VGG16, DenseNet121, and EfficientNetV2B2. All models were subsequently fine-tuned using transfer learning, with ImageNet pre-trained weights. The top layers were replaced with a custom-built classifier for the 31-class output. Models were trained with categorical cross-entropy loss and accuracy as the major evaluation factors.

Results of the Experiments

According to these aggregate metrics, EfficientNetV2B2 showed the best and most consistent performance across the 31 classes and most often returned endless values of 1.00 for precision, recall, and F1-scores. DenseNet121 also performed accurately across most categories but occasionally suffered some declines in terms of either precision or recall.VGG16, by contrast, exhibited great variability intuitively in disease classes with fewer examples or subtle visual distinctions.

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Table 3 summarizes the evaluation metrics: precision, recall, F1-score, and overall accuracy for all three models.

Model	**Precision**	**Recall**	**F1-score**	**Accuracy**
VGG16	0.95	0.95	0.95	94.83%
DenseNet121	0.96	0.96	0.96	96.25%
EfficientNetV2B2	1.00	1.00	1.00	99.29%

Such findings, shown through per-class performance tables and metrics, clearly indicate the effectiveness of the more modern, deeper architectures. EfficientNetV2B2, in particular, recorded the highest accuracy; it converged in fewer epochs while exhibiting almost no overfitting.

From the loss and accuracy plots, EfficientNetV2B2 is the fastest in convergence and lowest in validation loss, followed by DenseNet121. VGG16 is slower to converge with some minor signs of overfitting.

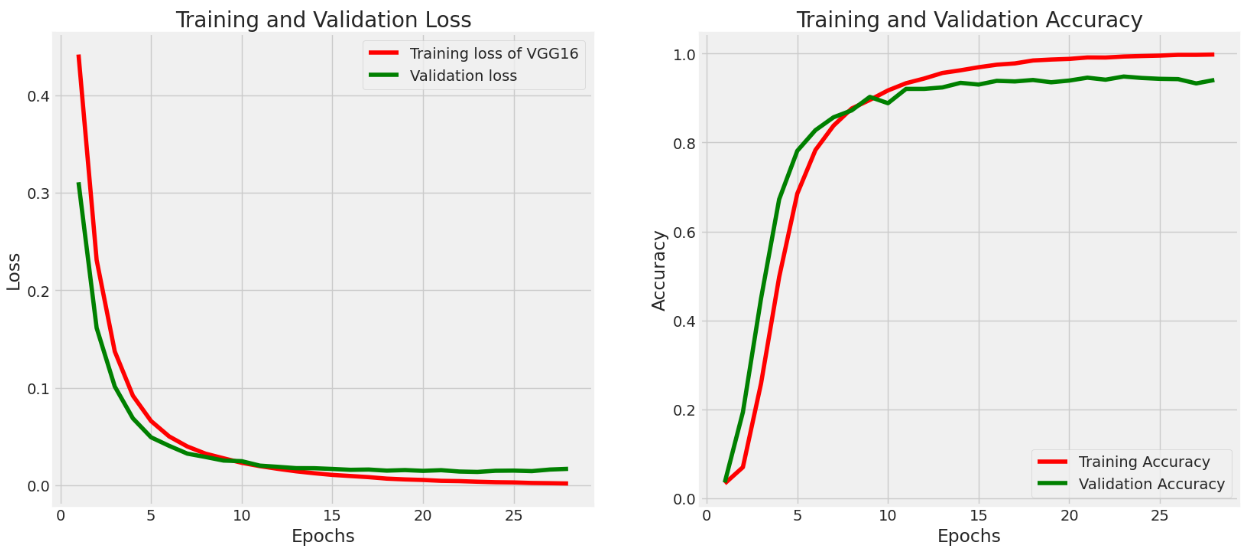

Figure 2: Training and validation accuracy and loss for the transfer learning network, using VGG16

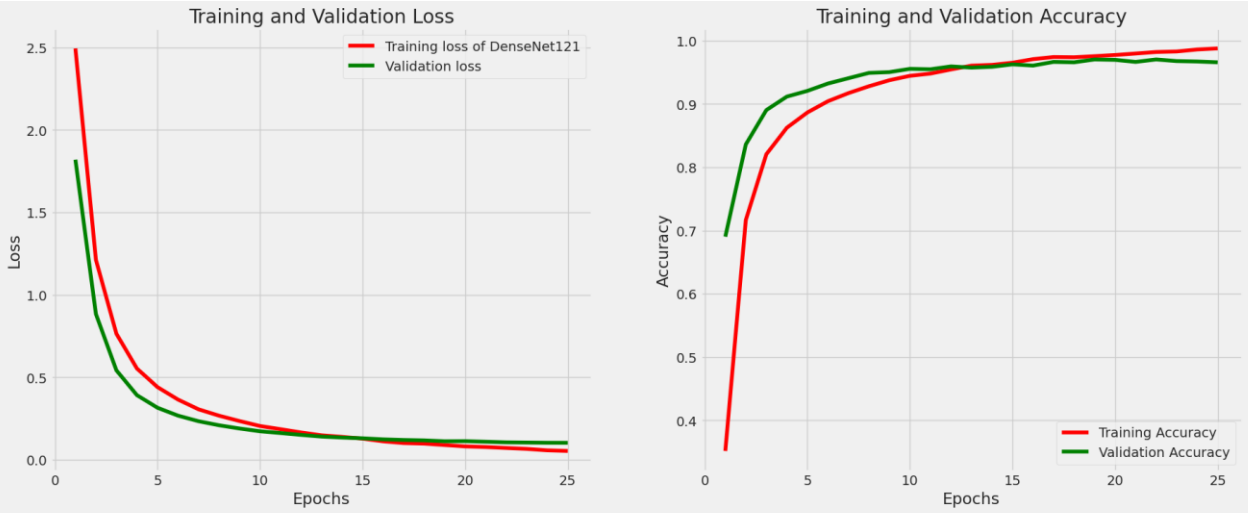

Figure 3: Training and validation accuracy and loss for the transfer learning network, using DensNet121

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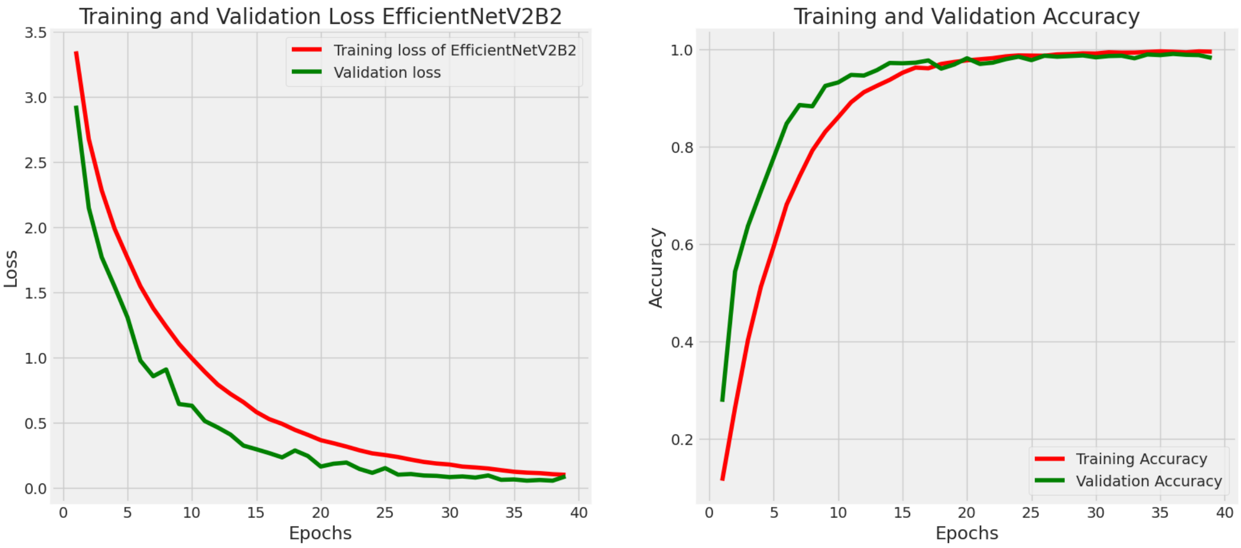

Figure 4: Training and validation accuracy and loss for the transfer learning network, using EfficientNetV2B2

Discussion

The three deep learning models—VGG16, DenseNet121, and EfficientNetV2B2—differed significantly in terms of training efficiency, convergence speed, and computation. VGG16, with its 15 million parameters, is the heaviest and shallowest, and this makes it slower in convergence. For instance, it takes about 88-90 seconds per epoch, and for 28 epochs, it arrives at roughly 46 minutes. Despite achieving a high training accuracy at the end, there were indications of overfitting as evidenced by lower test accuracy. DenseNet121 is most efficient at about 8 million parameters, thanks to its dense connectivity and reuse of features; its speed is also robust as it has completed 25 epochs in just 21 minutes, averaging 43-45 seconds per epoch to convergence at 96.

In a nutshell, VGG16 is slow and computationally heavy; DenseNet121, on the other hand, remains light, quick, and efficient; and EfficientNetV2B2 balances between depth and accuracy for deployment needing real-time results with high precision. Despite demonstrating better performance, one has to consider potential limitations and trade-offs that include higher computational cost and longer training times when compared to simpler models. Therefore, whether these findings will hold in the case of other plant species, diseases, and imaging conditions remains to be investigated, aside from their reliance on large, labeled datasets like PlantVillage. Nonetheless, irrespective of the drawbacks, EfficientNetV2B2 offers an excellent balance of accuracy and computational efficiency, thereby casting a potential solution for plant disease detection under confined environments or with adequate computational resources.

Conclusion

Under image classification, this work attempted a comparative account of three deep architectures, VGG16, DenseNet121, and EfficientNetV2B2 (Proposed Model), in plant disease identification. Being the deepest model, EfficientNetV2B2 was found able to land a classification accuracy of 99.29%, followed very closely by DenseNet121 at 96.25%, whereas VGG16 lagged at 94.83%.

By the class-wise analysis and checking the confusion matrices, the deeper models seemed to handle more complex disease patterns and leaf textures successfully. EfficientNetV2B2 missed none. Healthy leaf classes were classified right with certainty by all models because of their clear-cut and uniform visual traits.

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Overall, EfficientNetV2B2 is by far the most robust and scalable design for deployment in a real-world precision farming environment. This work stands to underpin how model depth, transfer learning, and data pre-processing are the major factors in strengthening the reliability in the automated classification of plant diseases.

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